

## Development of new software tools for phase equilibria modelling of open systems

Matthew Mayne

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## Titre de la thèse : Développement de nouveaux outils informatiques permettant de modéliser les équilibres de phases en système ouvert

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#### ABSTRACT

The investigation of metamorphic processes in the Earth's crust is integral to understanding the formation and evolution of the Earth. These processes control the preservation potential of the geochronological rock record and give us insight into, amongst others, the pressure and temperature conditions of the Earth's interior. Further, they control fluid generation and consumption within the crust which influences global geochemical cycles within the lithosphere, hydrosphere and atmosphere. This has important implications on the global climate and the creation of conditions conducive to life. The dominant mechanism of change both within and between these systems are compositional changes invoked by processes of mass transfer. Modern quantitative phase equilibrium modelling allows the calculation of the stable phase assemblage of a rock system at equilibrium given its pressure, temperature and bulk chemical composition. However, current software programs have limited functionalities for the sophisticated handling of a changing bulk composition. A new software tool (Rcrust) has been developed that allows the modelling of points in pressuretemperature-bulk composition space in which bulk compositional changes can be passed between points as the system evolves. This new methodology enables quantitative processoriented investigation of the evolution of rocks with a focus on mass transfer. Mass transfer within the crust generally occurs through partial melting and melt redistribution. These processes themselves are highly dependent on the chemical distribution of the crust in particular the water content of rocks undergoing metamorphism, thus the fluid state of rocks undergoing partial melting is investigated. It is found that metapelitic rocks begin melting at the fluid-saturated solidus regardless of their fluid state unless the subsolidus *P*-*T* path of the rock is sufficiently steep such that total water loss from the hydrous silicates of the rock cause the system to become less than fully-hydrated.

Further, as Earth's crustal differentiation proceeds largely by production and emplacement of granitic magmas (many of which are sourced from the melting of pelitic protoliths), a number of source controls are investigated for their relative effect on the bulk composition of melts produced by sequential melting and melt loss of a metapelitic starting bulk composition. It is found that the fluid state of the system is shown to have the strongest control on melt compositions with the pressure-temperature path having subordinate control on the volume and composition of melts produced.

This thesis presents key examples of the use of Rcrust to model the behaviour of open systems as well as the software developed in order to solve these problems and the graphical user interface built to enable its distribution and reuse in the petrology community.

**Keywords:** Rcrust, metamorphism; mass transfer, crustal differentiation, phase equilibrium modelling

#### **OPSOMMING**

Metamorfisme is die sleutel dryfkrag van die mineraalverspreiding binne en stabilisering van die kontinentale kors deur middel van chemiese differensiasie. As sodanig ondersoekende metamorfe prosesse in die kors is integraal om die vorming en evolusie van die Aarde te verstaan. Hierdie prosesse beheer die bewaringspotensiaal van die geochronologiese rotsrekord en gee ons insig in onder andere die druk en temperatuurtoestande van die Aarde se binnekant. Verder beheer hulle vloeistofopwekking en verbruik binne die kors wat globale geochemiese siklusse in die litosfeer, hidrosfeer en atmosfeer beïnvloed. Dit het belangrike implikasies op die globale klimaat en die skep van lewensverwante omstandighede. Die oorheersende meganisme van verandering binne en tussen hierdie stelsels is komposisionele veranderinge wat deur massaprosesse toegepas word. Moderne kwantitatiewe fase-ewewigsmodellering laat die berekening van die stabiele fase-samestelling van 'n rotsstelsel teen ewewig toe, gegee sy druk, temperatuur en grootmaat chemiese samestelling. Huidige sagteware programme het egter beperkte funksionaliteite vir die gesofistikeerde hantering van 'n veranderende grootmaat samestelling. 'n Nuwe sagteware-instrument (Rcrust) is ontwikkel wat die modellering van punte in druk-temperatuur-massasamestellingsruimte toelaat waarin grootmaat komposisionele veranderinge tussen punte verloop kan word as die stelsel ontwikkel. Hierdie nuwe metodologie stel kwantitatiewe proses-georiënteerde ondersoek in na die evolusie van rotse met die fokus op massa-oordrag. Massa-oordrag binne die kors kom gewoonlik voor deur middel van gedeeltelike smelt en smeltherverdeling. Hierdie prosesse self is hoogs afhanklik van die chemiese verspreiding van die kors, veral die waterinhoud van gesteentes wat metamorfose ondergaan. Die vloeistandstaat van rotse wat gedeeltelike smelting ondergaan, word dus ondersoek. Daar word bevind dat metapelitiese gesteentes begin smelt by die vloeistofversadigde solidus, ongeag hul vloeistand, tensy die subsolidus P–T-pad van die rots voldoende steil is, sodat totale waterverlies uit die waterige silikate van die rots veroorsaak dat die stelsel minder as ten volle gehidreer word.

Aangesien Aard se korsdifferensiasie hoofsaaklik deur produksie en inplanting van granietmagmas ontstaan (waarvan baie afkomstig is van die smelt van pelitiese protoliete), is 'n aantal bronkontroles ondersoek vir hul relatiewe effek op die grootmaat samestellings van smeltprodukte wat deur opeenvolgende smelting en smelt verlies van 'n metapeliet begin massa samestelling geproduseer word. Daar word bevind dat die vloeistoestand van die stelsel getoon word om die sterkste beheer op smeltkomposisies te hê, met die druktemperatuurpad ondergeskikte beheer op die volume en samestelling van smelt wat geproduseer word.

Hierdie proefskrif bied sleutel voorbeelde vir die gebruik van Rcrust om die gedrag van oop stelsels te modelleer, sowel as om die sagteware wat ontwikkel is om hierdie probleme op te los en die grafiese gebruikerskoppelvlak wat opgebou is om sy verspreiding en hergebruik in die petrolgemeenskap moontlik te maak, op te los.

**Sleutelwoorde:** Rcrust, metamorfose; massa-oordrag, korsdifferensiasie, faseewewigsmodellering

## RÉSUMÉ

Le métamorphisme est un phénomène majeur affectant la distribution des phases minérales au sein de la croûte continentale et participant à sa stabilisation. L'étude des processus métamorphiques est donc essentielle pour comprendre la formation et l'évolution de la Terre. Ces processus exercent un contrôle sur le potentiel de préservation des roches à sa surface et nous renseignent entre autres sur les conditions de pression-température régnant en profondeur. Ils contrôlent également la production et le stockage de fluides au sein de la croûte ce qui influence les cycles géochimiques au sein de la lithosphère, de l'hydrosphère et de l'atmosphère et a, de fait, des implications importantes sur le climat et l'apparition de la vie sur Terre.

La principale source de variabilité au sein de ces systèmes correspond à des changements de composition chimique résultant eux-mêmes de transferts de matière. Les techniques modernes de modélisation quantitative des équilibres de phases permettent de calculer l'assemblage minéralogique stable au sein d'un système à l'équilibre pour lequel les paramètres pression, température et composition chimique sont connus. Ceci étant, les programmes informatiques actuels ne possèdent que de fonctionnalités limitées pour modéliser et appréhender les conséquences de changements de composition chimique du système au cours du métamorphisme. Un nouvel outil informatique (Rcrust) a été développé pour permettre de calculer l'assemblage minéralogique stable dans un système soumis à des variations de composition lors de son évolution dans l'espace multidimensionnel pressiontempérature-composition chimique. Cette nouvelle approche méthodologique permet d'étudier de manière quantitative les processus métamorphiques et en particulier les conséquences des transferts de matière. Au sein de la croûte, ces derniers sont généralement associés à la fusion partielle des roches et à la migration des liquides magmatiques. Ces phénomènes sont tous deux fortement contrôlés par la composition chimique des roches crustales, en particulier leur teneur en eau. Ainsi, ce travail s'intéresse au rôle et à l'état des fluides présents dans les roches lors des phénomènes de fusion partielle. Il est ainsi montré que les métapélites commencent à fondre en franchissant leur solidus saturé en fluide, et ce, quel que soit leur état de saturation vis-à-vis de ce fluide. Une exception à ce comportement s'observe dans le cas où le trajet pression-température suivi par la roche comprend une importante décompression quasi-isotherme en conditions subsolidus. Ceci a pour conséquence d'entrainer une perte en eau du système qui présentera ainsi un assemblage minéralogique différent de celui observé lorsque la teneur en eau est maximisée au solidus

sans atteindre la saturation (conditions dites d'hydratation maximale).

La différenciation de la croûte continentale résulte de la production et migration de magmas granitiques dont une partie importante est issue de la fusion de protolithes pélitiques. Ainsi, les conséquences de variations compositionnelles au sein de telles sources sur la chimie des liquides produits par fusion partielle ont été appréhendées en modélisant une séquence d'évènements de fusion/extraction, reproduisant un comportement en système ouvert. Il est montré que l'état du système vis-à-vis des fluides est le paramètre qui exerce le plus fort contrôle sur la composition chimique des liquides produits.

Ce travail de thèse présente une série d'exemples illustrant l'utilisation de Rerust pour modéliser les systèmes ouverts tout en précisant la méthodologie suivie pour l'élaboration de l'outil ainsi que l'interface graphique construite afin de permettre sa distribution et son utilisation au sein de la communauté pétrologique.

**Mots-clés**: Rcrust, métamorphisme, transfert de matière, différenciation crustale, modélisation des équilibres de phases

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### LIST OF ABBREVIATIONS

#### Minerals:

Abbreviations for rock forming minerals were taken from Whitney & Evans (2010) as:

Bt	Biotite
Crd	Cordierite
Fsp	Feldspar (plagioclase and alkali)
Grt	Garnet
H <sub>2</sub> O	Water
Ilm	Ilmenite
Ку	Kyanite
Орх	Orthopyroxene
Qz	Quartz
Sil	Sillimanite
Spl	Spinel
St	Staurolite

#### **Terminology:**

*	Multiplication
/	Division
$\Delta P / \Delta T$ or $dP / dT$	Pressure versus temperature gradient
A/CNK	$Al_2O_3/(CaO+Na_2O+K_2O)$ by mol.%
aH <sub>2</sub> O	Water activity
An%	Anorthite percentage of feldspar as Ca/(Ca+Na)*100 by mol.%

Ca#	Calcium number of the bulk as $Ca/(Ca + Na)*100$ by mol.%
cos	trigonometric function cosine
IS	Isolated subsystem
E–HPG	Eclogite-high-pressure granulite
ES	Extract subsystem
FS	Full system
G–UHT	Granulite–ultrahigh temperature
GNU	GNU's Not Unix
Al	Aluminium
Ca	Calcium
°C	Degrees Celsius
Fe	Iron
FeOt	Total Iron as FeO + $0.89981*Fe_2O_3$ by wt.%
GCDkit	Geochemical Data Toolkit
GUI	Graphical user interface
Н	Hydrogen
IBH	Isobaric heating
ITD	Isothermal decompression
К	Potassium
kbar	kilobar
MAD	Metamorphic assemblage diagrams
МСТ	Melt Connectivity Transition
Mg	Magnesium

Mg#	Magnesium number as $Mg/(Fe + Mg)*100$ by mol.%
mol.%	molar percentage
Mn	Manganese
Na	Sodium
NCKFMASHTO	Na <sub>2</sub> O-CaO-K <sub>2</sub> O-FeO-MgO-Al <sub>2</sub> O <sub>3</sub> -SiO <sub>2</sub> -H <sub>2</sub> O-TiO <sub>2</sub> -O
0	Oxygen
ORCiD	Open Researcher and Contributor ID
P-T-X	Pressure-Temperature-Bulk composition
pi	mathematical constant ∏
RS	Reactive subsystem
Si	Silicon
sin	trigonometric function sine
Ti	Titanium
vol.%	volume percentage
wt.%	weight percentage
x_i	an increment in the vector direction x
y_i	an increment in the vector direction y

#### CHAPTER 1

#### **INTRODUCTION**

The formation of igneous and metamorphic rocks is fundamental to determining the chemistry of the Earth's crust. Processes of metamorphic devolatilisation, partial melting, magma emplacement, fractional crystallisation and hydrothermal alteration, amongst others, cause the redistribution of elements within the crust. Partial melting and melt migration into the upper crust, in particular, redistributes heat producing elements within the crust depleting the lower crust in these incompatible elements and enriching the upper crust. This in conjunction with the formation of the mantle lithospheric keel is fundamental to the stability of Earth's continents. These processes and their effects can extend to the Earth's surface through volcanic activity, hydrothermal venting and the tectonic exhumation of rocks leading to their exposure at the surface and weathering. Consequently, H<sub>2</sub>O and CO<sub>2</sub> can be released to the atmosphere/hydrosphere or re-absorbed into the lithosphere by weathering, sedimentation and lithification. Thus lithospheric processes can directly affect the hydrosphere and atmosphere as evidenced by major disturbances in the global geochemical cycles (Friend, 1973; Amiotte Suchet and Probst, 1995). This has important implications for secular changes in the Earth's climate and the availability of nutrients to the biosphere.

Since the majority of crustal processes occurring at depth are inaccessible to direct observation, observations of these processes must come from the incomplete sample set of rocks brought to the surface through erosion, uplift or transport through volcanic plumbing systems. In order to extend this dataset, laboratory experiments are conducted which aim to reproduce the conditions of the Earth's interior and then expose either natural or artificially created samples to these conditions. Other types of experiments commonly functioning in simple systems or using individual minerals measure the range of physical and chemical parameters necessary to define the thermodynamic properties of minerals and fluids. This thermodynamic data can be used to infer the conditions of a natural rock's formation (Spear et al., 2016).

Building on this dataset by cross referencing geochemical studies of natural rocks and experimental studies allowed individual mineral reactions to be identified (Berman, 1991). Compilations of reactions in a simple chemical system were first displayed on petrogenetic grids (Albee, 1965)(e.g. Fig. 1). The compilation of internally consistent thermodynamic

datasets allowed the quantitative calculation of subsolidus phase equilibria (Helgeson et al., 1978; Powell and Holland, 1985, 1988; Gottschalk, 1997; Holland and Powell, 1998).



**Fig. 1.** Petrogenetic grid in pressure (*P*)–temperature (*T*) space showing the location of selected reactions in the system  $K_2O-Al_2O_3-SiO_2-H_2O$  (KASH) taken from Spear et al. (1999). Abbreviations are given as follows: And = andalusite, As = Al\_2SiO\_5, IP1 = Invariant point, Kfs = K-feldspar, Ky = kyanite, L = liquid, Ms = muscovite, Qtz = quartz, Sil = sillimanite, V = H\_2O. Note: Reaction number 5 will only be observed in sillimanite absent rocks

In order to investigate the possible reactions that a single rock could experience, compositionally relevant phase diagrams were created from petrogenetic grids by considering a single bulk composition thereby creating isochemical phase diagrams of P-T-X space (Hensen and Essene, 1971; Hensen and Harley, 1990) (e.g. Fig. 2). These diagrams were initially termed 'pseudosections' but that name has recently been argued to be removed from common usage in favour of the term "metamorphic assemblage diagrams" (Spear and Pattison, 2017). Expansion of these data sets to include fluids and melts along with the creation of activity-composition models which describe phases by proportions of respective compositional endmembers has allowed more complicated systems to be investigated and for pressure-temperature conditions above the solidus to be investigated (Berman, 1988; Powell and Holland, 1988; Ghiorso and Sack, 1995; Holland and Powell, 2011; White et al., 2014).



**Fig. 2.** Pressure (P)–temperature (T) isochemical phase diagram calculated in the system  $K_2O$ –FeO–MgO–Al<sub>2</sub>O<sub>3</sub>–SiO<sub>2</sub>–H<sub>2</sub>O for a pelite composition: Al<sub>2</sub>O<sub>3</sub>=41.89, MgO=18.19, FeO=27.29, and  $K_2O=12.63$  (in mol.%) taken from Powell et al. (1998). Muscovite, quartz and water are in excess. Abbreviations are given as follows: and = andalusite; bi = biotite; chl = chlorite; g = garnet; ky = kyanite; sill = sillimanite; st = staurolite. Note: this diagram only shows phase assemblage fields applicable to this specific bulk composition.

Computer programs have been used to perform phase equilibrium modelling by either using the simultaneous solution of non-linear equations as is the case in THERMOCALC (Powell and Holland, 1988; Powell et al., 1998) or the minimization of Gibbs free energy of the system ( $\Delta G$ ) as is the case in Perple\_X (Connolly and Kerrick, 1987; Connolly, 2005) and Theriak/Domino (De Capitani and Petrakakis, 2010). This modelling traditionally focuses on considering one bulk composition in isochemical phase diagrams or on the linear scaling between two bulk compositions in isobaric or isothermic phase diagrams. Lab experiments also primarily focus on systems occurring in equilibrium and those that consider melting generally only simulate equilibrium batch melting due to the technical limitations of performing phase fractionations in an experimental capsule and the challenge of diminishing volumes of the products produced if fractionation is induced. However, in some cases the modelling of natural systems mandates a more sophisticated handling of a changing bulk composition.

Recent studies have begun to focus on the effects of compositional changes in open systems (Brown and Korhonen, 2009; Yakymchuk and Brown, 2014; Stuck, 2016; Webb et al.,

2015). As rocks are buried and subjected to processes of metamorphism they can dehydrate (White and Powell, 2010; Webb et al., 2015) or experience periods of fluid infiltration (Johnson et al., 2003; Korhonen et al., 2012) and hydrothermal alteration (White et al., 2003; Riesco et al., 2004; Nicoli and Dyck, 2018). If these systems reach sufficiently high temperatures, they can begin to melt and experience melt loss (Vigneresse and Burg, 2000; White et al., 2002; White and Powell, 2010; Brown and Korhonen, 2009; Johnson et al., 2011; Diener and Fagereng, 2014; Yakymchuk and Brown, 2014; Mayne et al., 2016; Morrissey et al., 2016; Stuck and Diener, 2018). The movement of melts or magmas can form complicated systems involving entrainment of minerals to melt (Taylor and Stevens, 2010; Garcia-Arias and Stevens; Stevens et al., 2007; Clemens and Stevens, 2012) as well as magma mixing, mingling and hybridisation (Beard et al., 2005; Clemens and Stevens, 2012). At sites of emplacement magma systems may differentiate further through processes of fractional crystallisation or assimilation (Blevin and Chappell, 1992; Linnen and Keppler, 2002). Throughout these processes chemical fractionation of major element, trace element and isotope systems occurs producing a complex array of chemical signatures which could provide insight into the mechanisms of compositional change in these rocks. López-Carmona et al. (2014) classify the potential changes to the effective bulk composition

of a rock (the portion of the rock that is available to the reacting assemblage of phases) into two mechanisms. "Open system behaviour" (discussed above) and "successive (re)equilibrations" which result from the growth of crystals with slow intracrystalline diffusion thereby temporarily removing their chemical constituents from the reactive system until diffusion may make them re-available. These two mechanisms can occur in conjunction with each other.

Lanari and Engi (2017) have presented a methodology (Lanari et al., 2018) and software tool (Lanari et al., 2014) for approximating and interrogating the volumes of equilibration in a rock which has compositionally zoned minerals. However, current thermodynamic modelling software has limited functionalities for dealing with the bulk compositional changes induced by "Open system behaviour". Here I classify bulk compositional changes occurring in open systems as phase manipulations consisting of phase additions (e.g. fluid infiltration, wall rock assimilation) and phase extractions (e.g. dehydration, melt loss). The functionalities of the three most commonly used thermodynamic modelling programs for metamorphic studies in performing phase manipulations are detailed below and summarised in Table 1.

# The use of current thermodynamic modelling software to model open system behaviour *THERMOCALC*

A "read bulk info" script can be used to manually change the abundance of a phase and recalculate a bulk composition. This can be iteratively used to increase the proportion of a phase or to fractionate a phase e.g. (Zeh, 2006). By calculating individual panels each time the bulk composition changes a stitched model of open system processes can be created e.g. (Yakymchuk and Brown, 2014) (Fig.3).



**Fig. 3.** Molar proportion of phases plotted against temperature for isobaric heating at 12 kbar starting with an average amphibolite-facies pelite composition calculated using THERMOCALC. The system is considered as conditionally open with melt loss induced by removing six-sevenths of the melt present wherever the P-T path intersects the 7 mol.% melt isopleth using the 'read-bulk-info' script. Abbreviations are as follows: Bt = biotite, Grt = garnet, Ilm = Ilmenite, Kfs = K-feldspar, Ky = kyanite, Liq = liquid, MLx = melt loss event, Ms = muscovite, Pl = plagioclase feldspar, Qtz = quartz. Taken from Yakymchuk and Brown (2014).

#### Theriak/Domino

Input commands in the "drv-file" can be specified to remove or add a set proportion of phase(s) from the system along a calculation path (De Capitani and Petrakakis, 2010) (Fig. 4). Commands can also be specified to remove or add set compositions along a path.



**Fig. 4.** Fractionation of garnet in a metapelite along a prograde P-T path calculated using Theriak/Domino. At incremental steps along the path the composition of the newly grown garnet is subtracted from the bulk composition. X shows the composition of the garnet in the reactive system as Alm = almandine, Gr = grossular and Py = pyrope. n shows the modal amount of phases in the reactive system as Bi = biotite, Chl = chlorite, Ctd = chloritoid, Grt = garnet, Ky = kyanite, Ms = muscovite, Parg = pargasite, Pg = paragonite, Pl = plagioclase, St = staurolite. The light-shaded area is a P-T segment where garnet is not growing and x is not defined. Taken from De Capitani and Petrakakis (2010).

#### Perple\_X

"Phase fractionation calculations" can be performed by selecting this option during creation of the build file. This fractionation can be along isobaric, isothermic or a user defined P-T path (Connolly, 2005) (Fig. 5). Fractionation must remove all of a given phase(s) and the independent variable used to increment the calculation path must increase or decrease continuously.



Fig. 5. Melt loss from an average metapelitic bulk composition along a clockwise

decompression path (red arrow in left panel on top of an isochemical phase diagram of pressure–temperature space of the same composition) calculated using Perple\_X. All melt is extracted from the system whenever it occurs as a stable phase. The volume percentage of the phases in the reactive system are shown in the right panel as AbPl = plagioclase feldspar, Bio = biotite, Gt = garnet, hCrd = cordierite, ky = kyanite, Pheng = phengite, q = quartz, San = sanadine, sill = sillimanite. Taken from (Connolly, 2018).

Table 1. Suitability of commonly used thermodynamic modelling programs for phase	e
equilibrium modelling in open systems	

Software	Calculation	Refinements	User Input	Phase manipulations
	method			
Thermocalc	Solution of	Not applicable	Command	At a single point, manually change
[1]	nonlinear	(individual	line and	proportion of phase(s)
	equations	reaction lines are	scripts	
		calculated)		
Theriak	Gibbs free	Reaction	Command	Along a single path, fractionation or
Domino [2]	energy	boundary	line or text	addition of a set proportion of
	minimisation	gridded	file input	phase(s) or set proportion of
		refinement		chemical components
Perple_X	Gibbs free	Fixed regular	Executable	Along a single path, fractionation of
[3]	energy	grid refinement	queries or	the full proportion of selected
	minimisation		text file	phase(s). Paths must be defined with
			input	one variable increasing or
				decreasing i.e. no loops

[1] http://www.metamorph.geo.uni-mainz.de/thermocalc/; [2]

https://titan.minpet.unibas.ch/minpet/theriak/theruser.html; [3] http://www.perplex.ethz.ch/

# The need for sophisticated handling of bulk compositional changes induced by phase manipulations

The presented thermodynamic modelling softwares have been shown to be able to model some open system processes however their use in this manner becomes restrictive when attempting to handle more complex open system behaviour that closer approximates the natural system. In such cases there may be a need to consider:

- Multiple phase fractionations concurrently (e.g. extraction of melt and peritectic minerals),
- Conditional phase manipulations (e.g. extraction of melt when a melt threshold is

exceeded)

- Phase manipulation proportions that are relative to the system (e.g. retention of melt on grain boundaries during melt extraction)
- Complex *P*–*T* paths (e.g. multi-stage metamorphism)
- A variety of conditional arguments in one modelling space (e.g. prograde devolatilisation of a subsolidus assemblage followed by melt loss of that assemblage above the solidus)
- Multiple potential *P*–*T* paths (e.g. the water content of a subsolidus rock is pressure dependent thus modelling in *P*–*T* space with a single water content introduces inherent inconsistencies)
- Compositional heterogeneity on the mineral, rock and crustal scale

#### Aims of this study

This study aims to present a methodology for the modelling of phase equilibrium in open systems. This methodology seeks to address the current limitations of thermodynamic software in the handling of bulk compositional changes induced by open system behaviour. Further, this study aims to use these new tools to build a model for crustal anatexis in which the effects of compositional change throughout this process is investigated. In order to accurately model anatexis this study will develop a methodology for the handling of the subsolidus fluid state of a system before anatexis. The combined effect of the pressure-temperature and bulk composition in this system, with sophisticated control of fluid state, will be investigated for its control on the position of the solidus. The controls of fluid state, P-T path and melt loss threshold will then be investigated for their effect on the resultant bulk composition of melts cumulatively extracted from a protolith. These source controls will be compared for their relative strength of influence and contrast with the effect of compositional heterogeneity in the source.

#### Structure of the thesis

This thesis presents the software program Rcrust (the name deriving from the fact that it is written in R and was developed to solve problems in crustal petrology) as a tool for the modelling of phase equilibrium in open systems.

#### Performing process oriented investigations

Chapter 2 presents the way in which the new functionalities of Rcrust allowed a methodology to be developed using mass transfer to perform process oriented investigations in open systems. These methodologies were built concurrently with further developments of Rcrust with the aim of creating a thermodynamically constrained model for crustal anatexis. The first challenge to this model was accurately determining the water content of a metamorphic rock. During the subsolidus prograde metamorphism of a rock the total water content of a rock may lie within the hydrous silicates of the rock, may exist as a free fluid phase in the limited pore space of the rock, or exceeding this, must leave the system. Rcrust models this behaviour by setting a maximum allowable amount of free water that can occur in the system and extracting all water that exceeds this amount. This allows the rock to progressively loose total water content from the reactive subsystem during its subsolidus evolution. Once the solidus is crossed melt is produced at the interface between reactant minerals. As this melt amount builds up an interconnected melt network may form and if it exceeds some critical threshold melt loss may occur. This process is thought to have a maximum critical threshold value by which it will occur estimated by the melt connectivity transition by Rosenberg and Handy (2005). Rcrust simulates this melt loss by extracting melt from the reactive subsystem whenever the melt threshold is exceeded and leaves a fraction of this melt behind to estimate melt retention on grain boundaries.

#### The effect of subsolidus water loss and its dependence on P-T path

Concurrent to building the methodology for performing process oriented investigations using Rcrust process-oriented investigations were undertaken to divulge the effects of compositional change on open systems. Chapter 3 presents a detailed study of the effect of subsolidus water loss on the position of the solidus in P-T space. When modelling subsolidus prograde water loss close to the solidus it is found that even fluid-absent rocks have the ability to melt at the fluid-saturated solidus as incremental heating before the solidus decreases the total water contained in the hydrous silicates freeing water to form a free phase in the porosity of the rock and participate in potential melting reactions. It seems that the fluid saturated solidus can only be crossed without melting if the subsolidus P-T path of the rock is sufficiently steep such that the increase in total water contained in the hydrous silicates as a function of pressure exceeds the decrease in total water contained in the hydrous silicates as a function of temperature, resulting in the rock becoming water deficient, i.e. not fully-hydrated.

#### The effect of source controls on open system melt compositions

These new tools and methodologies for modelling subsolidus water content, supersolidus melt threshold and varying P-T paths are used in Chapter 4 to investigate the effect of source controls on the composition of melt batches extracted sequentially from a metapelitic protolith. The resultant compositional effect of the source controls of fluid state, melt threshold and P-T path are compared and contrast to the effect of compositional variance in the protolith. It is found that the fluid state of the system is shown to have the strongest control on melt compositions with the pressure-temperature path having subordinate control on the volume and composition of melts produced.

#### A brief history of the development of Rcrust

Rcrust was developed following an iterative approach first implemented by Jean-François Moyen in response to extensive discussions with Arnaud Villaros and Gautier Nicoli which also culminated in a publication in the International Journal of Earth Sciences (Villaros et al., 2018). Phase stabilities are determined by calling and interpreting output from meemum from the Perple\_X suite (Connolly and Kerrick, 1987; Connolly, 2009) via calls from the R environment. These calls were first developed by Jean-François Moyen during a research stay at Stellenbosch University in January 2013 and further refined by Jean-François Moyen and Gautier Nicoli in late 2013. In January 2014 the project was handed over to Matthew Mayne who became the sole programming developer from that point forward. Compositional manipulations were split into two groups (phase additions and phase extractions) and sequenced within runs to allow path dependent processes with simultaneous additions and extractions. A graphical user interface was developed (Fig.3) using tcl/tk (Ousterhout and Jones, 2009) within R to handle user inputs and display processed outputs. In 2015 a new parsing method was employed in collaboration with Lars Kaislaniemi making use of a compiled form of meemum to speed up total calculation time (Mayne et al., 2016). A complete overhaul of the program began in 2016 in which a systematic methodology was employed to enable new modules to be activated or deactivated at points along the iterative loop. A new syntax was developed allowing a user defined modelling space to be built and conditions applied within this space to simulate the desired modelling output. The graphical user interface was redeveloped (Fig. 3) using the R package: Shiny (RStudio, 2014) in order to match these changes in functionality and to offer platform independence. File inputs of parameters were enabled and conditional inputs developed including phase thresholds and retention settings. A dependence solver was built to determine calculation order of points when points pass on compositional changes along user defined paths. Output routines were

built to process data and produce graphical outputs for contour diagrams of the modelling space, relative phase abundances along specific paths and for the creation of phase assemblage maps.

Rorust D:/Rorust			Projects Directory	):/Rerust/Projects	Working File Example1	Sav	e Li	oad F
Rcrust New Save Loa	d Run Close Working File Example	Rcrus	t				Clear	Cons
	Size	Loaded D:/Rcrust/Pro	ects/Example1/Inputs/E	cample1.txt				
	5.25	Input Parameters	Phase Manipulations	Modelling Options O	lutputs			
Steps	5							
Bulks	1	Size	Y					
Pressu	are and Temperature	4	3					
PT stages Pressure	1 Temperature Final step							
1 12000	690+60*(st-1)+273.15 5	Press and Tomo						
B	ulk Composition	Number of PT defi	nitions					
Major elements	H20, SiO2, AL2O3, CAO, MGO, FEO, K2O, NA2O, TI	1	-	Province distant	<b>-</b>			
Starting major elements bulk	1.96,56.96,20.44,1.56,3.27,8.50,4.09,1.82,1.05,0.31	(1:1)	(4:3)	7-v	670+x 1*20			
Bulk from file?	F							
Calculate trace elements	F							
	Phase Addition +	Bulk Composition						
F	Phase Extraction -							
Perform phase extraction	4	Major elements						
Phases	melt(HP)	NA20 MGO AL	203 SI02 K20 CAD TI	02 FEO 02 H2O				
Stages	1	Number of bulk de	finitions					
melt(HP) Conc	dition/Final Step	1						
1 1 melt()	HP),>=,7,wt%	From	То	NA20,MGO,AL203,810	02,K20,CA0,TI02,FE0,02,H20,mass			
	Output Mode	[1;1]	(4;3)	1.82,3.28,20.45,56.97	7,4.09,1.56,1.05,8.5,0.62,1.96,100			
Ad	ditional Settings	Import definitions	s from file					

**Fig. 6.** Old Tcl/Tk interface (left) built on Microsoft Windows "widgets" and new Shiny interface (right) operating platform independently from a browser.

#### Presentation of the modelling tool: Rcrust

The software program Rcrust is attached to this thesis as Addendum A: an electronic appendix. Addendum B present a user manual for installing and using the program and Addendum C present a fully commented description and presentation of the programming code.

#### Supplementary data

Addendum D provides the supplementary data for Chapter 4

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#### CHAPTER 2

## PRESENTATION OF RESEARCH PAPER 1: PERFORMING PROCESS-ORIENTED INVESTIGATIONS INVOLVING MASS TRANSFER USING RCRUST: A NEW PHASE EQUILIBRIUM MODELLING TOOL

This paper, first authored by Matthew Mayne, was accepted for publication in the Geological Society of London Special Issue: Making granites: petrogenetic processes, tectonic environments and secular variations.

The following aspects of the research were done independently by Matthew Mayne while receiving standard supervision by his supervisors Gary Stevens, Jean-François Moyen and Tim Johnson: (i) writing of programming code; (ii) conducting phase equilibrium modelling; (iii) generation of the figures; (v) writing of the manuscript

# Performing process-oriented investigations involving mass transfer using Rcrust: a new phase equilibrium modelling tool

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#### ABSTRACT

Modern quantitative phase equilibria modelling allows the calculation of the stable phase assemblage of a rock system given its pressure, temperature and bulk composition. A new software tool (Rcrust) has been developed that allows the modelling of points in pressure– temperature–bulk composition space in which bulk compositional changes can be passed from point to point as the system evolves. This new methodology enables quantitative process-oriented investigation of the evolution of rocks. Procedures are outlined here for using this tool to model: 1) the control of the water content of a subsolidus system based on available pore space; 2) triggering of melt loss events when a critical melt volume threshold is exceeded, while allowing a portion of melt retention; 3) entrainment of crystals during segregation and ascent of granitic magmas from its source; 4) modification of the composition of granite magmas due to fractional crystallization and 5) progressive availability (through dissolution) of slow diffusing species and their control on the effective bulk composition of a system. These cases collectively illustrate thermodynamically constrained methods for modelling systems that involve mass transfer.

**Keywords**: Phase equilibria modelling; Rcrust; effective bulk composition; water content; anatexis; melt loss; peritectic entrainment; fractional crystallization; volume of equilibration; dissolution–precipitation.
# **INTRODUCTION**

Given the pressure (P), temperature (T) and bulk composition (X) of a rock, quantitative phase equilibria modelling can predict the stable phase assemblages, the P-T fields of stability of these assemblages, phase modes and phase compositions, that characterize the system at equilibrium see THERMOCALC (Powell and Holland, 1988; Powell et al., 1998), Perple\_X (Connolly and Kerrick, 1987) and Theriak/Domino (De Capitani and Petrakakis, 2010). This technique has become a standard tool in metamorphic studies, most commonly involving analysis via calculation of isochemical phase diagram sections known as pseudosections e.g. Yakymchuk (2017) or metamorphic assemblage diagrams (MADs) (Spear and Pattison, 2017). Recent studies have begun to consider the effects of bulk compositional change in rocks undergoing metamorphism, e.g. through melt loss (Yakymchuk and Brown, 2014; Morrissey et al., 2016; Vigneresse and Burg, 2000; Brown and Korhonen, 2009; White and Powell, 2002, 2010; Diener and Fagereng, 2014; Mayne et al., 2016; Johnson et al., 2011), fluid loss (White and Powell, 2010), fluid infiltration (Korhonen et al., 2012; Johnson et al., 2003) and/or metasomatism (White et al., 2003; Riesco et al., 2004; Nicoli and Dyck, 2018). In these studies, isochemical phase diagram sections are limiting and alternative methods have been employed. To account for a changing bulk composition via subtraction or addition of portions of one or more phases, isothermal *P*–*X* or isobaric *T*–*X* diagrams are commonly used, in which bulk composition is allowed to vary between two predetermined endmembers. In cases where more than one compositional change is required, a number of individually calculated panels are stitched together (Yakymchuk and Brown, 2014; White and Powell, 2002; Brown and Korhonen, 2009; Johnson et al., 2011). However, when investigating processes that sequentially alter the bulk composition of a system within P-T space, manual calculation and stitching of diagrams becomes restrictive. An alternative, to this calculation of predetermined phase changes, is to include parameters for physical mechanisms of mass transfer within a calculation such that bulk compositional changes occur within a system based on properties that the system obtains such as phase abundances or phase compositions (Connolly, 2005; Karpov et al., 1997; Ghiorso and Sack, 1995). The need for increasingly more sophisticated models that allow this style of mass transfer prompted the creation of a path dependent thermodynamic modelling tool (called 'Rcrust') which automates the handling of bulk compositional change in a modelled P-T-X space (Mayne et al., 2016). This paper serves as a summary of the functionalities of this program and demonstrates some applications in

performing process-oriented investigations that inherently involve bulk compositional change. This provides a useful tool for reconciling petrographic observations and chemical analyses with thermodynamic modelling at a variety of scales within complex systems in order to better understand phase equilibria.

# **RCRUST: A NEW PHASE EQUILIBRIUM MODELLING TOOL**

# Path dependence of the reactive subsystem

Rcrust operates by assigning P-T-X conditions to a number of points that define a modelling space. A Perple\_X routine is then used which minimizes the Gibbs free energy of the system in order to predict the equilibrium phase assemblage at each point (Connolly, 2005, 2009). Modelling can be performed on compositions including pelites, greywackes, calc-silicates and mafic rocks as far as the available solution models in Perple\_X allow within the full *P-T* range of crustal metamorphism and magmatism. Further information about modelling tolerances can be found in the solution model files and references therein. What is unique in Rcrust's methodology is that the conditions of points in the modelling space can be assigned with reference to other points. If dependencies are assigned, then calculations first solve the hierarchy of dependence of points, after which calculations proceed sequentially along paths that connect the points. This 'path dependence' allows bulk compositional changes to be passed on from point to point, thereby permitting investigation of processes that are dependent on the evolving assemblage as the rock moves through pressure–temperature–bulk compositional space.

To best model the behaviour of rock systems that gain or lose material, it is helpful to consider the system as consisting of a number of subsystems which are, at least temporarily, in chemical isolation from one another. For example, the bulk composition of a rock, or the full system (FS), can be thought of as consisting of: 1. a reactive subsystem (RS) which represents the portion that is currently in chemical equilibrium at the P-T conditions of the system; 2. an extract subsystem (ES) which represents the portion that has been extracted from the RS, during the current and prior steps, and is no longer in chemical equilibrium with the RS. The ES is not subject to further phase equilibrium modelling; and 3. an isolated subsystem (IS) which represents that portion of the FS that has not yet contributed to the reactive subsystem but may later become part of it (Fig. 1). In this way a rock undergoing anatexis, for example, can be thought of as a portion which is currently melting (the reactive

subsystem), a portion which has been extracted through melt loss (the extract subsystem) and a portion, for example, the cores of compositionally zoned pre-anatectic porphyroblasts that have yet to contribute to the effective bulk composition of the reactive subsystem (the isolated subsystem). By transferring bulk material between these systems as the path progresses we can effectively model processes that effect a rocks evolution.



**Fig. 1.** Division of the bulk composition of the rock (full system) into a portion that is not yet incorporated into the chemical system (isolated subsystem); a portion that contains the chemical system currently in thermodynamic equilibrium (reactive subsystem) and a portion that is no longer part of the chemical system (extract subsystem). Effective bulk compositional change can be induced in the rock by moving crystals and/or melt and/or fluid between these subsystems.

# **Modelling setup**

The Rcrust program is operated through a graphical user interface written in R Copyright© 2016 the R Foundation for Statistical Computing (R Core Team, 2016) and therefore requires a working version of R which can be downloaded freely from http://www.R-project.org/. The Rcrust interface writes a text document which is read by the calculation routine when run. This enforces reproducibility between calculations as a record of all input parameters is saved with each calculation. These input files can be shared between users to allow direct correlation between calculations. For advanced users the GUI can be bypassed

by manually editing input files and accessing Rcrust directly from the console.

In a standard calculation the user first defines the size of the modelling space by setting the number of points in the P-T window to be considered. Once the number of points has been defined, P-T conditions are then attributed to each point by defining functions (Fig. 2b). These definitions can be as simple as individually assigning P-T values for each point or may be complex functions that define, for example a non-linear P-T path (e.g. the clockwise P-T loop in Mayne et al. fig. 5). Importantly, the axes of the modelling space do not have to be P and T, but may be a function of bulk composition or the progression of P-T-X paths or any other variable of interest. The next parameter that the user needs to define is the bulk composition (Fig. 2c). Again, this can be simple, for example comprising the weight percentage of each of the oxides that define the reactive subsystem, or a more complex function of the previous point along a P-T path). This functionality allows the user to create P-T paths that have path dependent bulk compositions.

At any point during a calculation, phase manipulations can be used to alter the bulk composition of subsystems by either adding or extracting phases to or from the reactive subsystem (Fig. 2d). Such manipulations can be statically defined prior to the calculation of phase assemblages (for example to add a set amount of water progressively into the system as a function of progress along a path) or dynamically defined in response to phase assemblage proportions (e.g. melt loss events triggered by exceeding a critical melt threshold). The latter also allows phase manipulations to respond to P-T dependent criteria, for example the volume of a phase in the phase assemblage (which itself is also dependent on pressure). The combination of phase manipulations and path dependence can be used to approximate mechanistic processes affecting the evolution of a rock. Output data can be viewed directly in the Rcrust interface or exported as text or postscript files for editing. Graphing routines are available in Rcrust, including an interpolation routine for projecting *P*-*T* paths onto a grid to allow contouring, and a routine for the creation of "phase assemblage maps", a term proposed here to describe graphs that show the change in phase assemblage of a system where pressure, temperature and bulk composition can be independently variable and path-dependent within the diagram (i.e. not a *pseudosection*) from a grid of points (Fig. 2e).



**Fig. 2.** Procedure for modelling using the phase equilibria tool Rcrust. (a) Define the number of points in the modelling space. (b) Assign pressure and temperature conditions. (c) Assign the bulk composition of the reactive subsystem. (d) Define any required phase additions or phase extractions. (e) project outputs to grids and export contour, phase diagram sections or phase assemblage maps.

# PERFORMING PROCESS-ORIENTED INVESTIGATIONS

To illustrate the methodology by which process-oriented investigations can be undertaken modelling was performed in Rcrust version 2017-10-26 (Mayne et al., 2016) with a compiled form of the meemum function from the Perple\_X suite of programs (Connolly,

2009). The NCKFMASHTO chemical system was utilized with the 2011 revised hp11ver.dat thermodynamic data file from the internally consistent dataset of (Holland and Powell, 2011). Solution models were chosen which are consistent with the slightly simplified chemistry of the bulk system (e.g. the chemical system does not account for Mn) yet takes into account substitutions that are important in stabilizing phases (e.g. Ti in biotite). The following solution models were used from solution\_model\_679.dat: Fsp(C1) for plagioclase and alkali-feldspar (Holland and Powell, 2003), Cpx(HP) for clinopyroxene (Holland and Powell, 1996), Ep(HP11) for epidote (Holland and Powell, 2011), Sp(WPC) for spinel (White et al., 2002), Ilm(WPH) for ilmenite (White et al., 2000) and the latest White *et al* (2014) set of models: Bi(W) for biotite, Crd(W) for cordierite, Gt(W) for garnet, melt(W) for melt, Mica(W) for micas, Opx(W) for orthopyroxene, St(W) for staurolite. Abbreviations for phases in figures except for melt and mica were taken from Whitney & Evans (2010) as Bt, Biotite; Crd, cordierite; Fsp, plagioclase and alkali-feldspar; Grt, garnet; H<sub>2</sub>O, liquid water; Ilm, ilmenite; Qz, quartz; Sil, sillimanite; Spl, spinel; St, staurolite.

# Dynamic setting of subsolidus water content of the Reactive System

The water content of the combined hydrous silicate phases of a subsolidus rock changes as a function of pressure and temperature as both the abundance and composition of those hydrous silicates changes. Any H<sub>2</sub>O that cannot be accommodated by the hydrous phases must either be contained within the pore space or must leave the rock system. To model this behaviour, the bulk composition of the system can be set to start with an excess of water and phase extraction routines set such that free water is extracted whenever its volume exceeds some value that is considered to represent a reasonable estimate of the porosity. Figure. 3 shows the phase relations for an average pelite bulk composition (Table 1) from Ague (1991) which evolved along an isobaric 7 kbar heating path from 670 to 920 °C. The bulk composition begins with an excess of water (10 wt.%) and all water that exceeds 0.1 vol.% is extracted in each step. Water extracted from the reactive subsystem is kept in isolation from the reactive subsystem and the abundance of phases are only shown relative to the phases within the reactive subsystem. This process is described in further detail in Mayne *et al* (2017).

	Average amphibolite facies pelite composition from Ague (1991)										
	SiO <sub>2</sub>	TiO <sub>2</sub>	Al <sub>2</sub> O <sub>3</sub>	FeO	MgO	CaO	Na <sub>2</sub> O	K₂O	0	H₂O	
wt.%	52.15	0.96	18.81	7.82	3.11	1.43	1.68	3.76	0.28	10.00	





**Fig. 3.** Modelling subsolidus water content by starting with excess water and then extracting all water that exceeds 0.1 vol.% (approximating a pore space). Phase abundance in wt.% of the reactive subsystem versus temperature for the isobaric heating path at 7 kbar from 670-920 °C starting with the pelite bulk composition in Table 1. The wt.% oxide in the bulk composition of the reactive subsystem is shown normalised to the starting bulk composition of the path.

# Melt loss through critical threshold values and retention amounts

When rocks melt, the melt initially forms along grain boundaries. As melting progresses, the volume of melt may reach some critical value such that it forms an interconnected network and can be extracted from the local rock system (Yakymchuk and Brown, 2014; Brown and Korhonen, 2009). To design a system which is open to melt loss, a critical melt threshold, upon which melt loss will occur, needs to be defined, for example when 80% of grain boundaries become melt bearing (the melt connectivity transition (MCT) proposed by (Rosenberg & Handy (2005). These thresholds can be approximated by volumetric constraints (MCT achieved at c. 7 vol.%) and incorporated into modelling parameters. When melt loss events occur they are very unlikely to be 100% efficient; some melt will inevitably remain within isolated pores/pockets and/or on grain boundaries. To model this behaviour, phase extraction routines can be defined to trigger when the volume of melt exceeds a set value, and to extract some proportion of that melt, perhaps leaving a small amount (e.g. 1 vol.%) in the reactive subsystem to account for melt retention on grain boundaries. This process is extensively discussed in the literature (Yakymchuk and Brown, 2014; Morrissey et al., 2016; Vigneresse and Burg, 2000; Brown and Korhonen, 2009; White and Powell, 2002, 2010; Diener and Fagereng, 2014; Johnson et al., 2011). Figure 4 shows the phase relations for the isobaric heating path with water extraction routines as described in Figure 3 but with an additional extraction routine set to occur whenever 7 vol.% melt is exceeded extracting all melt except 1 vol.%. The cumulative melt extracted from the reactive subsystem is labelled as "Melt es" and is isolated from the reactive subsystem. Rcrust's abilities in this regard are described further in Mayne et al. (2016). Farina et al. (2017) use this methodology to correlate multi-pulsed magmatism in the Monte Capanne pluton with multimodal distribution of zircon ages in order to estimate the duration of partial melting and the timescale of melt extraction from the source.



**Fig. 4.** Melt loss triggered when melt volume exceeds 7 vol.% and set to extract all melt except 1 vol.% (approximating melt retention on grain boundaries) for the isobaric heating path at 7 kbar from 670-920 °C. Handling of subsolidus water content and starting bulk composition as in Figure 3. The wt.% oxide in the bulk composition of the reactive subsystem is shown normalised to the starting bulk composition of the path.

# **Entrainment of phases to melt (magma loss)**

Melts often entrain crystals such as peritectic minerals on segregation from the source (Stevens et al., 2007). This creates magmas whose chemical composition is some combination of the volume of segregated melt and the composition and abundance of the entrained crystals. When these magmas segregate, the bulk composition of the reactive anatectic system is changed, with implications for subsequent melting behaviour. Phase extraction routines can be modified to model this behaviour by extracting proportions of additional phases whenever melt loss events are triggered. Within modelling functions, some peritectic mineral products formed by melting reactions may have the same name as pre-existing minerals e.g. plagioclase feldspar. In order to distinguish between the preexisting subsolidus phases and the newly formed peritectic phases a 'delta function' can be applied. The delta function allows the user to specify only the portion of a mineral phase that increased in mass during melting. This can be used, for example, to selectively extract peritectic minerals along with melt (Stevens et al., 2017). Figure 5 shows the phase relations for the isobaric heating path with water and melt extraction described in Figure 3 and Figure 4 respectively. Additional to these conditions, when melt extraction events occur 30% of the increase in mass, of any phase excluding melt, between the current point and either the last melt extraction event or the last melt absent point (whichever comes first) is extracted. The cumulative extract constituting the extract subsystem is shown in Figure 5 and its bulk composition is recorded in Table 2.



**Fig. 5.** Melt loss with entrainment of 30% of the increase in mass of all phases except melt between the current melt loss event and either the previous melt loss event or melt absent point (whichever is closer to the current event) for the isobaric heating path at 7 kbar from 670-920 °C. Melt threshold, handling of subsolidus water content and starting bulk composition as in Figure 4. The wt.% oxide in the bulk composition of the reactive subsystem is shown normalised to the starting bulk composition of the path.

	Cumulative extract subsystem formed in Figure 5										
	SiO <sub>2</sub>	TiO <sub>2</sub>	Al <sub>2</sub> O <sub>3</sub>	FeO	MgO	CaO	Na <sub>2</sub> O	K₂O	ο	H₂O	
wt.%	59.38	0.37	18.15	7.57	2.51	1.02	2.39	4.28	0.21	4.12	

**Table 2.** Bulk composition of the cumulative extract subsystem formed by subsolidus water

 loss, supersolidus melt loss and entrainment described in Figure 5

# **Fractional crystallisation**

Mechanisms of filter pressing or crystal settling may cause magma systems to fractionate, whereby a portion of crystalized phases are separated from the magma system (García-Arias and Stevens, 2017b). This loss of crystals changes the bulk composition of the magma and subsequent crystallization path followed by the remainder of the system. Depending on the mechanism involved, this process can be modelled by setting phase extraction routines to extract the crystals from the magma under several different circumstances. These extractions can be set relative to the cooling rate of the magma system or triggered when set criteria are met, such as when a threshold volume of crystals is exceeded (Bachmann and Bergantz, 2004; Stevens et al., 2017) or when the difference in density between a phase and melt exceeds a certain threshold. Figure 6 starts with the bulk composition of the cumulative extract system achieved in Figure 5 (Table 2) representing a magma emplaced at the same depth as extraction (7 kbar) which subsequently isobarically cools and crystallizes. To simulate a process of filter pressing, whenever, the total volume of solid phases (all phases excluding melt and H<sub>2</sub>O) in the reactive subsystem exceeds 20 vol.%, 90% of all solid phases are extracted.



**Fig. 6.** Fractional crystallisation of the cumulative extract subsystem formed by Figure 5 (representing a magma source), 90% of all solid phases (all phases except melt and H2O) are extracted whenever the cumulative solid phases exceed 20 vol.% of the reactive subsystem along the isobaric cooling path at 7 kbar from 920-640 °C. The wt.% oxide in the bulk composition of the reactive subsystem is shown normalised to the starting bulk composition of the path.

# Limited availability of phases

The diffusion of elements within crystals such as plagioclase or garnet is extremely slow (Morse, 1984; Zuluaga et al., 2005; Johannes and Koepke, 2001; Tajčmanová et al., 2007). Within anatectic systems, a dissolution-reprecipitation mechanism may operate that is orders of magnitude faster than intra-crystalline diffusion and may represent the rate limiting control on the availability of components from such phases to participate in melting reactions (García-Arias and Stevens, 2017a; Johannes and Koepke, 2001; Taylor et al., 2014). The role of this behaviour in changing the bulk composition of anatectic systems can be approximated by dividing each crystal into an inner core, whose components are effectively isolated from contributing to the chemical equilibrium of the full system, and an outer rim that contains the chemically available components. With increasing time and temperature and decreasing crystal size, components formerly contained within the unreactive core become available to participate in reactions (Nicoli et al., 2017; Tajčmanová et al., 2007; Madlakana and Stevens, 2018). This process can be modelled by removing a portion of the bulk composition of the rock (the cores of grains) thereby creating an isolated subsystem. Portions of this isolated subsystem can then be transferred back into the reactive subsystem, for example as a function of *P*, *T* or melt volume (Stevens et al., 2017). Figure 7 shows the phase relations for the isobaric heating path at 7 kbar from 670 to 920°C where 95% of all feldspar present in the first step of the calculation is extracted and then added progressively back into the reactive subsystem. The mass of feldspar returned in each step is given as  $0.01 \times (\text{melt}_{\text{vol}\%})^2$  until all feldspar is returned. Subsolidus water content is handled the same as in Figure 3.



