

Polymers in Solution

Dresden, 26th October 2022

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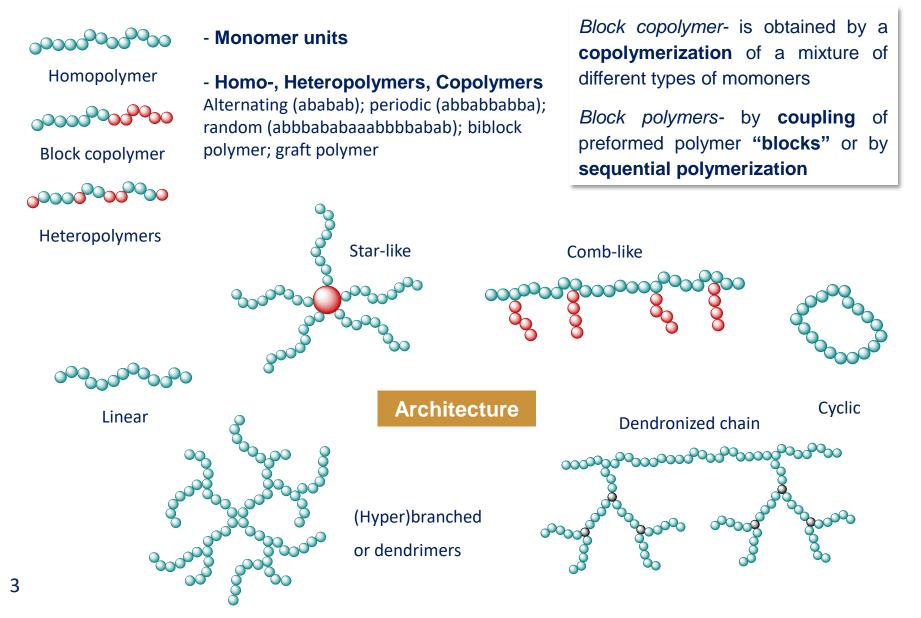


2. The isolated macromolecule: constitution, configuration, conformation

- 1. Constitution
- 2. Chemical configuration
- 3. Conformation → Microconformation
- 4. **Conformation** → Macroconformation
- 5. Example Questions
- 6. Books recommended

1. Constitution

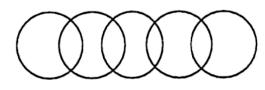


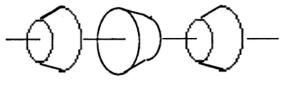


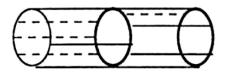
1. Constitution



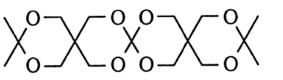
Higher constitution dimensions





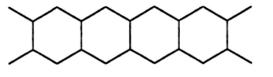


Polycatenane



Polyrotaxane

Polymer tube





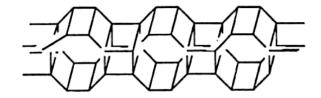
Spiro chain

Ladder polymer

Double helix



Spheroidal protein



Double ladder



Spherical molecule

Phyllo polymers- usually called layer or parquet polymers, form two-dimensional lattices- Graphene

1. Constitution

Higher constitution dimensions



COMMUNICATIONS CHEMISTRY

ARTICLE

https://doi.org/10.1038/s42004-019-0180-x OPEN

One-pot synthesis of cyclodextrin-based radial poly [n]catenanes

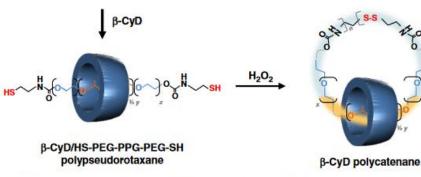
Taishi Higashi ^{1,2,3}, Kentaro Morita², Xia Song³, Jingling Zhu³, Atsushi Tamura ¹⁰, Nobuhiko Yui⁴, Keiichi Motoyama², Hidetoshi Arima⁵ & Jun Li ¹⁰

