

Extracting DNA twist rigidity from single molecule experiments

Sébastien Neukirch *CNRS & Université Paris 6 : Lab. de Modélisation en Mécanique*

Twisted Rods

Michael Thompson, Gert van der Heijden, Geoff Goss
Centre for Nonlinear Dynamics, Univ. College London, UK

Continuation algorithm

Michael Henderson
IBM, T.J. Watson Center, New York, USA

Mechanics of DNA

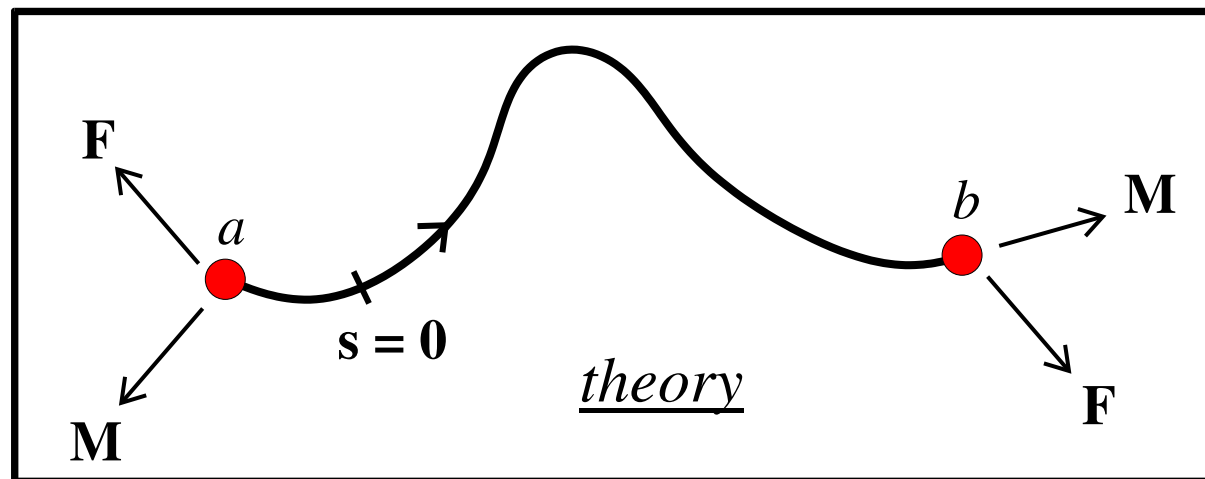
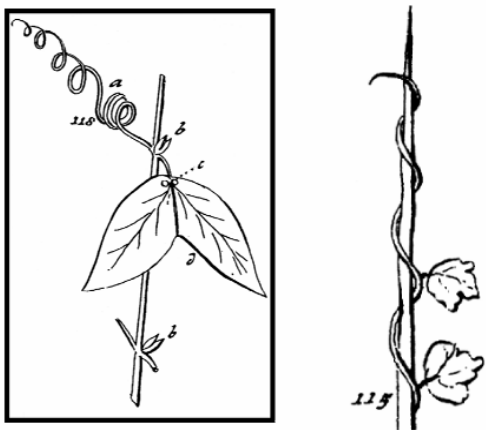
John H. Maddocks
Mathematics Institute, Ecole Polytechnique Fédérale, Lausanne

Single molecule experiments

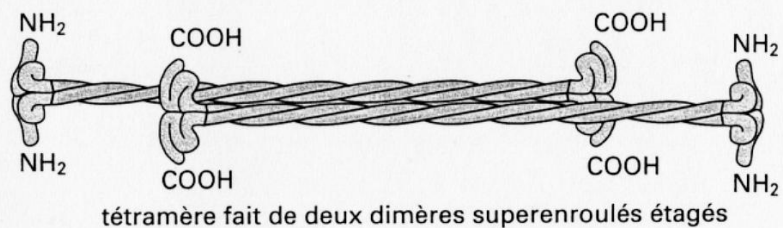
Vincent Croquette, David Bensimon, Gilles Charvin
Lab. Physique Statistique, Ecole Normale Supérieure, Paris

Elastic filaments

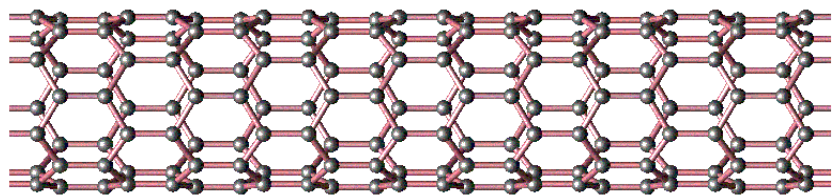
climbing plants



fibrous proteins



carbone nanotubes

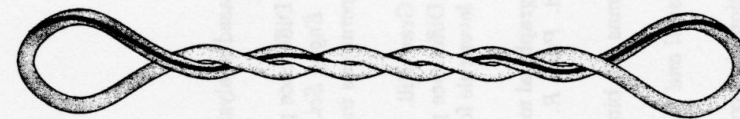


cables



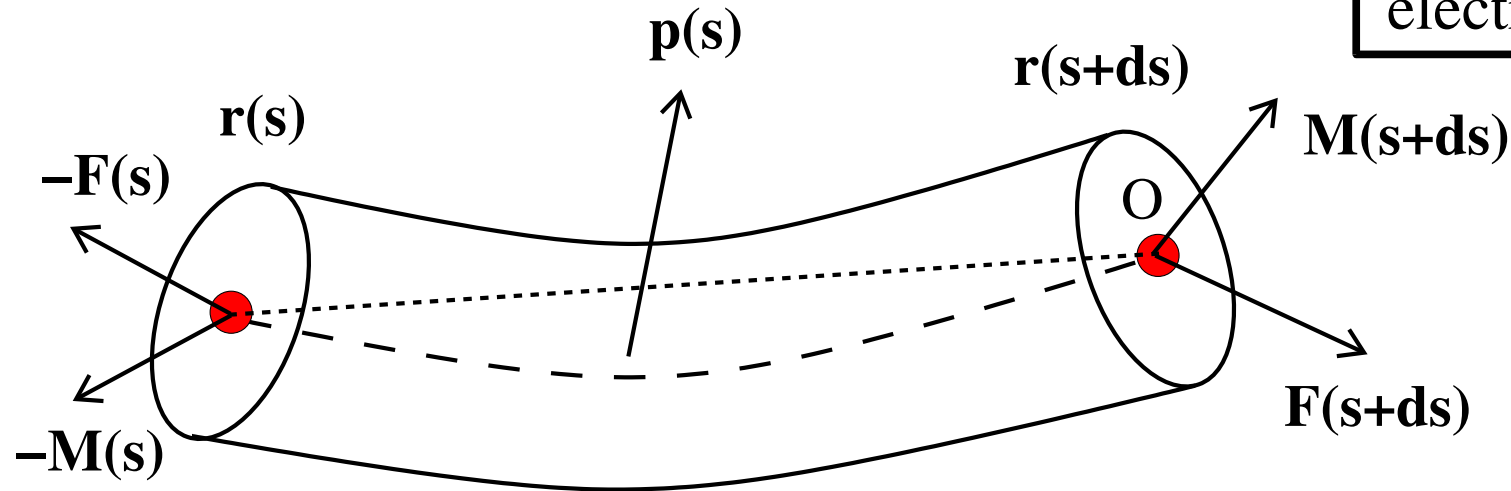
applications

DNA super-coiling



Elastic rod in equilibrium

$p(s)$ = external force
gravity, contact,
electrostatic, ...



force
balance

$$p(s) \delta s + F(s + \delta s) - F(s) = 0$$

$$p(s) + F'(s) = 0$$

momentum
balance

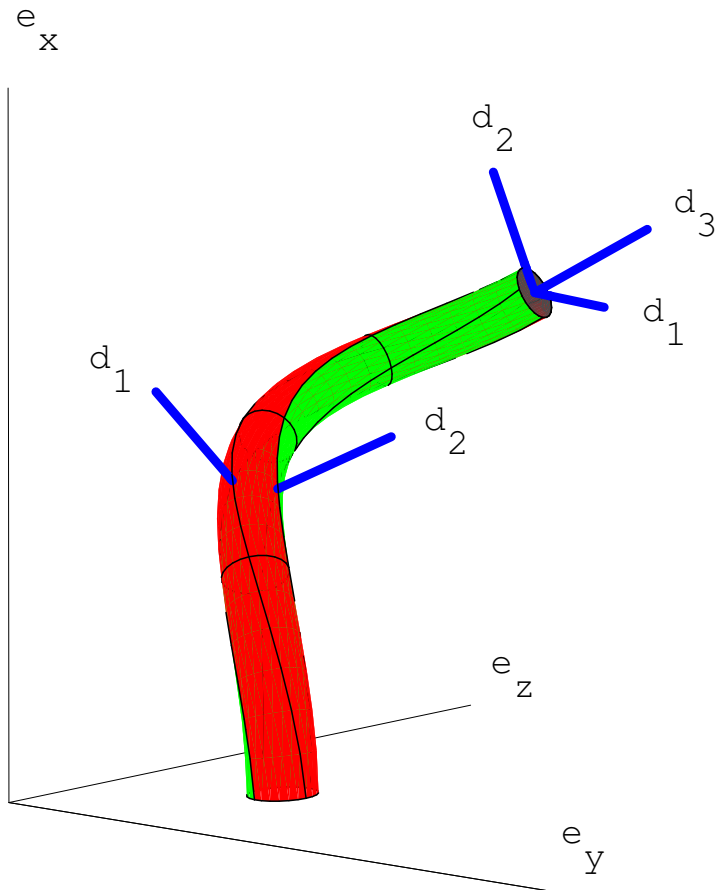
$$M(s + \delta s) - M(s) + \Pi_O[F(s + \delta s)] + \Pi_O[-F(s)] = 0$$

$$M(s + \delta s) - M(s) + 0 + (r(s) - r(s + \delta s)) \wedge (-F(s)) = 0$$

$$M'(s) + r'(s) \wedge F(s) = 0$$

Cosserat model for 1D elasticity

3 directors $\vec{d}_1, \vec{d}_2, \vec{d}_3$ on the top of $\vec{r}(s)$



no shear
no extension

$$\left. \begin{array}{l} \text{no shear} \\ \text{no extension} \end{array} \right\} \vec{r}'(s) = \vec{d}_3(s)$$

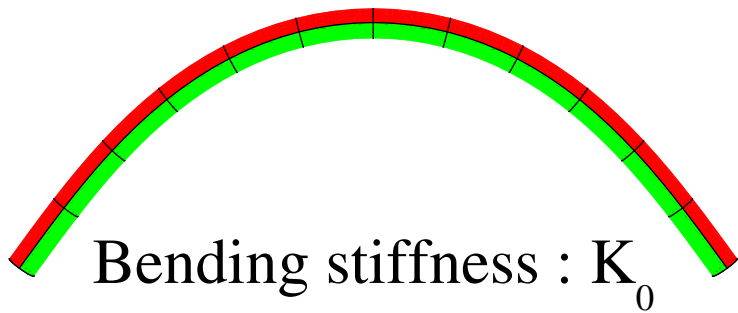
$$\left\{ \begin{array}{l} \vec{d}_1'(s) = \vec{u}(s) \wedge \vec{d}_1 \\ \vec{d}_2'(s) = \vec{u}(s) \wedge \vec{d}_2 \\ \vec{d}_3'(s) = \vec{u}(s) \wedge \vec{d}_3 \end{array} \right. \quad \text{evolution in SO(3)}$$

$$\vec{u}(s) = \{u_1, u_2, u_3\}_{\vec{d}_1, \vec{d}_2, \vec{d}_3}$$

$$\vec{u}(s) = \{\kappa_1, \kappa_2, \tau\}_{\vec{d}_1, \vec{d}_2, \vec{d}_3}$$

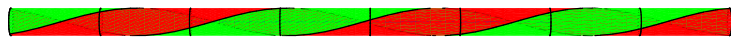
u_1, u_2 : curvature and u_3 : twist

Linear Constitutive Relations



$$\vec{M} \cdot \vec{d}_1 = K_0 u_1$$

$$\vec{M} \cdot \vec{d}_2 = K_0 u_2$$



Twist stiffness : K_3

$$\vec{M} \cdot \vec{d}_3 = K_3 u_3$$

$$K_0 = E I$$

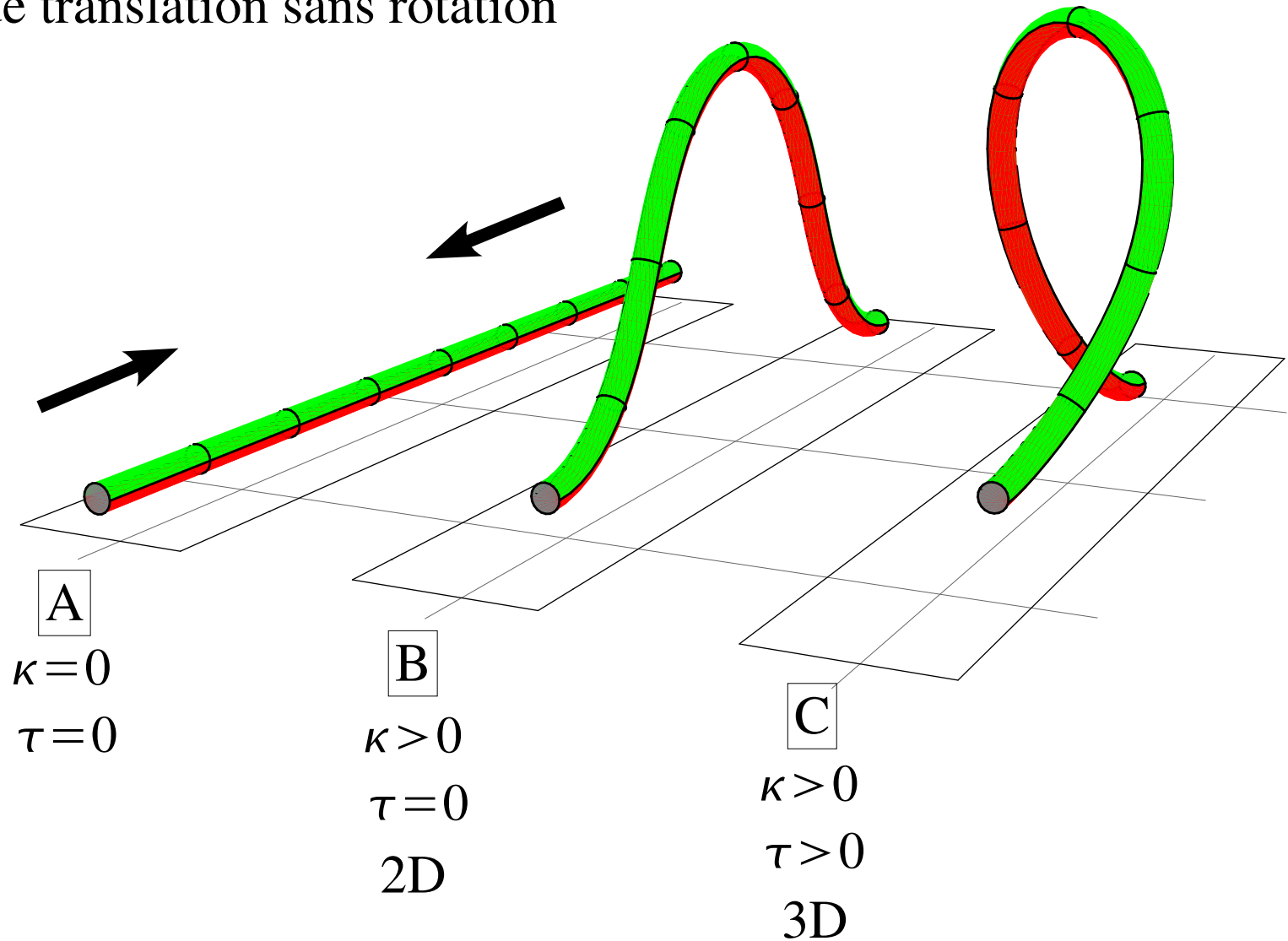
I : moment of inertia

E : Young's modulus

filament	E
Microtubule	1 GPa
DNA	1 GPa
Actine	2 GPa
Collagen	2 GPa
Rubber	2 GPa
Steel	200 GPa

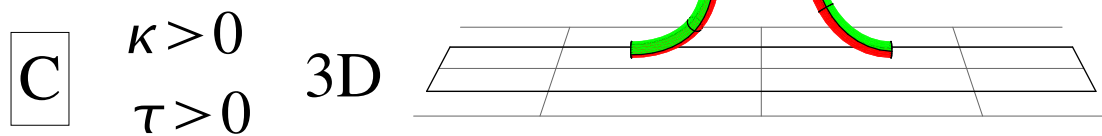
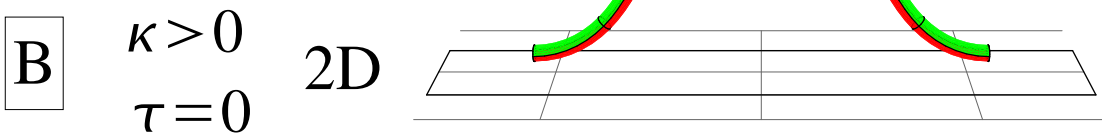
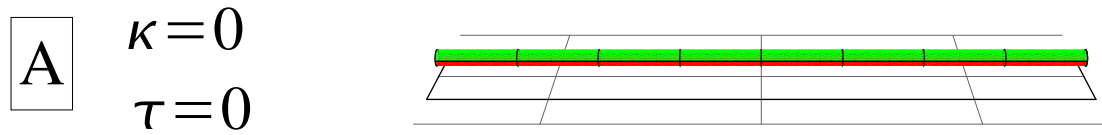
Courbure et torsion sont liées

