CO-SEGREGATION OF GENOMIC WINDOWS

**Reading assignment**

Read about linkage disequilibrium in the following sections of the GAM paper (<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5366070/>):

1. Section entitled “*Calculation of linkage matrices*”
2. Supplementary note 3.3
3. Supplementary note 3.4

Concepts to learn from the readings

1. Detection frequency of a genomic locus (window)
2. Co-segregation of a pair of genomic loci (windows)
3. Linkage
4. Normalized linkage

**Quiz**

Complete the blackboard quiz about these concepts before noon on Tuesday March 24.

Software Design & Implementation Activity

Design and develop software to calculate the normalized linkage table, containing the normalized linkage for all pairs of windows *in the Hist1 region*.

**PART1**: due on Thursday, March 26 before midnight (email to welch@ohio.edu)

Submit a design of the software:

* Page 1: Design diagram
* Page 2: Explanation of the design diagram (1-2 paragraphs)

**PART2**: due on Tuesday, March 31 before midnight (email to welch@ohio.edu)

Submit a demo of the software:

* Page 1: Screenshot of the core code that generates the normalized linkage table
* Page 2: Screenshot of the normalized linkage table produced by your program
* Page 3: A heatmap representation of the normalized linkage table
* Page 4: Explain the chromatin interactions shown in the heatmap (1 paragraph)

**NOTE**: I may respond to your email submissions with questions about your design, code, results, and/or interpretation. Please respond promptly to my questions.