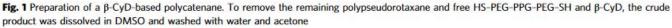




HS-PEG-PPG-PEG-SH

III





Commun Chem 2, 78 (2019). https://doi.org/10.1038/s42004-019-0180-x

1. Constitution

Higher constitution dimensions



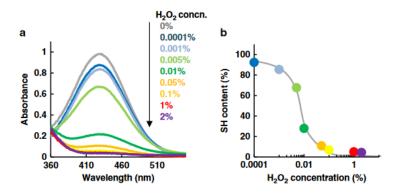


Fig. 2 Thiol-group content in the reaction suspensions. a Absorbance of 2-nitro-5-thiobenzoic acid and b thiol-group content in suspensions obtained by treating the prepared polycatenane with H_2O_2 solutions of varying concentration

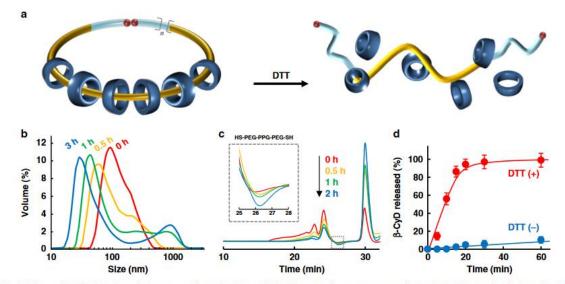
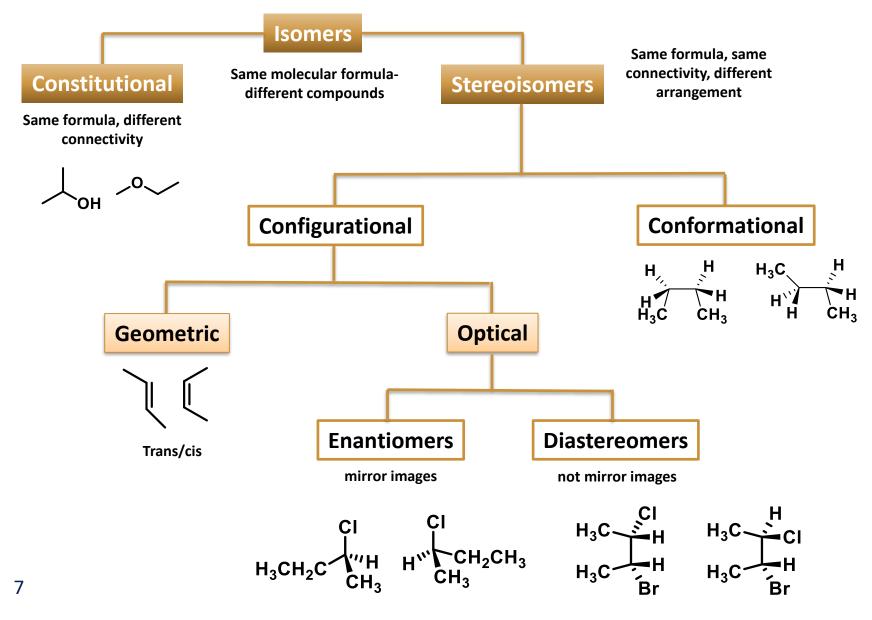


Fig. 4 Release of β -CyD from the polycatenane. **a** Schematic release of β -CyD from a polycatenane upon reduction. **b** Particle size distributions of β -CyD polycatenanes in the presence of DTT. **c** GPC profiles of β -CyD-based polycatenanes after treatment with DTT. **d** β -CyD-release profiles from polycatenanes in the absence/presence of DTT. Each data point corresponds to the mean ± standard error of three experiments

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2. Chemical configuration. Basic Terms





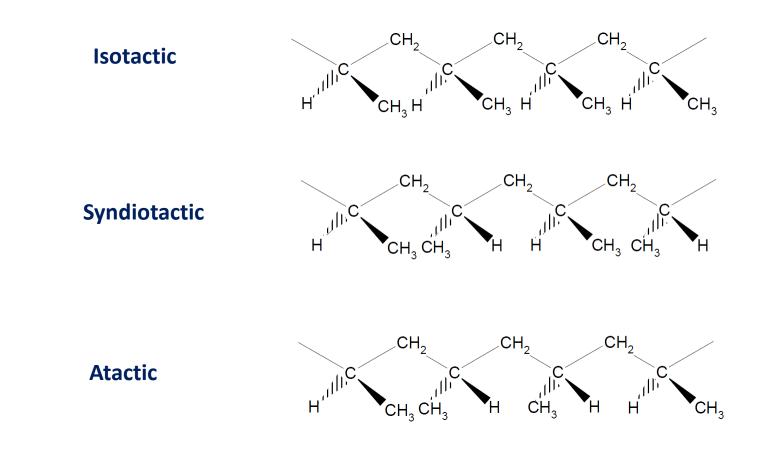
2. Chemical configuration Statistics



Configurational isomers- a large energy barrier (Isotactic/Syndiotactic or cis/trans)

