

Structure of DNA solutions

Surprisingly, there are no good tools to measure the structure of DNA polymers in solution structure in 50 nm to 1 μ m spatial range. Although this range should be accessible to the standard multi-angle static light scattering (SLS) technique, SLS does not give reliable data for DNA, mostly because DNA scatters light very poorly. Since DNA coil sizes (for DNA longer than \sim 3kbp) are similar to those of dust particles and since sample volumes in SLS are relatively large, it is impossible to avoid the presence of dust and of the associated noise in SLS measurements.

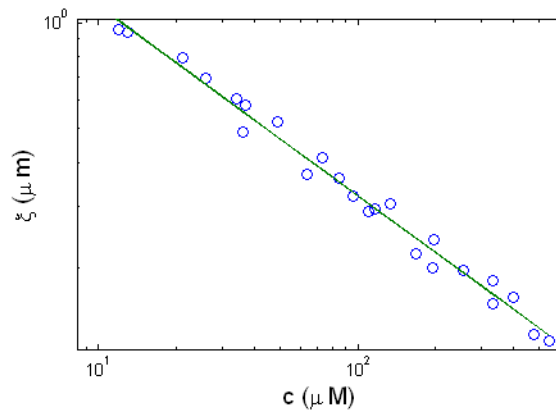
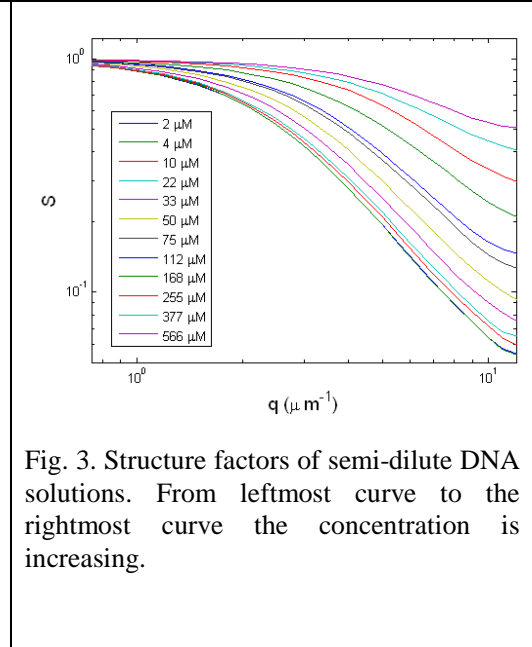
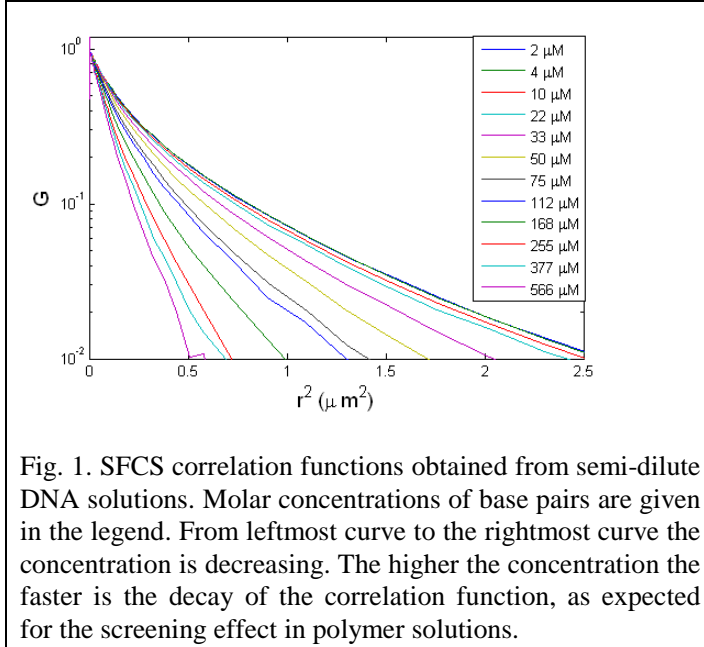
We found out [1] a surprisingly simple method to measure the structure factor of DNA solutions: we attach fluorescent labels to DNA and use scanning fluorescence correlation spectroscopy (SFCS) approach to measure spatial correlations between label positions.

The simplest way to understand our approach is to first imagine an isotropic spatially disordered system where fluorescent molecules are “frozen” in space. If we scan such a system through the confocal volume with a constant velocity \vec{V} , we will measure fluctuations in fluorescence resulting from the inhomogeneous spatial distribution of fluorophores. Then the temporal correlation function $G(t)$ of fluorescence fluctuations will just reflect the spatial correlations $g(r)$ in fluorophore positions with $r = Vt$ providing the conversion from temporal to spatial scale. Because of the final size of the sampling volume, the measured correlations will be a “smeared” version of actual spatial correlations. It is not difficult to show that in fact $G(r = Vt)$ is just a convolution of $g(r)$ with a “filter” function $F(r)$ that characterizes the illumination-detection profile: $G(\vec{r}) \propto \int d\vec{r}' g(\vec{r} - \vec{r}') F(\vec{r}')$. Since in Fourier space the convolution converts to a product, we have here a method of measuring the structure factor: $S(\vec{q}) \equiv g(\vec{q}) \propto G(\vec{q})/F(\vec{q})$.

We performed measurements of semi-dilute solutions of Lambda DNA (48.6 kbp) labelled with EtBr at 0.2 (bound EtBr)/bp ratio. The measured SFCS correlation functions and the respective structure factors are presented in Figs. 1 and 2. We observe screening effects due to the interactions between different chains evidenced by the more rapid decay of correlation functions corresponding to higher concentrations. This is the first measurement of polymer-type screening in DNA solutions. From the fits of $S(q)$ we obtain screening length for different concentrations.

Screening length dependence on concentration is presented in Fig. 3. The best power fit gives $\xi \propto c^{-0.53}$. This dependence is unusual for normal polymers for which $\xi \propto c^{-3/4}$ law is expected. In fact the dependence is very close to that predicted by Edwards’ theory [2] of semidilute solutions $\xi \propto c^{-0.5}$. Although this particular Edwards’ prediction is considered wrong for usual polymers, “marginal solution” theory by Schaefer, Joanny and Pincus [3] proposes that this law should hold for solutions of semiflexible polymers such as DNA

Thus we develop a new method to measure the structure of DNA solutions. Our first results support the conclusions of “marginal solutions” theory. We proceed to further develop our method by combining SFCS with specific labelling, an approach that allows us to measure e.g. end-to-end distributions in DNA polymers.



BIBLIOGRAPHY

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- 2) Edwards SF. "Theory of Polymer Solutions at Intermediate Concentration". *Proceedings of the Physical Society of London* (1966), **88**:265.
- 3) Schaefer DW, Joanny JF, Pincus P. "Dynamics of Semiflexible Polymers in Solution". *Macromolecules* (1980), **13**:1280-1289.