Boulder lecture references

P. C. Nelson

2007-06-29

1 Biopolymers

Handouts: Figures and text from Nelson, 2008.

Examples
Howard, 2001; Boal, 2001; Nelson, 2008; Phillips et al., 2008

Mechanics of elastic rods; harmonic vs non-harmonic elasticity models
Vologodskii, 1992; Marko & Siggia, 1994
Yan & Marko, 2004; Wiggins et al., 2005; Wiggins et al., 2006

Thermal motion; FJC as an approximate limit

Gene regulation via looping
General: Schleif, 1992; Rippe et al., 1995; Matthews & Nichols, 1998; Revet et al., 1999; Hochschild, 2002; Bintu et al., 2005; Saiz et al., 2005
More:
Dunn et al., 1984; Mossing & Record, 1986; Krämer et al., 1987; Bellomy et al., 1988; Adhya, 1989; Mossing & Record, 1986; Müller et al., 1996; Revet et al., 1999; Geanacopoulos et al., 2001; Vilar & Saiz, 2005; Becker et al., 2005a; Becker et al., 2005b; Swigon et al., 2006; Garcia et al., 2007
Why loop:
Vilar et al., 2002; Vilar & Leibler, 2003; Vilar et al., 2003

Tools: PDB files and viewers; the Lac repressosome
Lac structure: Lewis et al., 1996; Bell et al., 2001; Bell & Lewis, 2001b; Bell & Lewis, 2001c; Bell & Lewis, 2000; see PDB entry 1LBG.
Lambda structure: Bell et al., 2000; Bell & Lewis, 2001a.

2 Tethered particle motion as a diagnostic of DNA conformation

Handouts: Nelson review article; "`calibration`" notes; "`elasticity`" notes; "`J factor`" notes; "`loop simulation`" notes.

Brownian motion, Stokes–Einstein

Tethered brownian motion
TPM: Schafer et al., 1991; Yin et al., 1994; Finzi & Gelles, 1995; Segall et al., 2006; Nelson et al., 2006; Vanzi et al., 2006; Normanno et al., 2007
Applications to motors: Vanzi, 2003; Vanzi et al., 2003
More TPM: Zocchi, 2001; Singh-Zocchi et al., 2003; Tolic-Norrelykke et al., 2004; Dennis et al., 2004; Pouget et al., 2004; Blumberg et al., 2005; Dixit et al., 2005; Lambert et al., 2006
Application to DNA looping: Zurla et al., 2006; van den Broek et al., 2006; Wong et al., 2007

Tools: Monte Carlo evaluation of integrals

J factors, prediction versus experiment
Shimada & Yamakawa, 1984; Coleman et al., 1995; Zhang & Crothers, 2003; Spakowitz & Wang, 2004; Spakowitz & Wang, 2005; Yan et al., 2005; Becker et al., 2005a; Douarche & Cocco, 2005; Zhang et al., 2006; Czapla et al., 2006; Wiggins & Nelson, 2006; Spakowitz, 2006

3 Maximum likelihood methods

Handouts: Beausang et al., 2007a; and this document.

Tools: ML as the basis of least-squares fitting
Cox & Hinkley, 1974; Press et al., 1992; Bevington & Robinson, 2003

Applications
Blinking of fluorophores: Hoogenboom et al., 2006
Other applications: Myosin: Forkey et al., 2000; Quinlan et al., 2005; Forkey et al., 2005
Still more: Yang & Xie, 2002; Yang et al., 2003; Schroder & Grubmuller, 2003; Watkins & Yang, 2004; Watkins & Yang, 2005; Koster et al., 2006

Markov and Hidden Markov
Rabiner, 1989; Cowan, 2007
Milescu et al., 2006b; Milescu et al., 2006a; Qin et al., 2000a; Qin et al., 2000b; Smith et al., 2001; Andrec et al., 2003; McKinney et al., 2006
Cover & Thomas, 1993; Venkataramanan et al., 1998a; Venkataramanan et al., 1998b; Venkataramanan & Sigworth, 2002
Ion channels: Colquhoun & Sigworth, 1983
Genomics: Eddy, 2004
Networks: Newman and Leicht.

