Weekly Report

An outline with a bit more details

1. Background of nucleosome positioning (Literature reading)
   a. What is it and its importance
      Chromatin structures, relation to DNA methylation\(^1\), relation to variability of
      gene expression\(^2\), relation to replication origin in yeast\(^3\),
   b. Factors that influence nucleosome positioning
      i. Sequence affect: dinucleotide patterns\(^4,5\), A-tract\(^6\), G/C content\(^7\)
      ii. Chromatin remodelers and barriers: ACF assembly factor\(^8\), barrier
          model\(^9\)
   c. Goal of this manuscript: To compare nucleosome sequential positioning signals
      among different organisms: yeast, fly, and malaria parasite. And try to give an
      explanation for the signals from a structural perspective.

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Sampling sequences from malaria parasite genome with
bias to sequences that contain A-tract at end regions seems
not able to reproduce the observed A-tract distribution
observed
Method: scan the genome base by base and make nucleosome calls with probability $p_1$ and with probability $p_2$ if the following 147 bp contains A-tract at one of its ends (set $p_2 > p_1$ to cause the bias). If a nucleosome call is made, skip the following 147 bps and continue.

**MD simulation with GROMACS**

A new set of parameters has been worked out through communication with an MD expert. Technical problems with one node on the cluster have been solved. A new simulation with new parameters is now running on the cluster (600ps done).

**Reference**