**Fig. 7.** Limited availability of feldspar modelled by extracting 95% of all feldspar occurring in the reactive subsystem at the start of the path and then progressively reintroduced to the reactive subsystem as a function of melt volume (where mass of feldspar integrated in each step = 0.01 X (melt<sub>vol.%</sub>)2)) for the isobaric heating path at 7 kbar from 670-920 °C. Handling of subsolidus water content and starting bulk composition as in Figure 3. The wt.% oxide in the bulk composition of the reactive subsystem is shown normalised to the starting bulk composition of the path.

# CONCLUSIONS

The presented methodology illustrates how process-oriented investigations can be performed by splitting the effective bulk composition of a system into a number of subsystems and then manipulating bulk compositional proportions between these systems. Rcrust's unique ability to assign bulk compositions by dependence and dynamic phase manipulations allows path dependence to exist between points in modelling space. The consequence of this path dependence is the ability to model in simultaneously changing pressure, temperature and bulk compositional space. Path dependence restricts modelling results to be directional (along paths). This can be used as an advantage as this new form of modelling is suited for investigating processes that effect the progressive evolution of a rock system. By setting appropriate phase manipulations, processes of mass transfer can be simulated to gain insights into the controlling factors behind this chemical evolution. This style of modelling introduces a unique set of phase diagram sections in which any variable, including bulk composition may change independently within a calculation. I suggest terming these diagrams "phase assemblage maps" in order to distinguish the independence of their pressure, temperature and chemical variability from traditional pseudosections which are either isobaric, isothermal, isochemical or composite panel versions of these. This would prevent misinterpretations of these diagrams that do not take into account their path dependence and implications thereof. As a matter of convention to aid understanding of these diagrams I further suggest that complete descriptions of the modelled *P*-*T* paths and starting bulk composition should always accompany such diagrams to the point of reproducibility. Caution should be exercised when interpreting the accuracy of these diagrams as they are intrinsically limited by the accuracy of the thermodynamic datasets that they rely on as well as the accuracy of the activity-composition models which are used to predict variations in the thermodynamic properties of the solution phases (solid and liquid) as they change composition.

The methods presented in this paper exemplify the novel ability of path dependent P-T-X calculations to investigate processes of compositional change in a thermodynamically constrained manner. Future work could use the combination of phase manipulations and path dependence to investigate the mechanistic processes that affect the evolution of a rock by building models based on mass transfer between bulk compositions of subsystems. As these models become more sophisticated they could begin to consider crucial controls on phase equilibria such as kinetic obstacles to equilibration reactions (Nicoli et al., 2017;

Tajčmanová et al., 2007; Madlakana and Stevens, 2018) local bulk composition effects (Lanari and Engi, 2017) or the effect of local stress on equilibration volumes (Wheeler, 2018, 2014). Further, component partitioning between phases could be used to provide estimates of trace element and isotope compositions (Yakymchuk et al., 2018; Gardiner et al., 2018). These additional considerations come with their own uncertainties that the reader must be mindful of. Incrementally building on these methodologies opens up new lines of investigation into the studying of petrogenetic processes.

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# SUPPLEMENTARY MATERIAL\*

Files for reproducing figures 3-7 are contained in the zipped folder "Mayne\_et\_al\_2018\_1\_modelling\_files". To open these download Rcrust from https://www.sun.ac.za/english/faculty/science/earthsciences/rcrust and replace the "Projects" and "data" folders with those in the zipped folder. Open each project by double clicking the appropriate x.RData file.

\*For the thesis examiners' convenience these files are already copied into the electronic copy of Rcrust provided in Addendum A, to open them simply install Rcrust following the user manual in Addendum B, open the "Projects" directory of Rcrust, open the project of choice and double click on the .RData file contained in the project file

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# **CHAPTER 3**

# PRESENTATION OF RESEARCH PAPER 2: THE TRAJECTORY OF THE *P*–*T* PATH CONTROLS THE ONSET OF MELTING IN METASEDIMENTARY ROCKS.

This paper, first authored by Matthew Mayne, is under review for publication in the Journal of Metamorphic Geology.

The following aspects of the research were done independently by Matthew Mayne while receiving standard supervision by his supervisors Gary Stevens, Jean-François Moyen and Tim Johnson: (i) writing of programming code; (ii) conducting phase equilibirium modelling; (iii) generation of the figures; (v) writing of the manuscript

# The trajectory of the P–T path controls the onset of melting in metasedimentary rocks.

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# ABSTRACT

The partial melting behaviour of rocks is critically dependent on the pressure-temperature (P-T) location of the solidus. As rocks lose water during their subsolidus evolution, the higher the temperature at which the solidus is encountered, the lower the water content available to drive future anatexis of any given rock. Consequently, understanding the location of the solidus in P-T space is critical to understanding the metamorphic evolution of anatectic rocks and their fertility for the production of granitic melt. Despite wide application of these techniques, conventional phase equilibrium modelling that is based on a single or a limited number of "stitched" bulk compositions cannot handle bulk-rock water content realistically. The reason for this is that the water content of any fully-hydrated rock changes as a function of pressure and temperature. This study uses Rcrust, a new software tool that allows calculation of phase equilibria in systems with a continually changing bulk composition, to investigate the partial melting of an average metapelite composition. Three different fluid states are considered: fluid-saturated with an abundant H<sub>2</sub>O-rich fluid; fluidabsent, which has no fluid phase but begins calculations as fully-hydrated; and fluidrestricted which has a restricted quantity of free water (0.1 vol.%) filling pore spaces. The behaviour of the system under all three fluid states was investigated along a variety of linear prograde *P*–*T* paths that culminate in granulite and eclogite facies *P*–*T* conditions. Three fundamental aspects of partial melting behaviour were revealed that cannot be determined without the ability to continuously vary the bulk composition: (1) the fluid-absent solidus and the wet solidus are identical for all but steep P-T paths; (2) the bulk water content at the solidus of an average metapelite varies substantially as a function of pressure; (3) rocks following steep *P*–*T* paths ( $\Delta P/\Delta T > 6$  kbar/100 °C) will melt at significantly higher temperature than the wet solidus, because the increase in total water contained in the hydrous silicates as a function of pressure exceeds the decrease in total water contained in the hydrous silicates as a function of temperature, resulting in the rock becoming water deficient, i.e. not fully-hydrated.

Keywords: Rcrust, anatexis; bulk water content; pressure-temperature paths; wet solidus

# **INTRODUCTION**

The beginning of melting in the continental crust is controlled by pressure, temperature and bulk composition. Bulk compositions with sufficient H<sub>2</sub>O to contain a discrete fluid phase will melt at the appropriate fluid-saturated solidus e.g. (Thompson, 1982; Spear et al., 1999; Johannes and Koepke, 2001), whilst rocks with insufficient water to allow a fluid phase to form are considered to melt at the lowest temperature fluid-absent incongruent melting reaction that the metamorphic assemblage allows e.g. (Stevens and Clemens, 1993). For aluminous metapelites this will commonly be the fluid-absent incongruent melting reaction involving muscovite e.g. (Huang and Wyllie, 1981), which is located at significantly higher temperature than the pelite wet solidus. The fluid-absent solidus for biotite-bearing rocks without muscovite is located at even higher temperatures within the granulite facies (Vielzeuf and Montel, 1994; Stevens et al., 1995). Thus, there is general consensus that the presence of water in the subsolidus assemblage exerts the strongest control on the temperature at which partial melting begins in common crustal rocks e.g. (Waters, 1988; Weinberg and Hasalová, 2015; Clemens et al., 2016). However, the onset of fluid-absent melting is extremely difficult to define accurately.

Experimentally, the fluid-absent solidus is hard to identify because of the slow kinetics of the melting reactions, particularly those involving plagioclase e.g. (Johannes et al., 1994; Johannes and Koepke, 2001), and the difficulty of identifying small fractions of quenched melt in experimental run products. An additional challenge is the unavoidable inclusion of gas into the capsule (normally air), that must lower aH<sub>2</sub>O on the grain boundaries of the charge. Crystallization experiments suffer similar kinetic problems and are likely to systematically underestimate solidus temperatures.

Phase equilibria studies also have difficulty in investigating the onset of anatexis in fluidabsent systems across a range of pressures because established software for phase equilibria modelling have limited abilities for the automated handling of bulk compositional changes within pressure–temperature space. Most studies that assume fluid-absent conditions of anatexis determine bulk rock H<sub>2</sub>O content using isobaric  $T-X(H_2O)$  sections and set bulk H<sub>2</sub>O content at the maximum value possible before the appearance of melt without the presence of a free water phase. This commonly results in the first melt being produced through incongruent melting reactions that involve breakdown of micas, typically in the temperature range of 700 to 850 °C for mid– to lower crustal pressures (Vielzeuf and Holloway, 1988; Stevens et al., 1997; Brown and Korhonen, 2009; Yakymchuk and Brown,

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2014). Other studies make the assumption that there is a small amount of  $H_2O$  available in pore spaces leading to minor H<sub>2</sub>O-saturated melting at the wet solidus, and may also use isobaric  $T-X(H_2O)$  sections or modes of hydrous minerals coupled with stoichiometric amount of H<sub>2</sub>O in these minerals (Indares et al., 2008) to determine appropriate bulk rock H<sub>2</sub>O content at a specific pressure. However, if one considers the variations in assemblage and mineral mode inherent to any relevant pseudosection, it is clear that the water content of the subsolidus mineral assemblage varies as a function of both pressure and temperature. Fixed-composition pseudosections can therefore only constitute an accurate representation of the behaviour of the system at the specific pressure used to constrain the H<sub>2</sub>O content of the system; all pressures below and above that value must either over- or underestimate the H<sub>2</sub>O content (Webb et al., 2015). These inaccuracies in bulk H<sub>2</sub>O content are likely to cause significant discrepancies in melting behaviour as a function of pressure in pseudosections constructed in this way. Similarly, it is impossible for an experimental investigation of fullyhydrated, fluid-absent or fluid-restricted partial melting to be conducted at a range of pressures using the same starting material because the correct water content for defining this state is unique to a specific pressure. This study presents a new method for constraining the H<sub>2</sub>O content of the subsolidus system through progressive water loss during prograde metamorphism. This method is used to investigate the position of the solidus in pressuretemperature space, the bulk rock water content at the solidus as a function of pressure and the influence of the trajectory of the P-T path on the melting behaviour of such rocks under upper amphibolite, eclogite and granulite facies conditions for a single pelite bulk composition.

# METHODOLOGY

The phase equilibria tool Rcrust (Mayne et al., 2016) allows modelling to be conducted along P-T paths with bulk composition as a variable. It does this by breaking each P-T path into a number of points in P-T space. Each point passes on any bulk compositional changes induced by modelling functions to the next point on its respective path. Since these points are calculated in a progressive order, they have path dependent bulk compositions. In order to systematically evaluate the effect of the steepness of the P-T path on the partial melting behaviour of the system three different fanned arrays of linear prograde P-T paths were modelled, one projecting a fanned array from the P-T origin (0 °C; 0 kbar) (Fig. 1a), one starting at the origin and then following a P-T path till a fanned projection from 650 °C and 5 kbar (Fig. 1b) and one starting at the origin and then following a P-T path till a fanned projection from 650 °C and 10 kbar (Fig. 1c). This produced P-T paths that arrive at the same amphibolite, granulite and eclogite facies P-T conditions by travelling along different trajectories through P-T space.

The first set of paths start at the P-T origin (0 °C; 0 kbar) and increment pressure (in kbar) as  $sin((y_i-1+6)*pi/180)*10/140*(x_i-1)$  and temperature (in °C) as  $cos((y_i-1+6)*pi/180)*280/140*(x_i-1)$  where  $y_i$  increments the dP/dT of the individual paths in the set and  $x_i$  increments the steps along each respective path. From this fanned array of paths two points were chosen (650 °C;5 kbar and 650 °C;10 kbar) from which to project inflections of the P-T path. The bulk compositions achieved at these points by following the original P-T array from the origin were used as the initial compositions for two further fanned arrays projecting from these points. This ensures that bulk compositional changes from the P-T origin array are inherited by the paths originating at 650 °C;5 kbar and 650 °C;10 kbar.



**Fig. 1**. *P*–*T* diagrams illustrating the modelled path arrays and their intersections with the fields of eclogite–high–pressure granulite (E–HPG) and granulite–ultrahigh temperature (G–UHT) peak metamorphic conditions, as defined by (Brown, 2014). The 0 kbar array (grey dashed arrows) maintains a range of relatively flat *P*–*T* slopes from the origin across the modelled *P*–*T* space. The 5 kbar array (red lines) and 10 kbar array (green lines) begin with the bulk composition attained by the relative path on the 0 kbar array at 650 °C; 5 kbar (path for 5 kbar array) and 650 °C; 10 kbar (path for 10 kbar array) respectively. These arrays then propagate a range of changed  $\Delta P/\Delta T$  gradients while modelling continues to remove water to ensure a fully-hydrated, fluid-absent, or fluid-restricted subsolidus assemblage. The position of the fluid-saturated solidus (calculated in this study) is shown as a thick dashed line for reference.

Modelling was conducted in three different fluid modes (Table 1), fluid-saturated, fluidabsent and fluid-restricted with 0.1 vol.% water (approximating a water filled pore space). In the fluid-saturated mode, H<sub>2</sub>O content in the bulk rock was set to 17 wt.%, which produced a water-bearing assemblage under all P-T conditions investigated. In fluid-absent mode, phase assemblages were calculated for each P-T array with the fluid-saturated composition at the origin but with the software set to remove any free water and recalculate the composition at each step along the path. This maintains the subsolidus assemblage in a fully-hydrated, fluidabsent state, as long as subsolidus reactions encountered by prograde P-T paths do not consume H<sub>2</sub>O. In the fluid restricted mode exactly the same procedure was followed but with the software set to retain water sufficient to fill a nominal pore space, here taken as 0.1 vol.% of the rock, which likely represents a maximum value for high-grade metamorphic rocks e.g.(Thompson, 1983; Stevens and Clemens, 1993; Yardley, 2009; Brown and Korhonen, 2009; Yakymchuk and Brown, 2014). In fluid-absent or fluid restricted mode, if subsolidus reactions encountered by prograde P-T paths consume H<sub>2</sub>O the system may become fluidabsent as water is not added back in to the system.

Phase equilibrium modelling was performed on an average amphibolite–facies metapelite composition (Table 2) from (Ague, 1991) in the NCKFMASHTO (Na<sub>2</sub>O–CaO–K<sub>2</sub>O–FeO–MgO–Al<sub>2</sub>O<sub>3</sub>–SiO<sub>2</sub>–H<sub>2</sub>O–TiO<sub>2</sub>–O) chemical system. Calculations were performed using Rcrust (version 2017–02–14) (Mayne et al., 2016) based on a compiled form of *meemum* from Perplex 6.7.3 (Connolly, 2009) and the thermodynamic data file *hp11ver.dat* (Holland and Powell, 2011). Activity–composition (a–x) models from *solution\_model\_673.dat* were

used as follows: Bi(W), Crd(W), Gt(W), Ilm(W), melt(W), Mica(W), St(W) and Opx(W) from the internally consistent set of solution models produced by (White et al., 2014) for biotite, cordierite, garnet, ilmenite, melt, white mica, staurolite and orthopyroxene respectively; Fsp(C1) for feldspars (Holland and Powell, 2003); Ep(HP11) for epidote (Holland and Powell, 2011) and Sp(WPC) for spinel (White et al., 2002).

	Fluid-saturated	Fluid-absent	Fluid restricted
Starting bulk H <sub>2</sub> O			
content (wt.%)	17	17	17
			Remove all except
Phase extraction		Remove all water	0.1 vol.% of water
definition	None	present in each step	present in each step
		Subsolidus	
		assemblage is fluid-	Subsolidus
		absent.	assemblage begins
		Subsolidus	as water present, if
		assemblage is fully-	subsolidus reactions
		hydrated as long as	encountered by
	Water-bearing	subsolidus reactions	prograde <i>P</i> – <i>T</i> paths
	assemblage under all	encountered by	consume H <sub>2</sub> O the
	P-T conditions	prograde P-T paths	system may become
Fluid state	investigated	do not consume H <sub>2</sub> O	fluid-absent

**Table 1.** Modelling modes for handling of bulk H<sub>2</sub>O content in this study as fluid-saturated, fluid-absent and fluid restricted.

	Na <sub>2</sub> O	MgO	Al <sub>2</sub> O <sub>3</sub>	SiO <sub>2</sub>	K2O	CaO	TiO <sub>2</sub>	FeO	0	H <sub>2</sub> O*
wt.%	1.55	2.78	17.36	48.14	3.47	1.32	0.89	7.22	0.26	17.00
Note: Bulk composition taken from (Ague, 1991) as an average amphibolite-facies										
pelite.										
* $H_2O$ begins in excess (17 wt.%).										

**Table 2.** Starting bulk composition for modelling as the average amphibolite-facies pelite from Ague (1991) after H<sub>2</sub>O adjustment to ensure water begins in excess (17 wt.%).

# RESULTS

# Melting reactions as a function of fluid mode

Phase relations for the path marked "Path for 5 kbar array" (Fig. 1a) are shown in Figure 2. This system begins at the P-T origin with a bulk H<sub>2</sub>O content of 17 wt.%. In fluid-saturated mode this ensures a water-bearing assemblage for the entire length of the path with water abundance in the reactive subsystem beginning at ~ 15 wt.% rising to 16 wt.% at the solidus and then falling progressively during melting to 8 wt.% as the melt volume grows (Fig. 2a). In this system melting begins with a reaction involving white mica at 680 °C producing ~ 15 wt.% melt followed by melting involving biotite until 880 °C producing a further ~ 55 wt.% melt and finally melting involving cordierite producing ~ 13 wt.% melt, culminating in a total of 83 wt.% melt by 970 °C (Fig. 2d). When comparing this system to the other fluid modes it helps to note that the renormalized abundance of melt in the reactive subsystem excluding the abundance of water equates to approximately 17, 60 and 14 wt.% melt, respectively, producing a total of 91 wt.% melt in the reactive subsystem excluding the abundance of water. Further, note that in order to achieve this high degree of melting the average pelite composition used became quartz deficient by approximately 750°C. In fluid-absent mode there is no free water in the reactive subsystem (Fig. 2b). Water is extracted whenever it forms as a free phase (Fig. 2g) which occurs intermittently below the solidus culminating in just above 15.7 wt.% water extracted cumulatively by the solidus at 682°C. No further water is formed or extracted above the solidus. Melting begins at 682 °C producing less than 1 wt.% melt up till 688 °C, after which white mica is exhausted producing ~ 5 wt.% melt (Fig. 2b). From 688 °C onwards melting involving biotite produces ~ 17 wt.% melt by 825 °C after which melting involving cordierite produces a further ~ 25 wt.% melt by 910 °C and finally melting involving feldspar and quartz produces a further ~ 19 wt.% melt by the end of the path. This results in a total of ~ 66 wt.% melt by 1000 °C. Quartz is depleted by 940°C.

Modelling in the fluid restricted mode produced short intervals along the path with a water filled porosity resulting in <0.025 wt.% water in the reactive subsystem. This equates with the maximum allowable 0.1 vol.% pore space set in the modelling. The water extraction events follow a similar pattern to those in the fluid absent mode resulting in a cumulative 15.7 wt.% water extracted by the solidus at 680 °C. Overall, the partial melting behaviour is near identical to that observed in the fluid absent, mode with only a 2 °C lower solidus and slightly more melt produced before the exhaustion of white mica (also less than 1 wt.% by 688 °C) (Fig. 2c).



**Fig. 2.** Diagrams portraying the partial melting behaviour along the "Path for 5 kbar array" path shown in Figure 1a for the three fluid modes considered: (a-c) Water in the reactive subsystem (wt.%) as a function of temperature shows the difference between the three modelled fluid modes, i.e. fluid-saturated, fluid-absent and fluid restricted. Note the variation in scale for the y-axis. (d-f) Phase abundance as weight percentage of the reactive subsystem. (g-h) water extracted from the reactive subsystem as weight percentage of the full system. (i-j) cumulative water extracted from the reactive subsystem as weight percentage of the full system. Abbreviations for phases in figures except for melt, water and mica were taken from (Whitney and Evans, 2010) as Bt, Biotite; Crd, cordierite; Fsp, plagioclase and alkali-feldspar; Grt, garnet; Ilm, ilmenite; Opx, orthopyroxene; Qz, quartz; Sil, sillimanite; Spl, spinel; St, staurolite.

### Effect of fluid state and *P*–*T* trajectory on the position of the solidus

The solidi produced by the 3 fluid modes in combination with the path array originating at 0 °C;0 kbar, are all within 2 °C of each other despite the inclusion of a fluid-absent rock in the modelling (Fig. 3). This is in agreement with the findings of (Webb et al., 2015) who demonstrated using isobaric T-XH<sub>2</sub>O sections, that subsolidus water loss from rocks undergoing prograde metamorphism migrates the rock composition towards the minimum saturation point on the boundary of the wet-melting field. This study follows the same approach but in *P*–*T* space because bulk composition may vary simultaneously with *P* and T. The findings indicate that fully-hydrated fluid absent rocks do melt at the wet solidus, even in fluid-absent systems. In order to assess the potential effect of the P-T path trajectory on partial melting behaviour, each of the 3 fluid modes described above are modelled along the 3 P-T path arrays described in Figure 1. The results indicate that, for the fluid saturated case, the wet solidus is unaffected by the trajectory of the prograde P-T path; the solidus is located at ~ 680 °C between 2.5 and 15 kbar (Fig. 3a), irrespective of the path taken by the rock to reach the solidus. The position of this calculated solidus is in broad agreement with the results of experimental studies and other phase equilibrium investigations using a conventional pseudosection approach (Thompson, 1982; Spear et al., 1999; Johannes and Koepke, 2001). This behaviour contrasts strongly with the solidus behaviour for the two modes where water content is handled in a more petrologically realistic manner. In both the fluid-absent and fluid-restricted modes, the results in terms of phase assemblage and positions of the path dependent solidi were identical, so only the fluid-absent system is shown and discussed further. For these systems, the three modelled path arrays each produced a different solidus (Fig. 3e). The path array originating at 0 °C;0 kbar, underwent melting at the wet solidus as described above (Fig. 3b). However, evolution along the P-Tpath arrays originating at 5 and 10 kbar and 650 °C produced very different behaviour. Both these arrays contain P-T paths that are substantially steeper than those of the array originating at 0 kbar (Fig.3 c & d) and the fluid-absent and fluid-restricted rocks evolving along paths with  $\Delta P / \Delta T < 6$  kbar/100 °C melted at the wet solidus. However, for both systems, rocks evolving along steeper paths do not melt at the wet solidus, rather they map out a solidus which shifts to progressively higher temperature as pressure increases. For the array originating at 5 kbar this results in the solidus at 15 kbar being located at a temperature > 100 °C higher than the equivalent 0 kbar array's solidus. The portion of the solidus for the 5 kbar path arrays that is located at a temperature above the fluid-saturated solidus is located

within ~ 25 °C of the modelled white mica out boundary (Fig. 4c). Consequently, the steep P-T paths that produce this higher temperature solidus appear to record the fluid-absent incongruent melting reaction involving white mica at pressures above approximately 7 kbar. For both the fluid-restricted and fluid absent systems, the path array originating at 10 kbar records similar behaviour to the equivalent 5 kbar path array, matching the fluid-saturated solidus at lower pressure, and departing from it at higher pressure, but in this case the point of departure is located at ~11.5 kbar (Fig. 3d) because it is only above this pressure that the paths attain the prerequisite steepness. At 15 kbar the 10 kbar array is located >50 °C higher than the 0 kbar path array solidus.



**Fig. 3.** Melt abundance as weight percentage of the reactive subsystem (renormalized to 100% after excluding the abundance of water) for a) the fluid-saturated system; b) the fluid-

absent system originating at the P-T origin; c) the fluid-absent system beginning at the P-T origin but inflecting to a fanned array at 650 °C, 5 kbar; d) the fluid-absent system beginning at the P-T origin but inflecting to a fanned array at 650 °C, 10 kbar. e) Relative positions of the solidi produced by the fluid-saturated system and the fluid-absent system from the three arrays considered with respect to the fields of eclogite–high–pressure granulite (E–HPG) and granulite–ultrahigh temperature (G–UHT) peak metamorphic conditions, as defined by (Brown, 2014)

# Effect of fluid state and *P*–*T* trajectory on the melt production

Fluid saturated melting produces a large amount of melt close to the solidus with a tight grouping of melt wt.% contours near the solidus (calculated as melt abundance renormalized to 100% after excluding the abundance of water) (Fig. 3a). The system consists of up to 60 wt.% melt by 800 °C (Fig. 3a). For paths originating at the origin in the fluid-absent and fluid-restricted systems, the initial amount of melt produced is low with the 1 wt.% melt contour being separated from the solidus by 15 to >50 °C (Fig. 3b). A systematic increase in melt volume with temperature is observed in these paths above 800 °C with an average increase of approximately 10 wt.% melt per 30 °C.

Between approximately 3 and 4.5 kbar the solidus intersects a P-T field in which biotite is the only hydrous mineral, with white mica and cordierite present as an additional hydrous phase at higher and lower pressures respectively (Fig. 4 c- e). The H<sub>2</sub>O content of the rock along this portion of the solidus is constant at ~ 1 wt.% (Fig. 4b), indicating that the biotite mode and water content do not vary as a function of pressure in this area of the phase diagram. The consequences of this are visible as a bulge to higher temperatures in the melt isopleths (up to 30 °C) for paths that travelled through the pressure–temperature field of this assemblage (Fig. 3b). A maximum melt abundance of 80 wt.% is obtained for this system at low pressures (<8.5 kbar).

Melt abundance contours for paths originating at 650 °C, 5kbar in fluid-absent and fluid restricted systems show similar features to those originating at the origin. Contours are strongly temperature dependent, show systematic increases above 800 °C and are deflected to higher temperature at high pressures. A maximum of 80 wt.% melt is produced for pressures between 3. and 8.5 kbar at 1 100 °C. Below 800 °C, however, marked differences are found with the solidus, the 1, and the 10 wt.% melt contour all deflected at high pressure to near coincidence at 825 °C, 15 kbar. Additionally, the anomalous shift to higher

temperatures experienced by the 0.65 kbar/100 °C path from the origin is erased by the inflection of the P-T paths at 650 °C, 5kbar and an increase in temperature of contours is observed only for paths inflecting to a steepness less than -2 kbar/100 °C (Fig. 3c). Melt production for the paths originating at 650 °C, 10kbar in fluid-absent and fluid restricted systems are near identical to those produced by paths originating at 650 °C, 5kbar with the only significant differences being less deflected contours below 800 °C; at high pressure and a lack of any anomalous increase in temperature of contours for steeply downwards inflecting paths (Fig. 3d).



**Fig. 4.** P-T diagram showing the P-T path array originating at the P-T origin (grey dashed arrows). a) The grey shading represents the total H<sub>2</sub>O (as wt.% of the system) contained within the hydrous silicates white mica, biotite and cordierite, contoured from 0 (white) to 2.6 (dark grey) for the fluid absent system. Weight percentage of H<sub>2</sub>O in the entire system (including melt) is contoured in 0.2 wt.% increments (blue dotted lines) and the weight percentage of melt in the reactive subsystem is contoured (orange dashed lines). b) Weight percentage of H<sub>2</sub>O in the bulk system at the solidus for the fluid-absent and the fluid-restricted systems as a function of pressure. (c-e) Weight proportion of the solid system contained as H<sub>2</sub>O in white mica, biotite and cordierite. f) Degree of water saturation of melt given by the H<sub>2</sub>O in melt in the fluid-absent mode divided by the H<sub>2</sub>O in melt in fluid-saturated mode, expressed as a percentage.

# Rock water content at the solidus as a function of pressure

The H<sub>2</sub>O content of the fluid-absent system at the solidus produced by paths from the origin varies by 1.6 wt.% (from 0.8 to 2.4 wt.%) (Fig. 4b) over the pressure range investigated and generally increases as a function of pressure. This substantial range in water content clearly illustrates the deficiencies in trying to model anatexis over a pressure range using a single bulk composition. The water content of the fluid restricted system at this solidus is only minutely higher than the fluid-absent rock at the same pressure (Fig.4b). For both fluidabsent and fluid restricted systems above the solidus, bulk H<sub>2</sub>O content remains constant along each path as no supersolidus free water can form due to the presence of waterundersaturated melt (Fig. 4f). Above the solidus all H<sub>2</sub>O is accommodated either in melt or within melt and hydrous silicates (Fig. 4a). The hydrous silicates that are stable within this bulk composition in the relevant *P*–*T* range are white mica (Fig. 4c), biotite (Fig. 4d) and cordierite (Fig. 4e). With increasing pressure, the stability of the hydrous silicates accommodates larger total water content (up to 2.6 wt.% of the reactive subsystem) by increasing the phase abundance of the hydrous silicates and by preferentially forming hydrous silicates that contain more water (e.g. white mica rather than biotite) (Fig. 4a, c-e). If P-T paths are steeper than the H<sub>2</sub>O in hydrous silicate contours in Figure 4a (for example paths with  $\Box P / \Box T > 6$  kbar/100 °C in Figure 3c) then the abundance of white mica may increase and the abundance of biotite may decrease to such an extent that the rock system becomes fluid-deficient. If this happens the system may cross the position of the fluidsaturated solidus without melting and only begin melting at the first fluid absent melting reaction the path intersects
#### DISCUSSION AND CONCLUSIONS

The methodology presented allows phase equilibrium modelling to investigate the P-T path dependent partial melting of rocks with realistic H<sub>2</sub>O contents, over a range of pressures and temperatures. The results demonstrate that for rocks undergoing heating without a substantial pressure increase, all metapelitic rocks will melt at the wet solidus, irrespective of fluid state. The reason for this is that in the fluid-absent system, biotite H<sub>2</sub>O content decreases as a function of temperature (Fig. 4d). Once the rock reaches the position of the wet solidus, the decrease in biotite H<sub>2</sub>O content with the next increment of temperature increase allows for melt formation without the appearance of a fluid-phase. This liberation of water from biotite can also be seen in the water extraction behaviour of single paths in the fluid-absent and fluid restricted systems (Fig. 2 g,h). This is almost congruent fluid-absent anatexis as it is accompanied by only minor shifts in biotite and plagioclase compositions and it results in low melt volumes. Thus, phase equilibrium modelling using the best available models for activity-composition relations in the solid- and liquid-solution phases, in combination with a correct handling of H<sub>2</sub>O, demonstrates that the idea that fluid-absent rocks will only melt at the experimentally determined conditions of muscovite- and biotitedriven incongruent melting, is incorrect. As also detailed by (Webb et al., 2015), the main reasons why experimental studies have missed this behaviour are that experiments using a single composition cannot properly map out fluid-absent partial melting behaviour over a range of pressures, or the natural decrease in water content that occurs as subsolidus rocks evolve to higher temperature. The modelling predicts that melting at conditions at or close to the wet solidus is inevitable for most rocks. Possible examples of field areas where evidence of this type of low temperature anatexis are preserved are the Damara Belt of Namibia (Ward et al., 2008) and in the Famatinian Orogen of NW Argentina (Sola et al., 2017). With no melt loss, biotite bearing assemblages appear to melt progressively between the fluidabsent solidus and the point at which biotite disappears (Fig. 4a).

At common granulite facies temperatures, melt proportion appears to be a rather well defined function of temperature, with surprisingly little pressure influence at 800 °C the system contains ~ 10 wt.% melt, at 850 °C this figure is ~ 20 wt.%. Maximum melt proportions are attained in the fluid-saturated system at 90 wt.% with more than 60 wt.% of this melt being produced below 850 °C. The fluid-absent and fluid restricted system produces significantly less melt (with a maximum of 80 wt.%) only producing melt above 1 wt.% after 750 °C with a systematic increase in melt above 800 °C at an average of 10 wt.%

melt per 30 °C. Importantly, the melts present at relatively low temperatures are significantly water under-saturated (Fig. 4f) and consequently can ascend to achieve crustal differentiation if they are able to segregate from their sources. This implies that fluid-absent melting does makes a substantial contribution to low-temperature melting (< 850 C) and that these melts have significant assent potential due to their water-undersaturated character. Being able to adjust system water content incrementally to simulate fully-hydrated, fluidabsent conditions and fluid-restricted, water-present conditions over a range of pressures also allows the path dependency of partial melting behaviour to be investigated. This has demonstrated that if metapelitic rocks cross the position of the wet solidus in the field of white mica stability along a sufficiently steep positive P-T path, the solidus is displaced to significantly higher temperature than the fluid-saturated solidus. This appears to be a result of white mica mode growing at the expense of biotite as a function of pressure, as the rock progresses along the prograde path (Fig. 4 c,d). In the fluid-restricted case this results in the subsolidus rock consuming the 0.1 vol.% pore water through phengite producing reactions and the rock becoming fluid-absent before the water-saturated solidus is encountered (Fig. 4a). Under these conditions, the rocks in both fluid-absent and fluid restricted systems are less than fully-hydrated and the resultant decrease in water activity favours white mica stability over melt and melting is delayed to higher temperature. This phenomenon could effect a large number of rocks which undergo prograde evolution along steep P-T paths into the high pressure amphibolite facies and eclogite facies. This could provide a mechanism for such rocks to remain solid for a considerable time along these steep paths crossing the wet solidus after which shallowing of the P-T path and/or subsequent heating would produce substantial melt volumes (Fig. 3 c,d).

#### DOWNLOAD

Rcrust is free to download and use under the GNU copyleft. The latest version of the software can be found on either of the two institutional addresses at: http://www.univ-st-etienne.fr/rcrust or http://www.sun.ac.za/english/faculty/science/earthsciences/rcrust. Alternatively, the software can be downloaded by contacting the corresponding author.

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## SUPPLEMENTARY MATERIAL\*

Files for reproducing the results presented are contained in the zipped folder "Mayne\_et\_al\_2018\_2\_modelling\_files". PA0, PA5 and PA10 denote the path arrays originating from the P-T origin, from 650 °C; 5 kbar and from 650 °C; 10 kbar respectively. Fluid saturated calculations were performed using the PA0 array and fluid states of fluidabsent and fluid-restricted are shown for each of the possible path arrays. A process of gridded interpolation was performed on each array in order to plot a square regular gridded contour diagram, these files are presented with a suffix of "\_grid" added to their project name. To open the files download Rcrust from

https://www.sun.ac.za/english/faculty/science/earthsciences/rcrust and replace the "Projects" and "data" folders with those in the zipped folder. Open each project by double clicking the appropriate x.RData file.

\*For the thesis examiners' convenience these files are already copied into the electronic copy of Rcrust provided in Addendum A, to open them simply install Rcrust following the user manual in Addendum B, open the "Projects" directory of Rcrust, open the project of choice and double click on the .RData file contained in the project file

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# **CHAPTER 4**

# PRESENTATION OF RESEARCH PAPER 3: A PHASE EQUILIBRIUM INVESTIGATION OF SELECTED SOURCE CONTROLS ON THE COMPOSITION OF MELT BATCHES GENERATED BY SEQUENTIAL MELTING OF AN AVERAGE METAPELITE

This paper, first authored by Matthew Mayne, is accepted upon revision for publication in the Geological Society of London Special Issue: Making granites: petrogenetic processes, tectonic environments and secular variations.

The following aspects of the research were done independently by Matthew Mayne while receiving standard supervision by his supervisors Gary Stevens and Jean-François Moyen: (i) writing of programming code; (ii) conducting phase equilibrium modelling; (iii) generation of the figures; (v) writing of the manuscript

# A phase equilibrium investigation of selected source controls on the composition of melt batches generated by sequential melting of an average metapelite

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Abbreviated title: "Source controls on melting of a metapelite"

#### ABSTRACT

The ability of Rcrust (Mayne et al., 2016) to conduct path dependent phase equilibrium modelling with automated changing bulk compositions allows for a phase equilibrium approach to investigate an array of source controls for their effect on the bulk compositions of melts produced by sequential melting events. The following source controls of the rock system are considered: 1. Initial magnesium and iron content; 2. Initial sodium and calcium content; 3. fluid state; 4. Pressure-temperature path followed by the system and 5. threshold by which melt extractions in the system are triggered. The permutation of 3 cases for each of these source controls resulted in 243 different modelled pressure-temperature-bulk composition paths with which the melting of an average pelite composition is investigated. The resultant melt compositions are compared to that of a natural granite data set and provide a good fit for the incompatible elements Na<sub>2</sub>O and K<sub>2</sub>O with the allowance that granites most likely form as magmas consisting of melt and ferromagnesian rich crystals. The fluid state of the system is shown to have the strongest control on melt compositions with the pressure-temperature path having subordinate control on the volume and composition of melts produced.

**Keywords**: Phase equilibria modelling; Rcrust; source controls, fluid state, pressuretemperature path

#### **INTRODUCTION**

Granite plutons and batholiths (senso lato) commonly exhibit a substantial range in major and trace element compositions, within co-magmatic rocks e.g. (Brown and Pressley, 1999; Stevens et al., 2007). Studies seeking to explain this commonly propose a range of different processes that occur in the magma plumbing systems or in magma chambers, and that are interpreted to modify magmas of originally homogenous composition. Processes such as unmixing of entrained residuum e.g. (Chappell et al., 1987), fractional crystallization e.g. (Foden et al., 2002; Breaks, Frederick and Moore, 1992), assimilation of wall rocks e.g. (Beard et al., 2005; DePaolo, 1981), or mixing with other magmas e.g. (Barbarin, 1988; Collins, 1996), all feature prominently in the literature, yet as discussed by (Clemens and Stevens, 2012), are unlikely to provide viable explanations for the major element, trace element and isotopic variations recorded within large granite bodies.

Some petrogenetic processes proposed to account for the observed range of magma compositions do occur in the source. For example, the variable degrees of entrainment of the peritectic assemblage proposed by Stevens et al. (2007), Clemens et al. (2011) and Villaros and Stevens (2009) to explain compositional variation in the S-type granites of the Cape Granite Suite. These studies propose that incompatible major element concentrations in granites reflect the compositions and proportions of reactant minerals in the source, whilst compatible element concentrations principally reflect the amount of peritectic assemblage entrained to the magma in the source, during biotite fluid-absent melting. When combined with efficient extraction of magma from the source as different batches that do not mingle in the plumbing systems e.g. (Brown and Pressley, 1999), the changes in melting reaction stoichiometry that occur with increasing temperature and decreasing water content are recognised to produce a range of magma compositions e.g. (Farina and Stevens, 2011). The water content of rocks, as well as the absence or availability of a water-rich fluid phase, both have a profound effect on melt composition and the temperature of melt generation. The role of water content of the system in determining melt productivity is also dependant on the shape of the P-T path, through the control of pressure on the solubility of water in melt. Despite the fact that source compositional variation, including water content, P-T condition of anatexis, and the volume of melt that is retained in the source prior to magma extraction, all clearly may have a profound effect on magma chemistry, relatively few studies recognise that these factors may play a role in shaping the compositional range recorded in granites. The majority of studies that have attempted to interpret the origins of major element

chemical variation within granites assume the involvement of large volumes of melt of homogenous composition. For even relatively small sized bodies this is a highly unrealistic assumption for two reasons. Firstly, even if the source rocks retain melt until a single large batch is segregated and delivered to construct the pluton, it is very unlikely that the source rocks, and thus the melt, will be compositionally homogenous. This conclusion is based on the observations that all rock sequences that may represent fertile sources of granite magma, such as hydrated volcanic sequences of mafic to intermediate composition, as well as clastic sediments with a considerable hydrous mineral fraction, are typically compositionally variable on a metre to sub-metre scale; additionally, the volume of source rocks must be significantly larger than the volume of the magmatic rocks produced. Thus, for even small plutons, melt must drain from a sufficiently large volume of source rocks that compositional variation in the source is unavoidable. Secondly, it is very unlikely that the source rocks deliver melt in a single large batch (Clemens et al., 2016), potentially facilitating homogenization by mixing and diffusion after segregation. Both exposed granulite facies source rocks and granites contain compositional and textural evidence to support incremental or continual drainage of melt from the source e.g. (Coleman et al., 2004; de Saint Blanquat et al., 2011). Examples of restitic granulites that have yielded at least 25 vol.% melt, contain compositional layering at a decimetre to metre scale that is interpreted to represent compositional layering within the protolith e.g. (Taylor and Stevens, 2010). Contacts between layers are sharp and mineral assemblages within different layers are not in equilibrium e.g. orthopyroxene- and sillimanite-bearing assemblages in adjacent layers (Stevens and Reenen, 1992). Such rocks must have lost melt episodically, in small batches, or continuously. If not, they would have developed diatexitic textures, with disruption of regular layering. Evidence from some S-type leucogranites indicates that melt batches are indeed very rapidly transported from source to pluton and do not remain in the source for any significant time after formation. These rocks have bulk compositions that are zircon undersaturated at reasonable estimates for magma temperature, yet contain zircon inherited from the source, supporting estimates of melt residency in the source of no more than 500 years (Villaros et al., 2009). Continuous or episodic melt extraction will result in different melt compositions leaving the source, as the melting reactions change as anatexis of the source progresses e.g. (Farina and Stevens, 2011).

From the arguments above, granites derived from partial melting of the crust can be assumed to be principally constructed from melt batches that had different compositions at the point of segregation from the source. Investigation of the role of source composition in controlling melt compositions is hampered by the fact that almost all available data from experimental petrology represent the consequences of batch melting, mapped out over a range of pressures and temperatures. Typically, a single composition or a small number of different compositions is investigated e.g. (Stevens et al., 1997). The advent of Rcrust (Mayne et al., 2016), software which allows path dependant phase equilibrium modelling with changing bulk composition, allows the source control on the compositions of individual batches of melt leaving the source to be investigated using a phase equilibrium modelling approach. As there are an almost infinitely large number of potential variables that could be investigated. However, this study has aimed to investigate the control of Mg#, Na/Ca ratio and fluid state, as well as the effect of melt volume prior to melt extraction and the steepness of the P-T path on the compositions of melt batches produced from a metapelite undergoing progressive melting.

#### METHODOLOGY

The source parameters that were investigated in this study can be divided into compositional parameters and physical parameters. For the compositional parameters, the compositions used were based on the average pelite composition of Ague (1991) (Table 1). In order to approximate chemical heterogeneity in the metapelite source, the magnesium number (Mg#)= Mg/(Fe + Mg)\*100 [mol.%] and calcium number (Ca#) = Ca/(Ca + Na)\*100 [mol.%] of the bulk composition was varied. The Mg# of the Ague (1991) average is 20, two additional bulk compositions were generated by changing the atomic ratio of Mg to Fe to create Mg# =41 and 60. Similarly, the *Ca*<sup>#</sup> for the Ague (1991) average is 19 and the atomic proportions of Ca and Na were varied for each of the 3  $Mg^{\#}$  bulk compositions to produce additional bulk compositions with Ca = 32 and 42. Thus, excluding variations in water content, 9 different bulk compositions were used: the permutation of 3 magnesium numbers and 3 calcium numbers. At conditions just below the water-present solidus, these rock compositions are all characterized by assemblages dominated by quartz, plagioclase, biotite and muscovite, and at a reference P-T condition of 640 °C and 7 kbar, the mineral modes and plagioclase anorthite contents are indicated in Figure 1. Note that the plagioclase anorthite contents are higher than the Ca#'s of the rocks and also vary as a function of the  $Mg^{\#}$ . This is because Na is taken up by both muscovite and biotite, but in different amounts, and the mode of biotite and muscovite vary as a function of Mg#, whilst at this P-T condition, Ca is accommodated almost completely within plagioclase.

Water content was varied between three different fluid states  $(H_2O)$  across the 9 compositions described above. Firstly, each of the rocks was modelled as having 10 wt.% water in the bulk composition. This was sufficient to keep the assemblage water saturated to a temperature above 920 °C, the upper limit of the modelling conducted in this study. These compositions are termed water in excess. An additional set of compositions was modelled as fully-hydrated, fluid-absent. This was achieved by starting with the water in excess composition and setting the software to remove all water present as a free phase at each step of the prograde evolution of the rock. A final situation considered was for water to be porosity limited that is: water to be present at the water-saturated solidus only as a pore fluid filling a nominal porosity. In this case the software was set to start with water in excess and at each increment of prograde evolution to remove all free water except for 0.1 vol.%. The combination of the three different fluid states, with the variations in bulk rock Mg# and Ca#, produces 27 different sets of compositional parameters that were modelled. The 27 different sets of bulk compositional parameters were considered to evolve along three possible pressure-temperature paths (P-T). The first of these was an isobaric heating path at 7 kbar originating at 640 °C. The second, originating at the same point was a linear path to 920 °C and 9.5 kbar. The third, also originates at the same point and is a linear path to 920 °C and 12 kbar. In the discussion that follows these paths are referred to respectively as isobaric, gentle and steep. A second physical parameter considered in the modelling was the degree of melt retention in the source prior to melt extraction (Melt threshold). Values of 1, 7 and 10 vol.% melt were used as the trigger for melt extraction. Upon this threshold being exceeded, melt was extracted down to 1 vol.% which was assumed to represent the amount of melt retained on grain boundaries and therefore inaccessible to extraction. The combination of compositional parameters, with three P-T path scenarios and three Melt thresholds resulted in a total of 5 different source controls being investigated, each of which have 3 possible cases, culminating in  $3^5$  different models (Table 2).

	SiO <sub>2</sub>	TiO <sub>2</sub>	$Al_2O_3$	FeO	MgO	CaO	Na <sub>2</sub> O	K <sub>2</sub> O	0	H <sub>2</sub> O
wt.%	52.15	0.96	18.81	9.59	1.34	0.93	2.18	3.76	0.28	10

**Table 1.** Initial bulk composition used in the construction of path dependent *P*-*T*-*X* paths in wt.% as the average amphibolite-facies pelite from Ague (1991). The composition shown forms the baseline for calculating the 9 starting bulk compositions shown in Figure 1 with magnesium number (Mg#) and calcium number (Ca#) altered where applicable.

	2	Source controls					
			Compositional p	Physical parameters			
		Magnesium number ( <i>Mg</i> # )	Calcium number (Ca#)	Fluid state ( $H_2O$ )	Pressure- temperature path ( <i>P-T</i> )	Melt retention before extraction ( <i>Melt threshold</i> )	
Cases High Medium Low	Low	20	19	Fhfa: Fully-hydrated, fluid absent; water starting in excess but all liquid water present as a free phase removed from the reactive subsystem at each step	lsobaric: {640 °C;7 kbar}-> {920 °C;7 kbar}	1 vol.%	
	Medium	41	32	Porosity limited: water starting in excess but all liquid water exceeding 0.1 vol.% of the system removed at each step	Gentle: {640 °C;7 kbar}-> {920 °C;9.5 kbar}	7 vol.%	
	High	60	42	Water in excess: 10 wt.% H <sub>2</sub> O; water present as a free phase throughout	Steep:{640 °C;7 kbar}-> {920 °C;12 kbar}	10 vol.%	

Table 2. Summary of the *source controls* considered and each of their 3 *cases*.



**Fig. 1.** Starting 9 bulk compositions produced by altering the Mg# and Ca# of the average pelite composition of Ague (1991)(Table 1) expressed as wt.% oxides normalized to the Ague (1991) average with the phase assemblage produced by each bulk composition at 640 °C; 7 kbar expressed as wt.% of each phase present. The anorthite percentage as An%=Ca/(Ca+Na)\*100 [mol.%] of feldspar is reported above each phase assemblage. Abbreviations for phases except for melt and mica were taken from Whitney and Evans (2010) as Bt, Biotite; Fsp, plagioclase and alkali-feldspar; Grt, garnet; Ilm, ilmenite; Ky, kyanite; Qz, quartz; Spl, spinel; St, staurolite.

Calculations were performed in Rcrust version 2017-10-26 (Mayne et al., 2016) using a compiled form of the meemum function (version 6.7.9) from the Perple\_X suite of programs (Connolly, 2009) in the NCKFMASHTO chemical system utilizing the 2011 revised hp11ver.dat thermodynamic data file from the internally consistent dataset of Holland and Powell (2011). Solution models were chosen which are consistent with the slightly simplified chemistry of the bulk system (e.g. the chemical system does not account for Mn) yet takes into account substitutions that are important in stabilizing phases (e.g. Ti in biotite). The following solution models were used from solution\_model\_679.dat: Fsp(C1) for plagioclase and alkali-feldspar (Holland and Powell, 2003), Cpx(HP) for clinopyroxene (Holland and Powell, 1996), Ep(HP11) for epidote (Holland and Powell, 2011), Sp(WPC) for spinel (White et al., 2002), Ilm(WPH) for ilmenite (White et al., 2000) and the latest White et al. (2014) set of models: Bi(W) for biotite, Crd(W) for cordierite, Gt(W) for garnet,

melt(W) for melt, Mica(W) for micas, Opx(W) for orthopyroxene, St(W) for staurolite. All the *P-T* paths modelled start at 640 °C and 7 kbar with 10 wt.% H<sub>2</sub>O. This results in a free water phase being present at the beginning of each path, with water lost as appropriate to the model situation from the 642 °C step onwards.

#### RESULTS

The phase assemblage plots and melt production information as a function of temperature, for the Ague (1991) average Mg# and Ca# bulk composition, with 7 vol.% melt extraction threshold, evolving along the gentle prograde heating path (640°C; 7kbar to 920°C; 9.5 kbar) for three fluid cases are illustrated in Figure 2. The diagram illustrates some important fundamentals regarding the role of water during partial melting. The case with water limited to a nominal porosity and the fully-hydrated, fluid-absent case yield similar results because the bulk rock water contents of each of these water restricted cases at the solidus are similar. Each of the three cases considered undergoes melting at 684 °C, but the water restricted case predicts less than 3 vol.% melt in the system between 684 and approximately 735 °C, where there is a pulse of melt to >7 vol.% triggering the extraction of melt. This pulse of melt is the consequence of muscovite being consumed by an incongruent melting reaction. Sillimanite mode increases distinctly at the muscovite-out temperature as sillimanite is the primary crystalline product of the incongruent melting reaction which consumes muscovite. Following the disappearance of muscovite and the melt extraction event, melt modes increase very slightly as a function of temperature between 735 and 770 °C, where biotite mode begins to decrease as a function of temperature, with a corresponding increase in melt abundance. Biotite incongruent melting results in the appearance of peritectic garnet and triggers three melt extraction events between 770 and 850 °C, the temperature at which biotite disappears. Heating between 850 and 920 °C produces a single further melt extraction event. This last pulse of melt extraction occurs at a slightly higher temperature in the fully-hydrated, fluid-absent system, relative to the rock with 0.1 vol.% pore-water in the subsolidus assemblage. Thus, the melting of both water restricted rocks is controlled by the incongruent melting behaviour of the micas. Quartz and plagioclase remain in significant proportions in the residuum, despite the rocks having lost 20 vol.% melt.

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**Fig. 2.** Phase abundance and cumulative melt (both in wt.% relative to the full system) produced along *P-T-X* paths investigating water content ( $H_2O$ ) as a source control on melt production considering 3 *cases*: a) fully-hydrated, fluid-absent; b) porosity limited to 0.1 vol.% and c) water in excess. For the 3 paths shown here Mg# and Ca# are taken as the Ague (1991) average with melt extraction events triggered by a 7 vol.% *melt threshold* along the gentle prograde heating path (640°C; 7kbar to 920°C; 9.5 kbar). Step resolution of paths is set at 2°C. Abbreviations for phases except for melt and mica were taken from Whitney and Evans (2010) as Bt, Biotite; Fsp, plagioclase and alkali-feldspar; Grt, garnet; H<sub>2</sub>O, liquid water; Ilm, ilmenite; Ky, kyanite; Qz, quartz; Sil, sillimanite; Spl, spinel; St, staurolite.