Tethered Brownian motion as a Markov process
Beausang et al., 2007b

Tethered motion with looping
Beausang et al., 2007a; Beausang & Nelson, 2007; Han et al., 2007a; Han et al., 2007b; Han et al., 2007c

3.1 More Misc Refs

Cloutier & Widom, 2004; Cloutier & Widom, 2005; Du et al., 2005; Balaeff et al., 1999; Balaeff et al., 2004; Villa et al., 2004; Villa et al., 2005; Balaeff et al., 2006; Purohit & Nelson, 2006; Saiz & Vilar, 2006b; Saiz & Vilar, 2006a; Vilar & Saiz, 2006; Liang et al., 2007; Chen et al., 2007; Zhou et al., 2007
Dohoney & Gelles, 2001; Okonogi et al., 2002

Acknowledgements

NSF grants DGE-0221664, DMR04-25780, and DMR-0404674

Bibliography

Adhya, S. 1989. Multipartite Genetic-Control Elements — Communication by DNA Loop. *Annual Review of Genetics*, **23**, 227–250.

Andrec, M., Levy, R. M., & Talaga, D. S. 2003. Direct determination of kinetic rates from single-molecule photon arrival trajectories using hidden Markov models. *Journal of Physical Chemistry A*, **107**(38), 7454–7464. .

Balaeff, A., Mahadevan, L., & Schulten, K. 1999. Elastic rod model of a DNA loop in the *lac* operon. *Physical Review Letters*, **83**, 4900–4903.

Balaeff, A., Koudella, C. R., Mahadevan, L., & Schulten, K. 2004. Modelling DNA loops using continuum and statistical mechanics. *Philosophical Transactions of the Royal Society of London Series A—Mathematical Physical and Engineering Sciences*, **362**(1820), 1355–1371.

Balaeff, A., Mahadevan, L., & Schulten, K. 2006. Modeling DNA loops using the theory of elasticity. *Physical Review E*, **73**, 031919.

Beausang, J F, & Nelson, P C. 2007. *Diffusive Hidden Markov Model Characterization of DNA Looping Dynamics in Tethered Particle Experiments*. Submitted; available on `arXiv.org`.

Beausang, J. F., Zurla, C., Manzo, C., Dunlap, D., Finzi, Laura, & Nelson, P. C. 2007a. DNA Looping Kinetics Analyzed Using Diffusive Hidden Markov Model. *Biophys. J.*, **92**, L64–L66. Explicit *Mathematica* code implementing our method can be found in the online supplement `http://www.biophysj.org/cgi/content/full/biophysj.107.104828/DC1`.

Beausang, J. F., Zurla, C., Finzi, L., Sullivan, L., & Nelson, P.C. 2007b. Elementary simulation of tethered Brownian motion. *Am. J. Phys.*, **75**, 520–523.

Becker, N. A., Kahn, J. D., & Maher, L. J. 2005a. Bacterial repression loops require enhanced DNA flexibility. *Journal of Molecular Biology*, **349**(4), 716–730. Erratum ibid 353 (4): 924-926 2005.

Becker, N. B., Altmann, S. M., Scholz, T., Horber, J. K. H., Stelzer, E. H. K., & Rohrbach, A. 2005b. Three-dimensional bead position histograms reveal single-molecule nanomechanics. *Physical Review E*, **71**(2). Part 1.

Bell, C. E., & Lewis, M. 2000. A closer view of the conformation of the Lac repressor bound to operator. *Nature Structural Biology*, **7**(3), 209–214.

Bell, C. E., & Lewis, M. 2001a. Crystal structure of the lambda repressor C-terminal domain octamer. *Journal of Molecular Biology*, **314**(5), 1127–1136.

Bell, C. E., & Lewis, M. 2001b. Crystallographic analysis of *lac* repressor bound to natural operator O1. *Journal of Molecular Biology*, **312**(5), 921–926.

Bell, C. E., & Lewis, M. 2001c. The Lac repressor: a second generation of structural and functional studies. *Current Opinion in Structural Biology*, **11**(1), 19–25.

Bell, C. E., Frescura, P., Hochschild, A., & Lewis, M. 2000. Crystal structure of the lambda repressor C-terminal domain provides a model for cooperative operator binding. *Cell*, **101**(7), 801–811.

Bell, C. E., Barry, J., Matthews, K. S., & Lewis, M. 2001. Structure of a variant of *lac* repressor with increased thermostability and decreased affinity for operator. *Journal of Molecular Biology*, **313**(1), 99–109.

