

class: ExpressionSet

Slots

assayData

exprs: gene expression (mean of bead replicates)

featureData: identifier mapping and annotation

phenoData: sample information and experiment design

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class: LumiBatch

Slots

assayData

se.exprs: expression standard deviation of bead replicates

beadNum: bead replicate number of each gene

detection: p-value of expression detectability

QC: a list keeping the quality control information

controlData: a data.frame keeping control probe measurement

history: a data.frame recording previous operation over the object

Major methods

lumiR: input data from BeadStudio output text file

lumiB: background correction

lumiT: variance stabilizing transformation

lumiN: normalization

lumiQ: quality control evaluation

lumiExpresso: encapsulate all preprocessing functions

plot: MAplot, pairs, boxplot, density, sample relation, hist, cv

summary: summary of the data or QC information

getHistory: retrieve the previous operation over the object

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