

class: ExpressionSet

Slots

assayData

exprs: gene expression (bead replicate mean)

featureData: gene information

experimentData: experiment meta data

phenoData: experiment design

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class: LumiBatch

Slots

assayData

se.exprs: bead replicate standard deviation

beadNum: bead number of each gene

detection: detection probability

history: operation tracking

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Major methods

lumiR: initialization by reading raw data

lumiT: variance stabilizing transform

lumiN: normalization

lumiQ: quality control

getHistory

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class: LumiQC

Slots

assayData

cv: the coefficients of variance

mean, std, sampleCor,

detectionRate, sampleRelation,

outlier, history

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Major methods

plot:

MAplot, pairs, boxplot, density,

sample relation, outlier, cv,

hist

getHistory

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