Bellomy, G. R., Mossing, M. C., & Record, M. T. 1988. Physical-Properties of DNA In vivo as Probed by the Length Dependence of the *lac* Operator Looping Process. *Biochemistry*, **27**(11), 3900–3906.

Bevington, P. R., & Robinson, D. K. 2003. *Data reduction and error analysis for the physical sciences*. 3rd ed. Boston: McGraw–Hill.

Bintu, Lacramioara, Buchler, Nicolas E, Garcia, Hernan G, Gerland, Ulrich, Hwa, Terence, Kondev, Jané, & Phillips, Rob. 2005. Transcriptional regulation by the numbers: models. *Current Opinion in Genetics and Development*, **15**, 116–124.

Blumberg, S., Gajraj, A., Pennington, M. W., & Meiners, J. C. 2005. Three-dimensional characterization of tethered microspheres by total internal reflection fluorescence microscopy. *Biophysical Journal*, **89**(2), 1272–1281.

Boal, D. 2001. *Mechanics of the cell*. Cambridge, UK: Cambridge University Press.

Chen, H., Fu, H.X., Zhou, Z., Zhang, Z.H., & Yan, J. 2007. *Disagreement with WLC model revealed by DNA miniloop imaging*. In preparation.

Cloutier, T. E., & Widom, J. 2004. Spontaneous sharp bending of double-stranded DNA. *Molecular Cell*, **14**(3), 355–362.

Cloutier, T. E., & Widom, Jonathan. 2005. DNA twisting flexibility and the formation of sharply looped protein–DNA complexes. *Proc. Natl. Acad. Sci. USA*, **102**, 3634–3650.

Coleman, B. D., Tobias, I., & Swigon, D. 1995. Theory of the Influence of End Conditions on Self-Contact in DNA Loops. *Journal of Chemical Physics*, **103**(20), 9101–9109.

Colquhoun, D., & Sigworth, F. J. 1983. Fitting and statistical analysis of single-channel records. *Pages 191–263 of:* Sakmann, B., & Neher, E. (Eds.), *Single-Channel Recording*. New York: Plenum.

Cover, T. M., & Thomas, J. A. 1993. *Elements of information theory*. New York: Wiley.

Cowan, G. 2007. Data analysis: Frequently Bayesian. *Physics Today*, April.

Cox, D.R., & Hinkley, D.V. 1974. *Theoretical Statistics*. New York: Chapman and Hall.

Czapla, L., Swigon, D., & Olson, W. K. 2006. Sequence-dependent effects in the cyclization of short DNA. *Journal of Chemical Theory and Computation*, **2**(3), 685–695. .

Dennis, C., Fedorov, A., Kas, E., Salome, L., & Grigoriev, M. 2004. RuvAB-directed branch migration of individual Holliday junctions is impeded by sequence. *Embo Journal*, **23**(12), 2413–2422.

Dixit, S., Singh-Zocchi, M., Hanne, J., & Zocchi, G. 2005. Mechanics of binding of a single integration-host-factor protein to DNA. *Physical Review Letters*, **94**(11), 118101–(1–4).

Dohoney, K. M., & Gelles, J. 2001. chi-Sequence recognition and DNA translocation by single RecBCD helicase/nuclease molecules. *Nature*, **409**(6818), 370–374.

Douarche, N., & Cocco, S. 2005. Protein-mediated DNA loops: Effects of protein bridge size and kinks. *Physical Review E*, **72**(6), 061902–(1–10).

Du, Quan, Smith, Chaim, Shiffeldrim, Nahum, Vologodskaia, Maria, & Vologodskii, Alexander. 2005. Cyclization of short DNA fragments and bending fluctuations of the double helix. *Proc Natl Acad Sci USA*, **102**(15), 5397–402.

Dunn, T., Hahn, S., Ogden, S., & Schleif, R. 1984. An Operator at -280 Base Pairs that is Required for Repression of araBAD Operon Promoter: Addition of DNA Helical Turns between the Operator and Promoter Cyclically Hinders Repression. *Proc. Natl. Acad. Sci. USA*, **81**, 5017–5020.

Eddy, S. R. 2004. What is a hidden Markov model? *Nature Biotechnology*, **22**(10), 1315–1316.

