# Single Bivalent Level Metrics

- SC lengths (means and by class)

- Normalized CO positions (1CO) and telomere-centromere distance

- IFD, interference

**Pre-analysis questions**

1. What level is appropriate? (is mouse mean a valid level for these metrics? Or are single bivalents the right level)

**Driving questions for each metric:**

1. What are the main differences between males and females?

Are predictions for sexually dimorphic traits met?

1. What are the differences between high musc and low musc strains?

Use the Mixed model framework for analyzing / testing the HetC predictions.

Table 1

|  |  |  |
| --- | --- | --- |
| **Sexually dimorphic trait** | **Same across sexes** | **ref** |
| 1. SC lengths 2. Normalized CO positions | 1. Interference / IFD | 1.Lynn et al  2.Sardell-Kirkpatrick  3.PetkovBroman |

Table 2

|  |  |  |  |
| --- | --- | --- | --- |
| **trait** | **Pattern in High Musc** | **Pattern in Low Musc** | **ref** |
| SC Lengths | Longer SC | Shorter SC |  |
| IFD, spacing foci on single bivalents | Denser spacing, Shorter IFD | Greater average IFD |  |
| CO positions | ? | ? |  |
| DSB? (DSB on single chrms?) |  |  |  |

**First patterns to describe before test?**

Most logical approach for first examining the single bivalent patterns, is to split the data by subsp and sex, then apply post-hoc or selective pairwise comparisons.

1. Partitioning variance (cell, mouse, strain)
   1. How does the variance in each metric partition across the nested levels?
   2. What predictions or expectations should I have for these the partition of variance?
   3. (should I care since Chapter 2 will focus on means)
2. Subsampling / Permutations
   1. Might be easier to pick a certain number of mice and cells represented in the data, (but I would likely be leaving out data.
   2. For each of the tests, code a permutations of different subsamples

# CO position metrics

1. Rec landscape (1CO normalized positions)
2. Telomere distance and cent distance (all chrm classes)

-Main figure; density plots for each subspecies \* sex

-Rec landscape for 1CO: for all 1CO across a category, (subsp)

This metrics will be sexually dimorphic – only consider 1CO, because the REC landscape for multi-CO bivalents will be regulated by interference. \*\*I need to also consider the size effect for rec landscape, (shorter bivs are more uniformly distributed).

- t-tests for normalized positions (all pairwise tests between a subsp\*sex)

1CO: test between sexes, test between high-Rec and low-Rec

\*2CO/3CO, could test these, but interference would make the rec landscape converge to similar pattern.

2. Telomere and centromere distances, (another set of metrics that should help describe the biased positioning of Rec landscape). These metrics can be compared across all chromosome classes.

- same t-test framework as above for telomere and centromere distances.

# SC Lengths

Main figures

1. Scatter plot + boxplots for SC lengths by chrm class, facet by strain \* sex
2. Scatter plot to highlight, ‘missing’ 2CO

Metrics

1. Bivalent level SC length (by class)
2. ‘missing’ 2CO bivalent space (the cutoff / threshold in SC lengths for where there are 1COs, but no 2COs) \*\*this might be more of an interference metric?

\*\* Consider the issue of within cell covariation in SC length \*\*

# Interference

Main figure: scatter + boxplot of IFD distance (maybe cartoon/cropped 2CO biv)

-similar t-tests frame work IFDs (difference between sexes within strain, difference between high and low rec males.