Impute low expression

Single cell RNA-seq gene expression counts are zero inflated due to inefficient mRNA capture. This normalization task is based on MAGIC[1]—MArkov Affinity-based Graph Imputation of Cells), to recover gene expression lost due to drop-out. The limitation on using this method is up to 50K cells in the input data node.

To invoke this task, click on a normalized data node which has less than 50K cells, it will first compute PCA to use the number of PCs specified to impute.

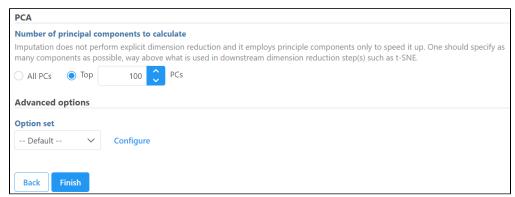


Figure 1. Select number of PCs to use for imputation

Click Finish to run the task, it will output low expression imputed matrix in the output report node.

References

1. Dijk D et al. MAGIC: A diffusion-based imputation method reveals gene-gene interactions in single-cell RNA-sequencing data

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.