Expérience de translation sans rotation

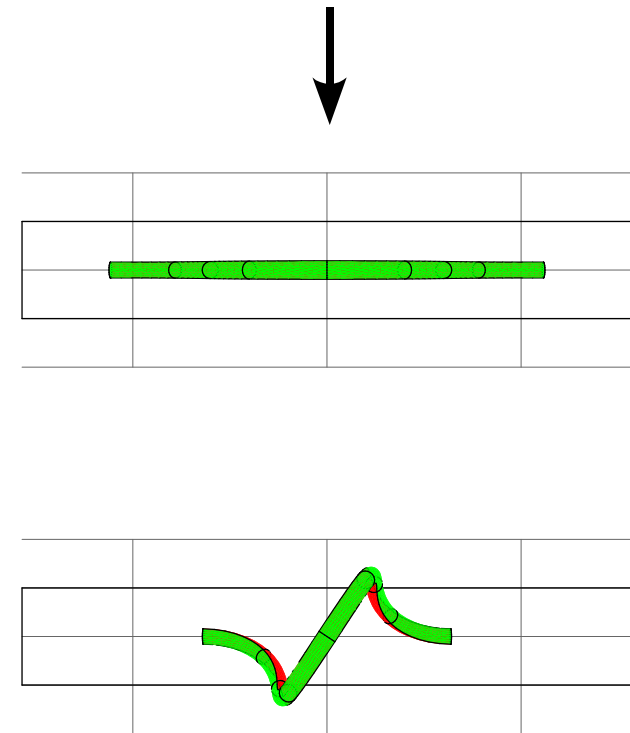


Courbure et torsion sont liées

Expérience de translation sans rotation



vues de dessus



Kirchhoff equations

21 ODEs with variable : s

ordinary differential equations

$$\frac{d}{ds} \vec{F} = \vec{p}$$

$$\frac{d}{ds} \vec{M} = \vec{F} \wedge \vec{d}_3$$

$$\frac{d}{ds} \vec{r} = \vec{d}_3$$

$$\frac{d}{ds} \vec{d}_i = \vec{u} \wedge \vec{d}_i$$

$$m_i = K_i u_i$$

linear elasticity

21 unknowns

$$\vec{F}(s)$$

$$\vec{M}(s)$$

$$\vec{r}(s)$$

$$\vec{d}_3(s)$$

$$\vec{d}_2(s)$$

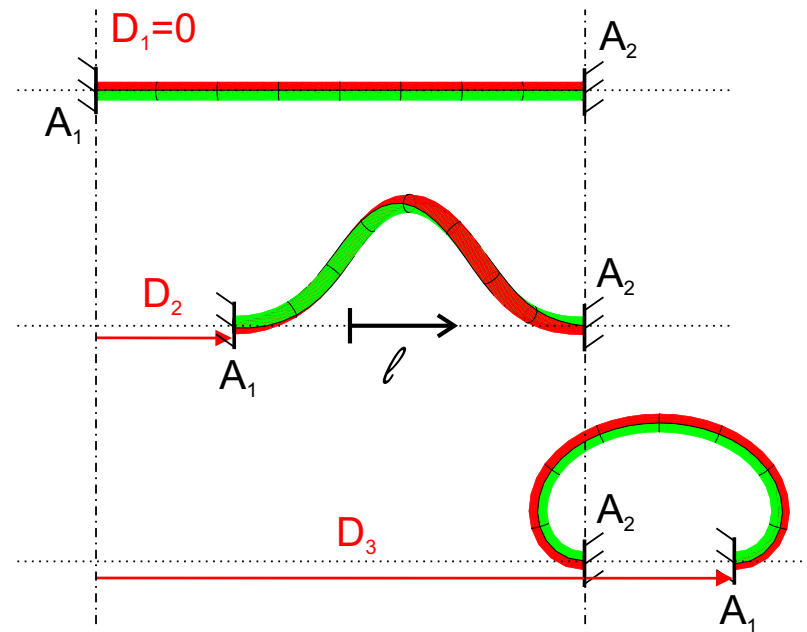
$$\vec{d}_3(s)$$

$$\vec{u}(s)$$

$$i = 1, 2, 3$$

boundary conditions

- how the rod is held
- few solutions are admissible



$$\vec{d}_3(A_1) = \vec{d}_3(A_2)$$

$$\vec{r}(A_2) - \vec{r}(A_1) = k \vec{d}_3(A_2)$$

$$(D = L - k)$$

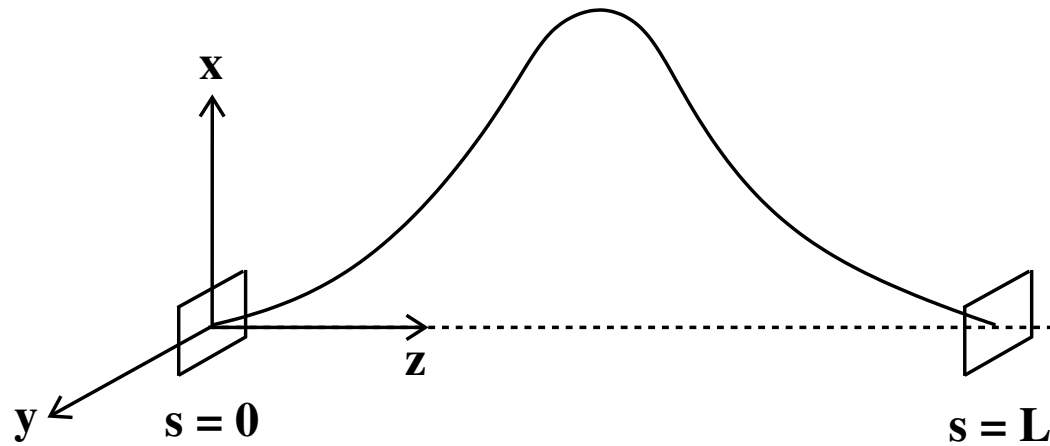
Find admissible equilibrium solutions : shooting method

initial conditions

$$\begin{aligned} r(0) &= (0,0,0) \\ d_1(0) &= (1,0,0) \\ d_2(0) &= (0,1,0) \\ d_3(0) &= (0,0,1) \end{aligned}$$

parameters

$$\vec{F}(0), \vec{M}(0)$$



end conditions

$$\left. \begin{aligned} x(L) &= 0 \\ y(L) &= 0 \\ d_3 x(L) &= 0 \\ d_3 y(L) &= 0 \end{aligned} \right\} \phi$$

solution of ODEs

$$\begin{aligned} \phi(\overbrace{\vec{F}(0), \vec{M}(0)}^u) &= 0 \\ \Leftrightarrow \phi(u) &= 0 \end{aligned}$$

$$\begin{aligned} \phi &\in \mathbb{R}^L \\ u &\in \mathbb{R}^P \end{aligned}$$

this defines a P - L solution manifold

1D solution manifold : path following predictor-corrector scheme

$$1D \text{ solution manifold } \begin{cases} \phi_1(u_1, u_2, u_3) = 0 \\ \phi_2(u_1, u_2, u_3) = 0 \end{cases}$$

At each point :

1-(**predictor**)

we take a guess : Z_i

2-(**corrector**)

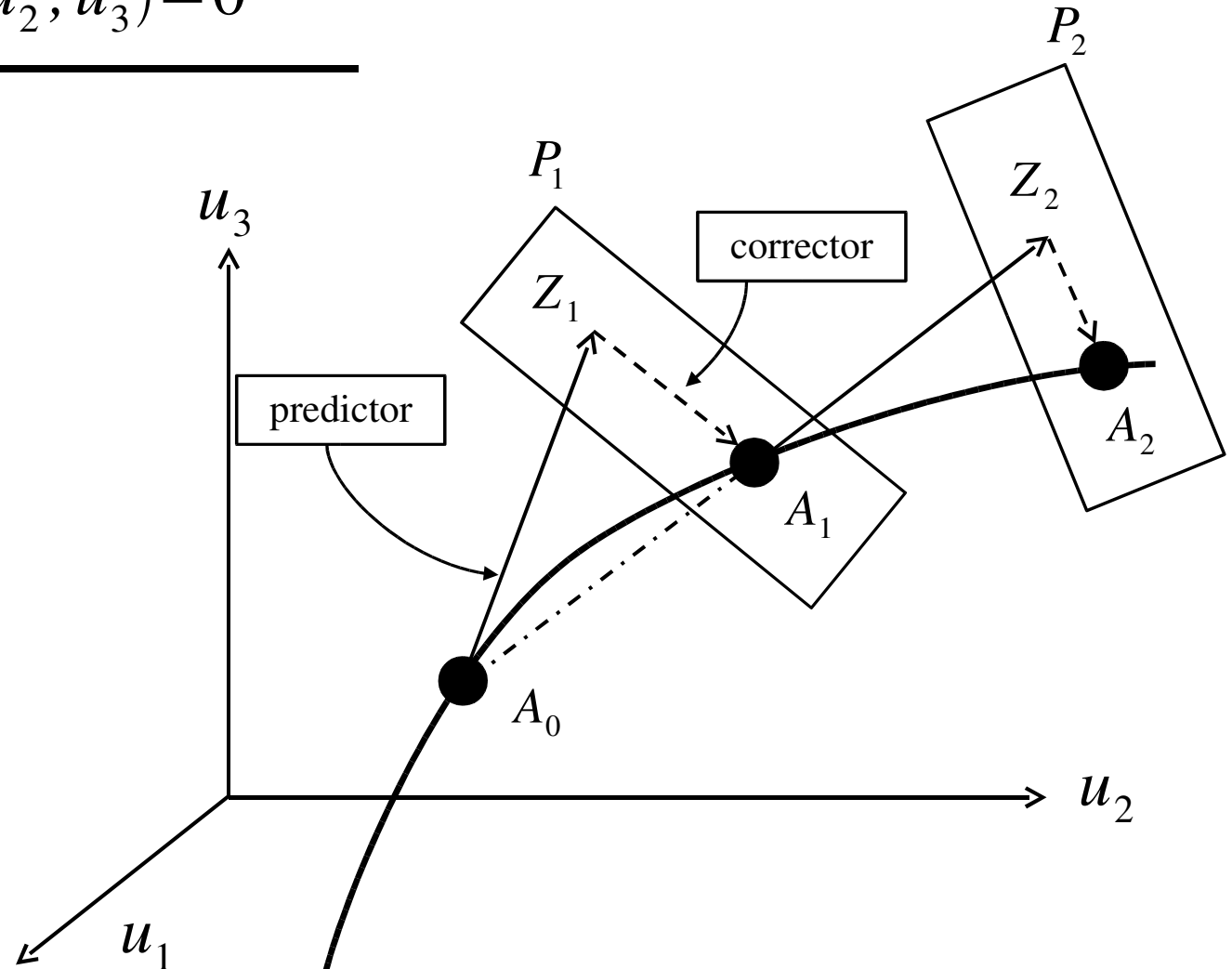
we define a projection :

$$P_i(u_1, u_2, u_3) = 0$$

and we solve :

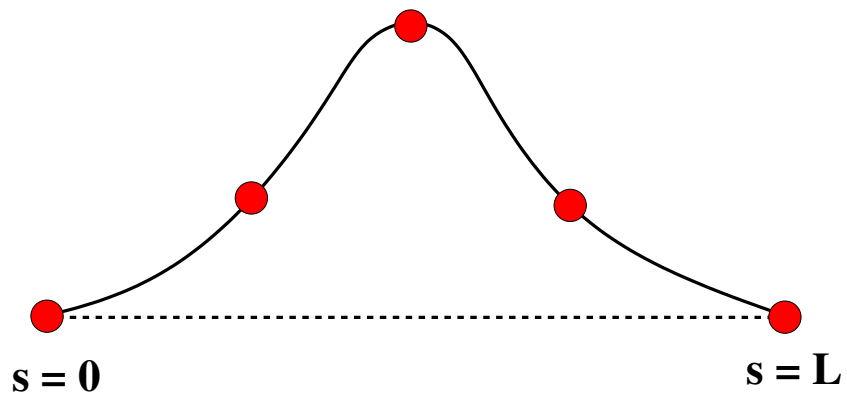
$$\begin{cases} \phi_1(u_1, u_2, u_3) = 0 \\ \phi_2(u_1, u_2, u_3) = 0 \\ P_i(u_1, u_2, u_3) = 0 \end{cases}$$

to obtain A_i



Find admissible equilibrium solutions : discretization methods

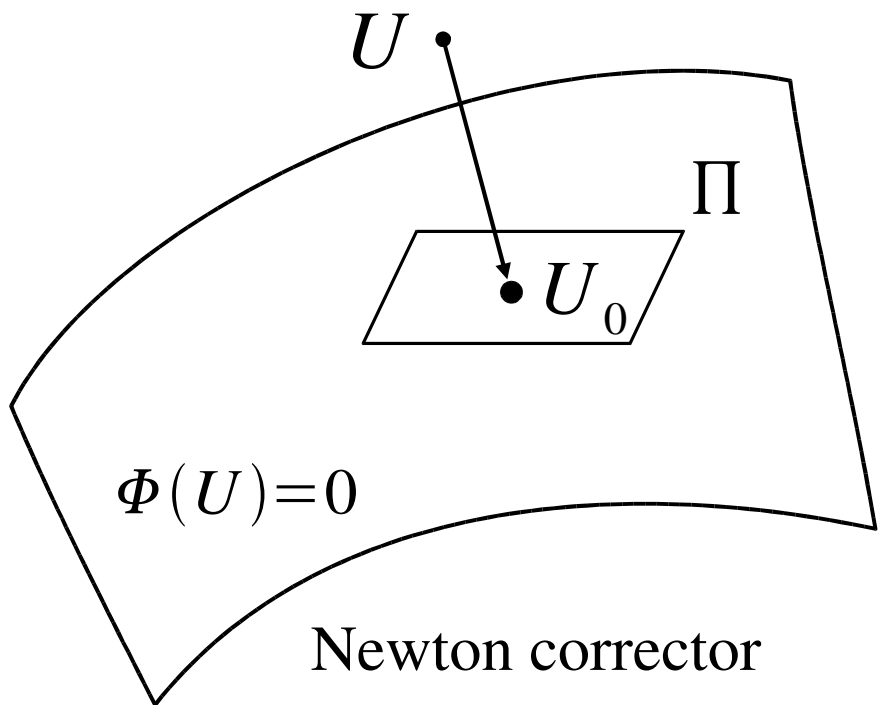
discretization over N intervals



$$\Phi(U) = 0$$

boundary conditions
matching conditions

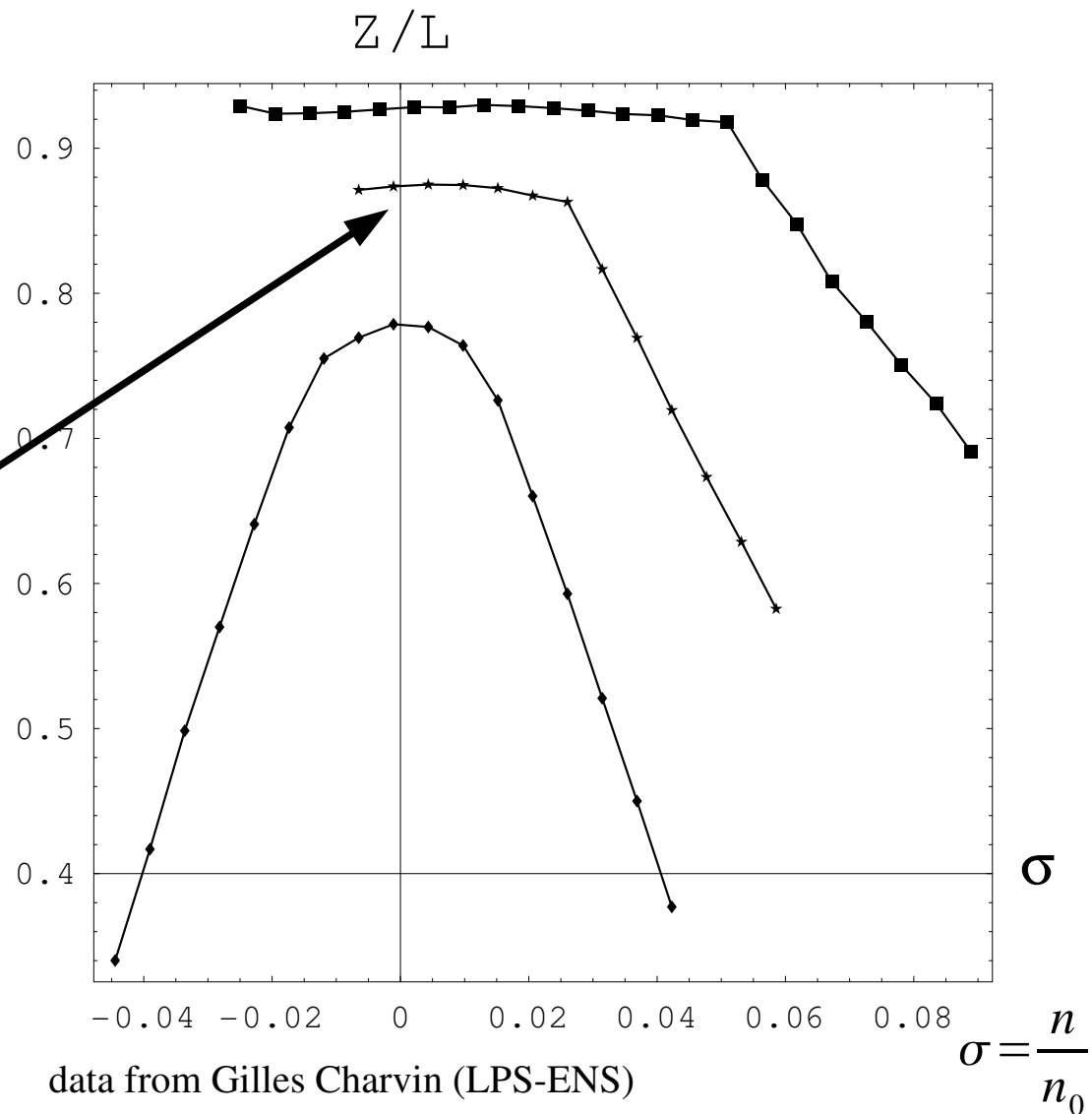
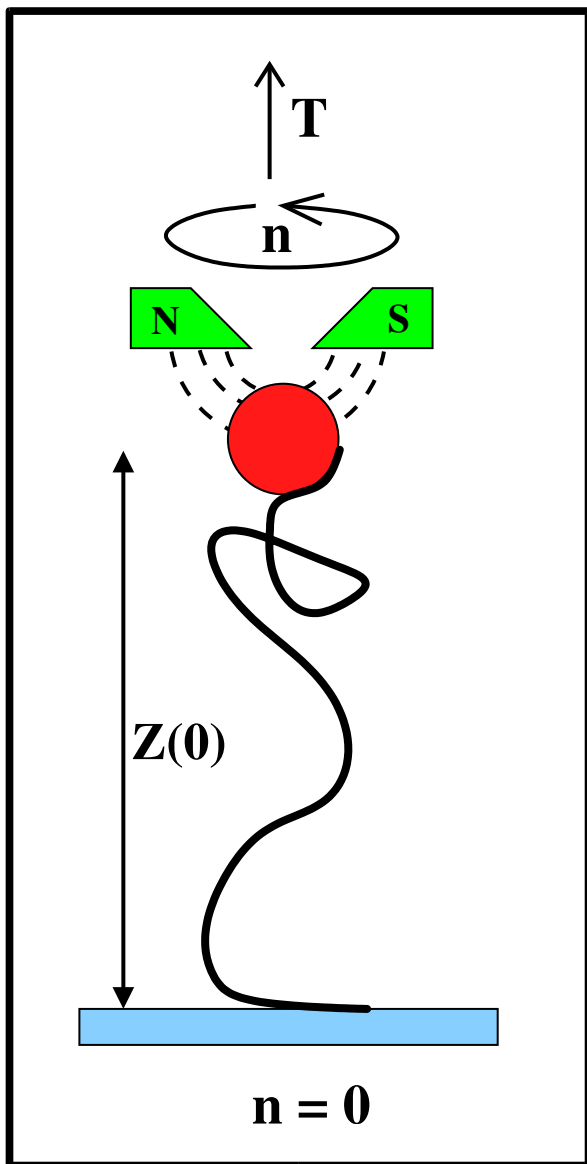
system of nonlinear algebraic equations