In contrast, the availability of water controls the melting behaviour of the rock in the water in excess case; there is always as much melt in the system as the temperature and melt depleted composition will allow. Muscovite mode reduces markedly at the solidus, as do the modes of quartz and plagioclase. Muscovite disappears at approximately 700 °C and sillimanite mode grows with the decrease in muscovite, reflecting the incongruent melting of muscovite. Peritectic garnet appears at approximately 710 °C, marking this temperature as the point at which biotite decomposition makes a significant contribution to incongruent melting. The mode of biotite, quartz and plagioclase decrease substantially from this temperature to approximately 750 °C. Melt extraction events occur with a frequency of approximately one per 10 °C between the solidus and 750 °C. At this temperature the plagioclase composition in the residuum becomes anorthite, supressing further biotite melting to approximately 780 °C. Significant reduction in biotite and quartz mode occurs between 780 and 800 °C, with a number of corresponding melt extraction events. At 800 °C quartz is depleted and no further melt extraction events are triggered until approximately 870 °C, where biotite and sillimanite participate in an incongruent melting reaction which produces peritectic spinel which ends when biotite is exhausted at 900 °C. The compositions of each melt extraction event produced along each of the possible P-T-Xpaths are plotted in Figures 3-4. The compositions of 548 bulk compositions reported for naturally occurring S-type granites (Euzen, 1993; Goad and Cerny, 1981; Scaillet et al., 1990; Nabelek et al., 1992; Solgadi et al., 2007; Williamson et al., 1996, 1997; Hine et al., 1978; Maas et al., 1997; Castro et al., 1999; Scheepers and Armstrong, 2002; Scheepers and Poujol, 2002; Bea et al., 1994; Ayres and Harris, 1997; Downes et al., 1990; Downes and Duthou, 1988; Chappell, 1978; Chappell and White, 1992; Birch, 1978; Bourne and Danis, 1987; Day and Weiblen, 1986; Georget and Martineau, 1986; Holtz and Johannes, 1991; Inger and Harris, 1993; Villaros, 2004; Sandeman and Clark, 2003; Scheepers, 1990) (Supplementary data: presented in Addendum D) are plotted for reference, although comparison between these rock compositions and the modelled melt compositions is only presented in the discussion. This dataset is filtered to only include samples that had been reported as being fresh and where possible thin section analysis was performed to ensure that only fresh samples were considered. Both the natural data and modelled data are normalised to the NCKFMAST chemical system where F is given as FeOt = FeO +0.89981\*Fe<sub>2</sub>O<sub>3</sub> by wt.% when FeO/Fe<sub>2</sub>O<sub>3</sub> data was available (all the modelled data and a subset of the natural data) or else assuming all iron is ferrous. Harker plots are shown for major elements in the chemical system modelled with exceptions of H<sub>2</sub>O and O as there is insufficient data on these components in the natural array considered to provide a comparison and TiO<sub>2</sub> as this component is not included in the current melt(W) solution model.

Modelled data is grouped by each of the 3 possible cases for each source control with colours assigned by Colorbrewer (Brewer, 2002). Alphahull approximation (Pateiro-López and Rodríquez-Casal, 2010) is performed on each case using an alpha value of 150 in order to calculate the bounding area for each subset of the modelled data in y vs SiO2 space for y as CaO, Na2O, K2O, Al2O3, MgO + FeOt, Mg#, A/CNK and Na/Ca using GCDkit (Janoušek et al., 2006). A vector connecting the centroid of each bounding area is drawn as an arrow pointing towards the highest valued case (e.g. highest water content considered). The length of the vector gives an indication of the magnitude by which the bounding areas

are shifted relative to one another by the source control of interest and therefore its relative strength in controlling the resultant melt composition. These vectors of source control are reproduced on the right of the diagram centred to a dimensionless panel for comparison.



Natural samples (S-type granite array)

OOO Modelled melt extracts (low, medium and high values for each source control)

Number of natural samples that plot in the shape defined by the low, medium, high or total groups of each source control

Compositional response to source control pointing to highest value of source contol

**Fig. 3.** Bulk compositions of natural data array of s-type granites and modelled melt extracts for the *source controls: Mg#*, Ca#,  $H_2O$ , P-T and *Melt threshold* expressed as wt.% oxide versus wt.% SiO<sub>2</sub>. Weight percentages are normalised to the NCKFMAST chemical system. Modelled points are coloured according to the *case* considered for each *source control* (see Table 2) as low (light blue), medium (blue) and high (dark blue). Arrows link the central points of the space defined by each modelling *case* and point towards the highest valued *case*. Arrows produced by each source control are copied and centred on a unit-less diagram to the right of the figure for comparison.



Natural samples (S-type granite array)

OOO Modelled melt extracts (low, medium and high values for each source control)

→ Compositional response to source control pointing to highest value of source control

**Fig. 4**. Bulk compositions of natural data array of s-type granites and modelled melt extracts for the *source controls*: Mg#, Ca#,  $H_2O$ , P-T and *Melt threshold* expressed as MgO + FeOt = MgO + FeO + 0.89981\*Fe<sub>2</sub>O<sub>3</sub> [wt.%]; Mg# = MgO/(FeOt + MgO)\*100 [mol.%]; A/CNK = Al<sub>2</sub>O<sub>3</sub>/(CaO+Na<sub>2</sub>O+K<sub>2</sub>O) [mol.%] and Na/Ca [mol.%] all versus wt.% SiO<sub>2</sub>. Weight percentages are normalised to the NCKFMAST chemical system. Modelled points are coloured according to the *case* considered for each *source control* (see Table 2) as low (light blue), medium (blue) and high (dark blue). Arrows link the central points of the space defined by each modelling *case* and point towards the highest valued *case*. Arrows produced by each source control are copied and centred on a unit-less diagram to the right of the figure for comparison.

In both the water in excess and water restricted cases, the details of the melting behaviour and assemblage evolution vary significantly with *P*-*T* path steepness and rock composition. This is because pressure has a strong control on water solubility in the melt and on the mineralogy of the anhydrous ferromagnesian assemblage, whilst Mg# and Ca# have a strong control on the relative proportions of biotite, muscovite and plagioclase in the rocks (Fig. 1). However, allowing for these variations, all the modelling conducted in this study produces behaviour which is generally consistent with that described above. Each of the water in excess rocks produce three pulses of melt production, irrespective of the melt extraction threshold. For the gentle prograde heating example illustrated in Figure 2, the first of these occurs between the solidus and 740 °C. In this temperature interval, a large volume of melt (~50 vol.%) is produced through water fluxed incongruent reactions that consume muscovite and biotite along with quartz and plagioclase. These melts have SiO<sub>2</sub> contents very close to 75 wt.% and are characterised by Na<sub>2</sub>O and K<sub>2</sub>O contents that, respectively, vary inversely and proportionally with temperature (Fig. 5). This reflects the change in the stoichiometry of the low-temperature water present incongruent melting reactions to consume increasing amounts of mica as temperature increases. A second pulse of melt production occurs between 770 and 790 °C due to biotite + quartz + anorthite +  $H_2O$ incongruent melting. The melts have SiO<sub>2</sub> contents that range from 75 down to 63 wt.%, as well as very low Na<sub>2</sub>O contents (<0.5 wt.%) and high K<sub>2</sub>O contents (> 6 wt.%). A third pulse of melt production occurs between 870 and 900 °C, where biotite, sillimanite, garnet and H<sub>2</sub>O melt incongruently to produce melt and peritectic spinel. This produces melts which range in SiO<sub>2</sub> content from 72 to 60 wt.% SiO<sub>2</sub>, with close to 0 wt.% Na<sub>2</sub>O, K<sub>2</sub>O between 6 and 12 wt.%, CaO between 2 and 5 wt.%, with very high Al<sub>2</sub>O<sub>3</sub>, between 17 and 25 wt.%. Note that the exceptions to this are the portion of the light blue data array in Figure 5 which extend to low  $K_2O$  contents. These data points represent low Mg# rocks which evolved along the isobaric heating path at 7 kbar with melt extraction at a 1 vol.% melt threshold (thus recording small melt extraction amounts). In this situation biotite is depleted at relatively low temperature and these melt compositions are produced by incongruent melting of garnet, sillimanite and H<sub>2</sub>O.

The water restricted models display considerably smaller compositional ranges of melt composition and two pulses of melt production (Fig. 5). The first is the consequence of incongruent melting reactions involving muscovite, the second is the result of incongruent melting reactions involving biotite. For both melt pulses, the melts range in composition between 72 and 75 wt.% SiO<sub>2</sub>, with K<sub>2</sub>O between 3 and 6.5 wt.%, Na<sub>2</sub>O between 3 and 6

wt.% and CaO < 1wt.%. The models with restricted water always produce approximately one third of the total melt volume produced by the water in excess rock at 920 °C. In the examples highlighted above, cumulative melt extracted from the system equates to 19.8 wt.% for the fully-hydrated, fluid-absent system; 20.0 wt.% for the porosity limited system and 71.4 wt.% for the water in excess system.



**Fig. 5.** Bulk compositions of natural data array of s-type granites and modelled melt extracts produced by varying the *source controls*: Mg#, Ca#, P-T and *Melt threshold* for the fluid case of water in excess (top) and fully-hydrated, fluid-absent (bottom). Modelled points are coloured according to the P-T path as isobaric (light blue), gentle (blue) and steep (dark blue). Melt extracts are grouped into 3 progressive temperature intervals with increasing temperature to the right of the figure. Weight percentages are normalised to the NCKFMAST chemical system.

#### DISCUSSION

The different source controls investigated in this study do not have equally significant influences on the composition of melt batches produced by progressive melting and melt extraction. The results indicate the hierarchy of influence on melt composition to be: 1. the presence or absence of water; 2. the pressure of melting; 3. the *Ca#* of the rock; 4. the *Mg#* of the rock; 5. *Melt threshold* (see size of compositional vectors on the right of Figs. 3&4). Ignoring the presence or absence of water, the nine bulk compositions investigated in this study vary substantially in terms of mode and composition of the reactant minerals, although all are metapelitic, with both muscovite and biotite present in the subsolidus assemblage along with quartz, plagioclase and aluminous minerals such as staurolite and/or aluminium silicates. Given the range in compositions it is noteworthy that on Figure 5, the different *P-T* path arrays are closely grouped, yet clearly discernible on almost every Harker plot. As the data for each *P-T* path include data on the compositions of the melt batches produced by all nine rock compositions, the variation in melt compositions produced by the compositional range covered is clearly subordinate to that induced by pressure of melting.

In making comparisons between the modelled melt compositions and the natural granite compositions, it needs to be considered that the granites are likely to represent mixtures of minerals and melts e.g. (Clemens and Stevens, 2012). Most hypotheses seeking to explain the petrogenesis of S-type granites can account for this. Restite entrainment and peritectic assemblage entrainment propose that a mineral load is carried out of the source during magma mobilization out of the source. Wall rock assimilation by melting can introduce peritectic minerals to the magma at the level of assimilation (Lackey et al., 2011). Mixing between hotter mafic magmas with a granitic melt will also produce an assemblage of ferromagnesian mineral in the resultant mixture. The results of this study, which covered the full range of temperature of anatexis that may be commonly attained in the mid to deep crust, also confirm the fact that common granites are mixtures of melt and a mineral assemblage. Despite the large number of permutations considered and the relatively high maximum temperatures used in the modelling, no melts are produced that have MgO and FeO contents as high as common granites (Fig. 4). Within the natural rock dataset FeO + MgO are inversely correlated with SiO<sub>2</sub> content ( $R^2 = 0.73$ ) and FeO and MgO are positively correlated with TiO<sub>2</sub> ( $R^2 = 0.74$ ). The modelled behaviour of TiO<sub>2</sub> could not be explored in this study because the activity-composition model for melts does not include TiO<sub>2</sub>. These correlations are considerably better if the population considered is a single co-magmatic

suite e.g. (Stevens et al., 2007). Stevens et al. (2007) have demonstrated that as K<sub>2</sub>O and TiO<sub>2</sub> are poorly correlated, and K<sub>2</sub>O decreases as a function of TiO<sub>2</sub> and FeO + MgO, it is extremely unlikely that these major element geochemical characteristics in granites are a function of mixing with mafic magma or biotite accumulation. Stevens et al. (2007) and Clemens and Stevens (2012) argue that such well correlated positive associations between compatible elements are a consequence of entrainment of the peritectic assemblage produced principally by incongruent melting reactions involving biotite in the case of S-type granites, and incongruent melting reactions involving biotite and hornblende in the case of I-type granites. In the case of S-type granites the peritectic assemblage would consist principally of garnet and ilmenite or garnet, ilmenite and plagioclase e.g. (Madlakana and Stevens, 2018), whereas in I-type granites it would consist of clinopyroxene, orthopyroxene and plagioclase. Consequently, on Harker plots such as FeO vs SiO<sub>2</sub>, modelled melt compositions do not coincide with the natural granite population. In contrast, where the element of interest is an incompatible element that is readily accommodated in the melt, e.g. Na<sub>2</sub>O or K<sub>2</sub>O, the agreement between the range of concentrations defined by the natural rocks and that defined by the modelled melts may be expected to be good, where the modelled scenario is appropriate to the genesis of the granites.

All of the permutations of physical parameters and rock chemistry considered in the case of the water-restricted modelling produce melt compositions that could conceivably be involved in S-type granite genesis. The melt compositions change slightly as a function of P-T path and slightly as a function of temperature (Fig. 5), but generally occupy space on major element bivariate plots that is within the range of compositions defined by the granites. Entrainment of an appropriate peritectic assemblage produces compositional trends that are very similar to those portrayed by the natural rocks e.g. (García-Arias and Stevens, 2017a). Very importantly, because mica decomposition regulates the reactions, the melt compositions map out very similar ranges in Na<sub>2</sub>O and K<sub>2</sub>O as defined by the granites. If dilution by a peritectic assemblage is also taken into account (García-Arias and Stevens, 2017a) the modelled magma compositions will agree very well with the natural granites with  $SiO_2 < 76$  wt.%. In the water in excess examples a substantial number of the melt compositions defined have no natural rock equivalents. These are compositions with SiO<sub>2</sub> in the range of granites and granodiorites, but with  $Na_2O < 1$  wt.% and/or with  $K_2O > 6$  wt.%. The low Na<sub>2</sub>O compositions are produced by melting once plagioclase in the residuum has become strongly enriched in anorthite, whilst the high K<sub>2</sub>O melts result from this melting, as well as further melting of biotite in the absence of quartz. The melt volumes produced are

substantial (> 20 vol.%) thus if such melting occurred in nature the results would be discernible in the rock record. Consequently, it can be concluded that such melting does not occur in nature. In Figure 5, water in excess melting of metapelites at relatively low temperature can be observed in terms of Na<sub>2</sub>O and K<sub>2</sub>O content in the melt as melting proceeds with increasing temperature. The melts produced close to the solidus have  $Na_2O >$ 6 wt.% and  $K_2O < 2$  wt.%, with SiO2 = 75 wt.%. Such compositions do occur in the natural rock population but they are rare. As melting progresses Na<sub>2</sub>O in successive melt batches decreases and K<sub>2</sub>O increases, as the stoichiometry of the melting reaction changes to consume less plagioclase and more muscovite. The melt compositions thus approach the compositions of common granites better. For melting along the gentle heating *P*-*T* path at 7 kbar, once approximately 40 vol.% melt has been extracted, the composition of the melt batches is sufficiently low in Na<sub>2</sub>O (< 1.5 wt.%) and high in K<sub>2</sub>O (> 7wt.%) that it can be concluded that no natural correlatives exist. This melt volume correlates with approximately 3.7 wt.% water consumed by the melting process and a temperature of only 740 °C. Further melting produces only increasingly more unusual extremely high  $K_2O$  melt compositions (Fig. 5).

The porosity of amphibolite facies metamorphic rocks is such that only a small amount of pore fluid may exist in the source prior to anatexis, as has been modelled in this study. The inclusion of this small amount of free water has a negligible effect on the melting history of the rock. Thus, melting with water in excess requires addition of water by some process. As it is not possible to move water through rocks above the water saturated solidus, such melting must occur at the interface between the hot rocks undergoing anatexis and the source of  $H_2O$ . This suggests that this process is likely to be most efficient at the solidus. The melt compositions produced are well characterised in this study, yet are rare in the natural rock record, leading to the conclusion that water fluxed melting of metapelites has not produced a significant proportion of the rocks reflected in the natural rock dataset used in this study. The melt compositions modelled in this study attain a maximum SiO<sub>2</sub> content of approximately 76 wt.%; many granites have higher SiO<sub>2</sub> contents than this. This is a function of the fact that this study has examined melt compositions in the source, at lower pressure melts are more SiO<sub>2</sub> rich. Alternatively, fractional crystallization in the upper crust could provide a mechanism for producing granites with SiO<sub>2</sub> between 76 wt.% and 79 wt.% SiO<sub>2</sub> from melts similar to those predicted in this study.

#### CONCLUSIONS

This study explored the compositions of melt batches produced by progressive melting for 243 permutations of bulk composition, *P*-*T* path steepness, fluid state and details of melt extraction. Of these 81 cases were for water in excess, with the other 2/3 of cases reflecting water restricted or internally buffered conditions. The findings of this study provide valuable insights into the role of source controls in creating major element geochemical diversity in granites. The presence or absence of a water rich fluid in the source and the *P*-*T* path followed by the rock exert the strongest controls on melt compositions. Within metapelitic sources, compositional factors such as bulk rock Ca# and Mg# exert a minor influence, as does the amount of melt retention in the source prior to melt extraction, assuming the threshold is not greater than 10 vol.%. The greatest impact of *P*-*T* path steepness, for the range investigated, is that steeper paths produce slightly lower melt SiO<sub>2</sub> contents. This occurs for sources that are both quartz-saturated and for melt depleted sources where all quartz has been consumed. Thus it is a consequence of pressure on the modelled melt composition, not solely a function of *a*SiO<sub>2</sub>.

Given that granite magmas predominantly represent mixtures of melts and crystals, with Fe, Mg, Ti, Ca and Al enriched in the crystal assemblage over melt, the most informative element concentrations in the modelled melts to compare with granite compositions are Na<sub>2</sub>O and K<sub>2</sub>O. These incompatible element concentrations in granites are likely to most closely approximate the compositions of the melts from which the granites formed. Water in excess melting of metapelites produces high melt yields (> 60 vol.%). A substantial volume of melt is produced at relatively low temperature (20 vol.% by 710 °C) and these melts have compositions that are unlike common granites as their K<sub>2</sub>O/Na<sub>2</sub>O ratios are low. Between 710 and 750 °C, water in excess melting occurs via the incongruent melting of muscovite and biotite and produced melt batches with compositions similar to normal granites. At higher temperature a number of incongruent melting reactions involving assemblages such as biotite, quartz and anorthite; biotite and quartz; biotite and sillimanite, produce melt batches with very low Na<sub>2</sub>O and high K<sub>2</sub>O that are unlike any common granites. In natural rocks, porosity considerations dictate that water in excess melting required addition of water to the rocks. Assuming geological circumstances that would allow for this, e.g. the thrusting of hot rocks over cold and then heating of both rock units to drive devolatilisation of the underlying rocks and melting of the overlying rocks, this modelling suggests that metapelites in the overlying unit would produce at least 20% of melts that are peraluminous

plagiogranites with K<sub>2</sub>O as low at 1 wt.%. That such rocks are uncommon in the rock record suggests that such water in excess melting does not contribute significantly to the inventory of granites. At moderate temperatures, 710 to 750 °C, this process does produce melts and peritectic assemblages that could lead to reasonable granite compositions. However, this portion of the melting behaviour cannot be accessed without prior melt depletion, so the paucity of low K peraluminous plagiogranites suggests that rocks never get there. Fluid restricted partial melting of metapelites in the P-T ranges investigated in this study produces melt compositions that generally fit well with the petrogenesis of common peraluminous granites, if allowance is made for a process such as peritectic assemblage entrainment to increase FeO, MgO and A/CNK and produce the characteristic good correlation between FeO + MgO and TiO<sub>2</sub>. The modelled melts have maximum  $SiO_2 = 76$ wt.% and this is lower than the value for many peraluminous leucocratic granites. These granites were either shaped by melt batches generated at substantially lower pressures than 7 kbar, or they have been shaped by crystal fractionation at low pressures. Some relatively low K<sub>2</sub>O/Na<sub>2</sub>O melt compositions also define the water restricted melt compositions produced at low temperature. This is a consequence of the fact that both the fully-hydrated, fluid-absent and pore water bearing rock compositions used do melt at the water-saturated solidus. However, the resultant melts that fall outside the range of normal granites make up a small fraction of the volume of melt produced from these rocks (< 3 vol.%)

#### DOWNLOAD

Rcrust is free to download and use under the GNU copyleft. The latest version of the software can be found on either of the two institutional addresses at: http://www.univ-st-etienne.fr/rcrust or http://www.sun.ac.za/english/faculty/science/earthsciences/rcrust. Alternatively, the software can be downloaded by contacting the corresponding author.

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# SUPPLEMENTARY MATERIAL\*

The full dataset of modelled melt compositions produced in this study and the array of s-type granite data used for comparison are contained in Addendum D. Files for reproducing figures 3-5 are contained in the zipped folder "Mayne\_et\_al\_2018\_3\_modelling\_files". To open these download Rcrust from

https://www.sun.ac.za/english/faculty/science/earthsciences/rcrust and replace the "Projects" and "data" folders with those in the zipped folder. Open each project by double clicking the appropriate x.RData file.

\*For the thesis examiners' convenience these files are already copied into the electronic copy of Rcrust provided in Addendum A, to open them simply install Rcrust following the user manual in Addendum B, open the "Projects" directory of Rcrust, open the project of choice and double click on the .RData file contained in the project file

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# **CHAPTER 5**

# **CONCLUSION AND FUTURE PERSPECTIVES**

Preliminary results from the creation and implementation of the Rcrust software tool appears to confirm that open system processes can be effectively investigated through path dependent modelling in P-T-X space. By altering the bulk composition of a number of subsystems in a defined modelling space, where compositional changes are inherited along dependent paths, processes of mass transfer have been simulated. This new methodology and its software implementation in Rcrust addresses the need for thermodynamically constrained modelling of complex open system behaviour (Table 1).

**Table 1.** Summary of the capabilities of Rcrust for comparison with information presented on other phase equilibrium modelling softwares presented in Chapter 1 Table 1 detailing the suitability of each respective software program for performing phase equilibrium modelling in open systems

Software	Calculation	Graphical	User Input	Phase manipulations
	method	refinements		
Rcrust [1]	Inherited from	None	Graphical	Along multiple paths,
	Perple_X		user	multiple concurrent phase
			interface,	manipulations as conditional
			text file	phase additions and
			input or R	extractions that can be set
			console	proportions or defined
			input	relative to system properties

[1] https://www.sun.ac.za/english/faculty/science/earthsciences/rcrust

The methodology presented can deal with phase fractionations or additions concurrently. These phase manipulations can be triggered by conditions on the reactive system and can effect multiple phases by proportional changes that are set prior to calculation or can be defined relative to system properties (e.g. melt retention). The procedure for defining dependent paths allows multiple complex P-T-X paths to be investigated simultaneously with calculations running sequentially through points within a path. Through these functionalities this new tool enables lines of investigation previously inaccessible to phase equilibrium modelling. The creation of these functions has focused on dealing with the most common chemical fluxes in metamorphic systems. These are the loss of subsolidus fluids
during prograde evolution; and at higher temperatures the loss of melts or magmas. Both of these processes have been accounted for in the modelling and the current software can handle their contributions to the effective bulk compostion of the system concurrently in modelling space.

The presented papers, that constitute this thesis, document methodologies for using Rcrust to perform process-oriented investigations that involve mass transfer. These methodologies address the dynamic setting of subsolidus water content in a system undergoing prograde metamorphism; the triggering of melt loss events in a conditionally open system with melt retention on grain boundaries; the entrainment of phases to melt during melt loss (including the possibility of phase selective entrainment); the fractional crystallisation of magmas whereby the proportion of solid crystals in a cooling magma can trigger crystal loss from that magma; and the limiting of the availability of slow diffusing phases from contributing to the bulk composition of the chemically reactive subsystem.

The methodology for dynamic setting of subsolidus water loss is investigated further for its effect on the onset of anatexis and the control of the P-T path on this behaviour. It is found that the trajectory of the P-T path of a rock can influence the conditions under which melting begins and can effect the melt fertility of a metasedimentary protolith. This is a result of the progression of the P-T path controlling which subsolidus reactions are experienced by the rock on its prograde path and thus determining the total water content of the rock once anatexis begins. The combination of fluid state and P-T path appear to be the dominant source control on the compositions of melts produced by sequential melt loss from a metasedimentary protolith. These controls appear stronger than both the effects of compositional heterogeneity of the source as well as of volumetric controls on melt loss events.

### **Potential limitations**

The main limitation for all metamorphic studies following a phase equilibrium approach is the delineation of equilibrium domains on the mineral and rock scale: the successive (re)equilibrations described by López-Carmona et al. (2014) as also evidence by the common observation of chemically zoned minerals. To determine what portions of the rock are in mutual equilibrium and what each of these domains could represent in the rock's complex P-T-X history presents the greatest challenge to its petrological interpretation (Lanari and Engi, 2017; Yakymchuk et al., 2017; Yakymchuk, 2017; Spear et al., 2016). Rcrust offers potential solutions for modelling this behaviour which are difficult to implement with other software programs. By considering each domain in the rock as a subsystem in Rcrust we may be able to unravel some of the complex relations inherent in these systems and find constraints for the mechanisms by which they interact. Further possible limitations to all phase equilibiium modelling lie in the restraints imposed by the compositional range of the available thermodynamic data and the activity–composition models developed from this data. In Rcrust since chemical fluxes can be large, for example when considering continuous melt loss from rocks attaining high temperatures (~1000 °C) the bulk compositional shifts experienced by the residium could take the composition of the effective bulk composition out of the range that the thermodynamic models were designed to handle.

#### New path dependent diagrams and a suggested protocol for reporting

Rcrust presents a functionally unique form of phase equilibrium modelling as it's methodology of setting path dependence allows the pressure temperature and bulk composition of the system to all vary simultaneously in modelling space. If composition is set to be constant traditional isochemical phase diagrams (metamorphic assemblage diagrams) of P-T space can be produced (e.g. Fig. 1a). However, if phase manipulations are applied to the system, then bulk compositional changes can occur within the defined P-T space and the resultant diagrams can no longer be read in the same way as isochemical phase diagrams (e.g. Fig. 1b). Instead the reader must be made aware of the direction of the constituent paths that produced the diagram and must take care to only interpret petrological changes invoked in these systems along each respective path rather than across paths. It is proposed that these compositionally variable diagrams be termed "phase assemblage maps" in order to avoid the confusion of them being interpreted as isochemical phase diagrams. Further it is proposed that by convention these diagrams must be accompanied by indicators of their paths' directions and positions in P-T space (e.g. the symbol above Fig.1b and the overprint arrows in Chapter 3: Figs 1, 3 & 4).



**Fig. 1.** (a) Isochemical phase diagram calculated using Rcrust in the system Na<sub>2</sub>O-CaO-K<sub>2</sub>O-FeO-MgO-Al<sub>2</sub>O<sub>3</sub>-SiO<sub>2</sub>-H<sub>2</sub>O-TiO<sub>2</sub>-O<sub>2</sub> for an average amphibolite facies metapelite. Individual isobaric heating and isothermal decompression paths in this P-T space are labelled as IBH and ITD respectively. (b) Phase assemblage diagram calculated in Rcrust by compiling multiple isobaric heating paths that all start with the same bulk composition described above. Melt extraction is set to occur along each path whenever a 7 vol.% threshold is exceeded and remove all melt present except 1 vol.% in order to approximate melt retention on grain boundaries. The bulk composition of each point within a path is passed to the next point in sequence thereby creating a path dependent bulk composition which inherits compositional changes invoked by previous melt loss events Both diagrams are taken from Mayne et al. (2016).

### **Documented uses of Rcrust**

Rcrust has been used by the following authors for phase equilibrium investigations. The projects I was personally involved in are identified with a \*. In these projects I programmed functional improvements to Rcrust in response to the respective author's requests. All other projects are solely the work of the respective authors and are listed here only to document the scope of the current use of the Rcrust software.

### **Entrainment of peritectic phases\***

Nicoli et al (2017) used Rcrust to simulate melt loss with entrainment of peritectic garnet. They used this model to explain the formation of K<sub>2</sub>O-poor leucosomes in the Southern Marginal Zone of the Limpopo Belt, South Africa as the result of multi-step disequilibrium partial melting. Rcrust allowed melt extractions to be triggered by a melt threshold and extract garnet in combination with melt at each of these events.

## **Fractional crystallisation\***

Soorajlal (2017) proposed a low temperature filter pressing model for Buddusò I-type granites and mafic enclaves in Sardinia, Italy in which melt is displaced from a crystal mush in order to produce a cumulate portion with granodioritic composition and an extract portion with leucogranitic composition. Soorajlal modelled the sequential extraction of melt from the reactive subsystem in equilibrium at a number of fixed P-T conditions in order to simulate a process of melt loss through filter pressing. Rcrust allowed melt loss events to be triggered by the cumulative proportion of crystals in the system. Work by Farina (2018) further develops the phase equilibrium constraints on this process of fractional crystallisation.

## **Crystallisation sequences**

Holness et al (2018) used Rcrust in their investigation of the conditions of alkali-feldspar crystallisation. They found an apparent disconnect between phase equilibrium modelling predicting alkali-feldspars to begin crystallising late at relatively low temperatures in contrast to the field evidence in many granites containing large subhedral-to-euhedral K-feldspar phenocrysts.

## **Compositional constraints in planetary sciences**

Mohit Melwani of the Jet Propulsion Laboratory of the Californian Institute of Technology used Rcrust to investigate melt formation and migration on early Mars in order to constrain the mass of volatile species (including SO<sub>2</sub>) degassed from volcanoes over time. Mohit has also used Rcrust to investigate melt production and migration from the melt source regions within Europa's silicate interior (Melwani Daswani and Vance, 2018a, 2018b)

# Estimating the duration of partial melting

Farina et al (2017) used Rcrust to correlate multi-pulsed magmatism in the Monte Capanne pluton with multimodal distribution of zircon ages in order to estimate the duration of partial melting and the timescale of melt extraction from the source

# Identifying fluid state during crustal melting

Schwindinger (2018) and Schwindinger et al (2018) used Rcrust to simulate a conditionally open system effected by melt loss events. They found that the main indicator for water present melting of metasedimentary sources undergoing anatexis is the melt fraction produced, with the composition of melt and peritectic phases appearing to be insensitive to the fluid state of the system.

# The role of thermal gradients in crustal melting

Juan David Montenegro of the National University of Colombia used Rcrust to model melt loss along different thermal gradients in order to assess the production and evolution of tonalite-trondhjemite-granodiorite magmas in the Archean and its implications for the generation of continental crust.

## **Future work**

The above projects demonstrate the broad scope of Rcrust's use and highlight its contribution to the petrological community. Up till now the development of Rcrust has largely focused on addressing compositional changes invoked by open system behaviour. Future work will build on expanding functionalities to the user and further developing these methodologies. In addition, there are a number of new directions that Rcrust can further develop:

## Kinetic restraints on equilibrium

The limiting of the availability of a phase from contributing to the effective bulk composition of the reactive system is only partly addressed in Chapter 2. Future work could build models to consider the effect of the kinetic speed of reactions in limiting the equilibration volume of a system (Lanari and Engi, 2017). Here the diffusion rate of chemical components within slow diffusing phases such as garnet (Caddick et al., 2010) or plagioclase feldspar (Tajčmanová et al., 2007) could be integrated into modelling procedures. This could control the rate at which chemical components from a chemically zoned phase are available to the reactive bulk.

### Consideration of trace elements in thermodynamic modelling

A major hesitation for igneous petrologists to adopt phase equilibrium modelling has been in the inability of current software to model trace element behaviour especially in magmatic systems. Including trace element data in thermodynamic databases and in the activity– composition models would require immense time, effort and resources. For processes occurring above the solidus, however, an easier alternative would be to use partition coefficients to approximate the fractionation of trace elements as the magmatic system evolves.

## Saturation model for zircon

Another major limitation to the modelling of trace elements is the lack of appropriate thermodynamic models for the accessory phases which are often the largest sinks for trace elements. Some of the accessory phases for example zircon could be approximated using saturation models which assume that all of a given trace element e.g. zirconium above that which the current stable phases of the system can accommodate must exist in a given accessory phase here zircon. This allows a thermodynamically unconstrained abundance of zircon to be approximated and manipulated by the modelling software as if it were determined phase.

Building on each of these procedures in an open source software platform will allow cumulative functionalities to be integrated into future modelling packages. In this way I aim to create an internally consistent, thermodynamically and kinetically constrained model for crustal anatexis.

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# ADDENDA

# **ADDENDUM A: Electronic copy of Rcrust software**

Included within the thesis files for evaluation is an electronic copy of the Rcrust program developed as part of the thesis by M.J. Mayne.

# **ADDENDUM B: User manual for Rcrust**

Included within the thesis files for evaluation is the user manual for the Rcrust program.



# Phase stabilities with path-dependence

Version 27 September 2018 (for help contact mjmayne@outlook.com)



# Getting started

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# **GETTING STARTED**

# Installation

Rcrust was developed using version 3.3.0 (2016-05-03) of R. Copyright © 2016 the R Foundation for Statistical Computing. To install Rcrust perform the following steps:

 Copy the Rcrust folder to a location of your choice (preferably a root directory for example C:\ or D:\). The result should be similar to the picture below with all the Rcrust files contained in single directory for example D:\\Rcrust\

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Figure 1 - Ro	ust file structure located in	the root direct		+\		

Install a working version of R on your system (at least version 3.3.0). The latest version of R used in the development of Rcrust is located in the folder "R installs" for your convenience.
 Warning: Rcrust requires the 64 bit version of R. When installing R please ensure "64-bit Files" is ticked.

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Figure 2 - R installation instruction ensuring at least "64-bit Files" is ticked

\*Alternatively newer versions of R (which may not be compatible with Rcrust) can be downloaded from <u>http://www.r-project.org/</u> or for windows can be found directly at <u>http://cran.r-project.org/bin/windows/base/</u>

3. Open the folder called code in the Rcrust folder.

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Deskton	libacc s seb-1 dll	06 Feb 2017 12:4		-
Documents	libgfortran-3.dll	06 Feb 2017 12:4		
Downloads	libperplex.dll	06 Feb 2017 12:4	Copy 4	
Musia	libquadmath-0.dll	06 Feb 2017 12:4	Create shortcut	
2) Music	libwinpthread-1.dll	06 Feb 2017 12:4	Delete	
Pictures	🚯 main.r	27 Sep 2018 10:4	Rename	
Videos	B meemum connect.r	27 Sep 2018 10:4	Properties	
Windows8_OS (C:)	Rcrust.RData	30 Oct 2017 2:49 PW	R workspace 2 KB	_
LENOVO (D:)	U run.Rcrust.R	27 Sep 2018 11:29	R File 25 KB	
DVD RW Drive (E:) HUMA	sandbox.r	17 Aug 2018 4:24	R File 65 KB	
Network	Server.k	27 Sep 2018 10:54	R File 113 KB	
22 items   1 item selected 4,94 KE	B	15 Sep 2018 10:00	IN FILE / ND	

Figure 3 – Rcrust file (circled in red) within code folder. The Rcrust file location here is D:\\Rcrust\code\Rcrust.RData

- 4. Copy the Rcrust file found in the code folder (~/Rcrust/code/Rcrust.RData). This can be done by right clicking on the file (circled in red above) and selecting "Copy" or by selecting the file and pressing "Ctrl"+"c".
- 5. Paste the Rcrust file as a **shortcut** on the Desktop. This can be done by right clicking on the Desktop and selecting "**Paste shortcut**".



Figure 4 – Paste shortcut option selected for Rcrust file

- 6. Rename this file to "Rcrust". Double click on this shortcut to open Rcrust.
- Rcrust requires the R package called "shiny", If this is not installed on your computer when you open Rcrust, Rcrust will try to install it (this requires an internet connection). Follow the prompts to complete installation of the package (it may ask you if you wish to create a personal library – choose yes). Alternatively, shiny can be downloaded here: <u>http://shiny.rstudio.com/</u>.

Each new project will be automatically saved in the "Projects" folder along with its associated inputs and outputs. To load a previously saved project simply double click the "xxx.RData" file in the associated project folder or open Rcrust from the desktop shortcut and load the project via the Rcrust GUI.

# Concept

Rcrust is an R program aimed at modelling with path dependence. The program functions by calculating a number of points in P-T-X space where a bulk composition is passed between points. This creates path dependence as points within the path rely on the outcomes of previous points for their calculation. The bulk composition can be altered at each point by phase manipulations consisting of phase additions and/or phase extractions. Phase stabilities for each point are calculated by using a compiled form of Perple\_X (Connolly & Kerrick, 1987; Connolly, 2005, 2009).

Rcrust manages calculations by splitting the full thermodynamic system (FS) into 3 subsystems: The reactive subsystem (RS) which contains the phases in thermodynamic equilibrium; The addition subsystem (AS) where phases are waiting to be added to the reactive subsystem; and the extract subsystem (ES) where phases extracted from the reactive subsystem are stored. The reactive subsystem is in thermodynamic equilibrium with the P-T-X conditions of each point and is re-equilibrated after each P-T-X change. The addition and extract subsystems are in thermodynamic isolation from other subsystems and from the P-T-X conditions of each point.



Figure 5 - Relationships between systems (left) and flow chart (right) illustrating the Rcrust program structure for a single path. The user inputs the calculation's resolution, starting bulk composition, P-T path and phase manipulation settings. Each step in a path consists of two runs and an output. The first run is shown in a solid line, the second run in a dashed line and the outputs in a dotted line. Circles show the system or subsystem involved in each step as AS (addition subsystem), ES (extract subsystem), FS (full system) or RS (reactive subsystem). Arrows show interactions between systems. From (Mayne et al., 2016)

Parameters for calculations are accessible to the user via the Rcrust Graphical User Interface (GUI). This GUI writes data to a text file which is then input to the program thus allowing the user to edit the file 'behind' the GUI as well as save inputs for re-use. The code files are extensively commented, and described in this document. The calculations routines are defined in several files, written in a modular way that should allow easy addition of features if required. For example, the Phase Extraction routine has been modified to suit the needs of magma extraction where additional capabilities allow melt extraction to leave a set melt retention amount behind.



Figure 6 - Flow chart of the magma extraction routine. Grey hexagon shaped boxes are decision points. Coding variables are in italics. The for phase loop (dotted line) is repeated until each phase tagged for extraction has been considered. If Retention mode is active melt is considered last so that other phases extracted are accounted for in its calculation. From (Mayne et al., 2016)

Rcrust results should easily be loaded into GCDkit and examined from there.

It is important to remember a few things:

- Rcrust is in development. It is not mature software. It is very unstable at the best of times, and very unforgiving in terms of improperly formatted inputs, etc. When Rcrust fails, it will try to generate some human-readable error messages: read them! It may well give you hints at things you can correct in your inputs.
- Most of the errors you will see are related to incorrect input (files with incorrect number of lines etc.); or to exotic phases being produced by meemum.

Rcrust calls a set of binary files containing the thermodynamic equations thus relying on published databases (Holland and Powell typically). The output will never be better than the underlying thermodynamic model. Since we focus on melting, we are tied to the capacities (and limitations) of the melt models. For example, melt(HP) does not include Titanium therefore its use in a system containing Ti can over/under estimate melt abundance.

# **Examples**

Below are 3 example simulations to get you started using Rcrust. All you need to do to complete the examples is to perform the actions written in bold numbered text. Explanations of what these actions achieve are given between steps.

Example1 - Simple

## Follow the bold numbered steps

To begin the first example open Rcrust via the desktop shortcut.

### 1. Double click the Rcrust desktop shortcut

This will launch the R console and an empty Rcrust Graphical User Interface (GUI) in your default web browser. The **"Working File**" (circled in red) shows you which file is currently being worked on and the **"Projects Directory**" (circled in green) shows you where the projects folder is located. The Rcrust toolbar (in grey) contains buttons for file management.

	Projects Directory
Projects Directory D:/Rcrust/Projects Working File Rcrust Save Load Run Clear Close	Working File
Input Parameters Phase Manipulations Modelling Options Outputs	Rcrust Toolbar
Size	
	R RGui (32-bit)         - □ ×           File Edit View Misc Packages Windows Help         - □ ×                ∭[2] ■ ● ● ● ● ●          ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ● ●
	R Console
Pressure and Temperature Number of PT definitions	R version 3.2.4 Revised (2016-03-16 r70336) "Very Secure Dishes" Copyright (C) 2016 The R Foundation for Statistical Computing Flatform: 1386-w64-mingw32/1386 (32-bi) R is free software and comes with ABSOLUTELY NO WARRANTY. You are velocme to redistribute it under certain conditions. Type 'license()' or 'licence()' for distribution details. Netural language sug
Bulk Composition Major elements	R is a collaborative p Type 'contributors()' ' 'citatio()' on how too Type 'demo()' for some demos, 'help()' for on-line help, or 'help.star()' for an HTML browser interface to help. Type 'd()' to quit R.
Number of bulk definitions	(Previously saved workspace restored)
Import definitions from file	Listening on http://127.0.0.1:6453

Figure 7 -Rcrust GUI and R Console (blue). Highlighted are the positions of the Projects Directory (green), Working File (red) and Rcrust toolbar (black).

# 2. Type "Example1" into the text box on the right of Working File and then click the Load button from the Rcrust toolbar

The data previously saved in the "Example1" file is now loaded into R and previously saved input parameters are loaded into the Rcrust GUI. To ensure that we do not overwrite any data lets rename the Working File.

# **3.** Rename Example1 by typing "Example\_simple" into the Working File textbox then click the Save button from the Rcrust toolbar

This will save the current Rcrust GUI inputs into a new file named "Example\_simple". The Rcrust GUI should now look similar to Figure 8.

	Projects Directory D:Rerust/Projects Working File Example1	Save Load Run
	Loaded D:/Rcrust/Projects/Example1/Inputs/Example1.txt	Clear Console
	Input Parameters Phase Manipulations Modelling Options Outputs	
Size	SizeY X Y 4 3	
Pressure and	Pressure and Temperature <- Number of PT definitions 1 From To Pressure (kbar) Temperature (C	;)
	Bulk Composition	
	Major elements NAZO MGO ALZOS SIOZ KZO GAO TIOZ FEO OZ HZO	
Bulk	Number of bulk definitions	
Composition	To NA20,M00,AL203,8102,K20,CA0,T102,FE0,02,H20,mass	
	(1;1) (4;3) 1.82,3.28,20,45,56,97,4.09,1.56,1.05,8.5,0.62,1.96,100	
	Import definitions from file	
	L	

Figure 8 - Rcrust GUI with Example1 (Example\_simple) parameters loaded. The GUI consists of a number of tabs. The Input Parameters tab sets the size, P-T conditions and bulk composition (X) of the simulation.

This example calculates the phases encountered at points in P-T-X space. Input parameters are grouped into collapsible panels:

• Size Panel

The **Size** panel sets the number of points in the simulation (here 4 points in the **X** direction multiplied by 3 in the **Y** direction). Points in the simulation space are identified by **tuples** written as  $\{x_i, y_i\}$  where i denotes the current point.



Figure 9 – Simulation space with point coordinates defined by tuples {x\_i ; y\_i}

• Pressure and Temperature Panel

Parameters in the simulation space are filled by a number of definitions. Each unique definition is applied over a range between the tuples **From** {  $x_a$  ;  $y_a$  } and **To** {  $x_b$  ;  $y_b$  } where a and b denote the start and end points of a rectangular range. Each definition sets its attributes as constants or as

functions of the point's position. **X** and **Y** positions of points are accessed by the variables x\_i and y\_i respectively. In the **Pressure and Temperature Panel** we set the Pressure in kilobars and Temperature in degrees Celsius for each point. In this example **Pressure** decreases along the y-axis by 1 kbar per point (7-y\_i) and **Temperature** increases along the x-axis by 20 °C per point (670+x\_i\*20).

• Bulk Composition Panel

The **bulk composition** of the system is made up of a number of major elements expressed as wt.% elemental oxides. For this simple example we define the bulk composition to be constant across the full P-T space, and we give it the value of the average amphibolite-facies pelite composition considered in (Mayne et al., 2016).

	Na₂O	MgO	Al <sub>2</sub> O <sub>3</sub>	SiO <sub>2</sub>	K <sub>2</sub> O	CaO	TiO <sub>2</sub>	FeO	<b>O</b> <sub>2</sub>	H₂O
wt.%	1.82	3.28	20.45	56.97	4.09	1.56	1.05	8.5	0.62	1.96
Table 1 – A	Average ar	nphibolite	facies pel	ite compo	sition co	nsidered ir	<mark>ո</mark> (Mayne e	et al., 2016	5).	

To get started let's run a reconnaissance simulation:

## 4. Click the Run button from the Rcrust toolbar

This will save inputs in the Rcrust GUI and launch the calculation procedure into the R console. Navigate to the R console now. The R console should now have a few lines of text in it (like the figure below): If your simulation successfully initialized like the one below then we are ready to start the calculation. If your console failed to initialize the program try reloading the original "Example1" file by closing Rcrust then starting from step 1 again, if problems persist try reinstalling Rcrust or report the problem to the developers (mjmayne@outlook.com).



Figure 10 - The Rcrust calculation is launched into the R Console which tracks the calculation progress and is currently waiting for a response to continue or to abort.

## 5. Click anywhere in the R console to activate it then press [enter] to continue

The calculation will run for 12 points :4 in the X direction by 3 in the Y direction. The results will automatically be saved to file and you will be prompted to select outputs.

# 6. Once the calculation is complete, navigate back to the Rcrust GUI and Select the Outputs tab

Here we see a compilation data file for the points in our simulation. To compare points, click the "Select Output" drop down and choose "Grid".

### 7. Choose "Grid" under "Select Output"

Grid allows easy comparisons between points for example choose:

- Select Output = Grid
  - Variable = wt% and Melt\_rs

### 8. Choose Variable="wt%" and "Melt\_rs"

The output should now match Figure 11. This shows us the amount of melt in the Reactive Subsystem (RS) over our point selection in P-T-X space. Remember we set temperature to increase along the x-axis and pressure to decrease along the y-axis. With that in mind, we see that the solidus (boundary between liquid and solid) at lower pressures is crossed by lower temperatures (this is a good illustration of the pressure dependence of melting). For further outputs you can deal directly with the data in the R console (hint: you can plot data directly into GCDkit). To access the data in R console, click the "Console" button on the Rcrust toolbar to launch a browser access. To return to the Rgui at any point type "c" then press [enter].

Melt	_rs wt%	6 on (X,	Y) grid	
	V1	V2	<b>V</b> 3	V4
1	6.48	19.21	21.92	25.48
2	12.91	14.75	17.01	21.45
3	5.06	13.18	14.86	16.96

To view a graphical output of this data toggle the "View" selection to "Plot". This will plot a filled contour graph of the selected data which can be saved directly as a .ps file through the "Save To File" button at the bottom of the selection panel.

9. Toggle the "View" selection from "Data" to "Plot" and choose "Bottom Axis" as "Temperature", "Left Axis" as "Pressure"



### Example2 – Phase extraction

Phase extractions can remove phases from the reactive subsystem. This is used to simulate scenarios such as melt loss or fractional crystallization.



Figure 13 – Example of melt extraction along a P-T-X path from (Mayne et al., 2016): Weight percentage of phases verses temperature in degrees Celsius for a fixed pressure of 12 kbar. Starting composition taken as an average amphibolite facies pelite (Table 1). Melt is extracted whenever a 7 vol.% threshold is met.

Let's perform melt extraction along a path in the P-T-X space explored by Example1.

**1.** Load Example2 by opening Rcrust, typing 'Example2' in working file and clicking "Load" To ensure that we do not overwrite any data lets rename the Working File.

# 2. Rename the file by typing "Example\_extract" into Working File then click the Save button from the Rcrust toolbar

This will save the current Rcrust GUI inputs into a new file named "Example\_extract". The Rcrust GUI should now look like the images below:

	Project	s Directory D	/Rorust/P	rojects	
Rcrust	Working File Example2	Save	Load	Run	Clear
					Console
ilculation complete, Resu ielect outputs throught t	ults saved to D:/Rcrust/Projects/Example2 the 'Outputs' tab	/Example2.RD	ata		
Input Parameters Phi	ase Manipulations Modelling Options	Outputs			
SizeX	¥ 1				
Descure and Temperatur	- C - C - C - C - C - C - C - C - C - C				
Number of PT definition	s				
1					
From To	Preccure (kbar)	Temperat	ure (C)		
(1;1) (25;	1} 12	760+x i	15		
Bulk Composition	e.				
Number of Component 1	Transformations				
Major elements					
NA20 MGD AL203 S	SI02 K20 CAO TI02 FEO 02 H20				
Number of bulk definitio	and				
1					
From To	NA20,MGO,AL203,8102,K20,C	AO,TIO2,FEO,	02,H2O,I	mass	
(1;1) (25;1	1} 1.82,3.28,20.45,56.97,4.09,1.56	6,1.05,8.5,0.75	1.96,100		
Import definitions from	fie				

Figure 14 - Rcrust GUI inputs for Example\_extract

This example calculates an open system dependent path in P-T-X space. The bulk composition of the Reactive Subsystem is altered by phase manipulations encountered along the path. Phase Manipulations are grouped into collapsible panels:

Phase Addition

Phases such as intruding fluids, segregated melts or residual crystals can be incorporated into the reactive subsystem. These additions are defined by the major elemental oxides chosen in "Bulk composition".

Phase Extraction

Phases in the reactive subsystem can be extracted when set conditions are met. These conditions are defined as logical arguments such as "TRUE"/"FALSE" to extract for every point/no points respectively. Alternatively a logical argument can be built of the form "phase,operand,value,unit" where phase = name of the phase/solution model, operand = (<,<=,==,>=,>,!=), value = a number and unit = the phase property to test. In this example we want to trigger extraction whenever a melt threshold is reached so our conditional argument is "Melt,>=,7,wt%". \*note that each argument in the condition is separated by a comma.

When the condition is met phase extraction is triggered on the reactive subsystem. For each phase listed in **Phases for Extraction** we need to define the amount of the phase to extract. This can be a numeric value (interpreted as grams relative to the starting mass in grams defined in the Bulk Composition Panel), or a percentage of the current value. In this example we extract all melt (100%).

1				
From	То	Condition	Phases	
{1;1}	{25;1}	ph{Melt,vol%}>=7	Melt	

Figure 15 - Phase extraction definition for Example\_extract

To save you time we have pre-run this calculation so you can directly view the results by selecting the **Outputs** tab.

# 3. Select the Outputs tab in the Rcrust GUI

A custom output selection is available for viewing phase abundances along a path.

# 4. Choose "Phase Abundance Along Path" under "Select Output"

Here you can select which axis the path traverses (axis), which path you wish to consider (path), select the (Start Point) and (End Point) of the path and add a label for the column names.

## 5. Set "End Point" as 25

The output should now match Figure 16.

