class: ExpressionSet

Slots
 assayData
   exprs: gene expression (bead replicate mean)
 featureData: gene information
 experimentData: experiment meta data
 phenoData: expreriment design
 ......

class: LumiBatch

Slots
 assayData
   se.exprs: bead replicate standard deviation
   beadNum: bead number of each gene
   detection: detection probability
 history: operation tracking
 ......

Major methods
 lumiR: initialization by reading raw data
 lumiT: variance stabilizing transform
 lumiN: normalization
 lumiQ: quality control
 getHistory
 ......

class: LumiQC

Slots
 assayData
   cv: the coefficients of variance
 mean, std, sampleCor,
 detectionRate, sampleRelation,
 outlier, history
 ......

Major methods
 plot:
   plot QC plots: MAplot,
   pairs, boxplot, sample relation,
   outlier, cv, densityPlot
 getHistory
 ......