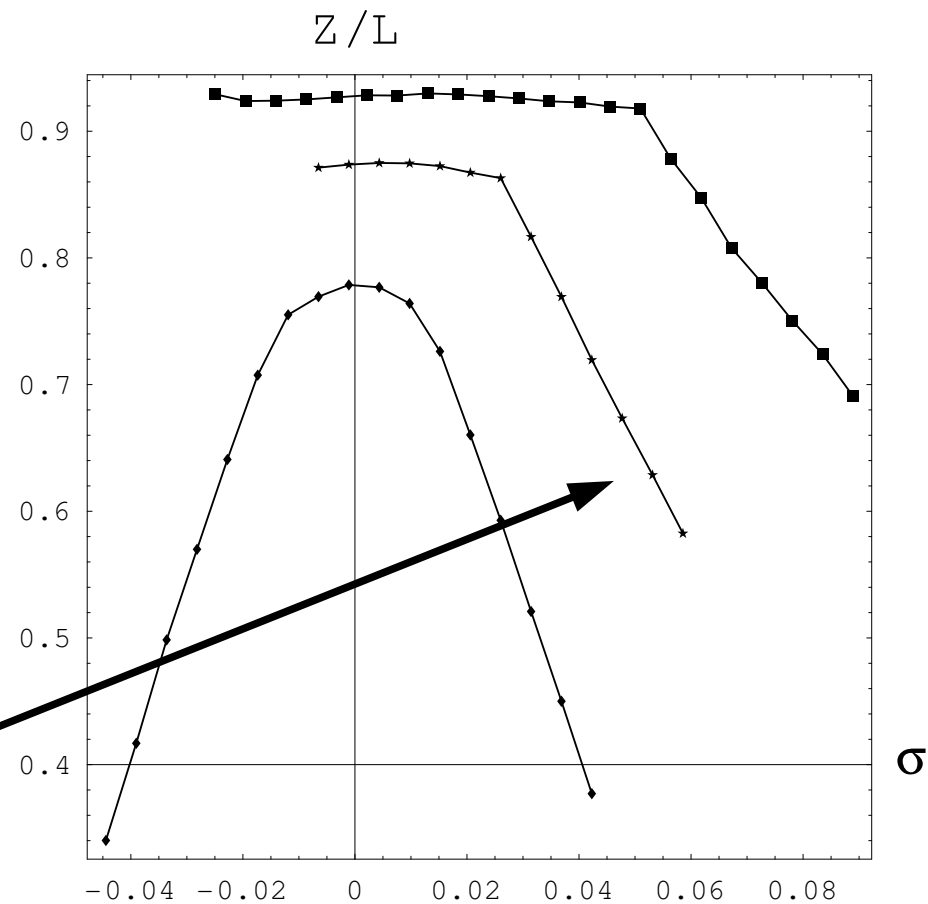
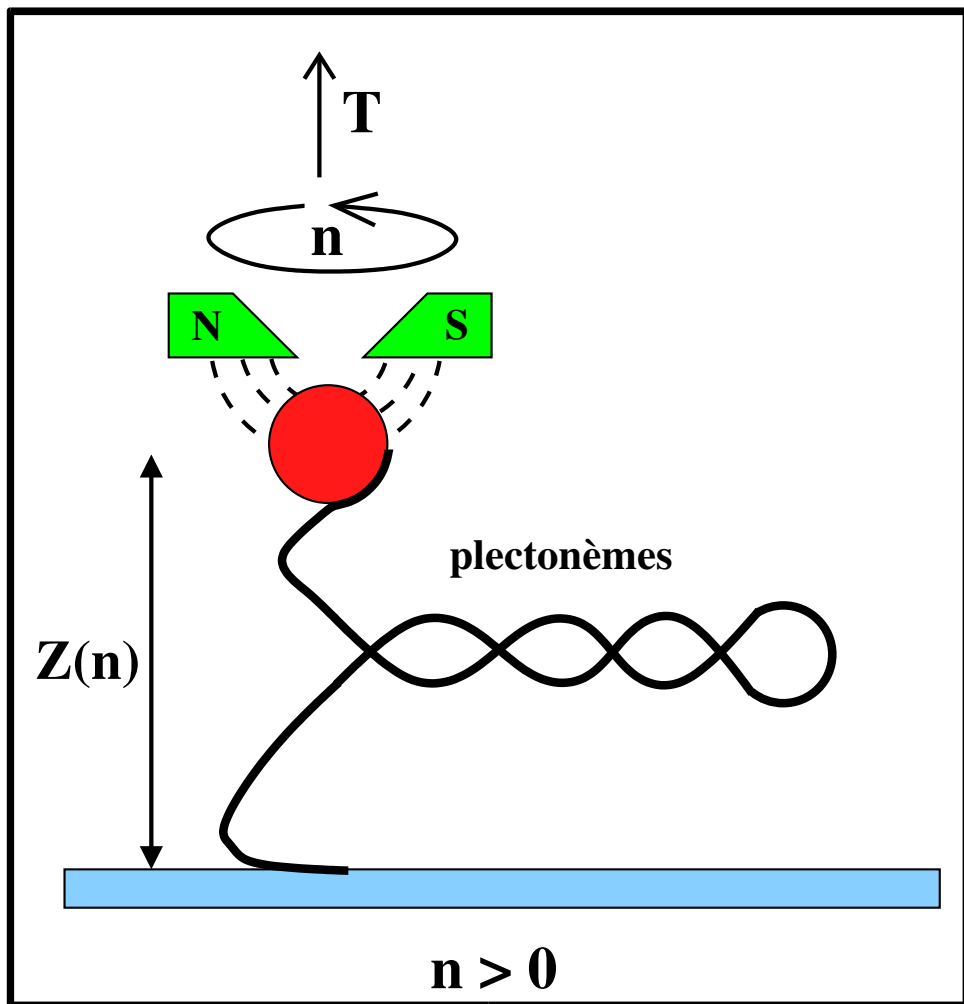
$$\underbrace{\Phi(U_0)}_{=0} = \Phi(U) + \frac{D\Phi}{DU}(U_0 - U) + \dots$$

- 1- we take a point U
- 2- compute Jacobian
- 3- kernel is tangent plane Π
- 4- we project orthogonally : $U \rightarrow U_0$

Pulling and twisting DNA



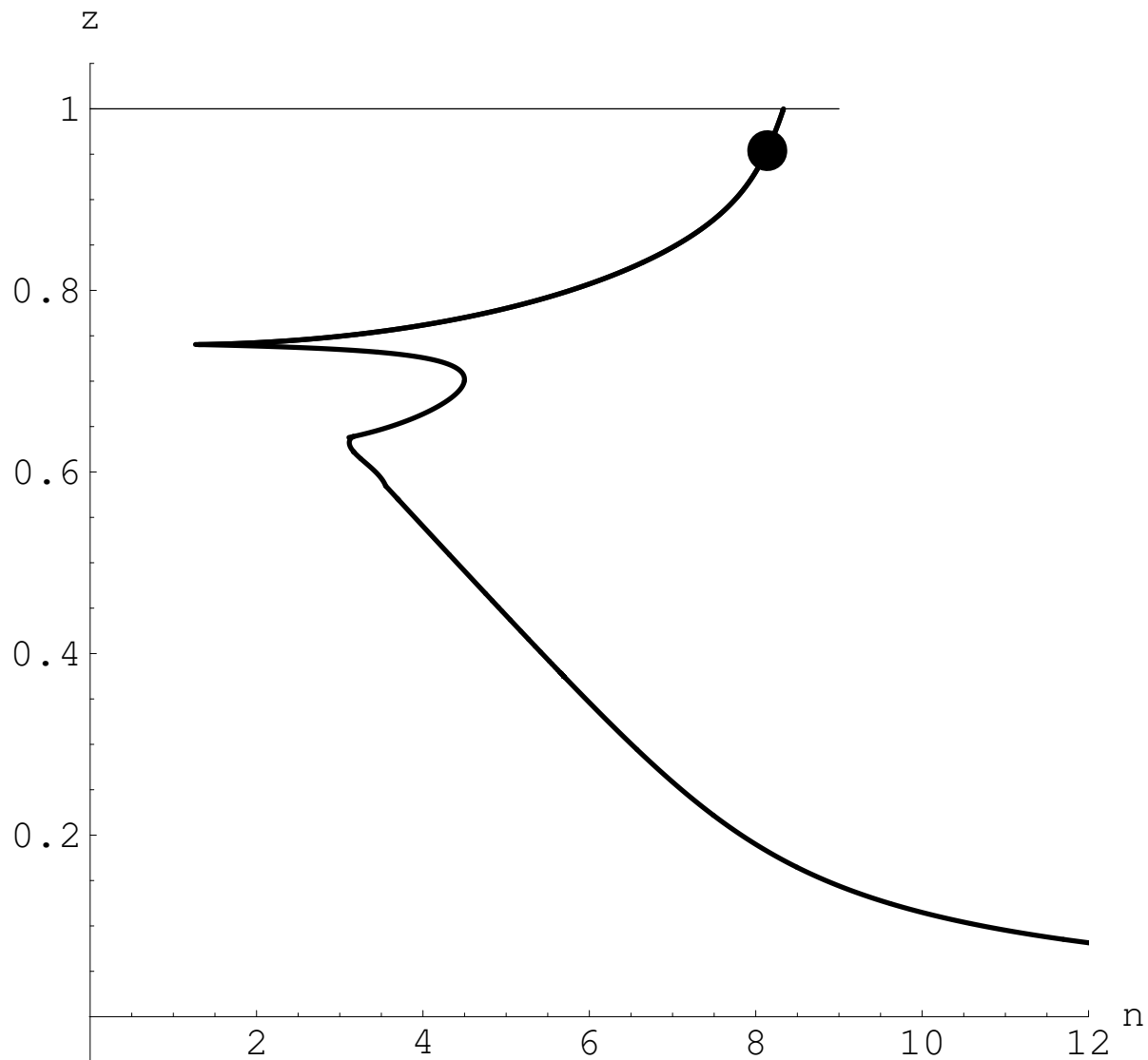
Pulling and twisting DNA



data from Gilles Charvin (LPS-ENS)

$$\sigma = \frac{n}{n_0}$$

Results : how a twisted rod coils



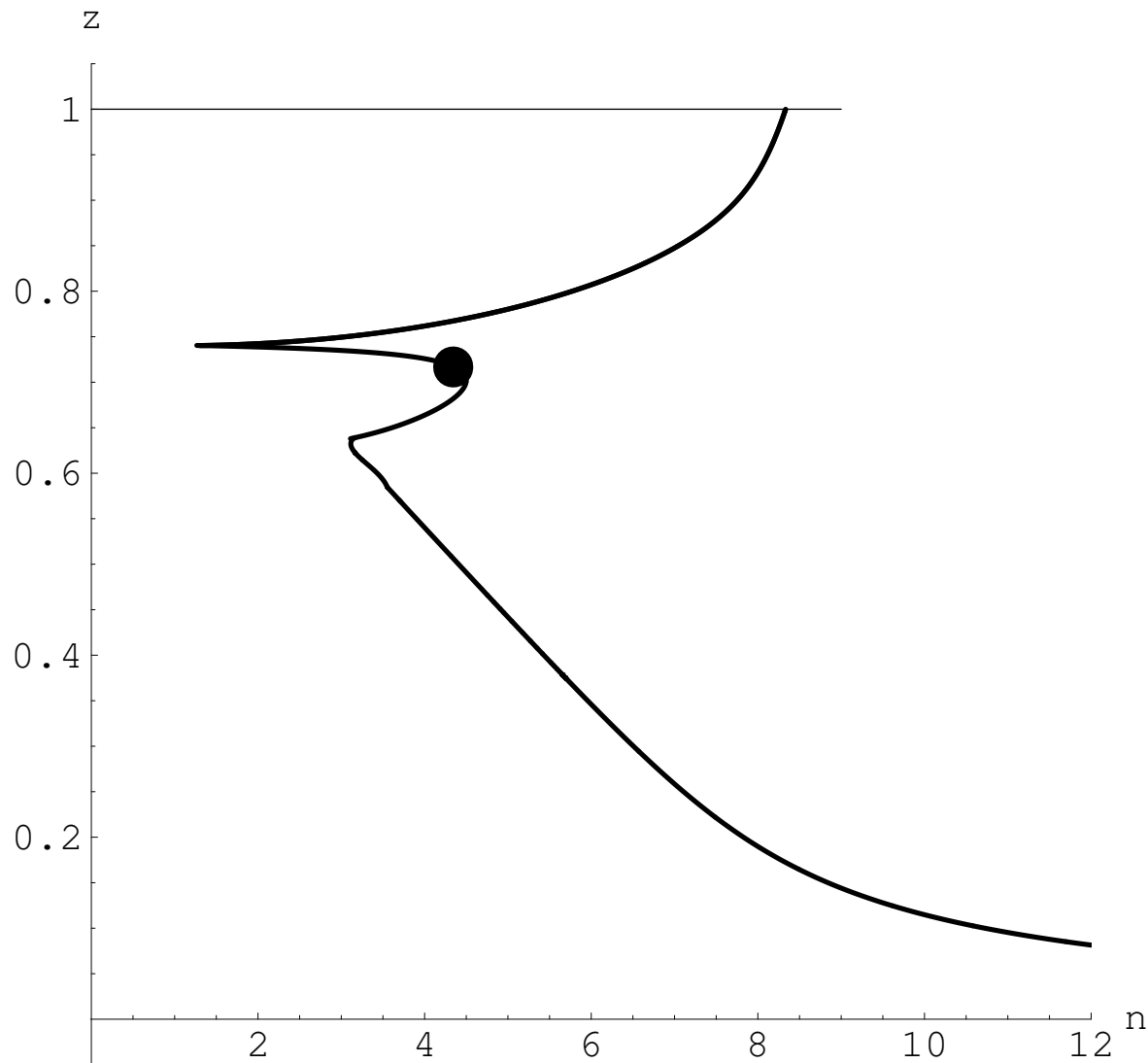
$$\frac{L}{2R} = 170$$
$$t = \frac{TL^2}{4\pi^2 K_0} = 6$$

0 contact(s)

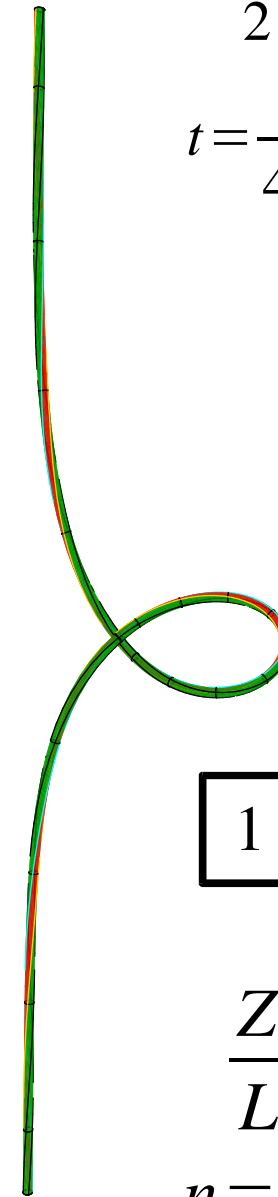
$$\frac{Z}{L} = 0.95$$

$n = 8.1 \text{ turns}$

Results : how a twisted rod coils



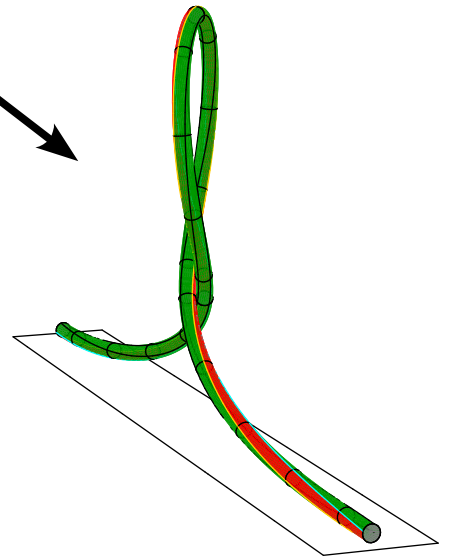
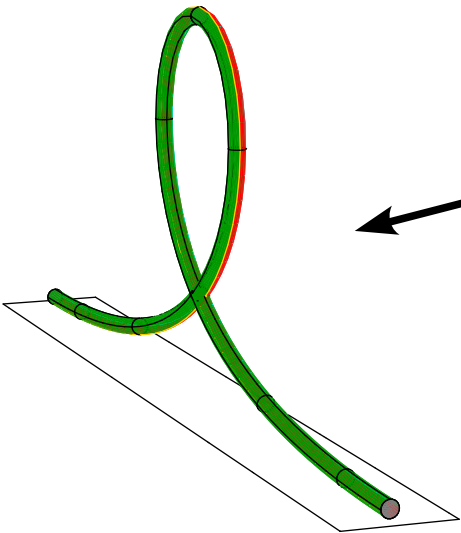
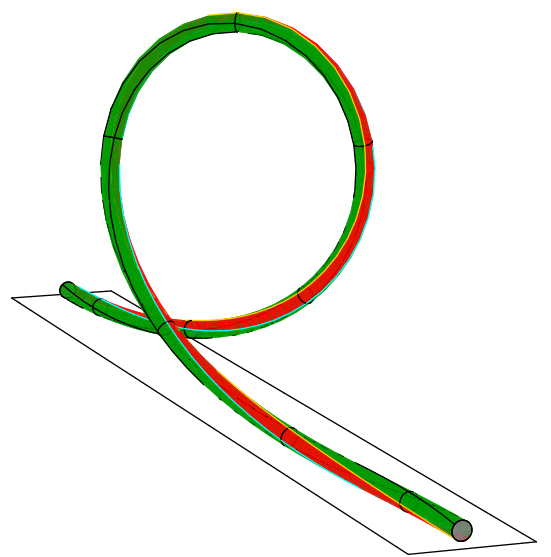
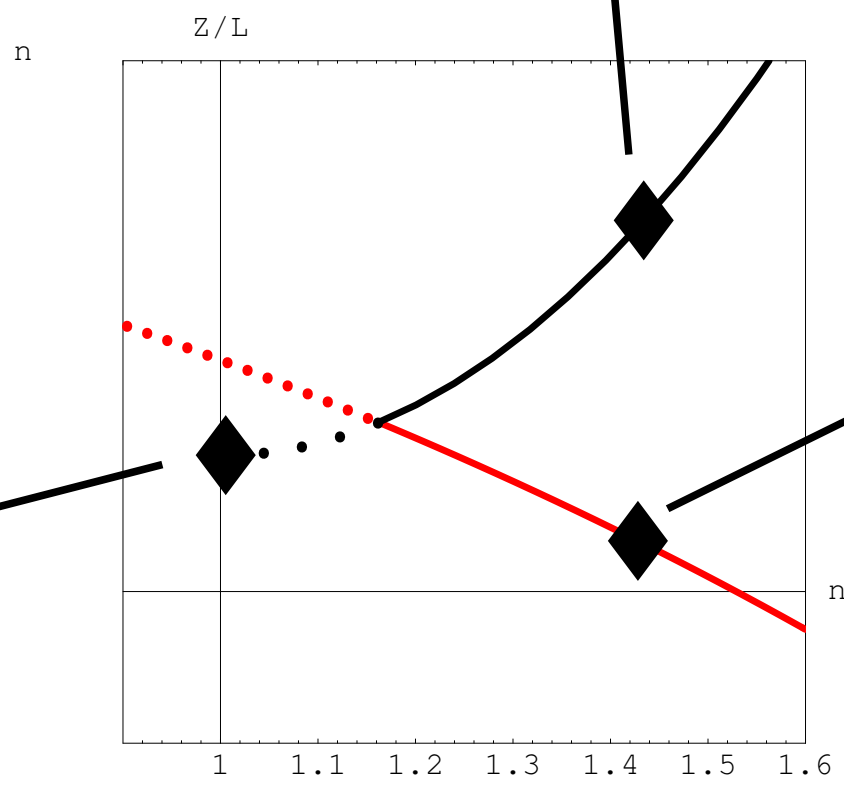
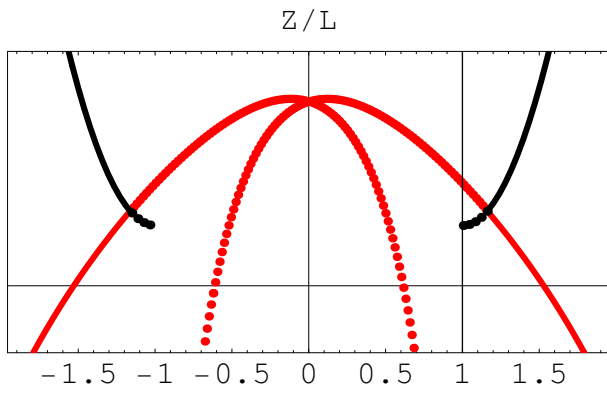
$$\frac{L}{2R} = 170$$
$$t = \frac{TL^2}{4\pi^2 K_0} = 6$$