Conformational isomers- a low energy barrier, they are interconverted rapidly into each other

Configurational statistics (1940s)



3. Microconformations

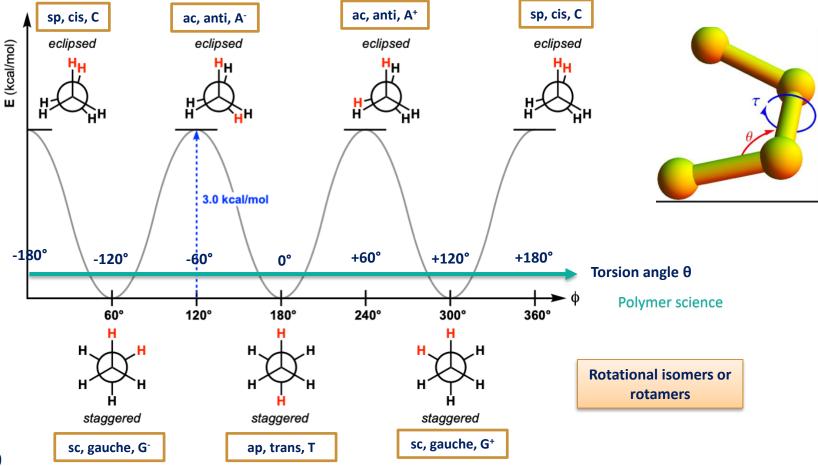


Local Conformations

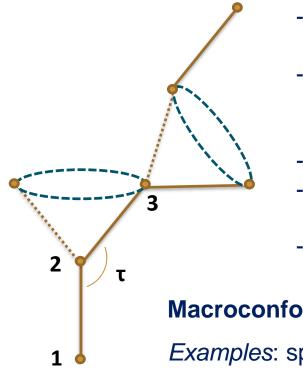
Torsion angle θ (conformational angle, rotational angle, dihedral angle)

Graphing the rotational barrier in ethane (C_2H_6) as a function of dihedral angle

The barrier to rotation in ethane is about 3.0 kcal/mol.







- Prefered positions are microconformations
- **Repeating sequences of microconformations** defining the macroconformation
- Very slow changes in crystalline state
- Very fast changes in dilute solution
- **Persistence** of prefered conformation

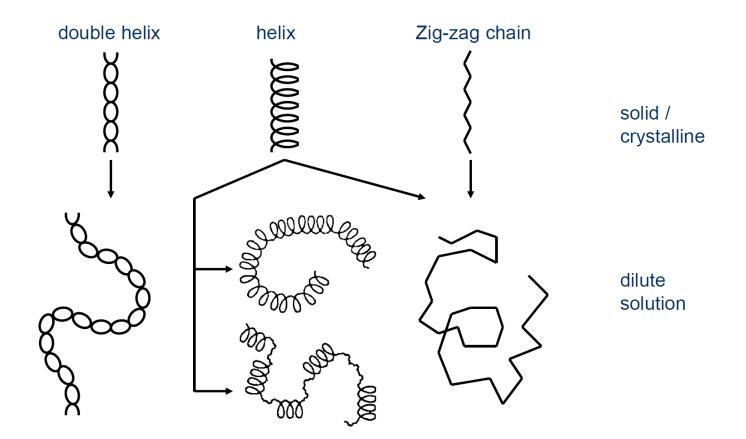
Macroconformations:

Examples: spheroidal proteins, rod like nucleic acids, stabilised by internal interactions constitution



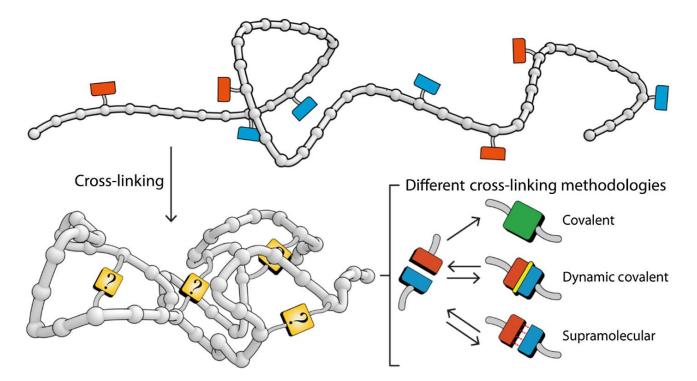


The shape of an isolated macromolecule is determinated by its molecular conformation (= macroconformation) which in turn depends on the type, proportion, and sequence of microconformations within the molecule.