Phase adundar	nce vs Te	emperatu	re(C) for	(1;1) to	{25;1}																				
	765	770	775	780	785	790	795	800	805	810	815	820	825	830	835	840	845	850	855	860	865	870	875	880	885
Melt_rs	3.90	4.04	4.37	4.71	5.09	0.00	0.00	0.00	0.00	0.00	0.00	0.20	0.59	0.95	1.35	1.66	2.32	2.89	3.48	4.38	0.00	0.73	1.62	2.37	2.44
Mica_rs	22.53	22.34	21.74	21.14	20.48	19.86	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bio_rs	13.49	13.49	13.63	13.79	13.93	14.09	14.19	14.19	14.19	14.19	14.19	13.70	12.92	12.15	11.30	10.68	9.47	8.43	7.34	5.85	4.14	2.83	1.23	0.00	0.00
PI_rs	12.59	12.91	13.39	13.92	14.44	14.81	2.71	2.86	2.98	3.03	3.31	3.14	2.91	2.85	2.58	2.36	1.79	2.51	1.98	1.21	0.28	0.00	0.00	0.00	0.00
Cpx_rs	6.27	6.05	5.72	5.35	5.00	4.74	7.84	7.74	7.64	7.62	7.36	7.27	7.08	6.76	6.61	6.49	6.39	5.86	5.80	5.81	5.80	5.55	5.19	5.02	4.74
llm_rs	7.40	7.42	7.46	7.52	7.57	7.57	7.32	7.35	7.38	7.38	7.42	7.44	7.47	7.53	7.56	7.61	7.64	7.73	7.76	7.80	7.86	7.93	8.02	8.09	8.10
ky_rs	9.37	9.41	9.46	9.47	9.53	9.61	17.57	17.55	17.52	17.52	17.38	17.29	17.17	16.95	16.78	16.69	16.52	16.16	16.02	15.84	15.68	15.44	15.10	14.84	14.76
q_rs	24.46	24.34	24.22	24.10	23.95	23.80	19.91	19.89	19.88	19.87	19.85	19.66	19.30	18.97	18.61	18.34	17.80	17.32	16.83	16.16	15.38	14.78	14.05	13.48	13.45
Kf_rs	0.00	0.00	0.00	0.00	0.00	0.00	15.44	15.42	15.40	15.37	15.38	15.74	16.27	16.78	17.37	17.79	18.62	18.65	19.39	20.36	21.46	22.19	22.82	23.23	23.40
Gt_rs	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.54	1.29	2.03	2.80	3.36	4.44	5.45	6.39	7.59	8.98	10.15	11.55	12.57	12.69
Bulk_rs	100.00	100.00	100.00	100.00	100.00	94.48	84.98	84.98	84.98	84.98	84.98	84.98	84.98	84.98	84.98	84.98	84.98	84.98	84.98	84.98	79.58	79.58	79.58	79.58	79.58
Melt_es	0.00	0.00	0.00	0.00	0.00	5.51	9.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.41	0.00	0.00	0.00	0.00
Bulk_es	0.00	0.00	0.00	0.00	0.00	5.51	9.50	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	5.41	0.00	0.00	0.00	0.00
Melt_es_cumul	0.00	0.00	0.00	0.00	0.00	5.51	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	20.41	20.41	20.41	20.41	20.41
Bulk_es_cumul	0.00	0.00	0.00	0.00	0.00	5.51	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	15.01	20.41	20.41	20.41	20.41	20.41

Phase adundance vs Temperature(C) for {1;1} to {25;1}



Figure 16 – Phase Abundance Along Path output for Example\_extract showing mass of each phase in the full system (FS) across the P-T-X points selected.

This output highlights a few key features of the phase extraction function:

- Outputs in the Phase Abundance along path plotter are expressed as wt.%
- The second melt extraction event extracts more than 7 vol.% melt (relative to the full system)(red box) even though the melt extraction threshold was set to be 7 vol.%

Reason -> Evaluations are only performed at each point thus if the resolution (number of points) is low then large changes can occur between each point.

• Subsequent melt extraction events may appear less than the melt extraction threshold (green boxes)

Reason -> The melt extraction threshold is evaluated relative to the Reactive Subsystem (which itself is shrinking due to melt extraction events) thus equivalent proportions of melt equate to different proportions when compared to the full system (FS).

## Example3 - Multi-path functionality

Multiple paths can be compiled in P-T-X space to produce path-dependent P-T mode diagrams. In these diagrams a plane in P-T space is filled with points originating from dependent paths.



Figure 17 – Example of a composite path-dependent P-T mode diagram from (Mayne et al., 2016): Colours scale the weight percentage of melt in the reactive subsystem (RS). Starting composition at 640 °C and 12 kbar taken as an average amphibolite facies pelite (Table 1). Melt is extracted whenever a 7 wt.% threshold is met and leaves behind 1 wt.% approximating melt retention on grain boundaries. The simulation space is filled by a number of isothermal decompression paths that each originate off a 12 kbar isobaric heating path.

Let's create a path-dependent P-T mode diagram by decompressing off of the path investigated in Example2.

**1.** Load Example3 by opening Rcrust, typing 'Example3' in working file and clicking "Load" To ensure that we do not overwrite any data lets rename the Working File.

2. Rename the file by typing "Example\_multi" into Working File then click the Save button from the Rcrust toolbar

This will save the current Rcrust GUI inputs into a new file named "Example\_multi". The Rcrust GUI should now look like Figure 18.

	P	rojects Directory D/Rcrust/Projec	ts			Projects Directo	ory D:/Rorust/Proje	cts
Rcrust	Working File Example3a	Save Load R	un Clear	Rcrus	Working File Exam	nple3a S	ave Load F	Run
			Console					Co
ation complete, Res contputs throught	ults saved to D:/Rcrust/Projects/Ex the 'Outputs' tab	ample3a/Example3a.RData		Calculation complete Select outputs three	e, Results saved to D:/Rcrus sught the 'Outputs' tab	t/Projects/Example3a/Examp	le3a.RData	
t Parameters Ph	ase Manipulations Modelling Option	s Outputs		Input Parameters	Phase Manipulations M	lodelling Options Outputs		
a 💶				Phase Addition				
	Y			Perform Phase	Addition?			
)	11							
ssure and Temperate				Phase Extraction	🗣			
nber of PT definition	nc			Perform Phase	Extraction?			
				📄 Re-equilibrate r	eactive subsystem after phase of	extraction?		
m To	Pressure (kbar)	Temperature (C)		Number of extrao	tion definitions			
;1) 19,	11 12-(y i-1)*0.3	660+(x i-1)*10+150		1				
				From	To Condition	Phases		
				(1;1)	(19;11) ph(Melt,vo	Mait		
k Composition	4			Melt				
mber of Component	Transformations			retain{1;wt%}				
or elements	5102 K20 CAO TIO2 EEO O2 H20							
100 M203	and the sho has the U2 h20							
mber of bulk definiti	ons							
m To	NA20,MGO,AL203,8102,F	K20,CA0,TI02,FE0,02,H20,mas	5					
(1)	1.82,3.28,20.45,56.97,4.0	9,1.56,1.05,8.5,0.75,1.96,100						
m To	NA20,MGO,AL203,8102,F	420,CA0,TI02,FE0,02,H20,masr						
.1 19,	t rs(x i-tay i)							
	NA 10 NO 11 101 NO1	K10 C 40 TIO2 EEO 02 H20 mar						
m To	NA20,MGO,AL206, 602,F	20,040,1102,120,02,120,1180	•					

This example creates a composite path-dependent P-T mode diagram. It does this by first calculating an open system isobaric heating path at 12 kbar (IBH12) and then calculating a number of isothermal decompression paths that each originate from a point on IBH12. Points along IBH12 are each dependent on the reactive subsystem of the point one to the left of itself on the x-axis. Points along decompression paths are each dependent on the point one above itself on the y-axis. Melt loss is defined to occur whenever a 7 vol.% melt threshold is met and melt is extracted until 1 wt.% melt is left behind (this is achieved using the "retain(amount,unit)" function).



Figure 19 - Grid output for Example\_multi showing volume percent of melt in the reactive subsystem (RS)



Figure 20 – Phase assemblage map for Example\_multi showing field labels as numbers

# **REFERENCE MANUAL**

# **Rcrust File Management**

The top line of the Rcrust GUI hosts a toolbar of file management buttons. User inputs are saved in a text document (**Working File**) which is located in the Projects folder of Rcrust (**Projects Directory**). This file is written, read or run in Rcrust by the **Save**, **Load** and **Run** buttons.

						Proiects
Projects Directory D:/Rcrust/Projects		orking Fil	le Examp	le1		Working File
Rcrust	Save	Load	Run	Clear	Close	
Loaded D:/Rcrust/Projects/Example1/Inputs/Example1.txt						Rcrust Toolbar
						Status

### Save

Saves the **Working File's** inputs and calculation results. Each working file is assigned its own project folder in the **Projects Directory**. Parameters currently in the Rcrust GUI are saved to the Inputs folder as a text document. Additional parameters can be passed to Rcrust by placing them in the text document after the line (# Additional Parameters). Calculation results are saved as an R workspace in the project folder.

## Load

Loads the **Working File's** inputs and calculation results. Reads the working file from the inputs folder and loads its options in the Rcrust GUI. Replaces the current workspace with that of the **Working File's**.

## Run

Saves the current Rcrust GUI inputs and runs the Rcrust calculation according to these parameters. Follow prompts in the R console to calculate the results. Once the results are complete you will be prompted to select outputs through the Rcrust GUI. Outputs written to file are saved in the Ouputs folder of the project Advanced users can access the results directly in the R console by pressing [esc] to activate the console (this is helpful for loading data into GCDkit). To relaunch the Rcrust GUI type 'runApp()' then press [Enter]

## Clear

Clears current values in the Rcrust GUI

## Console

Launches a browser in the R console giving you direct access to the coding environment and all calculated data

# **List of Parameters**

User inputs are listed here in a systematic fashion for clarity. The parameter name (the name that appears in the Rcrust GUI) is listed first followed by the variable name (the name of the variable accessible in the R console). The data type required for the parameter is listed in the second box. The third box contains possible values for the parameter and identifies any default value. Below this is a description as to what the parameter controls.



# **Input Parameters**

Tuple definitions		
From	Tuple	{1;1}<=
{pt_from_#}		pt_from_#<={x_n;y_n}
	The beginning of the definition selection	

To {pt_to_#}	Tuple	pt_from_#<=pt_to_#<={x_n;y_n}	
The end of the definition selection			

Size

Specify here the size of the simulation (resolution) you want to calculate: how many points in the X and Y directions.



X {x n}	Numeric	1< x_n
The total number of points in the	X direction	

Y	Numeric	1< y_n	
{y_n}			
The total number of points in the Y direction			

# Pressure and Temperature

	Pressure and Temperature Number of PT definitions 1						
	From {1;1}	<b>То</b> {19	;11}	Pressure (kbar)	Tempe 660+	rature (C) (x_i-1)*10	
Number of PT {n_pt_def}	definitions	/	Nun	neric		1< n_pt_def	
The number of definitions to use for assigning pressure and temperature values							

Pressure (kbar)	Numeric/Expression	0 <p< th=""></p<>	
{pressure_#}			
The pressure in kilobars of the Reactive Subsystem (RS). *(1 kbar = 0.1 GPa = 986,92 atm).			
This can be a constant or an expression built using the variables x_i, y_i, real numbers and			
Arithmetic Operators. e.g. 12-(y_i-1)*0.3 to decompress along the y-axis by 0.3kbar per step			
starting at 12 kbar.			

Temperature (°C)	Numeric/Expression	0 <t< th=""></t<>	
{temperature_#}			
The temperature in degrees Celsius of the Reactive Subsystem (RS). *(1 °C = 274.15 K = 33.8°F)			
This can be a constant or an expression built using the variables x_i, y_i, real numbers and			
Arithmetic Operators. e.g. 660+(x_i-1)*50 to heat along the x-axis by 50°C per step starting at			
660°C.			

PT definition	String	Options: input	
{pt_def}			
Advanced setting toggling the PT definition mode. Used to allow PT definition from file. *pt			
definition from file still to come			

{pt_definitions}	Listed Definition			
Pressure and temperature definitions of the form				
pt_definitions<-list("{x_a,y_a}_{x_b,y_b}"=c("pressure_#","temperature_#"),				
"{x_a,y_a}_{x_b,y_b}"=c("pressure_#","temperature_#"))				

# Additional Settings (main.r)

{PT_restrictions}	Comma-separated-strings	
P-T conditions which should not	be calculated. Use if projecting arr	ay through array where points
should be ignored		
### Bulk composition

Warmhar of Ca	manage Transfer	
Number of Co	mponent transfo	mations
1		
Replace	New	NA20, MGO, AL203, SIO2, K20, CA0, TIO2, MNO, FEO, NIO, ZRO2, CL2, O2, H20
component	component	0.0.0,0,0,0,0.0.0,0,0,0,0.5.0,0
02	0	
Major element	s	
Major element	AL203 SIO2 K2	O CAO TIOZ FEO O H2O
Major element	AL2O3 5102 K2	O CAO TIOZ FEO O H2O
Major element NA20 MG0 Number of bul	s AL2O3 SIO2 K2 Ik definitions	O CAO TIOZ FEO O H2O
Major element NA20 MG0 Number of bul 2	s AL2O3 SIO2 K2 Ik definitions	O CAO TIOZ FEO O HZO
Major element NA2O MGO Number of bul 2 From	is AL2O3 SIO2 K2 Ik definitions To	O CAD TIO2 FED O H20 NA20, MG0, AL 203, SIO2, K20, CAO, TIO2, FEO, O, H20, mass
Major element NA20 MG0 Number of bul 2 From {1:1}	s AL2O3 SIO2 K2 Ik definitions To {1:1}	O CAD TIO2 FEO O H20 NA20,MG0,AL203,SIO2,K20,CAO,TIO2,FEO,O,H20,mass 1.82,3,28,20,45,56.97,A09,1.56,1.05,8,5,0.31,1.96,100
Major element NA2O MGO Number of bul 2 From {1:1} From	s AL2O3 SIO2 K2 Ik definitions To {1:1} To	O CAD TIO2 FEO O H2O NA20,MGO,AL203,SIO2,K20,CAO,TIO2,FEO,O,H2O,mass 1.82,3,28,20,45,56,97,A.09,1,56,1.05,8,5,0,31,1,96,100 NA20,MGO,AL203,SIO2,K20,CAO,TIO2,FEO,O,H2O,mass

Number of Component	Numeric	0<= n_comp_trans		
Transformations				
{n_comp_trans}				
The number of component trans	formations to apply to the current	ly available chemical		
components: the possible compo	components: the possible components for transformation are set by the thermodynamic data file			

Replace component	String	
{old_comp_#}		
The current component to replace		

New component	String	<6 characters, All capitals
{new_comp_#}		
The name of the new compon	ent. This name must consist of les	s than 6 characters and must be
all in capital letters.		

NA2O,MGO,	Comma-separated numeric		
{comp_#}			
The value of the new component as a factor of the available components:. This must be a string			
of comma separated numbers of which a total of no-more-than 11 can be non-zero. For			
example, if we wish to use the component O instead of O2 and our starting chemical			
components are NA2O,MGO,AL2O3,SIO2,K2O,CAO,TIO2,MNO,FEO,NIO,ZRO2,CL2,02,H2O,CO2			
we would use: 0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0 If we wish to use FE2O3 we would use:			
0,0,0,0,0,0,0,0,2,0,0,0,0.5,0,0			

Major elements	Comma-separated-strings			
{major_elements}				
The major element components	The major element components used to define the bulk composition.			

Number of bulk definitions {n_bulk_def}	Numeric	1<= n_bulk_def	
The number of definitions to use for assigning bulk compositional values.			

NA2O,MGO,,mass	Comma-separated-	e.g. 1.5, 20.2, 40.8, 100			
	values/expressions	e.g. rs{x_i-1;y_i}			
The wt.% of each elemental oxide listed in "Major elements" (above) as well as the relative					
starting mass (in grams) of t	starting mass (in grams) of the Reactive Subsystem (RS).				
Expressions can use real numbers, Arithmetic Operators, x_i, y_i, x_n, y_n and any tuples of the					
form xs{#;#} where xs is any of rs,as,es,fs and # uses real numbers, Arithmetic Operators , x_i,					
y_i, x_n and/or y_n					
If xs{#;#} is of length 1 it will be repeated to fill the required terms.					
i.e. To make the full bulk composition of one point dependent on another first initialise the					
starting composition and th	starting composition and then set the dependent points as rs{x i-1; y i} for dependence on the				
x-axis or rs{x_i; y_i-1} for dependence on the y-axis					

Import definitions from file	Boolean	TRUE = Import from file		
{bulk_def_file}		FALSE = definition via input		
Choose whether bulk definitions are read from input or imported from a text file (.txt) located in				
the Inputs folder.				

Bulk file	Character string	e.g. bı	ulk.txt	
{bulk_file}				
The name of the input file cont	aining the bulk compos	sition definitions	(the name must end with	
tyt) The hulk file must be a tak	n delimited text file ( ty	t) containing the	· e columns "From" "To" vo	ur
				ui
selection of major elements an	d "Mass". For example	:		
📗 bulk.txt - Notepad		_		
File Edit Format View Hale				
<u>rite cut romat view H</u> eip				
FROM TO NA20 MG0	AL203 SI02	CAO FEO	MASS ^	
1;1 1;2 0.53 25.	8 6.93 48.15	7.02 10.93	100	
			<b>~</b>	
This text file can be easily expo	rted from an excel file	using File\Save A	As\Text (tab delimited) (* ty	xt)
	hulk visy - Evrel		bilder-fiel	~~)
File Home Insert Page Lavout Formulas Data Revi		€ Save As		
		New Save As		
	Wrap Text General	Cpen This PC	definition     definition     definition     definition     definition     definition     definition     definition     definition	Fill Save
* Sorrat Painter $B I \underline{U} * \underline{M} * \underline{A} * \equiv \equiv \equiv$	•= •= • Merge & Center • • • • • • •	Save Ac	Event Marcharde ("arlan) Event Marca-Enabled Workbard ("arlang) Event Marca-Enabled Workbard ("arlang)	
Clipboard Fa Font Fa	Alignment 🕞 Number	The second se	Does that any second (a loss) Event 77-2000 Workshow (ab) MAD, Bate ("web) Social (a Web Pase ("web" "social")	ed
A1 + FROM		Stare	United States (States (States)) (States) (States	643 PM
		Expert Datas	Exact ST-2003 Tensing in company. Exact ST-2003 Tensing Pack Feel (SS) Selenteel (2003) Unicode Feel (2005)	
A B C D E F	G H I J	Cose	MML Spreadsheet 2001 (*xml) Microsoft Kenel Sufy's Workdook (*xdq) CSN (Comman definited) (* noi)	
2 1;1 20;1 0.53 25.8 6.93 48.	15 7.02 10.93 100	Account	Formateul Text Space delimited) (*gmi) Text (Machina (*chr) Text (Machina ray)	
3 1;2 20;2 0.42 23.38 7.69 48.	08 7.76 12.23 100	Options	CSV (Macheolog) (*csv) CSV (Macheolog) (*csv)	
4 1;3 20;4 1.31 20.61 8.21 48.	76 8.62 11.96 100	Feedback	Die Gunta interchange Ferrarg (* 144) SVAX (Symbolie) (* 146) Excell Add-in (* slam)	
6			Exert 97-2003 Add vn (*ala)	
	k dofinitions for all noi	ate in the chocor	n modelling chace ly new n	1
The input file must provide bul	k deminitions for an poi	its in the chosei	Thoughing space $x_n, y_n$	ĵ
with numbers in the "From" an	d "To" arguments sena	irated by a semi	colon (·)	ĵ

The bulk definitions describe the wt.% of each elemental oxide as well as the relative starting mass (in grams) of the Reactive Subsystem (RS). Expressions can use real numbers, r operators, x\_i, y\_i, x\_n, y\_n and any tuples of the form xs{#;#} where xs is any of rs,as,es,fs and # uses real numbers, r operators, x\_i, y\_i, x\_n and/or y\_n

# **Phase Manipulations**

Phase Addition

Perioriti	Phase Addition?			
Number of a	addition definition	s		
1				
From	То	Condition	Phases	
1,1	30,1	TRUE	Water	

Perform Phase Addition?	Boolean	TRUE/FALSE
{ph_add}		
Add phases/components into	the Reactive Subsystem (RS) at	specified points?

Number of addition	Numeric	
definitions		
{n_ph_add_def}		
The number of definitions to use for assigning phase additions.		

Condition	Logical/expression	Options:
{ph_add_con_#}		TRUE
		FALSE
		ph{Melt,vol%}>=7
A conditional argument that evaluates to a Boolean answer of TRUE or FALSE.		
Note: if directly providing argument as TRUE or FALSE ensure all capitals.		
For example to add phases whenever melt exceeds a 7 vol% threshold you would use the		
following condition: ph{Melt,vol%}>=7 if "Melt" is the alias assigned in the solution model		
file used		

Comma-separated-strings		
Phases to be considered for phase addition in each definition. This can be any name as it is		
only the respective chemical components that are added to the system not the phase		
itself, thus the phase name is just a place holder for the user to remember what they are		
	Comma-separated-strings d for phase addition in each de emical components that are add ame is just a place holder for th	

#,#,mass	Comma-separated-values	
The wt.% of each elemental oxide listed in "Major elements" (Bulk composition tab) as well		
as the relative mass (in grams) of the phases/components to add.		

7 Destaur (	Share Entration 2			
enorm r	mase Extraction?			
Re-equilib	orate reactive subs	ystem after phase extraction?		
Number of e	straction definition	0.05		
Authori of a	Augenon dennin	5115		
1				
From	То	Condition	Phases	
{1;1}	{4;1}	ph{Melt,wt%}>=7	Melt	
Melt				

Perform Phase Extraction?	Boolean	TRUE/FALSE
{ph_extr}		
Extract phases from the Reactive Subsystem (RS) when specified criteria are met?		

Re-equilibrate reactive	Boolean	TRUE/FALSE
subsystem after phase		
extraction?		
{reequilibrate_steps}		
Use the bulk composition at the end of extraction to recalculate phase stabilities		

Number of extraction	Numeric	
definitions		
{n_ph_extr_def}		
The number of definitions to use for assigning phase extractions.		

Condition	Logical/expression	Options:	
{ph_extr_con_#}		TRUE	
		FALSE	
		ph{Melt,vol%}>=7	
A conditional argument that evaluates to a Boolean answer of TRUE or FALSE.			
Note: if directly providing argument as TRUE or FALSE ensure all capitals.			
Expressions should be of the form described in "Extraction expressions" below.			
For example to extract phases whenever melt exceeds a 7 vol% threshold you would use			
the following condition: p	the following condition: ph{Melt,vol%}>=7 if "Melt" is the alias assigned in the solution		
model file used			

Phases for extraction	Comma-separated-strings	
{ph_extr_phs_#}		
Phases to be considere	d for phase extraction in each o	definition. These can be any alias in
the solution model file chosen (Phase Models tab) or any pure phase output by Perple_X		
(see Perple_X		
http://www.perplex.ethz.ch/		
Perple_X Solution Model Glossary) and THERMOCALC's list of mineral abbreviations).		
*Can use "any_phase"	to set generic arguments	

[Dhase extraction	Numerie / nerecente de /	
[Phase extraction	Numeric / percentage /	e.g.
proportions]	expression	10%
{ph_extr_phs_#_ <i>phase</i> }		5 (mass relative to a starting
		mass of 100 for the full system)
		retain{2;vol%;Melt}
		delta{Melt ; x_i-1 ; y_i ; mass}*0.5

Define the proportion of phase to extract for each phase listed in "Phases for extraction". Proportions can be given as:

- 1. A percentage of what is present (e.g. 10%) \*you must include the percentage sign for this
- or
- 2. A set mass relative to the full system (100). If this amount is larger than what is present the full amount of the present phase will be extracted.
- or
- 3. As functions of the form described in "Extraction expressions" below.

\*Can use "any\_phase" to set generic arguments for all phases that are present but don't already have a phase extraction proportion set i.e. pre existing definitions take precedence.

Extraction	Numeric / percentage /		
expressions	expression		
Extraction expressions	can be evaluated for conditions	or proportions consisting of x_i, y_i,	
real numbers, Arithmet	tic Operators, Logical Operators	, {} and (). where {} separate terms	
for calculation order an	d () are reserved for solution m	odel names.	
The following functions	s can be called by placing the fu	nction name before {} with function	
terms inside the bracke	ets separated by commas (,) or s	emi-colons (;).	
<ul> <li>retain{amount</li> </ul>	; unit ; phase}		
o Retenti	tention extracts all but a set amount of a phase from the reactive		
subsystem where unit can be "mass","wt%" or "vol%". In phase proportion			
boxes can omit "phase" to extract current phase.			
<ul> <li>e.g. ret</li> </ul>	ain{2;vol%;Melt} will extract me	elt from the reactive subsystem until	
2 vol%	of melt remains, this is useful for	or approximating melt retention on	
grain boundaries. This can also be written as retain{2;vol%}			
o <b>*Warn</b> i	ing: when utilising multiple pha	se extraction definitions ensure that	
the retention definition is last in order to retain to the finalised bulk.			
<ul> <li>delta{phase ; x_a ; y_a ; unit}</li> </ul>			
<ul> <li>Delta calculates the incremental difference of a phase between the current</li> </ul>			
point (point b) and a previous point (point a) such that:			
	delta=phase_mode <sub>b</sub> - p	ohase_mode₄.	

*point a may be described as "prev_ext_X" where
X is the name of any phase or "prev_ext" to use the
name of the extracting phase as default
<ul> <li>phase = phase for extraction ; x_a and y_a describe the position of the</li> </ul>
previous calculated point and unit is one of "mass" or "wt%".
*phase may be described with "+" separating
individual phase terms e.g. to calculate deltas for
the alumina silicates phase would be "ky+and+sill"
• e.g. delta{Melt ; x_i-1 ; y_i ; mass}*0.5 to extract half of the delta mass for
Melt when paths progress with increasing x_i values.
<ul> <li>ph{phase;unit;x_i;y_i}</li> </ul>
o returns the requested variable (unit) for the given phase in the reactive
subsystem Where unit can be any column name in calc, phases and x i
subsystem. Where unit can be any column hame in calc_phases and x_r
and y_i are the current point by default, if ph{} is only given two arguments
the current point will be evaluated by default.

# **Modelling Options**

Modelling Data

Modelling Data
Meemum version
meemum_679.exe
Perple_X Option File
perplex_option_679.dat
Thermodynamic Data File
hp11ver_679.dat
Solution Models File
solution_model_679.dat
Solution models
BI(W) Cpx(HP) Crd(W) Ep(HP11) Fsp(C1) GI(W) IIm(WPH) melt(W) Mica(W) Opx(W) Sp(WPC) St(W)

Meemum version	String	Example = meemum.exe	
{meemum_path}			
The name of the meemum executable to be used in ~Rcrust/data for phase stability calculations.			

Perple_X Option File	Strings	Example = perplex_option.dat		
{perplex_option_file}				
The perplex option file present in ~Rcrust/data which controls extra settings for phase stability				
calculations.				

Thermodynamic Data File	String	Example = hp11ver.dat	
{thermodynamic_data_file}			
The thermodynamic data file present in ~Rcrust/data to be used for phase stability calculations.			

Solution Models File	String	Example = solution_model_673.dat	
{solution_models_file}			
The solution model file present in ~Rcrust/data from which solution models can be chosen.			

Solution models	Comma-separated-strings		
{use_sol_models}			
The solution models to use in phase stability calculations sourced from the Solution Models File.			
(see Perple_X			
http://www.perplex.ethz.ch/			
Perple_X Solution Model Glos	sary)		

Additional optional parameters

Additional optional parameters			
Saturated components			
Saturated phase components			
Independent potential/fugacity/activity			
Exclude phases			

Saturated components	String	
{saturated_components}		
Set saturated components		

Saturated phase components {saturated_phase_components}	String	
Set saturated phase components		

Independent potential/fugacity/activity	String		
{independent_potential_fugacity_activity}			
Set independent potentials fugacities or activities			

Exclude phases	String	
{exclude_phases}		
Set phases to be excluded from	n consideration during Gibbs er	nergy minimisation

### Extra Settings

Extra Settings When calculation is complete:	
Return to Interface	• ]

When calculation is complete: {end_of_calc}	String	Options: Return to interface Logout Shutdown Default = Return to interface
Action to be performed when a	a calculation is complete.	

Outputs		
Phase Aliases	Comma separated strings	e.g. TiBio(HP)=Bt,Gt(WPH)=Gt
{ phase_aliases}		
A list of aliases to use for rena	ming phases of the form TiBio(	HP)=Bt,Gt(WPH)=Gt,etc.
To hide a phase from plotting	use the alias "hide" e.g. TiBio(H	IP)=hide.

Select Output = Data File

View the output data as a single filtered table

Projects Dire	ectory D:/Ro	crust/Projects	Working File Exar	nple_m	ulti	Save	Load	Run	Clear	Console		
File saved to D:/Rcrust/Projects/Example_multi/Inpu	ts/Example_	multi.txt										
Input Parameters Phase Manipulations Model	ing Options	Outputs										
Phase Aliases	Compi	ilation data file	Dhave			Deserves(listers)	Trees					
	-	ID Mail as 4.4	Phase	y_1	×_1	Pressure(kbar)	enq	perature(C	.) mas	S W1%	4 204	4.45
Select Output		Rio m 1 1	Rio re	1	1	12	810		14.3	00 I 5 16.01	17.44	6.225
Data File -	3	Kfrs 1.1	Kf rs	1	1	12	810		14.5	7 17 17	20.13	8 575
	4	PLrs 1 1	PLis	1	1	12	810		3.47	4.089	4.67	2.087
View	5	Cox rs 1 1	Cox rs	1	1	12	810		7.24	8.532	7.531	5.203
Data	6	lim rs 1 1	llm rs	1	1	12	810		7.41	8.732	5.284	7.74
Select Columns	7	ky_rs_1_1	ky_rs	1	1	12	810		17.2	7 20.35	16.88	17.18
All	8	q_rs_1_1	q_rs	1	1	12	810		19.7	23.22	26.7	52.83
Select System/Phase	9	Bulk_rs_1_1	Bulk_rs	1	1	12	810		84.8	6 100	100	100
	10	Melt_es_1_1	Melt_es	1	1	12	810		15.1	4 0	0	0
	11	Bulk_es_1_1	Bulk_es	1	1	12	810		15.1	4 0	0	0
Select Points	12	Melt_es_cumul_1_1	Melt_es_cumul	1	1	12	810		15.1	4 0	0	0
{1:1}	13	Bulk_es_cumul_1_1	Bulk_es_cumul	1	1	12	810		15.1	4 0	0	0
File type												
CSV -												
Save To File												

Select Output = Grid

View the output data by selecting a single variable to express on a grid of x\_i and y\_i coordinates. Contour plotting can be achieved by selecting View>Plot.

Rerust	Projects Dire	ctory D:/F	Rcrust/P	rojects	v	Vorking	File Exa	mple_m	ulti		Save	Load	Run	Clea	r Co	onsole
le saved to D:/Rcrust/Projects/Exa	mple_multi/Input	s/Example	_multi.	txt												
Input Parameters Phase Manipula	ations Modellin	ng Options	s 0	utputs												
Phase Aliases		Melt	rs vol	% on ()	K,Y) gr	id										
			V1	V2	<b>V</b> 3	<b>V</b> 4	V5	<b>V</b> 6	<b>V</b> 7	<b>V</b> 8	<b>V</b> 9	V10	V11	V12	V13	V1
		1	0.00	0.00	0.00	0.00	2.63	0.00	0.00	0.00	1.76	1.86	1.97	2.08	2.21	2.3
Select Output		2	0.00	0.00	0.00	0.78	2.81	0.00	0.00	0.00	1.71	1.81	1.91	2.02	2.14	2.2
Grid	<b>^</b>	3	0.00	0.00	0.00	0.96	2.83	0.00	0.00	0.00	1.66	1.73	1.86	1.96	2.08	2.2
Data File		4	0.00	0.00	0.00	1.20	3.01	0.00	0.00	0.00	1.60	1.70	1.80	1.91	2.02	2.1
Grid		5	0.00	0.00	0.00	1.57	3.29	0.00	0.17	0.00	1.57	1.66	1.73	1.88	1.96	2.0
Phase Abundance Along Path		6	0.00	0.00	0.31	1.78	3.70	0.00	0.70	0.00	1.53	1.61	1.68	1.78	1.90	2.0
PAM		7	0.00	0.00	0.61	2.06	3.91	0.00	0.79	0.00	1.49	1.59	1.66	1.75	1.88	1.9
vol%	•	8	0.00	0.00	1.00	2.25	4.20	0.00	1.48	0.00	1.45	1.53	1.61	1.70	1.80	1.9
[		9	0.69	0.78	1.81	3.14	4.81	0.00	2.17	0.53	1.41	1.49	1.57	1.66	1.75	1.8
Meit_rs	·	10	1.11	1.46	2.60	3.95	5.75	0.60	3.51	1.36	1.38	1.45	1.53	1.63	1.72	1.8
Labelled axes		11	1.36	1.88	3.07	4.30	6.24	1.36	4.22	6.97	1.36	1.45	1.50	1.57	1.68	1.7
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Select Output = Phase Abundance Along Path

View phase abundance data by weight along a path in the x or y direction.

Phase abundance graphs can be viewed as 100% stacked column graphs by selecting View>Plot

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Select Output		Bio rs	14.35	13.65	12.20	10.62	8.48	5.72	2.66	0.00	0.00	0.00	0.00
Phase Abundance Along Path	-	Kf_rs	14.57	15.04	16.00	17.05	17.82	19.62	21.55	22.53	22.65	22.19	21.73
		PL <sub>I</sub> s	3.47	3.38	3.05	2.61	2.70	1.37	0.00	0.00	0.00	1.24	2.81
New Data O Plot		Cpx_rs	7.24	6.98	6.55	6.19	5.63	5.52	5.37	4.81	4.52	3.73	2.77
uia		llm_rs	7.41	7.47	7.54	7.63	7.73	7.82	7.93	8.09	8.11	8.16	8.25
AXIS	_	ky_rs	17.27	17.11	16.79	16.50	15.98	15.62	15.25	14.66	14.56	14.21	0.00
x	•	q_rs	19.70	19.39	18.74	18.05	17.06	15.81	14.44	13.18	13.11	13.05	12.97
Path		Gt_rs	0.00	0.65	2.06	3.50	5.50	7.78	10.36	12.63	12.78	13.09	13.39
1	-	sill_rs	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13.72
		Bulk_rs	84.86	84.86	84.86	84.86	84.86	80.07	80.07	80.07	76.50	76.50	76.50
Start Point		Melt_es	15.14	0.00	0.00	0.00	0.00	4.78	0.00	0.00	3.57	0.00	0.00
1	•	Bulk_es	15.14	0.00	0.00	0.00	0.00	4.78	0.00	0.00	3.57	0.00	0.00
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### Select Output = PAM

### Create a phase assemblage map by merging fields in x-y space with identical assemblages.

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Increments

# **File Management**

Functions for file management. See Rcrust File management for more details

Projects Directory	String	
{projects_directory}		
Absolute location of the projects	directory within the Rcrust folder	

Working File	String	
{working_file}		
Name of the current file under o	peration. Each file has its own fold	ler within the projects directory
containing results of simulations	(#.RData file), "Inputs" and "Outp	uts".

Save	Function call	
{on_save}		
Saves the current GUI inputs and	workspace to the working_file.	

Load	Function call	
{on_load}		
Loads the previously saved working_file into the GUI inputs and workspace.		

Run	Function call	
{manual_load}		
Saves the current GUI inputs and	workspace to the working_file. Tl	nen launches the Rcrust
calculation		

Clear	Function call	
{on_clear}		
Clears the current GUI inputs and workspace.		

Console	Function call	
{stopApp}		
Closes the current GUI to allow in	nteraction with the R console. To r	relaunch the Rcrust GUI type
'runApp()' then press [Enter].		

### Perple\_x options

Options parsed to wrapper calculation set in init\_meem.r

Number of chemical	Integer	Default = 15
components	-	
{number_components}		
The number of chemical components to build the major elements from.		

Unit for bulk	Integer	0 = molar %
composition		1 = weight %
definition		Default = 1
The unit proportion to use for bulk composition definition.		

Advanced user options Static variable options accessible through main.r

Calculation mode	Character vector	normal
{calc_mode}		Default = normal
Advanced setting toggling the calculation mode.		

Reaction buffering	Boolean	T (TRUE)
{reaction_buffering}		F (FALSE)
		Default = FALSE
Allows reaction buffering (threshold buffering) whereby phase extractions set on conditions are		
postponed by the number of reaction buffer steps to ensure continued exceedance of the		
threshold.		

### **Useful functions in the R Console**

-

. . . .

c Continue steps in a browser (if accessed by clicking "Console" in the Rcrust GUI then closes the browser and returns to the Rcrust GUI)

Rcrust()	Manually launches the Rcrust GUI
[Ctrl]+[w]	Toggles buffering of outputs
Q()	Quits the current session
ls(envir=.GlobalEnv)	List all objects in the global environment
ls()	List all objects in the current environment

To access the R console out of a browser click anywhere in the R console window and press [esc].

This will close the Rcrust GUI which has current control over the console. To relaunch the Rcrust GUI at any time simply type runApp() and press [enter].

Rcrust variables	
PT[[bulk]][[step]]\$press\$temp	list
List of pressure and temperature conditions for each step in each bulk	

crust[[bulk]][[step]][phase,detail]	list
The full system (FS). Contains details of the reactive subsystem (RS) at each step a	along with
cumulative extract (ES) and addition (AS) subsystems. Phases in crust are reporte	d as cumulative
weighted averages.	

c0[detail]	vector
Bulk composition passed between points	

workingfile	Character vector
The current Working File	

work_dir	Character vector
The current Working Directory. This is the location of the folder containing the W	/orking File

Running Rcrust		
Relaunch GUI	Function call	
{.First()} or {Rcrust()}		
Relaunches the Rcrust GUI from the R console		

Manually initiate calculation {manual load}	Function call	
Sends the current working file to be calculated		

### Rcrust Outputs

Data file	Function call	
{data_file()}		
Compiles calculation results into a table		

Write data file	Function call	
{write_data_file}		
Writes compilation table to file		

Grid data	Function call	
{grid_data()}		
Compiles an X Y grid of the values of a given variable		

Write grid file	Function call	
{write_grid_file}		
Writes X Y grid to file		

### R Syntax

Arit Ope	hmetic rators	2
	Operator	Description
	+	addition
	-	subtraction
	*	multiplication
	/	division
	^ or **	exponentiation
	x %% y	modulus (x mod y) 5%%2 is 1
	х %/% у	integer division 5%/%2 is 2

ogical Opera	ators	
Operator [	Description	
<	less than	
<=	less than or eq	ual to
> 0	greater than	
>= (	greater than or	r equal to
== 6	exactly equal t	0
!= r	not equal to	
!x 1	Not x	
x   y	x OR y	
x & v	x AND v	

### **Development**

Developers of new features should know a few things on the structure of the code. When developing custom functions please stick to these conventions.

The following files are required; they must all be in the same directory (these are contained within the Rcrust folder which should simply be copied to the desired location):

- 1) From **Perple\_X** suite (in the folder called "data"):
  - a. The various datafiles you wish to use, these include: thermodynamic datafiles and solution model files, typically hp04ver.dat and solution\_model.dat as well as the Perple X option file, *perplex option.dat*.
  - b. Meemum.exe
  - c. The rest of Perple\_X (vertex, build, werami, etc.) are not required.
- 2) From **Rcrust** (in the folder called "code"):
  - a. ui.r and server.r, these build the Rcrust Graphical User Interface (GUI)
  - b. main.r, this houses the main calls to run Rcrust
  - c. meemum\_connect.r, the functions for calling and interpreting outputs from meemum
  - d. Various init xxx files, used to transform user input in data structures that Rcrust can understand.

sets the phases to add

- i. init\_bulk.r
- ii. init pt.r
- iii. init\_ph\_add.r
- sets the P-T conditions

sets the bulk composition(s) of the system

- iv. init\_ph\_extr.r
- v. init meem.r
- vi. init\_dependence
- vii. init wrapper

sets the phases to extract writes user inputs into a meemum build file determines the calculation order of points the phase stability calculator from Perple X

e. parse\_meem, a temporary Perple\_X build file created to pass data into the wrapper f. run.Rcrust.r, the Rcrust calculation loop to be called for each point

Technically, each function works c0 which tracks the bulk compositional changes invoked by phase manipulations. main.r loops through each point, calculating and modifying the phases according to the chosen definitions and eventually stores the final product in a list called crust, whose structure is crust [[y i]] [[x i]]. So, for instance the SiO2 content in the melt of point y\_i=4 and x\_i=2 is crust[[4]][[2]]["melt(HP)","SIO2"]

g. Various xxx.dll files which contain compiled libraries needed to perform calculations within R

## Troubleshooting

A list of known errors that are unavoidable or are still to be fixed.

### Bulk\_ss system properties

Warning: some bulk system properties are reported as molar properties but perplex considers the bulk system to be one mol thus all molar properties need to be adjusted accordingly

### Molar phase proportions

Only weight definitions of bulk and phases is currently possible, read.meemum cannot read molar phase proportions. If molar proportions for bulk are entered, then bulk is molar but individual phases are weights thus phase extractions crash.

### **Buffered Output**

The R console by default returns a buffered output which forces the console to only refresh when flush.console() is called. To disable the buffering and view run data live deselect from R toolbar Misc/Buffered Output.

### **External Sources**

Perple\_X http://www.perplex.ethz.ch/

Perple\_X Solution Model Glossary http://www.perplex.ethz.ch/PerpleX\_solution\_model\_glossary.html

<u>THERMOCALC's list of mineral abbreviations</u> <u>http://www.metamorph.geo.uni-mainz.de/thermocalc/documentation/abbreviations/index.html</u>

### REFERENCES

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Connolly, J.A.D., 2005. Computation of phase equilibria by linear programming: a tool for geodynamic modeling and its application to subduction zone decarbonation. Earth and Planetary Science Letters, **236**, 524–541.

Connolly, J.A.D., 2009. The geodynamic equation of state: what and how. Geochemistry, Geophysics, Geosystems, **10**, 1–19.

Connolly, J.A.D. & Kerrick, D.M., 1987. An algorithm and computer program for calculating composition phase diagrams. Calphad, **11**, 1–55.

### **ADDENDUM C: Presentation of the programming code for Rcrust**

Included within the thesis files for evaluation is the programming code of the Rcrust program. This code is heavily commented throughout and is divided into a number of separate files for convenience. Each file is preceded by a brief description of its overall purpose and a summary of the tasks it performs.

File structure				
Purpose	File name	Page		
Initialise P-T conditions	init_pt.r	5		
Initialise bulk compositions	init_bulk.r	7		
Initialise phase additions	init_ph_add.r	10		
Initialise phase extractions	init_ph_extr.r	11		
Initialise dependence structure	init_dependence.r	11		
Initialise meemum	init_meem.r	14		
Rcrust launcher	main.r	16		
Rerust calculation loop	run.Rcrust.r	21		
Wrapper for phase stability calculations	init_wrapper.r	32		
Meemum connect	meemum_connect.r	34		
Server	server.r	36		
User interface	ui.r	80		

### Brief description of code

Rcrust operates by receiving user input through a graphical user interface (GUI built using server.r and ui.r) which writes parameters for modelling into a text file (the file is stored in the projects directory within the workingfile in the inputs folder). The text file itself can be altered and additional parameters accessed. This file is then loaded into the current environment and program initialisation begins. A modelling space is set up consisting of a number of points which record information including temperature, pressure and bulk composition of each point (init\_pt.r and init\_bulk.r). Phase manipulations are optionaly set on points to be analysed during the calculation of phase stabilities for each point (init\_ph\_add.r and init\_ph\_extr.r) which can alter the chemical composition of points. Input parameters are examined for possible dependence relations and these dependence relations are solved to determine the calculation order of points (init\_dependence.r). A dummy "meemum build file" is created to parse modelling settings to "meemum" from Perple X

(init\_meem.r). In sequential order Rcrust runs through each point (main.r): a calculation loop (run.Rcrust.r) is called which adds chemical contributions to the reactive bulk composition (c0) then calls a wrapper function (wrapper.r) that interrogates meemum with the pressure, temperature and bulk composition of the reactive bulk (meemum\_connect.r). Meemum then uses Gibbs free energy minimisation to predict the most stable phase assemblage for the system and returns results to Rcrust. Phase extractions are then performed on this assemblage and the new altered bulk composition is optionally recalculated for its new phase assemblage. This final data is stored at its point coordinates within the modelling space (crust) and the next point in the calculation order is calculated. Since points are calculated in sequential order determined by dependence relations, the reactive bulk composition of each subsystem can be passed between points thus inheriting compositional changes. Once all points are calculated focus is returned to the graphical user interface where outputs can be filtered, saved and graphed.

Tags to be used within code	
# fix-tag	requires urgent implementation critical to stability of program
# mod-tag	non-urgent addition that would improve program
Variables	
#variable-def	definition of a variable created and the syntax to be used within the variable structure
crust[[y_i]][[x_i]]	two dimensional array holding outputs for each point
input_pt[[y_i]][[x_i]]	two dimensional array holding pressure and temperature conditions of each point
input_bulk[[y_i]][[x_i]]	two dimensional array holding bulk composition and relative mass for each point
input_ph_add[[y_i]][[x_i]]	two dimensional array holding phase addition definitions for each point
input_ph_extr[[y_i]][[x_i]]	two dimensional array holding phase extraction definitions for each point

#### Methodology and syntax utilised in programming code

Tags

dependencies[[y_i]][[x_i]]	two dimensional array holding references for each dependent point (evaluates functions of the form rs{x_i- 1,y_i}+5-as{x_n-2,y_i*2})
available components	chemical components available for component transformations, set in thermodynamic data file
major_elements/comps	the current chemical components to use
c0	point specific bulk composition and relative mass (to be passed between points)
use_sol_models	the current solution models to use
calc_choice	selector for calculation method
comp_mat	matrix recording the status of calculation of all points
project_directory	folder storing all projects
working_file	the current project
tuples	vector notation for identifying points in x,y space
x_i	the current increment in the x direction
x_n	the maximum increment in the x direction
y_i	the current increment in the y direction
y_n	the maximum increment in the y direction
ions	

### Functions

#function-def	definition of a function and the syntax to be used within the
	function calls

wrapper(comps,c0,press,temp,calc\_choice="read.meemum")

run.Rcrust(comps,c0,press,temp,ph\_extr\_pnt,cumul\_extract\_pnt=NULL,ph\_add\_pnt,cumul\_add\_pnt
=NULL)

run.meemum(meemum.path="",build.file="",meemum.order="",press=press\*1000,temp=temp+273. 15,bulk="",components="",pt\_comp=pt\_comp)

get\_val(y\_i,x\_i,phase,variable,crust=crust,oxy\_num=24,site\_ocup="biotite",select=1)

eval\_expr(expr,calc\_phases=calc\_phases,crust=crust)

Evaluate expression given calc\_phases and crust, "()" are for solution models, "{}" are for function terms and bodmas. Evaluate any "{" and any word before it up until "}"

#### Evaluates the following subfunctions

ph{phase;unit;x\_i;y\_i}

delta{ph;x\_#;y\_#;unit}

retain{amount;unit;ph}

Calculate mass of retention phases to extract: extract till retention amount of retention phases is left, where ph can be omitted to take on the current ph

scale a composition incrementally across x-i

#### return{phase;amount}

where amount can be % or mass

### Triggers

scale\_bulk\_x\_i

	exit_calc	leave calculation	
	reequilibrate_steps	calculate point again after phase manipulations	
	pass	tag points to be left out	
	silent_calc	limit the messages to console	
System	labels		
	rs	reactive subsystem	
	is	isolated subsystem	
	es	extract subsystem	
	es_cumul	cumulative subsystem	
Advanced functionalities not yet worked into GUI			

### Initialise P-T conditions (init\_pt.r)

Creates a two dimensional data structure that will record pressure and temperature conditions of the form:

input\_pt[[y\_i]][[x\_i]]\$Pressure,\$Temperature

Reads either pressure and temperature definitions defined in the graphical user interface or imported from a file of the form:

 $pt_definitions <-list("{x_a,y_a}_{x_b,y_b}"=c("pressure_#","temperature_#"), "{x_a,y_a}_{x_b,y_b}"=c("pressure_#","temperature_#"))$ 

Populates pressure and temperature conditions for each point or assigns dependence

Performs error validation ensuring that all points have an assigned pressure and temperature conditions

```
*****
#
  Initialize PT conditions
#
****
cat("Initializing PT conditions...\n")
# fix-tag: error handling
input pt<-rep(list(rep(list(c(Pressure=NULL,Temperature=NULL)),x n)),y n)</pre>
****
#
  PT definition from configuration file
****
if(pt def=="input"){
cat("Calculating PT conditions from inputs...\n")
pnts<-unlist(strsplit(names(pt definitions)," "))</pre>
for(h in 1:length(pt definitions)){
a<-unlist(strsplit(gsub("\\{", "", gsub("\\}", "", pnts[h*2-1])), split=";"))
b<-unlist(strsplit(gsub("\\{", "", gsub("\\}", "", pnts[h*2])), split=";"))</pre>
for(x i in a[1]:b[1]){
for(y_i in a[2]:b[2]){
press<-eval(parse(text=paste0(pt definitions[[h]][1])))</pre>
temp<-eval(parse(text=paste0(pt_definitions[[h]][2])))</pre>
input_pt[[y_i]][[x_i]]<-matrix(c(press,temp),nrow=1,dimnames =</pre>
list("PT", c("Pressure", "Temperature")))
}
}
}
}
*****
  PT definition from input file
#
*****
if(pt def=="file"){
# mod-tag: cleanup below
cat("Reading PT conditions from file...\n")
PT file<-paste (work dir, "/Projects/", workingfile, "/Inputs/PT.txt", sep="")
PTO<-read.table(PT file, sep="\t")
    if(any(is.na(PT0[1,]))){
    warning("Error at init_pt.r\nError in PT file, NA found in column names,
probably a tab left at the end of the first row, will try to rectify and continue")
# mod-tag: Surely there's a better way to make a matrix numeric?
     make numeric mat<-function(x) {</pre>
  y<-matrix(as.numeric(as.vector(as.matrix(x))), nrow(x),)</pre>
  rownames(y)<-rownames(x)</pre>
```

```
colnames(y)<-colnames(x)</pre>
 return(y)
 }
 err<-length(PT0[1,])</pre>
 mat<-PT0[-1,-1]
 colnames(mat)<-as.character(unlist(PT0[1,1:(err-1)]))</pre>
 rownames(mat)<-1:(nrow(PT0)-1)</pre>
 PT0<-make_numeric_mat(mat)</pre>
 }
 for(i in 1:nrow(PT0)){
 PT[[PT0[i,1]]][[PT0[i,2]]]$press<-PT0[i,3]</pre>
 PT[[PT0[i,1]]][[PT0[i,2]]]$temp<-PT0[i,4]</pre>
 }
}
****
#
# Error validation
#
*****
for(y_i in 1:y_n){
 for(x i in 1:x n){
   if(is.null(input_pt[[y_i]][[x_i]])){cat("Error: No pt defined for x_i =",x_i,"
y_i =",y_i," \n");stop()}
   }
}
cat("Done with PT conditions\n")
cat(".....\n")
```

#### Initialise bulk compositions (init\_bulk.r)

Creates a two dimensional data structure that will record bulk chemical conditions of the form:

input\_bulk[[y\_i]][[x\_i]]\$major\_elements,\$mass

where major\_elements is a list of chemical components as wt.% oxides

and mass is a numeric value against which to scale the reactive subsystem

Reads either bulk compositional definitions defined in the graphical user interface or imported from a file of the form:

 $bulk\_definitions<-list("{x_a,y_a}_{x_b,y_b}"=c(major\_elements\_wt.\%,"mass"), "{x_a,y_a}_{x_b,y_b}"=c(major\_elements\_wt.\%,"mass"))$ 

where major\_elements\_wt.% is a comma separated list of real numbers as weight percentage of each chemical component or terms of the from  $rs{x_i;y_i}$  to assign dependence relations.

