

Modelling DNA Hairpins

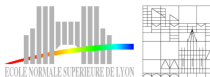
Jalal Errami¹

Supervisors: M. Peyrard¹ N. Theodorakopoulos²

¹Laboratoire de Physique
Ecole Normale Supérieure de Lyon

²TPCI/NHRF, Athens
Fachbereich Physik
Universität Konstanz

May 11, 2007/ Lyon



Outline

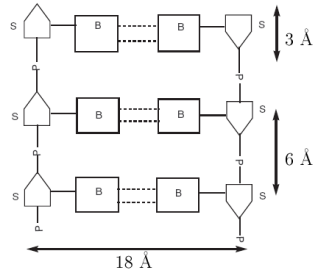
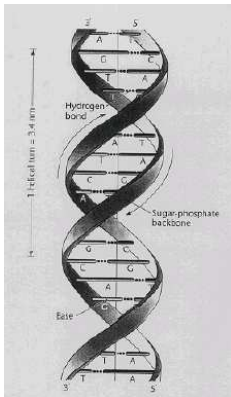
- 1 DNA molecule and Single-Stranded DNA
- 2 Experimental properties of DNA Hairpins
- 3 A two dimensional lattice model
- 4 PBD-Polymer model for DNA Hairpins

Outline

- 1 DNA molecule and Single-Stranded DNA**
- 2 Experimental properties of DNA Hairpins
- 3 A two dimensional lattice model
- 4 PBD-Polymer model for DNA Hairpins

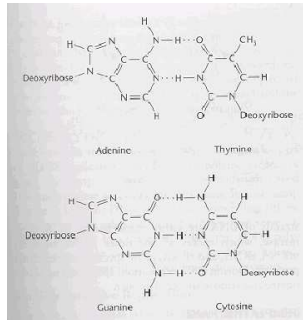
Structure and conformation

- DNA is a very long helicoidal molecule composed of two chains of deoxyribonucleotides:



Structure and conformation

- A nucleotide is composed of three molecular parts
 - A cyclic sugar (desoxyribose)
 - A purine or a pyrimidine base:
 - Adenine-Guanine-Cytosine-Thymine
 - A phosphate linked to the sugar



Properties

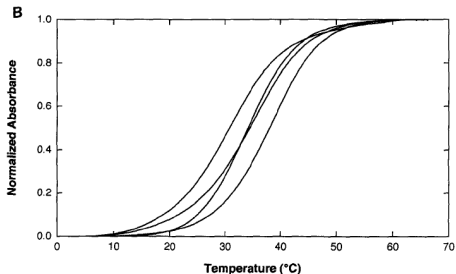
- The stability of DNA results from various interactions
 - Hydrogen bonding between complementary bases
 - Stacking interaction between base-pairs
- Melting of DNA
 - The two strands of the DNA can be dissociated by **heat**
 - The melting can be followed by the UV absorbance measurement

Properties

- The stability of DNA results from various interactions
 - Hydrogen bonding between complementary bases
 - Stacking interaction between base-pairs
- Melting of DNA
 - The two strands of the DNA can be dissociated by **heat**
 - The melting can be followed by the UV absorbance measurement

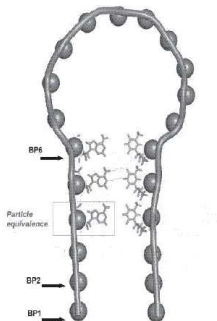
Properties

- The stability of DNA results from various interactions
 - Hydrogen bonding between complementary bases
 - Stacking interaction between base-pairs
- Melting of DNA
 - The two strands of the DNA can be dissociated by **heat**
 - The melting can be followed by the UV absorbance measurement



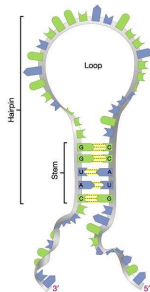
DNA Hairpins

- Single Strands of DNA with complementary bases at its two ends
→ 5'-CCCAA-(N)_n-TTGGG-3'
- Schematic secondary structure



Interest

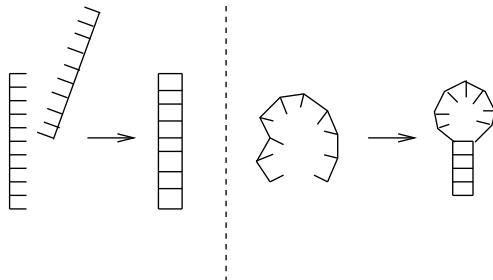
- Biological interest
 - Loop formation is a first step in the folding of the RNA



- DNA hairpins provide very sensitive probes for short DNA sequences

Interest

- Physical interest
 - DNA hairpins are simple systems for the understanding of the self-assembly of DNA



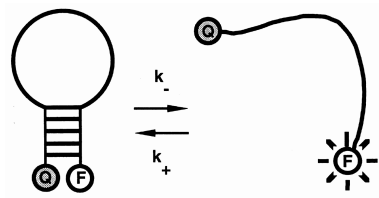
- Modelling the fluctuations of hairpins is more challenging than the thermal denaturation of DNA
 - it is not simply the reverse process of its opening

Outline

- 1 DNA molecule and Single-Stranded DNA
- 2 Experimental properties of DNA Hairpins**
- 3 A two dimensional lattice model
- 4 PBD-Polymer model for DNA Hairpins

Measurement Principle

- **Molecular Beacons** (G. Bonnet *et al*, Proc. Natl. Acad. Sci. USA **95**, 8602-8606)
 - Oligonucleotides with a fluorophore and a quencher attached at its two ends: 5'-CCCAA-(N)_n-TTGGG-3'