1 contact(s)

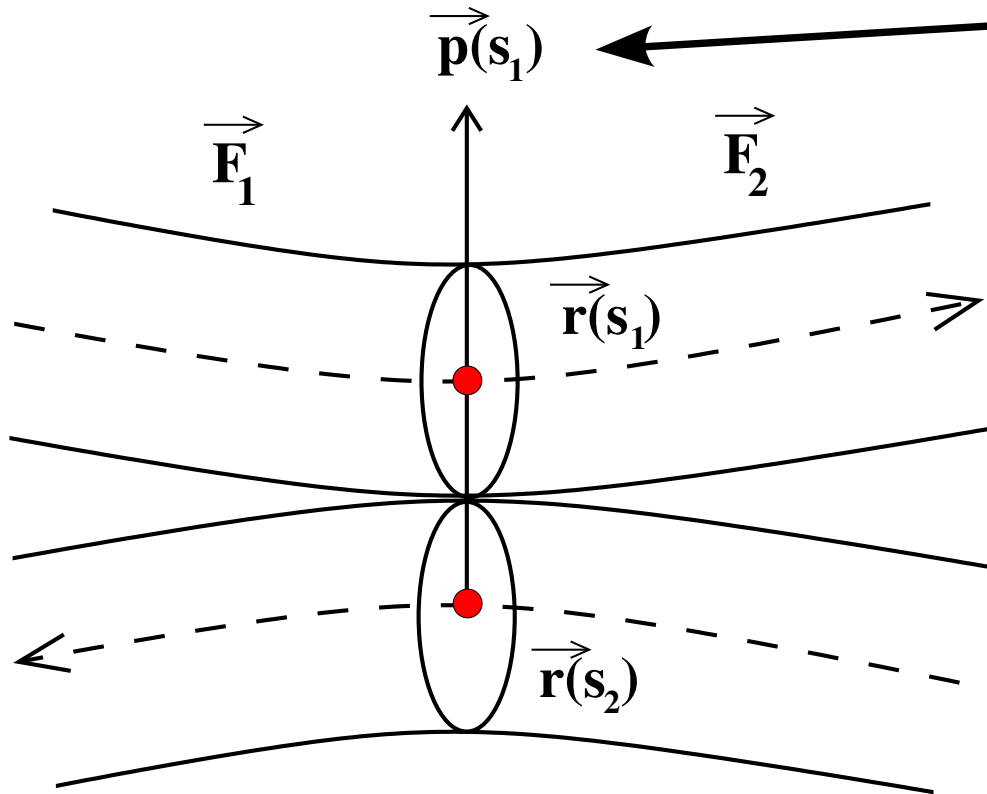
$$\frac{Z}{L} = 0.72$$
$$n = 4.3 \text{ turns}$$

Bifurcation : 0 contact -> 1 contact



Hard-wall contact, no friction

force from strand at s_2
acting on strand at s_1



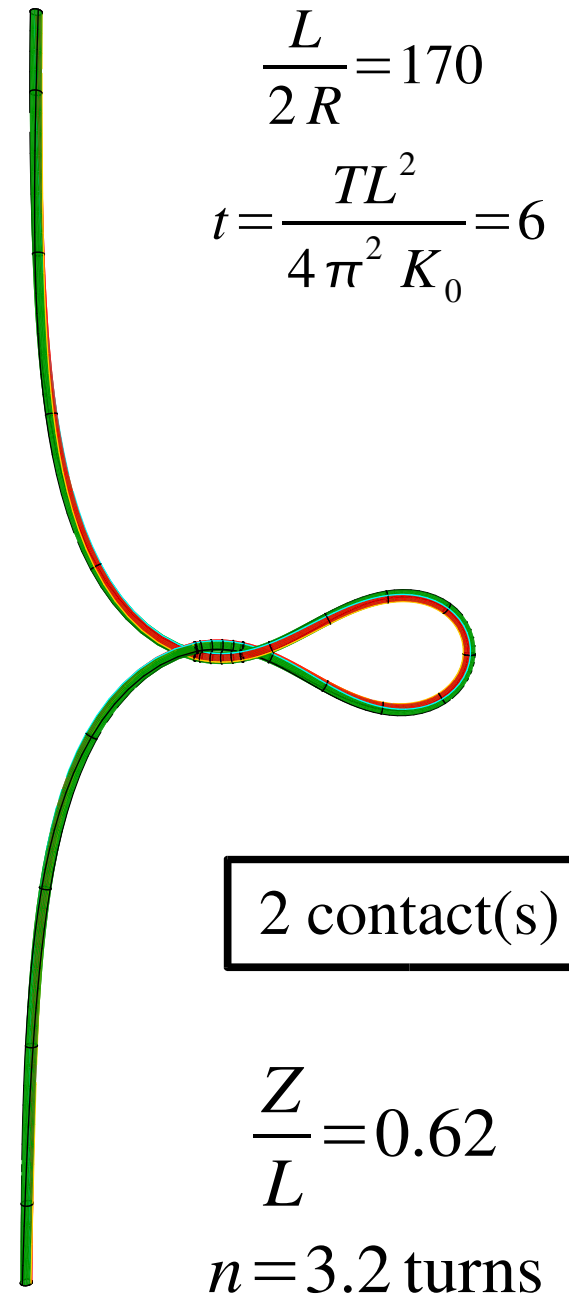
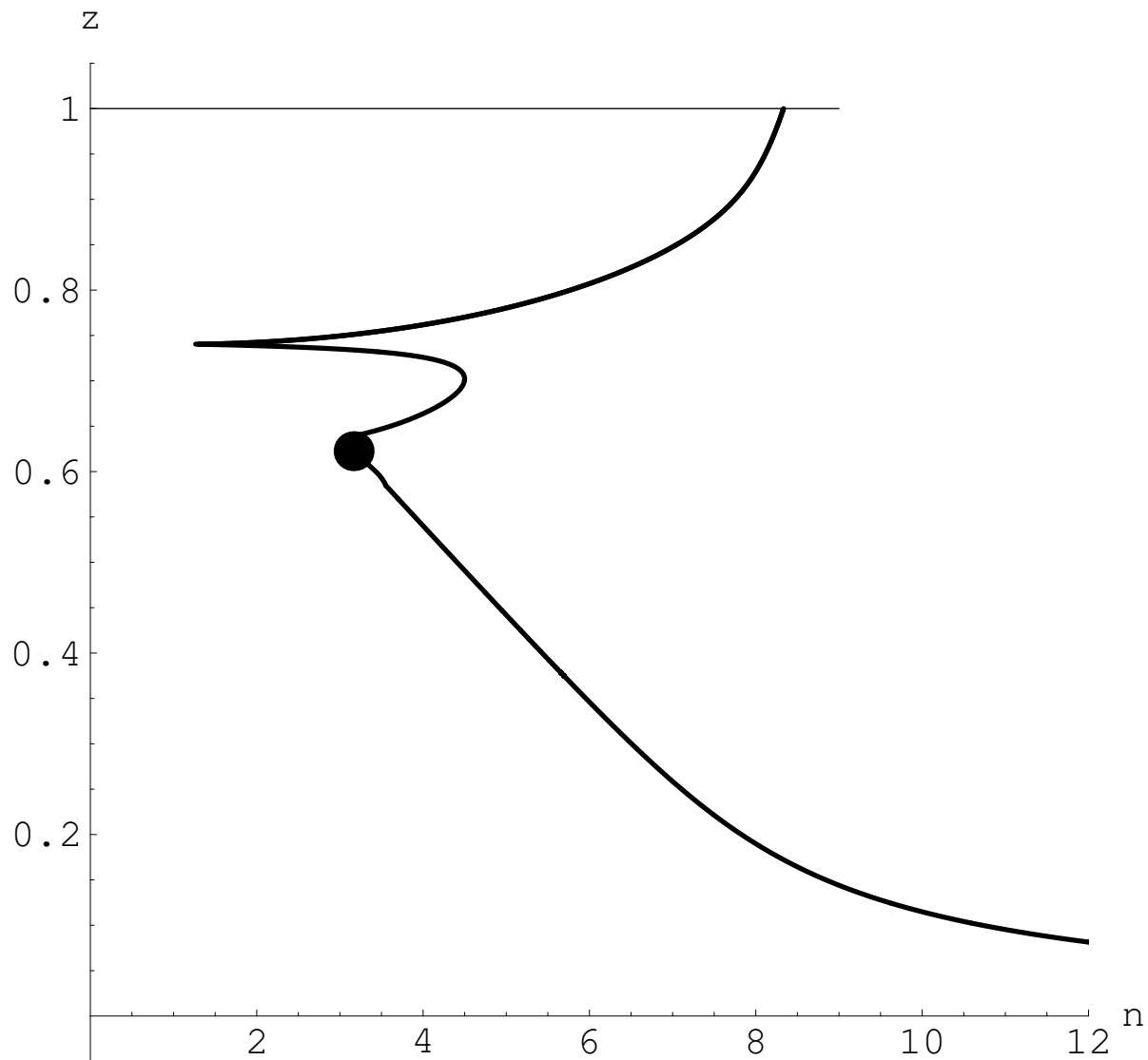
$$\vec{F}_1 = \vec{p} + \vec{F}_2$$

$$\vec{p} = p \frac{\vec{r}(s_1) - \vec{r}(s_2)}{|\vec{r}(s_1) - \vec{r}(s_2)|}$$

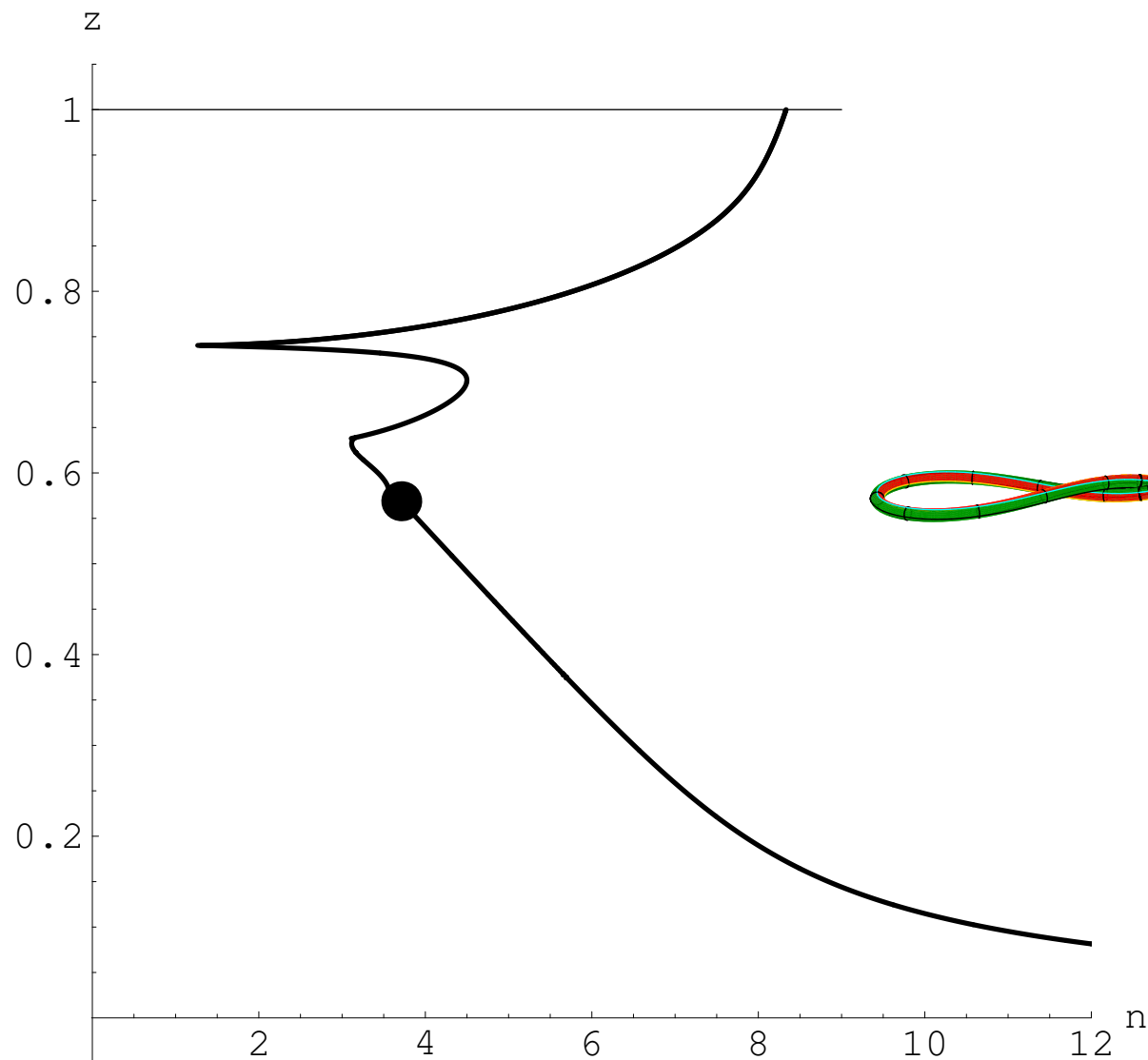
touching conditions :

$$\left\{ \begin{array}{l} |\vec{r}(s_1) - \vec{r}(s_2)| = \text{thickness} \\ (\vec{r}(s_1) - \vec{r}(s_2)) \perp \vec{d}_3(s_1) \\ (\vec{r}(s_1) - \vec{r}(s_2)) \perp \vec{d}_3(s_2) \end{array} \right.$$

Results : how a twisted rod coils



Results : how a twisted rod coils



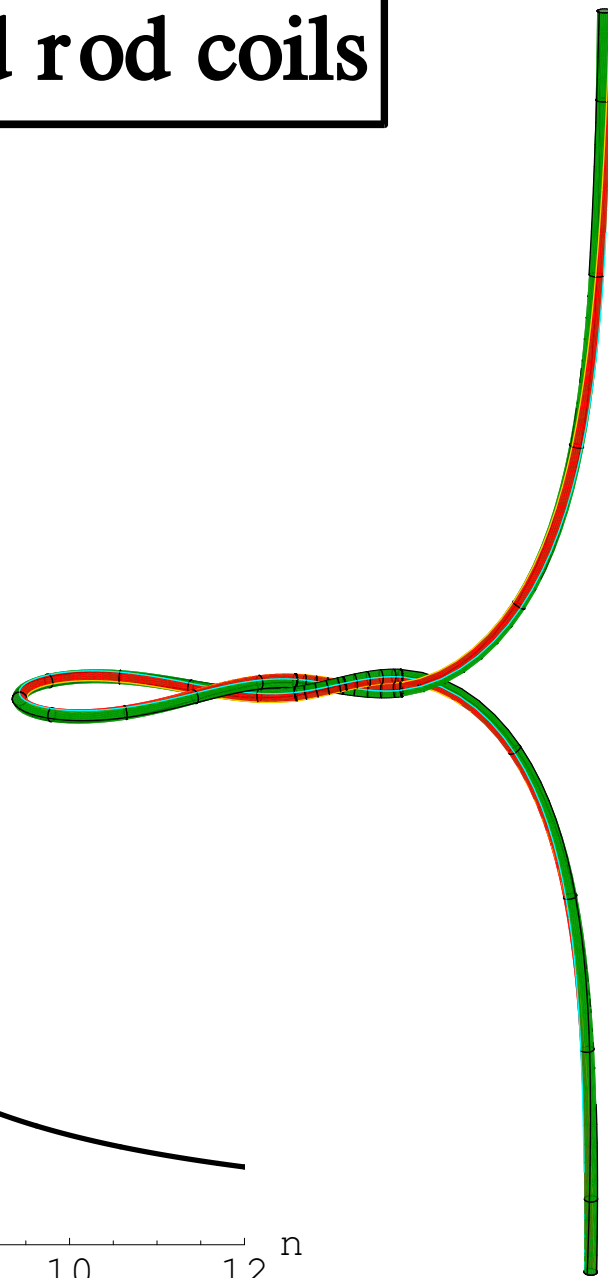
$$\frac{L}{2R} = 170$$

$$t = \frac{TL^2}{4\pi^2 K_0} = 6$$

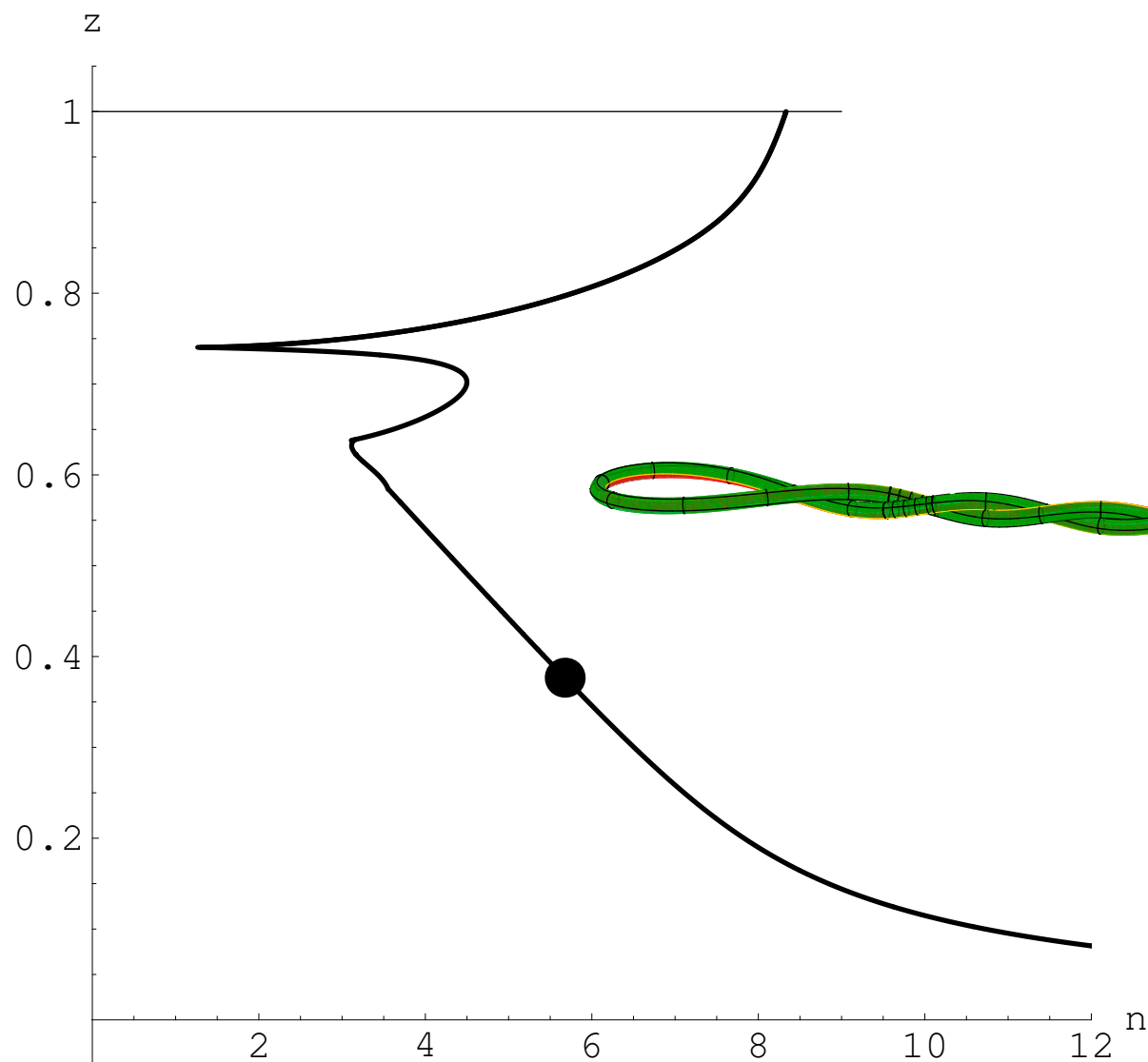
3 contact(s)