Possible dependents = rs, fs, es, as non-dependents =  $c0, x_i, y_i, x_n, y_n$ 

If the only one term is given e.g.  $rs{x_i;y_i}$  then this will be copied for all chemical components

Populates bulk composition conditions for each point or assigns dependence

Performs error validation ensuring that all points have an assigned bulk composition condition

```
*****
  Initialize bulk composition data (only major elements for now)
#
****
cat("Initializing bulk composition...\n")
#fix-tag: error handling
# Error handling
if(exists("bulk_def")){
if(bulk def=="input") {
cat("Bulk composition defined from inputs...\n")
}else{
if(bulk def=="file"){
cat("Bulk composition defined from file...\n")
}else{
cat("Error ! No valid option specified for major composition...\n")
stop()
}
}
}else{
cat("Error ! bulk def not specified...\n")
stop()
ł
# Create data structure
cat("P-T-X space under investigation with x =", x n, "and y =", y n, "\n")
input bulk<-rep(list(rep(list(NULL), x n)), y n)</pre>
*****
 Bulk definition from input
#
****
## Majors
```

```
if(bulk def=="input") {
cat("Creating bulk compositions from definitions in configuration file\n")
#fix-tag should set Mass and volume somewhere but can only normalise once
expressions have been evaluated before parsing to Rcrust()
pnts<-unlist(strsplit(names(bulk definitions)," "))</pre>
for(h in 1:(length(bulk definitions))){
a<-unlist(strsplit(gsub("\\{", "", gsub("\\}", "", pnts[h*2-1])), split=";"))
b<-unlist(strsplit(gsub("\\{", "", gsub("\\}", "", pnts[h*2])), split=";"))</pre>
for(x i in a[1]:b[1]){
for(y i in a[2]:b[2]){
  if(length(bulk definitions[[h]])==1){
    input_bulk[[y_i]][[x_i]]<-rep(bulk_definitions[[h]],length(major elements)+1)</pre>
  }else{
    input_bulk[[y_i]][[x_i]]<-c(bulk_definitions[[h]])</pre>
  ł
if(!length(c(major elements, "mass")) == length(input bulk[[y i]][[x i]]) {cat(paste0(
"Error number of entries in input_bulk (",length(input_bulk[[y_i]][[x_i]]),") is
not equal to major elements + 1 (",length(c(major_elements, "mass")),") for x_i =
",x i,"; y i = ",y i,"\n"));stop()}
names(input bulk[[y i]][[x i]])<-c(major elements, "mass")</pre>
#Apply Scaling on x i - Note if assigning dependence do not leave gaps while
scaling
#mod-tag: work this into GUI
scale bulk x i<-FALSE
if(scale_bulk_x_i){
if(x i>1){
leftmost<-0
for(i in 2:(x i-1)) {if(is.null(input bulk[[y i]][[i]])) {leftmost<-i</pre>
break
}}
incr<-1
for(i in leftmost:(x i-1)){
#scale proportionate value to distance
b prop<-incr/(length(leftmost:(x i-1))+1)</pre>
input_bulk[[y_i]][[i]]<-</pre>
as.numeric(input_bulk[[y_i]][[x_i]])*b_prop+as.numeric(input_bulk[[y_i]][[leftmost-
1]])*(1-b prop)
names(input bulk[[y i]][[i]])<-c(major elements, "mass")</pre>
class(input bulk[[y i]][[i]])<-"character"</pre>
incr<-incr+1
}
}
ł
}
ł
3
}
****
  Bulk definition from file
#
#
****
## Majors
if(bulk def=="file"){
cat("Bulk composition for majors defined from bulk file:",bulk file,"\n")
  bulk_file_loc<-paste0(projects_directory,"/",working_file,"/Inputs/",bulk_file)</pre>
  if(file.exists(bulk_file_loc)){
  table in<-as.matrix(read.table(bulk file loc, sep="\t"))</pre>
  table out<-table in[-1,,drop=FALSE]</pre>
  colnames(table out)<-table in[1,]</pre>
  major elements<-setdiff(table in[1,],c("from", "to", "mass"))</pre>
   for(h in 1:nrow(table out)) {
    a<-unlist(strsplit(table out[h,1],split=";"))</pre>
    b<-unlist(strsplit(table out[h,2],split=";"))</pre>
    for(x i in a[1]:b[1]){
      for(y i in a[2]:b[2]){
        input_bulk[[y_i]][[x_i]]<-table_out[h,c(-1,-2)]</pre>
```

```
names(input_bulk[[y_i]][[x_i]])<-c(major_elements, "mass")</pre>
    }
   }
   }
 }else{
   cat("Error during bulk initialisation\nBulk file: ",bulk file loc," not found")
   stop()
 }
}
****
#
# Error validation
#
*****
for(y_i in 1:y_n) {
 for(x_i in 1:x_n) {
if(is.null(input_bulk[[y_i]][[x_i]])){cat("Error: No bulk defined for x_i
=",x_i," y_i =",y_i," \n");stop()}
 }
}
cat("Done with bulk composition preparation\n")
```

### Initialise phase additions (init\_ph\_add.r)

Creates a two dimensional data structure that will record phase addition conditions of the form:

input\_ph\_add[[y\_i]][[x\_i]]

Reads either phase addition definitions defined in the graphical user interface or imported from a file of the form:

ph\_add\_definitions<list("{x\_a,y\_a}\_{x\_b,y\_b}"=c(major\_element\_proportions,"mass"), "{x\_a,y\_a}\_{x\_b,y\_b}"=c(major\_elements,"mass"))

where major\_element\_proportions is a comma separated list of real numbers for each phase

```
*****
#
  Initialize phase addition options
*****
#handles definitions of the form: ph add definitions <-
list("{1,1} {10,1}"=c(2.95,0.618,15.3,7.11,5.17,0.15,0.183,6.44,63.5,5),"{1,1} {10,
1 = c (2.95, \overline{0}. 618, 15.3, 7.11, 5.17, 0.15, 0.183, 6.44, 63.5, 2))
if(ph add){
  cat("Setting phase addition options...\n")
  # fix-tag: error handling
  # Create data structure
  input_ph_add<-rep(list(rep(list(NULL),x_n)),y_n)</pre>
  ****
  #
    Phase addition from input definitions
  #
  cat("Setting phase additions from definitions in configuration file\n")
  pnts<-unlist(strsplit(names(ph add definitions)," "))</pre>
  for(h in 1:length(ph add definitions)){
   a<-unlist(strsplit(gsub("\\{", "", gsub("\\}", "", pnts[h*2-1])), split=";"))
b<-unlist(strsplit(gsub("\\{", "", gsub("\\}", "", pnts[h*2])), split=";"))</pre>
   if(length(ph add definitions[[h]])==length(c(major elements, "mass"))){
   names(ph add definitions[[h]])<-c(major elements, "mass")}</pre>
   for(x_i in a[1]:b[1]){
     for(y i in a[2]:b[2]){
       if(is.null(input_ph_add[[y_i]][[x_i]])){
          input_ph_add[[y_i]][[x_i]]<-list(ph_add_definitions[[h]])</pre>
       }else{
         input ph add[[y i]][[x i]][length(input ph add[[y i]][[x i]])+1]]<-</pre>
ph add definitions[[h]]
       }
     }
   }
  }
}else{
  cat("No phase addition.\n")
}
cat("Done with phase addition options\n")
cat(".....\n")
```

### Initialise phase extractions (init\_ph\_extr.r)

Creates a two dimensional data structure that will record phase extraction conditions of the form:

input\_ph\_extr[[y\_i]][[x\_i]]

Reads either phase addition definitions defined in the graphical user interface or imported from a file of the form:

ph\_extr\_definitions<list("{x\_a,y\_a}\_{x\_b,y\_b}"=c(condition="expression",Ph\_#1,Ph\_#2,...,Ph\_#x), "{x\_a,y\_a}\_{x\_b,y\_b}"=c(condition="expression",Ph\_#1,Ph\_#2,...,Ph\_#x))

where ph\_# denotes a number of different phases and their proportion of phase proportion statement by which they should be extracted.

```
*****
#
  Initialize phase extraction options
#
****
#handles definitions of the form: ph_extr_definitions<-</pre>
list("{1,1}_{6,1}"=c(condition="melt(HP)>=8wt.%",Pl="20%",ky="3","melt(HP)"="rt(4,w
t.%)"),"{4,1} {9,1}"=c(condition="melt(HP)>=8wt.%",Pl="20%",ky="3","melt(HP)"="rt(4
,wt.%)"))
if(ph extr){
cat("Setting phase extraction options...\n")
 # fix-tag: error handling
  # Create data structure
 input ph extr<-rep(list(rep(list(NULL),x n)),y n)</pre>
 ***
 # Phase extraction from input definitions
  ****
cat("Setting phase extractions from definitions in configuration file\n")
 pnts<-unlist(strsplit(names(ph extr definitions)," "))</pre>
 for(h in 1:length(ph extr definitions)){
   a<-unlist(strsplit(gsub("\\{", "", gsub("\\}", "", pnts[h*2-1])), split=";"))
b<-unlist(strsplit(gsub("\\{", "", gsub("\\}", "", pnts[h*2])), split=";"))</pre>
   for(x i in a[1]:b[1]){
     for(y_i in a[2]:b[2]){
       if(is.null(input ph extr[[y i]][[x i]])){
       input_ph_extr[[y_i]][[x_i]]<-list(ph_extr_definitions[[h]])</pre>
       }else{
       input_ph_extr[[y_i]][[x_i]][[length(input_ph_extr[[y_i]][[x_i]])+1]]<-</pre>
ph extr definitions[[h]]
       }
     }
   }
 }
}else{
cat("No phase extraction.\n")
ł
cat("Done with phase extraction options\n")
cat(".....\n")
```

#### Initialise dependence structure (init\_dependence.r)

Creates a two dimensional data structure that will record dependence relations of the form: dependencies  $[[y_i]][[x_i]]$ 

Searches through points and for each chemical component in "major\_elements" evaluates the expression for dependence

Merges common dependence and determines tiers for hierarchy of dependence

Determines calculation order from tiers

Performs error validation to ensure all dependences have been resolves to a determinable element

```
****
#
#
   Determine the dependence relations between points
******
# Bulk Composition *For now dependence is only on composition
#possible handled variables dependents = rs,fs,es,as
                                                      non-dependents =
c0,x_i,y_i,x_n,y_n
#handles functions of the form"rs{x_i-1,y_i}+5-as{x_n-2,y_i*2}"
#fixtag error handling
dependencies<-rep(list(),x_n)),y_n)</pre>
#for each point
for(y_i in 1:y_n){
for(x i in 1:x n) {
dependence <- NULL
# for each major element
for(maj i in 1:length(major elements)){
#pull out tuples that major element for that point is dependent on
  #fix-tag: look at main.r for bulk comp to allow multiple rs calls in one tuple
n<-
gsub("rs", "", gsub("es", "", gsub("as", "", gsub("fs", "", input_bulk[[y_i]][[x_i]][maj_i]
))))
left_brac<-gregexpr("\\{", n)[[1]]</pre>
right brac<-gregexpr("\\}", n)[[1]]</pre>
tuples<-NULL
for(tup i in 1:length(left brac)){
tuples<-c(tuples, substr(n, left brac[tup i], right brac[tup i]))</pre>
}
if(tuples=="") {dependence="base"}else{
split tuples<-strsplit(gsub("\\{","",gsub("\\}","",tuples)),split=";")</pre>
for(split_i in 1:length(split_tuples)){
dependence<-
c(dependence, paste(eval(parse(text=split tuples[[split i]][1])), eval(parse(text=spl
it_tuples[[split_i]][2])), sep=";"))
ł
}
#Keep common dependence
dependencies[[y i]][[x i]]<-union(dependence, dependence)</pre>
}
}
# Determine tiers
tiers<-rep(list(rep(list(NULL), x n)), y n)</pre>
eval dep<-dependencies
for(y_i in 1:y_n) {
  for(x_i in 1:x_n) {
```

```
tier counter <- 0
while(is.null(tiers[[y_i]][[x_i]])){
if(eval_dep[[y_i]][[x_i]]=="base"){
  tiers[[y_i]][[x_i]]<-1+tier_counter</pre>
}else{
tier counter<-tier counter+1</pre>
#Evaluate dependencies
new_dep<-NULL
for(dep_i in 1:length(eval_dep[[y_i]][[x_i]])){
  dep_pos<-strsplit(eval_dep[[y_i]][[x_i]][dep_i], split=";")[[1]]</pre>
 new dep<-
c(new dep,dependencies[[as.numeric(dep pos[2])]][[as.numeric(dep pos[1])]])
}
#keep common dependence
eval dep[[y i]][[x i]]<-union(new dep,new dep)</pre>
3
}
}
ł
# Determine calculation order
tiers union<-union(unlist(tiers), unlist(tiers))</pre>
calc_order<-rep(list(rep(list(),1)),1)),length(tiers_union))</pre>
group_num<-0
for(i in tiers_union) {
  group_num<-group_num+1
 first_in_group<-TRUE</pre>
for(y_i in 1:y_n){
 for(x_i in 1:x_n) {
if(tiers[[y_i]][[x_i]]==i){
if(first_in_group) {
 calc num<-0
}
calc num<-calc num+1</pre>
first in group<-FALSE
calc_order[[group_num]][[calc_num]]<-list(x_i=x_i,y_i=y_i)</pre>
ł
}
}
}
****
#
  Error validation
#
#
****
for(y_i in 1:y_n){
  for(x i in 1:x n){
   if (is.null(dependencies[[y_i]][[x_i]])) {cat("Error: No dependence defined for
x_i =",x_i," y_i =",y_i," \n"); stop()}
  }
}
if(!length(unlist(calc order))/2==x n*y n){cat("Error: Calculation order could not
be determined\n");stop()}
cat("Done with dependence determination\n")
cat(".....\n")
```

#### Initialise meemum (init\_meem.r)

Creates component transformations from parameters parsed through GUI

Sets components matrix with placeholder composition

Writes dummy Perple\_X "build" file to be read by "meemum"

```
*****
#
#
  Create a meemum build file
****
cat("Creating meemum build file...\n")
# mod-tag: to be worked into Gui
number components <-15
molar_vs_wt<-1</pre>
#new name must be less than 6 characters
#can only build components with total of 11 or less components
#replace components each time
transformations<-NULL
n_comp_trans<-0</pre>
if(exists("comp transformations")){
  if(length(comp transformations)>=1&!all(comp transformations=="")){
n_comp_trans<-length(comp_transformations)</pre>
}
}
if(n comp trans>0){
for(i in 1:length(comp transformations)){
  new comp<-strsplit(names(comp transformations)[i], split=" ")[[1]][2]</pre>
  old_comp<-strsplit(names(comp_transformations)[i], split="_")[[1]][1]</pre>
transformations<-c(transformations, paste(new_comp, paste(rep(" ", 6-
nchar(new_comp)),collapse=""),which(available_components==old_comp)," component
"), sep=""))
}
}
#####################
# Create components matrix
comp mat<-NULL
 for(ox in major elements) {
comp_mat<-c(comp_mat,paste(ox,"</pre>
                                    1 1.00000 0.00000
",if(molar_vs_wt==1){"weight amount"}else{"molar amount"}, "\n", sep=""))
 }
# Write dummy meemum build file
dummy<-paste(
data directory,"/",thermodynamic data file,"
                                                thermodynamic data file
no_print | print generates print output
no plot
           | no plot suppresses plot output
data_directory,"/",solution_models_file,"
                                               solution model file, blank = none
parse meem
data_directory,"/",perplex_option_file," computational option file
5 calculation type: 0 - composition, 1 - Schreinemakers, 3 - Mixed, 4 - gwash,
5 - gridded min, 7 - 1d fract, 8 - gwash 9 - 2d fract, 10 - 7 w/file input
data_directory,"/",perplex_option_file,"
    0 unused place holder, post 06
    0 unused place holder, post 06
```

```
0 unused place holder, post 06
    ",n comp trans," number component transformations\n ",
    number components, " number of components in the data base\n",
    paste(transformations, collapse="\n"), "\n",
    molar vs wt," component amounts, 0 - molar, 1 weight
    0 unused place holder, post 06
    0 unused place holder, post 06
    0 unused place holder, post 05
    5 ifug EoS for saturated phase
    2 gridded minimization dimension (1 or 2)
    0 special dependencies: 0 - P and T independent, 1 - P(T), 2 - T(P)
 0.00000
           0.00000
                        0.0000
                                  0.00000 0.00000
                                                             Geothermal
gradient polynomial coeffs.
begin thermodynamic component list
", paste(comp_mat, collapse=""),
"end thermodynamic component list
begin saturated component list
", paste (unlist (strsplit (saturated components, split=",")), collapse="\n"), "
end saturated component list
begin saturated phase component list
",paste(unlist(strsplit(saturated phase components,split=",")),collapse="\n"),"
end saturated phase component list
begin independent potential/fugacity/activity list
", paste (unlist (strsplit (independent potential fugacity activity, split=",")), collaps
e="\n"),"
end independent potential list
begin excluded phase list
",paste(unlist(strsplit(exclude phases,split=",")),collapse="\n"),"
end excluded phase list
begin solution phase list
",paste(use_sol_models,collapse="\n"),
"\nend solution phase list
0.0000
            0.0000
                       0.0000000 0.0000
                                              0.0000
                                                         max p, t, xco2, u1, u2
0.0000
            0.0000
                       0.0000000 0.0000
                                              0.0000
                                                         min p, t, xco2, u1, u2
0.0000
            0.0000
                       0.0000000 0.0000
                                              0.0000
                                                         unused place holder post
06
2 1 4 5 3 indices of 1st & 2nd independent & sectioning variables
", sep="")
write(dummy,file=paste0(data_directory,"/parse_meem.dat"))
cat("Created meemum build file as
",paste0(data directory, "/parse meem.dat"), "\n", sep="")
cat(".....\n")
```

### Rcrust launcher (main.r)

Initialises packages and functions to be used on runtime

Applies additional settings accessible to advanced users (including functionalities not yet worked into GUI)

Sets data structures

Evaluates dependent values to populate all fields of required parameters

Sets up calculation loop to sequentially call "run.Rcrust" saving outputs in "crust" and reevaluate dependences by tier levels

Saves image of R environment on completion of calculation loop

```
## Rcrust (main.r)
# Function for shortcut
.First<-function() {
first load<<-FALSE
 #Load dependencies
 library(utils)
 if(!require(shiny)){
 install.packages("shiny")}
 library(shiny,quietly=TRUE)
   if(!require(raster)){
 install.packages("raster")}
   if(!require(rgeos)){
 install.packages("rgeos")}
     if(!require(grDevices)){
 install.packages("grDevices")}
 #Launch GUI
 Rcrust<<-function() {</pre>
   #Load dependencies
 library(utils)
 if(!require(shiny)) {
 install.packages("shiny")}
 library(shiny)
   if(!require(raster)){
 install.packages("raster")}
   if(!require(rgeos)){
 install.packages("rgeos")}
     if(!require(grDevices)){
 install.packages("grDevices")}
    #If working directory is x\Projects\y then set to x\code
 if(length(grep("Rcrust/Projects/",getwd()))==1){
 setwd(paste0(strsplit(getwd(), split="Projects")[[1]][1], "code"))
 }
   runApp()
 3
 #Launch without GUI
 manual load <<--
function(working file, projects directory=paste0(substring(getwd(),1,nchar(getwd())-
3), "Projects")) {
source(paste0(projects_directory,"/",working_file,"/Inputs/",working_file,".txt"))
   source("main.r")
 }
 #If working directory is x\Projects\y then set to x\code
 if(length(grep("Rcrust/Projects/",getwd()))==1){
 setwd(paste0(strsplit(getwd(), split="Projects")[[1]][1], "code"))
```

```
first load<<-TRUE
 -F
 runApp()
  Ł
 #Launch without GUI
 manual load <<--
function(working_file,projects_directory=paste0(substring(getwd(),1,nchar(getwd()))
3), "Projects")) {
source(paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"))
   source("main.r")
  }
****
#
# Additional Settings (Advanced users)
****
****
#Errors
run errors<<-NULL
exit calc <<- FALSE
pause on error <<- FALSE
# Calculation settings
request_readline<-FALSE
stop errors<-NULL
#Determine calculation mode #normal,parallel (still to come)
calc_mode<-"normal"</pre>
silent calc<-TRUE
cumulate on rs<-TRUE
# PT settings
pt_def<-"input"</pre>
PT restrictions<-c("Pressure > 0", "Temperature > 0")
#PT restrictions<-
c("Pressure > 2.5", "Pressure < 20", "Temperature > 600", "Temperature < 1100")
#Reaction buffering
reaction buffering<<-FALSE</pre>
reaction buffer steps <<-1
start_in_reaction <<- FALSE
merge duplicates<<-FALSE</pre>
# Sec to clock function
    sec_to_clock<-function(total sec) {</pre>
  hr<-floor(total sec/3600)</pre>
  mn<-floor((total_sec-hr*3600)/60)</pre>
  if(mn<10) {mn 0<-"0"}else{mn 0<-NULL}
  sec<-total_sec-hr*3600-mn*60
  if(sec<10) {sec 0<-"0"}else{sec 0<-NULL}</pre>
  clock<-paste(hr,":",mn 0,mn,":",sec 0,sec,sep="")</pre>
  return(clock)
  ł
****
# Set defaults
#
****
****
if(class(try(reequilibrate steps,silent=TRUE))=="try-error"){
reequilibrate_steps<-TRUE</pre>
}
if(class(try(calc choice, silent=TRUE)) == "try-error") {
calc choice <- "read.meemum"
                          #options = lars.wrap,read.meemum
if(class(try(data_directory,silent=TRUE))=="try-error"){
data directory<-gsub("/code", "/data", getwd())</pre>
****
#
# Initialize datastructures
#
```

```
****
cat("\n")
source("run.Rcrust.r")
                             # The function doing the job
chk valid<-try(
{source("init bulk.r")
                             # Bulk composition
source("init wrapper.r")
                             # Initialise wrapper function
source("meemum connect.r")
                                 # Initialise run and read meemum functions
source("init_meem.r")
                                 # Create meemum build file
source("init_pt.r")
                             # PT conditions
source("init_ph_add.r")
                             #phase addition
source("init_ph_extr.r")
                             #phase extraction
source("init dependence.r")
                                     # Determine dependence relations
}
)
#Input validation
input valid<-TRUE
if(class(chk valid)=="try-error") {
  cat("Initiation failed\n")
  input valid<-FALSE</pre>
  ÷.
if(input valid){
if(request_readline){
cat("Initiation succesful:\n Please read the above lines and make sure this is
what you wanted.\n")
rd<-readline (prompt="Choose \"n\" to abort or press [enter] to continue\n")
}else{
cat("Initiation succesful:\n Computation beginning\n")
rd<-"pass"}</pre>
if(!rd=="n"){
  #Normal calc by tiers
  #get values and pass them to run.Rcrust
  #Create calculation structures
  #variable-def: crust[[y_i]][[x_i]]
  crust<-rep(list(rep(list(NULL), x n)), y n)</pre>
  cumul extract<-rep(list(rep(list(NULL),x n)),y n)</pre>
  cumul add<-rep(list(rep(list(NULL),x n)),y n)</pre>
  calculation_matrix<-matrix(0,y_n,x_n)</pre>
  strt<<-proc.time()</pre>
  # Refresh input values for groups (j) and their members (i)
    for(j in 1:length(calc_order)){
    for(i in 1:length(calc_order[[j]])){
      #get and assign variables for each point in this calc group
    x i<-calc order[[j]][[i]]$x i</pre>
    y_i<-calc_order[[j]][[i]]$y_i</pre>
    #Get c0
      c0<-input_bulk[[y_i]][[x_i]]</pre>
      #replace rs,es,as,fs tuples with values
      for(k in 1:length(c0)){
        c0 k<-c0[k]
        left brac<-gregexpr("\\{", c0_k)[[1]]</pre>
        right_brac<-gregexpr("\\}", c0_k)[[1]]</pre>
        if(left brac[1]>0){
        subsystem<-NULL
        for(kk in 1:length(left_brac)){
          subsystem<-c(subsystem, substr(c0[k], (left brac[kk]-2), left brac[kk]-1))</pre>
        }
        tuples<-NULL
        for(tup i in 1:length(left brac)){
          tuples<-c(tuples,substr(c0_k, left_brac[tup_i], right_brac[tup_i]))</pre>
        1
        split tuples<-strsplit(gsub("\\{", "", gsub("\\}", "", tuples)), split=";")</pre>
        #Grab dependent point if cumulating extracts - caution this only works if
dependent entirely on one point
        if(k==1&ph extr&cumulate on rs){dep pnt<-</pre>
c(eval(parse(text=split tuples[[1]][1])),eval(parse(text=split tuples[[1]][2])))
        crust rows<-rownames(crust[[dep pnt[2]]][[dep pnt[1]]])
```

```
parse cumul extract<-
crust[[dep pnt[2]]][[dep pnt[1]]][crust rows[grep(" es cumul", crust rows)],, drop=FA
LSE]
        if(!length(parse cumul extract)==0) {cumul extract[[y i]][[x i]]<-</pre>
parse_cumul extract}
        }
        #Grab dependent point if cumulating additions - caution this only works if
dependent entirely on one point
        if(k==1&ph_add&cumulate_on_rs){dep_pnt<-</pre>
c(eval(parse(text=split_tuples[[1]][1])),eval(parse(text=split_tuples[[1]][2])))
        crust_rows<-rownames(crust[[dep_pnt[2]]][[dep_pnt[1]]])</pre>
        parse cumul addition <-
crust[[dep pnt[2]]][[dep pnt[1]]][crust rows[grep(" as cumul", crust rows)],, drop=FA
LSE]
        if(!length(parse cumul addition)==0){cumul add[[y i]][[x i]]<-</pre>
parse cumul addition}
        }
        #substitute in value
        c0_k<-gsub("rs", "", gsub("es", "", gsub("as", "", gsub("fs", "", c0_k))))
c0_k<-gsub("\\{", "", gsub("\\}", "", c0_k))</pre>
        for(split i in 1:length(split tuples)){
          outval<-
try(crust[[eval(parse(text=split tuples[[split i]][2]))]][[eval(parse(text=split tu
ples[[split_i]][1]))]][paste0("Bulk_", subsystem[split_i]), names(c0_k)], silent=TRUE)
           if(class(outval) == "try-error") {
           outval<-0
           ł
          if(is.null(outval)){
          c0_k_try<-0}else{
          c0_k_try<-
try(sub(paste0(unlist(split tuples[split i]),collapse=";"),outval,c0 k))
          if(class(c0 k try)!="try-error"){c0 k<-c0 k try}</pre>
        }
        }
         c0[k]<-eval(parse(text=c0 k))</pre>
      }
      # Make numeric
      nam<-names(c0)
      cO<-as.numeric(cO)
      names(c0)<-nam</pre>
       # Save to input bulk
      input_bulk[[y_i]][[x_i]]<-c0</pre>
    ł
      if(calc mode=="normal"){
      #run Rcrust in singular for each point in the calc group
      for(i in 1:length(calc order[[j]])){
        x i<-calc order[[j]][[i]]$x i</pre>
        y<sup>i</sup><-calc_order[[j]][[i]]$y_i
        if(silent calc){
             #Calculate times
             pull_time<-proc.time()-strt</pre>
             total sec<-round(pull time[3])</pre>
             run_time<-sec_to_clock(total_sec)</pre>
          cat("Computing Point", "x i=", x i," ; y i=", y i,"... Simulation
",round(sum(calculation matrix!=0)/(nrow(calculation matrix)*ncol(calculation matri
x))*100,2),"% complete\n")
           cat("Total run time:",run time,"\n")
           flush.console()
        }
        #Check if point should be calculated
        #variable-def: 0=remaining,1=calculated,2=aborted
        PT split<-strsplit(PT restrictions, split=" ")</pre>
        for(i in 1:length(PT restrictions)){
        chk<-
paste(input pt[[y i]][[x i]][,PT split[[i]][1]],PT split[[i]][2],PT split[[i]][3],c
ollapse="")
        if(!eval(parse(text=chk))){calculation_matrix[y_i,x_i]<-2</pre>
```
```
crust[[y i]][[x i]]<-matrix(c0,1,)</pre>
        rownames(crust[[y_i]][[x_i]])<-"Bulk_rs"</pre>
        colnames(crust[[y_i]][[x_i]])<-names(c0)</pre>
        }
        }
        strsplit(PT restrictions, split=" ")
        if(calculation_matrix[y_i,x_i]==0){
        crust[[y_i]][[x_i]]<-run.Rcrust(comps=comps,c0=input_bulk[[y_i]][[x_i]],</pre>
              press=input_pt[[y_i]][[x_i]][1],
              temp=input_pt[[y_i]][[x_i]][2],
              ph_extr_pnt=input_ph_extr[[y_i]][[x_i]],
              cumul_extract[[y_i]][[x_i]],
              ph_add_pnt=input_ph_add[[y_i]][[x_i]],
              cumul_add_pnt=cumul_add[[y_i]][[x_i]]
              )
              calculation_matrix[y_i,x_i]<-1</pre>
              }
              }
        }
        }
    }
#Save data
save.image(file=paste0(projects directory,"/",working file,"/",working file,".RData
"))
cat("\n\nDone with calculations:\nResults saved to
",paste0(projects_directory,"/",working_file,"/",working_file,".RData"),"\n\nSelect
outputs through the Rcrust GUI or press esc to edit data in the Rconsole\n")
flush.console()
}
```

## **Rcrust calculation loop (run.Rcrust.r)**

Loads functions for:

merging of phase lines (summing extensive properties and averaging intensive properties)

evaluating a Boolean condition that handles missing values as false

evaluating expressions parsed with "{}". This allows custom functions to be built and called from phase expressions

Runs until told to exit

Adds phases from the isolated subsystem into the reactive subsystem if applicable

Calculates stable phases of the system given the pressure, temperature and bulk composition of the system by calling a wrapper function that communicates with meemum from Perple\_X

Renames duplicate phases and splits feldspar phases into Pl or Kf based on CaO/K2O ratio

Extracts phases from reactive subsystem into extract subsystem where applicable

Creates extract subsystem and cumulative extract subsystem

Compiles full system to be saved as a point in "crust"

Flushes response to console

```
*****
# Main Rcrust Loop (run.Rcrust.r)
****
#function-def:run.Rcrust<-</pre>
function(comps,c0,press,temp,ph extr pnt,cumul extract pnt=NULL,ph add pnt,cumul ad
d pnt=NULL)
run.Rcrust<-
function(comps,c0,press,temp,ph_extr_pnt,cumul_extract_pnt=NULL,ph_add_pnt,cumul_ad
d pnt=NULL, ...) {
  ****
 # Ancillary function to merge several lines (by mass)
 *****
  .wtd.add<-function(thelines, prop="mass", avname="Averaged") {
   if(nrow(thelines)==1){
     foo<-thelines
   }else{
     # Two sets of cols
     if(exists and true(calc mol)){
      extensive.cn<-c("wt%", "vol%", "mol%", "mol")  # Extensive properties (mass</pre>
dependant) -- add the others if required
     }else{
      extensive.cn<-c("wt%")</pre>
     }
```

intensive.cn<-setdiff(colnames(thelines),c(prop,extensive.cn))

```
foo<-matrix(rep(0, length(colnames(thelines))), nrow=1)</pre>
      colnames(foo)<-colnames(thelines)</pre>
      # Intensive
      foo[,intensive.cn]<-</pre>
thelines[,prop]%*%thelines[,intensive.cn,drop=F]/sum(thelines[,prop])
      # Extensive
      foo[,prop]<-sum(thelines[,prop])</pre>
      if(!length(intersect(extensive.cn,thelines))==0){
        foo[,extensive.cn]<-colSums(thelines[,extensive.cn])}</pre>
    ł
    rownames (foo) <- avname
    return(foo)
  ł
  #exists and true
exists and true<<-function(x) {
chk<-try(x, silent=TRUE)</pre>
if(class(chk) == "try-error") {return(FALSE) }else{
return(x)
}
}
  *****
  #
  # Expression evaluator
  #
  #function-def: eval expr<-function(expr,calc phases=calc phases,crust=crust)</pre>
  #Evaluate expression a given calc_phases and crust
          #() are for solution models, {} are for function terms and bodmas
          #evaluate any { and word before it up until }
          eval expr<-function(expr, calc phases=calc phases, crust=crust) {
          #wrap outside for evaluation
          a<-paste0("{",expr,"}")</pre>
          while(!unlist(gregexpr("[{]",a}))[1]==-1){
          letters<-gregexpr("[a-z]",a)</pre>
          left bracs<-unlist(gregexpr("[{]",a))</pre>
          names(left bracs) <- rep("left", length(left bracs))</pre>
          right_bracs<-unlist(gregexpr("[]]",a))</pre>
          names(right bracs)<-rep("right", length(right bracs))</pre>
          bracs<-sort(c(left bracs, right bracs))</pre>
          #Find inner brackets
          i<-1
          while(!(names(bracs)[i]=="left"&names(bracs)[i+1]=="right")){
          i<-i+1
          ł
          #evaluate inner brackets
          #If require function call find name
          j<-1
          while((bracs[i]-j)%in%letters[[1]]){
          j<-j+1
          #if j==1 dont require function call, else j+1 is first letter of function
name
          if(!j==1){
          funct_name<-substr(a,bracs[i]-j+1,bracs[i]-1)</pre>
          #apply function
          if(funct name=="ph"){
          #arguments of the form ph{phase;unit;x_i;y_i} where unit can be any
column name in calc_phases and x_i and y_i are the current point by default
          ph args<-strsplit(substr(a, bracs[i]+1, bracs[i+1]-1), "[;,]")[[1]]</pre>
          if(length(ph args)==2){
          #current variable
          chk var<-
try(eval(parse(text="calc phases[ph args[1],ph args[2]]")),silent=TRUE)
            if(class(chk var)=="try-error"){
              out<-0
            }else{
              out<-chk_var
            ł
```

```
}else{
            #past variable
            #default look in rs
            if(length(grep(" rs", ph args[1]))==0&length(grep(" es",
ph_args[1]))==0){
            ph args[1]<-paste0(ph args[1], " rs")</pre>
          chk_var<-
try (eval (parse (text="crust[[eval (parse (text=ph args[[4]]))]][[eval (parse (text=ph ar
gs[[3]]))]][ph args[1],ph args[2]]")),silent=TRUE)
            if(class(chk_var) == "try-error") {
              out<-0
            }else{
              out<-chk var
            }
            }
          3
          if(funct name=="delta") {
          skip_delta<-FALSE
          #arguments of the form delta { ph;x #;y #;unit } where unit can be wt% or
mass
          delta_args<-strsplit(substr(a,bracs[i]+1,bracs[i+1]-1),"[;,]")[[1]]</pre>
          delta phs<-delta args[1]</pre>
          if(substring(delta_args[2],1,8)=="prev_ext"){
          find ph<-substring(delta args[2],10)</pre>
          pnt<-"find"
          1<-1
          while(pnt=="find") {
          #find earliest of phase extraction or phase absent point, if neither show
warning and take pnt=1
          #find previous increase in es cumul
          chk_pnt<-try(crust[[y_i]][[x_i-
1]][paste0(find_ph,"_es"),"mass"],silent=TRUE)
          if(class(chk pnt) == "try-error") {
          chk_pnt<-try(crust[[y_i]][[x_i-
l]][paste0(find ph, " rs"), "mass"], silent=TRUE)
          if(class(chk_pnt) == "try-error") {
          pnt<-x i-l
          cat (paste0 ("Delta calculated to previous phase absent point at x i =
", pnt, "\n"))
          }else{
          pnt<-x i-l
          cat(paste0("Delta calculated to previous extract at x i = ",pnt,"\n"))
          ł
          if((x i-1)==1&pnt=="find"){
          pnt<-x i-l
          cat(paste0("Delta calculated to first point at x i = ",pnt,"\n"))
          Ł
          1<-1+1
          }
          delta_index_x<-pnt
          }else{
          delta_index_x<-eval(parse(text=delta_args[2]))}</pre>
          if(!(delta_index_x<=x_n&delta_index_x>=1)){cat("Warning delta_index_x not
<x n and >=1, skipping this delta calculation\n");skip delta<-TRUE}</pre>
          delta_index_y<-eval(parse(text=delta_args[3]))</pre>
          if(!(delta_index_y<=y_n&delta_index_y>=1)){cat("Warning delta_index_y not
<y n and >=1, skipping this delta calculation\n");skip delta<-TRUE}
          delta unit<-delta args[4]</pre>
          if(!(delta unit=="mass"|delta unit=="wt%")){
          cat("Error delta only currently accepted as mass or wt%\n")
          stop() }
          if(!skip delta){
            current mode<-0
            previous mode<-0
            #Check for plus sign (e.g. aluminosilicate given as sill+ky+and)
            delta_phases<-strsplit(delta_args[1],"+",fixed=TRUE)[[1]]</pre>
```

```
for(each ph in delta phases) {
             #current mode
             chk var<-
try(eval(parse(text="calc phases[each ph,delta unit]")),silent=TRUE)
             if(!class(chk var)=="try-error"){
             current mode<-current mode+chk var
             }
             #previous mode
             delta phase rs<-paste(each ph, " rs", sep="")</pre>
             chk var<-
try(eval(parse(text="crust[[delta_index_y]][[delta_index_x]][delta_phase_rs,delta_u
nit]")),silent=TRUE)
             if(!class(chk var)=="try-error"){
             previous mode <- previous mode+chk var
             }
           #delta
           if(current mode>previous mode) {
           out<-current mode-previous mode}else{</pre>
           out<-0
           }else{out<-0}</pre>
           }
           if(funct_name=="retain"){
          #c# If Retention Mode - Calculate mass of retention phases to extract
             #c# Extract till retention amount of retention phases is left
             #arguments of the form retain{amount;unit;ph} where ph can be omitted
to take on the current ph
           retain args<-strsplit(substr(a,bracs[i]+1,bracs[i+1]-1),"[;,]")[[1]]</pre>
           ret<-as.numeric(retain args[1])</pre>
           retention_unit<-retain_args[2]
if(!is.na(retain_args[3])) {ph<-retain_args[3]}</pre>
             bulk no<-which (rownames (calc phases) == "Bulk rs")
             ph no<-which(rownames(calc phases)==ph)</pre>
             if(retention_unit=="mass") {
             system less ret<-calc phases[-c(bulk no,ph no),"mass"]</pre>
               if(calc_phases[ph,"mass"]<=ret){</pre>
               out<-0
               }else{
               out<-calc phases[ph, "mass"]-ret</pre>
               }
             }
             if(retention_unit=="vol%"){
             system less ret<-calc phases[-c(bulk no,ph no),"vol%"]</pre>
             if(calc phases[ph, "vol%"]<=ret){</pre>
             out.<-0
             }else{
             new ret vol<-(ret*(sum(system less ret)))/(100-ret)</pre>
             new_ret_mass<-new_ret_vol*calc_phases[ph,"mass"]/calc_phases[ph,"vol%"]</pre>
             out<-calc phases [ph, "mass"]-new ret mass
               }
             }
                          if(retention unit=="wt%"){
             system_less_ret<-calc_phases[-c(bulk_no,ph_no),"wt%"]</pre>
               if(calc phases[ph, "wt%"]<=ret){</pre>
               out<-0
               }else{
               new_ret_wt<-(ret*(sum(system_less_ret)))/(100-ret)</pre>
               new_ret_mass<-new_ret_wt*calc_phases[ph,"mass"]/calc_phases[ph,"wt%"]</pre>
               out<-calc phases [ph, "mass"] - new ret mass
               }
             }
           }
           if(funct name=="return") {
             #arguments of the form return{phase;amount} where amount can be % or
mass
           return args<-strsplit(substr(a,bracs[i]+1,bracs[i+1]-1),"[;,]")[[1]]</pre>
           #check if phase is in extract cumul subsystem
```

```
chk var<-
try(eval(parse(text=paste0("cumul extract pnt[\"", return args[1]," es cumul\", \"mas
s\"]"))),silent=TRUE)
           if(class(chk var)!="try-error"){
          if(!is.null(chk var)){
          percentage<-FALSE
                   #if percentage tag to calculate
          if(length(grep("%", return_args[2]))!=0){
          percentage<-TRUE
          return args[2]<-gsub("%","",return args[2])</pre>
           ł
           #evaluate for number
            chk num<-try(eval(parse(text=return args[2])), silent=TRUE)</pre>
             if(class(chk num)=="try-error"){
           cat ("Error phase addition could not evaluate isolated function
correctly")
          stop()
            }
           #calculate
          if(percentage) {
           take<-chk_num/100*chk var
           leave<-(100-chk_num)/100*chk_var</pre>
           }else{
           take<-chk num
           leave<-as.numeric(chk var)-chk num</pre>
          if(leave<0) {</pre>
           take<-chk var
           leave<-0}</pre>
           #transfer
           cumul extract pnt[paste0(return args[1]," es cumul"),"mass"]<<-leave</pre>
           #leave calc
          a<-
paste(c(cumul extract pnt[paste0(return args[1]," es cumul"),comps],take),collapse=
",")
          break
           }else{
            cat(paste0("Phase ",return args[1]," not found in extract cumul\n"))
            a<-paste(rep(0, length(comps)+1), collapse=",")</pre>
           break
           out<-""
           ł
           }else{
           cat(paste0("Phase ", return args[1]," not found in extract cumul\n"))
            a<-paste(rep(0, length(comps)+1), collapse=",")</pre>
           break
           out<-""
           Ł
           ł
           #replace inner brackets with function output
           a<-paste(substr(a,1,bracs[i]-</pre>
j),out,substr(a,bracs[i+1]+1,nchar(a)),sep="")
           }else{
           #evaluate inner brackets for bodmas output
          out<-eval(parse(text=substr(a, bracs[i]+1, bracs[i+1]-1)))</pre>
           a<-paste(substr(a,1,bracs[i]-</pre>
j),out,substr(a,bracs[i+1]+1,nchar(a)),sep="")
           }
           ł
          return(a)
           }
calc<-TRUE
pass<-1
extract<-NULL
addition subsystem<-NULL
  while(calc) {
    # Phase addition
    if(ph_add){
```

```
if(pass==1){
      if(!is.null(ph add pnt)){
         # mod-tag:DFM addition (Disequilibrium Fractional Melting calculation)
        if(ph add pnt[[1]][[1]]=="dfm"){
           #Disequilibrium Fractional Melting calculation
          current pnt<-run.Rcrust(comps=comps,c0=c0,</pre>
                                    press=input_pt[[y_i]][[x_i]][1],
                                    temp=input_pt[[y_i]][[x_i]][2],
                                    ph_extr_pnt=NULL,
                                    cumul_extract_pnt=NULL,
                                    ph_add_pnt=NULL
          )
          next pnt<-run.Rcrust(comps=comps,c0=c0,</pre>
                                 press=input_pt[[y_i]][[x_i+1]][1],
                                 temp=input_pt[[y_i]][[x_i+1]][2],
                                 ph extr pnt=NULL,
                                 cumul extract pnt=NULL,
                                 ph add pnt=NULL
          )
          #Pl dfm calculation... X(Pl consum) = (Na(melt 2) X(melt 2) + Na(Kfs 2)
X(Kfs 2) - Na(Ms 1) X(Ms 1))/Na(Pl 2)
          Na_melt_2<-try(next_pnt[paste0(melt.name,"_rs"),"NA20"], silent=TRUE)</pre>
           if(class(Na_melt_2) == "try-error") {Na_melt_2<-0}</pre>
          X_melt_2<-try(next_pnt[paste0(melt.name,"_rs"),"wt%"],silent=TRUE)</pre>
          if(class(X_melt_2) == "try-error") {X_melt_2<-0}</pre>
          Na_Kf_2<-try(next_pnt["Kf_rs", "NA20"], silent=TRUE)
          if(class(Na_Kf_2) == "try-error") {Na_Kf_2<-0}</pre>
          X_Kf_2<-try(next_pnt["Kf_rs","wt%"],silent=TRUE)
          if(class(X_Kf_2)=="try-error"){X_Kf_2<-0}
          Na_Ms_1<-try (current_pnt["Mica(CHA) rs", "NA20"], silent=TRUE)
          if(class(Na Ms 1)=="try-error") {Na Ms 1<-0}</pre>
          X_Ms_1<-try(current_pnt["Mica(CHA)_rs", "wt%"], silent=TRUE)
          if(class(X Ms 1)=="try-error"){X_Ms_1<-0}
          Na Pl 2<-try (next pnt["Pl rs", "NA20"], silent=TRUE)
          if (class (Na Pl 2) == "try-error") {cat ("Error, Plagioclase not found in
second point") }else{
             X_Pl_consm<- (Na_melt_2*X_melt_2+Na_Kf_2*X_Kf_2-Na_Ms_1*X_Ms_1)/Na_Pl_2
             X Pl 1<-try(current pnt["Pl rs", "mass"], silent=TRUE)
             if(class(X Pl 1)=="try-error"){cat("Error, Plagioclase not found in
first point") }else{
               if(X_Pl_consm<X_Pl_1){</pre>
                 #Place unreacted Pl in addition subsystem
                 addition_subsystem<-current_pnt["Pl_rs",,drop=FALSE]
                 addition subsystem["Pl rs", "mass"]<-
addition subsystem["Pl rs", "mass"]-X Pl consm
                 rownames(addition_subsystem) <-"Pl_as"</pre>
                 #recalculate new c0 with only the reactive Pl amount
                 current pnt["Pl rs", "mass"] <-X Pl consm
                 current_pnt["Bulk rs", "mass"]<-0</pre>
                 c0<-.wtd.add(current pnt)[, names(c0)]</pre>
              ł
            }
          }
        }
        else{
        #Standard addition
    grab<-c(major_elements,"mass")</pre>
    grab phases <- NULL
  for(add_def_no in 1:length(ph_add_pnt)) {
   #Evaluate if addition is required
    statement<-ph_add_pnt[[add_def no]]["condition"]</pre>
  #if statement is true
  if(is.na(as.logical(eval_expr(statement,calc_phases,crust)))){cat(paste0("Error
condition for phase addition definition number ",add def no," as ",statement," does
not evaluate to logical output\n"));stop()}
  if(as.logical(eval expr(statement, calc phases, crust))){
        for(add_ph in 2:length(ph_add_pnt[[add_def_no]])){
         #Evaluate expression unless numeric comma seperated vector
```

```
if (any (is.na (suppressWarnings (as.numeric (strsplit (ph add pnt [[add def no]][add ph],
",")[[1]]))))){
        ph add pnt[[add def no]][add ph] <-
eval expr(ph add pnt[[add def no]][add ph], calc phases, crust)
        }
        }
           add_mat<-matrix(c(as.numeric(unlist(strsplit(ph_add_pnt[[add_def_no]][-</pre>
1], ", "))), c0), length (ph add pnt[[add def no]]), byrow=TRUE)
           colnames(add_mat) <-c(major_elements, "mass")</pre>
           # Calculate new c0
           c0[c(major elements, "mass")]<-</pre>
c(.wtd.add(add mat,prop="mass",avname="Bulk rs"))
  }else{
    if (!silent calc) {cat ("\nNo addition at this point for this condition\n") }
  3
  }
        }
          }
      }
      }
  #Calculate phases
comps<<-names(c0[-length(c0)])</pre>
calc_phases<-try(wrapper(comps,c0,press,temp,calc_choice),silent=TRUE)</pre>
if(class(calc_phases) == "try-error") {
cat("Oops, an error occured while calculating phases\n at ",press," kbar and
",temp," C for the bulk composition:\n ",major_elements,"\n",c0,"\n")
run errors<<-c(run errors,y i,x i)</pre>
if(pause_on_error) {
browser()
}else{
exit_calc<<-TRUE
- F
}
calc<-FALSE
    #mod-tag: calculate traces here and then zircon and monazite saturation
    #fix-tag: renaming felspars twice (need to work this into earlier position so
that renamed phases are extractable)
if(!exit calc){
if(!is.na(match("Bulk rs", rownames(calc phases)))){
  #rename kf
  if(length(intersect(major elements,c("CAO", "K2O")))==2){
  split_names<-strsplit(rownames(calc_phases),"_","")</pre>
  first names<-NULL
  for(i in 1:length(split names)){
  first names<-c(first names, split names[[i]][1])</pre>
  - J-
  for(ph in which(first names=="Fsp")) {
    if(calc phases[ph,"K20"]<=0) {calc phases[ph,"K20"]<-0.0001}
    if(calc phases[ph,"CAO"]/calc phases[ph,"K2O"]>1) {
      rownames(calc_phases)[ph]<-"Pl"</pre>
    }else{
    rownames(calc phases)[ph]<-"Kf"</pre>
    }
  }
  }
  #number duplicates
    for(ph in rownames(calc phases)[which(duplicated(rownames(calc phases))]){
        rownames (calc_phases) [which (rownames (calc_phases) == ph) [-1]]<-
paste0(ph," ",1:length(which(rownames(calc phases)==ph)[-1]))
    3
}
}
if(!exit calc){
  #Phase Extraction
if(ph extr){
    #pass 1 extraction
if(!is.null(ph_extr_pnt)){
```

```
if(pass==1){
    grab<-c(major elements, "mass")</pre>
    grab_phases<-NULL
  for(ex def no in 1:length(ph extr pnt)){
   #Evaluate if extraction is required
    statement<-ph extr pnt[[ex def no]]["condition"]</pre>
  #if statement is true
  if(is.na(as.logical(eval_expr(statement,calc_phases,crust)))){cat(paste0("Error
condition for phase extraction definition number ",ex def no," as ",statement,"
does not evaluate to logical output\n"));stop()}
  if(as.logical(eval expr(statement,calc_phases,crust))){
    #must evaluate conditions in order then phases in order, retain phases must be
last, cannot have overlapping extract conditions that target the same phase
    extr_phases<-
names(ph extr pnt[[ex def no]])[2:length(ph extr pnt[[ex def no]])]
    if(any(extr phases=="any phase")){
    #old extr phases<-extr phases</pre>
    while(length(which(extr phases=="any phase"))!=0) {
    rep no<-which (extr_phases=="any_phase") [1]</pre>
    #Remove bulk
    cur phases<-rownames(calc phases)[-nrow(calc phases)]</pre>
    #Remove phases with existing definitions
    existing defs<-NULL
    for(i in 1:length(ph_extr_definitions)){
    existing defs<-union(existing defs, names(ph extr definitions[[i]]))
    cur_phases<-setdiff(cur_phases,existing_defs)</pre>
    x<-as.list(extr phases)</pre>
    x[[rep_no]]<-cur_phases
    extr phases<-unlist(x)</pre>
    extr vals<-unlist(lapply(1:length(extr phases), function(i){</pre>
    gsub("any_phase",extr_phases[i],ph_extr_pnt[[ex_def_no]]["any_phase"])}
    ))
    names(extr vals)<-extr phases</pre>
    ex def<-names(ph extr pnt[[ex def no]])[-1]</pre>
    ex_def<-ex_def[-which(ex_def=="any_phase")]</pre>
    extr_vals[ex_def]<-ph_extr_pnt[[ex_def_no]][ex_def]</pre>
    }else{
    extr vals<-ph extr pnt[[ex def no]][extr phases]</pre>
    for(ph in extr phases) {
    #If extract phase is present
      if(length(which(rownames(calc_phases)==ph))>0){
      #grab phase details
        chk<-try(calc phases[ph,grab,drop=FALSE],silent=TRUE)</pre>
        if(!class(chk) == "try-error") {
           grab phases <- rbind (grab phases, calc phases [ph, grab, drop=FALSE])
        }
        #Evaluate for extraction value unless ending in % sign
        a<-extr_vals[ph]
if(!substring(extr vals[ph],nchar(extr vals[ph]),nchar(extr vals[ph]))=="%"){
        a<-eval_expr(a,calc_phases,crust)</pre>
        ł
        #Evaluate unless extraction value is non numeric
        if(!is.na(suppressWarnings(as.numeric(gsub("%","",a))))){
        #If number then take smallest of number or mass present
        if(regexpr("%",a)[1]==-1){
        class(a) <- "numeric"</pre>
         if(a<calc phases[ph, "mass"]){</pre>
                   grab phases[ph, "mass"]<-as.numeric(a)</pre>
                   calc phases[ph, "mass"]<-calc phases[ph, "mass"]-</pre>
grab_phases[ph,"mass"]
                 }else{
                   calc phases[ph,"mass"]<-0</pre>
        }else{
```

```
#If percentage then take as proportion
        grab phases[ph, "mass"]<-</pre>
round(calc_phases[ph, "mass"]*as.numeric(gsub("%", "", a))/100,6)
        calc phases[ph, "mass"] <- round (calc phases[ph, "mass"], 6) -</pre>
grab_phases[ph,"mass"]
        ł
        }else{
        cat("Error in expression used for extraction\n")
        stop()
        }
     }
    }
  }else{
    if (!silent calc) {cat ("\nNo extraction at this point for this condition\n") }
  }
  }
   #Check for negatives
    if(any(calc_phases[, "mass"]<0)|any(grab_phases[, "mass"]<0)){</pre>
    cat("Error negative mass produced upon extraction\n")
    }
  #h# Create Extract
  if(!sum(grab phases[, "mass"])==0){
    #c# Place extracts into extract and calculate Bulk es
    extr bulk<-.wtd.add(grab phases,prop="mass",avname="Bulk es")</pre>
    rownames(grab_phases) <-paste0(rownames(grab_phases), "_es")</pre>
    extract<-rbind(grab_phases,extr_bulk)</pre>
    #c# Calculate new c0
    c0[c(major_elements, "mass")]<-c(.wtd.add(calc_phases[-</pre>
which(rownames(calc_phases) == "Bulk_rs"), c(major_elements, "mass")]))
    #Recalculate mass dependent properties in calc phases if not re-equilibrating
    if(!reequilibrate steps){
    calc phases[,"mol"][-which(rownames(calc phases)=="Bulk rs")]<-</pre>
calc phases[,"mass"][-
which (rownames (calc phases) == "Bulk rs")]/(calc phases [, "wt%"] [-
which(rownames(calc_phases) == "Bulk_rs")]/calc_phases[, "mol"][-
which (rownames (calc_phases) == "Bulk_rs")])
    calc_phases[, "mol%"][-which(rownames(calc_phases)=="Bulk_rs")]<-</pre>
calc phases[,"mol"][-
which(rownames(calc_phases) == "Bulk_rs")]/sum(calc_phases[, "mol"][-
which(rownames(calc_phases) == "Bulk_rs")])*100
    calc phases[,"wt%"][-which(rownames(calc phases)=="Bulk rs")]<-</pre>
calc phases[,"mass"][-
which(rownames(calc_phases) == "Bulk_rs")]/sum(calc_phases[, "mass"][-
which(rownames(calc phases) == "Bulk rs")])*100
    vols<-calc phases[, "mass"][-</pre>
which (rownames (calc_phases) == "Bulk_rs") ]/calc_phases [, "Density (kg/m3)"] [-
which (rownames (calc_phases) == "Bulk rs")]
    calc phases[, "vol%"][-which(rownames(calc phases)=="Bulk rs")]<-
vols/sum(vols)*100
    calc_phases["Bulk_rs", names(c0)]<-c0</pre>
    #mod-tag: check that changed all mass dependent properties
    }
    ł
  #if(changed c0 comp) then trigger for recalculation
  if(reequilibrate steps){
  if(!all(calc_phases["Bulk_rs", names(c0)]==c0)){
    calc<-TRUE
    }
    }
}
ł
#end extraction
}
  pass<-pass+1
}
 }
#end calculation
```

```
#if successful calc phases
if(!exit calc){
if(!is.na(match("Bulk rs", rownames(calc phases)))){
  #rename kf
  if(length(intersect(major elements,c("CAO", "K2O")))==2){
  for(ph in which(rownames(calc phases) == "Fsp")) {
    if(calc_phases[ph,"K20"]<=0) {calc_phases[ph,"K20"]<-0.0001}</pre>
    if(calc_phases[ph,"CAO"]/calc_phases[ph,"K2O"]>1) {
      rownames(calc_phases)[ph]<-"Pl"
    }else{
    rownames(calc phases)[ph]<-"Kf"</pre>
    ł
  }
  }
  #number duplicates
    for(ph in rownames(calc phases)[which(duplicated(rownames(calc phases)))]){
        rownames(calc phases)[which(rownames(calc phases)==ph)[-1]]<-</pre>
paste0(ph,"_",1:length(which(rownames(calc_phases)==ph)[-1]))
    ł
  #add rs labels
  rownames(calc phases)[-match("Bulk rs", rownames(calc phases))]<-</pre>
paste0(rownames(calc_phases)[-match("Bulk_rs", rownames(calc_phases))],"_rs")
}
#Update combined extracts
combined_extracts<-NULL
#Expand extract
if(!is.null(extract)){
expanded<-matrix(0, nrow(extract), ncol(calc phases))</pre>
rownames (expanded) <- rownames (extract)</pre>
colnames(expanded)<-colnames(calc phases)</pre>
expanded[rownames(extract), colnames(extract)]<-extract</pre>
extract<-expanded
ł
#Calculate new cumul extract pnt
if(is.null(cumul_extract_pnt)){
  new cumul extract<-extract</pre>
}else{
rownames(cumul_extract_pnt)<-gsub("_cumul", "", rownames(cumul extract pnt))</pre>
all extr<-union (rownames (extract), rownames (cumul extract pnt))
new cumul extract<-matrix(0,length(all extr),ncol(calc phases))</pre>
rownames(new_cumul_extract)<-all_extr</pre>
for(nam i in all extr){
  #In extract and cumul - .wtd.add
if (length (which (rownames (extract) == nam i) >>0& length (which (rownames (cumul extract pn
t)==nam i))>0){
    new cumul extract[nam i,]<-</pre>
.wtd.add(rbind(cumul extract pnt[nam i,],extract[nam i,]))
  1
  #In extract- extract
if(length(which(rownames(extract)==nam i))>0&!length(which(rownames(cumul_extract_p
nt)==nam i))>0){
    new_cumul_extract[nam_i,]<-extract[nam_i,]</pre>
  ł
  #In cumul- cumul
if (!length (which (rownames (extract) == nam i) > 0 & length (which (rownames (cumul extract p
nt)==nam i))>0){
    new cumul extract[nam i,]<-cumul extract pnt[nam i,]</pre>
  }
}
#Calculate new Bulk es cumul
colnames(new cumul extract)<-colnames(cumul extract pnt)</pre>
new cumul extract<-rbind(new cumul extract[-</pre>
(which (rownames (new cumul extract) == "Bulk es")),, drop=FALSE],.wtd.add (new cumul ext
ract[-(which(rownames(new_cumul_extract)=="Bulk_es")),,drop=FALSE],,"Bulk_es"))
}
```

```
if(!is.null(new cumul extract)){
rownames (new cumul extract) <- paste0 (rownames (new cumul extract), " cumul")
¥.
combined extracts<-rbind(extract, new cumul extract)</pre>
#Update IS
#Calculate new cumul add pnt
if(is.null(cumul_add_pnt)){
 new cumul add - addition subsystem
}else{
  rownames(cumul add pnt)<-gsub(" cumul", "", rownames(cumul add pnt))</pre>
  all add<-union(rownames(addition subsystem), rownames(cumul add pnt))
  new cumul add<-matrix(0,length(all add),ncol(calc phases))</pre>
  rownames(new_cumul_add)<-all_add</pre>
  for(nam i in all add){
    #In add and cumul - .wtd.add
if(length(which(rownames(addition subsystem)==nam i))>0&length(which(rownames(cumul
add pnt)==nam i))>0){
     new_cumul_add[nam_i,]<-</pre>
.wtd.add(rbind(cumul add pnt[nam i,],addition subsystem[nam i,]))
    }
                                      - addition_subsystem
    #In addition subsystem
if(length(which(rownames(addition_subsystem)==nam_i))>0&!length(which(rownames(cumu)))
1 add pnt)==nam i))>0){
      new_cumul_add[nam_i,]<-addition_subsystem[nam_i,]</pre>
    3
    #In cumul
                           - cumul
if (!length (which (rownames (addition subsystem) == nam i))>0 & length (which (rownames (cumu
l add pnt)==nam i)>>0){
     new cumul add[nam i,]<-cumul add pnt[nam i,]</pre>
    ł
  }
}
if(!is.null(new cumul add)){
  rownames (new cumul add) <- paste0 (rownames (new cumul add), " cumul")
ł
combined add<-rbind(addition subsystem, new cumul add)</pre>
  #Compile Full System
full system<-rbind(calc phases, combined extracts, combined add)</pre>
}else{
# Return Blank Comp
full system<-
matrix(0,2,length(c0)+1,dimnames=list(c("Error","Bulk error"),c("wt%",names(c0))))
ł
  #Output results to console
if(silent calc){
#flush.console()
}else{
cat("-----\n","Input:\n",paste0("x_i = ",x_i,"y_i =
",y_i,"P = ",press," kbar"," ; T = ",temp," C\n"))
print(c0)
cat("-----\n", "Output:\n")
print(full system[,c(major elements, "mass")])
flush.console()
}
return(full system)
}
```