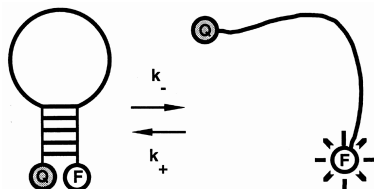


- Fluorescence Resonance Energy Transfer
 - The conformational state is directly reported by the fluorescence
 - The fraction of open beacons can be measured

$$f(D) = \frac{(D) - b}{b - a}$$

Measurement Principle

- **Molecular Beacons** (G. Bonnet *et al*, Proc. Natl. Acad. Sci. USA **95**, 8602-8606)
→ Oligonucleotides with a fluorophore and a quencher attached at its two ends: 5'-CCCAA-(N)_n-TTGGG-3'

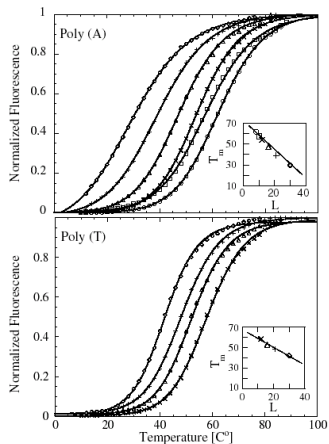


- **Fluorescence Resonance Energy Transfer**
 - The conformational state is directly reported by the fluorescence
 - The fraction of open beacons can be measured

$$f(T) = \frac{I(T) - I_c}{I_0 - I_c}$$

Results

- Melting curves for different loop sequences



- The melting temperature T_m decreases with the loop length
- The decay is most important for poly(A)
- T_m is higher for a poly(T) than a poly(A)-loop

Measurement principle

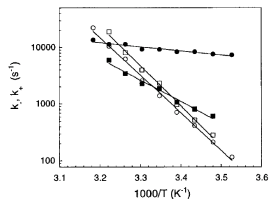
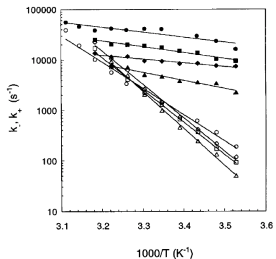
- **Fluorescence Correlation Spectroscopy**
→ Measurement of the autocorrelation function that gives the sum of the kinetic rates k_- and k_+
- The equilibrium constant gives the ratio of the kinetic rates

$$K(T) = \frac{f(T)}{1 - f(T)}$$

$$K(T) = \frac{k_-(T)}{k_+(T)}$$

Results

● Rates of opening and closing in Arrhenius plot

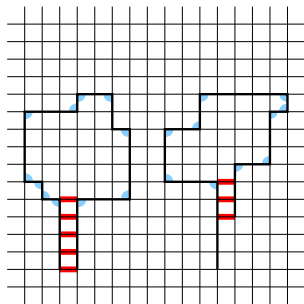


- Kinetics of opening do not depend on the loop sequence
- The rate of closing decreases with the loop length
- The activation energy is only affected by the nature of the loop

Outline

- 1 DNA molecule and Single-Stranded DNA
- 2 Experimental properties of DNA Hairpins
- 3 A two dimensional lattice model**
- 4 PBD-Polymer model for DNA Hairpins

Description of the model



(S. Cuesta-López, J. Errami, F. Falo,
and M. Peyrard, J. Biol. Phys. **31**,
273-301)

- Total energy of the chain

$$E = n_A E_A + \frac{1}{2} \sum_{j=1}^{n_s} \sum_{j'=1}^{n_s} e(j, j')$$

$$e(j, j') = \delta(t_j - t_{j'}) \delta(d_{jj'} - 1) a(j) a(j') E_{HB}(t_j)$$

- **Hydrogen bonds** between complementary bases

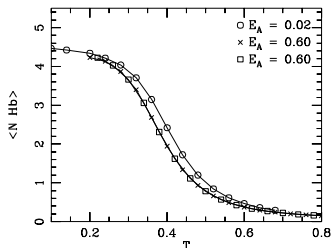
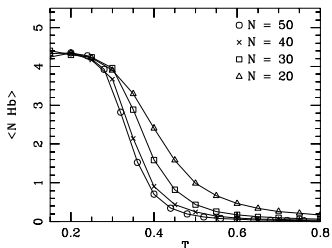
$$E_{HB} < 0$$

- **Flexibility** of the chain and stacking interaction

$$E_A > 0$$

Thermodynamics of the opening-closing transition

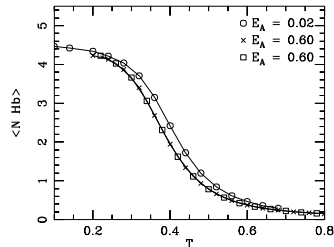
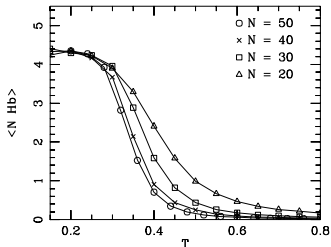
● Transition in the absence of mismatch



- The melting temperature T_m decreases with the loop length
→ Good agreement with the experiments
- The melting temperature T_m decreases with the increase of the rigidity
→ The effect is too small to model (T)-loop and (A)-loop
- Role of the mismatches

Thermodynamics of the opening-closing transition

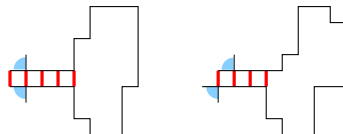
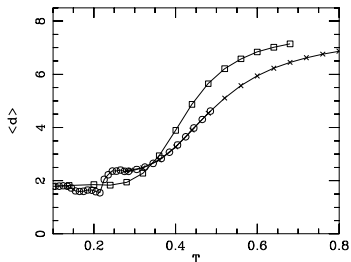
● Transition in the absence of mismatch



- The melting temperature T_m decreases with the loop length
→ Good agreement with the experiments
- The melting temperature T_m decreases with the increase of the rigidity
→ The effect is too small to model (T)-loop and (A)-loop
- Role of the mismatches

