**Comparison of within mouse MLH1 variance**

**Expectations under gamma model**

**-no interference = mean and variance will be equal**

**-higher mean, higher variance**

**Chap 3 results outline**

1. Does CO count per cell, SC length, IFD, CO position covary across bivalents within cells?

(is there a within nucleus / cell effect similar to the Wang paper)

1. Does the packing ratio (of SC length) reflect the underlying physical size variation across chromosomes?
2. Are there chromosome specific effects ( cov(ChmrY,ChrmZ) which are significantly different from all other pairs? Post-hoc pairwise comparisons – MAJOR CAVEAT – RANKED SC estimates
3. Comparisons of groups
   1. (what happens with the high recombining strains? High musc and molf have more 2CO bivs – are there predictions for these cell effects?
   2. What’s the differences across sexes? (females have more total variance, is this driven by increased cell effects or intrinsic chrm effects

<characterize cell level effects on bivalent observations>

<examine among cell variation> (main hypothesis is that total variation across cells (all data) is driven by nucleus specific effects (within cell covariation).>

**Framework**

1A. COMPARE DISTRIBUTIONs. Quantify cell effects from empirical data based on difference from randomized / simulated distributions. (simulated distribution for a panel of metrics (CO count, SC biv lengths, CO position, telomere – centromere position, rbar)

1B. C/A – decompose total variance to cell effect and chrm specific (intrinsic effect) for the same metrics.

2. compare ratio of within cell SC variance to chrm size variance (account for missing cent and telomere sequence with permutations)

3. (Scatter plot of all pairwise covariance) --- HOW will pairwise covariance work when all I have is SC rank?

**Data**

Hand measured whole cell data

Automated Biv data (missing 4 bivs)