erccdashboard Package Vignette

1   201

i gete e ea gtea tn
n kntateete etg
ta genea tote t
egh e

ntgeta tte gete e
te tabkn

- tgtateea

- me a e e nee
  anne

  e egateinte teieeae et
e eba

  tg egeta

  egeta

  age teba

$mmn\ mmn$

$$m$$

$$m$$

ategeta

```
> data(SEQC.Example)
```

e ta nn te eteagete
ne

- a teta annaae
  t n ie tt

- ta eta atgt

- ta eta a ine tt t
  n

ettoac ba e eg

- ta toea enntgbe
  etta

- ta tenaente
  tta

notbadbaut tabg eie
th tigtbpie

```
> datType = "count" # "count" for RNA-Seq data, "array" for microarray data
> isNorm = FALSE # flag to indicate if input expression measures are already
>                 # normalized, default is FALSE
> exTable = MET.CTL.countDat # the expression measure table
> filenameRoot = "RatTox" # user defined filename prefix for results files
> sample1Name = "MET" # name for sample 1 in the experiment
> sample2Name = "CTL" # name for sample 2 in the experiment
> erccmix = "RatioPair" # name of ERCC mixture design, "RatioPair" is default
> erccdilution = 1/100 # dilution factor used for Ambion spike-in mixtures
> spikeVol = 1 # volume (in microliters) of diluted spike-in mixture added to
>                 #   total RNA mass
> totalRNAmass = 0.500 # mass (in micrograms) of total RNA
> choseFDR = 0.05 # user defined false discovery rate (FDR), default is 0.05
```

e ttg e betaidta n e
te t aaie a eigie
tieean tei tton
e ahiein eigteet eti
th tniee aab g t ea ge
teidgtin en alR
eitg e itiena
keakatetta

```
> head(MET.CTL.countDat)
        Feature MET_1 MET_2 MET_3 CTL_1 CTL_2 CTL_3
16499 ERCC-00002 16629 18798 26568 36600 45436 25163
16500 ERCC-00003  1347  1565  1983  3048  3447  2195
16501 ERCC-00004  4569  5570  6755  1240  1484   902
16502 ERCC-00009   811   869  1123   909  1073   537
16503 ERCC-00012     0     0     0     0     0     0
16504 ERCC-00013     3     1     2     1     5     1
```

e tn eiet e tem atbt
eh eintt egytet tia e n
tieabttei e atnei e
meittatean tbegin i
onbta   _eie ten ntineat n
oe   _   eeibton
eti teg edtnaiete
ig iteteta edatait
te abaet th tihtieat et
btgeitgie caate ba e
te enbateieeei t et
tenint etbta nteieeaa
iibt en e iietteaein
t
noteakt i ienteakt
i ie ntiba ne

[1] "Analyzing Gene # 2"
[1] "Analyzing Gene # 10"
[1] "Analyzing Gene # 2"
[1] "Analyzing Gene # 10"
Note: 'test.mat' not provided. Comparing each model
from 'design.list ' to first model in 'design.list ', which must be the full model
[1] "Spline scaling factor: 0.933720469163937"
[1] "Finished DE testing"
[1] "Spline scaling factor: 0.933720469163937"

Finished examining dispersions

Threshold P-value
0.00775934

Generating ROC curve and AUC statistics...

Area Under the Curve (AUC) Results:

Ratio	AUC	Detected	Spiked
4:1	1.000	16	23
1:1.5	0.950	16	23
1:2	0.971	16	23

Estimating ERCC LODR
....

Ratio	LODR Estimate	90% CI Lower Bound	90% CI Upper Bound
4:1	26	19	32
1:1.5	Inf	<NA>	<NA>
1:2	270	140	390

LODR estimates are available to code ratio-abundance plot

Saving main dashboard plots to pdf file...

Saving exDat list to .RData file...
Analysis completed.

eabigatee tatc etiiie
a tiagttaegtth e on ta
tatite,

```
> summary(exDat)
            Length Class      Mode
sampleInfo    11   -none-     list
plotInfo       9   -none-     list
erccInfo       4   -none-     list
Transcripts    7   data.frame list
designMat      3   data.frame list
sampleNames    2   -none-     character
```