Nature has unparalleled control over the conformation and dynamics of its folded macromolecular structures. Nature's ability to arrange amino acids into a precise spatial organization by way of folding allows proteins to fulfill specific functions in an extremely efficient manner. Chemists and materials scientists have used the delicate structure–function relationships observed in proteins to elucidate nature's design principles.



4. Macroconformations

The ideal chain

No correlation between polymer monomers separated by long distances along the polymer.

- Short range correlations between neighboring monomers are not excluded
- Ideal chain models do not take interactions caused by conformations in space into account
- Ideal chains allow the polymer to cross itself

Modeling a polymer

Imagining a blown up picture of a section of the polymer in a certain conformation, could look like this:

 $\vec{R}_{n} = \sum \vec{r}_{i}$

a) Conformations:

Torsion angle $\pmb{\theta}$

Bond angle $\pmb{\tau}$

b) Bond vectors:

Starting from one end we use vectors \boldsymbol{r}_i to represent the bonds

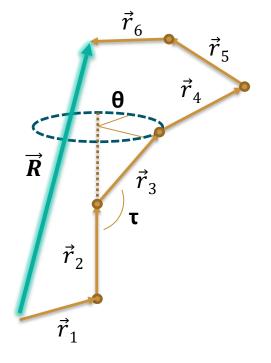
c) End-to-end vector:

The sum of all bond vectors

The ensamble average of $\langle \vec{R}_n \rangle = 0$ due to isotropy

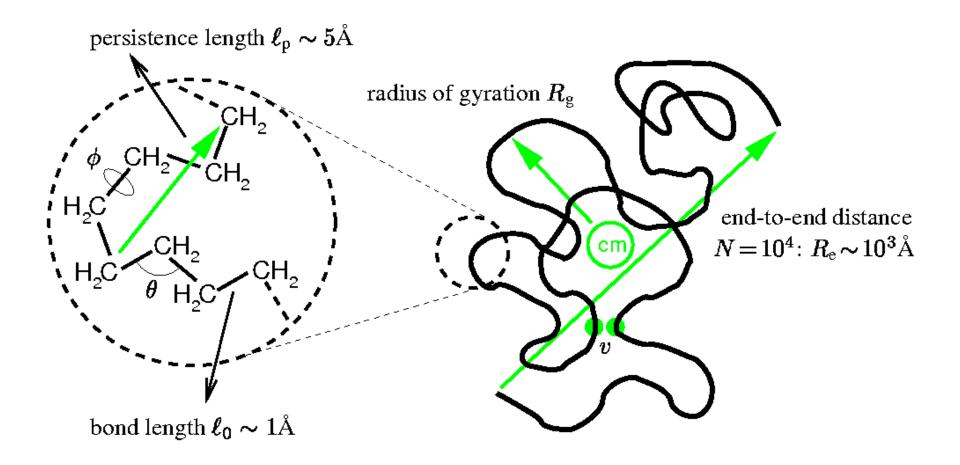
d) Mean square end-to-end distance:

Simplest non-zero average $\langle R^2 \rangle = \langle \vec{R}_n * \vec{R}_n \rangle = \sum_{i=1}^n \sum_{j=1}^n \langle \vec{r}_i * \vec{r}_j \rangle$ 13

