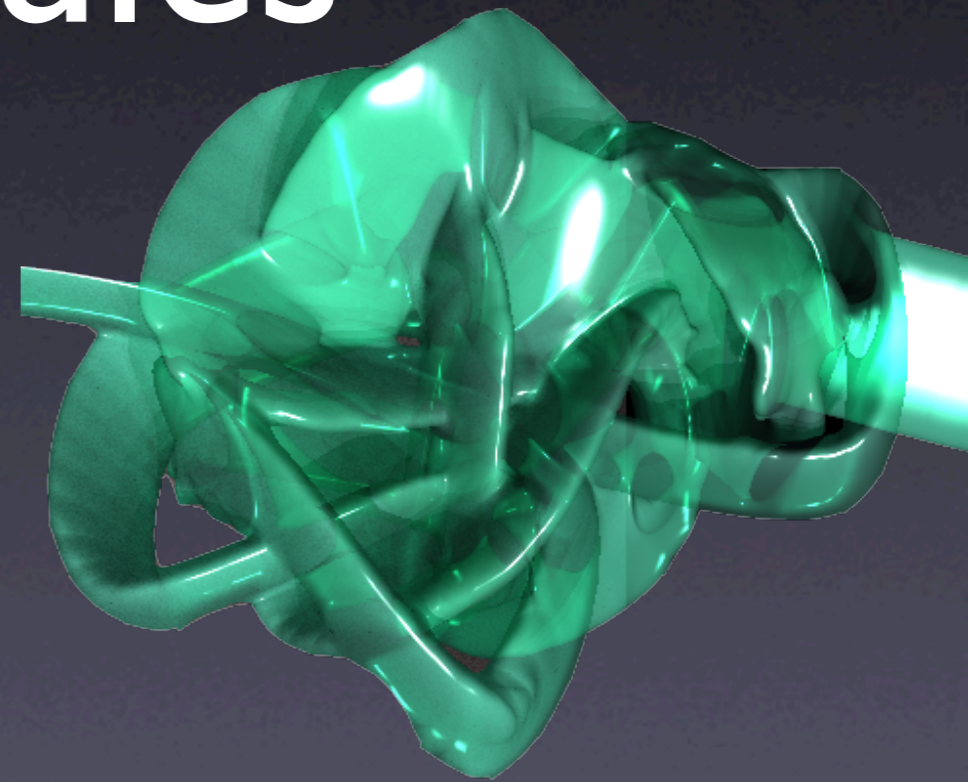
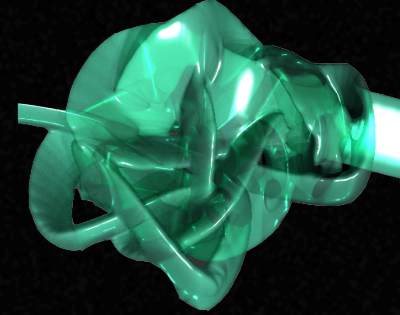


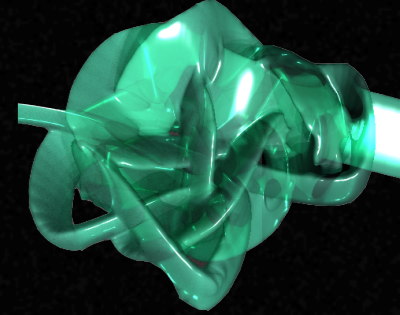
Knots in Macromolecules



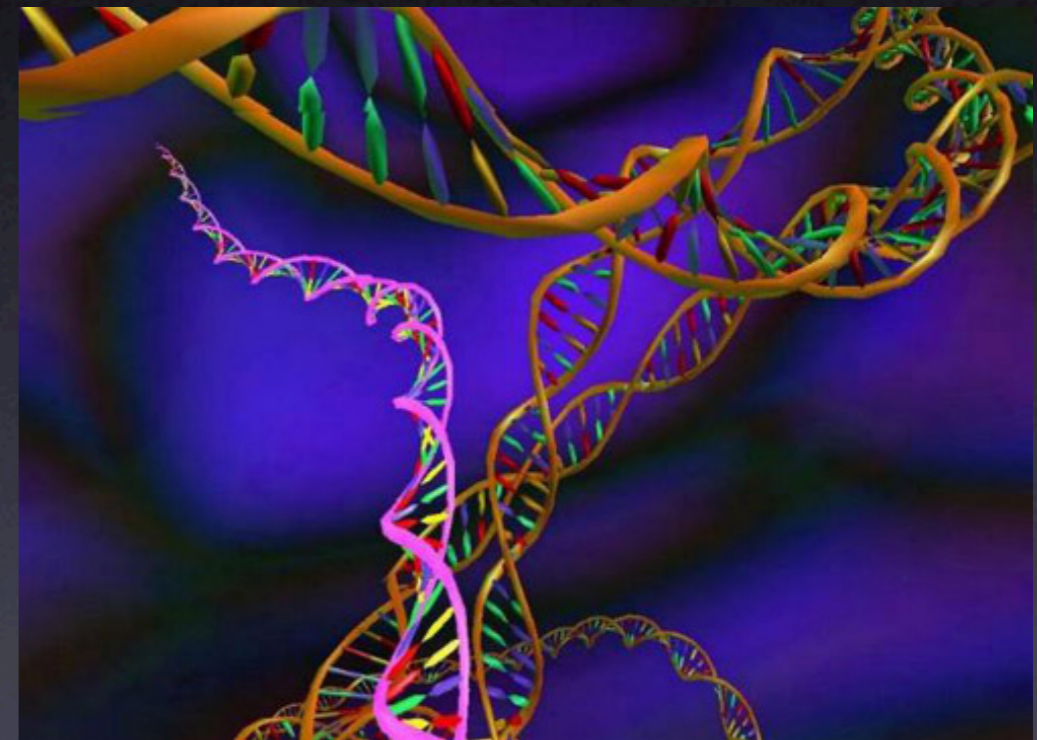
Introduction



Introduction

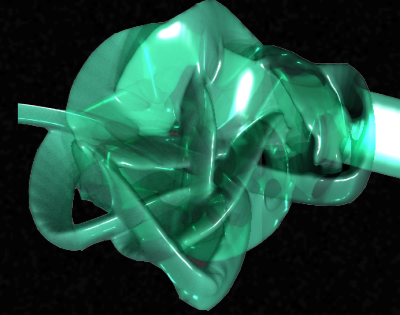


- DNA packing can be visualized as two very long strands that have been intertwined millions of times, tied into knots, and subjected to successive coiling.
- Replication and transcription are much easier to accomplish if the DNA is neatly arranged rather than tangled up in knots.
- Enzymes are essential to unpacking DNA.
- Enzymes act to slice through individual knots and reconnect strands in a more orderly way.

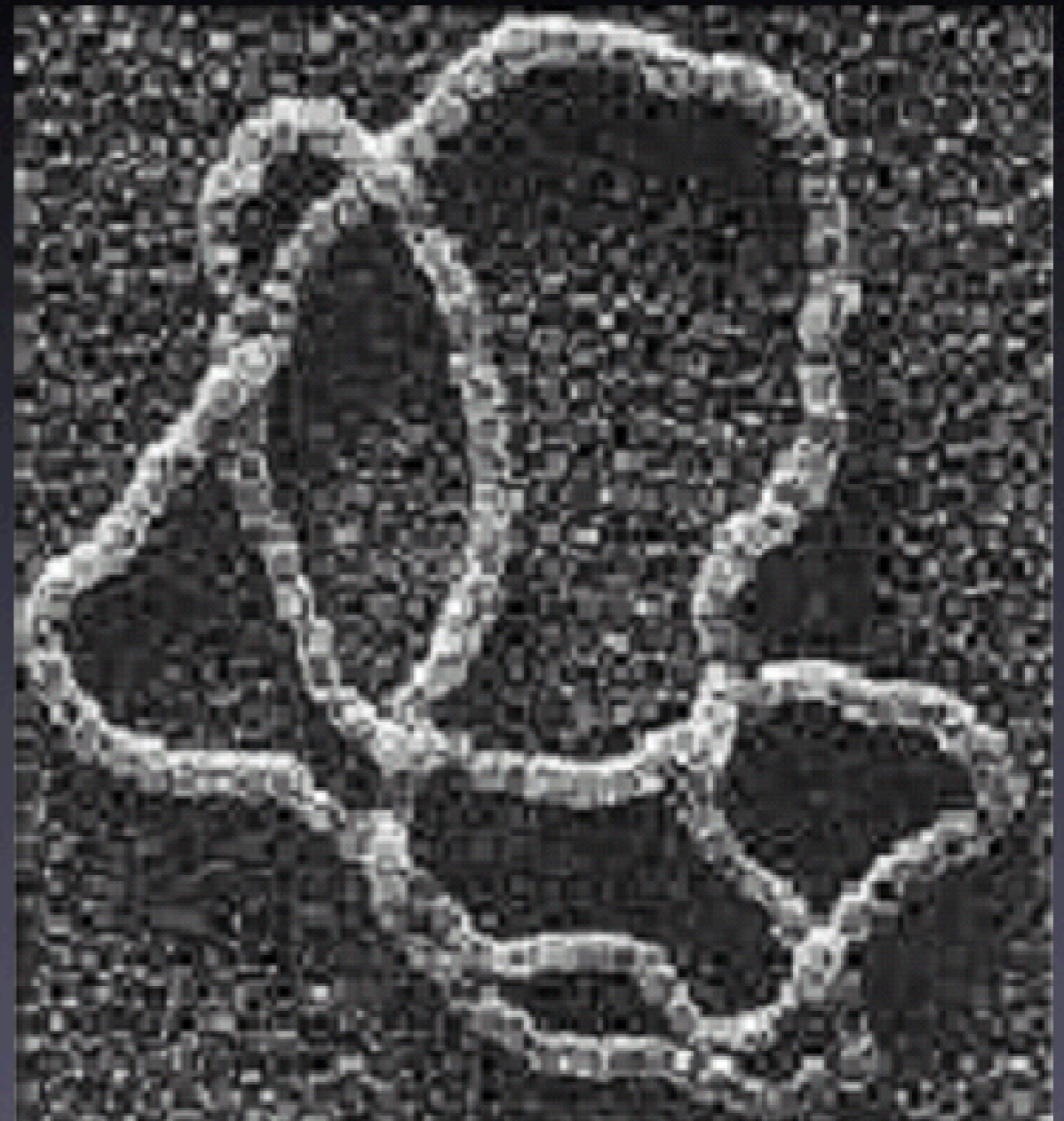


Taken from http://www.smoothbrothers.com/design/design_3d.htm

Introduction

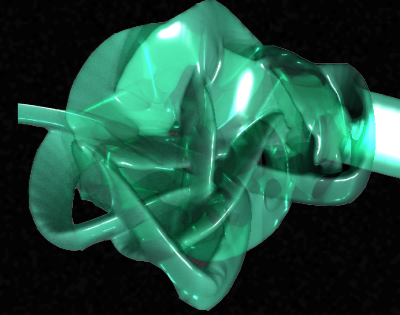


- How can knot theory help us understand DNA packing?
- How can we estimate the rates at which enzymes unknot DNA?

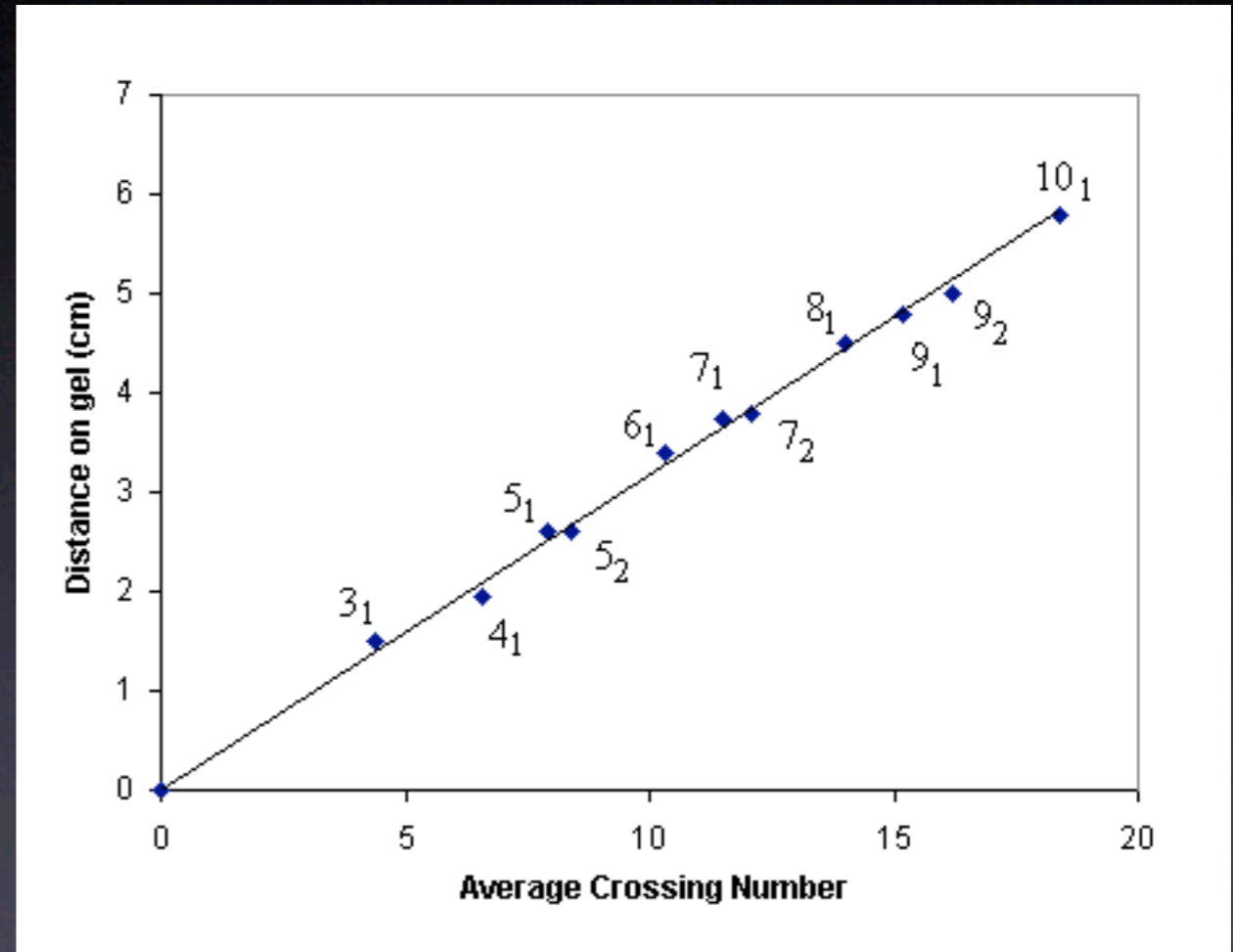


Picture taken from Sumners, D. 1995. Lifting the curtain: Using topology to probe the hidden action of enzymes. Notices of the AMS 42:528-537.