Finzi, L., & Gelles, J. 1995. Measurement of Lactose Repressor-Mediated Loop Formation and Breakdown in Single DNA-Molecules. *Science*, **267**(5196), 378–380. .

Forkey, J. N., Quinlan, M. E., & Goldman, Y. E. 2000. Protein structural dynamics by single-molecule fluorescence polarization. *Progress in Biophysics and Molecular Biology*, **74**(1-2), 1–35.

Forkey, J. N., Quinlan, M. E., & Goldman, Y. E. 2005. Measurement of single macromolecule orientation by total internal reflection fluorescence polarization microscopy. *Biophysical Journal*, **89**(2), 1261–1271.

Garcia, H. G., Grayson, P., Han, L., Inamdar, M., Kondev, J., Nelson, P. C., Phillips, R., Widom, J., & Wiggins, P. A. 2007. Biological consequences of tightly bent DNA: The other life of a macromolecular celebrity. *Biopolymers*, **85**(2), 115–130.

Geanacopoulos, M., Vasmatzis, G., Zhurkin, V. B., & Adhya, S. 2001. *gal* repressosome contains an antiparallel DNA loop. *Nature Structural Biology*, **8**(5), 432–436.

Han et al., L. 2007a. *[[calibration]].* In preparation (to appear on `arXiv.org`).

Han et al., L. 2007b. *[[sequence]].* In preparation (to appear on `arXiv.org`).

Han et al., L. 2007c. *[[short DNA; concentration]].* In preparation (to appear on `arXiv.org`).

Hochschild, A. 2002. The λ switch: cI closes the gap in autoregulation. *Current Biology*, **12**, R87–R89.

Hoogenboom, J. P., den Otter, W. K., & Offerhaus, H. L. 2006. Accurate and unbiased estimation of power-law exponents from single-emitter blinking data. *J. Chem. Phys.*, **125**, 204713–(1–12).

Howard, J. 2001. *Mechanics of motor proteins and the cytoskeleton.* Sunderland, MA: Sinauer Press.

Koster, D. A., Wiggins, C. H., & Dekker, N. H. 2006. Multiple events on single molecules: Unbiased estimation in single-molecule biophysics. *Proceedings of the National Academy of Sciences of the United States of America*, **103**(6), 1750–1755.

Krämer, H., Niemöller, M., Amouyal, M., Revet, B., von Wilcken-Bergmann, B., & Müller-Hill, B. 1987. *lac* Repressor Forms Loops with Linear DNA Carrying 2 Suitably Spaced *lac* Operators. *Embo Journal*, **6**(5), 1481–1491.

Lambert, M. N., Vocker, E., Blumberg, S., Redemann, S., Gajraj, A., Meiners, J. C., & Walter, N. G. 2006. Mg2+-induced compaction of single RNA molecules monitored by tethered particle microscopy. *Biophysical Journal*, **90**(10), 3672–3685.

Lewis, M., Chang, G., Horton, N., Kercher, M., Pace, H., Schumacher, M., Brennan, R., & Lu, P. 1996. Crystal Structure of the Lactose Operon repressor and its complexes with DNA and inducer. *Science*, **271**, 1247–1254.

Liang, D., Maarel, J. R. C. Van Der, , & Yan, J. 2007. *Dynamical simulation study of base pair opening by sharp bending*. In preparation.

Marko, J.F., & Siggia, E.D. 1994. Bending and twisting elasticity of DNA. *Macromolecules*, **27**, 981–988. Erratum *Ibid.* **29** (1996) 4820.

Matthews, KS, & Nichols, JC. 1998. Lactose repressor protein: Functional properties and structure. *Prog. Nucleic Acid Res. Mol. Biol.*, **58**, 127–164.

McKinney, S. A., Joo, C., & Ha, T. 2006. Analysis of single-molecule FRET trajectories using hidden Markov modeling. *Biophysical Journal*, **91**(5), 1941–1951. .

Milescu, L. S., Yildiz, A., Selvin, P. R., & Sachs, F. 2006a. Extracting dwell time sequences from processive molecular motor data. *Biophysical Journal*, **91**(9), 3135–3150.

Milescu, L. S., Yildiz, A., Selvin, P. R., & Sachs, F. 2006b. Maximum likelihood estimation of molecular motor kinetics from staircase dwell-time sequences. *Biophysical Journal*, **91**(4), 1156–1168.

