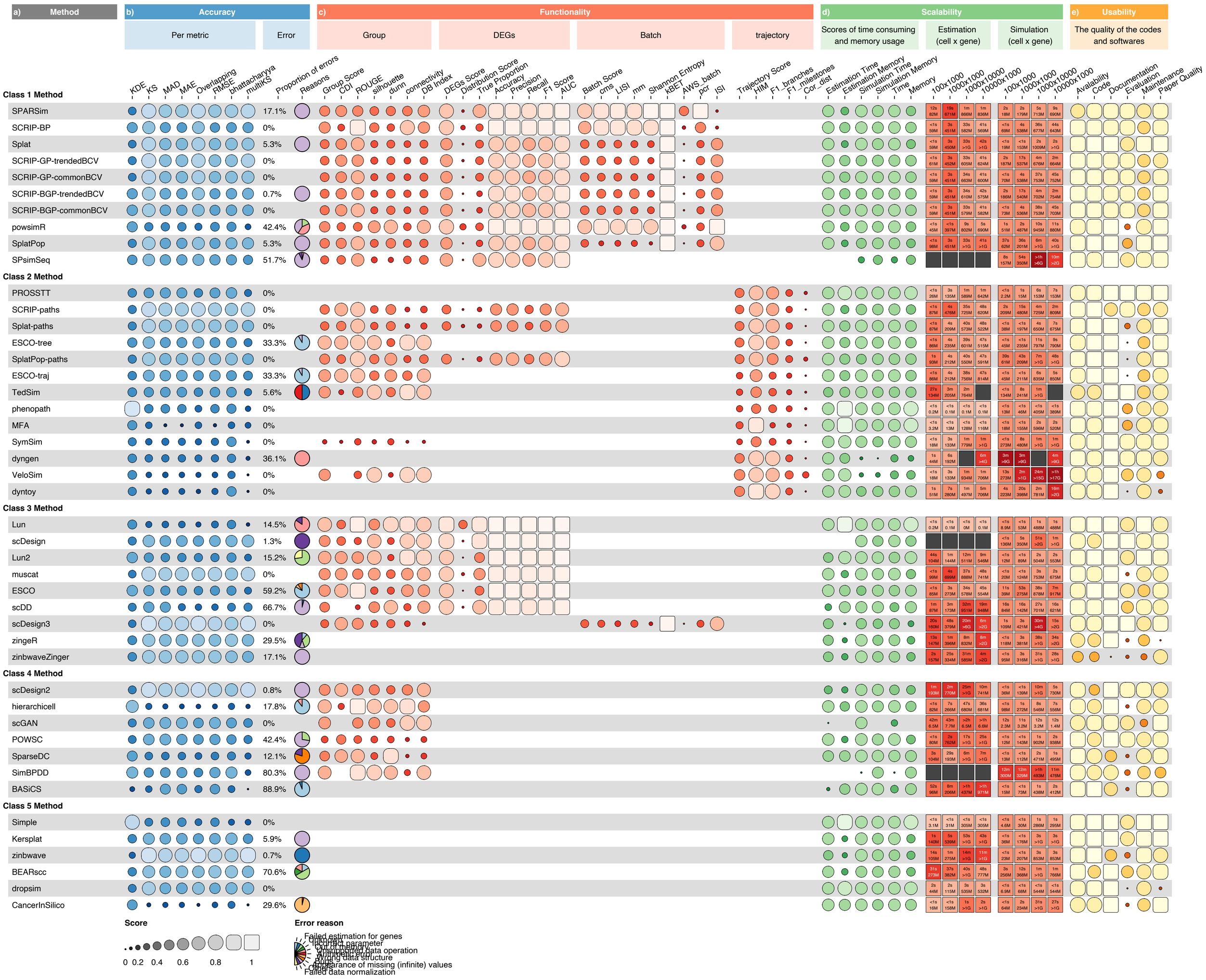
a) Method
b) Accuracy
Per metric
Error
c) Functionality
Group
DEGs
Batch
trajectory
d) Scalability
Scores of time consuming and memory usage
Estimation (cell x gene)
Simulation (cell x gene)
e) Usability
The quality of the codes and softwares
KDE KS MAD MAE Overlapping RMSE bhattacharyya multiKS Proportion 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 Estimation Memory Simulation Time Simulation Memory Time Memory
100x1000 1000x1000 1000x10000 10000x1000 100x1000 1000x1000 1000x10000 10000x1000
Avalability Code Documentation Evaluation Maintenance Paper Quality
Class 1 Method
SPARSim 17.1%
SCRIP-BP 0%
Splat 5.3%
SCRIP-GP-trendedBCV 0%
SCRIP-GP-commonBCV 0%
SCRIP-BGP-trendedBCV 0.7%
SCRIP-BGP-commonBCV 0%
powsimR 42.4%
SplatPop 5.3%
SPsimSeq 51.7%
Class 2 Method
PROSSTT 0%
SCRIP-paths 0%
Splat-paths 0%
ESCO-tree 33.3%
SplatPop-paths 0%
ESCO-traj 33.3%
TedSim 5.6%
phenopath 0%
MFA 0%
SymSim 0%
dyngen 36.1%
VeloSim 0%
dyntoy 0%
Class 3 Method
Lun 14.5%
scDesign 1.3%
Lun2 15.2%
muscat 0%
ESCO 59.2%
scDD 66.7%
scDesign3 0%
zingeR 29.5%
zinbwaveZinger 17.1%
Class 4 Method
scDesign2 0.8%
hierarchicell 17.8%
scGAN 0%
POWSC 42.4%
SparseDC 12.1%
SimBPDD 80.3%
BASiCS 88.9%
Class 5 Method
Simple 0%
Kersplat 5.9%
zinbwave 0.7%
BEARscc 70.6%
dropsim 0%
CancerInSilico 29.6%
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
Wrong data structure
Bugs
Appearance of missing (infinite) values
Failed data normalization
Others