## Wrapper for phase stability calculations (init\_wrapper.r)

Contains functions for calculating the stable phases of a system given its pressure, temperature and bulk composition

Older versions called a compiled form of meemum from Perple\_X to save calculation time however the documented experience of users prefers accessibility to multiple versions of Perple\_X so that a wider choice of solution models and chemical systems is available.

Thus the dominant calculation method is now a direct call to meemum from Perple\_X

Placing this call within a wrapper assists in handling error response and allows outputs to be formatted to be readable by Rcrust

Replaces placeholder composition in parse\_meem.dat with composition of the given point to be calculated (c0)

Calls run.meemum to calculate results and read.meemum to format results

```
****
#
  Wrapper.r containing calls to meemum from Perple X
#
*****
#function-def:wrapper<-function(comps,c0,press,temp,calc choice="read.meemum")</pre>
wrapper<-function(comps,c0,press,temp,calc choice="read.meemum"){</pre>
****
# Wrapper function, gives some exception handling
# So an error in the calc does not necessarily kill all the previous results !
****
if(!(calc_choice=="read.meemum"|calc_choice=="lars.wrap")){
cat ("\nError: ", calc choice, "Is not an appropriate calculation choice
(calc choice)\n")
stop()
}
if(calc_choice=="read.meemum"){
#control comps order
input file<-
readLines (paste0 (gsub ("Projects", "data", projects directory), "/parse meem.dat"))
comp mat<-NULL
 for(ox in major elements) {
comp_mat<-c(comp_mat,paste0(ox,"</pre>
                                   1 ",c0[which(major elements==ox)]," 0.00000
",if(molar vs wt==1) {"weight amount"}else{"molar amount"}, sep=""))
 ł
start write<-grep("begin thermodynamic component list", input file)+1</pre>
end write<-grep ("end thermodynamic component list", input file) -1
input_file[start_write:end_write]<-comp_mat</pre>
write (input file, file =
paste0(gsub("Projects", "data", projects_directory), "/parse_meem.dat"))
# mod-tag: have to bring c0 into global, look for alternative
c0<<-c0
calc out<-read.meemum(run.meemum(comps,c0,press,temp,meemum path))</pre>
}
# mod-tag: Do we still need "lars.wrap"?
if(calc choice=="lars.wrap"){
#mod-tag: check if need to normalise c0 or if perplex does this
#a (Options: P, T, bulk composition in given order)
 a <- .Call("R phaseq", as.numeric(press*1000), as.numeric(temp+273.15),
as.numeric(c0[comps]))
  #'a' is a list, with following components:
```

```
1 - Return value (should be zero in case of successful minimization
#
#
     2 - Amounts of stable phases (wt% or mol, depending on PerpleX options)
     3 - Names of the stable phases
#
     4 - Compositions of stable phases (a[[4]][[i]][j] for phase a[[3]][[i]],
#
         element comps[j] (wt% or mol, depending on PerpleX options) * PerpleX
#
options not editable
     5 - Bulk properties
#
     6 - System properties of stable phases (a[[6]][[i]][j] for phase a[[3]][[i]],
#
system property [j]
#Check for error
error<<-FALSE
chk call<-try(length(a[[3]])==length(a[[4]]),silent=TRUE)</pre>
if(class(chk call)=="try-error"){
error<<-TRUE
}
else{
if(!chk call){
error<<-TRUE
Ł
}
out colnames <<-
c("wt%","vol%",comps,"mass","V(J/bar)","H(J)","Gruneisen T","Ks(bar)","Mu(bar)","V0
(km/s)", "Vp(km/s)", "Vs(km/s)", "Vp/Vs", "Rho(kg/m3)", "Cp(J/K)", "alpha(1/K)", "beta(1/b
ar)","S(J/K)","N(g)","Cp/Cv")
if(!error){
  #compile phases
phases<-NULL
for(ii in 1:length(a[[3]])){
one<-matrix(a[[4]][[ii]],1,length(a[[4]][[ii]]))</pre>
prop_one<-matrix(a[[6]][[ii]],1,length(a[[6]][[ii]]))</pre>
phases<-rbind(phases, cbind(one, prop one))</pre>
ł
colnames(phases)<-
c(comps, "V(J/bar)", "H(J)", "Gruneisen T", "Ks(bar)", "Mu(bar)", "V0(km/s)", "Vp(km/s)", "
Vs(km/s)", "Vp/Vs", "Rho(kg/m3)", "?", "Cp(J/K)", "alpha(1/K)", "beta(1/bar)", "S(J/K)", "?
?", "N(g)", 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, "Cp/Cv")
# Create mass and wt columns
wt<-matrix(a[[2]],length(a[[3]]),1)</pre>
colnames(wt)<-"wt%"
mass<-matrix(a[[2]]/100*c0["mass"],length(a[[3]]),1)</pre>
colnames(mass)<-"mass"</pre>
# Create vol% columns
vol<-(wt/phases[,"Rho(kg/m3)",drop=FALSE])/(100/a[[5]][10])*100
colnames(vol)<-"vol%"</pre>
#Create Bulk
bulk row<-matrix(c(100,100,c0[],a[[5]]),1)
rownames(bulk row) <- "Bulk rs"</pre>
# Compile calc out
calc out<-
cbind(wt,vol,phases[,names(c0[1:length(comps)])],mass,phases[,(length(comps)+1):nco
l(phases)])
rownames(calc_out) <-a[[3]]</pre>
calc out<-rbind(calc out, bulk row)</pre>
calc_out<-calc_out[,out_colnames,drop=FALSE]</pre>
}else{
# Return Blank Comp
colmns<-c("wt%",out_colnames)
calc_out<-matrix(0,2,length(out_colnames))</pre>
rownames(calc out)<-c("Error", "Bulk error")</pre>
colnames(calc_out)<-out colnames</pre>
÷.
}
return (calc out)
}
```

## Meemum connect (meemum\_connect.r)

Compile matrix of phases

Number duplicate phases

Run.meemum calls meemum.exe in the code folder of Rcrust with the current pressure, temperature and bulk composition of the system

Read.meemum formats the outputs from meemum.exe to be readable by Rcrust

Merge data tables of parameters for each phase Create Bulk\_rs \*\*\*\*\* # Run meemum with parameters \*\*\*\* #function-def:run.meemum<-</pre> function(meemum.path="",build.file="",meemum.order="",press=press\*1000,temp=temp+27 3.15, bulk="", components="", pt comp=pt comp) run.meemum<-function(comps=comps,c0=c0,press=press,temp=temp,meemum path=""){ parms<c(paste0(data\_directory,"/parse\_meem"),"n",c(temp+273.15,press\*1000),"0","0") res<system(shQuote(paste0(data\_directory,"/",meemum\_path)),invisible=T,input=parms,inte rn=T) return (res) } # Parse meemum .prn file \*\*\*\* read.meemum<-function(meemum in=meemum in){</pre> #Grab data matrix after line given line text data matrix from line<-function(line text) {</pre> ln given<-grep(line text, meemum in)</pre> nm phases<-which (nchar (meemum in [-(1:ln given)])==0) [1]-2</pre> text\_given<-meemum\_in[(ln\_given+1):(ln\_given+nm\_phases+1)]</pre> text altered<-trimws(text given)</pre> text\_altered<-gsub(" %", "%", text\_altered)</pre> # mod-tag: remove system - fluid for now, may be useful in future to have access to this data text\_altered<-gsub("System - fluid", "System-fluid", text\_altered)</pre> text altered <- qsub ("Poisson ratio", "Poisson ratio", text altered) text altered<-strsplit(text altered, split="\\s{1,}")</pre> col\_names<-c("Phase",text\_altered[[1]])</pre> mat\_out<-matrix(unlist(text\_altered)[-c(1:(length(col\_names)-</pre> 1))],nm phases,byrow=TRUE) colnames (mat out) <- col names</pre> #number duplicates for(ph in mat out[which(duplicated(mat out[,1])),1]){ mat out[which(mat out[,1]==ph)[-1],1]<-</pre> paste0(ph,"\_",1:length(which(mat\_out[,1]==ph)[-1])) } return (mat out) } #merge data tables by common first field with rows in same order merge matrix<-function(a,b) {</pre> full\_rows<-union(a[,1],b[,1])</pre> #add extra row of NA to any table that needs it max row<-max(nrow(a), nrow(b))</pre> if(nrow(a)<max row){</pre> a<-rbind(a, matrix(NA, max row-nrow(a), ncol(a)))</pre> ł

```
if(nrow(b)<max row){</pre>
b<-rbind(b, matrix(NA, max row-nrow(b), ncol(b)))</pre>
÷.
#rename first row
a[,1]<-full rows
#delete key row in second table
b<-b[,-1]
#merge
return(cbind(a,b))
÷.
#grab crust output by merging tables
#reorder major elements
ph comp mat<-data matrix from line ("Phase Compositions")
ph comp mat<-
ph comp mat[,c(setdiff(colnames(ph comp mat),major elements),major elements),drop=F
ALSE1
#merge info
merge 1<-merge matrix (ph comp mat, data matrix from line ("Molar Properties and
Density"))
merge 2<-merge matrix (merge 1, data matrix from line ("Seismic Properties"))</pre>
#make numeric and set phase column as row names
meemum_out<-merge_2[,-1]</pre>
meemum out<-matrix (as.numeric (meemum out), nrow (meemum out))</pre>
rownames(meemum_out)<-merge_2[,1]</pre>
colnames(meemum out)<-colnames(merge 2)[-1]</pre>
# mod-tag: remove system - fluid properties for now, may be useful in future to
have access to this data
chk call<-try(meemum out["System-fluid",], silent=TRUE)</pre>
if(class(chk call)!="try-error"){
meemum out<-meemum out[-grep("System-fluid", rownames(meemum out)),]</pre>
ł
#merge phases with the same name
if(merge duplicates){
rownames(meemum out) <- qsub(" [0-9]", "", rownames(meemum out))</pre>
while(any(duplicated(rownames(meemum out)))){
ph<-rownames (meemum out) [which (duplicated (rownames (meemum out))) [1]]
thelines<-meemum_out[which(rownames(meemum_out)==ph),]</pre>
prop<-"wt%"
new<-.wtd.add(thelines,prop,ph)</pre>
meemum out<-rbind(new,meemum out[-which(rownames(meemum out)==ph),])</pre>
- F
}
#Create Bulk rs with system
new names<-rownames(meemum out)</pre>
new_names[which(new names=="System")]<-"Bulk rs"</pre>
rownames (meemum_out) <-new_names</pre>
meemum_out["Bulk_rs", comps]<-c0[comps]</pre>
#Set % to 100 for Bulk rs
chk call<-try(meemum out["Bulk rs", "vol%"], silent=TRUE)
if(class(chk call)!="try-error"){
meemum_out["Bulk_rs", "wt%"]<-100</pre>
ł
chk call<-try (meemum out ["Bulk rs", "vol%"], silent=TRUE)
if(class(chk_call)!="try-error"){
meemum_out["Bulk_rs", "vol%"]<-100</pre>
}
chk_call<-try(meemum_out["Bulk_rs", "vol%"], silent=TRUE)</pre>
if(class(chk_call)!="try-error"){
meemum_out["Bulk_rs","mol%"]<-100</pre>
- F
mass<-matrix(meemum out[,"wt%"]/100*c0["mass"],nrow(meemum out),1)</pre>
colnames(mass)<-"mass"</pre>
meemum out<-cbind(mass,meemum out)</pre>
return (meemum out)
}
```

## Server (server.r)

Define functions for manipulating data in Rcrust Define functions to be used for formatting and plotting outputs Set reactive values and build reactive stores for GUI Define save function to write GUI inputs into text file