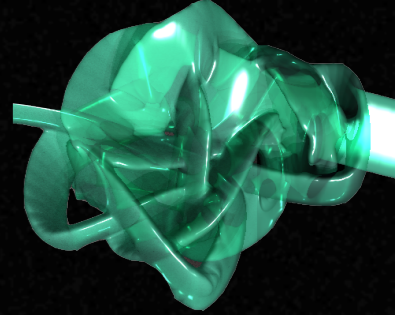
Introduction



- Determining the crossing number of DNA knots involves using gel electrophoresis.
- The distance DNA fragments move on an electrophoretic gel is highly correlated with the average crossing number.



Content



- **Average Crossing Number**

Key questions:

Predict behaviour for chains with excluded volume.

Distinguish between $\ln N$ and a power law.

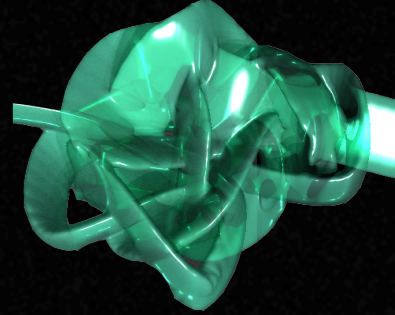
- **Statistics of knots**

Key questions:

Distribution of knots.

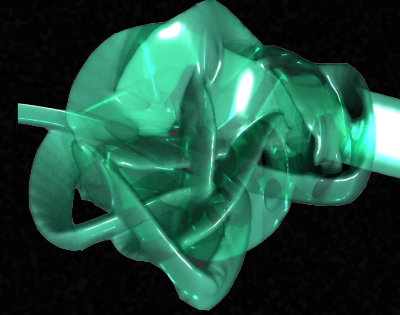
Average number of monomers in a knot.

Average Crossing Number

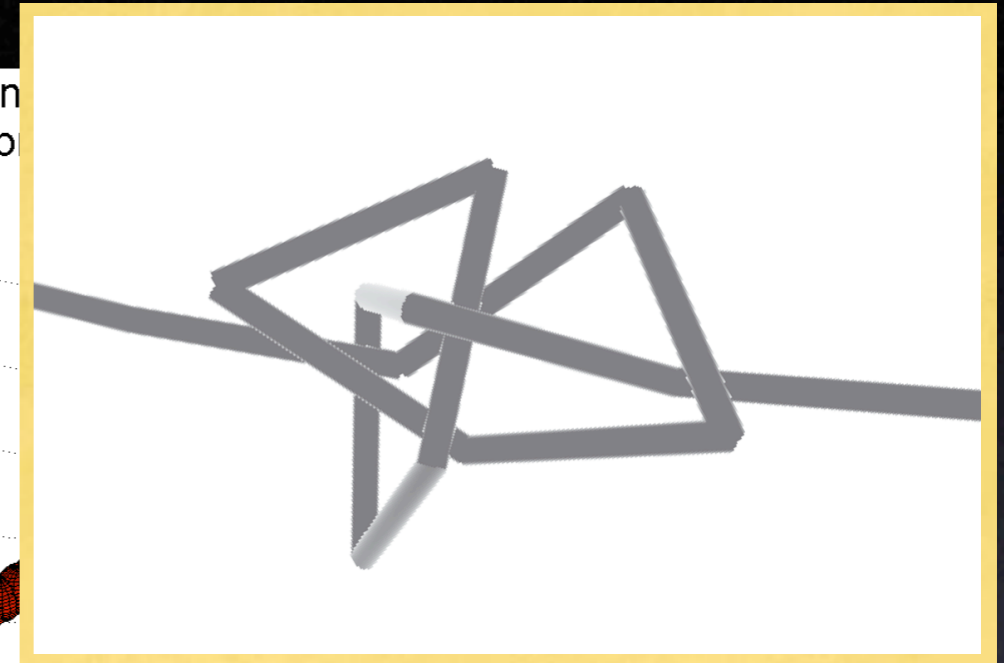
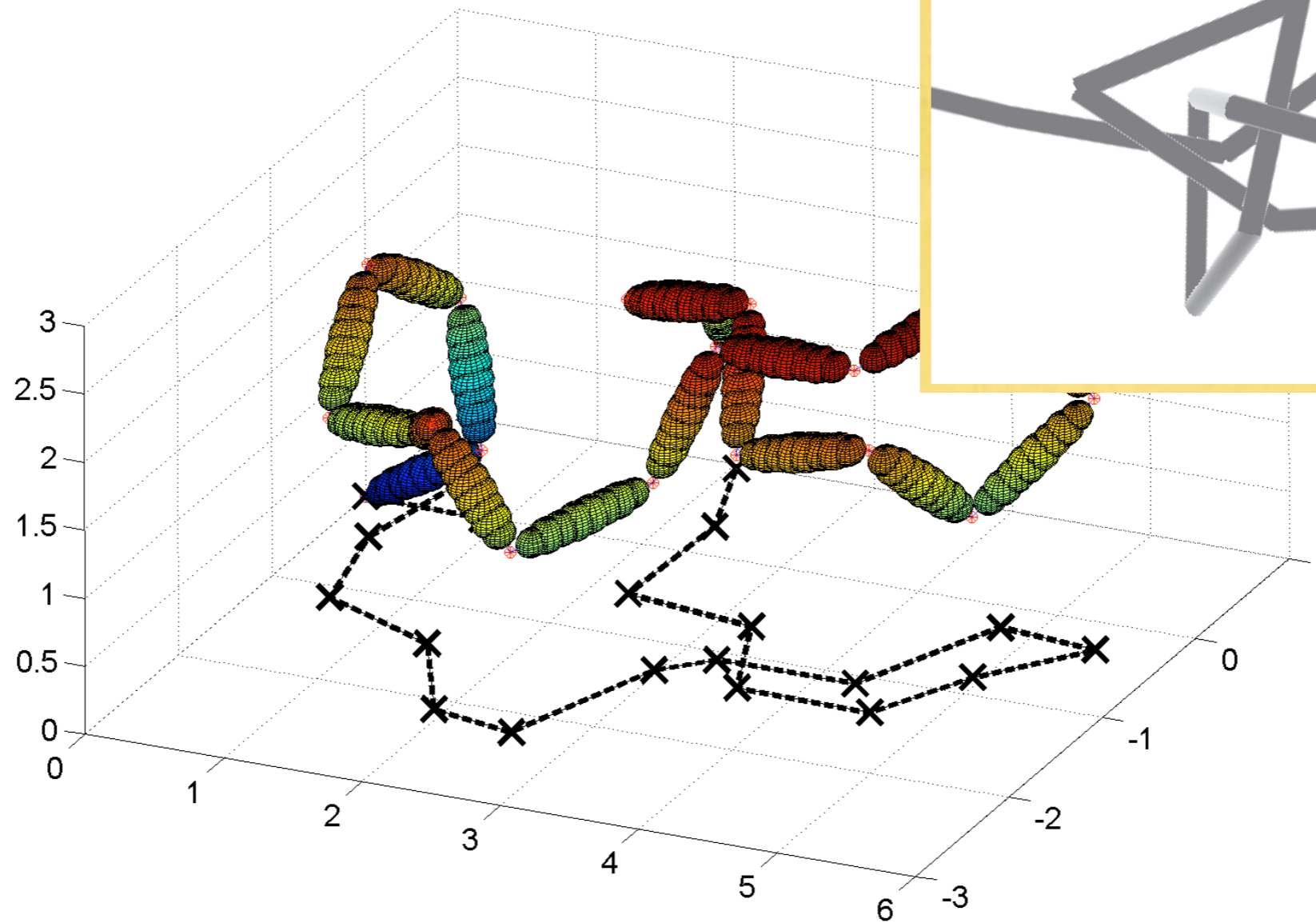


- Investigate the effects of excluded volume interactions on the average crossing number (ACN)
- Look at two kinds of chains:
 - Equilateral and
 - Gaussian random walks

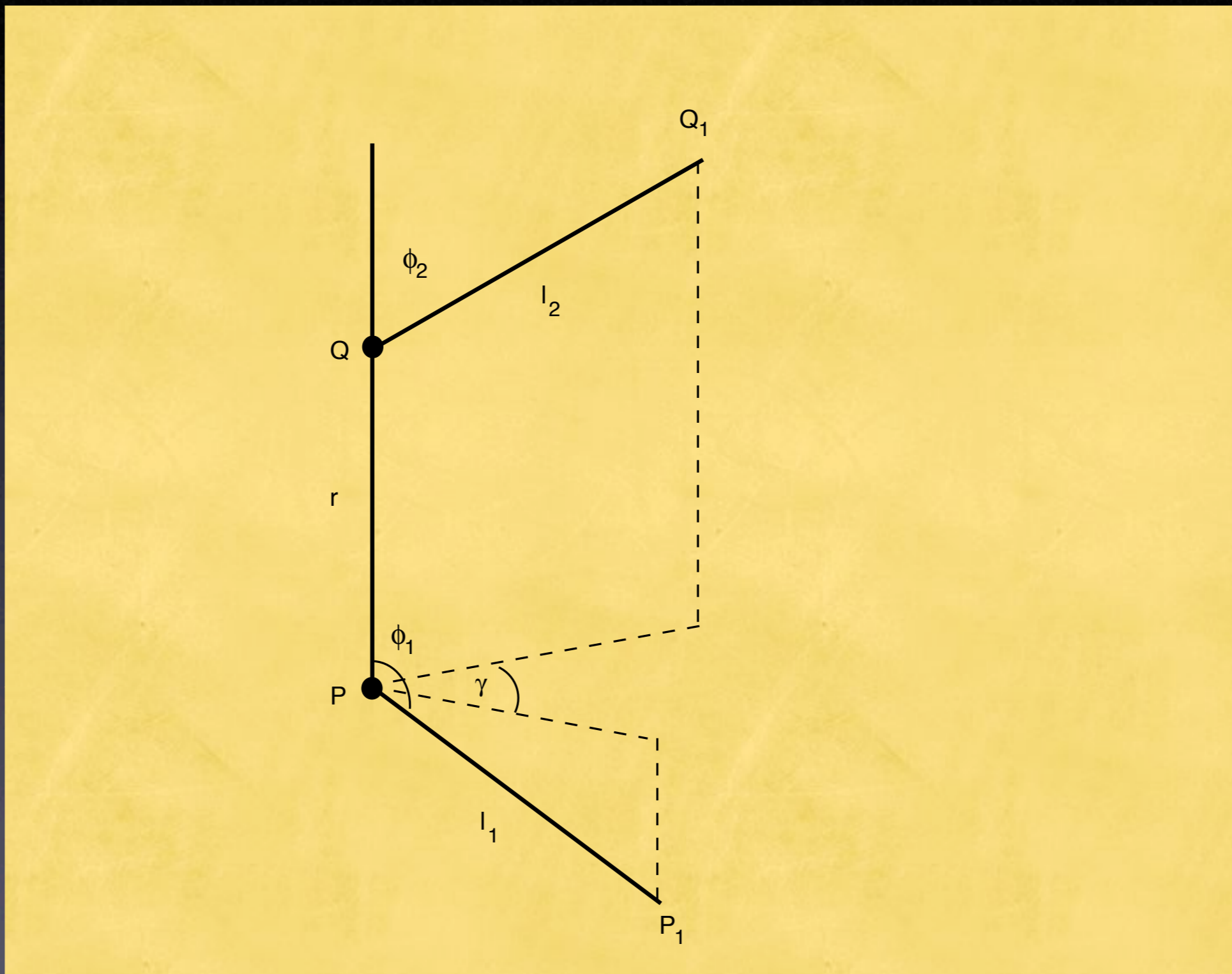
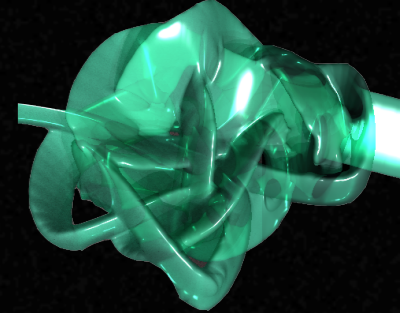
Average Crossing Number



