

## 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.

### PCA

**Number of principal components to calculate**

Imputation does not perform explicit dimension reduction and it employs principle components only to speed it up. One should specify as many components as possible, way above what is used in downstream dimension reduction step(s) such as t-SNE.

☐ All PCs

☒ Top

100

↑

↓

PCs

**Advanced options**

**Option set**

-- Default --

▼

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Finish

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.



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