Mossing, M. C., & Record, M. T. 1986. Upstream Operators Enhance Repression of the *Lac* Promoter. *Science*, **233**(4766), 889–892.

Müller, Johannes, Oehler, Stefan, & Müller-Hill, Benno. 1996. Repression of *lac* Promoter as a Function of Distance, Phase and Quality of an Auxiliary *lac* Operator. *Journal of Molecular Biology*, **257**(1), 21–29.

Nelson, P. C., Zurla, C., Brogioli, D., Beausang, J. F., Finzi, L., & Dunlap, D. 2006. Tethered particle motion as a diagnostic of DNA tether length. *Journal of Physical Chemistry B*, **110**(34), 17260–17267.

Nelson, Philip. 2008. *Biological Physics: Energy, Information, Life*. Updated first ed. New York: W. H. Freeman and Co.

Normanno, D., Vanzi, F., & Pavone, F. S. 2007. Unpublished.

Okonogi, T. M., Alley, S. C., Reese, A. W., Hopkins, P. B., & Robinson, B. H. 2002. Sequence-dependent dynamics of duplex DNA: The applicability of a dinucleotide model. *Biophysical Journal*, **83**(6), 3446–3459.

Phillips, R., Kondev, J., & Theriot, J. 2008. *Physical Biology of the Cell*. New York: Garland Science.

Pouget, N., Dennis, C., Turlan, C., Grigoriev, M., Chandler, M., & Salomé, L. 2004. Single-particle tracking for DNA tether length monitoring. *Nucl. Acids Res.*, **32**, e73.

Press, W. H., Flannery, B. P., Teukolsky, S. A., & Vetterling, W. T. 1992. *Numerical Recipes in C*. 2nd ed. Cambridge: Cambridge University Press.

Purohit, P. K., & Nelson, P. C. 2006. Effect of supercoiling on formation of protein-mediated DNA loops. *Physical Review E*, **74**(6), Art. No. 061907. Erratum ibid. 75, Art. No. 039903, 2007.

Qin, F., Auerbach, A., & Sachs, F. 2000a. A direct optimization approach to hidden Markov modeling for single channel kinetics. *Biophysical Journal*, **79**(4), 1915–1927.

Qin, F., Auerbach, A., & Sachs, F. 2000b. Hidden Markov modeling for single channel kinetics with filtering and correlated noise. *Biophysical Journal*, **79**(4), 1928–1944.

Quinlan, M. E., Forkey, J. N., & Goldman, Y. E. 2005. Orientation of the myosin light chain region by single molecule total internal reflection fluorescence polarization microscopy. *Biophysical Journal*, **89**(2), 1132–1142.

Rabiner, L. R. 1989. A Tutorial on Hidden Markov-Models and Selected Applications in Speech Recognition. *Proceedings of the IEEE*, **77**(2), 257–286. .

Revet, B., von Wilcken-Bergmann, B., Bessert, H., Barker, A., & Müller-Hill, B. 1999. Four dimers of lambda repressor bound to two suitably spaced pairs of lambda operators form octamers and DNA loops over large distances. *Current Biology*, **9**(3), 151–154.

Rippe, K., von Hippel, P. H., & Langowski, J. 1995. Action at a distance: DNA-looping and initiation of transcription. *TIBS*, **20**, 500–506.

Saiz, L., & Vilar, J. M. G. 2006a. DNA looping: the consequences and its control. *Current Opinion in Structural Biology*, **16**(3), 344–350.

Saiz, L., & Vilar, J. M. G. 2006b. Stochastic dynamics of macromolecular-assembly networks. *Molecular Systems Biology*.

Saiz, L., Rubi, J. M., & Vilar, J. M. G. 2005. Inferring the in vivo looping properties of DNA. *Proceedings of the National Academy of Sciences of the United States of America*, **102**(49), 17642–17645.

Schafer, D. A., Gelles, J., Sheetz, M. P., & Landick, R. 1991. Transcription by Single Molecules of RNA–Polymerase Observed by Light-Microscopy. *Nature*, **352**(6334), 444–448. .

Schleif, R. 1992. DNA Looping. *Annual Review of Biochemistry*, **61**, 199–223.

