

a) Method

b) Accuracy

Per metric	Error
KDE KS MAD MAE Overlapping RMSE phatacharyya multiks	Proportion of errors Reasons Group Score CCI ROUGE silhouette dunn connectivity DB index DEGs Score Distribution Proportion True Accuracy Precision Recall F1 Score AUC

c) Functionality

Group	DEGs	Batch	trajectory
Batch Score cns tS1 mm Shannon KBE1 AWS_batch per ISI Trajectory Score HLM F1 branches F1 milestones Cor_estim	Correlation Time Estimation Memory Simulation time Cor(simulation memory)	Estimation (cell x gene) Simulation (cell x gene)	The quality of the codes and softwares Availability Code Documentation Evaluation Maintenance Paper Quality

d) Scalability

Scores of time consuming and memory usage	Estimation (cell x gene)	Simulation (cell x gene)
Time Memory 100x1000 100x1000 100x1000 100x1000 100x1000 100x1000 100x1000	<1s <1s <1s <1s <1s <1s <1s <1s	<1s <1s <1s <1s <1s <1s <1s <1s

e) Usability

Class 1 Method

- SPARSim
- SCRIP-BP
- Splat
- SCRIP-GP-trendedBCV
- SCRIP-GP-commonBCV
- SCRIP-BGP-trendedBCV
- SCRIP-BGP-commonBCV
- powsimR
- SplatPop
- SPsimSeq

Class 2 Method

- PROSTTT
- SCRIP-paths
- Splat-paths
- ESCO-tree
- SplatPop-paths
- ESCO-traj
- TedSim
- phenopath
- MFA
- SymSim
- dyngen
- VeloSim
- dyntoy

Class 3 Method

- Lun
- scDesign
- Lun2
- muscat
- ESCO
- scDD
- scDesign3
- zingeR
- zinbwaveZinger

Class 4 Method

- scDesign2
- hierarchicell
- scGAN
- POWSC
- SparseDC
- SimBPDD
- BASICS

Class 5 Method

- Simple
- Kersplat
- zinbwave
- BEARssc
- dropsin
- CancerInSilico

Score: 0 0.2 0.4 0.6 0.8 1

Error reason:

- Failed estimation for genes
- Wrong parameter
- Wrong operation
- Wrong data structure
- Absence of missing (infinite) values
- Failed data normalization