

IMPORT Single Cell raw data

create fluidSCraw S3 object

From custom dataframe: **fluidSCraw()**

From Biomark table format output: **read_Fluidigm()**

Remove assays or samples: **remove_data()**



PRE-PROCESSING in order

functions on fluidSCraw S3 object

(optional) generate quality call based on list with ideal melt temperatures of all assays: **decide_Call_meltTemp()**

1. Identify bad and low expressed assays based on resp. ratio and number of quality calls: **identifyBadAssays()**

2. Identify bad samples based on missing data and assay expression probabilities: **identifyBadSamples()**

3. Check expression distributions between conditions to decide LoD value: **merge_fluidSCraw()**, **visualize_distribution()**, **display_parameters_distribution()**



4. normalize raw Ct data and calculate log2 expression score: **normalize_fluidSC()**

create fluidSCproc S3 object



ANALYSIS AND VISUALIZATION

functions on fluidSCproc S3 object

A. Identify sample outliers: **identifyOutlierSamples()**



B. Assay expression distribution: **dotplotSC()**, **violinplotSC()**



C. Data clustering and reduction:

- Hierarchical, Kmeans, correlation clustering: **cluster_SC()**, **heatmapSC()**
- Data reduction: **PCA_SC()**, **wcmds_SC()**



D. Expression range: **show_IQRexpression_Range()**, **multi_IQR_expression_range()**



E. Assay correlation: **scatterplot_SC()**, **ellipseCorrPlot_SC()**, **matrixplot_SC()**, **ternaryplot_SC()**



F. Abundance vs variation: **meanExpression_vs_variance_SC()**, **meanExpression_vs_COV_SC()**, **meanExpression_vs_standardDeviation_SC()**



INTEGRATION & ADVANCED ANALYSIS



MONOCLE

WGCNA

Network
analysis