Schroder, G. F., & Grubmuller, H. 2003. Maximum likelihood trajectories from single molecule fluorescence resonance energy transfer experiments. *Journal of Chemical Physics*, **119**(18), 9920–9924.

Segall, D. E., Nelson, P. C., & Phillips, R. 2006. Volume-exclusion effects in tethered-particle experiments: Bead size matters. *Physical Review Letters*, **96**(8), 088306–(1–4). .

Shimada, J., & Yamakawa, H. 1984. Ring-closure probabilities for twisted wormlike chains – applications to DNA. *Macromolecules*, **17**, 689–698.

Singh-Zocchi, M., Dixit, S., Ivanov, V., & Zocchi, G. 2003. Single-molecule detection of DNA hybridization. *Proceedings of the National Academy of Sciences of the United States of America*, **100**(13), 7605–7610.

Smith, D.A., Steffen, W., Simmons, R.M., & Sleep, J. 2001. Hidden-Markov methods for the analysis of single-molecule actomyosin displacement: The Variance-Hidden-Markov Method. *Biophys. J.*, **81**, 2795–2816.

Spakowitz, A. J. 2006. Wormlike chain statistics with twist and fixed ends. *Europhys. Lett.*, **73**, 684–690.

Spakowitz, A. J., & Wang, Z. G. 2004. Exact results for a semiflexible polymer chain in an aligning field. *Macromolecules*, **37**(15), 5814–5823.

Spakowitz, A. J., & Wang, Z. G. 2005. End-to-end distance vector distribution with fixed end orientations for the wormlike chain model. *Physical Review E*, **72**(4). Part 1.

Swigon, D., Coleman, B. D., & Olson, W. K. 2006. Modeling the Lac repressor-operator assembly: The influence of DNA looping on Lac repressor conformation. *Proceedings of the National Academy of Sciences of the United States of America*, **103**(26), 9879–9884.

Tolic-Norrelykke, S. F., Engh, A. M., Landick, R., & Gelles, J. 2004. Diversity in the rates of transcript elongation by single RNA polymerase molecules. *Journal of Biological Chemistry*, **279**(5), 3292–3299.

van den Broek, B., Vanzi, F., Normanno, D., Pavone, F. S., & Wuite, G. J. L. 2006. Real-time observation of DNA looping dynamics of type IIE restriction enzymes NaeI and NarI. *Nucleic Acids Research*, **34**(1), 167–174. .

Vanzi, F. 2003. *Mechanical Studies of Single Ribosome/mRNA Complexes*. Ph.D. thesis, University of Pennsylvania.

Vanzi, F., Vladimirov, S., Knudsen, C. R., Goldman, Y. E., & Cooperman, B. S. 2003. Protein synthesis by single ribosomes. *RNA*, **9**, 1174–1179.

Vanzi, F., Broggio, C., Sacconi, L., & Pavone, F. S. 2006. Lac repressor hinge flexibility and DNA looping: Single molecule kinetics by tethered particle motion. *Nucleic Acids Research*, **34**(12), 3409–3420.

Venkataramanan, L., & Sigworth, F. J. 2002. Applying hidden Markov models to the analysis of single ion channel activity. *Biophysical Journal*, **82**(4), 1930–1942.

Venkataramanan, L., Walsh, J. L., Kuc, R., & Sigworth, F. J. 1998a. Identification of hidden Markov models for ion channel currents - Part I: Colored background noise. *IEEE Transactions on Signal Processing*, **46**(7), 1901–1915.

Venkataramanan, L., Kuc, R., & Sigworth, F. J. 1998b. Identification of hidden Markov models for ion channel currents - Part II: State-dependent excess noise. *IEEE Transactions on Signal Processing*, **46**(7), 1916–1929.

Vilar, J. M. G., & Leibler, S. 2003. DNA looping and physical constraints on transcription regulation. *Journal of Molecular Biology*, **331**(5), 981–989.

Vilar, J. M. G., & Saiz, L. 2005. DNA looping in gene regulation: From the assembly of macromolecular complexes to the control of transcriptional noise. *Current Opinion in Genetics and Development*, **15**(2), 136–144.

Vilar, J. M. G., & Saiz, L. 2006. Multiprotein DNA looping. *Physical Review Letters*, **96**(23).