$$\frac{Z}{L} = 0.57$$

$$n = 3.7 \text{ turns}$$



Results : how a twisted rod coils



$$\frac{L}{2R} = 170$$

$$t = \frac{TL^2}{4\pi^2 K_0} = 6$$

1L1 contact(s)

$$\frac{Z}{L} = 0.38$$

$n = 5.7$ turns

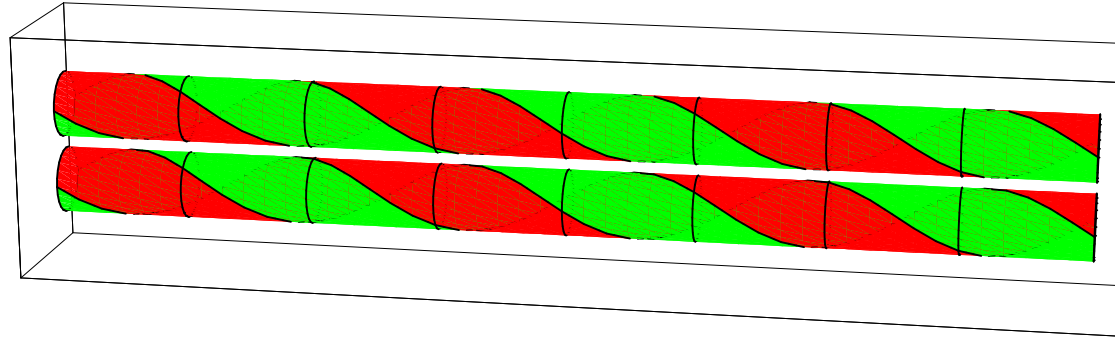
Filaments coiled in helical structures

Previous work : Fraser & Stump (1998) , Coleman & Swigon (2000)

$$Lk = 6$$

$$Tw = 6$$

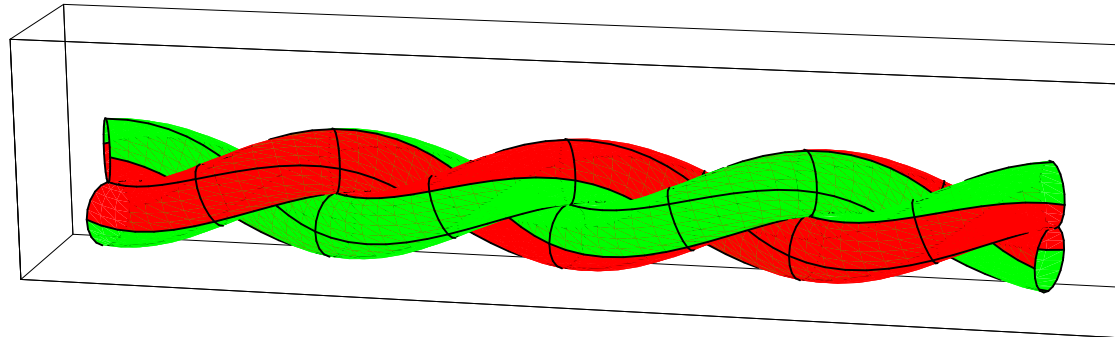
$$Wr = 0$$



$$Lk = 6$$

$$Tw = 2.35$$

$$Wr = 3.65$$

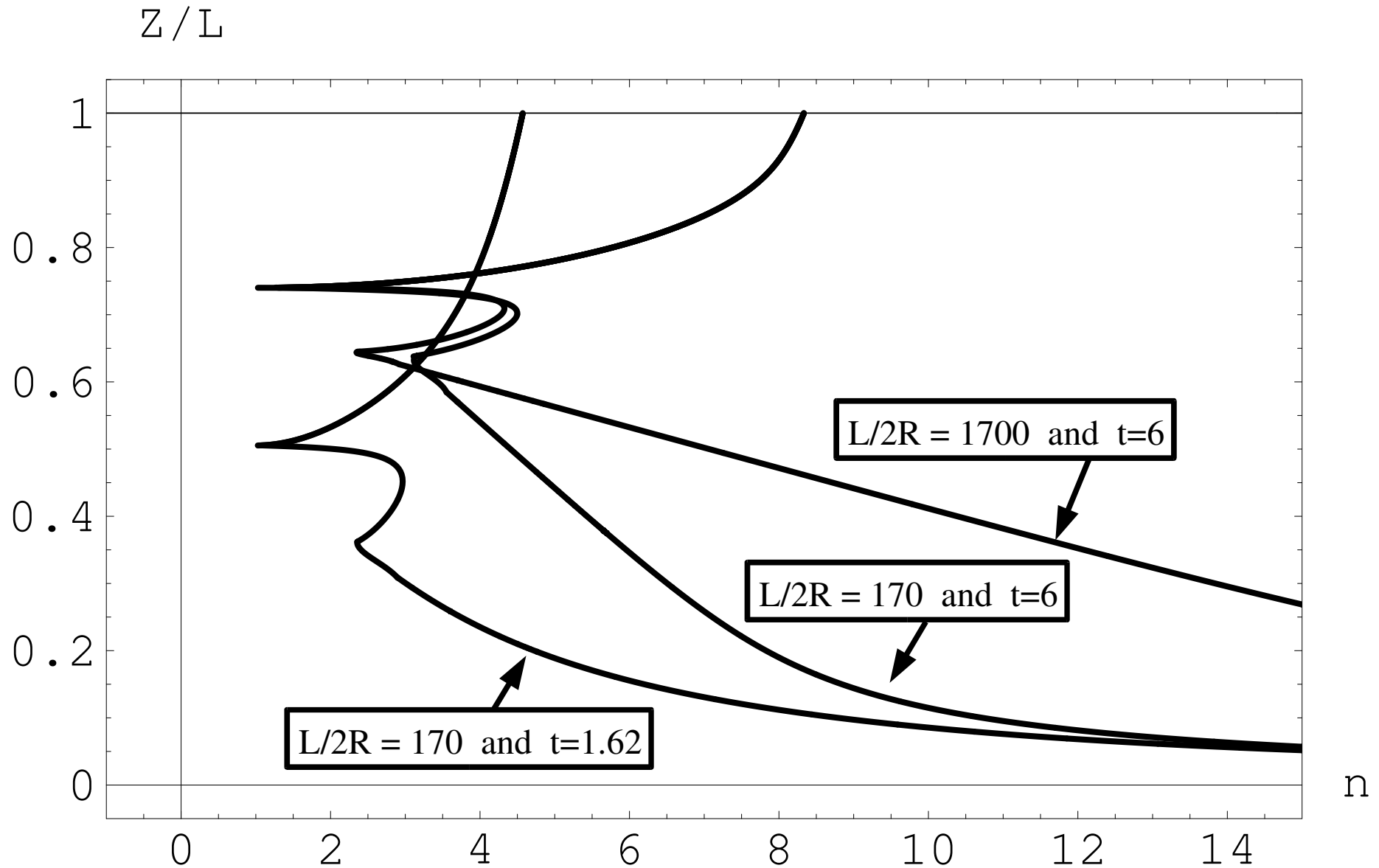


$$2 K_0 n \sin^3 \theta \cos \theta + \epsilon n K_3 R \tau \cos 2 \theta + R^2 F \sin \theta - \epsilon R M \cos \theta = 0$$

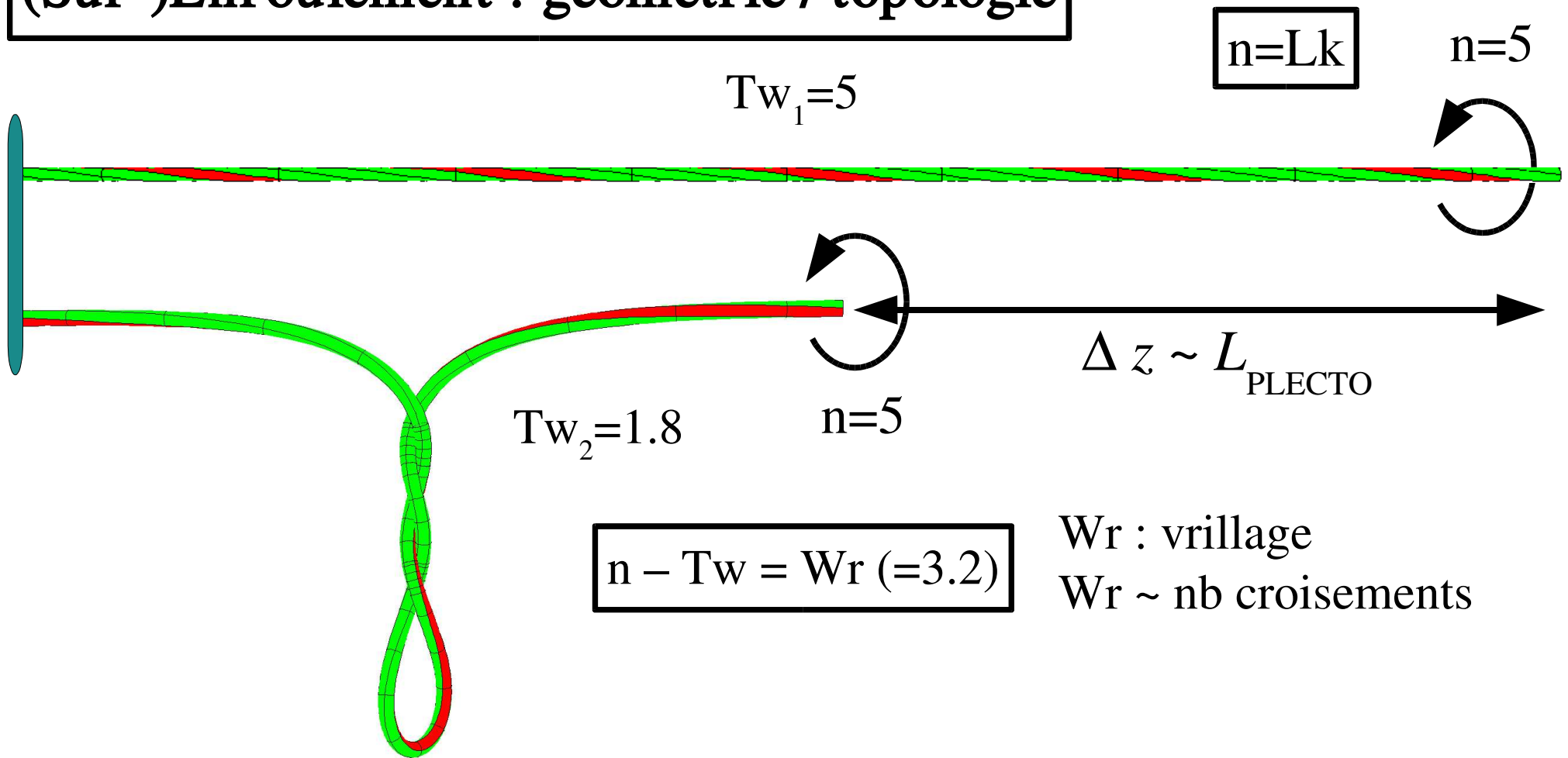
$$p R^3 = \frac{\sin^2 \theta}{\cos 2 \theta} \left(K_0 \sin^2 \theta + \frac{R^2 F}{n} \cos \theta - \epsilon \frac{R M}{n} \sin \theta \right)$$

$\epsilon = \pm 1$: handedness
 n : nb of strands
 F, M : external stress

Slope of linear part : fonction of t and L/R



(Sur-)Enroulement : géométrie / topologie



$n=Lk$

$n=5$

$Tw_1=5$

$Tw_2=1.8$

$n=5$

$n - Tw = Wr (=3.2)$

Wr : vrillage
Wr ~ nb croisements

$\Delta z \sim L_{PLECTO}$

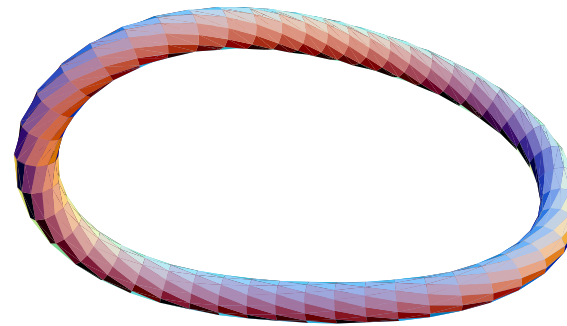
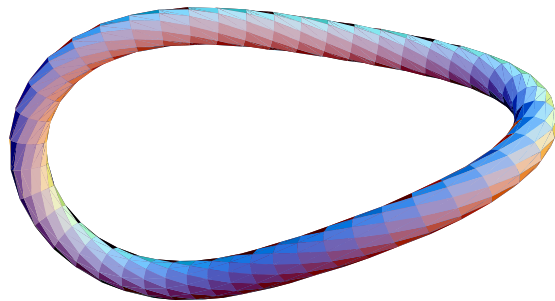
$$\frac{1}{2\pi} \int_0^L \dot{\psi} (1 - \cos \theta) ds = 1.2 = Wr \text{ mod } 1$$

$$\frac{1}{2\pi} \int_0^L (\dot{\psi} + \dot{\phi}) ds = 3 = Lk \text{ mod } 1$$

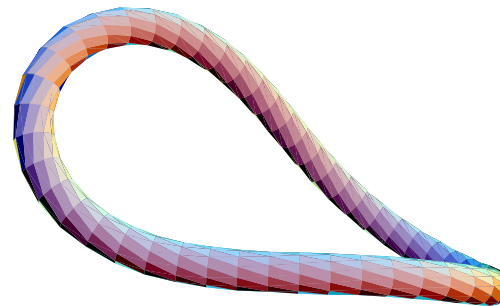
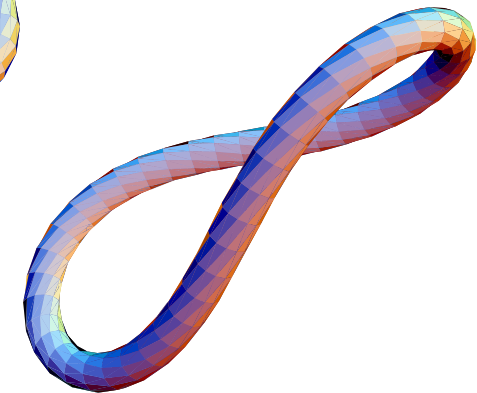
Vrillage d'une courbe : writhe

$$W_r(C) = \frac{1}{4\pi} \iint \frac{(r(s_1) - r(s_2)) \cdot (t(s_1) \times t(s_2))}{|r(s_1) - r(s_2)|^3} ds_1 ds_2$$

$$C : s \rightarrow r(s) \quad s \in [0, L]$$



$$W_r = 0.24$$



- $W_r \in \mathbb{R}$
- invariant géométrique
- PAS invariant topologique
- nombre moyen de croisements vus sous tous les angles

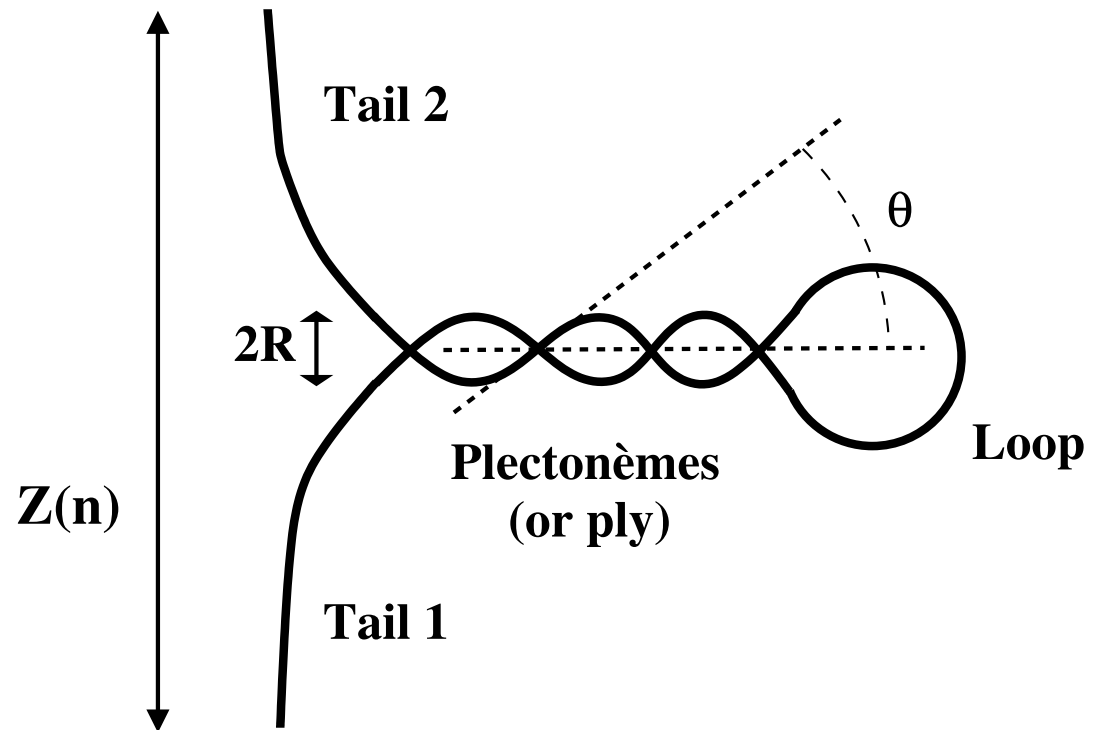
Topology : Writhe

Wr is given by a double integral, hence not additive (a priori).

