a) Method
b) Accuracy
Per metric
Error
c) Functionality
Group
DEGs
Batch
trajectory
d) Scalability
Scores of time consuming and memory usage
Estimation (cell x gene)
Simulation (cell x gene)
e) Usability
The quality of the codes and softwares
KDE KS MAD MAE Overlapping RMSE bhattacharyya multiKS Proportion of errors Reasons
Group Score CDI ROUGE silhouette dunn connectivity DB Index DEGs Score Distribution Score True Proportion Accuracy Precision Recall F1 Score AUC
Batch Score cms LISI mm Shannon Entropy kBET AWS_batch pcr ISI
Trajectory Score HIM F1_branches F1_milestones Cor_dist
Estimation Time Cor(estimation time) Estimation Memory Cor(estimation memory) Simulation Time Cor(simulation time) Simulation Memory Cor(simulation memory) Time Memory
100x1000 1000x1000 1000x10000 10000x1000 100x1000 1000x1000 1000x10000 10000x1000
Avalability Code Documentation Evaluation Maintenance Paper Quality
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
PROSSTT
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
BEARscc
dropsim
CancerInSilico
Score
0 0.2 0.4 0.6 0.8 1
Error reason
Failed estimation for genes
Unknown
Incorrect parameter
Out of memory
Unsupported data operation
Unknown error
Wrong data structure
Bugs
Appearance of missing (infinite) values
Other
Failed data normalization