

# PBMC\_cluster\_accuracy

Coefficient

0.15  
0.10  
0.05  
0.00  
-0.05  
-0.10

## Processing steps

- clustering method
- normalization method
- preprocess workflow

salmon\_SA  
zUMIs  
kallisto bustools  
Cell Ranger  
scPipe  
salmon\_splici  
dropSeqPipe  
sctransform  
sctransform\_poi  
DESeq2  
linnorm  
scone  
scrna  
sc3\_SVM  
scrna\_fastgreedy  
seurat\_slm  
seurat\_louvain  
sc3  
scrna\_louvain  
scrna\_walktrap