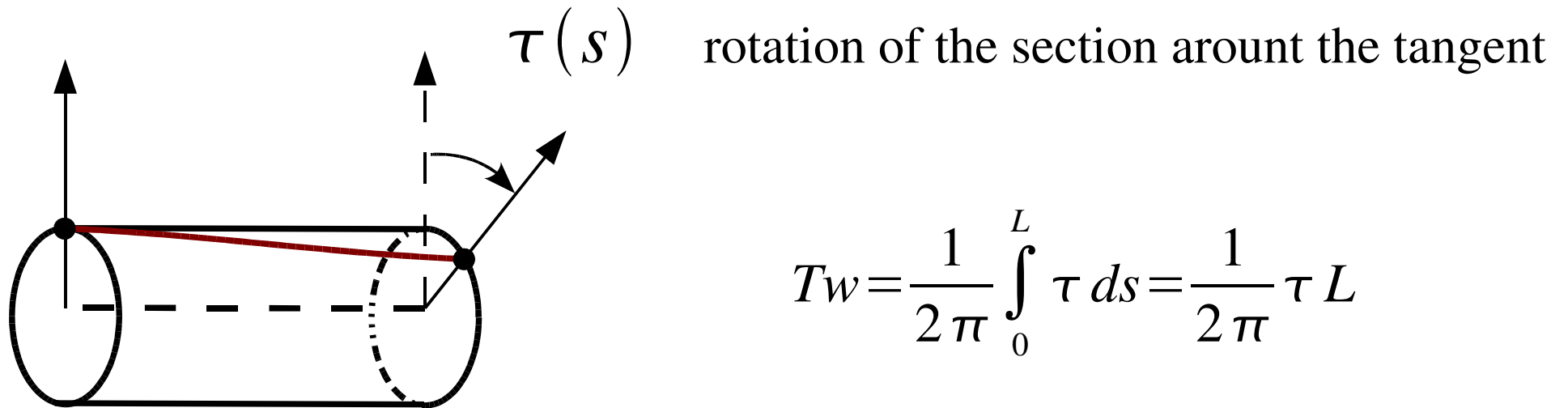
But there is Fuller theorem (1978) : $\int_0^L \int_0^L \dots ds ds' \rightarrow \int_0^L \dots ds$

$$Wr = Wr_{Plecto} + Wr_{Loop} + Wr_{Tails} \quad (\text{we neglect } Wr_{Loop} \text{ et } Wr_{Tails})$$

$$Wr \approx Wr_{Plecto} = -\epsilon \frac{L_{Plecto}}{4 \pi R} \sin(2\theta)$$



Twist of a curve



$$Tw = \frac{1}{2\pi} \int_0^L \tau ds = \frac{1}{2\pi} \tau L$$

$$Tw \in \mathbb{R}$$

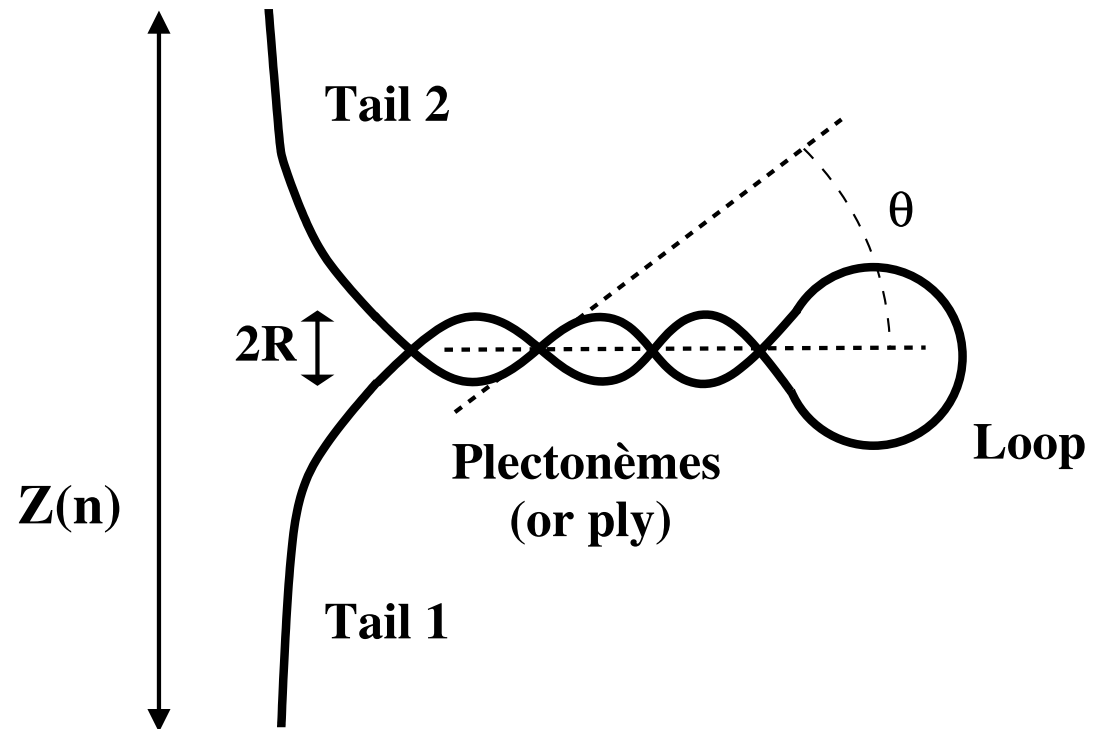
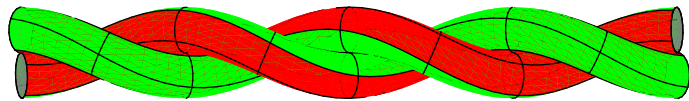
Tw not topologically invariant

Tw is additive (single integrale)

Topology : Twist

$$Tw = \frac{1}{2\pi} \int_0^L \tau ds = \frac{1}{2\pi} \tau L \quad (\tau \text{ constant \% } s)$$

Equilibrium of plectonemic part yields : $\tau = -\epsilon \frac{1}{2R} \frac{K_0}{K_3} (\tan 2\theta - \sin 2\theta)$



Nombre d'enlacements d'un ruban : Link

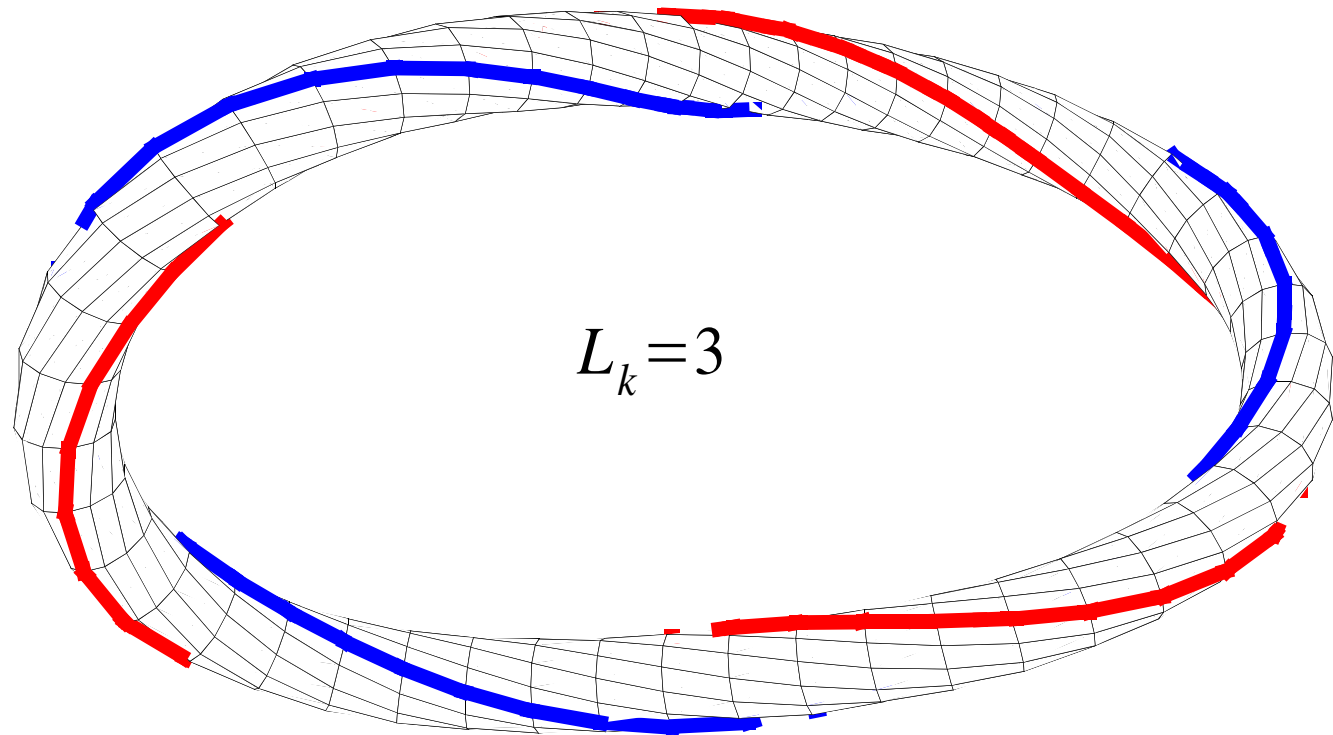
$$L_k(C_1, C_2) = \frac{1}{4\pi} \iint \frac{(r_1(s_1) - r_2(s_2)) \cdot (t_1(s_1) \times t_2(s_2))}{|r_1(s_1) - r_2(s_2)|^3} ds_1 ds_2$$

C_1 et C_2 : bords du ruban

$$C_1 : s \rightarrow r(s) + \epsilon d_1(s)$$

$$C_2 : s \rightarrow r(s) - \epsilon d_1(s)$$

$$s \in [0, L]$$



$$L_k = 3$$

- normalement $L_k \in \mathbb{Z}$
- invariant géométrique
- invariant topologique
- nombre de rotations d'une boucle autour de l'autre

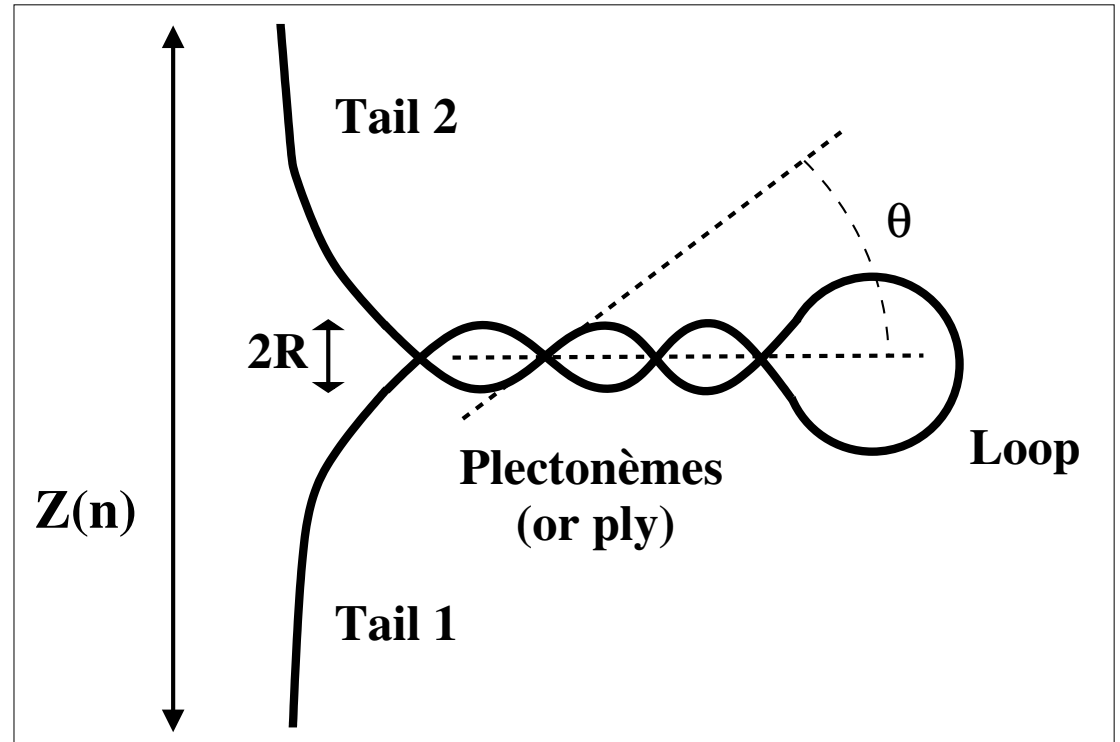
Topology : Twist, Writhe and Link

Calugareano, White, Fuller

$$n = Lk = Tw + Wr$$

$$Tw = -\epsilon \frac{L}{4 \pi R} \frac{K_0}{K_3} (\tan 2\theta - \sin 2\theta)$$

$$Wr \approx -\epsilon \frac{L_{Plecto}}{4 \pi R} \sin(2\theta)$$



$$L = L_{Plecto} + \cancel{L_{Loop}} + L_{Tails}$$

$$L_{Tails} = Z \cdot \frac{L}{Z(0)}$$

$$n = \frac{L}{4 \pi R} \left\{ \frac{K_0}{K_3} (\tan 2\theta - \sin 2\theta) + \sin 2\theta \left(1 - \frac{Z}{Z(0)} \right) \right\}$$

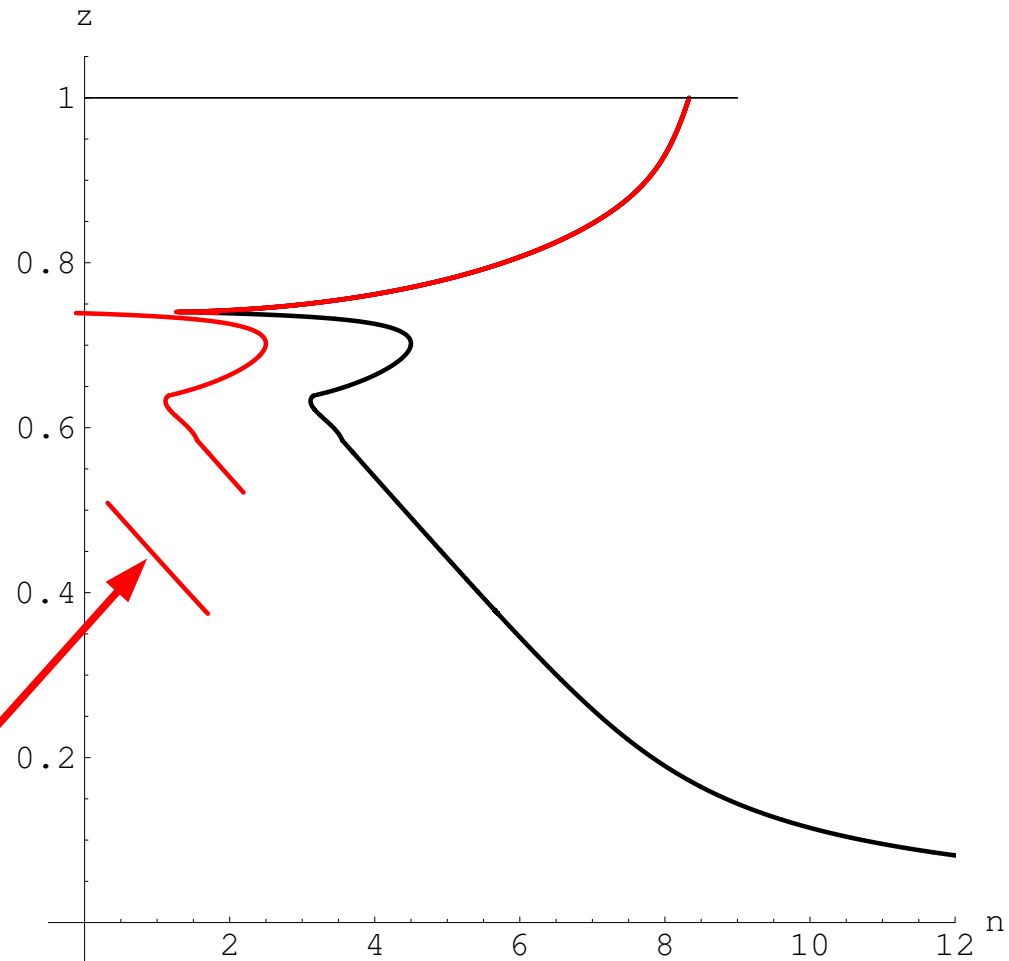
($\epsilon = -1$)

