Single Cell Toolkit

R Package and Shiny App for Complete Workflow for scRNA-seq Analysis

• Upload Raw Counts, Filtered or Normalized Data
• Easy Import/Export of R/Bioconductor objects
• Data Summary, Data Filtration, Normalization
• Batch Correction
• Clustering and Annotation
• Differential Expression Analysis
• Pathway Activity Prediction
• Experimental Design, Sample Size, Power
Creates SingleCellExperiment object, stores counts and annotations as "reactiveValues" objects. Can be modified and triggers functions to run.

You can also upload a SingleCellExperiment or SummarizedExperiment object here or from the R console when you load the app.
Future Development

• Release pending, available on Github:
  • https://github.com/combiomed/singleCellTK
• Feature requests, bug reports, questions
• Develop with us! Join us on slack:
  • https://combiomed.slack.com/

• Novel methods/tools for the following:
  • R console and Shiny App integration
  • Modifications to SingleCellExperiment
  • Clustering/topic modeling
  • Batch correction (ComBat-SCSeq)
  • Differential expression for nested designs
  • Pathway activity analysis