

Single-nucleus multimodal sequence

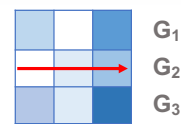


snRNA-seq

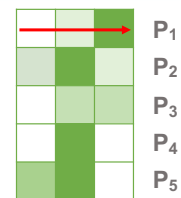
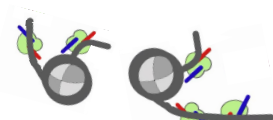
snATAC-seq

- scRNA and scATAC co-assays

Gene expression matrix



Open chromatin intensity matrix

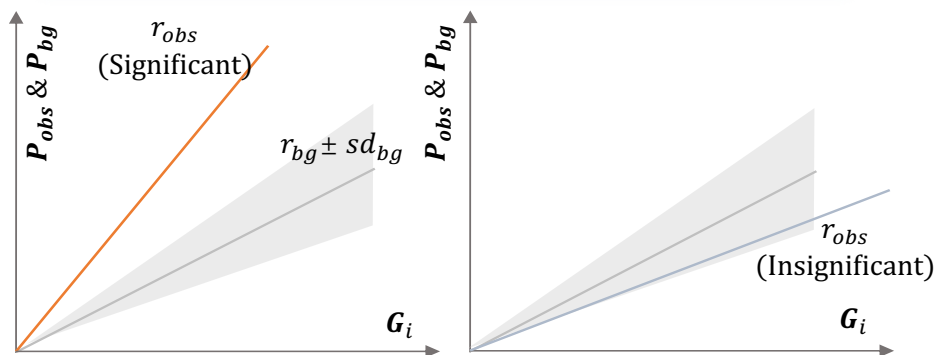


Embedded scRNA and scATAC datasets

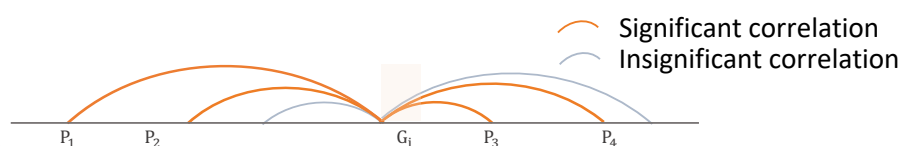
The cell counts **must** be identical in scRNA and scATAC dataset.

- Using **scJoint** to unify cell type annotations, and pairing individual cells using **scOptmatch** is highly recommended.
- Make sure the samples can be embedded reasonably,

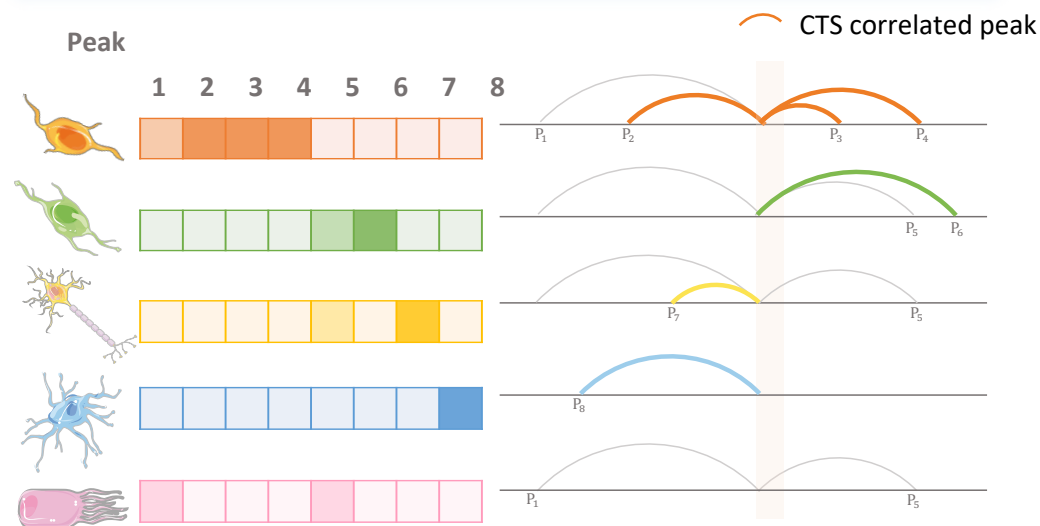
Obtaining significant correlated peaks in the genomic window size of 500kb



All correlated peaks for G_i



Obtaining cell type specific (CTS) correlated peaks for G_i



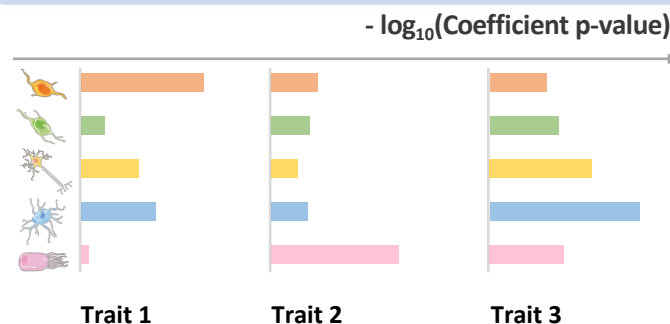
Functional regions in different cells



SNPs under peaks

S-LDSC

Heritability enrichment of GWAS loci in functional regions of different cells



Inferring phenotype-relevant cell types