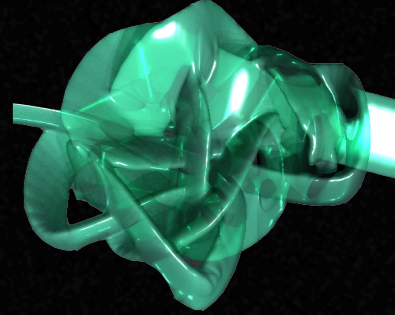
An equilateral 20-segments chain
with excluded volume and one possible p



Average Crossing Number



Average Crossing Number



$$a(l_1, l_2) = \frac{1}{2\pi} \int_{\gamma_1} \int_{\gamma_2} \frac{|\dot{\gamma}_1(t), \dot{\gamma}_2(s), \gamma_1(t) - \gamma_2(s)|}{\|\gamma_1(t) - \gamma_2(s)\|^3} dt ds$$

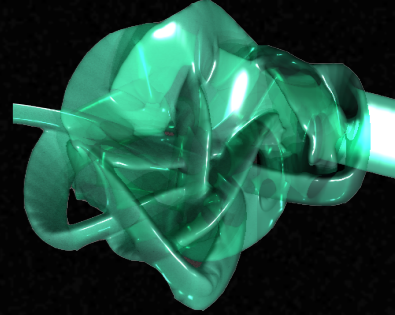
For Gaussian phantom chains

$$\langle a(l_1, l_2) \rangle = \frac{1}{2\pi d^2} + O\left(\frac{1}{d^{2.5}}\right)$$

For equilateral phantom chains

$$\langle a(l_1, l_2) \rangle = \frac{1}{16d^2} + O\left(\frac{1}{d^3}\right)$$

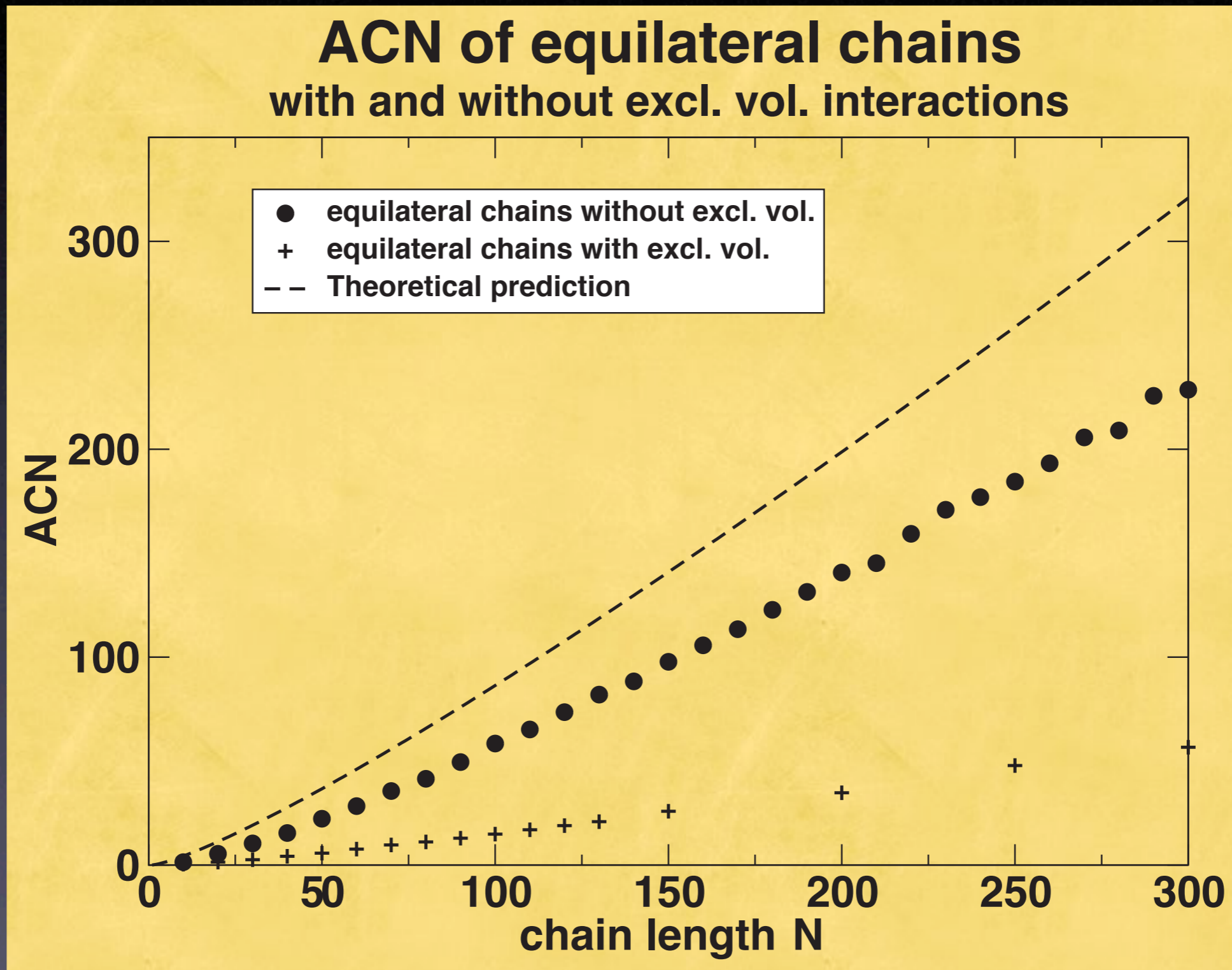
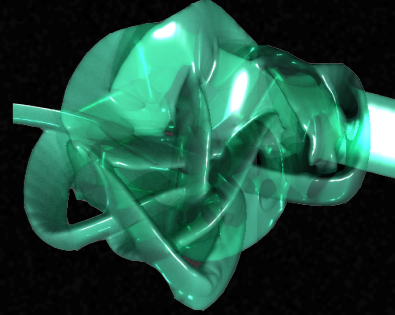
Average Crossing Number



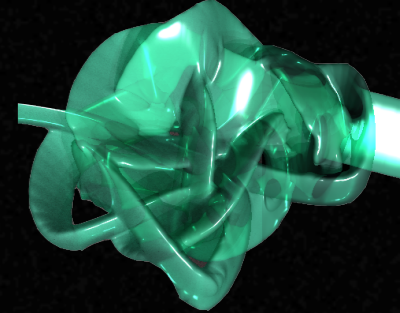
$$\begin{aligned} \text{ACN}_{\text{Gaussian}}(N) &= \frac{1}{2\pi} N \log(N) + O(N) \\ &\approx \frac{1}{2\pi} N \log(N) + c_1 \cdot N \end{aligned}$$

$$\begin{aligned} \text{ACN}_{\text{Equilateral}}(N) &= \frac{3}{16} N \log(N) + O(N) \\ &\approx \frac{3}{16} N \log(N) + c_2 \cdot N \end{aligned}$$

Average Crossing Number

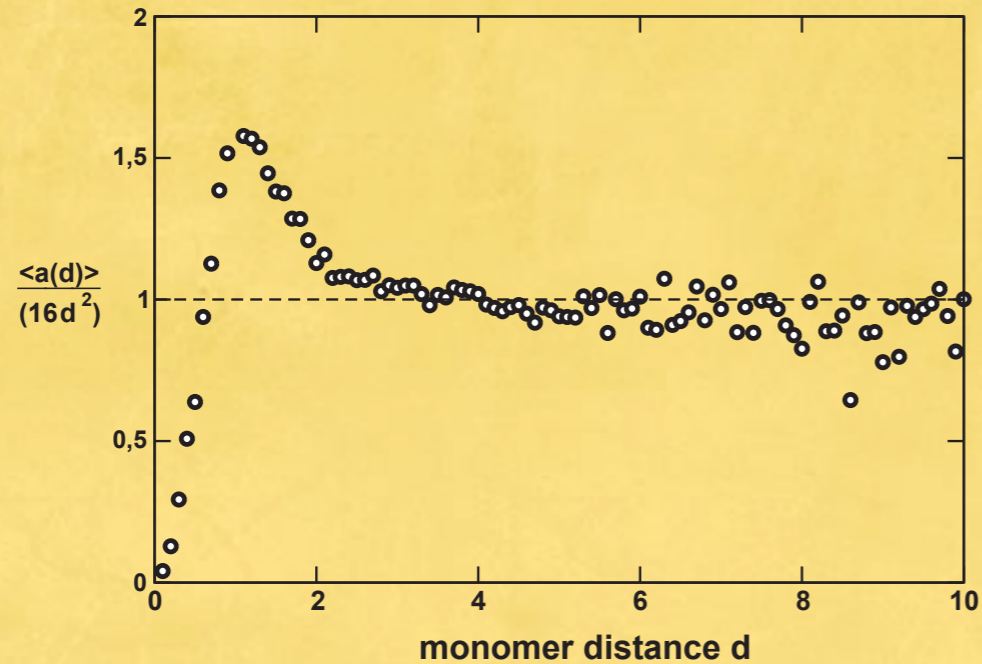


Average Crossing Number

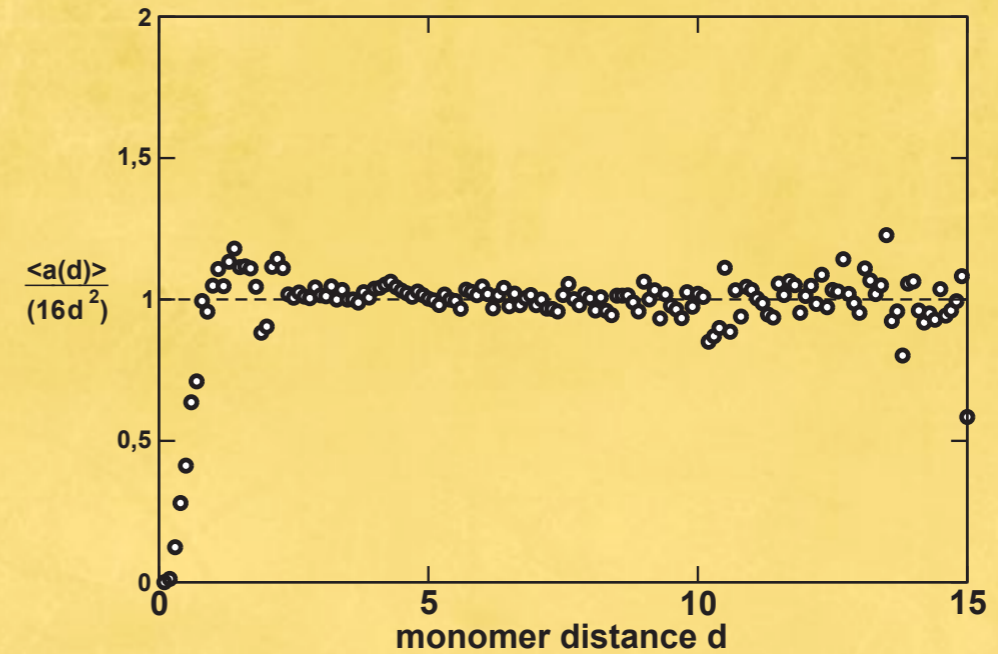


Ratio of simulation results with the leading term from the theoretical prediction