Thermodynamics of the opening-closing transition

● Role of the mismatches



- The melting curve is smoother
- The melting curve shows an additional fairly sharp kink
→ The mismatched closings are metastable states

Kinetics of opening and closing

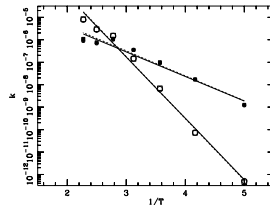
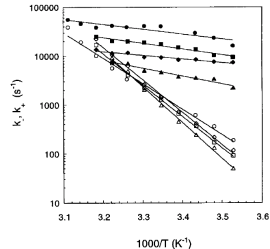
- Chemical equilibrium between closed and open states

$$\frac{d[C]}{dt} = -k_o[C] + k_{cl}[O]$$

$$\frac{d[O]}{dt} = +k_o[C] - k_{cl}[O]$$

$$k_o = \frac{1}{\tau} \frac{1}{1 + K_e} \quad k_{cl} = \frac{1}{\tau} \frac{K_e}{1 + K_e}$$

→ Studying the opening of the hairpins we can also get the kinetics of closing



Discussion

- Thermodynamic and kinetic results are in qualitative agreement with respect to the experiments
- No quantitative comparisons are possible
 - There is not enough degrees of freedom in the model
 - The difference between poly(T) and poly(A) is not well described
 - To get good statistics the calculation could become very long

Discussion

- Thermodynamic and kinetic results are in qualitative agreement with respect to the experiments
- No quantitative comparisons are possible
 - There is not enough degrees of freedom in the model
 - The difference between poly(T) and poly(A) is not well described
 - To get good statistics the calculation could become very long

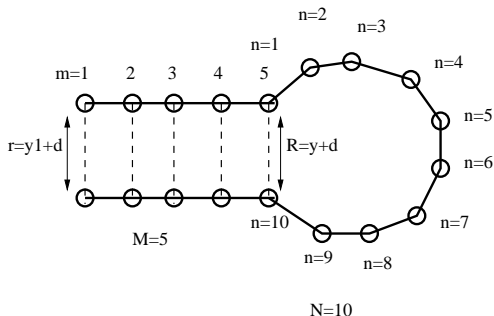
Outline

- 1 DNA molecule and Single-Stranded DNA
- 2 Experimental properties of DNA Hairpins
- 3 A two dimensional lattice model
- 4 PBD-Polymer model for DNA Hairpins**

Presentation of the model

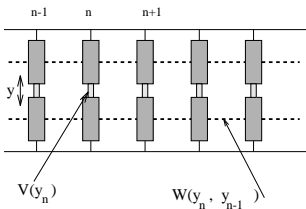
- The model of the hairpin contains two parts
 - The loop which is treated as a polymer in three dimensions
 - The stem which is an extension of the ends of the loop with additional interactions: PBD-model

(J. Errami, N. Theodorakopoulos and M. Peyrard, *Modelling DNA beacons at the mesoscopic scale*, submitted to European Physical Journal E)



PBD-Model for melting

- PBD model



- Modelling the interactions at the scale of the base
 - Hydrogen bonding between complementary bases

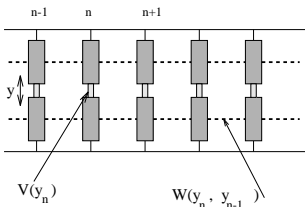
$$V(y_n) = D(e^{-\alpha y_n} - 1)^2$$

- Coupling between consecutive base-pairs

$$W(y_n, y_{n-1}) = \frac{K}{2} \left[1 + \rho e^{-\alpha(y_n + y_{n-1})} \right] (y_n - y_{n-1})^2$$

PBD-Model for melting

- PBD model



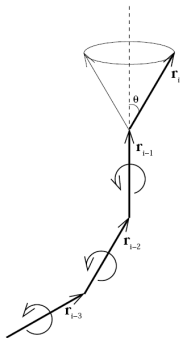
- Modelling the interactions at the scale of the base
 - Hydrogen bonding between complementary bases

$$V(y_n) = D (e^{-ay_n} - 1)^2$$

- Coupling between consecutive base-pairs

$$W(y_n, y_{n-1}) = \frac{K}{2} \left[1 + \rho e^{-\alpha(y_n + y_{n-1})} \right] (y_n - y_{n-1})^2$$

Freely Rotating Chain



The root mean square distance scales as \sqrt{N} for large N

$$\langle R^2 \rangle = Nl^2 \frac{1 + \cos \theta}{1 - \cos \theta}$$

The chain has a “stiffness”

$$\lim_{N \rightarrow \infty} \langle R \cdot u_0 \rangle \equiv l_p = \frac{l}{1 - \cos \theta}$$

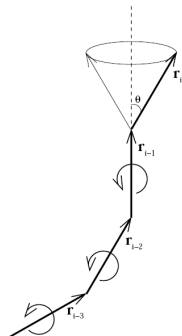
→ It also corresponds to the correlation length in the continuum limit approximation

End-to-end distance probability distribution

R scales as \sqrt{N} for large N

→ The probability distribution is Gaussian for large N

Freely Rotating Chain



The root mean square distance scales as \sqrt{N} for large N

$$\langle R^2 \rangle = Nl^2 \frac{1 + \cos \theta}{1 - \cos \theta}$$

The chain has a “stiffness”

$$\lim_{N \rightarrow \infty} \langle \mathbf{R} \cdot \mathbf{u}_0 \rangle \equiv l_p = \frac{l}{1 - \cos \theta}$$

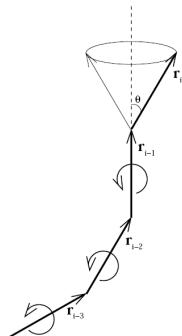
→ It also corresponds to the correlation length in the continuum limit approximation

