**Simulation**

1. Identify pericentromeric regions to split chr1 into arms

Hg38 – bins 3043-3580

Hg19 – bins 3038-3565

I will be masking 3039-3563 because we see no contacts across tissues

Zahra: Repeat simulation, which will probably take two weeks

Liezel: She is still working on 4.2 and latest she can give it to me is by next week. If this is the case and given that maybe I can start working with corrections on the other plots next week, I think it’s okay to repeat.

2. Key parameters

a. Cut-off – Zahra’s worried that using 1.0 or 1.5 results to a sparse matrix, but I think it’s fine cause because we are not trying to replicate the whole matrix and the comparison method using the MCC was made to deal with sparse matrix.

<2 is fine

b. Parameter set for 3.2 and 4.2

Zahra’s determining the best parameter set by comparing with the slope of the contact-distance line form all 21 tissues.

If repeating the simulations, maybe she can just use the best parameter set based on current available matrices and let’s not mention that we tried different parameter sets for applying complementarity scores as attractive strengths.

c. Arm-interaction type

Zahra recommends doing comparison using both but to only present non-interacting arm results in the main text. If reviewers question the lack of non-interacting arms control and set2 then we act on it.

Set2 (cp only) – why no non-interacting version?

3. Timescale of simulation per type

Simulation maps contain frequency of contact not distance. Maps are generated for roughly 72 hours but different timescales (until it converges).

Normalise to number of snapshots taken during equilibrium.

Analysis of simulation maps

1. Discuss scaling done during comparison

I should probably asked for simulation method explanation.