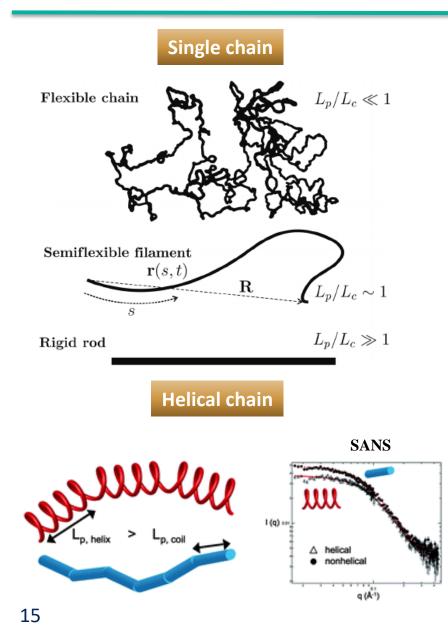




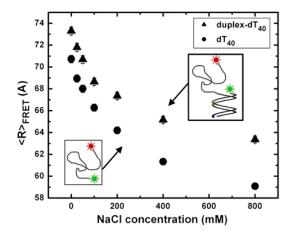




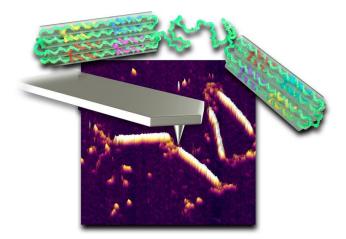




Ionic strength-dependent persistence lengths of single-stranded RNA and DNA



Measuring the Conformation and Persistence Length of Single-Stranded DNA Using a DNA Origami Structure

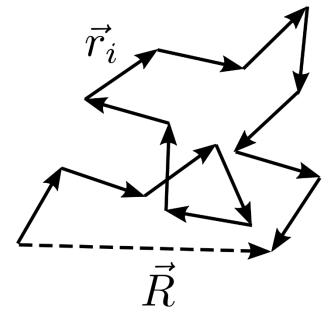


Freely jointed chain Kuhn 1934

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The **end-to-end distance** is the **distance** between the first particle and the last particle of one molecular chain. It has

no physical meaning for cyclic or branched molecules.



It can be only determinated experimentally for chains with specially marked end groups (fluorescent groups).

Undisturbed dimension (θ state)

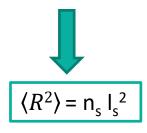
No correlation between the directions of different bond vectors. θ and τ are free to rotate. All bond vectors have: I_s (segment lenght) and n_s (number of segments), R (end-to-end distance)

$$\vec{R}^2 \rangle = \langle \vec{R}_n * \vec{R}_n \rangle = \sum_{i=1}^n \sum_{j=1}^n \langle \vec{r}_i \ast \vec{r}_j \rangle$$

$$\langle \vec{r}_{i_{*}} \vec{r}_{j} \rangle = \langle l_{s} l_{s} con \tau_{ij} \rangle \Rightarrow \langle \vec{R}^{2} \rangle = |s^{2} \sum_{i=1}^{n} \sum_{j=1}^{n} \langle con \tau_{ij} \rangle$$

No correlation between different bond vectors, i≠j

$$\langle \vec{r}_{i}, \vec{r}_{j} \rangle = \langle \vec{r}_{i} \rangle * \langle \vec{r}_{j} \rangle = 0$$



Maximum R- the most probable end-toend distance Kuhn segment

$$L_k = R_{max} = n_s I_s$$

$$M \sim n_s \quad \langle R^2 \rangle \sim M$$

4. Macroconformations

Freely rotating chain and characteristic ratio (C_{∞})

Bond angle τ is fixed. Torsion angle θ still free to rotate.

$$\langle \vec{R}^2 \rangle = \sum_{i=1}^n \sum_{j=1}^n \langle \vec{r}_i \ast \vec{r}_j \rangle \implies \langle \vec{r}_i \ast \vec{r}_j \rangle =?$$

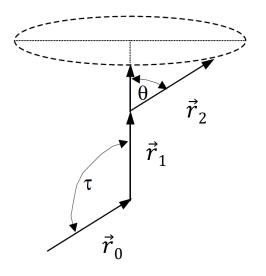
Ex: What is the correlation between vector \vec{r}_3 and \vec{r}_{0_2}

Due to the free rotation around the torque angle, only the perperdicular component of r_3 is paased down.

$$\langle \vec{r}_3 * \vec{r}_0 \rangle = l_{cc} \langle con\tau \rangle^2 * l_{cc} \langle con\tau \rangle = l_{cc}^2 \langle con\tau \rangle^3$$

 $\langle \vec{r}_{i}, \vec{r}_{j} \rangle = lcc^{2} \langle con\tau \rangle^{|i-j|}$

The general expession becomes:



