

# 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 of the three additive or either of the three multiplicative PMP (Partial Mean Polish) methods (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, Anderson-Darling or Cramer-von-Mises 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

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correct_bias	<i>Correct the bias present in the assay, previously detected by the detect_bias() method</i>
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## Description

correct\_bias() (1) uses either of the three additive or either of the three 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, Anderson-Darling or Cramer-von-Mises 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)
```

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create_assay	Create a new assay
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## 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 contains 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, initialized 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). It is computed by counting the number of bias models (additive or mutliplicative) which agree together.

## Examples

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

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detect_bias	<i>Detect the type of bias present in the assay</i>
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### 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)
```

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m	<i>Artificially generated HTS assay</i>
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### 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	<i>Plate 7 of raw measurements obtained by Carralot et al. 2012 (Institut Pasteur Korea)</i>
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**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 array of dimension 16 x 20 x 1.

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plot.assay	<i>Plot assay plate-wise</i>
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**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	<i>Print assay summary</i>
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**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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