Define load function which reads text file input to populate GUI inputs

Define clear function to reset GUI inputs

Define console function to give access to the direct environment

Define run function to source Rcrust calculation loop with saved input variables

Dynamically create GUI inputs based on current selections

Dynamically create view outputs and filter data relative to the intended output

```
## Rcrust (server.r)
##
# Functions
##
#function-def:
get val(y i,x i,phase,variable,crust=crust,oxy num=24,site ocup="biotite",select=1)
get val<-
function(y i,x i,phase,variable,crust=crust,oxy num=24,site ocup="biotite",select=1
) {
if(variable=="Temperature"|variable=="Pressure"){
chk<-
try(input pt[[y i]][[x i]][which(colnames(input pt[[1]][[1]])==variable)],silent=TR
UE)
if(class(chk) == "try-error") {val<-0}else{</pre>
val<-input_pt[[y_i]][[x_i]][which(colnames(input_pt[[1])[[1]))==variable)]}</pre>
return (val)
}
if(variable=="Min formula"){
return (Min_formula(y_i,x_i,phase,oxy_num,site_ocup,crust=crust)[as.numeric(select)]
)}
chk<-try(crust[[y_i]][[x_i]][phase,variable],silent=TRUE)
if(class(chk) == "try-error") {val<-0}else{</pre>
if(class(chk) == "NULL") {val<-NA}else{</pre>
val<-crust[[y_i]][[x_i]][phase,variable]</pre>
}}
return(val)
3
#function-def:sub brackets(x)
#substitute brackets for obrac and cbrac
sub brackets<-function(x) {</pre>
return(gsub("\\("," obrac ",gsub("\\)"," cbrac ",x)))
}
#function-def:ret brackets(x)
#return brackets from place holders obrac and cbrac
ret brackets<-function(x) {</pre>
return(gsub(" obrac ", "\\(", gsub(" cbrac ", "\\)", x)))
}
#function-def:.wtd.add(thelines,prop="mass",avname="Averaged")
```

```
.wtd.add<<-function(thelines,prop="mass",avname="Averaged") {
    if(nrow(thelines)==1){
      foo<-thelines
    }else{
     #fix-tag: is N(g) extensive or intensive
      extensive.cn<-c("wt%", "vol%", "mol%", "mol", "mass")</pre>
      extensive.cn<-intersect(extensive.cn, colnames(thelines))</pre>
      intensive.cn<-setdiff(colnames(thelines),c(prop,extensive.cn,"Phase"))</pre>
      foo<-matrix(rep(0, length(colnames(thelines))), nrow=1)</pre>
      colnames(foo)<-colnames(thelines)</pre>
      suppressWarnings(class(thelines) <- "numeric")</pre>
      # Intensive
      foo[,intensive.cn]<-</pre>
thelines[,prop]%*%thelines[,intensive.cn,drop=F]/sum(thelines[,prop])
      # Extensive
      for(i in extensive.cn) {
      foo[1,i]<-sum(thelines[,i])</pre>
      }
    ł
    rownames(foo)<-avname</pre>
    return(foo)
  ł
#function-def:check tuple(tuple)
check_tuple<-function(tuple="") {</pre>
  if(Tuple=="") {return(list("Valid tuple", ""))}
  split tuple<-unlist(strsplit(gsub("\\{", "", gsub("\\}", "", tuple)), split=", |;"))</pre>
  if(!length(split_tuple)==2) {return(list("Error: Tuple is invalid", NULL))}
  for(k in 1:length(split tuple)) {
    if(is.na(suppressWarnings(as.numeric(split tuple[k])))){return(list("Error:
Tuple argument is non-numeric", NULL))}
    if(as.numeric(split tuple[k])<1) {return(list("Error: Tuple argument is less
than 1", NULL)) }
    if (!as.numeric (split tuple [k]) %%1==0) { return (list ("Error: Tuple argument is not
a whole number", NULL))}
  }
  return(list("Valid tuple",paste0("{",paste(split tuple,collapse=";"),"}")))
}
#function-def:flip_y(mat)
#matrix reflection in y direction
flip y<-function(mat){</pre>
mat out<-mat[nrow(mat):1,,drop=FALSE]</pre>
return (mat out)
   }
#function-def:flip_x(mat)
#matrix reflection in x direction
flip x<-function(mat){</pre>
mat out<-mat[,ncol(mat):1,drop=FALSE]</pre>
return (mat out)
    }
#function-def:rotate(x)
#Matrix rotation
rotate<-function(x)t(apply(x, 2, rev))</pre>
substrRight <- function(x, n) {</pre>
  substr(x, nchar(x)-n+1, nchar(x))
}
#function-
def:phase_abundance(crust,axis,path=1,p_a=1,p_b=p_a,path_label="Point",input_pt=NUL
T.)
phase abundance <-
function(crust,axis,path=1,p a=1,p b=p a,path label="Point",input pt=NULL){
  #Header
  outname<-switch(axis,</pre>
         x=paste0("Phase adundance vs ",path label," for {",p a,";",path,"} to
{",p_b,";",path,"}"),
          y=paste0("Phase adundance vs ",path label," for {",path,";",p a,"} to
{",path,";",p b,"}")
  )
  #Abundance rows
```

```
switch(axis,
           x={pnt_y<-"path";pnt_x<-"p_i"},</pre>
           y={pnt y<-"p i";pnt x<-"path"}</pre>
           )
    all phases<-NULL
    for(p i in p a:p b){
      all_phases <-
union(all phases, rownames(crust[[eval(parse(text=pnt y))]][[eval(parse(text=pnt x))
11))
    ł
    #reorder into rs,es,es cumul,as
    rs phases<-all phases[grep1(".* rs",all phases)]</pre>
    rs bulk<-grep("Bulk rs", rs phases)</pre>
    es_phases<-all_phases[grepl(".*_es",all_phases)]</pre>
    es_cumul<-grep(".*_es_cumul",es_phases)
as_phases<-all_phases[grep1(".*_as",all_phases)]</pre>
    all phases <- c (rs phases [-rs bulk], rs phases [rs bulk], es phases [-
es cumul], es phases[es cumul], as phases)
    abundance_rows<-NULL
    for(ph in all phases) {
      abundace phase <- NULL
      for(p_i in p_a:p_b){
        chk phase <-
try(crust[[eval(parse(text=pnt_y))]][[eval(parse(text=pnt_x))]][ph,"mass"],silent=T
RUE)
        if(class(chk_phase) == "try-error") {
           abundace_phase<-c(abundace_phase,0)
        }else{
           abundace phase <-
c(abundace phase,crust[[eval(parse(text=pnt y))]][[eval(parse(text=pnt x))]][ph,"ma
ss"])
      }
      abundance rows<-rbind (abundance rows, matrix (abundace phase, 1))
    }
    rownames(abundance rows)<-all phases</pre>
    col_nms<-p_a:p_b</pre>
    if(!path label=="Point") {
    if(path label=="Pressure(kbar)"|path label=="Temperature(C)"){
    switch(path label,"Pressure(kbar)"=slct<-1,"Temperature(C)"=slct<-2)</pre>
    if(!is.null(input pt)){
      col nms<-NULL
      for(p_i in p_a:p_b) {
        col nms<-
c(col nms,input pt[[eval(parse(text=pnt y))]][[eval(parse(text=pnt x))]][slct])
      }
    }
    ł
    colnames(abundance rows)<-col nms</pre>
  return(list(outname, abundance_rows))
}
#function-
def:write phase abundance(data,working file=working file,projects directory=project
s directory,file type)
write phase abundance <-
function(data,working_file=working_file,projects_directory=projects_directory,file_
type){
  outfile path<-
paste0 (projects directory,"/",working file,"/Outputs/",working file,"
", data[[1]], file type)
  if(file type==".txt") {
    write.table(data[[2]],outfile path,sep="\t",quote=F,row.names = TRUE)
  }
  if(file_type==".csv"){
    write test<-try(write.csv(data[[2]],outfile path,row.names = TRUE),silent=TRUE)</pre>
    if(class(write_test) == "try-error") {
```

```
cat ("Error cannot write to ",outfile path,", please close all programs that
may be accessing the file then try again\n")
      return (paste0 ("Error could not save phase abundance file: ",outfile path,",
file may be open in another program, please
      close all programs that may be accessing the file then try againn")
    }
  }
  cat("File written to ",data[[1]],"\n")
return (paste0 ("Phase abundance file saved to
",projects directory,"/",working file,"/Outputs/\n"))
÷.
#function-def:get PAM names(crust, PAM system)
get PAM names<-function(crust, PAM system) {</pre>
y_n<-length (crust)</pre>
x n<-length(crust[[1]])</pre>
#Group phases
PAM<-matrix(0, y n, x n)</pre>
for(x i in 1:x n){
for(y_i in 1:y_n){
#Grab phases from system under consideration
if(PAM system=="Reactive Subsystem"){
grab<-
rownames(crust[[y i]][[x i]])[which(substrRight(rownames(crust[[y i]][[x i]]),3)=="
rs")]
}
if(PAM_system=="Extract Subsystem"){
grab<-
rownames(crust[[y i]][[x i]])[which(substrRight(rownames(crust[[y i]][[x i]]),3)=="
 es")]
ł
if(PAM system=="Full System") {
grab<-rownames(crust[[y i]][[x i]])</pre>
ł
if(length(grab)>0){
#Remove bulk arguments
grab<-grab[-which(grab=="Bulk rs"|grab=="Bulk es"|grab=="Bulk es cumul")]
if(!PAM_system=="Full System"){
#remove identifiers
for(i in 1:length(grab)){
grab[i]<-substr(grab[i], 1, nchar(grab[i]) -3)</pre>
}
}
        #Reorder alphabetically
        grab<-sort(grab)</pre>
}
        collapsed<-paste(grab,collapse="+")</pre>
        if(collapsed=="") {collapsed<-"No Phases"}</pre>
        PAM[y i,x i]<-collapsed
}
}
PAM_names<-setdiff(intersect(PAM, PAM), "0")</pre>
return(list(PAM_names,PAM))
}
#function-def:PAM calc(crust,PAM system,compile PAM=FALSE,PAM compilation=NULL)
PAM calc<-function(crust, PAM system, compile PAM=FALSE, PAM compilation=NULL) {
PAM data<-get PAM_names(crust, PAM_system)</pre>
PAM<-PAM_data[[2]]</pre>
if(compile PAM){
validate (need (file.exists (paste0 (sub ("/code", "/Projects", getwd ()), "/Compile/", PAM c
ompilation, " compilation legend.txt"), paste0 (PAM compilation, " compilation
legend.txt not found in ",sub("/code","/Projects",getwd()),"/Compile/","\nPlease
compile legend first")))
compilation names<-
read.table(paste0(sub("/code", "/Projects", getwd()), "/Compile/", PAM compilation,"
compilation legend.txt"))
class(compilation names) <- "vector"</pre>
PAM_names<-as.character(compilation_names[[2]])}else{</pre>
PAM_names<-PAM_data[[1]]</pre>
```

```
}
# Shade by number of phases (variance)
        no_phs<-NULL
for(i in 1:length(PAM names)){
        no phs<-c(no phs,length(strsplit(PAM names,split="+",fixed=TRUE)[[i]]))
    }
PAM_names<-PAM_names[rev(order(no_phs,PAM_names))]</pre>
#Populate grid
    for(y_i in 1:length(crust)){
            for(x i in 1:length(crust[[1]])){
            if(!PAM[y_i,x_i]==0){
            PAM[y_i,x_i]<-which(PAM_names==PAM[y_i,x_i])</pre>
}
}
}
mode(PAM) <- "numeric"</pre>
# Pull common phases from legend
nam<-strsplit(PAM names, split="+", fixed=TRUE)</pre>
inter<-nam[[1]]</pre>
if(length(PAM names)>1){
for(i in 1:length(PAM names)){
inter<-intersect(inter,nam[[i]])</pre>
}
}
all_pres<-paste(inter,collapse="+")</pre>
internam<-list()</pre>
for(i in 1:length(PAM_names)){
internam[[i]]<-setdiff(nam[[i]],inter)</pre>
}
new nam<-list()</pre>
for(i in 1:length(PAM names)){
if(length(internam[[i]])>0){
new nam[i]<-paste(internam[[i]], collapse="+")</pre>
}else{
new_nam[i]<-"-"
}
}
PAM names<-unlist(new nam)
PAM legend<-1:length(PAM names)</pre>
names(PAM legend) <- PAM names</pre>
#if compiling save individual legend (phases relevant to this specific section)
compile PAM legend <- NULL
if(compile PAM){
compile PAM legend <- PAM legend
PAM legend<-PAM legend[sort((setdiff(intersect(PAM, PAM), "0")))]</pre>
}
    #Flip y-axis for matrix drawing
    PAM<-flip y(PAM)
    library (raster)
    library(rgeos)
    x<-raster::raster(PAM)
    pol <- raster::rasterToPolygons(x,dissolve=TRUE)</pre>
    #create label ids
    pol_ex<-extract(x,pol)</pre>
    pol id<-NULL
    for(i in 1:length(pol ex)){
    pol_id<-c(pol_id,pol_ex[[i]][1])</pre>
    ł
return(list(PAM, PAM_legend, all_pres, pol, pol_id, compile_PAM_legend))
÷.
#function-
def:data file(crust, x n=length(crust[[1]]), y n=length(crust), choose columns=NULL, ch
oose rows=NULL, choose points="All")
data file<-
function(crust,x_n=length(crust[[1]]),y_n=length(crust),choose_columns=NULL,choose_
rows=NULL, choose points="All") {
  *****
  #Outputs select_data list
```

```
#Settings for outputing data file
  # choose columns
                       options =
                                    from crust
("wt%", comps, "mass", "V(J/bar)", "H(J)", "Gruneisen T", "Ks(bar)", "Mu(bar)", "V0(km/s)",
"Vp(km/s)", "Vs(km/s)", "Vp/Vs", "Rho(kg/m3)", "Cp(J/K)", "alpha(1/K)", "beta(1/bar)", "S(
J/K)", "N(q)", "Cp/Cv")
  #
                                     from other
("Phase", "y_i", "x_i", "Pressure(kbar)", "Temperature(C)")
  #
                                     Brief
  #
                                      A11
  #
                        default = All
  #choose columns<-c("All")</pre>
  #choose columns<-c("Brief")</pre>
                       default = All
  #choose rows
                       options = Reactive subsystem
  #choose rows
  #
                                   Extract subsystem
                                   Addition subsystem
  #
  #choose_rows<-c("All")</pre>
  #choose rows<-c("Bio(TCC) rs", "Bulk rs")</pre>
  #choose points
                              default = All
  *****
  #fix-tag: number duplicate names (feldspar, mica)
validate(need(!choose_points=="","To select points enter arguments seperated by
commas of the form \{x_a; y_a\} for single points or \{x_a; y_a\}: \{x_b; y_b\} for ranges
where a<=b<=n"))
  if(choose points=="All"){choose points<-paste("{1;1}:{",x n,";",y n,"}",sep="")}</pre>
  choose points<-unlist(strsplit(choose points, split=","))</pre>
  choose points <-
unlist(strsplit(gsub("\\{","",gsub("\\}",",choose points)),split=","))
  choose points<-strsplit(choose points, split=":|;")</pre>
  data out<-NULL
  for(i in 1:length(choose points)){
  x a<-as.numeric(choose points[[i]][1])</pre>
  y_a<-as.numeric(choose_points[[i]][2])</pre>
  if(length(choose_points[[i]])>2){
  x b<-as.numeric(choose points[[i]][3])</pre>
  y_b<-as.numeric(choose_points[[i]][4])</pre>
  }else{
  x b<-as.numeric(choose points[[i]][1])</pre>
  y b<-as.numeric(choose points[[i]][2])</pre>
  3
  #error validation on selection (range must be possible i.e. b>=a,b<=n)</pre>
  validate(need(all(x_a<=x_b,y_a<=y_b,x_b<=x_n,y_b<=y_n),"To select points enter</pre>
arguments seperated by commas of the form \{x_a; y_a\} for single points or \{x_a; y_a\}: \{x_b; y_b\} for ranges where a \le b \le n")
  for(y_i in y_a:y_b){
    for(x i in x a:x b){
    #fix-tag: create validation here for erronous pixels
    #error validation for point existence
    if(is.null(crust[[y i]][[x i]])){
    #fix-tag: only works if point 1;1 is populated - dont know how many columns
otherwise
    new pnt<-matrix(NA,1,(ncol(crust[[1]][[1]])+6))</pre>
    new_pnt[1,1]<-paste("Blank",y_i,x_i,sep="_")</pre>
    }else{
      ID<-matrix(paste(rownames(crust[[y_i]][[x_i]]),y_i,x_i,sep="_"),ncol=1)</pre>
      colnames(ID)<-"ID"</pre>
      phase<-matrix(rownames(crust[[y i]][[x i]]),ncol=1)</pre>
      colnames(phase)<-"Phase"</pre>
      pnt<-matrix(c(y_i,x_i),nrow=nrow(crust[[y_i]][[x_i]]),ncol=2,byrow=TRUE)</pre>
      colnames(pnt)<-c("y_i","x_i")
if(exists("input_pt")){</pre>
      p t<-
matrix(input_pt[[y_i]][[x_i]], nrow=nrow(crust[[y_i]][[x_i]]), ncol=2, byrow=TRUE)
      }else{
```

```
p t<-matrix(0, nrow=nrow(crust[[y i]][[x i]]), ncol=2, byrow=TRUE)</pre>
      ł
      colnames(p_t)<-c("Pressure(kbar)", "Temperature(C)")</pre>
      new pnt<-cbind(ID,phase,pnt,p t,signif(crust[[y i]][[x i]],4))</pre>
      rownames(new pnt)<-ID</pre>
      }
      data_out<-rbind(data_out,new_pnt)</pre>
    }
    }
  }
   if(is.null(choose columns)){
    choose columns<-colnames(data out)
  }
  if(any(choose columns=="Brief")){
    choose columns<-union(choose columns[-
which (choose columns=="Brief")], c ("ID", "Phase", "y i", "x i", "Pressure (kbar)", "Temper
ature(C)", "wt%", comps, "mass"))
  }
    if(is.null(choose_rows)){
      select rows<-1:nrow(data out)</pre>
    }else{
    if(choose rows=="All"){
    select rows<-1:nrow(data out)}else{</pre>
      select_rows<-NULL</pre>
      if(!is.na(match("Reactive subsystem", choose rows))){
      rs rows<-grep("_rs", rownames(data_out))</pre>
      choose_rows(-choose_rows[-match("Reactive subsystem", choose_rows)]
      select rows<-union(select rows,rs rows)</pre>
      ł
      if(!is.na(match("Extract subsystem", choose rows))){
        rs rows<-grep(" es", rownames(data out))</pre>
        choose rows<-choose rows[-match("Extract subsystem", choose rows)]</pre>
        select rows<-union(select rows, rs rows)</pre>
      }
      for(row arg in choose rows) {
      chk names<-NULL
      for(i in 1:length(rownames(data_out))){
      chk_names<-c(chk_names,paste(strsplit(rownames(data_out),"_")[[i]][c(-3,-
4)],collapse=" "))
      }
        select_rows<-union(select_rows, which(chk_names==row_arg))</pre>
      }
      }
    ł
    data out<-data out[sort(select rows), choose columns, drop=FALSE]</pre>
    rownames(data_out) <-NULL</pre>
  return (data out)
}
#function-
def:write data file(data out,working file=working file,projects directory=projects
directory, file type=".csv")
write_data_file<-
function (data out, working file=working file, projects directory=projects directory, f
ile_type=".csv") {
  #file_type
                         options = ".csv", ".txt"
   #
                         default = ".csv"
outfile_path<-
paste0 (projects_directory, "/", working_file, "/Outputs/", working file, " data file", fi
le type)
  if(length(data out)>0){
  if(file type==".txt"){
    write.table(data out,outfile path,sep="\t",quote=F,row.names = FALSE)
    cat("File written to ",outfile path,"\n")
  }
  if(file type==".csv"){
    write test<-try( write.csv(data out,outfile path,row.names =</pre>
FALSE), silent=TRUE)
    if(class(write_test) == "try-error") {
```

```
cat ("Error cannot write to ",outfile path,", please close all programs that
may be accessing the file then try again\n")
      return (paste0 ("Error could not save Data File: file may be open in another
program, please close all programs that may be accessing the file then try
again\n"))
    }
    cat("File written to ",outfile path,"\n")
  ł
  if(file type==".ps"){
  cat("Error cannot write Data File to .ps format\n")
  return(paste0("Error cannot write Data File to .ps format\n"))
  }
  ł
  return(paste0("Data File saved to
",paste0(projects_directory,"/",working_file,"/Outputs/"),"\n"))
}
#function-
def:grid data(Grid variable,Grid variable phase="Bulk rs",crust in=crust out(),inpu
t_pt_in=input_pt,oxy_num=24,site_ocup="biotite",select=1)
grid data <-
function(Grid variable,Grid variable phase="Bulk rs",crust in=crust out(),input pt
in=input_pt,oxy_num=24,site_ocup="biotite",select=1) {
                 x n<-length(crust in[[1]])</pre>
                 y_n<-length(crust_in)</pre>
                 if(!is.null(Grid_variable)){
                 grid_out_mat<-matrix(0,y_n,x_n)</pre>
                  for(x_i in 1:x_n){
                  for(y_i in 1:y_n){
                  grid out mat[y i,x i] <-
get_val(y_i,x_i,Grid_variable_phase,Grid_variable,crust_in,oxy_num,site_ocup,select
                  }
                 ł
                 #Flip matrix so origin is bottom left (psuedosection convention)
                grid out mat<-flip y(grid out mat)
if(Grid_variable=="y_i"|Grid_variable=="x_i"|Grid_variable=="Temperature"|Grid_vari
able=="Pressure") {
                 grid out title<-Grid variable
                 }else{
                 grid out title<-paste(Grid variable phase,Grid variable)</pre>
                 suppressWarnings(mode(grid out mat)<-"numeric")</pre>
                 return(list(grid out title,grid out mat))
ł
#function-def:.First()
# Function for shortcut
.First<-function() {
  library(utils)
    if(!require(shiny)){
  install.packages("shiny")}
  library(shiny)
  #Launch with GUI function
  Rcrust<<-function() {</pre>
   #If working directory is x\Projects\y then set to x\code
    if(length(grep("Rcrust/Projects/",getwd()))==1){
    setwd(paste0(strsplit(getwd(), split="Projects")[[1]][1], "code"))
    -F
    runApp()
  ł
  #function-
def:manual load(working file, projects directory=paste0(substring(getwd(),1,nchar(ge
twd())-4), "Projects"))
  #Launch without GUI function
  manual load<<-</pre>
function(working_file,projects_directory=paste0(substring(getwd(),1,nchar(getwd())-
4), "Projects")) {
```

```
source (paste0 (projects directory, "/", working file, "/Inputs/", working file, ".txt"))
    source("main.r")
  }
  #launch the GUI
  #If working directory is x\Projects\y then set to x\code
  if(length(grep("Rcrust/Projects/",getwd()))==1){
  setwd(paste0(strsplit(getwd(), split="Projects")[[1]][1], "code"))
  ł
  runApp()
  ÷.
  #function-def:Rcrust()
  #Launch with GUI function
  Rcrust<<-function() {</pre>
   #If working directory is x\Projects\y then set to x\code
    if(length(grep("Rcrust/Projects/",getwd()))==1){
    setwd(paste0(strsplit(getwd(), split="Projects")[[1]][1], "code"))
    }
    runApp()
  }
  #Launch without GUI function
  manual load <<--
function(working file,projects directory=paste0(substring(getwd(),1,nchar(getwd())-
4), "Projects")) {
source(paste0(projects_directory,"/",working_file,"/Inputs/",working_file,".txt"))
    source("main.r")
  }
#function-def:error handling(working file, projects directory)
#error handling on button press
error handling<-function(working file, projects directory) {</pre>
  if (projects directory=="") {return ("Error: no projects directory specified") }
  if (!dir.exists (projects directory)) {return ("Error: projects directory does not
exist")}
  if(working_file=="") {return("Error: no working file specified")}
  return("error handling passed")}
#function-def:bl(x)
#blank function : returns a value or quotes "" if blank
bl<-function(x) {</pre>
  if(is.null(x)){return("\"\")}else
  {if(x=="") {return("\"\"") }else{
    return(x)
  }}
#function-def:bl(str to phases)
#string to phases function : takes a string e.g. "melt(HP),Pl,q" and returns a
vector of the phases e.g. "melt(HP)", "Pl", "q"
str to phases<-function(x) {</pre>
    list<-strsplit(x,",")</pre>
  if(length(x list)==0){
    x out<-NULL
  }else{
    x_out<-x_list[[1]][1]</pre>
    if(length(x list[[1]])>1){
      for(mi in 2:length(x_list[[1]])){
        x_out<-c(x_out,x_list[[1]][mi])</pre>
      }
    }
  }
  return(x_out)
}
#function-def:pasteq(x)
#pasteq fubction: collapse vector into comma seperated terms with quotes around
them
pasteq<-function(x) {</pre>
      if(length(x)==0) {paste0("\"", x, "\"", collapse=", ") }else{
          a<-""
          y<-NULL
      for(i in 1:length(x)){
```

```
if(is.null(x[i])){y<-c(y, "")}else{</pre>
           if(x[i]==a) {y<-c(y, "") }else{</pre>
             #if want to remove all quotes (dont know if I want this) then
gsub('"',"",x)
             #remove enclosing quotes if present
             x split<-strsplit(as.character(x[i]), split="")[[1]]</pre>
             if(x split[1]=="\""){x_split[1]<-""}</pre>
             if(x_split[length(x_split)]=="\""){x_split[length(x_split)]<-""}</pre>
             x[i]<-paste(x split, collapse="")</pre>
             y<-c(y,x[i])}}
                 paste0("\"",y,"\"",collapse=",")
      }}
##
# Shiny Server
##
shinyServer(function(input, output, session) {
  #Stop app when browser closed
  session$onSessionEnded(stopApp)
  #Global Variables (all variables that must be kept between load events needs to
be in the vector keep on load)
 keep on load<<-c("from clear button", "from copy", "first load")</pre>
  from clear button<<-FALSE</pre>
  from_copy<<-FALSE</pre>
  #Reactive variables (globally accessed)
  #Reactive stores
  pt_definitions_r<-reactiveValues(data = "")</pre>
  bulk definitions r<-reactiveValues (data = NULL)
  ph add definitions r<-reactiveValues(data = NULL)
  ph_extr_definitions_r<-reactiveValues(data = NULL)</pre>
  solution models_file_r<-reactiveValues(data = NULL)
available_components_r<-reactiveValues()</pre>
  comp transformations r<-reactiveValues (data = NULL)
  current components r<-reactiveValues(data= NULL)
  major elements r<-reactiveValues(data= NULL)</pre>
  #mod-tag - this is a quick fix
  use sol models r<-reactiveValues(data = NULL)
  #store_r contains output data from runs
  store r<-
reactiveValues(crust r=NULL, input pt r=NULL, input bulk r=NULL, major elements r=NULL
)
  #initialise a passing message for error checking and reporting
  reactive message <- reactiveValues(data = NULL)</pre>
  load_pt_r<-reactiveValues(data = NULL)</pre>
  #save data reactive
  save data file <- reactive({</pre>
    #Grab working file and projects directory
    working file<-input$working file
    projects directory<-input$projects directory</pre>
    #error handling
    reactive_message$data <-error_handling(working_file,projects_directory)</pre>
    if(reactive_message$data=="error handling passed"){
      #if error handling is passed
      #Return success message
      return(paste0("File saved to
",projects directory,"/",working file,"/Inputs/",working file,".txt"))
    }else{
      #Return error message
      return (reactive message$data)
    }
    })
  #Save function
  on save <- reactive({</pre>
    #Grab working file and projects directory
    working file<-input$working file
    projects directory <- input $ projects directory
    #Replace projects directory if from copy
    if(!exists("from_copy")){from_copy<<-FALSE}</pre>
```

```
if(from copy){
    projects directory <- copy directory
    from copy<<-FALSE
    #error handling
    reactive message$data <-error handling(working file, projects directory)
    if(reactive message$data=="error handling passed"){
      #if error handling is passed
      w file<-paste0("################\n#\n#
                                            Rcrust input
file\n#\n################ Location of project files\n",
                     "working file<-", pasteq (working_file), "\n",
                     "projects directory<-", pasteq (projects directory ), "\n")
if(!input$x n=="") {if(is.na(suppressWarnings(as.numeric(input$x n))) {return("Error
: X must be numeric")}
      if(as.numeric(input$x n)<1) {return("Error: X must be greater than 1")}
      if(!as.numeric(input$x n)%%1==0){return("Error: X must be a whole number")}}
if(!input$y_n==""){if(is.na(suppressWarnings(as.numeric(input$y_n)))}{return("Error
: Y must be numeric")}
      if(as.numeric(input$y n)<1) {return("Error: Y must be greater than 1")}</pre>
      if(!as.numeric(input$y_n)%%1==0){return("Error: Y must be a whole number")}}
        "y n<-", bl(input$y_n), "\n")
        if(input$n_pt_def=="load") {
          if(!all(pt definitions r$data=="")){
          list pt<-NULL
          for(i in 1:length(pt definitions r$data)){
          list pt<-
c(list pt,pasteo("\"",names(pt definitions r$data)[i],"\"=c(",pasteq(pt definitions
r$data[[i]]),")"))
          }
          pt definitions<-paste0("list(",paste0(list pt,collapse=","),")")</pre>
          }else{
          pt definitions<-""</pre>
          ł
          }else{
        if(!input$n_pt_def==""){
          #Error validation
        if (is.na (suppressWarnings (as.numeric (input$n pt def)))) {return ("Error:
Number of PT definitions must be numeric") }
        if (as.numeric (input $n pt def) <1) {return ("Error: Number of PT definitions
must be greater than 0")}
        if(!as.numeric(input$n pt def)%%1==0){return("Error: Number of PT
definitions must be a whole number") }
        list pt<-NULL
      for(i in 1:as.numeric(input$n pt def)){
        #check tuples
        from<-check_tuple(eval(parse(text=paste0("input$pt from ",i))))</pre>
        if(!from[[1]]=="Valid tuple"){
        return(paste0("Error in PT Definition:
                                                  ", from[[1]]))
        3
        to<-check tuple(eval(parse(text=paste0("input$pt to ",i))))</pre>
        if(!to[[1]]=="Valid tuple"){
          return (paste0 ("Error in PT Definition:
                                                     ",to[[1]]))
        }
        list pt<-
c(list pt,paste0("\"",from[[2]]," ",to[[2]],"\"=c(",pasteq(eval(parse(text=paste0("))))))
input$pressure ",i)))), ", ", pasteq(eval(parse(text=paste0("input$temperature ",i))))
,")"))
      }
        pt definitions<-paste0("list(",paste0(list pt,collapse=","),")")</pre>
      }else{
       pt definitions<-""
      ł
        }
```

```
w pt<-paste0("#######################" PT data\n#\n###############",",
                   "pt_def<-\"input\"
                                                               #input,file\n",
                  "pt_definitions<-",bl(pt_definitions),"\n"
      if(input$n comp trans=="load"){
        if(!all(comp transformations r$data=="")){
          list trans<-NULL
          for(i in 1:length(comp transformations r$data)){
            list trans<-
c(list trans,paste0("\"",names(comp transformations r$data)[i],"\"=c(",pasteq(comp
transformations r$data[[i]]),")"))
          -F
          comp transformations<-paste0("list(",paste0(list trans,collapse=","),")")</pre>
        }else{
          comp transformations<-""</pre>
        1
      }else{
        if(!input$n comp trans=="") {
          #Error validation
if (is.na(suppressWarnings(as.numeric(input$n comp trans)))) {return("Error: Number
of Component transformations must be numeric")
          if(as.numeric(input$n comp trans)<1){return("Error: Number of Component
transformations must be greater than 0")}
          if(!as.numeric(input$n_comp_trans)%%1==0){return("Error: Number of
Component transformations must be a whole number") }
          list trans<-NULL
          for(i in 1:as.numeric(input$n comp trans)){
            list trans<-
c(list_trans,paste0("\"",eval(parse(text=paste0("input$old_comp_",i))),"_",eval(par
se(text=paste0("input$new comp ",i))),"\"=c(",pasteg(eval(parse(text=paste0("input$
comp_",i))),")"))
          -F
          comp transformations<-paste0("list(",paste0(list trans,collapse=","),")")</pre>
        }else{
          comp transformations<-""</pre>
        }
      }
      if(input$n bulk def=="load"){
        if(!all(bulk definitions r$data=="")){
        list bulk<-NULL
        for(i in 1:length(bulk definitions r$data)){
          list bulk<-
c(list bulk,paste0("\"",names(bulk definitions r$data)[i],"\"=c(",pasteq(bulk defin
itions r$data[[i]]),")))
        ł
        bulk definitions<-paste0("list(",paste0(list bulk,collapse=","),")")</pre>
        }else{
        bulk definitions<-""
        }
      }else{
        if(!input$n bulk def==""){
          #Error validation
          if(is.na(suppressWarnings(as.numeric(input$n_bulk_def)))){return("Error:
Number of Bulk definitions must be numeric") }
          if(as.numeric(input$n bulk def)<1){return("Error: Number of Bulk
definitions must be greater than 0") }
          if(!as.numeric(input$n_bulk_def)%%1==0) {return("Error: Number of Bulk
definitions must be a whole number") }
          list bulk<-NULL
          for(i in 1:as.numeric(input$n bulk def)){
            #check tuples
            from<-check tuple(eval(parse(text=paste0("input$bulk from ",i))))</pre>
            if(!from[[1]]=="Valid tuple"){
              return(paste0("Error in Bulk Definition:
                                                             ", from[[1]]))
            ł
            to<-check tuple(eval(parse(text=paste0("input$bulk to ",i))))</pre>
            if(!to[[1]]=="Valid tuple"){
```

```
return(paste0("Error in Bulk Definition:
                                                             ",to[[1]]))
            3
            bulk eval<-
strsplit(eval(parse(text=paste0("input$bulk ",i))),split=",")[[1]]
            #place in quotes
            for(j in 1:length(bulk eval)){
                bulk_eval[j]<-pasteq(bulk_eval[j])</pre>
            }
            list bulk<-
c(list bulk,paste0("\"",from[[2]]," ",to[[2]],"\"=c(",paste(bulk eval,collapse=",")
,")"))
          bulk definitions<-paste0("list(",paste0(list bulk,collapse=","),")")</pre>
        }else{
          bulk definitions<-""</pre>
        }
      3
      if(!is.null(input$major elements)){
      if(any(input$major elements=="load")){
        major elements <- major elements r$data
      }else{
        major elements<-unlist(strsplit(input$major elements, split=","))</pre>
        }
      }else{
        major elements<-""</pre>
      if(input$bulk def file==FALSE) {bulk def<-"input"}else{bulk def<-"file"}</pre>
      Bulk composition data
\n#\n#############/n",
                                  "comp_transformations<-
c(",bl(comp transformations),")\n",
                                  "bulk def<-",pasteq(bulk_def),"
#input,file\n",
                                  "major elements<-c(",pasteq(major elements),") \n",</pre>
                                  "bulk definitions<-c(", bl (bulk definitions), ") \n",
                                  "bulk file<-", pasteq (input $bulk file), "\n"
      )
      if(input$ph add){
        if(input$n ph add def=="load"){
          if(!all(ph add definitions r$data=="")){
          list_ph_add<-NULL
          for(i in 1:length(ph add definitions r$data)){
            qt names<-unlist(lapply(names(ph add definitions r$data[[i]]),pasteq))</pre>
            qt_values<-unlist(lapply(ph_add_definitions_r$data[[i]],pasteq))</pre>
            list ph add<-
c(list ph add, paste0("\"", names(ph add definitions r$data)[i], "\"=c(", paste(qt name
s,qt values,collapse=",",sep="="),"))
          ph add definitions<-paste0("list(",paste0(list ph add,collapse=","),")")</pre>
          }else{
          ph_add_definitions<-""
          Ł
        }else{
          if(!input$n_ph_add_def==""){
            #Error validation
if (is.na(suppressWarnings(as.numeric(input$n_ph_add_def)))) {return("Error: Number
of Phase Addition definitions must be numeric") }
            if(as.numeric(input$n_ph_add_def)<1){return("Error: Number of Phase</pre>
Addition definitions must be greater than 0") }
            if (!as.numeric (input $ n ph add def) % 1==0) { return ("Error: Number of
Phase Addition definitions must be a whole number") }
            list ph add<-NULL
            for(i in 1:as.numeric(input$n ph add def)){
              ph add defs<-NULL
              #check tuples
              from<-check tuple(eval(parse(text=paste0("input$ph add from ",i))))</pre>
              if(!from[[1]]=="Valid tuple"){
```

```
return(paste0("Error in Phase Addition Definition:
", from[[1]]))
              ł
              to<-check tuple(eval(parse(text=paste0("input$ph add to ",i))))</pre>
              if(!to[[1]]=="Valid tuple"){
                return(paste0("Error in Phase Addition Definition:
                                                                        ",to[[1]]))
              }
               ph_add_con<-
paste0("condition=",pasteq(eval(parse(text=paste0('input$ph add con ',i)))))
              phases<-
unlist(strsplit(eval(parse(text=paste0('input$ph add phs ',i))),split=","))
               for(j in 1:length(phases)){
               ph add defs<-
c (ph add defs,paste0(pasteq(phases[j]), "=", pasteq(eval(parse(text=paste0('input$ph
add_phs_',i,'_',phases[j])))))
              3
              list ph add <-
c(list ph add,paste0("\"",from[[2]],"_",to[[2]],"\"=c(",paste0(c(ph_add_con,ph_add_
defs), collapse=","),")))
            ph add definitions<-
paste0("list(", paste0(list_ph_add, collapse=","),")")
          }else{
           ph_add_definitions<-""
          }
        }
      }else{ph_add_definitions<-""}</pre>
      Phase
addition\n#\n#############\n".
                               "ph_add<-",input$ph_add,"\n",
                               "ph add definitions <-
c(",bl(ph add definitions),")\n"
      )
      if(input$ph extr){
        if(input$n ph extr def=="load"){
          if(!all(ph extr definitions r$data=="")){
            list_ph_extr<-NULL
            for(i in 1:length(ph_extr_definitions_r$data)){
              qt names<-
unlist(lapply(names(ph_extr_definitions_r$data[[i]]),pasteq))
              qt_values<-unlist(lapply(ph_extr_definitions_r$data[[i]],pasteq))</pre>
              list ph extr<-
c(list_ph_extr,paste0("\"",names(ph_extr_definitions_r$data)[i],"\"=c(",paste(qt_na
mes,qt_values,collapse=",",sep="="),")")
            }
           ph extr definitions <-
paste0("list(", paste0(list_ph_extr, collapse=", "), ")")
          }else{
            ph_extr_definitions<-""
          ł
        }else{
          if(!input$n_ph_extr_def==""){
            #Error validation
if(is.na(suppressWarnings(as.numeric(input$n_ph_extr_def)))){return("Error: Number
of Phase Extraction definitions must be numeric") }
            if(as.numeric(input$n_ph_extr_def)<1){return("Error: Number of Phase</pre>
Extraction definitions must be greater than 0") }
            if(!as.numeric(input$n_ph_extr_def)%%1==0){return("Error: Number of
Phase Extraction definitions must be a whole number") }
            list ph extr<-NULL
            for(i in 1:as.numeric(input$n ph extr def)){
              ph_extr_defs<-NULL
              #check tuples
              from<-check tuple(eval(parse(text=paste0("input$ph extr from ",i))))</pre>
              if(!from[[1]]=="Valid tuple"){
                return (paste0 ("Error in Phase Extraction Definition:
", from[[1]]))
```

```
}
              to<-check tuple(eval(parse(text=paste0("input$ph extr to ",i))))</pre>
              if(!to[[1]]=="Valid tuple"){
                return(paste0("Error in Phase Extraction Definition:
",to[[1]]))
              }
             ph_extr con<-
paste0("condition=", pasteq(eval(parse(text=paste0('input$ph_extr_con_',i)))))
             phases<-
unlist(strsplit(eval(parse(text=paste0('input$ph extr phs ',i)),split=","))
              for(j in 1:length(phases)){
               ph extr defs<-
c(ph_extr_defs,paste0(pasteq(phases[j]), "=",pasteq(eval(parse(text=paste0('input$ph)))))
              _', sub_brackets (phases [j])))))))
_extr_phs_',i,'
             ł
             list_ph_extr<-</pre>
c(list ph extr,paste0("\"",from[[2]]," ",to[[2]],"\"=c(",paste0(c(ph extr con,ph ex
tr defs), collapse=","),")))
           ł
           ph extr definitions <-
paste0("list(", paste0(list_ph_extr, collapse=","),")")
         }else{
           ph extr definitions<-""</pre>
          }
       }
      }else{ph_extr_definitions<-""}</pre>
      Phase
extraction\n#\n###############"
                                 "ph extr<-",input$ph_extr,"\n",
                                 "reequilibrate_steps<-
",input$reequilibrate_steps,"\n",
                                 "ph_extr_definitions<-
c(", bl(ph extr definitions), ") \n"
      )
       if(input$solution_models_file=="load"){
          if(!exists("solution models file")){solution models file<-""}</pre>
        }else{
          solution_models_file<-input$solution_models_file</pre>
         use sol models r$data<-input$use sol models</pre>
       }
    #error validation for meemum path
    if (input $meemum path == "") {return ("Error: No meemum path defined") }
if (!file.exists (paste0 (data directory, "/", input$meemum path))) {return (paste0 ("Error
: Meemum not found at ",paste0(data directory,"/",input$meemum path)))}
      Modelling
Options\n#\n###############",n",
                                 "thermodynamic data file <-
", pasteq(input$thermodynamic_data_file), "\n",
                                 "solution models file --
", pasteq(solution_models_file), "\n",
                                  "meemum_path<-",pasteq(input$meemum_path),"\n",</pre>
                                 "perplex option file <-
", pasteq(input$perplex_option_file), "\n",
                                 "use sol models<-
c(",pasteq(use sol models r$data),")\n",
                                 "saturated_components<-
",pasteq(input$saturated components),"\n",
                                 "saturated phase components <-
",pasteq(inputsaturated_phase_components),"\bar{n}",
                               "independent potential_fugacity_activity<-
", pasteq(input$independent_potential_fugacity_activity), "\n",
                                 "exclude phases<-
", pasteq(input$exclude phases), "\n",
                                 "end_of_calc<-",pasteq(input$end_of_calc),"\n")
      Options\n#\n##############\n",
```

```
C:50
```

```
"phase aliases<-
", pasteq (input$phase aliases), "\n",
                                   "PAM compilation <-
", pasteq(input$PAM compilation), "\n",
                                   "compile_PAM<-",pasteq(input$compile_PAM),"\n")
      #Compile all tabs into a page
      thepage <-
c(w_file,w_size,w_pt,w_bulk_composition,w_phase_addition,w_phase_extraction,w_model
ling_options,w_output_options)
       If directory doesnt exist, create it
      if(!dir.exists(paste0(projects directory,"/",working file))){
        dir.create(paste0(projects directory, "/", working file))
      }
      if(!dir.exists(paste0(projects directory,"/",working file,"/Inputs/"))){
        dir.create(paste0(projects directory, "/", working file, "/Inputs/"))
      if(!dir.exists(paste0(projects directory,"/",working file,"/Outputs/"))){
        dir.create(paste0(projects directory, "/", working file, "/Outputs/"))
      ł
      #Grab additional parameters if file already exists
      add text<-NULL
if (file.exists (paste0 (projects directory, "/", working file, "/Inputs/", working file, "
.txt"))){
      scanned <-
scan(file=paste0(projects_directory,"/",working_file,"/Inputs/",working_file,".txt"
),what="character",sep="\n",quiet=TRUE)
      break line<-which (scanned=="#</pre>
                                      Additional Parameters")
      if(length(break line)==1){
        add text<-scanned[break line:length(scanned)]</pre>
      }
      3
      #Save .txt file
      write(c(thepage,add text), file =
paste0 (projects_directory, "/", working_file, "/Inputs/", working file, ".txt"))
      #Save workspace
      working file<<-input$working file</pre>
save.image(file=paste0(projects directory,"/",working file,"/",working file,".RData
"))
      #Return success message
      return(paste0("File saved to
", projects directory, "/", working file, "/Inputs/", working file, ".txt"))
    }else{
      #Return error message
      return(reactive message$data)
    }
  1)
  #Load function
  on load <- reactive({</pre>
    working_file<-input$working_file</pre>
    #error handling
    reactive_message$data <-error_handling(working_file,projects_directory)</pre>
    if(reactive message$data=="error handling passed") {
      #Remove current workspace but keeping marker: from clear button
      #mod-tag: should we really be clearing workspace? can't we just overwrite
values for load?
      rm(list=ls())
      rm(list=setdiff(ls(envir=.GlobalEnv),c("keep on load",keep on load)),envir =
.GlobalEnv)
      #clear reactive stores
      pt definitions r$data<-NULL
      bulk definitions r$data<-NULL
      ph add definitions r$data<-NULL
      ph extr definitions r$data<-NULL
      #Load .txt unless from clear button
      if(from_clear_button){
```

```
projects directory<-input$projects directory</pre>
        working file<-input$working file
        }else{
source(paste0(input$projects_directory,"/",input$working file,"/Inputs/",input$work
ing file,".txt"))
      #Values to load
      load variables<-</pre>
c("x n"="inp","y n"="inp","n pt def"="reactive","n comp trans"="reactive","bulk def
 file"="checkbox", "major elements"="reactive select", "n bulk def"="reactive", "bulk
file"="inp","ph_add"="checkbox","n_ph_add_def"="reactive","ph_extr"="checkbox","ree
quilibrate_steps"="checkbox", "n_ph_extr_def"="reactive", "thermodynamic_data_file"="
inp","saturated_components"="inp","saturated_phase_components"="inp","independent_p
otential fugacity activity"="inp", "exclude phases"="inp", "end of calc"="inp", "solut
ion models file"="reactive", "perplex option file"="inp", "meemum path"="inp", "phase
aliases"="inp","PAM compilation"="inp","compile PAM"="checkbox")
      #load reactive stores
      if(exists("pt_definitions")){
        pt definitions r$data<-pt definitions
      if(exists("bulk definitions")){
      bulk definitions r$data<-bulk definitions
      ł
      if(exists("comp transformations")){
        comp transformations r$data<-comp transformations
      if(exists("ph add definitions")){
        ph add definitions r$data<-ph add definitions
      ો
      if(exists("ph extr definitions")){
        ph extr definitions r$data<-ph extr definitions
      if(exists("solution models file")){
        solution models file r$data<-solution models file
      ł
      if(exists("use sol models")){
        use sol models r$data<-use sol models
      if(exists("major_elements")){
        major elements r$data<-major elements</pre>
      }
      #custom loads
      #bulk def
      if(exists("bulk def")){if(bulk def=="input"){bulk def file<-
FALSE}else{bulk def file<-TRUE}}else{bulk def file<-FALSE}</pre>
      #get addition phases
      if(is.null(ph add definitions r$data[[1]][1])){add phases<-""}else{</pre>
        add_phases<-
paste(setdiff(names(ph add definitions r$data[[1]]), "condition"), collapse=", ")
      }
      #get extract phases
      if(is.null(ph extr definitions r$data[[1]][1])){extr phases<-""}else{</pre>
        extr_phases<-
paste(setdiff(names(ph extr definitions r$data[[1]]), "condition"), collapse=",")
      }
      #load values
      for(i in 1:length(load variables)){
        if(load variables[i]=="reactive"){
            updateTextInput(session, names(load variables)[i], value="load")
        if(load variables[i]=="reactive select"){
          updateSelectizeInput(session, names(load variables)[i], selected="load")
        }
        if(load_variables[i]=="inp"){
            if(exists(names(load variables)[i])){
```

```
updateTextInput(session, names(load variables)[i], value=eval(parse(text=names(load v
ariables)[i])))
             }else{
              updateTextInput(session, names(load variables)[i], value="")
            3
        }
        #modtag - remove this
        if(load variables[i]=="def count"){
          def name<-
sub("n ","",sub(" def"," definitions",names(load variables)[i]))
         if(exists(def name)){
            if(is.null(eval(parse(text=def_name))[[1]][1])){val_out<-""}</pre>
            else{if(eval(parse(text=def_name))[[1]][1]==""){val_out<-""}</pre>
              else{val_out<-length(eval (parse(text=def_name)))}}}else{val_out<-""}</pre>
                    updateTextInput(session, names(load variables)[i], value=val out)
        if(load variables[i]=="checkbox"){
          if(exists(names(load variables)[i])){
        updateCheckboxInput(session, names(load variables)[i], value =
eval(parse(text=names(load variables)[i])))
          }else{
          #False is default for all load checkboxes
        updateCheckboxInput(session,names(load_variables)[i],value = FALSE)
          }
            }
        if(load_variables[i]=="select"){
          if(exists(names(load variables)[i])){
        updateSelectInput(session,
names(load variables)[i], selected=eval(parse(text=names(load variables)[i])))
          }else{
        updateSelectInput(session, names(load variables)[i],selected="")
          ł
      }
      #Return success message
      if(from clear button) {
        from clear button <<- FALSE
        return(paste0("Inputs and workspace cleared"))
      }else{
        return (paste0 ("Loaded
",projects directory, "/", working file, "/Inputs/", working file, ".txt"))
    }else{
      #Return error message
      return(reactive message$data)
    ¥
    1)
  #Toolbar buttons
    #Load button
  observeEvent(input$load, {
    #load the file from input$working file
    working file<-input$working file
  projects_directory<-input$projects_directory</pre>
    #error handling
    reactive message$data <-error handling(working file, projects directory)
      if(reactive_message$data=="error handling passed"){
         #load
if (file.exists (paste0 (projects directory, "/", working file, "/Inputs/", working file, "
.txt"))){
        reactive message$data <- paste0(on load())</pre>
        }else{
        reactive_message$data <- paste0("No input file found at</pre>
",paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"))
        }
        #Load workspace if it exists (previous calculation results)
```

```
if (file.exists (paste0 (projects directory, "/", working file, "/", working file, ".RData"
))){
load(paste0(projects directory,"/",working file,"/",working file,".RData"),envir=.G
lobalEnv)
        #Refresh reactive outputs if they exist
        if(exists("crust")){store r$crust r<-crust}</pre>
        if(exists("input pt")){store r$input pt r<-input pt}</pre>
        if(exists("input_bulk")){store_r$input_bulk_r<-input_bulk}</pre>
        if (exists ("major elements")) {store r$major elements r<-major elements}
    }else{
      reactive message$data
    }
  1)
    #Clear button
  observeEvent(input$clear, {
      #delete selection inputs
    from clear button<<-TRUE</pre>
    reactive message$data <- paste0(on load())</pre>
})
    #Console button
  observeEvent(input$console, {
  cat ("To regain access to the Rcrust GUI type \'c\' then press enter\n")
    browser()
3.)
    #Run Button
  observeEvent(input$run, {
    #Grab working file and projects directory
    working file<-input$working file
    projects directory<-input$projects directory</pre>
    #error handling
    reactive message$data <-error handling(working file, projects directory)
    if(reactive message$data=="error handling passed") {
      #if error handling is passed
      #GUI level validation check that have at least minimum of P,T, and X
definitions in GUI
      var_missing<-NULL
      chk_variables<-
c("input$x n", "input$y n", "input$n pt def", "input$n bulk def", "input$major elements
")
      for(i in rev(chk variables)) {if(any(eval(parse(text=i))=="")) {var missing<-</pre>
i}}
      if(!is.null(var missing)){reactive message$data <- paste0("Error: Cannot run
calculation. Missing ",var missing);return(reactive message$data)}
      #Save
      reactive message$data <- paste0(on save())</pre>
      # source the saved variables into the workspace
source(paste0(projects_directory,"/",working_file,"/Inputs/",working_file,".txt"))
      #Run
      source("main.r")
      reactive_message$data <- paste0("Calculation complete, Results saved to</pre>
",projects_directory,"/",working_file,"/",working_file,".RData\n Select outputs
throught the 'Outputs' tab")
      #Save copy to directory
        if(FALSE) {copy_directory<<-"H:/Rcrust/Projects"</pre>
        from_copy<<-TRUE
        reactive message$data <- paste0(on save())</pre>
      #End of Calculation
if (!exists ("end of calc")) {end of calc<-"Return to Interface"}
      #Email report
      if(FALSE) {
      library(gmailr)
      mime() %>%
        to("mjmayne@outlook.com") %>%
```

```
from("matt.mayne.1992@gmail.com") %>%
        html body("Body text") -> html msg
        html_msg %>%
        subject (paste0 (working file, " completed successfully after ", run time, "with
finish option ",end_of_calc)) %>%
#attach_file(paste0(projects_directory,"/",working_file,"/",working_file,".RData"))
-> file attachment
        #attach file(paste0(projects directory,"/Yak PT fh any all/Yak PT fh
any all.RData")) -> file attachment
        send message()
if(end of calc=="Logout") {system('shutdown -l')}
if(end of calc=="Shutdown") {system('shutdown -s')}
      #Refresh reactive outputs if they exist
      if(exists("crust")){store_r$crust_r<-crust}</pre>
      if(exists("input pt")){store_r$input_pt_r<-input_pt}</pre>
      if(exists("input_bulk")){store_r$input_bulk_r<-input_bulk}</pre>
      if(exists("major_elements")){store_r$major_elements_r<-major_elements}</pre>
      ł
})
    #Save button
  observeEvent(input$save, {
  reactive_message$data <- paste0(on_save())</pre>
})
    #Send error/success messages to GUI
  output$print_message <- renderText({</pre>
  if (is.null(reactive message$data)) return()
  paste0(reactive message$data)
})
  # Dyanmically use number of PT definitions to create the correct number of
From, To, P, T inputs
    output$pt <- renderUI({</pre>
    if(input$n pt def=="load"){
      if(all(pt definitions r$data=="")|is.null(pt definitions r$data)){
        def num<-"'
      }else{
      def_num<-length(pt_definitions_r$data)</pre>
      ł
      updateTextInput(session, "n pt def", value=def num)
    }else{
      def num<-input$n pt def</pre>
    }
      if(!(is.null(def num)|def num==""|def num==0)){
      validate(if(is.na(suppressWarnings(as.numeric(def num)))){"Error: Number of
PT definitions must be numeric"}else{NULL})
      validate(if(as.numeric(def num)<1){"Error: Number of PT definitions must be</pre>
greater than 0"}else{NULL})
      validate(if(!as.numeric(def num)%%1==0){"Error: Number of PT definitions must
be a whole number"}else{NULL})
      fixedRow(
        lapply(1:(as.numeric(def_num)*4), function(i) {
          a<-1; ii<-i
          while(ii>4) {ii<-ii-4;a<-a+1}</pre>
          if(ii==1) {chk From<-</pre>
try(unlist(strsplit(names(pt definitions r$data)[a],split=" "))[1],silent=TRUE)
                     if(class(chk_From) == "try-error") {chk_From<-NULL}</pre>
column(2,textInput(paste0('pt from ',a),'From',value=chk From))}else{
          if(ii==2) {chk To<-
try(unlist(strsplit(names(pt definitions r$data)[a],split=" "))[2],silent=TRUE)
                     if (class (chk To) == "try-error") {chk To<-NULL}
                     column(2,textInput(paste0('pt_to_',a),'To',value=chk_To))}else{
          if(ii==3){chk pressure<-try(pt definitions r$data[[a]][1],silent=TRUE)</pre>
                     if(class(chk pressure) == "try-error") {chk pressure<-NULL}</pre>
                     column(4,textInput(paste0('pressure ',a), 'Pressure
(kbar) ',value=chk_pressure))}else{
          if(ii==4) {chk_temperature<-try(pt_definitions_r$data[[a]][2],silent=TRUE)</pre>
```
```
if (class (chk temperature) == "try-error") {chk temperature -NULL}
                      column(4,textInput(paste0('temperature ',a),'Temperature
(C) ', value=chk temperature))
                  }}})
      )
      }
      })
        #Import P-T definitions button
  observeEvent(input$import pt, {
  #bugtag - try rather updating text to have only a local load
#updateTextInput(session,input$n_ph_add def,value="load")
  reactive message$data <- paste0(on save())</pre>
  #Import definitions from file (csv of definitions or txt as Rcrust input file)
  #read Rcrust Input file
  if(input$file_pt["type"]=="text/plain"){
  data in<-readLines(paste(input$file pt[4]))</pre>
  input file<-
readLines (paste0 (projects directory, "/", working file, "/Inputs/", working file, ".txt"
))
  if(!length(grep("pt definitions<-",data in))==0){</pre>
  if(length(grep("pt definitions<-",input file))==0){</pre>
  input_file<-c(input_file,grep("pt_definitions<-",data_in))</pre>
  }else{
  input_file[grep("pt_definitions<-",input_file)]<-data_in[grep("pt_definitions<-</pre>
",data in)]
  ł
  write(input file, file =
paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"))
  }else{
  #read csv of definitions
  data in<-as.matrix(read.csv(paste(input$file pt[4])))</pre>
  lines all<-NULL
  for(line no in 1:nrow(data in)) {
  line i<-
paste("\"{",data_in[line_no,1],";",data_in[line_no,2],"}_{",data_in[line_no,3],";",
data_in[line_no,4],"}\"=c(\"",data_in[line_no,5],"\",\"",data_in[line_no,6],"\")",s
ep="")
  if(line no==1) {lines all <- paste ("pt definitions <- list (", line i, sep="") }else {
  lines all<-paste(lines all,line i,sep=",")</pre>
  if(line no==nrow(data in)){
  lines_all<-paste(lines_all,")", sep="")</pre>
  ł
  }
  input file<-
readLines (paste0 (projects directory, "/", working file, "/Inputs/", working file, ".txt"
))
  if(length(grep("pt definitions<-",input file))==0){</pre>
  input file<-c(input file, lines all)</pre>
  }else{
  input_file[grep("pt_definitions<-",input_file)]<-lines_all</pre>
  write(input_file, file =
paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"))
  }
  reactive_message$data <- paste0(on_load())</pre>
})
    # Dyanmically use number of component transformations to create the correct
number of inputs
    output$trans <- renderUI({</pre>
      if(input$n comp trans=="load"){
if (all (comp transformations r$data=="") is.null (comp transformations r$data)) {
           def num<-""
         }else{
           def_num<-length(comp_transformations_r$data)</pre>
         }
```

```
updateTextInput(session, "n comp trans", value=def num)
      }else{
        def num<-input$n comp trans</pre>
      if(!(is.null(def num)|def num==""|def num==0)){
        validate(if(is.na(suppressWarnings(as.numeric(def num)))){"Error: Number of
Component transformations must be numeric" }else{NULL})
        validate(if(as.numeric(def_num)<1){"Error: Number of Component</pre>
transformations must be greater than 0"}else{NULL})
        validate(if(!as.numeric(def num)%%1==0){"Error: Number of Components
transformations must be a whole number"}else{NULL})
        fixedRow(
          lapply(1:(as.numeric(def num)*3), function(i) {
             a<-1; ii<-i
             while(ii>3) {ii<-ii-3;a<-a+1}</pre>
             if(ii==1) {chk_old<-</pre>
try(unlist(strsplit(names(comp transformations r$data)[a], split=" "))[1], silent=TRU
E)
             if(class(chk_old) == "try-error") {chk old<-NULL}</pre>
             column(2,textInput(paste0('old comp ',a),'Replace
component',value=chk old))}else{
               #mod-tag: better to have a select input but for some reason it doesnt
work well with column()
#column(2,selectizeInput(paste0('old comp ',a),'Replace',c("",available components
r$data), selected=chk old))}else{
             if(ii==2) {chk new<-</pre>
try(unlist(strsplit(names(comp transformations r$data)[a],split=" "))[2],silent=TRU
E)
                       if(class(chk new) == "try-error") {chk new<-NULL}</pre>
                       column(2,textInput(paste0('new comp ',a),'New
component',value=chk new))}else{
             if(ii==3){
                   comp label<-paste(available components r$current,collapse = ",")</pre>
                   chk comp<-try(comp transformations r$data[[a]], silent=TRUE)</pre>
                   if(class(chk comp) == "try-error") {chk comp<-NULL}</pre>
column(8,textInput(paste0('comp_',a),comp_label,value=paste(chk_comp,collapse=","))
)}else{
                   }}})
        )
      }
    })
     #Component transformation
    observe({
    available components <-NULL
    suppressWarnings(qq_try<-</pre>
try (scan (file=gsub ("Rcrust/code", paste0 ("Rcrust/data/", input$thermodynamic data fil
e),getwd()),what="character",sep="\n",quiet=TRUE),silent=TRUE))
    if(class(qq_try)!="try-error"){
    qq<-qq_try
    start_foo<-grep("begin_components",qq)</pre>
    end foo<-grep("end components", qq)
    qq<-qq[(start_foo+1):(end_foo-1)]</pre>
    qq<-strsplit(qq," ")</pre>
    for(i in 1:length(qq)){
    available_components<-c(available_components,qq[[i]][1])</pre>
    ÷.
    }
    available components r$current<-available components
    })
    #Component transformation
    observe({
      #use current component transformation inputs to update current components r
and selection in major elements
      current components <- available components r$current
      chk trans<-FALSE
      if(!is.na(suppressWarnings(as.numeric(input$n_comp_trans)))){
```

```
if(!as.numeric(input$n comp trans)<1){</pre>
           if(as.numeric(input$n comp trans)%%1==0){
             chk trans<-TRUE
           }
        }}
      if(chk trans) {
        for(i in 1:input$n_comp_trans) {
          pos<-
which(current components==eval(parse(text=paste0("input$old comp ",i))))
           current components[pos]<-eval(parse(text=paste0("input$new comp ",i)))</pre>
        }
      ł
      current components r$data<-current components
        - } )
    output$maj <- renderUI({</pre>
      #fix-tag: does not work if have multiple component transformations, scoping
means we come here after first transformation is complete because we alter "current
components"
      if(!input$n_comp_trans=="load"){
      if(any(input$major elements=="load")){
      selectizeInput('major elements', 'Major elements',
c(major elements r$data, setdiff(current components r$data, major_elements_r$data),"1
oad"), selected=major elements r$data, multiple=TRUE)
      }else{
selectizeInput('major_elements', 'Major elements',
c(input$major_elements, setdiff(current_components_r$data, input$major_elements), "loa
d"), selected=input$major elements, multiple=TRUE)
      }
      })
    # Dyanmically use number of bulk definitions to create the correct number of
From, To, bulk inputs
    output$bulk <- renderUI({</pre>
      if(input$n bulk def=="load"){
        if(all(bulk_definitions_r$data=="")|is.null(bulk_definitions_r$data)){
           def num<-""
         }else{
           def num<-length(bulk definitions r$data)</pre>
        ł
        updateTextInput(session,"n bulk def",value=def num)
      }else{
        def num<-input$n bulk def</pre>
      if(!(is.null(def num)|def num==""|def num==0)){
        validate(if(is.na(suppressWarnings(as.numeric(def num)))){"Error: Number of
Bulk definitions must be numeric" }else {NULL})
        validate (if (as.numeric (def num) <1) { "Error: Number of Bulk definitions must
be greater than 0" }else{NULL})
        validate (if (!as.numeric (def num) %%1==0) {"Error: Number of Bulk definitions
must be a whole number"}else{NULL})
        fixedRow(
           lapply(1:(as.numeric(def num)*3), function(i) {
             a<-1; ii<-i
             while(ii>3) {ii<-ii-3; a<-a+1}</pre>
             if(ii==1) {chk From<-</pre>
try(unlist(strsplit(names(bulk definitions r$data)[a],split=" "))[1],silent=TRUE)
             if(class(chk_From) == "try-error") {chk_From<-NULL}</pre>
             column(2,textInput(paste0('bulk_from_',a),'From',value=chk_From))}else{
               if (ii==2) { chk To<-
try(unlist(strsplit(names(bulk definitions r$data)[a], split=" "))[2], silent=TRUE)
               if(class(chk To) == "try-error") {chk To<-NULL}</pre>
               column(2,textInput(paste0('bulk to ',a),'To',value=chk To))}else{
                 if(ii==3){
                   if(is.null(input$major elements)){
                     bulk label<-"Please choose major elements above"</pre>
                   }else{
                     bulk_label<-paste(c(input$major_elements, "mass"), collapse =</pre>
",")
```

```
}
                   chk bulk<-try (bulk definitions r$data[[a]], silent=TRUE)
                 if(class(chk bulk) == "try-error") {chk bulk<-NULL}</pre>
column(8,textInput(paste0('bulk_',a),bulk_label,value=paste(chk_bulk,collapse=","))
)}else{
    }}})
        )
      }
    })
 #Import bulk definitions button
  observeEvent(input$import bulk, {
  #mod-tag: try rather updating text to have only a local load
#updateTextInput(session,input$n ph add def,value="load")
  reactive message$data <- paste0(on save())</pre>
  #Import definitions from file (csv of definitions or txt as Rcrust input file)
  #read Rcrust Input file
  if(input$file_bulk["type"]=="text/plain"){
  data in<-readLines(paste(input$file bulk[4]))</pre>
  input file <-
readLines(paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"
))
  if(!length(grep("comp transformations<-",data in))==0){</pre>
  if(length(grep("comp_transformations<-",input_file))==0){</pre>
  input file<-c(input file,grep("comp transformations<-",data in))</pre>
  }else{
  input_file[grep("comp_transformations<-",input_file)]<-</pre>
data in[grep("comp transformations<-",data in)]</pre>
  }
  ł
    if(!length(grep("major elements<-",data in))==0){</pre>
  if(length(grep("major elements<-",input file))==0){</pre>
  input file<-c(input file,grep("major elements<-",data in))</pre>
  }else{
  input file[grep("major elements<-", input file)]<-data in[grep("major elements<-
",data in)]
  }
  if(!length(grep("bulk definitions<-",data in))==0){</pre>
  if(length(grep("bulk definitions<-", input file))==0) {</pre>
  input_file<-c(input_file,grep("bulk_definitions<-",data_in))</pre>
  }else{
  input file[grep("bulk definitions<-",input file)]<-</pre>
data in[grep("bulk definitions<-",data in)]</pre>
  }
  }
 write(input file, file =
paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"))
  }else{
  #read csv of definitions
  data_in<-as.matrix(read.csv(paste(input$file_bulk[4])))</pre>
  lines all<-NULL
  for(line no in 1:nrow(data in)){
  line i<-
paste("\"{",data in[line_no,1],";",data_in[line_no,2],"}_{{",data_in[line_no,3],";",
data_in[line_no, 4],"}\"=c(\"", paste(data_in[line_no, c(-1, -2, -3, -
4)],collapse="\",\""),"\")",sep="")
  if (line no==1) {lines all <- paste ("bulk definitions <- c (list (", line i, sep="") }else {
  lines all<-paste(lines all, line i, sep=",")</pre>
  1
  if(line no==nrow(data in)){
  lines all<-paste(lines all,"))", sep="")</pre>
  ł
  input file<-</pre>
readLines(paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"
))
  if(length(grep("bulk definitions<-",input file))==0){</pre>
```

```
input file<-c(input file,lines all)</pre>
  }else{
  input file[grep("bulk definitions <- ", input file)] <- lines all
  }
  write(input_file, file =
paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"))
  }
  reactive message$data <- paste0(on load())</pre>
1)
    # Dyanmically use number of Phase Addition definitions to create the correct
number of From, To, P, T inputs
    output$ph add <- renderUI({</pre>
      if(input$n_ph_add_def=="load"){
        if(all(ph add definitions r$data=="")|is.null(ph add definitions r$data)){
           def num<-""
        }else{
          def_num<-length(ph add definitions r$data)</pre>
        }
        updateTextInput(session, "n ph add def", value=def num)
      }else{
        def num<-input$n ph add def
      if(!(is.null(def num)|def num==""|def num==0)){
        validate(if(is.na(suppressWarnings(as.numeric(def_num)))){"Error: Number of
Phase Addition definitions must be numeric" }else{NULL})
        validate (if (as.numeric (def num) <1) { "Error: Number of Phase Addition
definitions must be greater than 0"}else{NULL})
        validate (if (!as.numeric (def num) %%1==0) {"Error: Number of Phase Addition
definitions must be a whole number" }else{NULL})
        fixedRow(
           lapply(1:(as.numeric(def num)*5), function(i) {
            a<-1; ii<-i
             while(ii>5){ii<-ii-5;a<-a+1}</pre>
             if(ii==1) {chk From<-</pre>
try(unlist(strsplit(names(ph_add_definitions_r$data)[a], split=" "))[1], silent=TRUE)
             if(class(chk From) == "try-error") {chk From<-NULL}</pre>
column(2,textInput(paste0('ph add from ',a),'From',value=chk From))}else{
               if(ii==2) {chk To<-
try(unlist(strsplit(names(ph add definitions r$data)[a],split=" "))[2],silent=TRUE)
               if(class(chk_To) == "try-error") {chk_To<-NULL}</pre>
               column(2,textInput(paste0('ph_add_to_',a),'To',value=chk_To))}else{
                 if(ii==3) {chk Condition<-</pre>
try(ph add definitions r$data[[a]][["condition"]],silent=TRUE)
                 if(class(chk Condition) == "try-error") {chk Condition<-NULL}</pre>
column(3,textInput(paste0('ph add con ',a),'Condition',value=chk Condition))}else{
                 if(ii==4) {
                 chk Phases<-try(paste(names(ph_add_definitions_r$data[[a]][-</pre>
1]), collapse=","), silent=TRUE)
                 if(class(chk_Phases) == "try-error") {chk_Phases<-NULL}</pre>
column(4,textInput(paste0('ph add phs ',a),'Phases',value=chk Phases))
                 }else{
                 if(ii==5){
                  column(12,uiOutput(paste0("ph add ",a)))
                 3
                 }}
                   }})
        )
      }
    })
    #auto create phase addition inputs given number of phases
             observe({
if (all (!input$n ph_add_def=="load", !is.null (input$n_ph_add_def), !input$n_ph_add_def
```

```
=="",!input$n_ph_add_def==0)){
```

```
lapply(1:input$n ph add def, function(i) {
    eval(parse(text=paste0("output$ph_add_",i,"<-renderUI({</pre>
    a<-i
    chk Phases<-try(eval(parse(text=paste0(\'input$ph add phs \',a))),silent=TRUE)
                     if(!is.null(chk Phases)) {
                     if(!chk Phases=\"\"){
                     phases<-unlist(strsplit(chk Phases, split=\", \"))</pre>
                          fixedRow(
                          lapply(1:(length(phases)), function(j) {
                          chk_in_ph<-
try(ph_add_definitions_r$data[[a]][phases[j]], silent=TRUE)
                          if(class(chk in ph) == \"try-error\") {chk in ph<-NULL}</pre>
column(3,textInput(paste0(\'ph add phs \',a,\' \',phases[j]),phases[j],value=chk in
ph))
                          }))
                          } }
                          })")))
    })
    }
    })
   #Import addition definitions button
  observeEvent(input$import ph add, {
  #mod-tag: try rather updating text to have only a local load
#updateTextInput(session, input$n ph add def, value="load")
  reactive_message$data <- paste0(on_save())</pre>
  #Import definitions from file (csv of definitions or txt as Rcrust input file)
  #read Rcrust Input file
  if(input$file_ph_add["type"]=="text/plain"){
  data in<-readLines(paste(input$file ph add[4]))</pre>
  input file<-
readLines (paste0 (projects directory, "/", working file, "/Inputs/", working file, ".txt"
))
  if(!length(grep("ph add<-",data in))==0){</pre>
  if(length(grep("ph add<-",input file))==0){</pre>
  input file<-c(input file,grep("ph add<-",data in))</pre>
  }else{
  input_file[grep("ph_add<-",input_file)]<-data_in[grep("ph_add<-",data_in)]</pre>
  }
  }
  if(!length(grep("ph_add_definitions<-",data_in))==0){</pre>
  if(length(grep("ph add definitions<-",input file))==0){</pre>
  input file<-c(input file,grep("ph add definitions<-",data in))</pre>
  }else{
  input file[grep("ph add definitions<-",input file)]<-</pre>
data in[grep("ph add definitions<-",data in)]</pre>
  }
  }
 write(input file, file =
paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"))
  }else{
  #read csv of definitions
  data in<-as.matrix(read.csv(paste(input$file ph add[4])))</pre>
  lines_all<-NULL</pre>
  for(line no in 1:nrow(data in)){
  line i<-
paste("\"{", data_in[line_no, 1], "; ", data_in[line_no, 2], "}_{", data_in[line_no, 3], "; ",
data in[line no,4],"}\"=c(condition=\"",data in[line no,5],"\",",data in[line no,6]
 ")",sep="")
  if(line_no==1){lines_all<-paste("ph_add_definitions<-</pre>
c(list(",line i,sep="")}else{
  lines all<-paste(lines all, line i, sep=",")</pre>
  if(line no==nrow(data in)){
  lines_all<-paste(lines_all,"))", sep="")</pre>
  }
  }
```

```
input file<-</pre>
readLines(paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"
))
    if(length(grep("ph add<-",input file))==0){</pre>
  input file<-c(input_file, "ph_add<-TRUE")</pre>
  }else{
  input file[grep("ph add<-",input file)]<-"ph add<-TRUE"</pre>
  ł
  if(length(grep("ph add definitions<-",input file))==0){</pre>
  input file<-c(input file,lines all)</pre>
  }else{
  input file[grep("ph add definitions<-",input file)]<-lines all</pre>
  }
 write(input file, file =
paste0(projects directory,"/",working_file,"/Inputs/",working_file,".txt"))
  }
  reactive message$data <- paste0(on load())</pre>
  updateTextInput(session, input$file ph add, value="")
})
    #Import extraction definitions button
  observeEvent(input$import ph extr, {
  #mod-tag: try rather updating text to have only a local load
#updateTextInput(session,input$n ph extr def,value="load")
  reactive_message$data <- paste0 (on_save())</pre>
  #Import definitions from file (csv of definitions or txt as Rcrust input file)
  #read Rcrust Input file
  if(input$file_ph_extr["type"]=="text/plain"){
  data in<-readLines(paste(input$file ph extr[4]))</pre>
  input file <-
readLines(paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"
))
  if(!length(grep("ph extr<-",data in))==0){</pre>
  if(length(grep("ph extr<-", input file))==0){</pre>
  input file<-c(input file,grep("ph extr<-",data in))</pre>
  }else{
  input file[grep("ph extr<-", input file)]<-data in[grep("ph extr<-", data in)]</pre>
  }
  if(!length(grep("reequilibrate steps<-",data in))==0){</pre>
  if(length(grep("reequilibrate steps<-",input file))==0){</pre>
  input_file<-c(input_file,grep("reequilibrate_steps<-",data_in))</pre>
  }else{
  input file[grep("reequilibrate steps<-",input file)]<-</pre>
data_in[grep("reequilibrate_steps<-",data_in)]</pre>
  ł
  ł
  if(!length(grep("ph extr definitions<-", data in))==0) {</pre>
  if(length(grep("ph extr definitions<-",input file))==0){</pre>
  input file<-c(input file,grep("ph extr definitions<-",data in))</pre>
  }else{
  input_file[grep("ph_extr_definitions<-",input_file)]<-</pre>
data_in[grep("ph_extr_definitions<-",data_in)]</pre>
  }
  }
  write(input file, file =
paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"))
  }else{
  #read csv of definitions
  data in<-as.matrix(read.csv(paste(input$file ph extr[4])))</pre>
 lines all<-NULL
  for(line no in 1:nrow(data in)) {
  line i<-
paste("\"{",data in[line no,1],";",data in[line no,2],"} {",data in[line no,3],";",
data in[line no,4],"}\"=c(condition=\"",data in[line no,5],"\",",data in[line no,6]
,")",sep="")
 if(line no==1) {lines all<-paste("ph extr definitions<-</pre>
c(list(",line_i,sep="")}else{
  lines_all<-paste(lines_all,line_i,sep=",")</pre>
```

```
}
  if(line no==nrow(data in)){
  lines all<-paste(lines all,"))", sep="")</pre>
  }
  input file<-
readLines (paste0 (projects directory, "/", working file, "/Inputs/", working file, ".txt"
))
  input file[grep("ph extr definitions", input file)]<-lines all</pre>
  write(input file, file =
paste0(projects directory,"/",working file,"/Inputs/",working file,".txt"))
  }
  reactive message$data <- paste0(on load())</pre>
  updateTextInput(session, input$file ph extr, value="")
})
    # Dyanmically use number of Phase Extraction definitions to create the correct
number of From, To, P, T inputs
    output$ph extr <- renderUI({</pre>
      if(input$n ph extr def=="load"){
if(all(ph_extr_definitions_r$data=="")|is.null(ph extr definitions r$data)){
          def num<-""
        }else{
          def_num<-length(ph_extr_definitions_r$data)</pre>
        }
        updateTextInput(session, "n ph extr def", value=def num)
      }else{
        def num<-input$n ph extr def</pre>
      if(!(is.null(def num)|def num==""|def num==0)){
        validate(if(is.na(suppressWarnings(as.numeric(def num)))){"Error: Number of
Phase Extraction definitions must be numeric" }else{NULL})
        validate(if(as.numeric(def num)<1){"Error: Number of Phase Extraction</pre>
definitions must be greater than 0" }else {NULL })
        validate(if(!as.numeric(def_num)%%1==0){"Error: Number of Phase Extraction
definitions must be a whole number" }else{NULL})
        fixedRow(
           lapply(1:(as.numeric(def num)*5), function(i) {
             a<-1; ii<-i
             while(ii>5) {ii<-ii-5;a<-a+1}</pre>
             if(ii==1) {chk From<-
try(unlist(strsplit(names(ph extr definitions r$data)[a], split=" "))[1], silent=TRUE
)
             if(class(chk From) == "try-error") {chk From<-NULL}</pre>
column(2,textInput(paste0('ph extr from ',a),'From',value=chk From))}else{
               if (ii==2) {chk To<-
try(unlist(strsplit(names(ph_extr_definitions_r$data)[a],split=" "))[2],silent=TRUE
)
               if(class(chk To) == "try-error") {chk To<-NULL}</pre>
               column(2,textInput(paste0('ph_extr_to_',a),'To',value=chk_To))}else{
                 if(ii==3) {chk_Condition<-</pre>
try(ph extr definitions r$data[[a]][["condition"]],silent=TRUE)
                 if(class(chk_Condition) == "try-error") {chk_Condition<-NULL}</pre>
column(3,textInput(paste0('ph extr con ',a),'Condition',value=chk Condition))}else{
                 if(ii==4){
                 chk Phases<-try (paste (names (ph extr definitions r$data[[a]][-
1]),collapse=","),silent=TRUE)
                 if(class(chk Phases) == "try-error") {chk Phases<-NULL}</pre>
column(4,textInput(paste0('ph extr phs ',a),'Phases',value=chk Phases))
                 }else{
                 if(ii==5){
                  column(12,uiOutput(paste0("ph extr ",a)))
                 ÷.
                 }}})
        )
```

```
}
    1)
#auto create phase extraction inputs given number of phases
            observe({
if(all(!input$n ph extr def=="load",!is.null(input$n ph extr def),!input$n ph extr
def=="",!input$n_ph_extr_def==0)){
    lapply(1:input$n_ph_extr_def, function(i) {
    eval(parse(text=paste0("output$ph extr ",i,"<-renderUI({</pre>
    a<-i
    chk_Phases<-try(eval(parse(text=paste0(\'input$ph_extr_phs_\',a))),silent=TRUE)</pre>
                    if(!is.null(chk Phases)){
                    if(!chk_Phases=\"\") {
                    phases<-unlist(strsplit(chk Phases, split=\", \"))</pre>
                         fixedRow(
                         lapply(1:(length(phases)), function(j) {
                         chk in ph<-
try(ph extr definitions r$data[[a]][phases[j]], silent=TRUE)
                         if(class(chk_in_ph) == \"try-error\") {chk in ph<-NULL}</pre>
column(3,textInput(paste0(\'ph extr phs \',a,\' \',sub brackets(phases[j])),phases[
j],value=chk in ph))
                         }))
                         })
    ł
    })
    # Dyanmically use solution model file to build phase models selection
    output$solution models <- renderUI({</pre>
      if(input$solution models file=="load"){
if(all(solution models file r$data=="")|is.null(solution models file r$data)){
          solution models file<-""
        }else{
          solution models file<-solution models file r$data
        }
        updateTextInput(session,"solution_models_file",value=solution_models_file)
      ł
      if(!(is.null(input$solution models file)|input$solution models file=="")){
        data directory<-gsub("/code", "/data", getwd())</pre>
        if(!input$solution models file=="load"){
        validate(if(!dir.exists(data directory)){return("Error: data directory does
not exist") }else {NULL})
validate(if(!file.exists(paste0(data directory,"/",input$solution models file))){re
turn("Error: Solution model file does not exist")}else{NULL})
        selectizeInput('use sol models', 'Solution models',
solution models available r(), selected=use sol models r$data, multiple=TRUE)
      }
      }
    })
        # Dyanmically use abundance phases to select which phases to show
    output$select_abundance_phases <- renderUI({</pre>
    selectizeInput('show_abundance_phases', 'Show phases',
c(abundance phases available r(), "Reactive Subsystem", "Extract
Subsystem", "Cumulative Extract Subsystem", "Full
System"), multiple=TRUE, selected="Reactive Subsystem")
    })
            abundance phases available r<- reactive({
     if(!is.null(input$axis)){
    rownames(switch(input$axis,
x=phase abundance(store r$crust r,input$axis,as.numeric(input$path y),input$start x
, input$end x, input$path label, input pt = store r$input pt r),
```

```
y=phase_abundance(store_r$crust_r,input$axis,as.numeric(input$path_x),input$start_y
,input$end_y,input$path_label,input_pt = store_r$input_pt_r)
```

```
)[[2]])}
    })
     #Create Compilation button
    observeEvent(input$create compilation,{
    #Compile PAM fields (corelation to other PAMs)
    validate(need(!input$PAM compilation=="","Please provide a comma seperated list
of working files in PAM compilation"))
    cat("Creating Compilation Legend for", input$PAM compilation, "\n")
    flush.console()
    #mergers must contain the current file
    mergers<-
sort(union(unlist(strsplit(input$PAM compilation,",")),input$working file))
if (!dir.exists(paste0(input$projects directory, "/Compile"))) {dir.create(paste0(inpu
t$projects directory, "/Compile"))}
    compile names<-NULL
    for(i in mergers) {
attach (paste0 (input$projects directory, "/", i, "/", i, ".RData"), warn.conflicts=FALSE)
    pull crust<-
get("crust",which(search()==paste0("file:",input$projects directory,"/",i,"/",i,".R
Data")))
detach(pos=which(search()==paste0("file:",input$projects_directory,"/",i,"/",i,".RD
ata")))
    compile names<-
union (compile_names,get_PAM_names(neaten_crust(pull_crust,input$phase_aliases),inpu
t$PAM system)[[1]])
    -F
write.table(compile names,paste0(input$projects directory,"/Compile/",input$PAM com
pilation, " compilation legend.txt"), sep="\t", quote=F, col.names=FALSE)
    cat("Compilation successfully created for", input$PAM compilation, "\n")
    flush.console()
    })
    #Save Data button
    observeEvent(input$save data, {
      switch(input$output_type,
             "Data File"=
               reactive message$data <-
write_data_file(data_file(crust_out(),x_n=length(crust_out()[[1]]),y_n=length(crust
 out()), input$choose columns, input$choose rows, input$choose points), input$working f
ile, input$projects directory, input$file type),
             "Grid"=
            if(TRUE) { reactive message$data <-"Saving"</pre>
               reactive message$data <-draw Grid r()},</pre>
             "Phase Abundance Along Path"=
            if(TRUE) { reactive message$data <-"Saving"</pre>
               reactive_message$data <-draw abundance r()},</pre>
             "PAM"=
            if(TRUE) {reactive_message$data <-"Saving"</pre>
               reactive_message$data <-draw_PAM_r() }</pre>
             )
      })
          #GCDkit button
    observeEvent(input$send_gcdkit, {
    #mod-tag: perform maintenance on this functionality
    library (GCDkit)
    setwd("D:\\Rcrust\\code")
    Rcrust()
    eqq<-
data file(crust, x n=length(crust[[1]]), y n=length(crust), choose columns=NULL, choose
rows=NULL, compile=c("y i", "x i"))
    eqq mat<-eqq[[1]]</pre>
    bb<-apply(eqq mat,FUN=as.numeric,MARGIN=1)</pre>
    accessVar("bb",GUI=FALSE)
    #needs data frame with samples as lines and info as columns
```

```
#accessVar("eqq",GUI=FALSE)
      F)
    solution_models_available_r <- reactive({</pre>
    solution models available <- NULL
    data directory <- qsub ("/code", "/data", getwd())</pre>
    qq<-
scan(file=paste0(data_directory,"/",input$solution_models_file),what="character",se
p="\n", quiet=TRUE)
    foo<-grep("begin_model",qq)</pre>
    for(i in 1:length(foo)){
      if(i==length(foo)){
        toto<-substr(qq[foo[i]:length(qq)],1,1)</pre>
      }else{
        toto<-substr(qq[foo[i]:foo[i+1]],1,1)</pre>
      }
      modrow<-grep("[A-Za-z]", toto)[2]</pre>
      line<-gg[foo[i]+modrow-1]</pre>
      solution models available <- c (solution models available, strsplit (line, "
")[[1]][1])
    }
    return(sort(solution models available))
    })
     grid data r <- reactive({</pre>
        if(input$Grid_variable=="Custom"){
        grid in<-eval(parse(text=input$Custom selection))</pre>
        }else{
        grid in<-
grid data(input$Grid variable,input$Grid variable phase,crust out(),input pt)
        ł
        #Remove values
        if(input$remove values!=""){
        for (val in unlist (strsplit (input$remove values, split=", |;"))) {
        for(i in 1:length(grid in[[2]])){
        if(!is.na(grid in[[2]][i])){
             if(length(unlist(strsplit(val,split="-")))>1){
                 if(grid in[[2]][i]>=unlist(strsplit(val,split="-
"))[1]&grid_in[[2]][i]<=unlist(strsplit(val,split="-"))[2]){grid_in[[2]][i]<-NA}
             }else{
             if(grid in[[2]][i]==val){grid in[[2]][i]<-NA}}}</pre>
        }
        ł
        #apply matrix rotations
        if(input$rotation!=0){
        for(i in 1:input$rotation) {
        grid in[[2]]<-rotate(grid in[[2]])</pre>
        }
        #apply matrix reflections
        if(any(input$reflection=="Horizontal")){grid in[[2]]<-flip y(grid in[[2]])}</pre>
        if (any (input $reflection=="Vertical")) {grid in [[2]] <- flip x (grid in [[2]])}
        validate(need(nrow(grid_in[[2]])>1,"Cannot plot a grid with only 1 row"))
validate(need(ncol(grid_in[[2]])>1,"Cannot plot a grid with only 1
column"))
    if(any(input$Grid axes=="bottom")){bottom<-</pre>
create_Axes(input$Grid_bottom_axis,input$Grid_bottom_axis_grid_phase,input$Grid_bot
tom_axis_increments, "x", crust_out(), input_pt) }else{bottom<-NULL}</pre>
    if(any(input$Grid axes=="left")){left<-</pre>
create_Axes(input$Grid_left_axis,input$Grid_left_axis_grid_phase,input$Grid_left_ax
is_increments, "y", crust_out(), input_pt) }else{left<-NULL}</pre>
    if(any(input$Grid_axes=="top")){top<-
create_Axes(input$Grid_top_axis,input$Grid_top_axis_grid_phase,input$Grid_top_axis_
increments, "x", crust out(), input pt, y n) }else {top<-NULL}</pre>
    if(any(input$Grid axes=="right")){right<-</pre>
create Axes (input$Grid right axis, input$Grid right axis grid phase, input$Grid right
_axis_increments,"y",crust_out(),input_pt,x_n)}else{right<-NULL}
    #mod-tag: look into rotations
    #Apply rotations
    #if(any(input$Grid axes=="bottom")){colnames(grid in[[2]])<-</pre>
paste0(create_Axes(input$Grid_bottom_axis,input$Grid_bottom_axis_grid_phase,length(
```

```
crust[[1]])+1, "x", crust out(), input pt)[[2]][-
(length(crust[[1]])+1)],"_{",1:length(crust[[1]]),";1}")}
    #if(any(input$Grid_axes=="left")){rownames(grid_in[[2]])<-</pre>
paste0(create Axes(input$Grid left axis,input$Grid left axis grid phase,length(crus
t)+1, "y", crust out(), input pt) [[2]][-
(length(crust)+1)]," {1;",1:length(crust),"}")}
    return(list(grid_in[[1]],grid_in[[2]],bottom,left,top,right))
    })
    phase abundance r<-reactive({
    if(!is.null(input$axis)){
    switch(input$axis,
x=phase_abundance(store_r$crust_r,input$axis,as.numeric(input$path_y),input$start_x
, input$end x, input$path label, input pt = store r$input pt r),
y=phase abundance(store r$crust r,input$axis,as.numeric(input$path x),input$start y
, input$end y, input$path label, input pt = store r$input pt r)
    )
    }
    })
        PAM r<-reactive({
PAM calc(crust out(), input$PAM system, input$compile PAM, input$PAM compilation)
    })
    neaten crust<-function(crust neat=NULL, phase aliases=NULL) {</pre>
    #rename using aliases if given
    if(!phase aliases==""){
    split aliases<-strsplit(strsplit(phase aliases,c(","))[[1]],"=")</pre>
    phase_aliases<-NULL
    phase_aliases_names<-NULL
    for(i in 1:length(split aliases)){
    phase aliases<-c(phase aliases, split aliases[[i]][1])</pre>
    phase aliases names<-c(phase aliases names, split aliases[[i]][2])
    }
    names(phase aliases)<-phase aliases names</pre>
    #seperate merge commands
    merge_aliases<-grep("&",phase_aliases,value=TRUE)</pre>
    if(length(merge aliases)!=0){
    phase aliases[-grep("&",phase aliases)]
    }
    merge_aliases<-strsplit(merge_aliases,"&")</pre>
    if(length(merge aliases) == 0) {merge aliases<-""}</pre>
    if(length(phase_aliases) == 0) {phase_aliases<-""}</pre>
    if(all(phase aliases!="")|all(merge aliases!="")){
    for(x i in 1:length(crust[[1]])){
    for(y i in 1:length(crust)){
    delete<-NULL
    grab<-rownames(crust neat[[y i]][[x i]])</pre>
    if(length(grab)>0){
    grab_split<-strsplit(grab, " ")</pre>
    grab_sys<-grab_name<-grab</pre>
    for(ph in 1:length(grab)){
    grab name[ph]<-grab split[[ph]][1]</pre>
    #if first part of system is numeric extract up to end of
    if(!is.na(suppressWarnings(as.numeric(grab split[[ph]][-1][1])))){
    grab sys[ph]<-paste(grab split[[ph]][c(-1,-2)],collapse=" ")</pre>
    }else{
    grab sys[ph] <- paste (grab split[[ph]][-1], collapse="")</pre>
    }
    #rename using aliases
    if(all(phase_aliases!="")){
    for(ph in 1:length(grab)){
    if(any(grab name[ph]==phase aliases)){
    #Rename feldspars
        if(names(which(grab name[ph]==phase aliases))=="Pl|Kf"){
        if(length(intersect(major_elements,c("CAO", "K2O")))==2){
```

```
# fix-tag: currently rename feldspars in two places, in order ot allow
phase extraction, simplify this
        if(crust_neat[[y_i]][[x_i]][ph,"CAO"]>crust_neat[[y_i]][[x_i]][ph,"K2O"]){
        grab name[ph]<-"Pl"</pre>
        }else{grab name[ph]<-"Kf"}</pre>
        }
        }else{
    #Rename phases using aliases
    grab name[ph] <- names (which (grab name[ph] == phase aliases) [1])</pre>
    }
    #label unwanted phases (phases of zero mass or phases labelled as "hide")
        if(crust neat[[y i]][[x i]][ph,"mass"]==0|grab name[ph]=="hide"){
        delete<-c(delete,ph)</pre>
        }
         }
        }
    #number duplicates within systems
    renamed<-paste(grab_name,grab_sys,sep="_")</pre>
    num<-1
    while(any(duplicated(renamed))){
    renamed[which(duplicated(renamed))]<-</pre>
paste(grab_name[which(duplicated(renamed))],num,grab_sys[which(duplicated(renamed))
],sep=" ")
    num<-num+1
    }
    rownames(crust_neat[[y_i]][[x_i]])<-renamed</pre>
    3
    #merge if required
    if(all(merge_aliases!="")){
        systems<-c("rs", "es", "cumul")</pre>
        for(sys in systems) {
        for(merge try in 1:length(merge aliases)){
        merge nos<-NULL
        for(i in 1:length(merge aliases[[merge try]])){
if(any(paste(grab name,grab sys,sep=" ")==paste(merge aliases[[merge try]][i],sys,s
ep=""))){
        merge_nos<-union(merge_nos,which(grab_name==merge_aliases[[merge_try]][i]))</pre>
        ł
        }
        merger<-NULL
        if(!is.null(merge nos)){
        for(i in merge nos){
        merger<-rbind(merger,crust_neat[[y_i]][[x_i]][i,,drop=FALSE])</pre>
        }
        merged<-.wtd.add(merger,avname=names(merge aliases)[merge try])</pre>
        crust_neat[[y_i]][[x_i]][merge_nos[1],]<-merged
rownames(crust_neat[[y_i]][[x_i]])[merge_nos[1]]<-</pre>
paste(names(merge_aliases)[merge_try], sys, sep="_")
        if(length(merge nos)>1){
        delete<-c(delete,merge_nos[-1])</pre>
        ł
        }
        }
        }
        }
    #remove unwanted phases
    if(!is.null(delete)){
    crust_neat[[y_i]][[x_i]]<-crust_neat[[y_i]][[x_i]][-delete,]</pre>
    ł
    ł
    ł
    ł
    }
    }
    return(crust neat)
    }
    crust_out<-reactive({</pre>
```

```
return(neaten crust(store r$crust r,input$phase aliases))
    })
        create Axes<-
function (axes variable, axes variable phase, axes increments, axes direction, crust=NUL
L, input pt=NULL, axes line=1) {
    #Given axes variable, axes variable phase, axes increments, axes direction create
axis values
    if(axes_increments=="Increments"){axes_increments<-11}else{axes increments<-</pre>
as.numeric(axes increments)}
    if(axes direction=="y"){
    i n<-length(crust)/(axes increments-1)*(0:(axes increments-1))+1</pre>
    }else{i n<-length(crust[[1]])/(axes increments-1)*(0:(axes increments-1))+1}</pre>
    if(axes_variable=="y_i"|axes_variable=="x_i"){
    axis values<-i n[-length(i n)]</pre>
    }else{
    axis_values<-NULL
    for(i in i n[-length(i n)]){
    if(axes direction=="y"){
    if(axes_variable=="Temperature"|axes_variable=="Pressure"){
    axis_values<-c(axis_values, input pt[[i]][[axes line]][, axes variable])</pre>
    }else{
    chk<-
try(crust[[i]][[axes line]][axes variable phase,axes variable],silent=TRUE)
    if(class(chk) == "try-error") {
    axis_values<-c(axis_values,0)}else{</pre>
    axis values<-
c(axis_values,crust[[i]][[axes_line]][axes_variable_phase,axes_variable])}
    Ł
    }else{
    if(axes variable=="Temperature"|axes variable=="Pressure"){
    axis values<-c(axis values, input pt[[axes line]][[i]][,axes variable])
    }else{
    chk<-
try(crust[[axes line]][[i]][axes variable phase,axes variable],silent=TRUE)
    if(class(chk)=="try-error"){
    axis values<-c(axis values,0)}else{</pre>
    axis values<-
c(axis_values,crust[[axes_line]][[i]][axes_variable_phase,axes_variable])
    }
    ł
    ł
    }
    axis values<-
c(axis values,axis values[length(axis values)]+axis values[length(axis values)]-
axis values[length(axis values)-1])
if(axes variable=="y i"|axes variable=="x i"|axes variable=="Temperature"|axes vari
able=="Pressure") {
        axis title<-axes variable
        }else{
        axis_title<-paste(axes_variable_phase,axes variable)</pre>
    return(list(axis_title, signif(axis_values, digits=4)))
        }
        draw Grid r<-reactive({
        library(graphics)
        library (grDevices)
        validate (need (nrow (grid data r() [[2]])>1, "Cannot plot a grid with only 1
row"))
        validate (need (ncol (grid data r() [[2]])>1, "Cannot plot a grid with only 1
column"))
        bottom<-grid data r()[[3]]</pre>
        left<-grid data r()[[4]]</pre>
        top<-grid data r()[[5]]
        right<-grid data r()[[6]]
        action<-"View"
```

```
if (!is.null (reactive message$data)) {if (reactive message$data=="Saving") {action<-
"Save"}
        if(action=="Save"){
        outfile path<-
paste0(input$projects directory,"/",input$working file,"/Outputs/",input$working fi
le, " grid_", gsub("\\/", " per ", grid_data_r()[[1]]), input$file_type)
        if(input$file_type==".txt"){
        write.table(grid data r()[[2]],outfile path,sep="\t",quote=F)
        if(input$file_type==".csv"){
        write test<-try(write.csv(grid data r()[[2]],outfile path),silent=TRUE)</pre>
        if(class(write test) == "try-error") {
        cat("Error cannot write to ",outfile_path,", please close all programs that
may be accessing the file then try again\n")
        return(paste0("Error could not save Grid File: ",grid data r()[[1]],", file
may be open in another program, please close all programs that may be accessing the
file then try again\n"))
        ł
        }
        if(input$file type==".ps"){
        outfile path<-gsub("%", "%%", outfile path)</pre>
        postscript(file=outfile path,onefile=TRUE,horizontal=TRUE)
        }
        }
        if(action=="View"|(action=="Save"&input$file type==".ps")){
        filled.contour(t(flip_y(grid_data_r()[[2]])),
        plot.axes={
        if(!is.null(bottom)) {axis(1, (0:(length(bottom[[2]])-
1))/(length(bottom[[2]])-1),bottom[[2]])}else{NULL};
        if(!is.null(left)) {axis(2, (0: (length(left[[2]])-1))/(length(left[[2]])-
1),left[[2]])}else{NULL};
        if(!is.null(top)) {axis(3,(0:(length(top[[2]])-1))/(length(top[[2]])-
1),top[[2]])}else{NULL};
        if(!is.null(right)) {axis(4, (0: (length(right[[2]])-1))/(length(right[[2]])-
1), right[[2]]) }else{NULL}},
        color.palette=eval(parse(text=input$Grid colours)))
        #Colour options =
gray.colors, heat.colours, terrain.colours, rainbow, topo.colours
        if(!is.null(bottom)) {mtext(bottom[[1]],1,line=3)}
        if(!is.null(left)) {mtext(left[[1]], 2, line=3)}
        if(!is.null(top)) {mtext(top[[1]],3,line=3)}
        if(!is.null(right)) {mtext(right[[1]], 4, line=3)}
        if(action=="Save"){
        title(paste("Grid of ",gsub("\\/"," per ",grid data r()[[1]])," for
",input$working_file))
        dev.off()
        }
        }
        detach("package:graphics")
        detach("package:grDevices")
        if(action=="Save"){
        cat("File written to ",outfile path,"\n")
        return(paste0(paste("Grid of",gsub("\\/"," per ",grid_data_r()[[1]])),"
saved to ", input$projects directory, "/", input$working file, "/Outputs/\n"))
    }
3.)
draw abundance r<-reactive({</pre>
        #Plot phase abundance versus path cumulative column graph
        library(graphics)
        library(RColorBrewer)
        library(grDevices)
        #All RColorBrewer palettes display.brewer.all()
        #Display a specific pallette display.brewer.pal(12,"Set3")
        action <- "View"
if(!is.null(reactive_message$data)){if(reactive_message$data=="Saving"){action<-
"Save"}}
```

```
if(action=="Save"){
        outfile_path<-
paste0(input$projects_directory,"/",input$working_file,"/Outputs/",input$working_fi
le,"_phase_abundance_",gsub("\\/"," per
", phase abundance r() [[1]]), input$file type)
        if(input$file type==".txt"){
write_phase_abundance(phase_abundance_r(),input$working_file,input$projects_directo
ry,input$file type)
        if(input$file_type==".csv"){
        write test<-
try (write phase abundance (phase abundance r(), input$working file, input$projects dir
ectory, input$file type), silent=TRUE)
        if(class(write test) == "try-error") {
        cat("Error cannot write file please close all programs that may be
accessing the file then try again\n")
        return (paste0 ("Error could not save Phase abundance File: file may be open
in another program, please close all programs that may be accessing the file then
try again\n"))
        }
        ł
        if(input$file type==".ps"){
        cat("Error Functionality not available yet\n")
        return(paste0("Error Functionality not available yet\n"))
         # mod-tag: look into saving phase abundance directly to .ps
        #outfile_path<-gsub("%","%%",outfile_path)</pre>
        #postscript(file=outfile path,onefile=TRUE,horizontal=TRUE)
        3
        ł
        if(action=="View"|(action=="Save"&input$file type==".ps")){
        phase abundance data <- phase abundance r() [[2]]
        #subset phases
        if(!is.null(input$show abundance phases)){
        phases to show <- input $ show abundance phases
        phases present <- rownames (phase abundance data)
        if(any(phases_to_show=="Reactive Subsystem")){
        phases_to_show<-
union(phases_to_show,phases_present[setdiff(which(substrRight(phases present,3)=="
rs"), which (phases_present=="Bulk_rs"))])
        phases_to_show<-phases_to_show[-grep("Reactive Subsystem", phases_to_show)]</pre>
        if(any(phases to show=="Extract Subsystem")){
        phases to show <-
union (phases to show, phases present[setdiff (which (substrRight (phases present, 3) =="
es"), which (phases present=="Bulk es"))])
        phases to show <- phases to show [-grep ("Extract Subsystem", phases to show)]
        if(any(phases_to_show=="Cumulative Extract Subsystem")){
        phases to show <-
union (phases_to_show, phases_present[setdiff(which(substrRight(phases_present,9)=="
es_cumul"), which (phases_present=="Bulk_es_cumul"))])
        phases to show <- phases to show [-grep ("Cumulative Extract
Subsystem", phases_to_show)]
        - }
        if(any(phases to show=="Full System")){
        phases_to_show<-union(phases_to_show,phases_present)</pre>
        phases to show <- phases to show [-grep ("Full System", phases to show)]
        phase_abundance data <-
phase abundance data[match(phases to show, rownames(phase abundance data)),, drop=FAL
SE]
         #Normalise to percentage
        phase abundance data <- apply (phase abundance data, 2,
function(x) {x*100/sum(x, na.rm=T)})
        #Set colour pallette
        cols<-brewer.pal(min(nrow(phase_abundance_data),12), "Set3")</pre>
```