Restricted rotation

$$\langle R^2 \rangle_{0f} = n_{cc} l_{cc}^2 \frac{1 - \cos \tau}{1 + \cos \tau}$$

$$\frac{\langle R^2 \rangle_{_{0r}}}{\langle R^2 \rangle_{_{0f}}} = \sigma^2 \quad \sigma$$
 restriction parameter

 C_{∞} is called Flory's characteristic ratio, and can be seen as a measure of the stiffness of the polymer in a given ideal chain model.

$$\langle R^2 \rangle = n_{cc} l_{cc}^2 C_{\infty}$$





Freely rotating chain and characteristic ratio

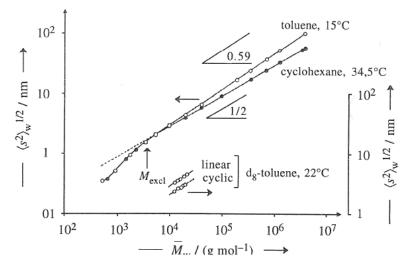
Polymer	Solvent	T (°C)	C∞	I _s /I _{cc}	σ
at-Polystyrol	cyclohexane	34	10.2	12	2.3
at-Polypropylen	diphenylether	153	5.3	6.5	1.61
Polyisobutylen	benzene	24	6.6	8.0	1.80
at-Polymethylmethacrylat	different	4 - 70	6.9	8.4	2.08
at-Polymethylmethacrylat	butyl chloride	35	7.2	8.8	1.74
Polysimethylsiloxan	2-butanone	20	6.2	-	1.39
Polyvinylchlorid	benzyl alcohole	155	9.2		2.08
Polyethylen	diphenyl methane	142	6.7	8.2	

 l_{C-C} = length of C-C bond



Scaling of the Radius of Gyration

 $\langle s^2 \rangle$ scattering methods deliver the average square of the **radius of gyration** $\langle R^2 \rangle$ not easy to determine; problems in case of branching –**end-to-end distance**



 $\langle s^2 \rangle_0 = \frac{1}{2n^2} \sum_i \sum_j \mathbf{r_{ij}}^2 = \frac{1}{n+1} \sum_i \mathbf{s_i}^2$

For n >> 10 $\langle S^2 \rangle_0 = \frac{\langle R^2 \rangle_0}{6}$ $\langle S^2 \rangle = \frac{\langle R^2 \rangle_0}{(2+\varepsilon)(3+\varepsilon)}$ O state

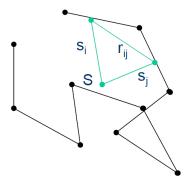
 $s^2
angle \sim M^{2\nu}$ $\varepsilon = 2n - 1$, depends on the quality of the solvent

$$s^2\rangle^{1/2} \sim M^{\nu}$$

$$\langle s^2 \rangle = R_g$$

Radius of Gyration

S center of mass; s_i distance center of mass-segment; r_{ij} distance segment-segment



Unperturbed chain $\rightarrow \nu = 0.5$

1. Polymer chain is collapsed onto itself and is very dense object $\rightarrow \nu = 0.33$ 2. Polymer chain is in a solution and the polymer prefers the solution to itself, thermodinamically good solvent $\rightarrow \nu = 0.60$

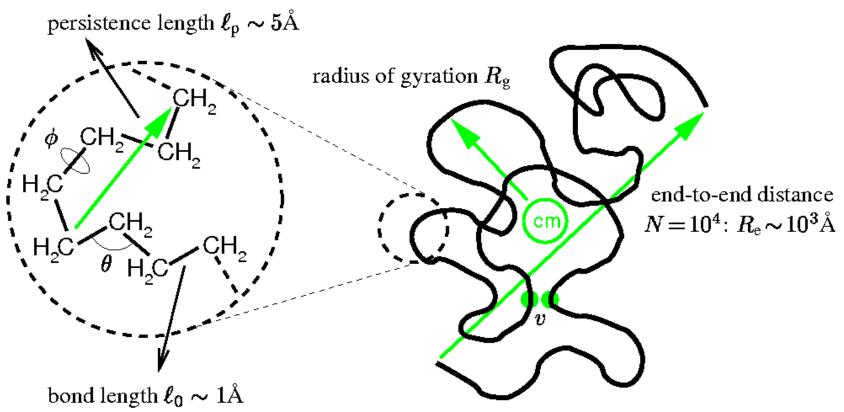
3. Polymer chain is rod-like $\rightarrow \nu = 1.00$