**Writhe (and link):
wrong formula**

slenderness ratio: $\frac{L}{2R} = 170$

constant tension: $t = \frac{TL^2}{4\pi^2 K_0} = 6$

$$n = Lk = \frac{1}{2\pi} \int_0^L (\dot{\psi} + \dot{\phi}) ds \pmod{1}$$

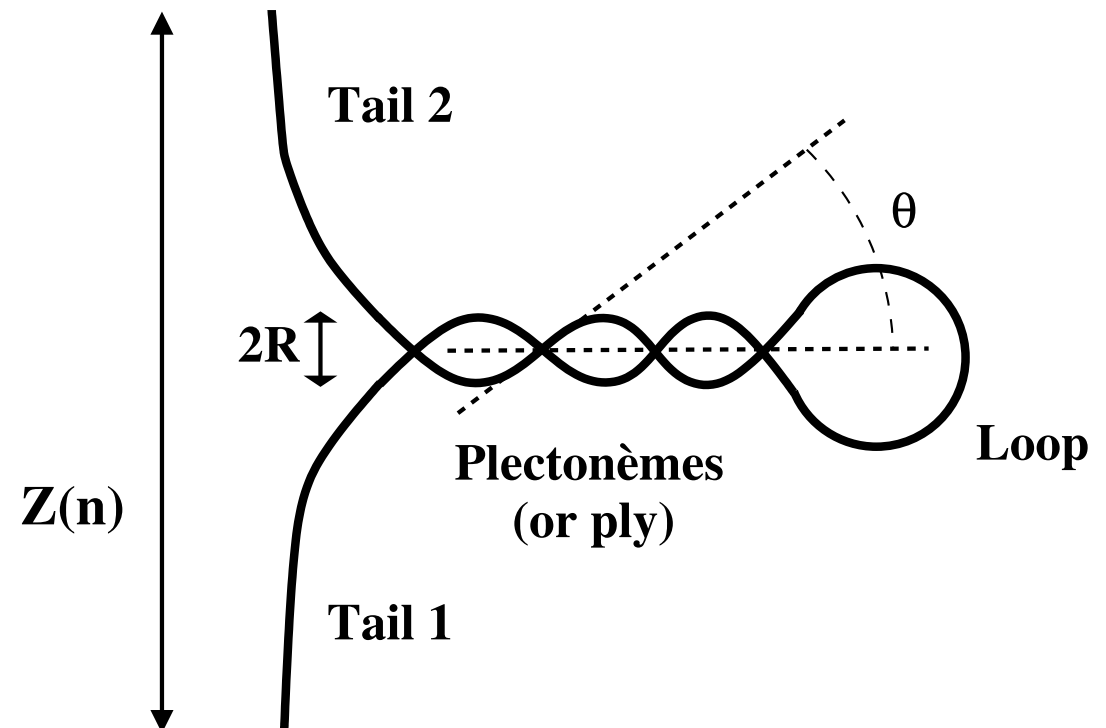
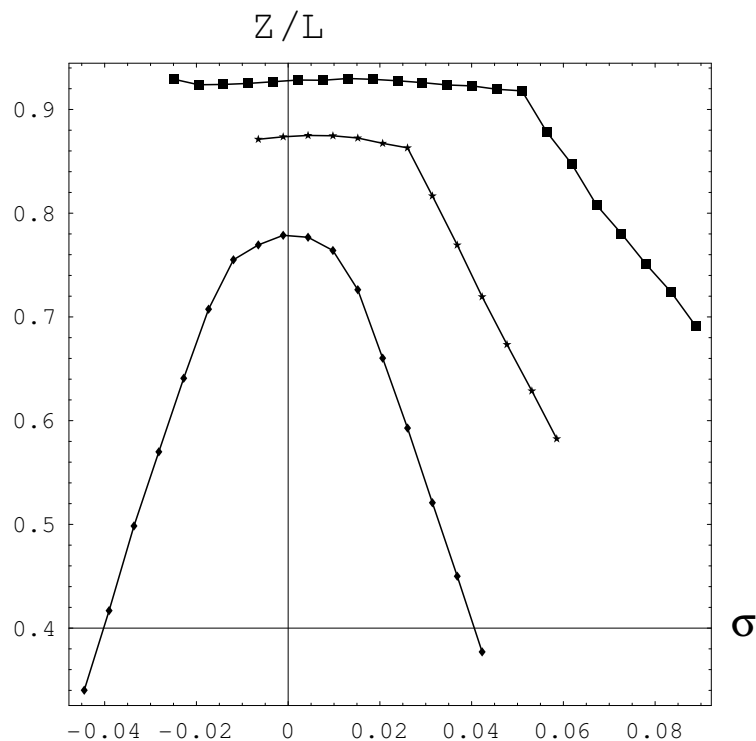


Helical angle θ : fonction of t and L/R

Helix angle θ is almost constant for all configurations in the linear part of the response curve (same for Twist)

θ does not depend on K_3 (centre line $\mathbf{r}(s)$ does not depend on K_3)

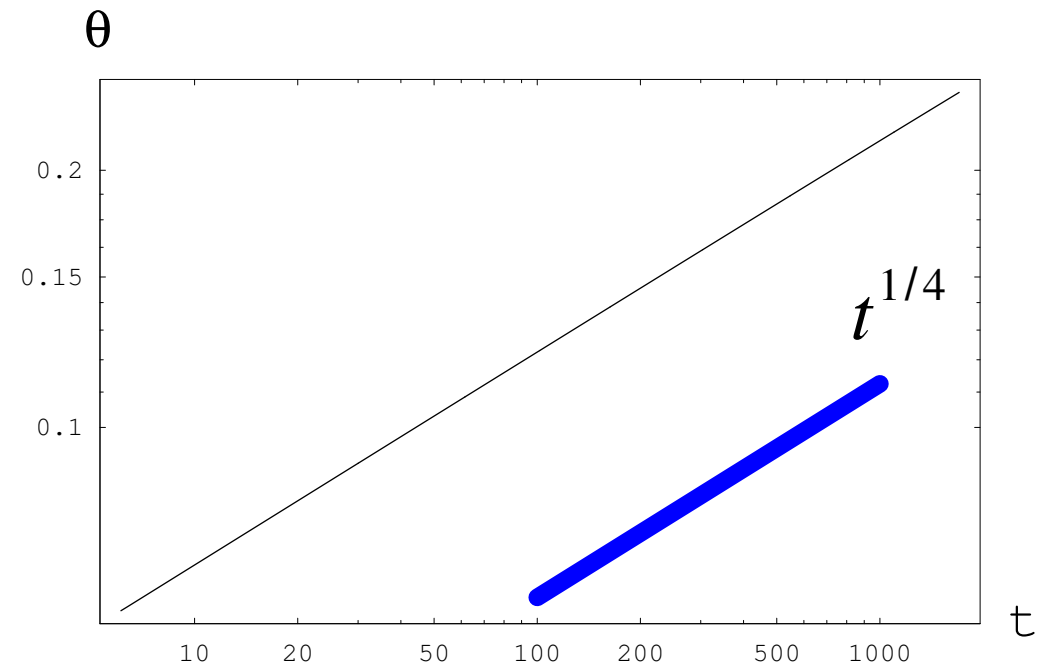
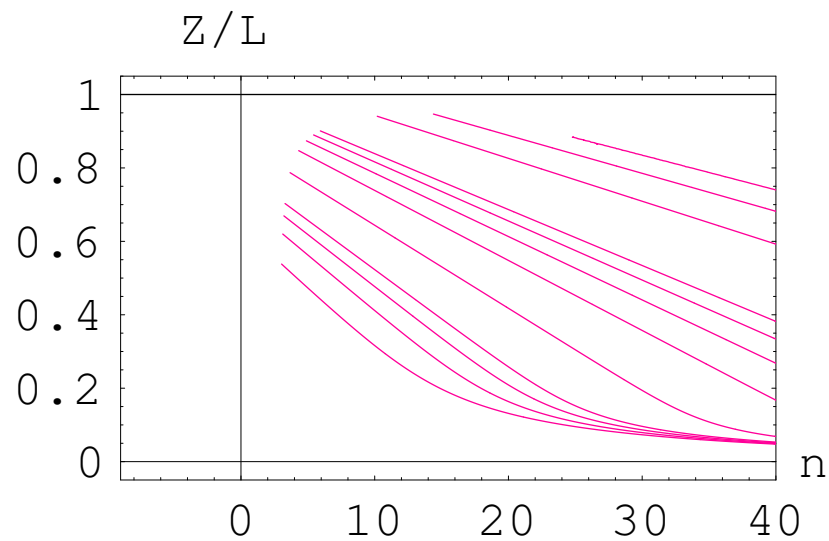
$$\theta = \theta(t, L/R)$$



Helical angle θ : fonction of t and L/R

we vary t while keeping L/R fixed

$$\frac{L}{2R} = 1700$$

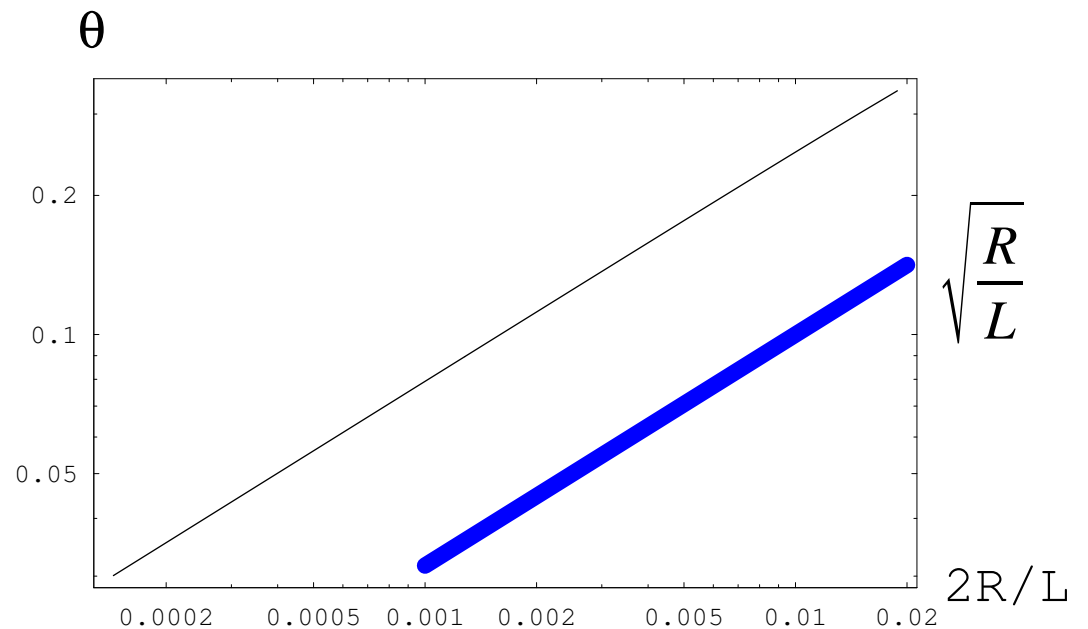
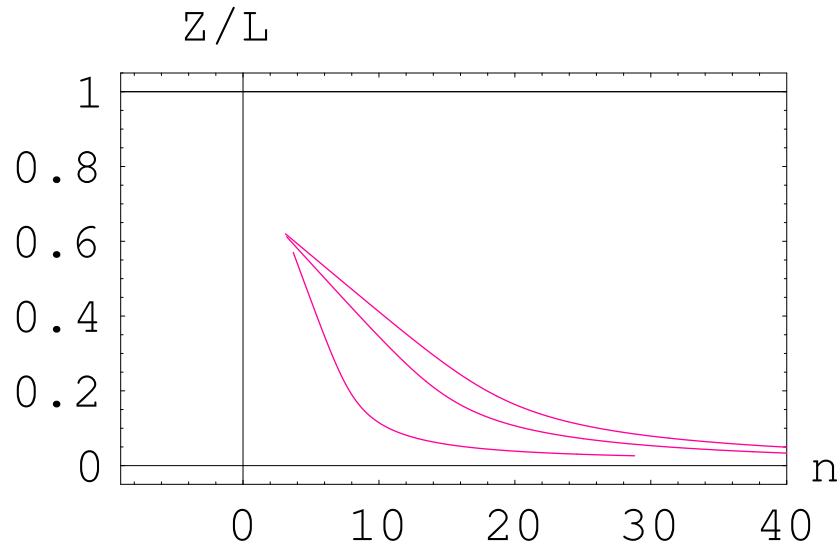


$$t = \frac{TL^2}{(2\pi)^2 K_0}$$

Helical angle θ : fonction of t and L/R

we vary L / R while keeping t fixed

$$t = \frac{T L^2}{(2 \pi)^2 K_0} = 6$$



polynomial interpolation : $\frac{R^2 T}{K_0} = \varphi(\theta) = 1.66 \theta^4$

Approximate equation for the linear part

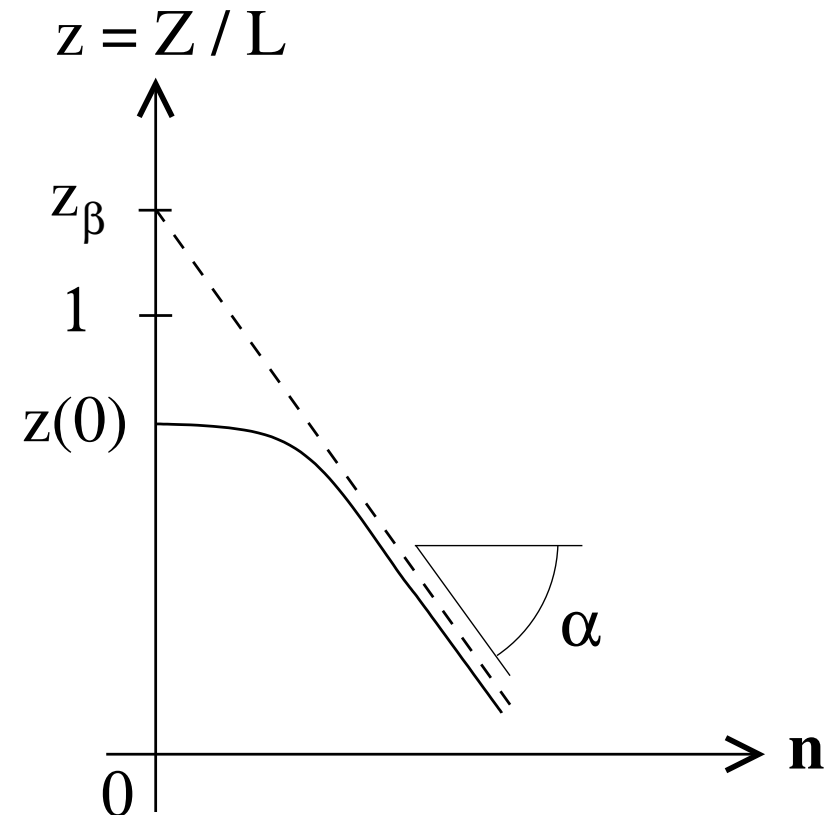
$$z = z(0) \underbrace{\left\{ 1 + \frac{K_0}{K_3} \left(\frac{1}{\cos 2\theta} - 1 \right) \right\}}_{Z_\beta} - \underbrace{\frac{4 \pi R}{\sin 2\theta} \frac{z(0)}{L}}_{\alpha} n \qquad \frac{\sigma}{H} = \frac{n}{L}$$

$H = 3.57 \text{ nm}$

this is not a fit !

$$\left\{ \begin{array}{l} \frac{R^2 T}{K_0} = \varphi(\theta) = 1.66 \theta^4 \\ \alpha = \frac{4 \pi R}{\sin 2\theta} \frac{z(0)}{L} \\ z_\beta = z(0) \left\{ 1 + \frac{K_0}{K_3} \left(\frac{1}{\cos 2\theta} - 1 \right) \right\} \end{array} \right.$$

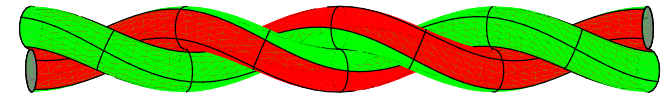
3 unknowns : (R , θ , K_0 / K_3)



Repulsive force in the plectonemic part



Mechanical equilibrium implies $\frac{p R^3}{K_0} = \frac{\sin^4 \theta}{\cos 2 \theta}$



with $\frac{R^2 T}{K_0} = 1.66 \theta^4$ this yields $p \simeq \frac{T}{1.66 R}$

careful :
T and R
are related

How does this compare with Debye Huckel electrostatic repulsion of two charged (straight) helices ?

$$p \simeq 4 k_B T \frac{L_B}{\lambda_D} \nu^2 \frac{e^{(-2 R/\lambda_D)}}{\sqrt{2 R/\lambda_D}}$$

L_B : Bjerrum length (0.7 nm)

λ_D : Debye length (0.8 nm)

ν : Poisson – Boltzmann effective charge per unit length 10 – 40 nm⁻¹

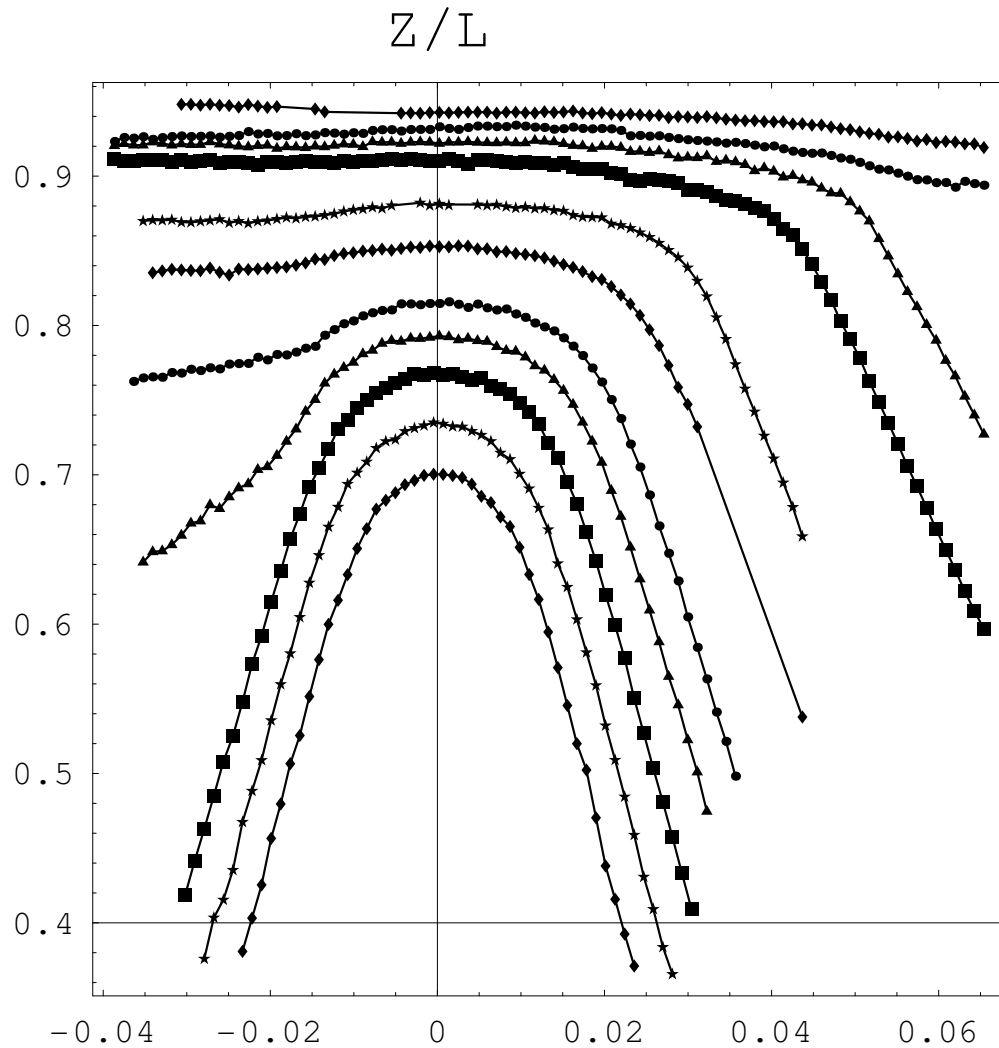
Ubbink + Odijk [1999] also in Marko+Siggia [1995]

Results

buffer solution = monovalent salt (phosphate) 10mM

molecule ~ 48kb

$$B = \frac{K_0}{k_B T} = 51 \text{ nm} \quad (\text{worm-like chain})$$



data from Vincent Croquette (LPS-ENS)