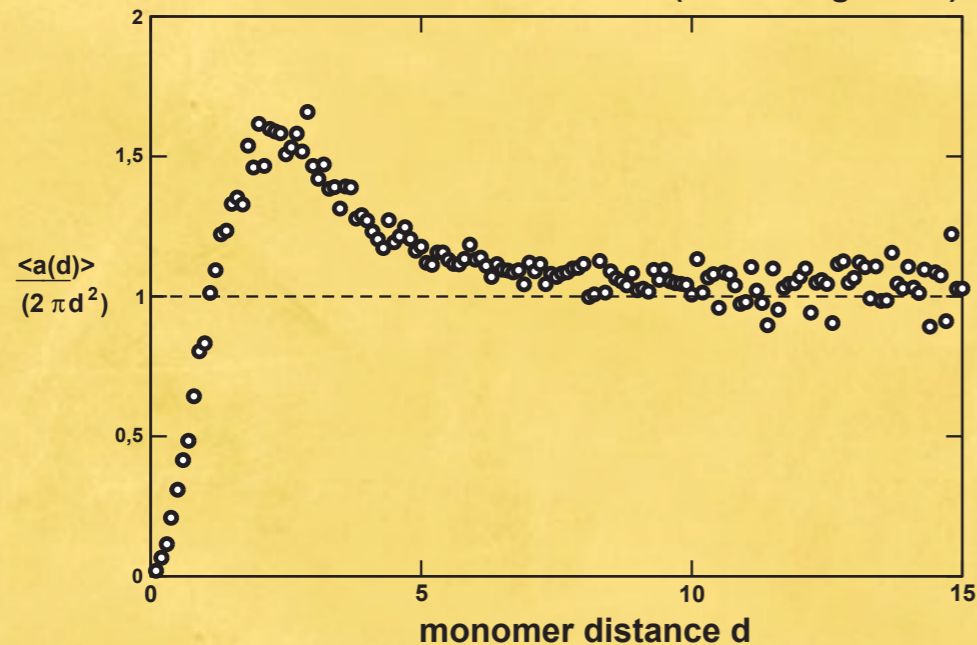
Equilateral chains without excl. vol. (chain length 100)



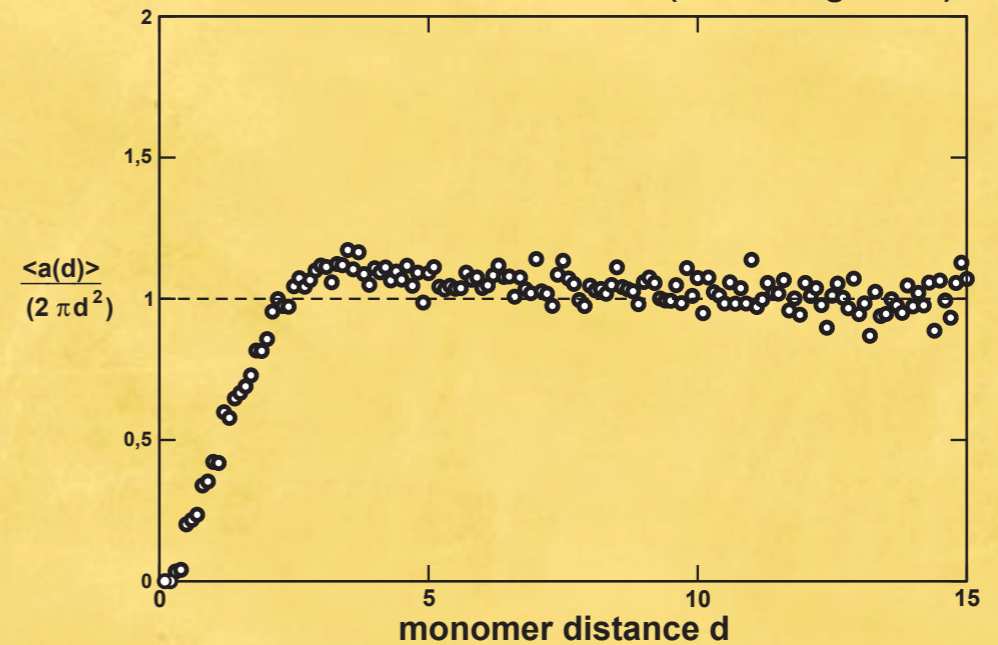
Equilateral chains with excl. vol. (chain length 100)



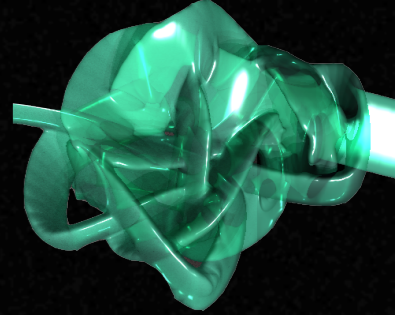
Gaussian chains without excl. vol. (chain length 100)



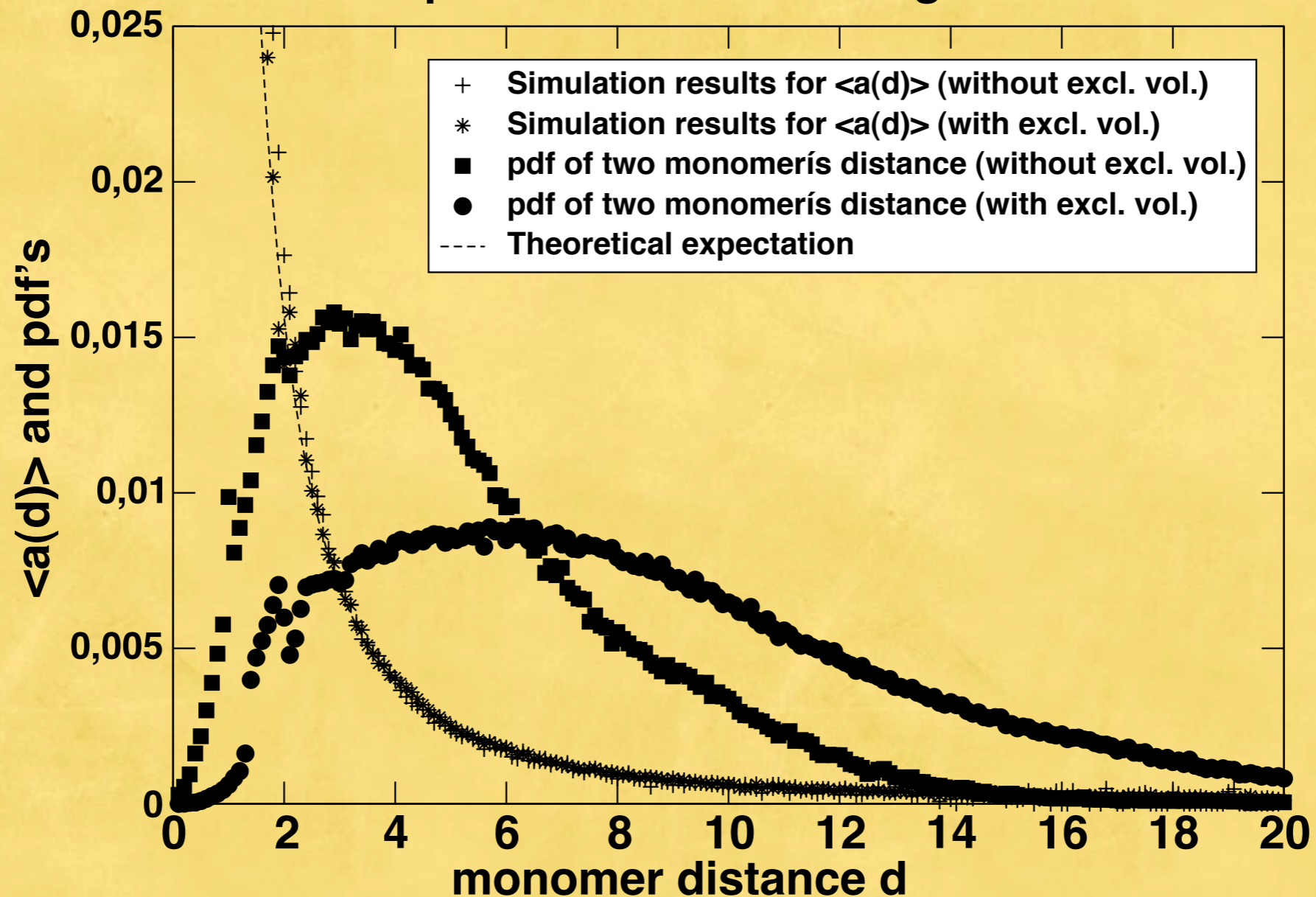
Gaussian chains with excl. vol. (chain length 100)



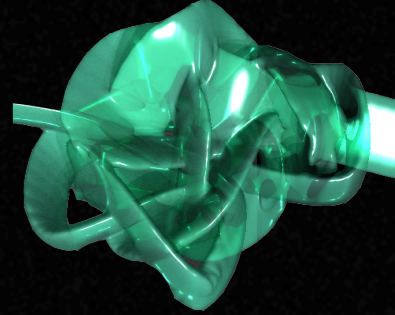
Average Crossing Number



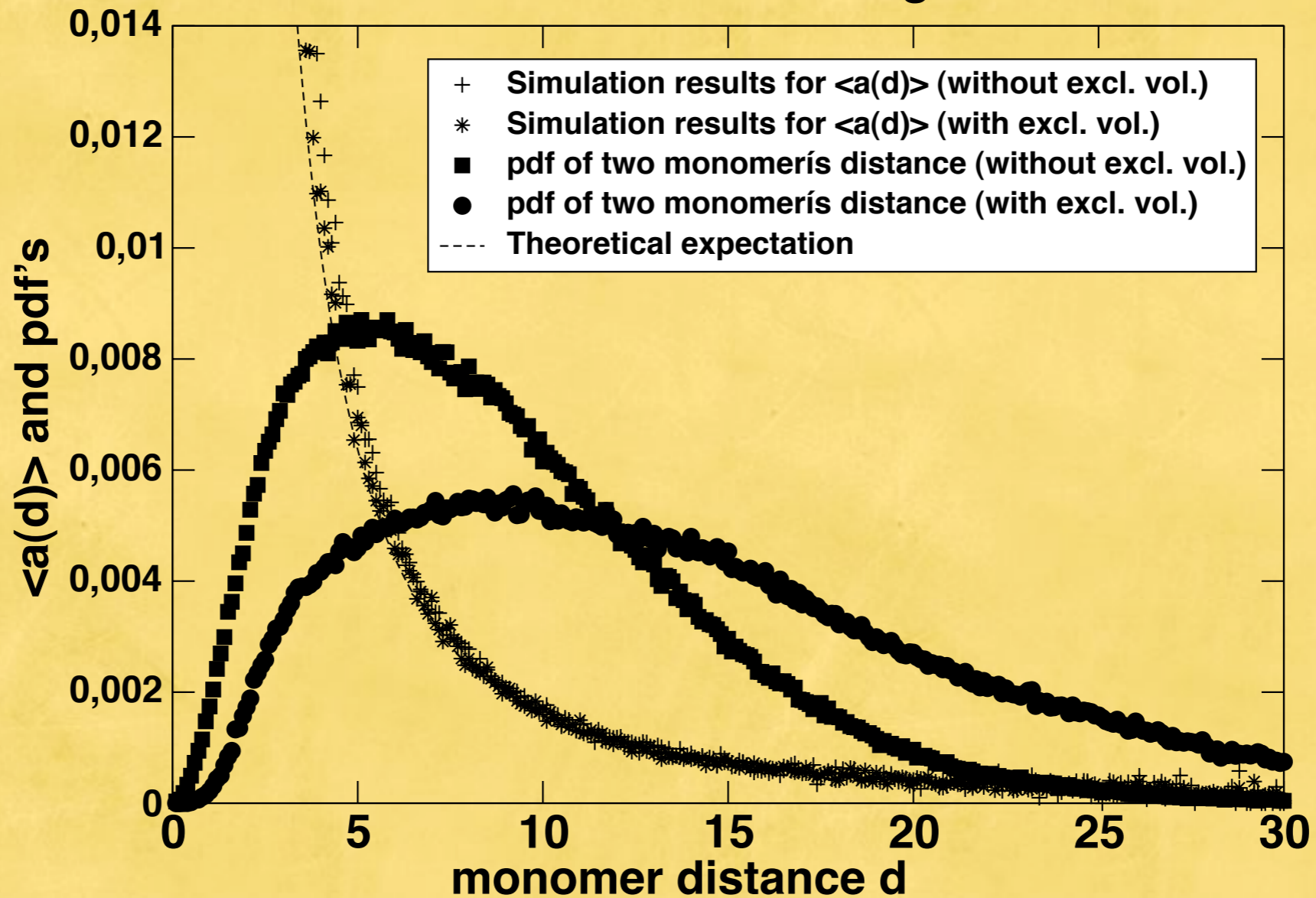
Probability density function for distance d
between two monomers and $\langle a(d) \rangle$
equilateral chains of length 100