Radius of gyration and molar mass

Shape of macromolecule	Characteristic dimension – radius of gyration	Characteristic dimension – molecular weight
unperturbed coil	$< h^2 >_o = 6 < r^2 >_o$	$< h^2 >_o \sim M$
random coil, good solvent	$=(2+\varepsilon)(3+\varepsilon)$	$<\!\!h^2\!\!>\sim M^{1+\epsilon}$
thin rod, length L	$< L^2 > = 12 < r^2 >$	$L \sim M$
hard sphere, radius R *)	$< R^2 > = (5/3) < r^2 >$	$R \sim M^{1/3}$
disc, radius R	$< R^2 > = 2 < r^2 >$	$R \sim M^{1/2}$
0	$\langle R^2 \rangle_0 = 6 \langle s^2 \rangle_0$	$\langle R^2 \rangle_0 \sim M$





→ Conformational analysis and estimation of the persistence length of DNA using atomic force microscopy in solution DOI: 10.1039/c0sm01160f
 → Flexibility of single-stranded DNA measured by single-molecule FRET https://doi.org/10.1016/j.bpc.2014.08.004



The dynamics of solvation dictates the conformation of polyethylene oxide in aqueous, isobutyric acid and binary solutions

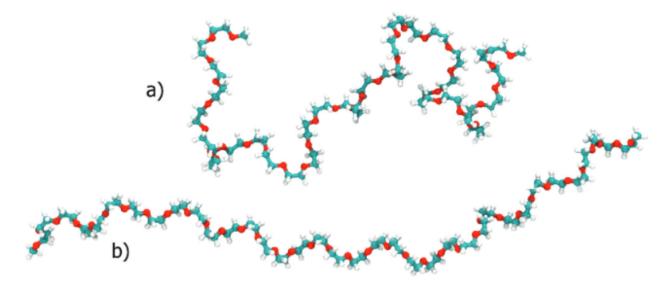


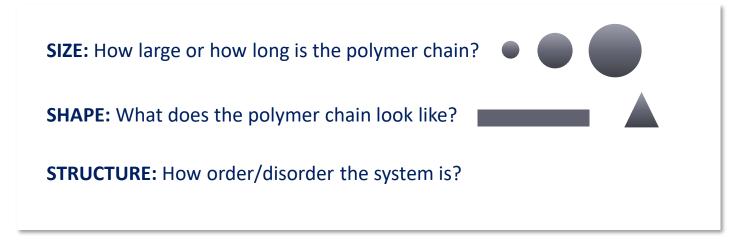
Fig. 1 Simulation snapshots of typical PEO (*n* = 36) conformation in (a) water and (b) isobutyric acid. Solvent is not shown. Carbons, oxygens and hydrogens are shown in cyan, red and white, correspondingly.

Table 1 The average end-to-end distance, R_{end} , radius of gyration, $R_{q'}$ aspect ratio, $R_{end}/R_{q'}$ and asphericity (eqn (1)) for F	or PEO in different solvents
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Solvent	R _{end} (nm)	R_{g} (nm)	$R_{\rm end}/R_{\rm g}$	Asphericity (nm ²)
Hexane	1.61 ± 0.6	0.75 ± 0.08	$\textbf{2.15} \pm \textbf{0.78}$	0.21 ± 0.13
Benzene	3.08 ± 1.3	1.30 ± 0.30	$\textbf{2.32} \pm \textbf{0.71}$	$\textbf{1.18} \pm \textbf{0.87}$
Water	3.42 ± 1.0	1.35 ± 0.19	2.50 ± 0.51	1.31 ± 0.62
Isobutyric acid	5.95 ± 0.46	$\textbf{2.07} \pm \textbf{0.08}$	$\textbf{2.87} \pm \textbf{0.22}$	3.50 ± 0.70

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Size, shape, and structure. Gyration tensor and measures of asphericity



Isotropic system: no differences in dimension $R_g^2 = R_x^2 + R_y^2 + R_z^2$

Anisotropy system → no differences in dimension, gyration tensor Desviation form the ideal sphere