End-to-end distance probability distribution

R scales as \sqrt{N} for large N

→ The probability distribution is Gaussian for large N

Freely Rotating Chain



The root mean square distance scales as \sqrt{N} for large N

$$\langle \mathbf{R}^2 \rangle = Nl^2 \frac{1 + \cos \theta}{1 - \cos \theta}$$

The chain has a “stiffness”

$$\lim_{N \rightarrow \infty} \langle \mathbf{R} \cdot \mathbf{u}_0 \rangle \equiv l_p = \frac{l}{1 - \cos \theta}$$

→ It also corresponds to the correlation length in the continuum limit approximation

End-to-end distance probability distribution

\mathbf{R} scales as \sqrt{N} for large N

→ The probability distribution is Gaussian for large N

Kratky-Porod Chain (KP)

Hamiltonian of the chain

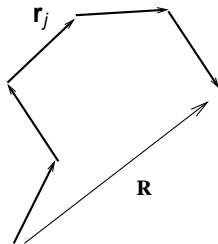
$$H = -\epsilon \sum_{j=1}^{N-1} (\mathbf{r}_j \cdot \mathbf{r}_{j+1} - l^2)$$

The persistence length depends on the temperature

$$l_p = -\frac{l}{\ln [\coth b - \frac{1}{b}]} \approx lb = l \times \frac{\epsilon l^2}{k_B T}$$

No analytical expression for the end-to-end probability distribution

→ Powerful numerical calculation in terms of a finite sum of Bessel functions



Kratky-Porod Chain (KP)

Hamiltonian of the chain

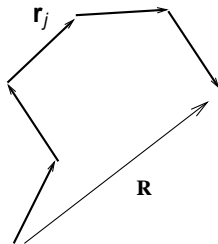
$$H = -\epsilon \sum_{j=1}^{N-1} (\mathbf{r}_j \cdot \mathbf{r}_{j+1} - l^2)$$

The persistence length depends on the temperature

$$l_p = -\frac{l}{\ln [\coth b - \frac{1}{b}]} \approx lb = l \times \frac{\epsilon l^2}{k_B T}$$

No analytical expression for the end-to-end probability distribution

→ Powerful numerical calculation in terms of a finite sum of Bessel functions



Kratky-Porod Chain (KP)

Hamiltonian of the chain

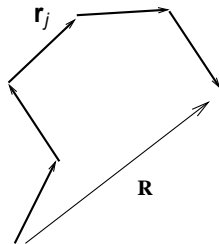
$$H = -\epsilon \sum_{j=1}^{N-1} (\mathbf{r}_j \cdot \mathbf{r}_{j+1} - l^2)$$

The persistence length depends on the temperature

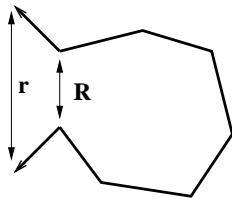
$$l_p = -\frac{l}{\ln [\coth b - \frac{1}{b}]} \approx lb = l \times \frac{\epsilon l^2}{k_B T}$$

No analytical expression for the end-to-end probability distribution

→ Powerful numerical calculation in terms of a finite sum of Bessel functions



Growth of a polymer chain $S(r|R)$



Probability of the growth chain $P_{N+2}(r)$
 → derived from $P_N(R)$

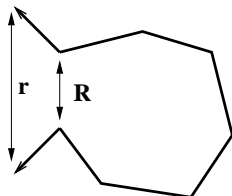
$$\int_0^{\infty} dR P_N(R) S(r|R) = P_{N+2}(r) \quad \forall r, N$$

The conditional probability distribution $S(r|R)$

$$\int_0^{\infty} dr S(r|R) = 1 \quad \forall R$$

Distribution of the added bond vectors assumed to be **Gaussian**

Growth of a polymer chain $S(r|R)$



Probability of the growth chain $P_{N+2}(r)$
 \rightarrow derived from $P_N(R)$

$$\int_0^\infty dR P_N(R) S(r|R) = P_{N+2}(r) \quad \forall r, N$$

The conditional probability distribution $S(r|R)$

$$\int_0^\infty dr S(r|R) = 1 \quad \forall R$$

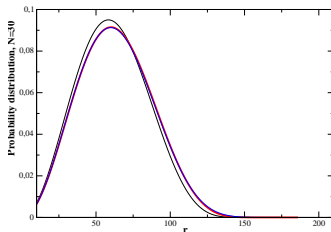
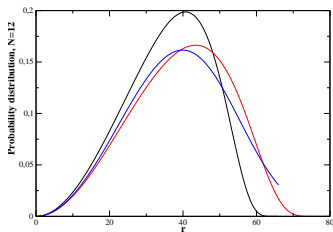
Distribution of the added bond vectors assumed to be **Gaussian**

Conditional probability distribution $S(r|R)$

Effective Gaussian approach

→ Approximate $P_N(R)$ by a Gaussian chain that gives the correct **persistence length**

The Gaussian approximation can be rough for small N but quite good for the extension of the chain



Partition function

- Construction of the reduced partition function of the hairpin
 - Partition function of a chain for a given end-to-end distance R

$$Z_N(R) = Z_N^{\text{tot}} P_N(R)$$

- Suppose that we add one bond at each end

$$Z_{N+2}(r_{M-1}) = P_{N+2}(r_{M-1}) Z_{N+2}^{\text{tot}}$$

- Introducing the S function

$$Z_{N+2}(r_{M-1}) = Z_{N+2}^{\text{tot}} \int dr_M S(r_{M-1} | r_M) P_N(r_M)$$

Partition function

- Construction of the reduced partition function of the hairpin
 - Partition function of a chain for a given end-to-end distance R

