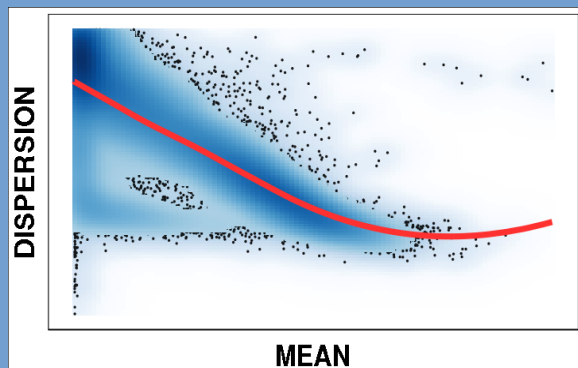


A ESTIMATION

RNA-seq read
counts of bulk or
single cells*

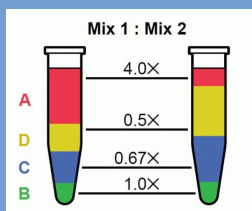
estimateParam()

Distribution
(Zero-Inflated) Negative Binomial



plotParam()

evaluateDist()



estimateSpike()

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

B SIMULATION

**Differential Expression
Settings**

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

DESetup()

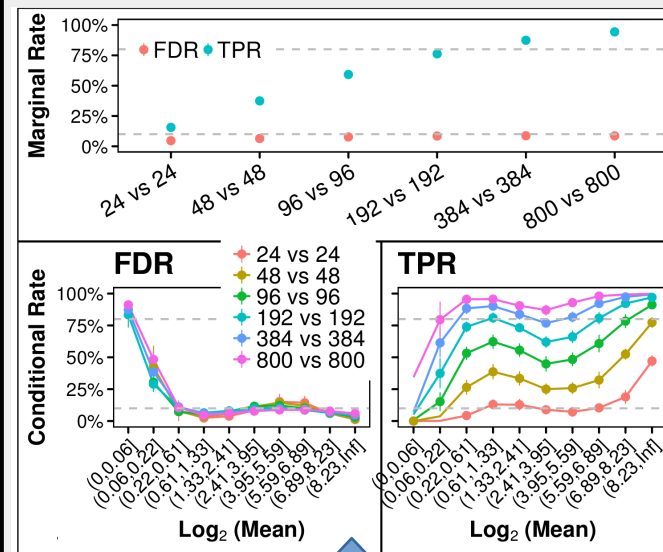
SimSetup()

Simulation Settings

- Number of replicates
- Normalisation method
- DE method
- Parallel computing
- Spike-ins
- Downsampling

simulateDE()

C EVALUATION



plotEvalDE()

Power Analysis

- MTC method
- Cutoff
- Stratification by moments
- Filtering

evaluateDE()

Simulation Analysis

evaluateSim()