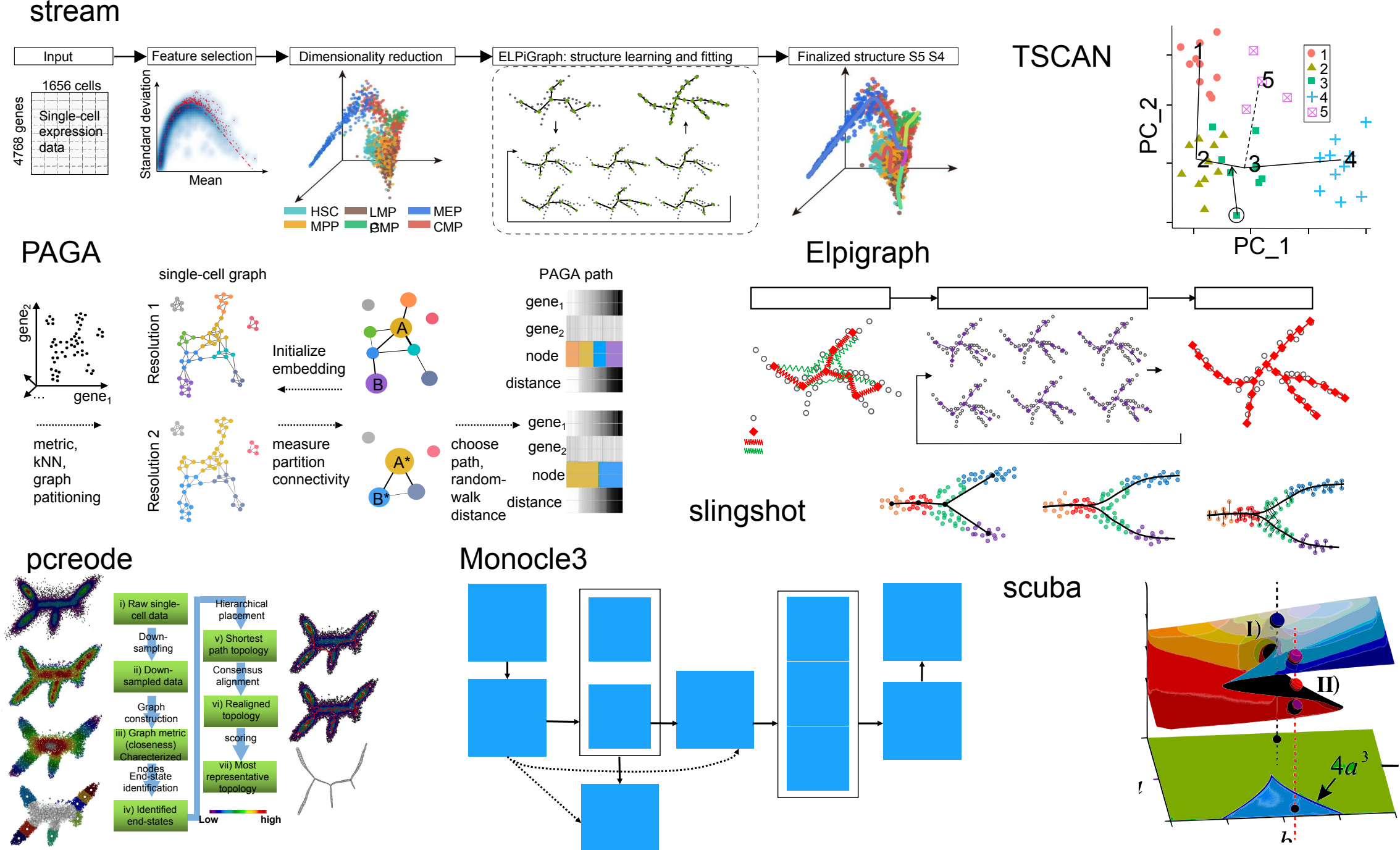
stream
Input
Feature selection
Dimensionality reduction
ELPiGraph: structure learning and fitting
Finalized structure S5 S4
1656 cells
4768 genes
Single-cell expression data
Standard deviation
Mean
HSC
MPP
LMP
BMP
MEP
CMP
TSCAN
PC_2
PC_1
PAGA
single-cell graph
Resolution 1
Resolution 2
Initialize embedding
metric, kNN, graph patitioning
measure partition connectivity
choose path, random-walk distance
PAGA path
gene1
gene2
node
distance
Elpigraph
slingshot
pcreode
i) Raw single-cell data
Down-sampling
ii) Down-sampled data
Graph construction
iii) Graph metric (closeness) Charecterized nodes
End-state identification
iv) Identified end-states
Hierarchical placement
v) Shortest path topology
Consensus alignment
vi) Realigned topology
scoring
vii) Most representative topology
Low
high
Monocle3
scuba