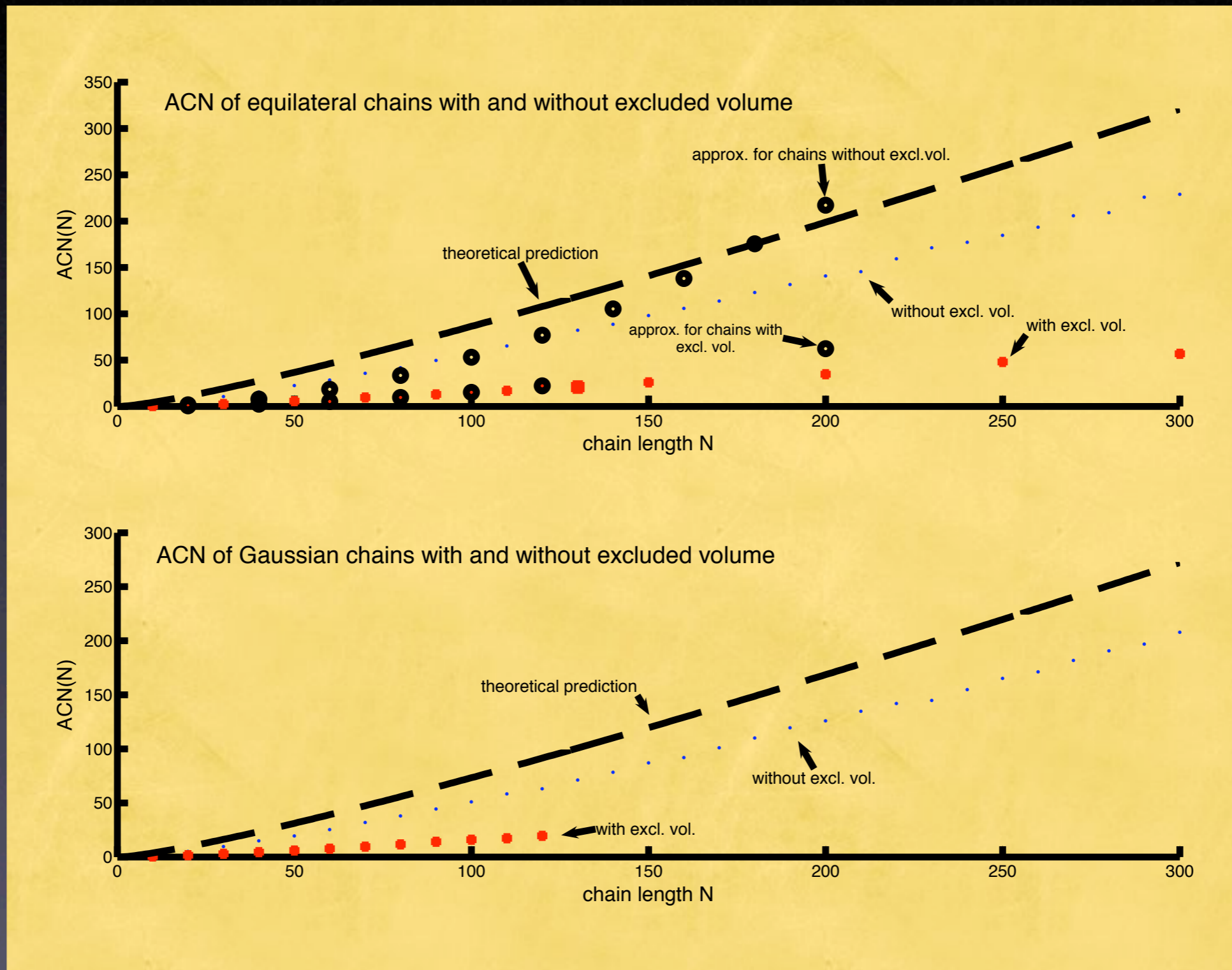
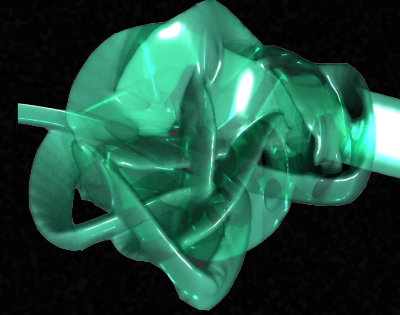
Average Crossing Number



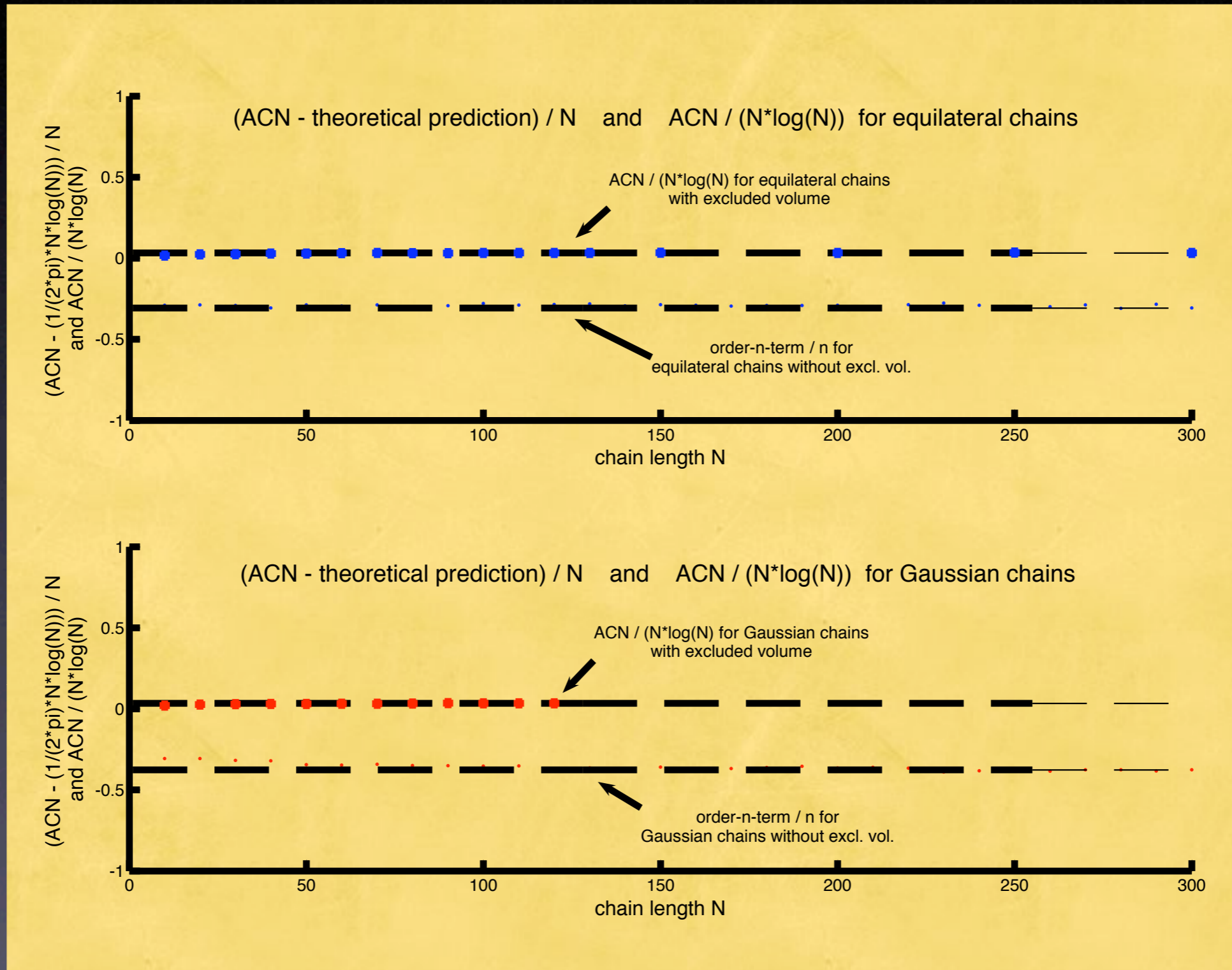
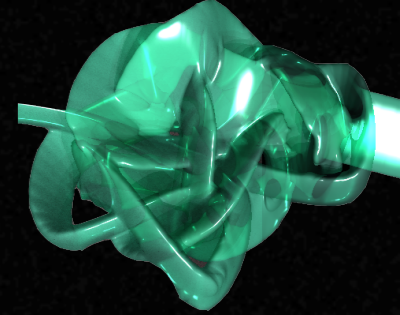
Probability density function for distance d
between two monomers and $\langle a(d) \rangle$
Gaussian chains of length 100



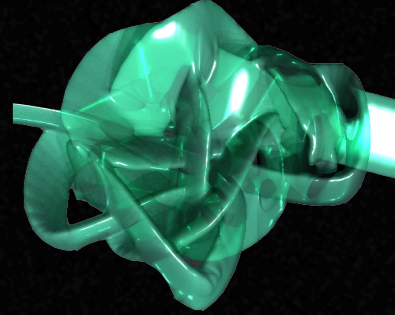
Average Crossing Number



Average Crossing Number



Average Crossing Number

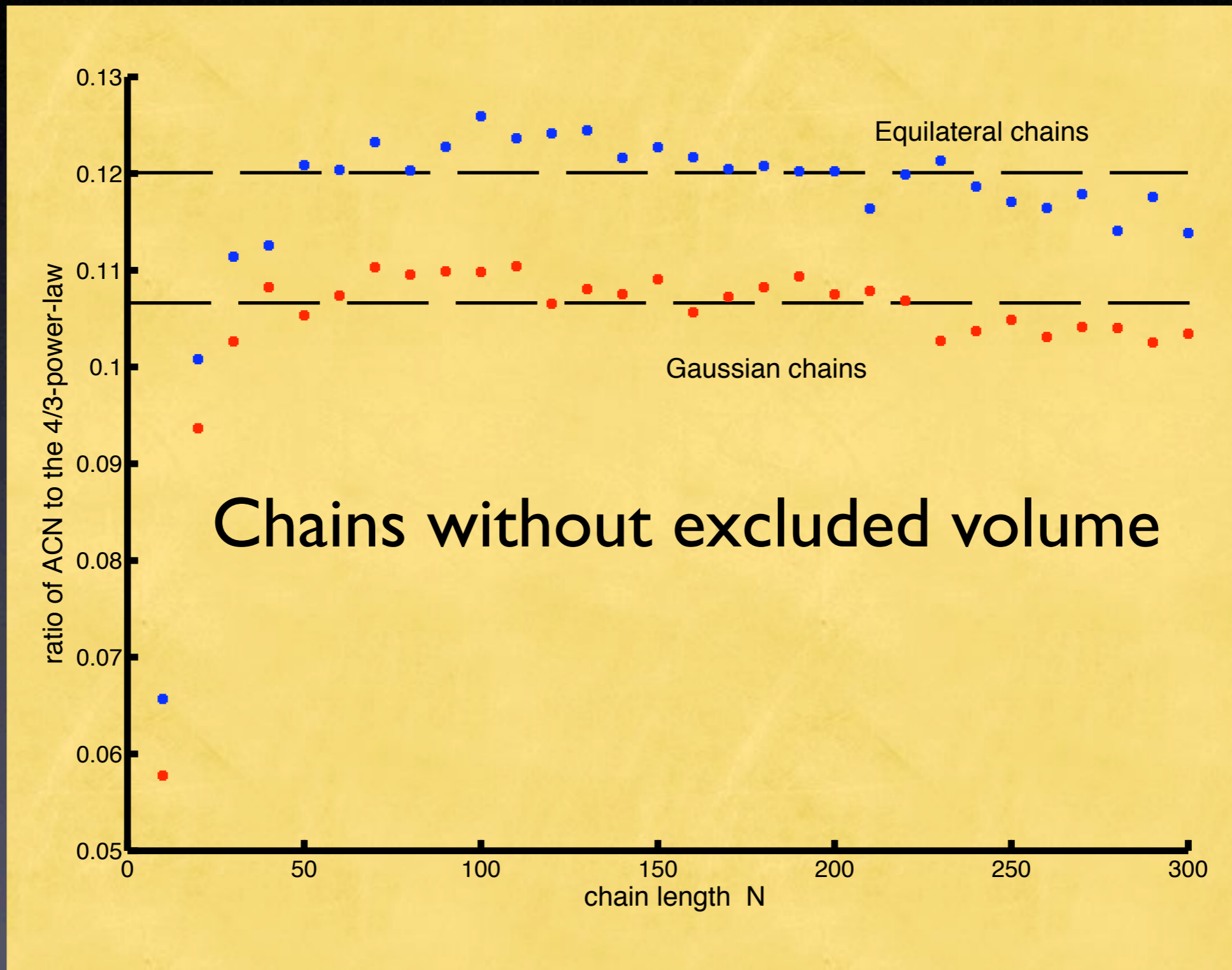
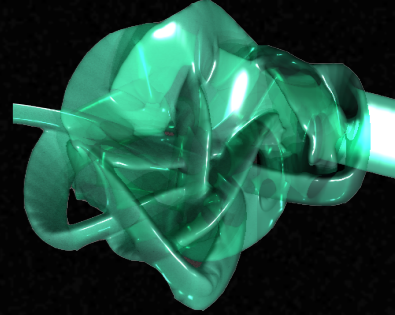


