Package 'AssayCorrector'

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Type Package

Title Detection and Correction of Spatial Bias in HTS Screens

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Description (1) Detects plate-specific spatial bias by identifying rows and columns of all plates of the assay affected by this bias (following the results of the Mann-Whitney U test) as well as assay-specific spatial bias by identifying well locations (i.e., well positions scanned across all plates of a given assay) affected by this bias (also following the results of the Mann-Whitney U test); (2) Allows one to correct plate-specific spatial bias using either the additive or multiplicative PMP (Partial Mean Polish) method (the most appropriate spatial bias model can be either specified by the user or determined by the program following the results of the Kolmogorov-Smirnov two-sample test) to correct the assay measurements as well as to correct assay-specific spatial bias by carrying out robust Z-scores within each plate of the assay and then traditional Z-scores across well locations.

Depends R (>= 3.3.0),
RColorBrewer,
lattice,
latticeExtra,
kSamples,
RVAideMemoire

License GPL-3

LazyData TRUE

RoxygenNote 6.0.1

R topics documented:

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correct_bias	*Correct the bias present in the assay, previously detected by the* `detect_bias()` *method*

Description

`correct_bias()` (1) uses either the additive or multiplicative PMP (Partial Mean Polish) methods (the most appropriate spatial bias model can be either specified or determined by the program following the results of the Kolmogorov-Smirnov two-sample test) to correct the assay measurements if the plate-specific correction is specified; (2) carries out the assay-specific correction if specified.

Usage

```
correct_bias(assay, method = NULL, alpha = 0.05, type = "PA")
```

Arguments

assay	The assay to be corrected. Has to be an `assay` object.
method	NULL:autodetect (default), 1:additive, 2:multiplicative
alpha	Significance level threshold (defaults to 0.05)
type	P:plate-specific, A:assay-specific, PA:plate then assay-specific, AP:assay then plate-specific

Value

The corrected assay (`assay` object)

Examples

```
assay<-create_assay(m)
detected<-detect_bias(assay)
corrected<-correct_bias(detected,method=2)
```

---

create_assay	*Create a new* `assay`

Description

`create_assay` makes a new object of class assay. You should pass this object to `detect_bias()` and `correct_bias()` methods

Usage

```
create_assay(m, ctrl = NA)
```

Arguments

`m`	The assay you want to be corrected
`ctrl`	An optional boolean array of the same dimensions as m. Each entry is 1 if the well is a control well, 0 otherwise. All control wells are excluded from all computations

Value

assay The created assay object. It containts the following fields:

n The HTS matrix of raw measurements

ctrl The binary matrix of control wells

biasPositions The binary matrix where 1:well is biased, 0:well is unbiased, as suggested by Mann-Whitney test

mCorrected The HTS matrix of corrected measurements, initilized to a zero array, and subsequently storing the corrected version of m via `correct_bias()`

biasType Vector of length p, where p is the number of plates. It tells, for each plate of the assay, A:Additive trend, M:Multiplicative trend, U:Undetermined trend and C:Error-free plate.

biasModel Vector of length p, where p is the number of plates. It tells, for each plate of the assay, the most likely spatial bias model (1 through 6)

biasConf Vector of length p, where p is the number of plates. It tells, for each plate of the assay, the confidence in the model, (0 - lowest to 3- highest).

Examples

```
# Fictive 8x12x5 assay
assay<-create_assay(m)
# Plate 7 taken from Carralot et al. 2012
assay<-create_assay(plate7)
```

---

detect_bias	*Detect the type of bias present in the assay*

Description

detect (1) identifies rows and columns of all plates of the assay affected by spatial bias (following the results of the Mann-Whitney U test); (2) identifies well locations (i.e., well positions scanned across all plates of a given assay) affected by spatial bias (also following the results of the Mann-Whitney U test).

Usage

```
detect_bias(assay, alpha = 0.01, type = "P", test = "AD")
```

Arguments

`assay`	The assay to be corrected. Has to be an `assay` object.
`alpha`	Significance level threshold (defaults to 0.01)
`type`	P:plate-specific, A:assay-specific, PA:plate then assay-specific, AP:assay then plate-specific
`test`	KS:Kolmogorov-Smirnov (1933), AD:Anderson-Darling (1952), CVM:Cramer-von-Mises (1928)

Value

The corrected assay (`assay` object)

Examples

```
assay<-create_assay(m)
detected<-detect_bias(assay)
```

---

m	*Artificially generated HTS assay*

Description

A 8x12x5 assay (class array) that was generated with partial column bias in the last column. Gaussian noise was then added

Usage

```
m
```

Format

An object of class `array` of dimension 8 x 12 x 5.

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plate7	*Plate 7 of raw measurements obtained by Carralot et al. 2012 (Institut Pasteur Korea)*

Description

The seventh plate take from an experimental assay, which showed the evidence of existence of multiplicative kind of bias in screening technologies.

Usage

```
plate7
```

Format

An object of class `matrix` with 16 rows and 20 columns.

---

plot.assay   *Plot assay plate-wise*

Description

plot.assay plots a hit map of the assay (only one plate at a time)

Usage

```
## S3 method for class 'assay'
plot(x, ..., plate = 1, type = "R")
```

Arguments

x	The assay you want to plot
...	Ellipsis to be passed to the levelplotplot() function from the lattice package
plate	The plate number (Default:1)
type	Either "R" - raw assay, "C" - corrected assay (if it exists) or "P" - spatial bias position

Value

None

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print.assay   *Print assay summary*

Description

print.assay simply prints a summary of the HTS assay

Usage

```
## S3 method for class 'assay'
print(x, ..., plate = 1)
```

Arguments

x	The assay you want to print
...	Ellipsis to be passed to the default print() function
plate	The plate number (Default:1)

Value

None

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