Finding Sequence Paired Sites in the *Drosophila* genome -- Weirauch Lab Rotation

Aims

1. Gain competency in managing large datasets
2. Become familiar with new programming languages (Python, R, etc.)
3. Design a method to identify/predict SPS-sites in the *Drosophila* *melanogaster* genome
4. Apply method to other *Drosophilids*

Significance

Using available or generating new tools with which to identify Sequence Paired Sites (SPS) is a key component in gaining understanding of their endogenous behavior.

Background

The Notch signaling pathway is highly conserved and the key player in several human developmental diseases. Upon ligand binding, the Notch transmembrane receptor (auto-phos?) permits cleavage by gamma-secretase, releasing the Notch intracellular domain (NICD) signaling molecule to be transported to the nucleus. Upon arrival,

Methods

References[1-3]

1. Hass, M.R., et al., *SpDamID: Marking DNA Bound by Protein Complexes Identifies Notch-Dimer Responsive Enhancers.* Molecular cell, 2015. **59**(4): p. 685-97.

2. Nam, Y., et al., *Cooperative assembly of higher-order Notch complexes functions as a switch to induce transcription.* Proceedings of the National Academy of Sciences of the United States of America, 2007. **104**(7): p. 2103-8.

3. Severson, E., et al., *Genome-wide identification and characterization of Notch transcription complex-binding sequence-paired sites in leukemia cells.* Science signaling, 2017. **10**(477).