$$Z_N(R) = Z_N^{\text{tot}} P_N(R)$$

- Suppose that we add one bond at each end

$$Z_{N+2}(r_{M-1}) = P_{N+2}(r_{M-1}) Z_{N+2}^{\text{tot}}$$

- Introducing the S function

$$Z_{N+2}(r_{M-1}) = Z_{N+2}^{\text{tot}} \int dr_M S(r_{M-1} | r_M) P_N(r_M)$$

Partition function

- Construction of the reduced partition function of the hairpin
 - Partition function of a chain for a given end-to-end distance R

$$Z_N(R) = Z_N^{\text{tot}} P_N(R)$$

- Suppose that we add one bond at each end

$$Z_{N+2}(r_{M-1}) = P_{N+2}(r_{M-1}) Z_{N+2}^{\text{tot}}$$

- Introducing the S function

$$Z_{N+2}(r_{M-1}) = Z_{N+2}^{\text{tot}} \int dr_M S(r_{M-1} | r_M) P_N(r_M)$$

Partition function

- Construction of the reduced partition function of the hairpin
 - Then we put the additional interactions according to the PBD model

$$Z_{N+2}(r_{M-1}) = Z_{N+2}^{tot} e^{-\beta V(r_{M-1})} \int dr_M e^{-\beta(W(r_{M-1}, r_M) + V(r_M))} S(r_{M-1}|r_M) P_N(r_M)$$

- Finally we extend the process to the hairpin

$$Z(r) = Z_{loop(N+2(M-1))} e^{-\beta V(r)} \times \int_0^{+\infty} \prod_{i=2}^M dr_i \prod_{i=2}^M S(r_{i-1}|r_i) e^{-\beta[V(r_i) + W(r_{i-1}, r_i)]} P_N(r_M)$$

Partition function

- Construction of the reduced partition function of the hairpin
 - Then we put the additional interactions according to the PBD model

$$Z_{N+2}(r_{M-1}) = Z_{N+2}^{tot} e^{-\beta V(r_{M-1})} \int dr_M e^{-\beta(W(r_{M-1}, r_M) + V(r_M))} S(r_{M-1} | r_M) P_N(r_M)$$

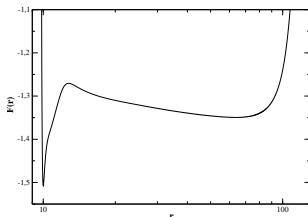
- Finally we extend the process to the hairpin

$$Z(r) = Z_{loop(N+2(M-1))} e^{-\beta V(r)} \times \int_0^{+\infty} \prod_{i=2}^M dr_i \prod_{i=2}^M S(r_{i-1} | r_i) e^{-\beta[V(r_i) + W(r_{i-1}, r_i)]} P_N(r_M)$$

Melting curves

- Free energy landscape

$$F(r) = -k_b T \ln Z(r)$$



→ The shape of $F(r)$ justifies the image of the two-state system

- Melting curves

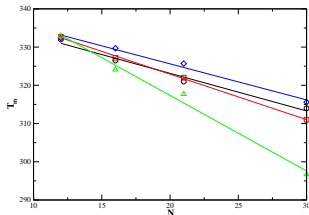
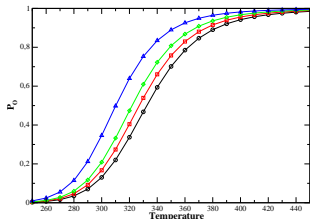
$$f = \frac{K_{eq}}{1 + K_{eq}} = \frac{\frac{P_0}{P_C}}{1 + \frac{P_0}{P_C}} = P_0 = \frac{\int_{r_c}^{+\infty} dr Z(r)}{\int_0^{+\infty} dr Z(r)}$$

FRC Model

- Melting curves equivalent to poly(T)

$k=0.025 \text{ eV}\cdot\text{\AA}^{-2}$, $\alpha=6.9 \text{ \AA}^{-1}$,
 $\delta = 0.35$, $\rho = 5$. $D=0.112 \text{ eV}$,
 $\theta = 50^\circ$, ○: $N=12$; □: $N=16$;
 ◇: $N=21$; △: $N=30$

□: $D=0.112 \text{ eV}$, $\theta = 50^\circ$;
 ◇: $D=0.119 \text{ eV}$, $\theta = 45^\circ$;
 △: $D=0.100 \text{ eV}$, $\theta = 64^\circ$

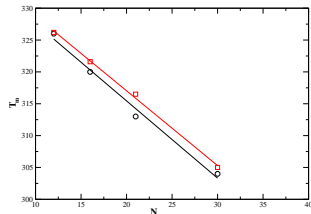
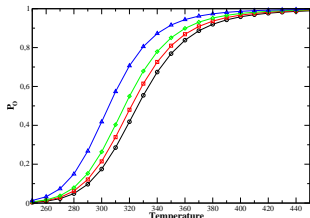


FRC model

- Melting curves equivalent to poly(A)

$$D=0.112 \text{ eV}, k=0.025 \text{ eV}\cdot\text{\AA}^{-2}, \alpha=6.9 \text{ \AA}^{-1}, \delta = 0.35, \rho = 5,$$

$$\theta = 48^\circ, \circ: N=12; \square: N=16; \diamond: N=21; \triangle: N=30$$



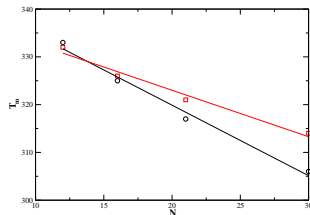
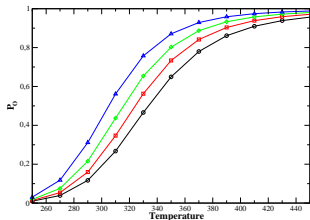
N	$\theta = 50^\circ, \frac{\Delta P}{\Delta T} T_m$	$\theta = 48^\circ, \frac{\Delta P}{\Delta T} T_m$	Poly(T) (Exp)	Poly(A) (Exp)
12	3.6	3.7	11	9
16	3.7	3.8	11	8.5
21	3.7	3.8	11	8.5
30	3.9	4.0	11	7.5