Vilar, J. M. G., Kueh, H. Y., Barkai, N., & Leibler, S. 2002. Mechanisms of noise-resistance in genetic oscillators. *Proceedings of the National Academy of Sciences of the United States of America*, **99**(9), 5988–5992.

Vilar, J. M. G., Guet, C. C., & Leibler, S. 2003. Modeling network dynamics: The lac operon, a case study. *Journal of Cell Biology*, **161**(3), 471–476.

Villa, E., Balaeff, A., Mahadevan, L., & Schulten, K. 2004. Multiscale method for simulating protein-DNA complexes. *Multiscale Modeling and Simulation*, **2**(4), 527–553.

Villa, E., Balaeff, A., & Schulten, K. 2005. Structural dynamics of the *lac* repressor-DNA complex revealed by a multiscale simulation. *Proceedings of the National Academy of Sciences of the United States of America*, **102**(19), 6783–6788.

Vologodskii, A. V. 1992. *Topology and physics of circular DNA*. Boca Raton: CRC Press.

Watkins, L. P., & Yang, H. 2004. Information bounds and optimal analysis of dynamic single molecule measurements. *Biophysical Journal*, **86**(6), 4015–4029.

Watkins, L. P., & Yang, H. 2005. Detection of intensity change points in time-resolved single-molecule measurements. *Journal of Physical Chemistry B*, **109**(1), 617–628.

Wiggins, P. A., & Nelson, P. C. 2006. Generalized theory of semiflexible polymers. *Phys. Rev. E*, **73**, 031906–(1–13).

Wiggins, P. A., Nelson, P. C., & Phillips, R. 2005. Exact Theory of Kinkable Elastic Polymers. *Phys. Rev. E*, **71**, 021909–(1–19). .

Wiggins, P. A., Van der Heijden, T., Moreno-Herrero, F., Spakowitz, A., Phillips, R., Widom, J., Dekker, C., & Nelson, P. C. 2006. High flexibility of DNA on short length scales probed by atomic force microscopy. *Nature Nanotechnology*, **1**(2), 137–141.

Wong, O. K., Guthold, M., Erie, D. A., & Gelles, J. 2007. *Interconvertible lactose repressor–DNA looped complexes revealed by single-molecule experiments*. unpublished.

Yan, J., & Marko, J. F. 2004. Localized Single-Stranded Bubble Mechanism for Cyclization of Short Double Helix DNA. *Phys. Rev. Lett.*, **93**, 108108–(1–4). .

Yan, Jie, Kawamura, Ryo, & Marko, John F. 2005. Statistics of loop formation along double helix DNAs. *Phys. Rev. E*, **71**, 061905–(1–17).

Yang, H., & Xie, X. S. 2002. Statistical approaches for probing single-molecule dynamics photon-by-photon. *Chemical Physics*, **284**(1-2), 423–437.

Yang, H., Luo, G. B., Karnchanaphanurach, P., Louie, T. M., Rech, I., Cova, S., Xun, L. Y., & Xie, X. S. 2003. Protein conformational dynamics probed by single-molecule electron transfer. *Science*, **302**(5643), 262–266.

Yin, H., Landick, R., & Gelles, J. 1994. Tethered Particle Motion Method for Studying Transcript Elongation by a Single RNA-Polymerase Molecule. *Biophysical Journal*, **67**(6), 2468–2478.

Zhang, Y., McEwen, A. E., Crothers, D. M., & Levene, S. D. 2006. Statistical-mechanical theory of DNA looping. *Biophysical Journal*, **90**(6), 1903–1912.

Zhang, Y. L., & Crothers, D. M. 2003. Statistical mechanics of sequence-dependent circular DNA and its application for DNA cyclization. *Biophysical Journal*, **84**(1), 136–153.

Zhou, Z., Chen, H., & Yan, J. 2007. *Bend-induced flexible hinge mechanism for short DNA anomalous elasticity*. Submitted.

Zocchi, G. 2001. Force Measurements on Single Molecular Contacts through Evanescent Wave Microscopy. *Biophys. J.*, **81**, 2946.

Zurla, C., Franzini, A., Galli, G., Dunlap, D. D., Lewis, D. E. A., Adhya, S., & Finzi, L. 2006. Novel tethered particle motion analysis of cI protein-mediated DNA looping in the regulation of bacteriophage lambda. *Journal of Physics-Condensed Matter*, **18**(14), S225–S234.