

## Description

The R Scripts are for generating some figures for data distribution scatter plots etc.

### 1. drawInput.R: generating density plots for distribution of methylation scores

Requirement: ggplot2 (see details at <http://www.ggplot2.org>)

Usage:

RScript drawInput.R <input path> <index>

- <input path>: input data path, tab-eliminated.
- <index> [integer]: column index which contains the methylation score

Running Example:

RScript drawInput.R /somewhere/input.bed 5

### 2. drawMixtureDistribution.R: generation density plot of methylation score distribution estimated from mixture model

Requirement: easyGgplot2 (see details at <http://www.sthda.com/english/wiki/easyggplot2>)

Usage:

RScript drawMixtureDistribution.R <CCR mean> <CCR std> <OCR mean> <OCR std>

- <CCR mean>: mean methylation score of GCHs in CCR
- <CCR std>: standard deviation of methylation score of GCHs in CCR
- <OCR mean>: mean methylation score of GCHs in OCR
- <OCR std>: standard deviation of methylation score of GCHs in OCR

Running Example:

Rscript drawMixtureDistribution.R 0.1 0.1 0.9 0.1

### 3. drawPredictedDistribution.R: generation of density plot of methylation score distribution predicted by CAME

Requirement: easyGgplot2 (see details at <http://www.sthda.com/english/wiki/easyggplot2>)

Usage:

RScript drawPredictedDistribution.R <input path>

- <input path>: Path for input file. After running CAME, there will be an output.bed.pred to be generated. This file could be the input for drawing.

Running Example:

Rscript drawPredictedDistribution.R /somewhere/output.bed.pred

#### **4. drawScatterPlot.R: generating a scatter plot in terms of length and average methylation score**

Usage:

Rscript drawScatterPlot.R <input path>

- <input path>: Path for input file. The output BED file of CAME will be the input data format.

Running Example:

Rscript drawScatterPlot.R /somewhere/output.bed