T (pn)	θ (rad)	R (nm)	C/B	P pN/ μm
0,25	0,42	6,73	1,75	28
0,33	0,44	6,46	1,71	39
0,44	0,45	6,02	1,72	56
0,57	0,45	5,33	1,64	82
0,74	0,48	5,37	1,71	108
1,10	0,47	4,10	1,62	208
1,31	0,45	3,54	1,41	284
σ 2,20	0,48	3,11	1,40	556

$$\sigma = \frac{n}{n_0} \quad C = \frac{K_3}{k_B T} = 80 \pm 10 \text{ nm}$$

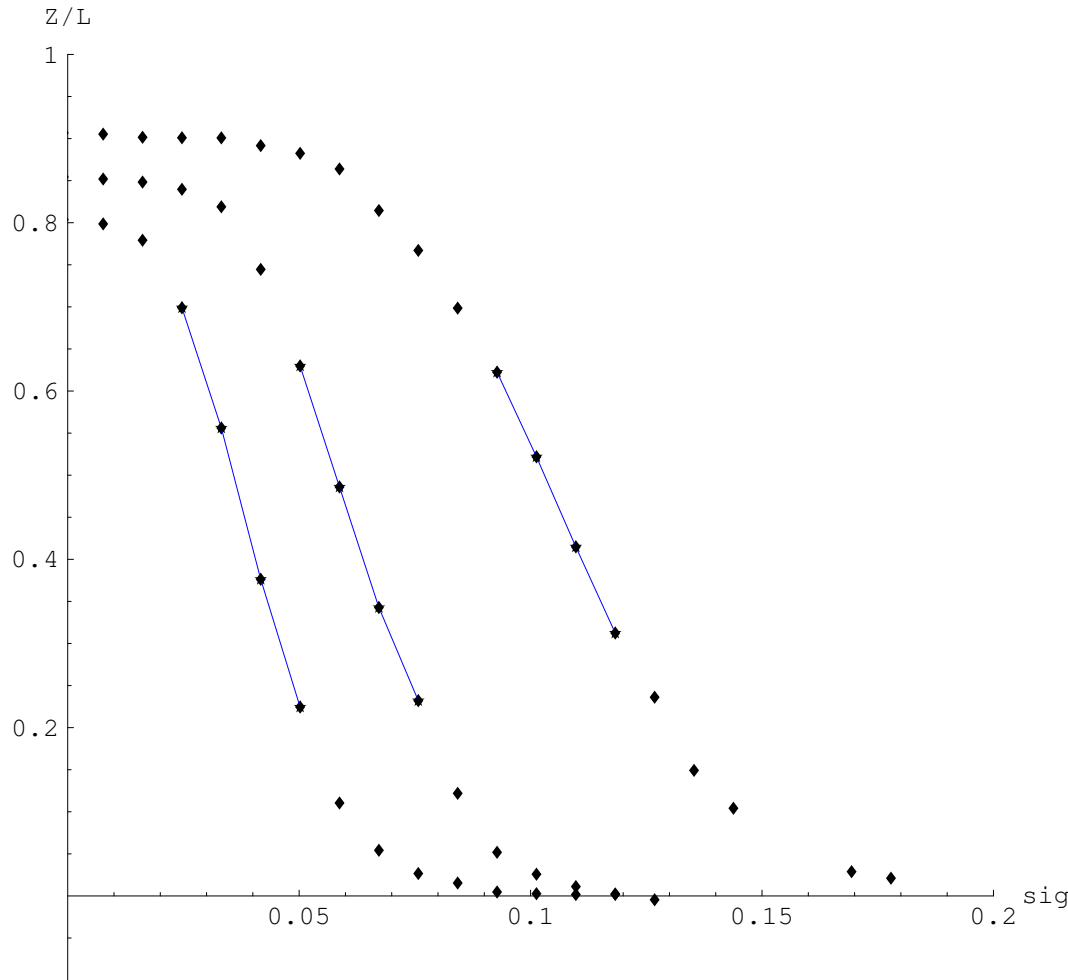
Results

buffer solution = monovalent salt (PB) 10mM

molecule ~ 6kb

$$B = \frac{K_0}{k_B T} = 46 \text{ nm} \quad (\text{worm-like chain})$$

T (pn)	θ (rad)	R (nm)	C/B	P pN/ μm
0,45	0,43	5,03	1,13	64
0,90	0,46	4,14	0,98	145
3,00	0,54	3,37	1,21	646



$$C = \frac{K_3}{k_B T} = 50 \pm 5 \text{ nm}$$

data from Gilles Charvin (LPS-ENS)

$$\sigma = \frac{n}{n_0}$$

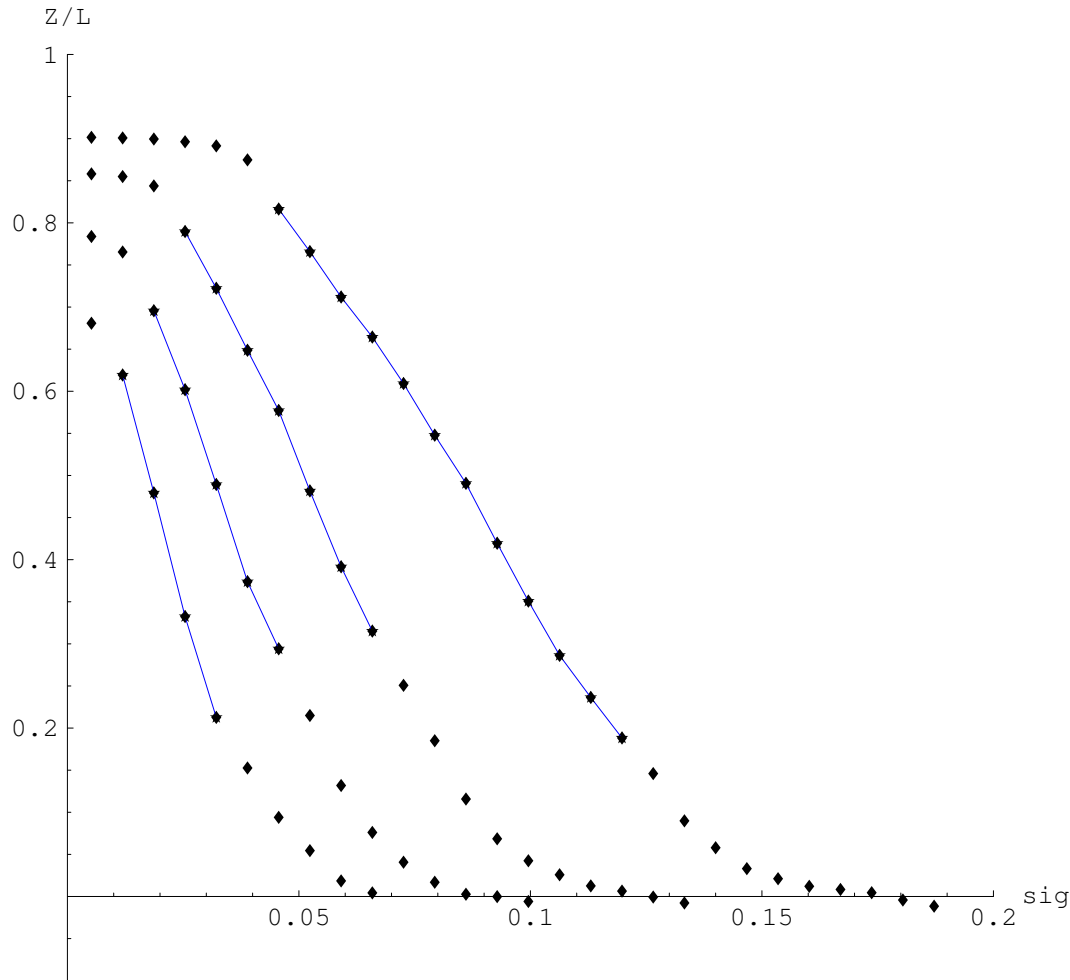
Results

buffer solution = monovalent salt (PB) 100mM

molecule ~ 6kb

$$B = \frac{K_0}{k_B T} = 49 \text{ nm} \quad (\text{worm-like chain})$$

T (pn)	θ (rad)	R (nm)	C/B	P pN/ μm
0,20	0,37	5,56	1,35	26
0,45	0,37	3,72	1,31	87
0,90	0,37	2,67	1,19	242
3,00	0,44	2,12	1,54	1 007



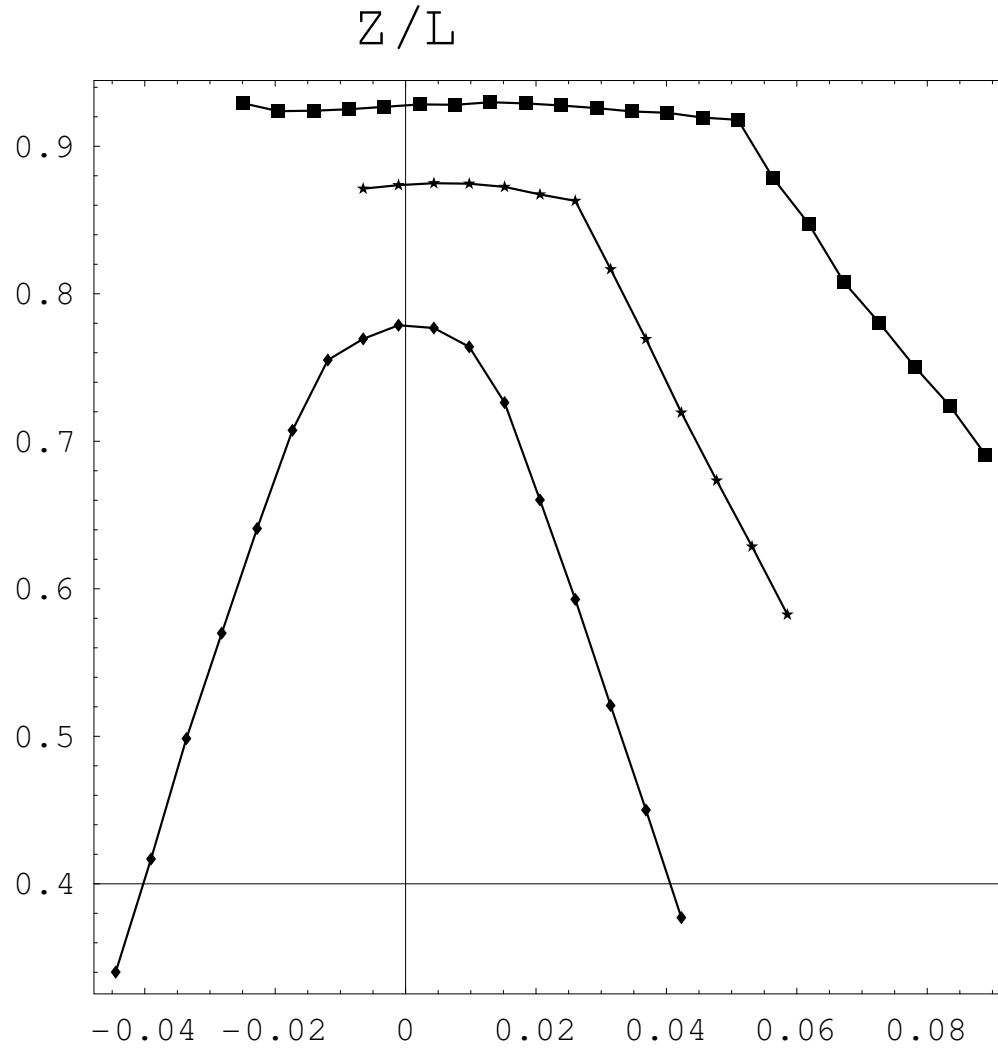
$$C = \frac{K_3}{k_B T} = 66 \pm 8 \text{ nm}$$

data from Gilles Charvin (LPS-ENS)

$$\sigma = \frac{n}{n_0}$$

Results

buffer solution = monovalent salt (phosphate) 150mM
+ divalent salt (magnésium) 5mM



data from Gilles Charvin (LPS-ENS)

molecule ~ 11kb

$$B = \frac{K_0}{k_B T} = 57 \text{ nm} \quad (\text{worm-like chain})$$

T (pn)	θ (rad)	R (nm)	C/B	P pN/ μm
0,45	0,31	2,81	1,08	114
1,45	0,32	1,68	1,01	615
4,30	0,35	1,16	0,99	2 690

σ

$$C = \frac{K_3}{k_B T} = 59 \pm 2.5 \text{ nm}$$

$$\sigma = \frac{n}{n_0}$$

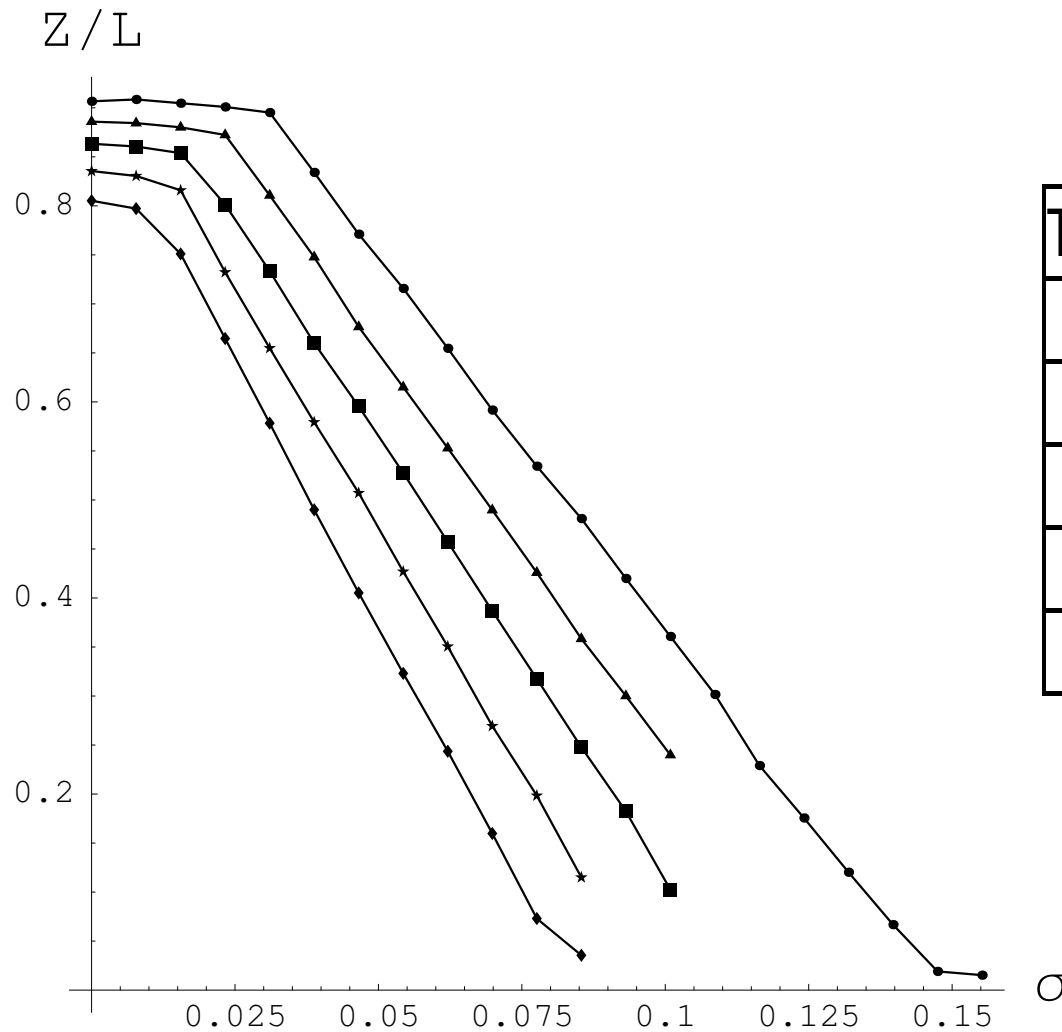
Results

buffer solution = monovalent salt (NaCl) 500mM

molecule ~ 9kb

$$B = \frac{K_0}{k_B T} = 40 \text{ nm} \quad (\text{worm-like chain})$$

T (pn)	θ (rad)	R (nm)	C/B	P pN/ μm
0,62	0,34	2,38	2,02	187
0,95	0,36	2,23	2,12	310
1,30	0,37	1,95	2,02	485
1,80	0,38	1,81	1,90	729
2,70	0,41	1,76	1,92	1 150



data from par R. Fulconis (Institut Curie)

$$C = \frac{K_3}{k_B T} = 80 \pm 4 \text{ nm}$$

$$\sigma = \frac{n}{n_0}$$

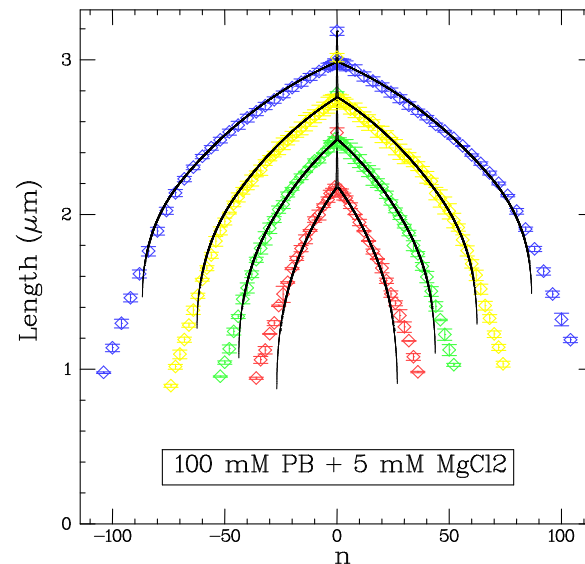
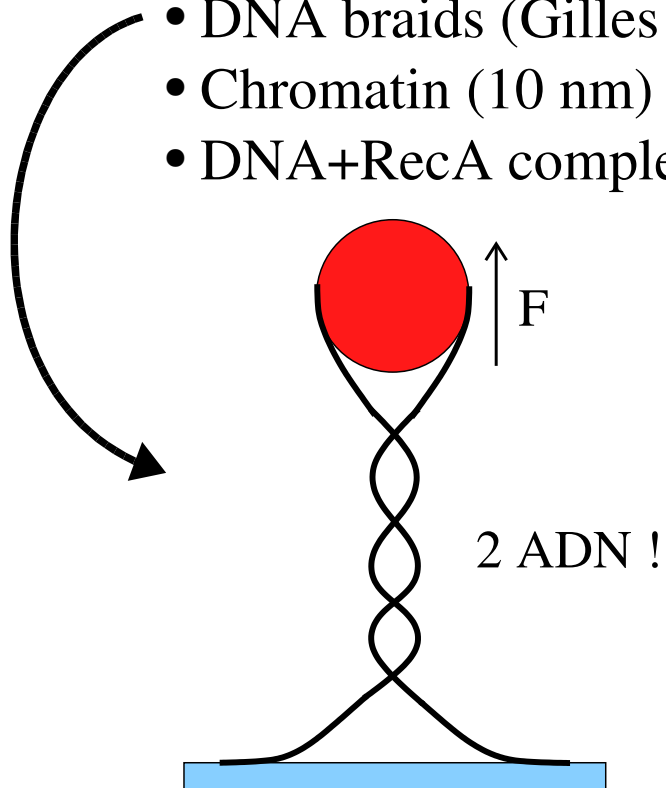
Futur work

→ Include :

- chirality and twist-extension coupling
- electrostatic repulsion

→ Model other experiments :

- DNA braids (Gilles Charvin)
- Chromatin (10 nm) fiber (A. Bancaud & J.-L. Viovy)
- DNA+RecA complex (R. Fulconis & J.-L. Viovy)



Relation between n and σ

$$\sigma = \frac{n}{n_0} = n \frac{H}{L}$$

$$L = 0.34 \text{ nbp nm}$$

σ : super-coiling ratio

n : number of turns applied on the magnetic bead

$n_0 = L / H$: intrinsic twist of the DNA double helix

$H = 3.57 \text{ nm}$: pitch of the DNA double helix

L : total contour length of the DNA molecule