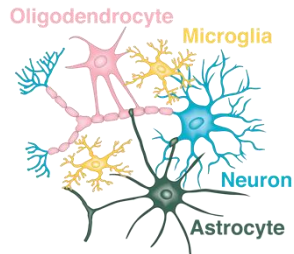
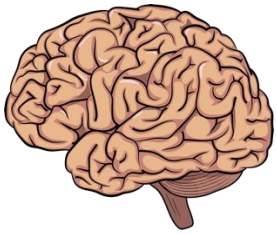


CHAS input

Bulk tissue H3K27ac peaks

Bulk tissue H3K27ac counts

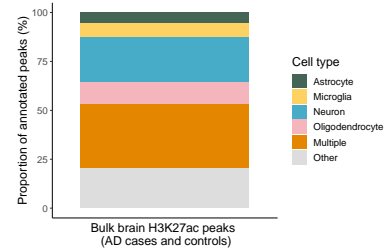
Cell type H3K27ac reference peaks



CHAS

CHAS-MF

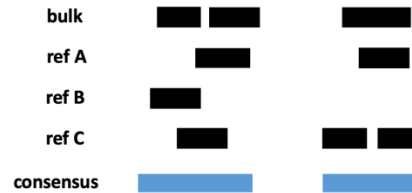
Step 1: cell type annotation



Step 2: calculate CHAS score

$$CHAS_{x,y} = \frac{\sum_{p \in P_x} s_{p,y}}{|P_x|} \cdot q_x$$

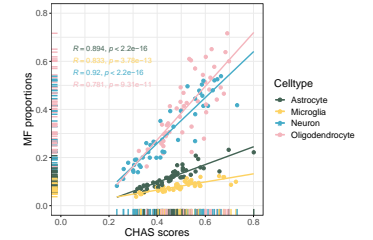
Step 1: read counting for bulk-ref consensus peaks



Step 2: run MF using EPIC

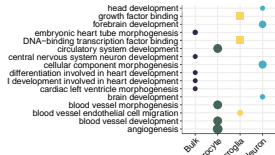
$$f(\bar{p}^*) = \sum_{i \in S} w_i [\bar{b}_i - (\bar{C}^* \times \bar{p}^*)_i]^2$$

Correlate CHAS and CHAS-MF

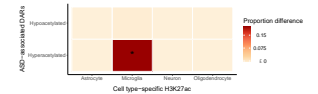


Biological mechanisms

Functional enrichment analysis at cell type resolution



Cell type enrichment in DARS



S-LDSC using cell type H3K27ac and GWAS