$$N \ln N + c \cdot N$$

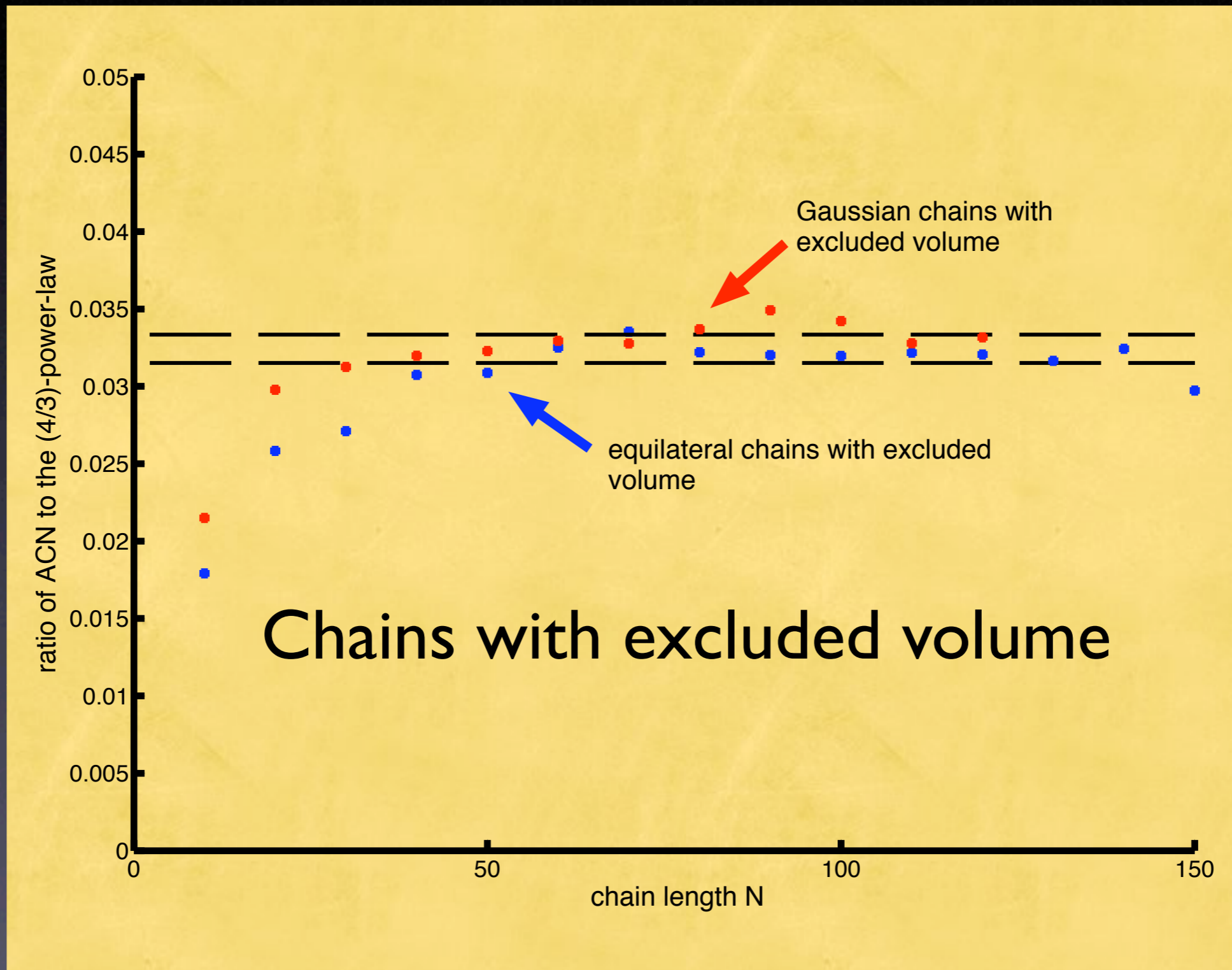
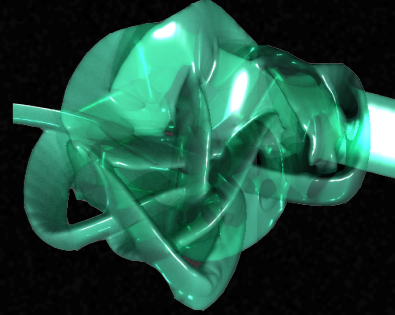
vs.

$$N^{4/3}$$

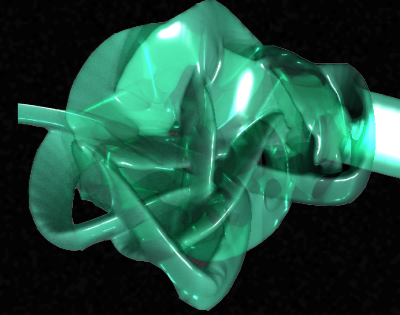
Average Crossing Number



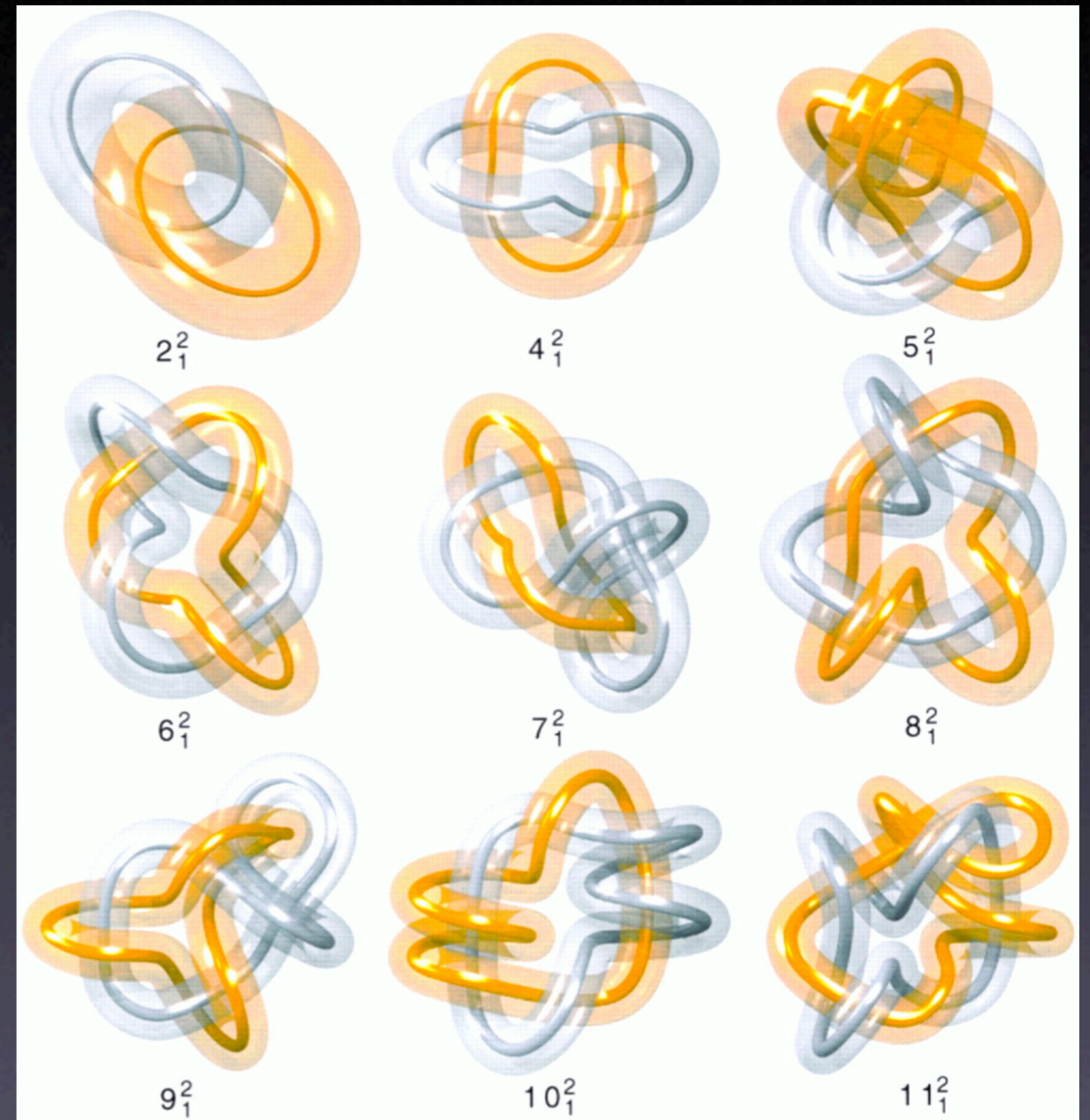
Average Crossing Number



Statistics of Knots

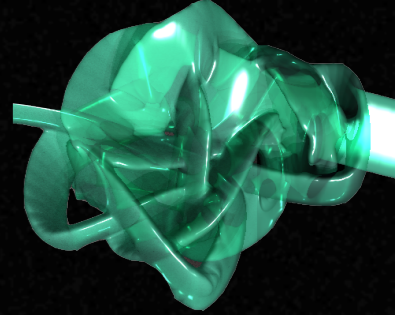


- Topological characterization of knots.
- Alexander, HOMFLY, ... Polynomials
- Here not interested; Chains are open.



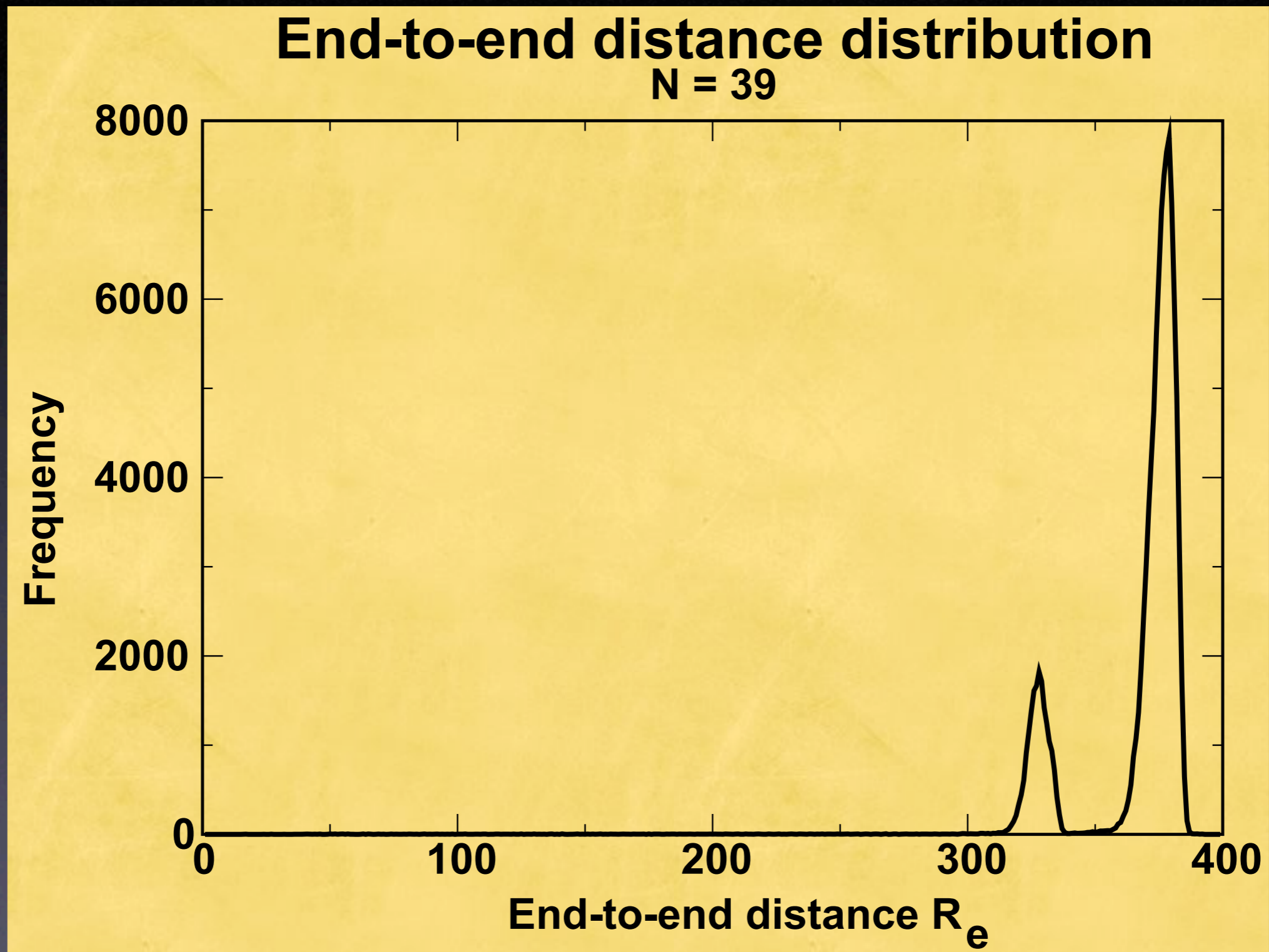
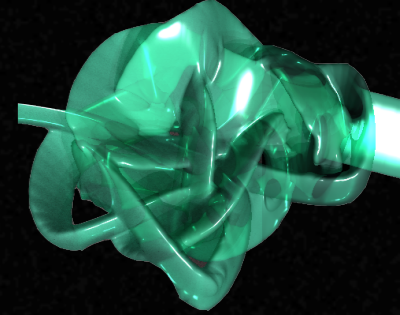
Taken from Geometry and Physics of Catenanes Applied to the Study of DNA Replication
Ben Laurie, Vsevolod Katritch, Jose Sogo, Theo Koller, Jacques Dubochet, and Andrzej Stasiak

