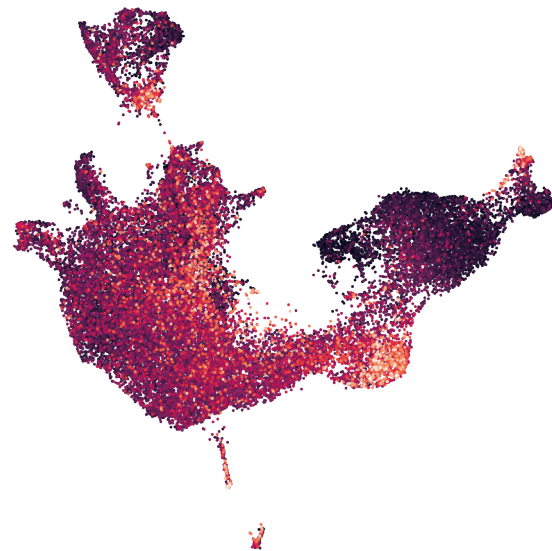


batch



- WT_1
- Fezf2_KO_1
- WT_2
- Aire_KO_2
- WT_3

total_counts



n_genes_by_counts

