1085-92-261      **Thomas C Bishop\*** (`bishop@latech.edu`), Louisiana Tech University, Biomedical Engineering Center/BEC 103, 818 Nelson Ave, P.O. Box 10157
, Ruston, LA 71272. *DNA and chromatin as space curves constructed with 1 to 1,000,000 base pairs.* Preliminary report.

Given a sequence representing 1 to 1,000,000 base pairs of DNA, a model of double stranded DNA can be constructed by stacking successive base pairs together using known biophysical data. The integration is sufficiently fast to support interactive modeling. If nucleosome locations are also known, either from experiment or theory, then it is possible to construct models of entire chromosomes in near real time. Conformations of DNA and chromatin for the mouse mammary tumor virus promoter complex and for all sixteen chromosomes of the yeast genome are presented as case studies to demonstrate the utility and problems with this approach.

A web based version of these tools is available via the Chromatin Folding tab at `www.latech.edu/~bishop`. (Received September 11, 2012)