Statistics of Knots

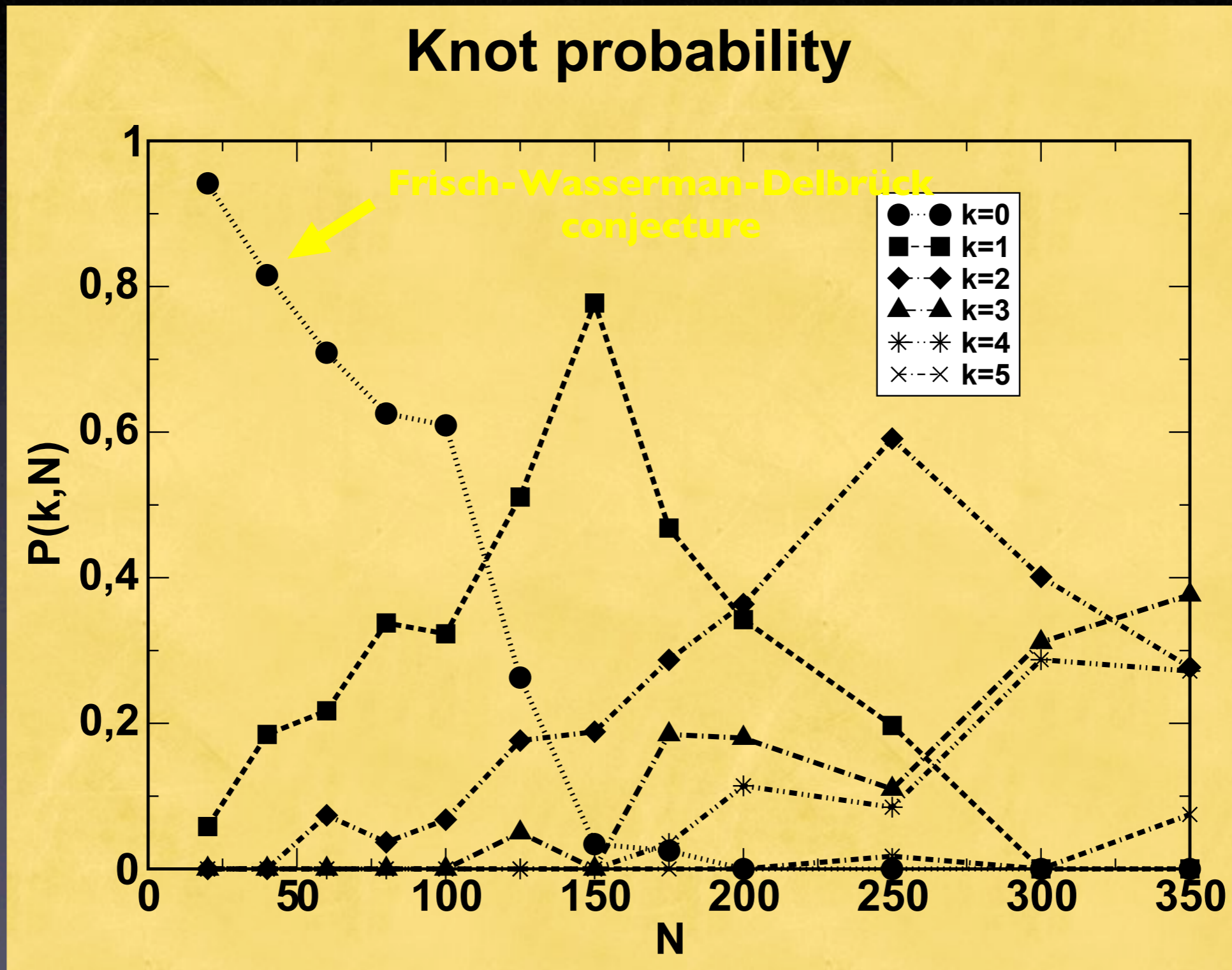
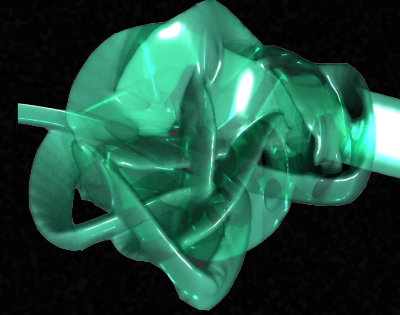


- Here we apply a heuristic approach to the identification of a knot.
- We employ the notion of polymers with entanglement which cannot be reduced to a straight polymer chain.
- Knots are an effect of the self-avoiding property of the macromolecules and they do only occur when we stretch the chain.
- Frisch-Wasserman-Delbrück conjecture

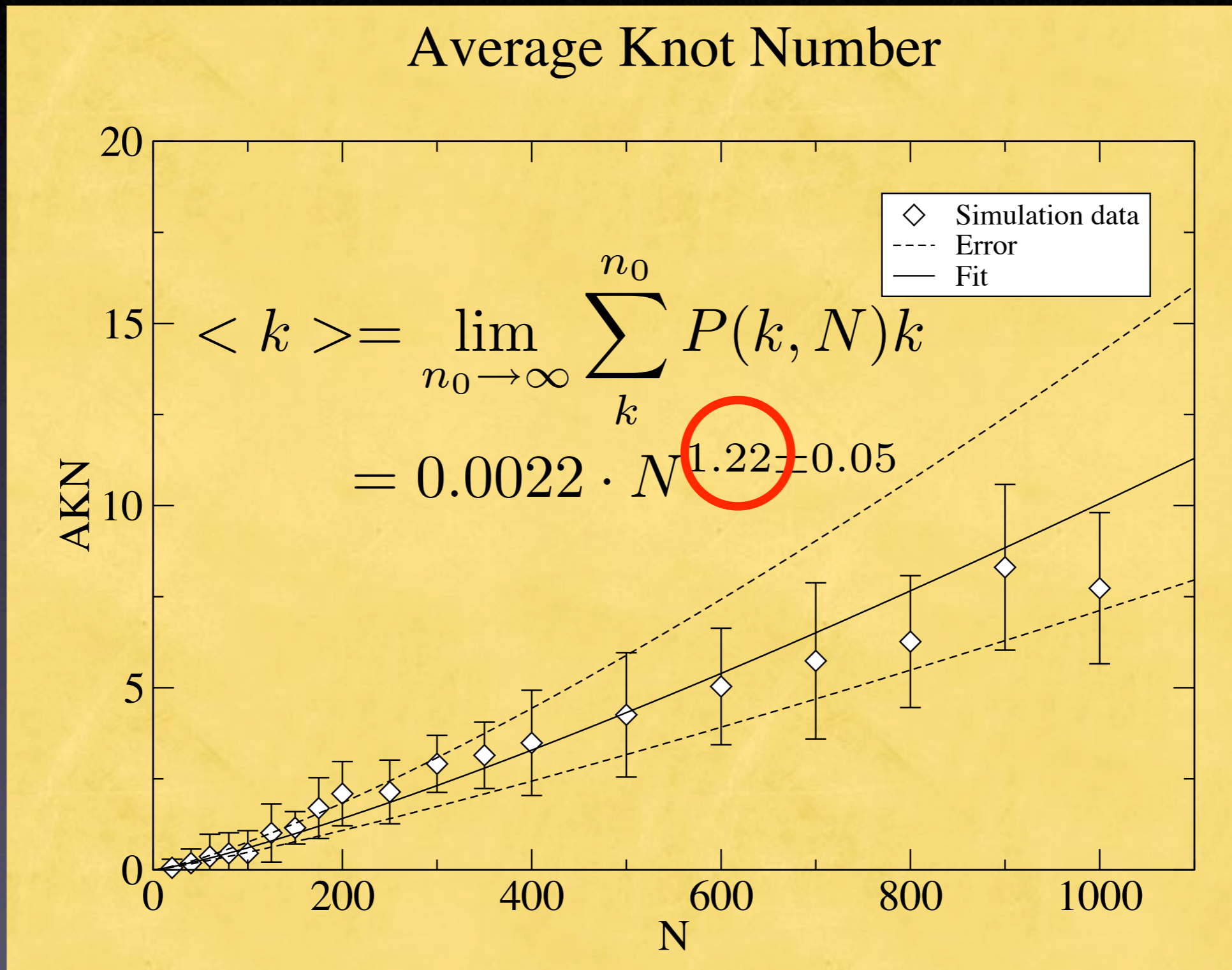
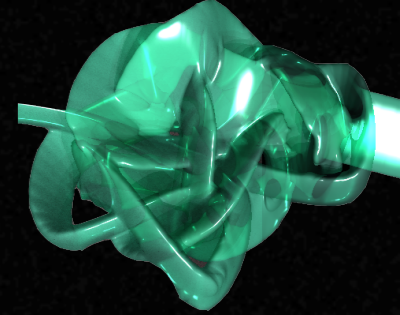
Statistics of Knots



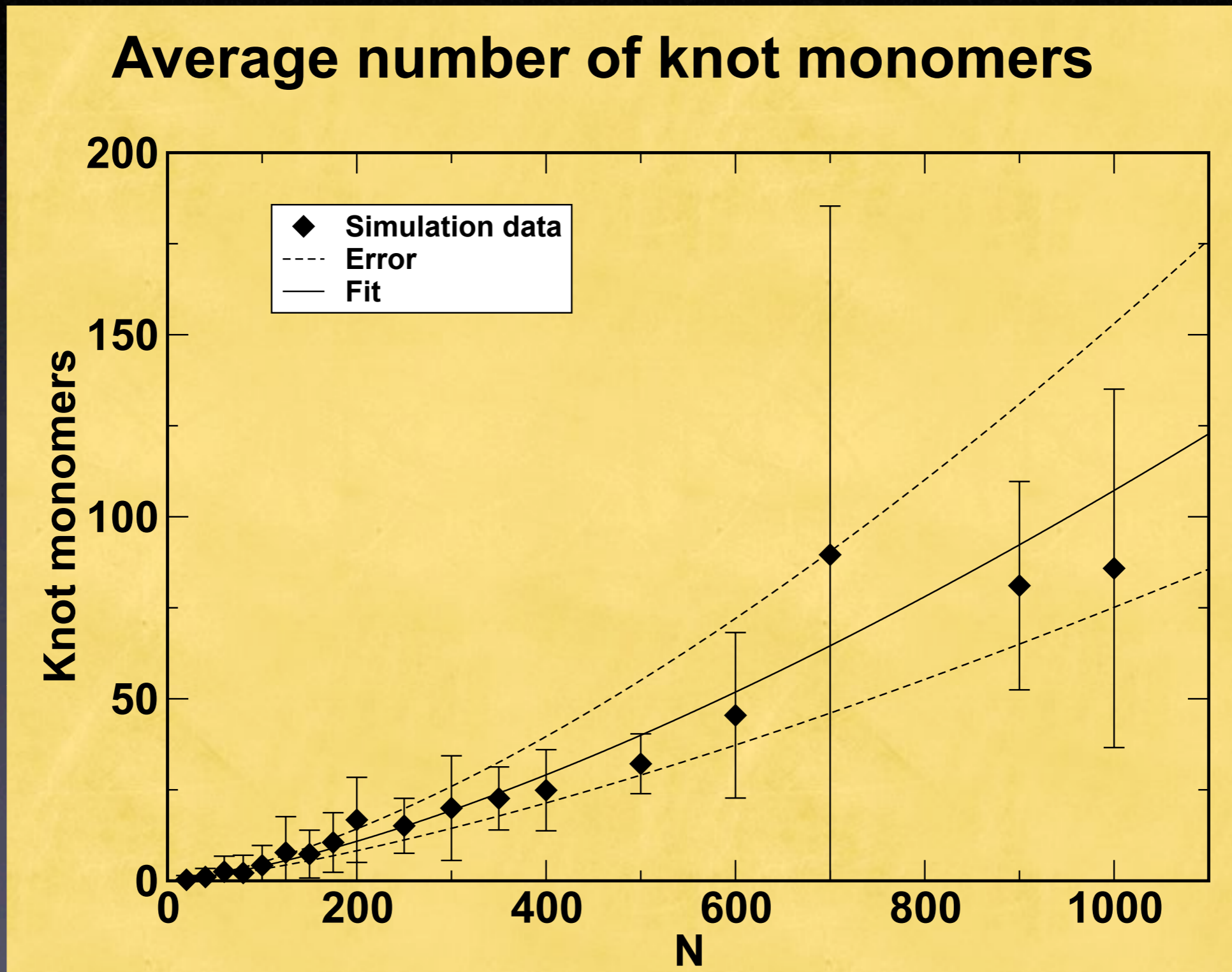
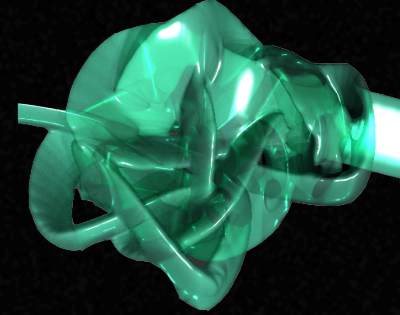
Statistics of Knots