KP model

- Melting curves equivalent to poly(T)

$$D=0.107 \text{ eV}, k=0.025 \text{ eV}\cdot\text{\AA}^{-2}, \alpha=6.9 \text{ \AA}^{-1}, \delta = 0.35, \rho = 5,$$

$$\epsilon = 0.0018 \text{ eV}\cdot\text{\AA}^{-2}. \bullet: N=12; \square: N=16; \diamond: N=21; \triangle: N=30$$

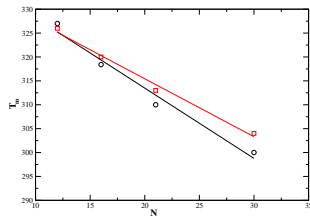
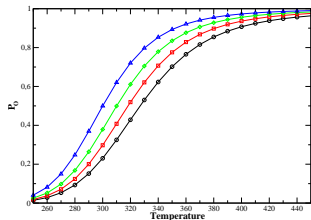


N	$\epsilon=0.0018 \text{ eV}\cdot\text{\AA}^{-2}, \frac{\Delta P}{\Delta T} T_m$	Poly(T) (Exp), $\frac{\Delta P}{\Delta T} T_m$
12	3.2	11
16	3.4	11
21	3.45	11
30	3.8	11

KP model

- Melting curves equivalent to poly(A)

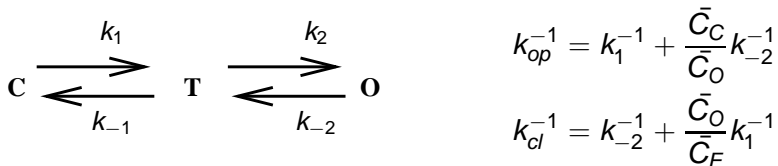
$D=0.107$ eV, $k=0.025$ eV.Å⁻², $\alpha=6.9$ Å⁻¹, $\delta = 0.35$, $\rho = 5$,
 $\epsilon = 0.00195$ eV.Å⁻²; ●: $N=12$; □: $N=16$; ◇: $N=21$; △: $N=30$



N	$\epsilon=0.00195$ eV.Å ⁻² , $\frac{\Delta P}{\Delta T} T_m$	Poly(A) (Exp), $\frac{\Delta P}{\Delta T} T_m$
12	3.25	9
16	3.45	8.5
21	3.6	8.5
30	3.8	7.5

Theoretical predictions

- Transition state theory



- The system is evolving on a one-dimensional free energy surface

$$k_{op}^{-1} = Z_C \int_{-\infty}^{+\infty} dr \frac{e^{-\beta F(r)} J^2(r)}{D(r)} = \frac{Z_C}{Z_O} k_{cl}^{-1}$$

$$J(r) = \begin{cases} \int_{-\infty}^r dx \frac{e^{-\beta(F(x)-F(r))}}{Z_C} & \forall r < r_T \\ \int_r^{+\infty} dx \frac{e^{-\beta(F(x)-F(r))}}{Z_O} & \forall r > r_T \end{cases}$$

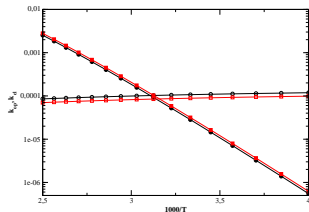
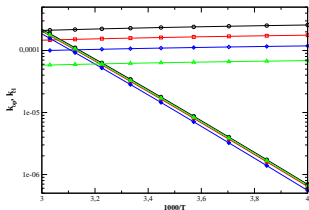
FRC model

- Rates of opening and closing

$D=0.112$ eV, $k=0.025$ eV.Å⁻², $\alpha=6.9$ Å⁻¹, $\delta = 0.35$, $\rho = 5$.

Left: $\theta = 50^\circ$; ●: $N=12$; □: $N=16$; ◇: $N=21$; △: $N=30$.

Right: $N=21$, black: $\theta = 50^\circ$, red: $\theta = 48^\circ$



	E_{op} , model	E_{cl} , model	E_{op} , exp	E_{cl} , exp
Poly(T)	11.5	-0.33	32	3.4
Poly(A)	11.5	-0.33	32	17.4

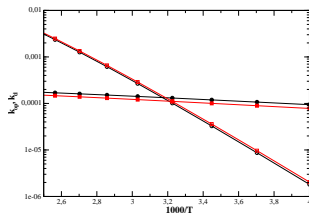
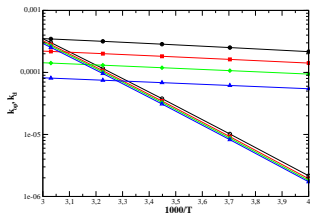
KP model

- Rates of opening and closing

$D=0.107$ eV, $k=0.025$ eV.Å⁻², $\alpha=6.9$ Å⁻¹, $\delta = 0.35$, $\rho = 5$.

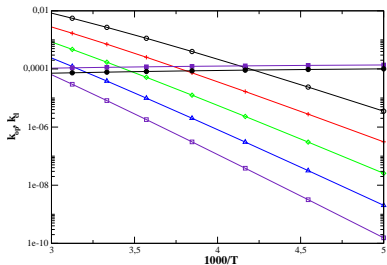
Left: $\epsilon=0.0018$ eV.Å⁻²; ○: $N=12$; □: $N=16$; ◇: $N=21$; △: $N=30$.

