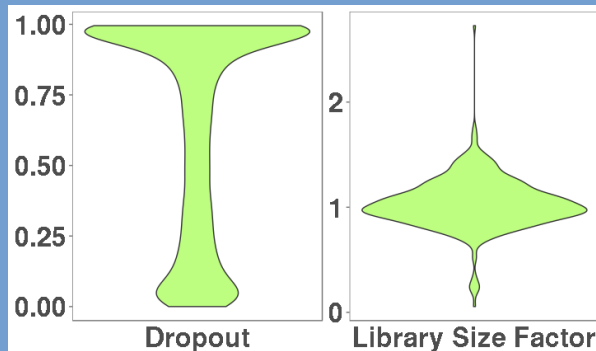
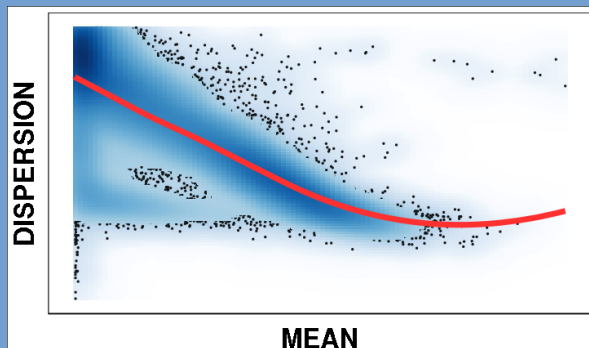


A ESTIMATION

RNA-seq read counts of bulk
or single cells*

estimateParam()

**Distribution
(Zero-Inflated) Negative Binomial**



plotParam()

evaluateDist()

*source: user-provided,
recount data base,
predefined examples

B SIMULATION

**Differential Expression
Settings**

- Number of genes
- Percentage DE genes
- Effect size (fold change)
- Number of simulations

DESetup()

SimSetup()

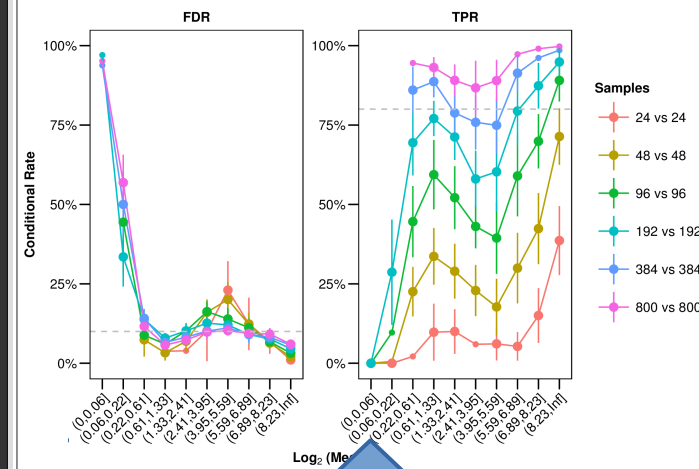
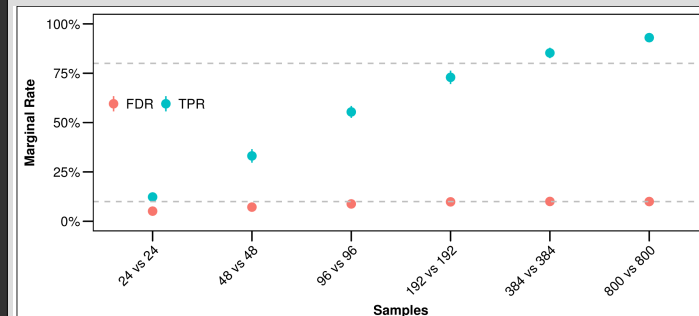
Simulation Settings

- Number of replicates
- Parallel computing
- Differential testing method

simulateDE()

Wrapper function PowSim()

C EVALUATION



plotEvalRes()

Power Analysis

- MTC method
- Cutoff
- Stratification by moments
- Filtering

evaluateSim()