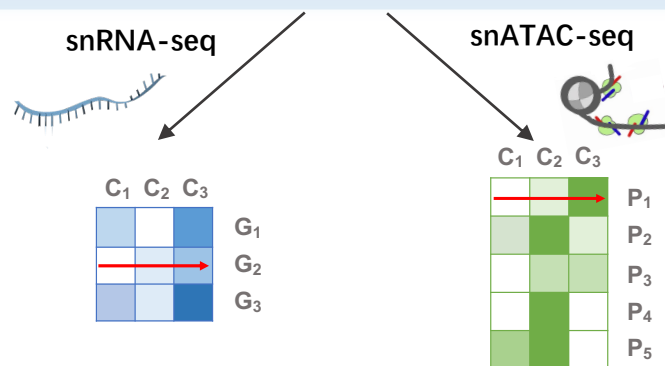


## Single-nucleus multimodal sequence



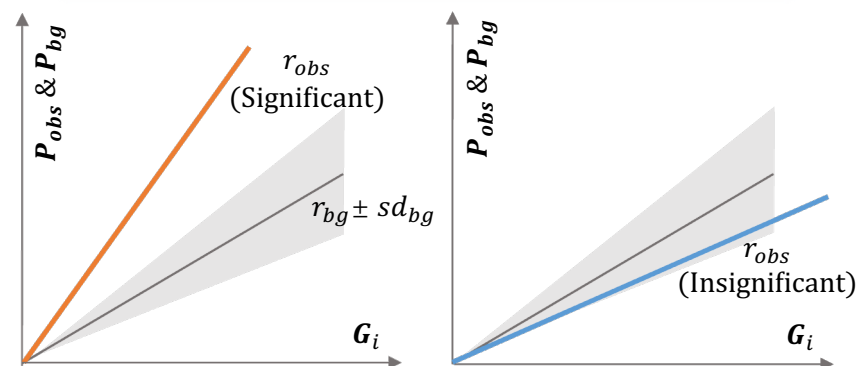
scRNA and scATAC co-assays

OR

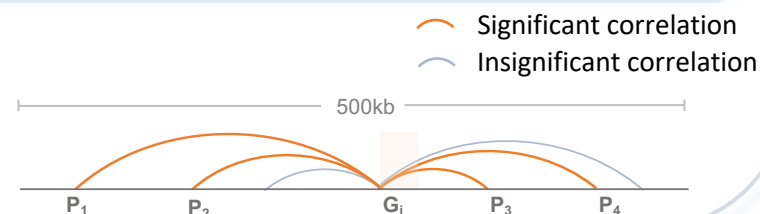
Embedded scRNA and scATAC datasets

- 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,

## Significance of correlated peaks for each expressed genes

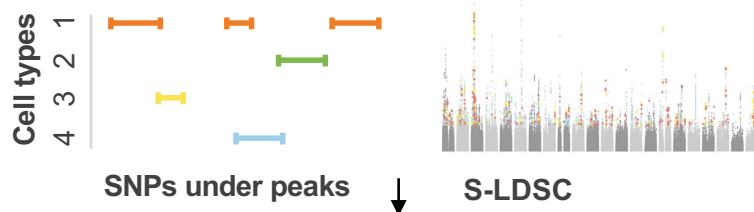


## All correlated peaks for $G_i$

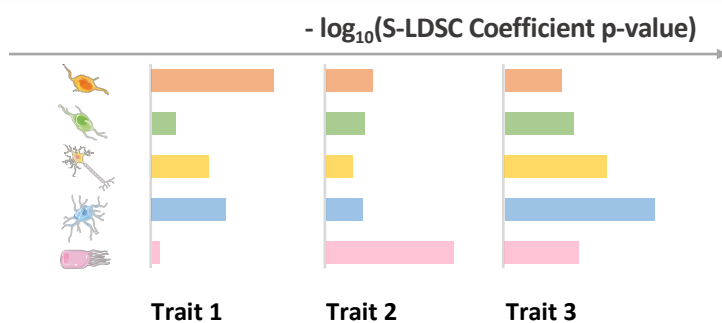


## Functional regions

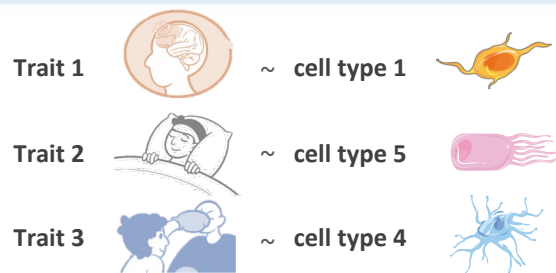
## Summarized GWAS



## Trait heritability enrichment



## Inferring phenotype-relevant cell types



## Obtaining cell type specific (CTS) correlated peaks for $G_i$