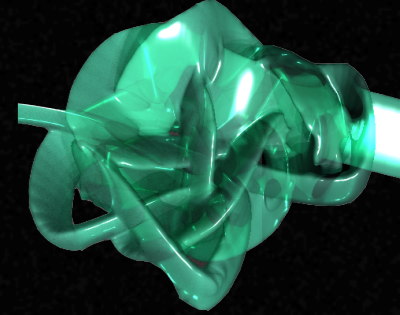
Statistics of Knots



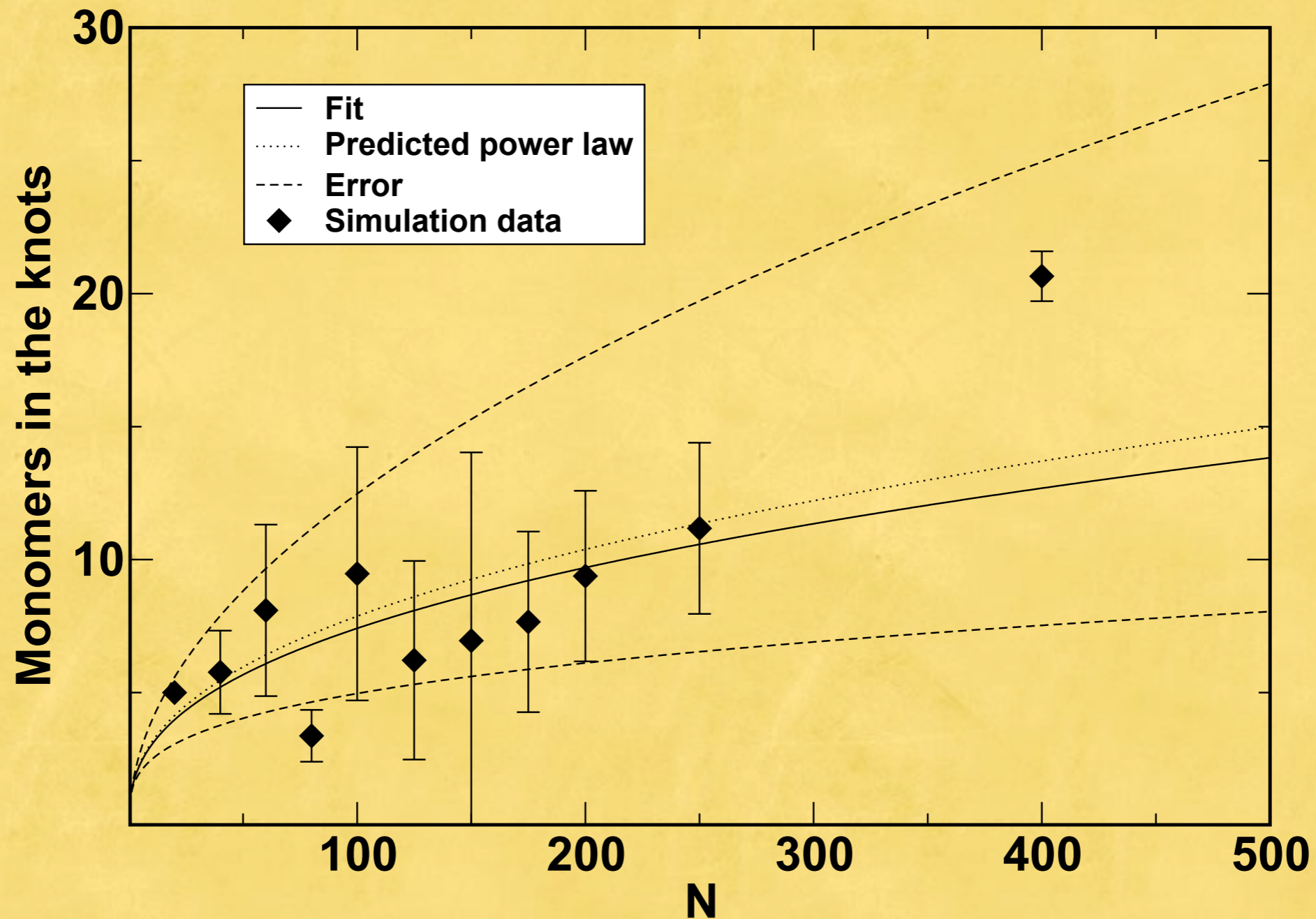
Statistics of Knots



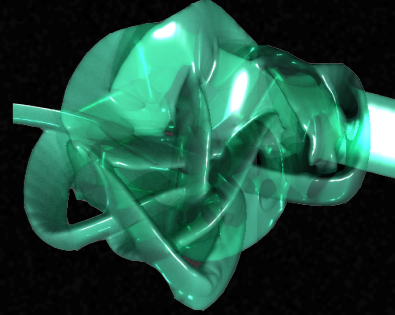
Statistics of Knots



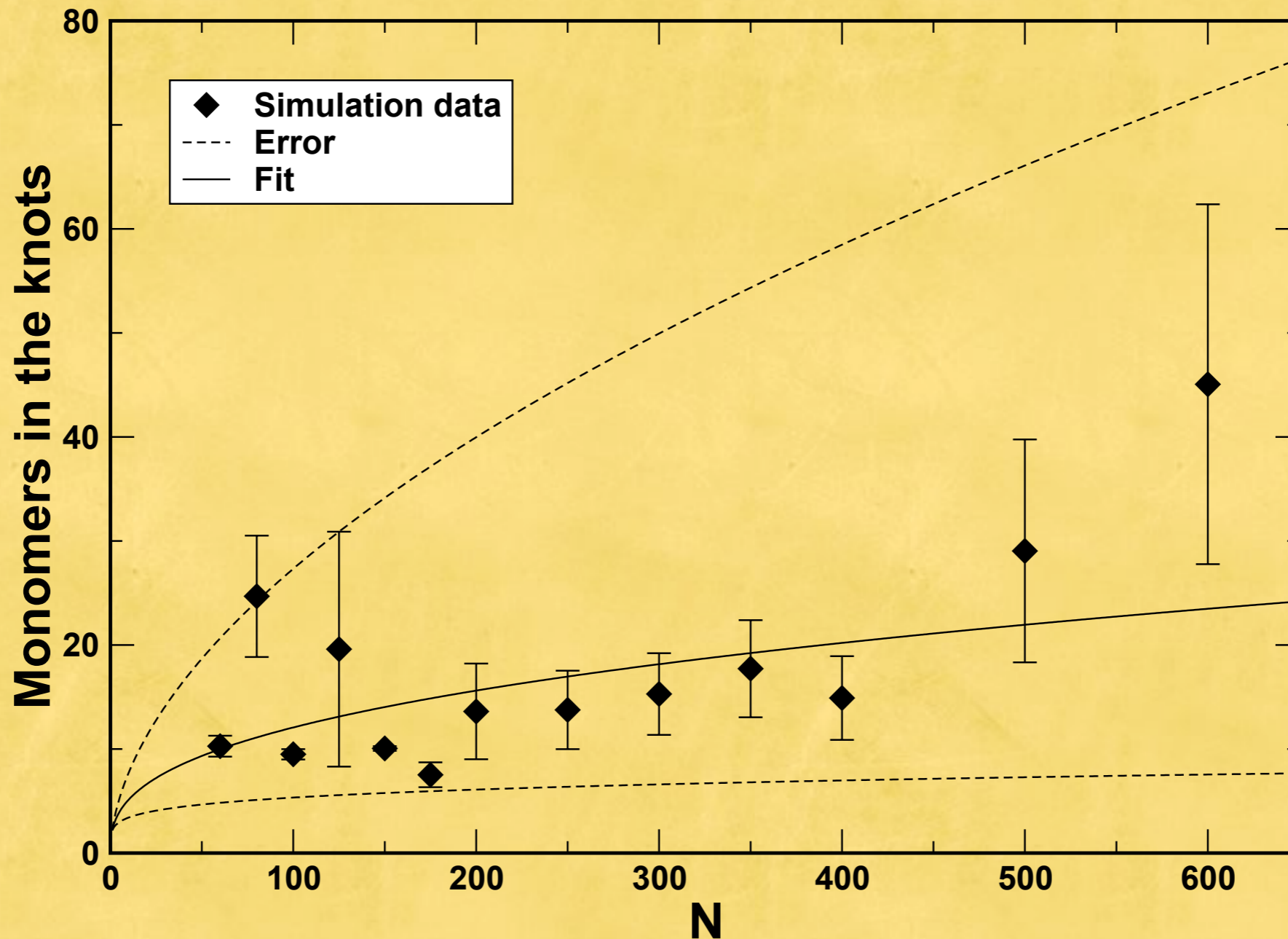
Knot-monomers in chains with one knot



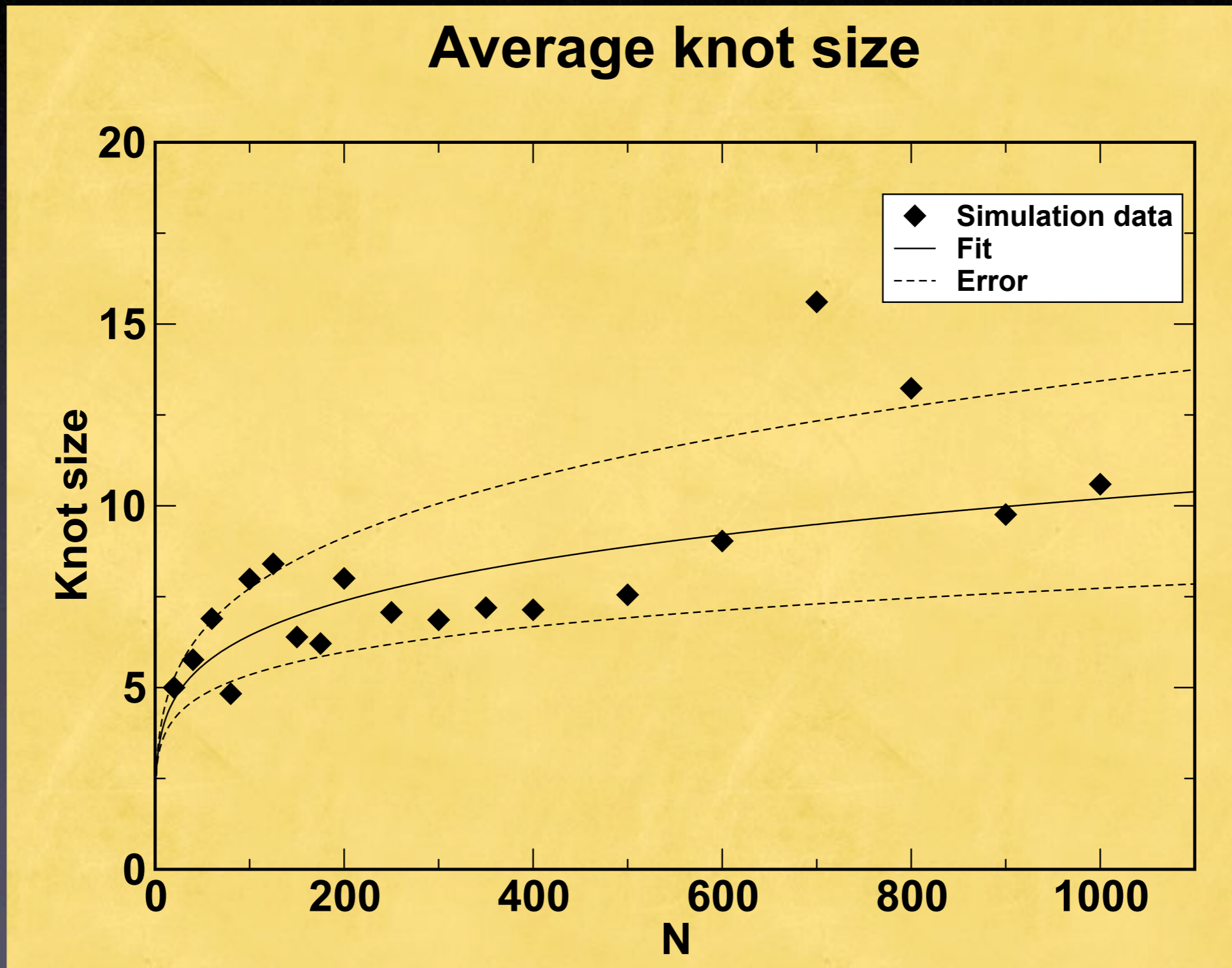
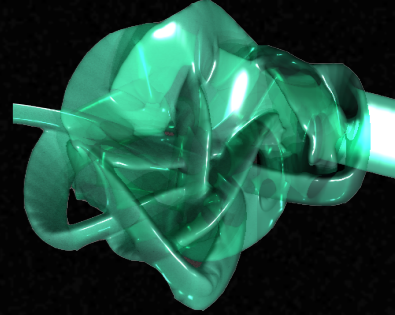
Statistics of Knots



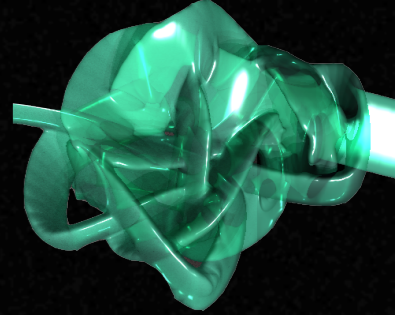
Knot-monomers in chains with two knots



Statistics of Knots



Summary



- Situation still undecided concerning the average crossing number.
- Knot statistics also needs to be improved.

Knots in Macromolecules

Thank you for your attention!