## #Plot

```
barplot (phase abundance data, space=0, col=cols, border=NA, legend.text=(input$legend!=
"None"), args.legend=list(x =input$legend,bty =
"n"), xlab=input$path label, ylab="Phase abundance (wt.%)")
        if(action=="Save"){
        title(paste("Grid of ",gsub("\\/"," per ",grid_data_r()[[1]])," for
", input $working file))
        dev.off()
        ł
        ł
        detach("package:graphics")
        detach("package:grDevices")
        if(action=="Save"){
        cat("File written to ",outfile path,"\n")
        return(paste0(paste("Grid of", gsub("\\/", " per ", grid_data_r()[[1]])),"
saved to ", input$projects directory, "/", input$working file, "/Outputs/\n"))
    }
1)
        draw PAM r<-reactive({
        #Bind all pres to PAM legend
        PAM legend<-c(PAM_r()[[3]], names(PAM_r()[[2]]))</pre>
        names(PAM legend) <-c("\"All fields are +\"", as.numeric(PAM r()[[2]]))</pre>
        compiled_legend<-c(PAM_r()[[3]], names(PAM_r()[[6]]))</pre>
        names(compiled legend)<-c("\"All fields are +\"",as.numeric(PAM r()[[6]]))</pre>
        action<-"View"
if(!is.null(reactive message$data)){if(reactive message$data=="Saving"){action<-
"Save"}}
        if(action=="Save"){
        outfile path<-
paste0(input$projects directory,"/",input$working file,"/Outputs/",input$working fi
le," PAM", input$file type)
        outfile legend path <-
paste0(input$projects directory,"/",input$working file,"/Outputs/",input$working fi
le," PAM legend", input$file type)
        outfile compile legend path <-
paste0 (input$projects_directory, "/Compile/", paste (sort (union (unlist (strsplit (input$
PAM compilation,",")),input$working file)),collapse=",")," compile
legend", input$file type)
         if(input$file_type==".txt"){
    write.table(PAM r()[[1]],outfile path,sep="\t",quote=F,row.names = TRUE)
    write.table(PAM legend,outfile legend path,sep="\t",quote=F,row.names =
TRUE, col.names = FALSE)
if (input$compile PAM) {write.table (compiled legend,outfile compile legend path,sep="
\t", quote=F, row.names = TRUE, col.names = FALSE) }
  if(input$file type==".csv"){
    write test<-try(write.csv(PAM r()[[1]],outfile_path,row.names =</pre>
TRUE), silent=TRUE)
    if(class(write_test) == "try-error") {
      cat ("Error cannot write to ",outfile path,", please close all programs that
may be accessing the file then try again\n")
     return (paste0 ("Error could not save phase assemblage map: ",outfile path,",
file may be open in another program, please close all programs that may be
accessing the file then try again\n"))
    ł
    write test<-try(write.csv(PAM legend,outfile legend path,row.names =</pre>
TRUE, col.names = FALSE), silent=TRUE)
    if(class(write test) == "try-error") {
      cat ("Error cannot write to ",outfile legend path,", please close all programs
that may be accessing the file then try again\n")
      return (paste0 ("Error could not save phase assemblage map legend:
",outfile legend path,", file may be open in another program, please close all
programs that may be accessing the file then try again \n"))
    }
```

```
if(input$compile PAM) {write test<-</pre>
try (write.csv (compiled legend, outfile compile legend path, row.names =
TRUE, col.names = FALSE, silent=TRUE)
    if(class(write_test) == "try-error") {
      cat ("Error cannot write to ", outfile compile legend path,", please close all
programs that may be accessing the file then try again\n")
      return(paste0("Error could not save phase assemblage map legend:
",outfile_compile_legend_path,", file may be open in another program, please close
all programs that may be accessing the file then try again n")
    }
    }
  }
          if(input$file type==".ps"){
        library(grDevices)
        postscript(file=outfile path,onefile=TRUE,horizontal=TRUE)
        3
        3
        if(action=="View"|(action=="Save"&input$file type==".ps")){
    library(graphics)
    par(mar=c(5, 4, 4, 5)+.1)
    library(grDevices)
    library(raster)
    library(rgeos)
    max_pol<-max(length(PAM_r()[[2]]),length(PAM_r()[[6]]))</pre>
    raster::plot(PAM r()[[4]],col=gray(1:max pol/max pol)[PAM r()[[5]]])
    if(input$PAM labels=="Numbers"){
    raster::text(gCentroid(PAM_r()[[4]], byid = TRUE),labels=PAM_r()[[5]],col =
"Black")
    }else{
    if(input$compile_PAM){
    raster::text(gCentroid(PAM r()[[4]], byid =
TRUE),labels=compiled_legend[PAM_r()[[5]]],col = "Black")
    }else{
    raster::text(gCentroid(PAM r()[[4]], byid =
TRUE),labels=PAM legend[PAM r()[[5]]],col = "Black")
    }
        # Create axes
    if(length(input$PAM axes)>0){
    for(j in 1:length(input$PAM axes)){
    #get variable and increment choice
    var choice <-
eval(parse(text=paste("input$PAM ",input$PAM axes[j]," axis",sep="")))
if(!(var choice=="y i"|var choice=="x i"|var choice=="Temperature"|var choice=="Pre
ssure")){
    grid_phase_choice <-
eval(parse(text=paste("input$PAM ",input$PAM axes[j]," axis grid phase",sep="")))
    ł
    increment choice<-
eval(parse(text=paste("input$PAM_", input$PAM_axes[j], "_axis_increments", sep="")))
        if(increment_choice=="Increments"){increment_choice<-</pre>
11}else{increment choice<-as.numeric(increment choice)}</pre>
    if(input$PAM_axes[j]=="left"|input$PAM_axes[j]=="right"){
    i n<-length(crust)/(increment choice-1)*(0:(increment choice-1))+1</pre>
    }else{i n<-length(crust[[1]])/(increment choice-1)*(0:(increment choice-1))+1}</pre>
    if(var_choice=="y_i"|var_choice=="x_i"){
    axis values<-i n[-length(i n)]</pre>
    }else{
    axis values<-NULL
    for(i in i n[-length(i n)]){
    if(input$PAM axes[j]=="left"|input$PAM axes[j]=="right"){
    if(var choice=="Temperature"|var choice=="Pressure") {
    axis values<-c(axis values, input pt[[i]][[1]][, var choice])</pre>
    }else{
    chk<-try(crust[[i]][[1]][grid phase choice,var choice],silent=TRUE)</pre>
    if(class(chk) == "try-error") {
    axis_values<-c(axis_values,0)}else{</pre>
```

```
axis values<-c(axis values,crust[[i]][[1]][grid phase choice,var choice])}
    ł
    }else{
    if(var choice=="Temperature"|var choice=="Pressure"){
    axis values<-c(axis_values,input_pt[[1]][[i]][,var_choice])</pre>
    }else{
    chk<-try(crust[[1]][[i]][grid_phase_choice,var_choice],silent=TRUE)</pre>
    if(class(chk) == "try-error") {
    axis values<-c(axis values,0)}else{</pre>
    axis_values<-c(axis_values,crust[[1]][[i]][grid_phase_choice,var_choice])</pre>
    ł
    }
    }
    ł
    axis_values<-
c(axis values,axis values[length(axis values)]+axis values[length(axis values)]-
axis values[length(axis values)-1])
    #round to 2 significant figures
    axis_values<-signif(axis_values,digits=4)
side_no<-switch(input$PAM_axes[j],"bottom"=1,"left"=2,"top"=3,"right"=4)</pre>
    axis(side_no, (0: (increment_choice-1))/(increment_choice-1), axis_values)
if(var choice=="y_i"|var_choice=="Temperature"|var_choice=="Press
ure"){
    mtext(var choice, side=side no, line=3)
    }else{
    mtext(paste(grid phase choice,var choice), side=side no, line=3)
    ł
    ł
    }
    if(!PAM_r()[[3]]==""){
    title(, paste("All fields are +", PAM r()[[3]]))
  }
#Add contour
    if(!input$PAM contour=="None") {
                 grid_out_mat<-matrix(0,y_n,x_n)</pre>
                 if(input$PAM contour=="Pressure"|input$PAM contour=="Temperature"){
                 for(x i in 1:x n){
                  for(y_i in 1:y_n){
             grid_out_mat[y_i,x_i]<-input_pt[[y_i]][[x_i]][, input$PAM_contour]</pre>
                  ł
                  }
                 }else{
                  for(x i in 1:x n){
                  for(y_i in 1:y_n){
                  chk<-
try(crust_out()[[y_i]][[x_i]][input$PAM_contour_grid phase,input$PAM contour],silen
t=TRUE)
    if(class(chk) == "try-error") { grid out_mat[y_i,x_i] <-0 }else{</pre>
    grid_out_mat[y_i,x_i]<-chk</pre>
    ł
                  }
                  }
                  }
                 x<-raster::raster(flip y(grid out mat))</pre>
                 if(input$PAM_contour_increments=="Default")
Increments") {raster::contour(x,add=TRUE,col="red") }else{
if (input$PAM contour increments=="In/Out") {raster::contour(x,add=TRUE,levels=0.0000
0000000000001, col="red") }else{
raster::contour(x,add=TRUE,nlevels=as.numeric(input$PAM contour increments),col="re
d")
                 }
                 }
                 }
```

```
if(action=="Save") {
```

```
title(paste("Phase Assemblage Map for", input$working file),)
  dev.off()
    write.table(PAM legend,outfile legend path,sep="\t",quote=F,row.names =
TRUE, col.names = FALSE)
if (input$compile PAM) {write.table (compiled legend,outfile compile legend path,sep="
\t",quote=F,row.names = TRUE,col.names = FALSE) }
 1
  detach("package:graphics")
  detach("package:rgeos")
  detach("package:raster")
  detach("package:sp")
  detach("package:grDevices")
  }
    if(action=="Save"){
    cat("File written to ",outfile path,"\n")
    cat("File written to ",outfile legend path,"\n")
return(paste0("Phase Assemblage Map saved to
",input$projects directory,"/",input$working file,"/Outputs/\n"))
    }
    })
    output$output header<-renderText(</pre>
      switch(input$output type,
              "Data File"=if(!is.null(store_r$crust_r)){"Compilation data file"},
             "Grid"=if(!is.null(grid data r())) {paste0(grid data r()[[1]]," on
(X,Y) grid")},
             "Phase Abundance Along
Path"=if(!is.null(phase abundance r())){phase abundance r()[[1]]},
             "PAM"=if(!is.null(store_r$crust_r)){"Phase Assemblage Map"}
    ))
    # Dyanmically create output for viewing
    output$output view <- renderUI({</pre>
    if(!is.null(input$output form)){
    switch(input$output form,
    "Data"=tableOutput("table"),
    "Legend"=tableOutput("table"),
    switch(input$output_type,
              "PAM"=plotOutput("plot"),
              "Grid"=plotOutput("plot"),
              "Phase Abundance Along Path"=plotOutput("plot")
    )
    )
    }
    1)
    output$table <- renderTable(</pre>
      switch(input$output type,
              "Data
File"=data file(crust out(), x n=length(crust out()[[1]]), y n=length(crust out()), in
put$choose columns, input$choose_rows, input$choose_points),
               "Grid"=if(!is.null(grid data r())){grid data r()[[2]]},
              "Phase Abundance Along Path"= phase abundance r() [[2]],
"PAM"=matrix(names(PAM r()[[2]]),,1,byrow=FALSE,dimnames=list(PAM r()[[2]],paste("A
ll fields are +", PAM_r()[[3]]))
    ), rownames=TRUE
    )
        output$plot <- renderPlot(</pre>
      switch(input$output type,
             "PAM"=draw PAM r(),
             "Grid"=draw Grid r(),
             "Phase Abundance Along Path"=draw abundance r()
    )
    )
            # Dyanmically create output form selections
    output$output_form_selection <- renderUI({</pre>
    form selection<-switch(input$output type,</pre>
             "Data File"="Data",
             "PAM"=c("Legend", "Plot"),
```

```
c("Data", "Plot")
    )
    radioButtons ('output form', "View", form selection, inline=TRUE)
    })
     # Dyanmically create output selections
    output$output selection <- renderUI({</pre>
           #Refresh reactive outputs if they exist
      if(exists("crust")){store_r$crust_r<-crust}</pre>
      if(exists("input pt")){store r$input pt r<-input pt}</pre>
      if(exists("input_bulk")){store_r$input_bulk_r<-input_bulk}</pre>
      if(exists("major elements")){store_r$major_elements_r<-major_elements}</pre>
      if(is.null(store r$crust r))
      return("To select ouputs: first run calculation or load previously saved
calculation
              *(variables 'crust' and 'major elements' must be present")
      all columns<-NULL
      all phases<-NULL
      for(y i in 1:length(crust out())){
        for(x i in 1:length(crust out()[[1]])){
          all columns<-union(all columns, colnames(crust out()[[y i]][[x i]]))
          all phases<-union(all phases, rownames(crust_out()[[y_i]][[x_i]]))</pre>
        }
      }
      #mod-tag: figure out better way of parsing multiple panels
      conditionalPanel("true",
      conditionalPanel("input.output_type == 'Data File'",
selectizeInput('choose_columns', 'Select Columns',
c("All"="", "Brief", "ID", "Phase", "y_i", "x_i", "Pressure(kbar)", "Temperature(C)", "wt%"
,"vol%",major elements,"mass","V(J/bar)","H(J)","Gruneisen T","Ks(bar)","Mu(bar)","
V0(km/s)","Vp(km/s)","Vs(km/s)","Vp/Vs","Rho(kg/m3)","Cp(J/K)","alpha(1/K)","beta(1
/bar)", "S(J/K)", "N(q)", "Cp/Cv"), multiple=TRUE),
      selectizeInput('choose_rows', 'Select System/Phase', c("All"="", "Reactive
subsystem", "Extract subsystem", all phases), multiple=TRUE),
      textInput('choose points', 'Select Points', "{1;1}")
      ),
      conditionalPanel("input.output_type == 'Grid'",
   selectInput('Grid_variable', 'Variable',
c("Pressure", "Temperature", all columns, "Custom"),
selected="Pressure", selectize=TRUE),
        conditionalPanel(condition= "input.Grid variable.indexOf('Custom') != -1",
        textInput('Custom selection', "Custom Selection")
        ),
conditionalPanel("['Pressure', 'Temperature', 'Custom'].indexOf(input.Grid variable)
== -1",
        selectInput('Grid variable phase', NULL, sort(all phases),
selected="Bulk_rs", selectize=TRUE)),
        # mod-tag: allow incrments setting
        #selectizeInput('Grid variable increments', NULL,
c("Increments", 3:y n), "Increments") ,
        selectInput('Grid_axes', 'Labelled axes', c("bottom","left","top","right"),
selected=c("bottom", "left"), selectize=TRUE, multiple=TRUE),
                        conditionalPanel (condition=
"input.Grid axes.indexOf('bottom') != -1",
                         selectInput('Grid bottom axis', 'Bottom Axis',
c("x i","Pressure","Temperature",colnames(crust[[1]][[1]])),
selected="x i", selectize=TRUE),
conditionalPanel("['x i', 'Pressure', 'Temperature'].indexOf(input.Grid bottom axis)
== -1",
                         selectInput('Grid bottom axis grid phase', NULL,
sort(all_phases), selected="Bulk_rs", selectize=TRUE)),
                         selectizeInput('Grid bottom axis increments', NULL,
c("Increments", 3:x n), "Increments")
                          ),
                         conditionalPanel (condition=
"input.Grid axes.indexOf('left') != -1",
```

```
selectInput('Grid left axis', 'Left Axis',
c("y i","Pressure","Temperature",colnames(crust[[1]][[1]])),
selected="v i", selectize=TRUE),
conditionalPanel("['y i', 'Pressure', 'Temperature'].indexOf(input.Grid left axis) ==
-1",
                        selectInput('Grid_left_axis_grid_phase', NULL,
sort(all_phases), selected="Bulk_rs", selectize=TRUE)),
                        selectizeInput('Grid left axis increments', NULL,
c("Increments", 3:y n), "Increments")
                         ),
                          conditionalPanel (condition=
"input.Grid axes.indexOf('top') != -1",
                        selectInput('Grid top axis', 'Top Axis',
c("x i", "Pressure", "Temperature", colnames(crust[[1]][[1]])),
selected="x_i", selectize=TRUE),
conditionalPanel("['x i', 'Pressure', 'Temperature'].indexOf(input.Grid top axis) ==
-1",
                        selectInput('Grid top axis grid phase', NULL,
sort(all phases), selected="Bulk rs", selectize=TRUE)),
                        selectizeInput('Grid_top_axis_increments', NULL,
c("Increments", 3:x n), "Increments")
                         ),
                          conditionalPanel (condition=
"input.Grid axes.indexOf('right') != -1",
                        selectInput('Grid right axis', 'Right Axis',
c("y i","Pressure", "Temperature", colnames(crust[[1]][[1]])),
selected="y i", selectize=TRUE),
conditionalPanel("['y i', 'Pressure', 'Temperature'].indexOf(input.Grid right axis)
== -1",
                        selectInput('Grid right axis grid phase', NULL,
sort(all phases), selected="Bulk rs", selectize=TRUE)),
                        selectizeInput('Grid right axis increments', NULL,
c("Increments", 3:y n), "Increments")
                         ),
      textInput('remove_values',"Remove Values"),
      selectInput('Grid colours', 'Colour Scheme',
c("gray.colors", "heat.colors", "terrain.colors", "rainbow", "topo.colors"),
selected="gray.colors", selectize=TRUE),
      radioButtons ("rotation", "Rotation", c ("0"=0, "90"=1, "180"=2, "270"=3), selected
=0, inline = TRUE, width="200px"),
      checkboxGroupInput("reflection", "Reflection", c("Horizontal", "Vertical"))
      ),
      conditionalPanel("input.output type == 'Phase Abundance Along Path'",
                       selectInput('axis', 'Axis', c("x", "y"),
selected="x", selectize=TRUE),
                       conditionalPanel("input.axis == 'x'",
                                         selectInput('path y', 'Path',
1:length(crust), selected=1, selectize=TRUE),
                                         selectInput('start x', 'Start Point',
1:length(crust[[1]]), selected=1, selectize=TRUE),
                                         selectInput('end x', 'End Point',
1:length(crust[[1]]), selected=1, selectize=TRUE)
                       ),
                       conditionalPanel("input.axis == 'y'",
                                         selectInput('path x', 'Path',
1:length(crust[[1]]), selected=1, selectize=TRUE),
                                         selectInput('start y', 'Start Point',
1:length(crust), selected=1, selectize=TRUE),
                                         selectInput('end y', 'End Point',
1:length(crust), selected=1, selectize=TRUE)
                       ),
                       uiOutput("select abundance phases"),
                       selectInput('path label', 'Path Label',
c("Point", "Pressure(kbar)", "Temperature(C)"), selected="Point", selectize=TRUE),
```

```
selectInput('legend', 'Legend', c("None", "bottomright",
"bottom", "bottomleft", "left", "topleft", "top", "topright", "right", "center"),
selected="topright", selectize=TRUE)
      ),
      conditionalPanel("input.output type == 'PAM'",
                       selectInput('PAM system', 'System', c("Reactive
Subsystem", "Extract Subsystem", "Full System"), selected="Reactive
Subsystem", selectize=TRUE),
                       selectInput('PAM labels', 'Field Labels',
c("Phases", "Numbers"), selected="Phases", selectize=TRUE),
                       selectInput('PAM axes', 'Labelled axes',
c("bottom","left","top","right"),
selected=c("bottom", "left"), selectize=TRUE, multiple=TRUE),
                       conditionalPanel (condition=
"input.PAM axes.indexOf('bottom') != -1",
                        selectInput('PAM bottom axis', 'Bottom Axis',
c("x i", "Pressure", "Temperature", colnames(crust[[1]][[1]])),
selected="x i", selectize=TRUE),
conditionalPanel("['x i', 'Pressure', 'Temperature'].indexOf(input.PAM bottom axis)
== -1",
                        selectInput('PAM bottom axis grid phase', NULL,
sort(all phases), selected="Bulk rs", selectize=TRUE)),
                        selectizeInput('PAM_bottom_axis_increments', NULL,
c("Increments", 3:x n), "Increments")
                         ),
                         conditionalPanel(condition= "input.PAM axes.indexOf('left')
! = -1",
                        selectInput('PAM left axis', 'Left Axis',
c("y i","Pressure","Temperature", colnames(crust[[1]][[1]])),
selected="y i", selectize=TRUE),
conditionalPanel("['y i', 'Pressure', 'Temperature'].indexOf(input.PAM left axis) ==
-1",
                        selectInput('PAM left axis grid phase', NULL,
sort(all phases), selected="Bulk rs", selectize=TRUE)),
                         selectizeInput('PAM_left_axis_increments', NULL,
c("Increments", 3:y n), "Increments")
                          ),
                          conditionalPanel (condition=
"input.PAM axes.indexOf('top') != -1",
                        selectInput('PAM top axis', 'Top Axis',
c("x i","Pressure","Temperature",colnames(crust[[1]][[1]])),
selected="x_i", selectize=TRUE),
conditionalPanel("['x i', 'Pressure', 'Temperature'].indexOf(input.PAM top axis) == -
1",
                        selectInput('PAM top axis grid phase', NULL,
sort(all phases), selected="Bulk rs", selectize=TRUE)),
                        selectizeInput('PAM top axis increments', NULL,
c("Increments", 3:x n), "Increments")
                         ),
                          conditionalPanel (condition=
"input.PAM axes.indexOf('right') != -1",
                        selectInput('PAM right axis', 'Right Axis',
c("y i","Pressure","Temperature",colnames(crust[[1]][[1]])),
selected="y i", selectize=TRUE),
conditionalPanel("['y i', 'Pressure', 'Temperature'].indexOf(input.PAM right axis) ==
-1",
                        selectInput('PAM right axis grid phase', NULL,
sort(all phases), selected="Bulk rs", selectize=TRUE)),
                        selectizeInput('PAM right axis increments', NULL,
c("Increments", 3:y n), "Increments")
                         ),
                         selectInput('PAM contour', 'Contour',
c("None", "Pressure", "Temperature", colnames (crust[[1]][[1]])),
selected="None", selectize=TRUE),
```

```
conditionalPanel("['None', 'Pressure', 'Temperature'].indexOf(input.PAM contour) == -
1",
                         selectInput('PAM contour grid phase', NULL,
sort(all_phases), selected="Bulk_rs", selectize=TRUE)),
                         selectizeInput('PAM contour increments', NULL, c("Default
Increments","In/Out","Set Levels","Set Contours", 3:y_n),"Default Increments"),
                         textInput('PAM_compilation', 'PAM Compilation'),
                         actionButton("create compilation", "Compile/Refresh
Legend"),
                         checkboxInput("compile PAM", "Apply compilation?",value =
FALSE)
      ),
      selectInput('file type', 'File type', c(".csv",".txt",".ps"),
selected=".csv", selectize=TRUE),
      actionButton("save data", "Save To File")
      # mod-tag: allow this functionality
      #actionButton("send gcdkit", "Send To GCDkit")
      )
    })
        #if working file is not blank on first opening, load file
        observe({
        if(!exists("first load")){first load<<-TRUE}</pre>
        if(first_load){
        projects_directory<-input$projects directory</pre>
        working_file<-input$working file
         #error handling
    reactive message$data <-error handling (working file, projects directory)
      if(reactive message$data=="error handling passed"){
         #load
if (file.exists (paste0 (projects directory, "/", working file, "/Inputs/", working file, "
.txt"))){
        reactive message$data <- paste0(on load())</pre>
        }else{
        reactive message$data <- paste0("No input file found at</pre>
",paste0(projects_directory,"/",working_file,"/Inputs/",working file,".txt"))
        }
        #Load workspace if it exists (previous calculation results)
if (file.exists (paste0 (projects directory, "/", working file, "/", working file, ".RData"
))){
load(paste0(projects directory,"/",working file,"/",working file,".RData"),envir=.G
lobalEnv)
        }
        #Refresh reactive outputs if they exist
        if(exists("crust")){store r$crust r<-crust}</pre>
        if(exists("input_pt")){store_r$input_pt_r<-input_pt}</pre>
        if(exists("input bulk")){store r$input bulk r<-input bulk}</pre>
        if(exists("major_elements")){store_r$major_elements_r<-major_elements}</pre>
    }else{
      reactive message$data
    }
    }
        first load<<-FALSE
        1)
})
```

.

## User interface (ui.r)

Build the skeleton of the user interface with a top toolbar and multiple conditional panels contained in grouped tabs as follows:

- Toolbar
  - o Projects directory
  - o Working file
  - o Save
  - o Load
  - o Run
  - o Clear
  - o Console
- Input parameters tab
  - o Size
  - Pressure and temperature
  - o Bulk composition
- Phase manipulations
  - Phase addition
  - Phase extraction
- Modelling options
  - Modelling data
  - o Additional optional parameters
  - o Extra Settings
- Outputs
  - Data file
  - o Grid
  - o Phase abundance
  - Phase assemblage maps

```
## Rcrust (ui.r)
#function-def: textInputRow(inputId, label, value = "")
textInputRow<<-function (inputId, label, value = "")</pre>
ł
  div(style="display:inline-block",
     tags$label(label, `for` = inputId),
     tags$input(id = inputId, type = "text", value = value,class="input-small"))
}
shinyUI(fixedPage(
# Add custom CSS & Javascript for Progress Indicator
  tagList(
   tags$head(
     tags$link(rel="stylesheet", type="text/css",href="style.css"),
     tags$script(type="text/javascript", src = "busy.js")
   )
  ),
  div(class = "busy",
     p("Busy.."),
     img(src="35.gif")
 ),
# Logo for Rcrust
 titlePanel(img(src="Rcrust_logo.png", align =
"left",width=150,height=60),windowTitle = "Rcrust"),
 fixedRow(textInputRow("projects directory", "Projects
Directory", value=paste0 (substring (getwd(), 1, nchar (getwd()) - 4), "Projects")),
```

```
textInputRow("working file", "Working File", working file),
actionButton("save", "Save"), actionButton("load", "Load"), actionButton("run", "Run"), a
ctionButton ("clear", "Clear"), actionButton ("console", "Console"), align="right"),
  fixedRow(verbatimTextOutput("print message")),
#Define Tabs
    tabsetPanel(id = "inTabset",
#Input Parameters UI Tab
tabPanel ("Input Parameters",
  #Size Panel
  wellPanel("Size", actionButton("size panel minimiser", label = "..."),
  conditionalPanel("(input.size panel minimiser)%2 == 0",
  fixedRow(
  column(3,textInput("x n","X")),
  column(3,textInput("y<sup>n</sup>","Y"))
  )
  )
  ),
  #PT Panel
 wellPanel ("Pressure and Temperature", actionButton ("pt panel minimiser", label =
"..."),actionButton("pt_import_panel_minimiser", label = "<-"),
  conditionalPanel("(input.pt panel minimiser)%2 == 0",
    conditionalPanel("(input.pt_import_panel_minimiser)%2 == 1",
        fileInput("file_pt", "Import P-T definitions"),
        actionButton("import pt", "Import")
  ),
                    textInput("n pt def", "Number of PT definitions"),
    # Dynamic PT definition input boxes
    uiOutput("pt")
  )),
  #Bulk Composition Panel
  wellPanel ("Bulk Composition", actionButton ("bulk comp panel minimiser", label =
"..."),actionButton("bulk import panel minimiser", label = "<-"),
  conditionalPanel ("(input.bulk comp panel minimiser) %2 == 0",
        conditionalPanel("(input.bulk import panel minimiser)%2 == 1",
            fileInput("file bulk", "Import bulk composition definitions"),
            actionButton("import bulk", "Import")
  ),
     textInput("n comp trans", "Number of Component Transformations"),
    # Dynamic transformation input boxes
    uiOutput("trans"),
    conditionalPanel("input.bulk def file == false",
    uiOutput("maj"),
    textInput("n bulk def", "Number of bulk definitions"),
    # Dynamic bulk definition input boxes
    uiOutput("bulk")
  ),
  conditionalPanel("input.bulk def file == true",
                   textInput("bulk file", "Bulk file")
  ),
  checkboxInput("bulk_def_file", "Import definitions from file",value = FALSE)
 ))
),
#End of Input Parameters UI Tab
#Phase Manipulations UI Tab
tabPanel ("Phase Manipulations",
  #Phase Addition Panel
 wellPanel("Phase Addition",actionButton("phase_addition_panel_minimiser", label =
"..."), actionButton ("phase addition import panel minimiser", label = "<-"),
  conditionalPanel("(input.phase_addition_panel_minimiser)%2 == 0",
   conditionalPanel("(input.phase addition import panel minimiser) %2 == 1",
    fileInput("file_ph_add", "Import phase addition definitions"),
    actionButton("import ph add", "Import")
  ),
  checkboxInput("ph add", "Perform Phase Addition?",value = FALSE),
    conditionalPanel("input.ph add == true",
    textInput("n_ph_add_def", "Number of addition definitions"),
      # Dynamic phase addition definition input boxes
```

```
uiOutput("ph add")
  ))),
  #Phase Extraction Panel
  wellPanel ("Phase Extraction", actionButton ("phase extraction panel minimiser",
label = "..."), actionButton("phase extraction import panel minimiser", label = "<-</pre>
"),
  conditionalPanel("(input.phase_extraction_panel_minimiser)%2 == 0",
  conditionalPanel("(input.phase_extraction_import_panel_minimiser)%2 == 1",
    fileInput("file_ph_extr", "Import phase extraction definitions"),
    actionButton("import ph extr", "Import")
  ).
  checkboxInput("ph extr", "Perform Phase Extraction?",value = FALSE),
    conditionalPanel("input.ph_extr == true",
    checkboxInput("reequilibrate steps", "Re-equilibrate reactive subsystem after
phase extraction?", value = TRUE),
    textInput("n ph extr def", "Number of extraction definitions"),
      # Dynamic phase extraction input boxes
      uiOutput("ph extr")
    )))
),
#End of Phase Manipulations UI Tab
#Modelling Options UI Tab
tabPanel("Modelling Options",
  #Modelling data Panel
  wellPanel ("Modelling Data", actionButton ("modelling data panel minimiser", label =
"···"),
   conditionalPanel("(input.modelling data panel minimiser) %2 == 0",
      textInput("meemum path", "Meemum version", "meemum.exe"),
      textInput("perplex_option_file", "Perple_X Option File", "perplex option.dat"),
      textInput("thermodynamic_data_file", "Thermodynamic Data File", "hpllver.dat"),
textInput("solution_models_file", "Solution Models
File", "solution model 673.dat"),
      # Dynamic solution models input boxes
      uiOutput("solution models")
               )),
#Additional optional parameters Panel
        wellPanel ("Additional optional
parameters", actionButton ("additional optional parameters panel minimiser", label =
"..."),
conditionalPanel("(input.additional_optional_parameters_panel_minimiser)%2 == 0",
                 textInput ("saturated components", "Saturated components"),
                 textInput ("saturated phase components", "Saturated phase
components"),
                 textInput ("independent potential fugacity activity", "Independent
potential/fugacity/activity"),
                 textInput("exclude phases", "Exclude phases")
                 )),
  #Extra Settings Panel
 wellPanel ("Extra Settings", actionButton ("extra settings panel minimiser", label =
"..."),
  conditionalPanel("(input.extra_settings_panel_minimiser)%2 == 0",
      selectInput("end of calc", "When calculation is complete:", c("Return to
Interface"="Return to
Interface", "Logout"="Logout", "Shutdown"="Shutdown"), selected="Return to
Interface", selectize=TRUE)
               ))
  ),
#End of Modelling Options UI Tab
#Outputs UI Tab
tabPanel("Outputs",
         sidebarLayout(
           sidebarPanel(
            textInput('phase aliases', "Phase Aliases"),
            selectInput('output_type', 'Select Output', c("Data File", "Grid", "Phase
Abundance Along Path", "PAM"), selected="Data File", selectize=TRUE),
            uiOutput("output_form_selection"),
            # Dynamic output selection boxes
```

```
uiOutput("output_selection")
),
mainPanel(
    h4(textOutput("output_header", container = span)),
uiOutput("output_view")
    )
),
,selected = "Input Parameters")
#End of tabs
)
#End of page
)
#End of Shiny
```

## **ADDENDUM D: Supplementary data for Research Paper 3**

Included within the thesis files for evaluation is an excel document containing compositions of a natural s-type granite array and the modelled melt compositions produced by the study "A phase equilibrium investigation of selected source controls on the composition of melt batches generated by sequential melting of an average metapelite" developed as part of the thesis by M.J. Mayne.