scImpute

We used the R package of scImpute v0.0.9.

VIPER

We used the R package of VIPER (GitHub commit 0170c27). Following its README (https://github.com/ChenMengjie/VIPER/blob/master/README.md), we used its gene based imputation.

deepImpute

We used the Python package of deepImpute v1.0.0.

### Mean absolute error (MAE)

MAE measures the difference of gene expressions of the observed or imputation data to the reference data, given by

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where *n* is the number of positive-count genes in cell c from the reference data,  is the observed / imputed mRNA counts,  is the mRNA counts before down-sampling and .