ASPHERICITY VALUE

$$< A > = 1/2 \frac{\Sigma < (R_{gi}^2 - R_{gj}^2) >}{(< \Sigma R_{gi}^2 >)^2}$$

Higher A, higher < A > = 0anisotropy < A > = 1

$$A >= 0 \quad \text{Perfect sphere} \quad R_{g1} = R_{g2} = R_{g3}$$
$$A >= 1 \quad \text{Perfect rod} \qquad R_{g1} = R_g \quad R_{g2} = R_{g3} \sim 0$$



Size, shape, and structure. Gyration tensor and measures of asphericity

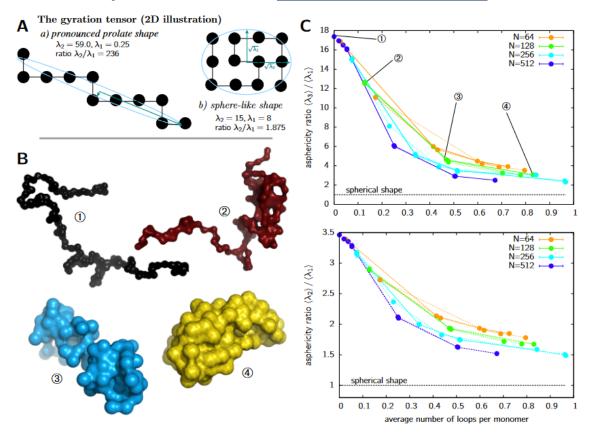
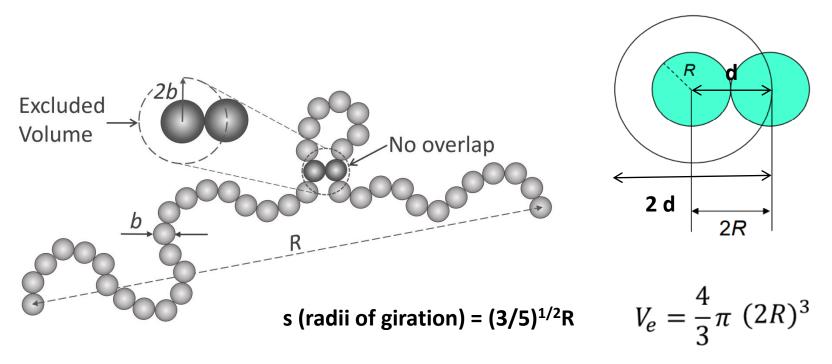


Figure 6: Elongated shape of the chromatin model polymers. A. Illustration of the gyration tensor. The gyration ellipsoid is shown for an elongated and a compact polymer conformations in two dimensions. The ratio λ_2/λ_1 is large for the elongated polymer, indicating strong devations from a sphere-like shape. B. Example conformations for a chain of length N = 128 and loop lifetime τ_1 (see eq. ??) for different looping probabilities. The shown conformations are one sample of the ensemble of conformations belonging to the data point marked in figure C. C. The ratios between the gyration tensor's main axes. The upper graph shows the ratio between the largest and smallest main axis, the lower graph the ratio between the second largest and smallest main axis. The data is shown for chain length up to N = 512, different lifetimes of the loops ($\tau = \tau_1$ solid line, $\tau = \tau_2$ dotted line, $\tau = \tau_3$ dashed line) and different looping probabilities p.



Volume excluded – hard sphere



u (excluded volume) = $4\pi d^3/3 = 32\pi R^3/3 = 8V$

Collects all interactions on an inter- and intramolecular level



- Define end-to-end distance, radius of gyration and persistence length
- Polystyrene with molar mass 5x10⁵ g/mol has <h²>_o = 300 nm², calculate <h²>_o for a PS with molar mass of 1x10⁶ g/mol; calculate <r²>_o for both molar masses
- How can you measure <r²>_o?
- How can you measure persistence length?

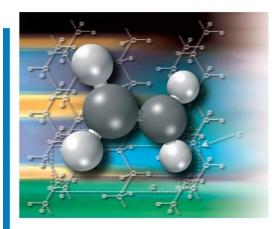
6. Recommended Books



Macromolecules Volume 3: Physical Structures and Properties Hans-Georg Elias Wiley-VCH GmbH & Co. KGaA, Weihnheim 2008



Volume 3: Physical Structures and Properties



Polymer Solutions An introduction to physical properties Iwao Teraoka Wiley-Interscience 2002