Right: $N=21$, black: $\epsilon=0.0018$ eV.Å⁻², red: $\epsilon=0.00195$ eV.Å⁻²

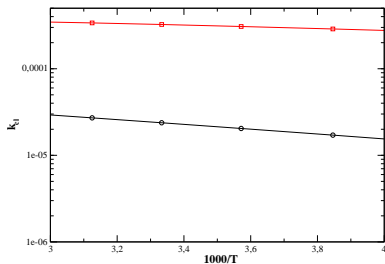


	E_{op} , model	E_{cl} , model	E_{op} , exp	E_{cl} , exp
Poly(T)	10	+1	32	3.4
Poly(A)	10	+1	32	17.4

● Effect of D and ϵ on the kinetics



○: $D=0.08$ eV; □: $D=0.09$ eV;
 ◇: $D=0.10$ eV; △: $D=0.11$ eV,
 ×: $D=0.12$ eV



○: $\epsilon=0.0040$ $\text{eV} \cdot \text{\AA}^{-2}$,
 □: $\epsilon=0.0010$ $\text{eV} \cdot \text{\AA}^{-2}$

Discussion

● Thermodynamics

- We are able to describe the dependance of T_m with the loop length for poly(T) and poly(A)
- We get too large transition widths

● Kinetics

- Our results are in qualitative agreements with the experiments
- We can describe the kinetics of poly(T)
- We are missing something to deal with the problem of poly(A)

Discussion

- Thermodynamics
 - We are able to describe the dependance of T_m with the loop length for poly(T) and poly(A)
 - We get too large transition widths
- Kinetics
 - Our results are in qualitative agreements with the experiments
 - We can describe the kinetics of poly(T)
 - We are missing something to deal with the problem of poly(A)

Discussion

- Thermodynamics
 - We are able to describe the dependance of T_m with the loop length for poly(T) and poly(A)
 - We get too large transition widths
- Kinetics
 - Our results are in qualitative agreements with the experiments
 - We can describe the kinetics of poly(T)
 - We are missing something to deal with the problem of poly(A)

- We have studied the self assembly of DNA Hairpins with two models
- Lattice model
 - The results are qualitatively good
 - It helps us in the understanding of the physics of the system
- PBD-Polymer model
 - The results are in semi-quantitative agreement with the experiments
 - It shows some limitations
 - The behavior of a single strand of DNA depends on its sequence
 - Poly(T) can be viewed as a polymer
 - Poly(A)?

- We have studied the self assembly of DNA Hairpins with two models
- Lattice model
 - The results are qualitatively good
 - It helps us in the understanding of the physics of the system
- PBD-Polymer model
 - The results are in semi-quantitative agreement with the experiments
 - It shows some limitations
 - The behavior of a single strand of DNA depends on its sequence
 - Poly(T) can be viewed as a polymer
 - Poly(A)?

- We have studied the self assembly of DNA Hairpins with two models
- Lattice model
 - The results are qualitatively good
 - It helps us in the understanding of the physics of the system
- PBD-Polymer model
 - The results are in semi-quantitative agreement with the experiments
 - It shows some limitations
 - The behavior of a single strand of DNA depends on its sequence
 - Poly(T) can be viewed as a polymer
 - Poly(A)?

DNA and ssDNA

ooooo

Experimental results

oooo

Lattice model

oooo

PBD-Polymer model

oooooooooooooooooooo

Conclusion

- Microscopic model

→Modelling of all the interactions between the atoms

- Potential describing the stretching of covalent bonds

$$k_{\text{bond}} (r - r_0)^2$$

- Potential of angular rigidity

$$k_f (\theta - \theta_0)^2$$

- Potential of torsion

$$k_g (1 + \cos \phi)$$

- Lennard-Jones potential for non-bonding interactions

$$4\epsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 \right]$$

- Microscopic model

→Modelling of all the interactions between the atoms

- Potential describing the stretching of covalent bonds

$$k_{\text{bond}} (r - r_0)^2$$

- Potential of angular rigidity

$$k_f (\theta - \theta_0)^2$$

- Potential of torsion

$$k_g (1 + \cos \phi)$$

- Lennard-Jones potential for non-bonding interactions

$$4\epsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 \right]$$

- Microscopic model

→Modelling of all the interactions between the atoms

- Potential describing the stretching of covalent bonds

$$k_{\text{bond}} (r - r_0)^2$$

- Potential of angular rigidity

$$k_f (\theta - \theta_0)^2$$

- Potential of torsion

$$k_g (1 + \cos \phi)$$

- Lennard-Jones potential for non-bonding interactions

$$4\epsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 \right]$$

- Microscopic model

→Modelling of all the interactions between the atoms

- Potential describing the stretching of covalent bonds

$$k_{\text{bond}} (r - r_0)^2$$

- Potential of angular rigidity

$$k_f (\theta - \theta_0)^2$$

- Potential of torsion

$$k_g (1 + \cos \phi)$$

- Lennard-Jones potential for non-bonding interactions

$$4\epsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 \right]$$

- Microscopic model

→Modelling of all the interactions between the atoms

- Potential describing the stretching of covalent bonds

$$k_{\text{bond}} (r - r_0)^2$$

- Potential of angular rigidity

$$k_f (\theta - \theta_0)^2$$

- Potential of torsion

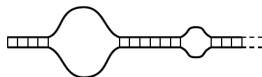
$$k_g (1 + \cos \phi)$$

- Lennard-Jones potential for non-bonding interactions

$$4\epsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 \right]$$

● Poland-Scheraga model

- Model consists on an alternating sequence of ordered and unordered states



- The ordered state is energetically favoured over an unordered state

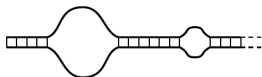
$$\rightarrow \psi = \exp\left(-\frac{E}{kT}\right)$$

