Single-Cell Analysis of the 3D Topologies of Genomic Loci Using Genome Architecture Mapping

We will study on the largest portion of the HLB – the HIST1 region.

HIST1 is located on mouse chromosome 13 at the following coordinates:

Start:21.7 Mb

Stop: 24.1 Mb

Once you have

1. extracted the HIST1 region from the segmentation table
2. extracted relevant NPs for HIST1 (contain at least one window in the region of interest)

Then you should

1. compute the Jaccard index (aka the Jaccard similarity coefficient) for each pair of relevant NPs
2. store the computed values in a matrix; the matrix should contain similarities for all pairs of relevant NPs