- The probability of the ordered state decreases exponentially with the length

- The phase transition is governed by the value of c

- Poland-Scheraga model

- Model consists on an alternating sequence of ordered and unordered states



- The ordered state is energetically favoured over an unordered state

$$\rightarrow w = \exp\left(-\frac{E}{k_b T}\right)$$

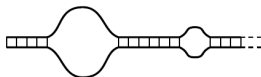
- The entropy of the unbound state depends solely on its length

$$\rightarrow S \propto \frac{s'}{l^c}$$

- The phase transition is governed by the value of c

- Poland-Scheraga model

- Model consists on an alternating sequence of ordered and unordered states



- The ordered state is energetically favoured over an unordered state

$$\rightarrow w = \exp\left(-\frac{E}{k_b T}\right)$$

- The entropy of the unbound state depends solely on its length

$$\rightarrow S \propto \frac{s'}{l_0}$$

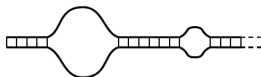
- The phase transition is governed by the value of c

• $c \leq 1$ no phase transition

• $c > 1$ phase transition

- Poland-Scheraga model

- Model consists on an alternating sequence of ordered and unordered states



- The ordered state is energetically favoured over an unordered state

$$\rightarrow w = \exp\left(-\frac{E}{k_b T}\right)$$

- The entropy of the unbound state depends solely on its length

$$\rightarrow S \propto \frac{s'}{l^c}$$

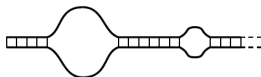
- The phase transition is governed by the value of c

- $c \leq 1$ no phase transition

- $1 < c \leq 2$ continuous phase transition

● Poland-Scheraga model

- Model consists on an alternating sequence of ordered and unordered states



- The ordered state is energetically favoured over an unordered state

$$\rightarrow w = \exp\left(-\frac{E}{k_b T}\right)$$

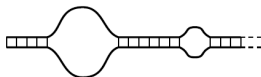
- The entropy of the unbound state depends solely on its length

$$\rightarrow S \propto \frac{s'}{l^c}$$

- The phase transition is governed by the value of c
 - $c \leq 1$ no phase transition
 - $1 < c \leq 2$ continuous phase transition
 - $c \geq 2$ first order phase transition

● Poland-Scheraga model

- Model consists on an alternating sequence of ordered and unordered states



- The ordered state is energetically favoured over an unordered state

$$\rightarrow w = \exp\left(-\frac{E}{k_b T}\right)$$

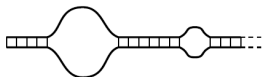
- The entropy of the unbound state depends solely on its length

$$\rightarrow S \propto \frac{s'}{l^c}$$

- The phase transition is governed by the value of c
 - $c \leq 1$ no phase transition
 - $1 < c \leq 2$ continuous phase transition
 - $c \geq 2$ first order phase transition

● Poland-Scheraga model

- Model consists on an alternating sequence of ordered and unordered states



- The ordered state is energetically favoured over an unordered state

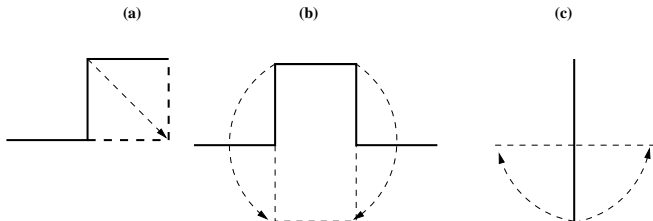
$$\rightarrow w = \exp\left(-\frac{E}{k_b T}\right)$$

- The entropy of the unbound state depends solely on its length

$$\rightarrow S \propto \frac{s^l}{l^c}$$

- The phase transition is governed by the value of c
 - $c \leq 1$ no phase transition
 - $1 < c \leq 2$ continuous phase transition
 - $c \geq 2$ first order phase transition

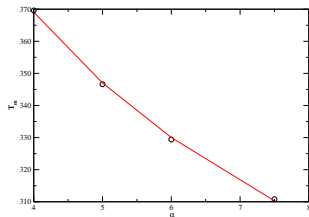
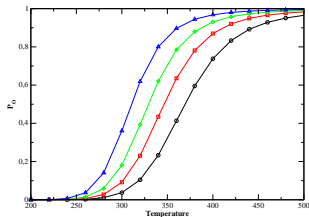
- Monte Carlo simulation in the canonical ensemble
 - Minimization of the Free Energy
 - Find the **Thermodynamic** properties of the system
 - Try to deduce the **Kinetics** using MC-step
 - Selection of local motions of the chain



● Effect of the width of the Morse potential

$D=0.112$ eV, $k=0.025$ eV.Å⁻², $\delta = 0.35$, $\rho = 5$, $\theta = 50^\circ$ and

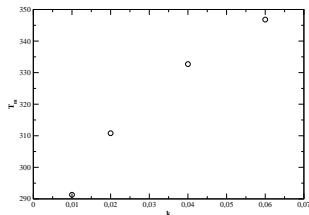
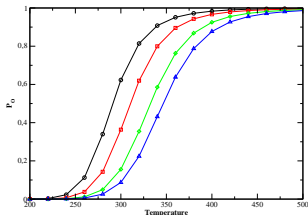
$N=21$. ●: $\alpha=4.0$ Å⁻¹; □: $\alpha=5.0$ Å⁻¹; ◇: $\alpha=6.0$ Å⁻¹; △: $\alpha=7.5$ Å⁻¹



a (Å ⁻¹)	$S \neq 1, \frac{\Delta P}{\Delta T} T_m$
4	3.4
5	3.5
6	3.8
7.5	4.1

● Effect of the rigidity of the stem

$D=0.112$ eV, $\alpha=6.9$ Å⁻¹, $\delta = 0.35$, $\rho = 5$, $\theta = 50^\circ$ and $N=21$. ●: $k=0.010$ eV.Å⁻²; □: $k=0.020$ eV.Å⁻²; ◇: $k=0.040$ eV.Å⁻²; △: $k=0.060$ eV.Å⁻²



$k(\text{eV.Å}^{-2})$	$S \neq 1, \frac{\Delta P}{\Delta T} T_m$
0.01	4.1
0.020	4
0.040	3.8
0.06	3.7