Package ‘detrendr’

September 3, 2020

Type Package
Title Detrend Images
Version 0.6.9
Maintainer Rory Nolan <rorynoolan@gmail.com>
Description Detrend fluorescence microscopy image series for fluorescence fluctuation and correlation spectroscopy ('FCS' and 'FFS') analysis. This package contains functionality published in a 2016 paper <doi:10.1093/bioinformatics/btx434> but it has been extended since then with the Robin Hood algorithm and thus contains unpublished work.
License BSD_3_clause + file LICENSE
BugReports https://github.com/rorynolan/detrendr/issues
Depends R (>= 3.1)
Imports arrayhelpers (>= 1.1.0), autothresholdr (>= 1.3.3), checkmate (>= 1.9.3), doParallel, dplyr, filestrings (>= 3.1.5), foreach, ijtiff (>= 2.0.2), iterators, magrittr (>= 1.5), parallel, plyr, purrr, Rcpp (>= 1.0.1), RcppParallel (>= 5.0.0), rlang (>= 0.3.3), stringr (>= 1.4.0), tools, withr (>= 2.1.0)
Suggests abind, covr, ggplot2, glue (>= 1.3.0), graphics, gridExtra, knitr, lattice, MASS, matrixStats, mgcv, pacman, rmarkdown, spelling, testthat, tidyR
LinkingTo Rcpp (>= 1.0.1), RcppParallel (>= 5.0.0)
VignetteBuilder knitr
Encoding UTF-8
Language en-US
LazyData true
RoxygenNote 7.1.1
**System Requirements** GNU make

**NeedsCompilation** yes

**Author** Rory Nolan [aut, cre] (<https://orcid.org/0000-0002-5239-4043>),
Luis Alvarez [ctb, cph] (<https://orcid.org/0000-0003-1316-1906>),
Sergi Padilla-Parra [ctb, ths, cph]
(<https://orcid.org/0000-0002-8010-9481>)

**Repository** CRAN

**Date/Publication** 2020-09-03 05:20:03 UTC

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---

**apply_on_pillars**  
*Apply a function to each pillar of a 3-dimensional array.*

**Description**

Define a 'pillar' of a 3-dimensional array as pillar i,j off array arr being arr[i,j,]. This function applies a specified function to each pillar.

**Usage**

`apply_on_pillars(arr3d, FUN)`

**Arguments**

- `arr3d`  
  A 3-dimensional array.

- `FUN`  
  A function which takes a vector as input and, for a given input length, outputs a vector of constant length (can be 1).
**best_degree**

Find the best polynomial degree for polynomial detrending.

**Value**

If `FUN` is returning length 1 vectors, a matrix whereby `mat[i, j] = FUN(arr3d[i, j,])`. If `FUN` is returning vectors of length `l > 1`, a 3-dimensional array whereby `arr[i, j,] = FUN(arr3d[i, j,])`.

**Description**

Use Nolan’s algorithm to find the ideal polynomial degree for polynomial detrending.

**Usage**

```r
best_degree(img, parallel = FALSE, purpose = c("FCS", "FFS"))
```

**Arguments**

- `img`  
  A 4-dimensional array in the style of an `ijtiff_img` (indexed by `img[y, x, channel, frame]`) or a 3-dimensional array which is a single channel of an `ijtiff_img` (indexed by `img[y, x, frame]`).

- `parallel`  
  Would you like to use multiple cores to speed up this function? If so, set the number of cores here, or to use all available cores, use `parallel = TRUE`.

- `purpose`  
  What type of calculation do you intend to perform on the detrended image? If it is an FFS (fluorescence fluctuation spectroscopy) calculation (like number and brightness), choose ‘FFS’. If it is an FCS (fluorescence correlation spectroscopy) calculation (like cross-correlated number and brightness or autocorrelation), choose ‘FCS’. The difference is that if `purpose` is ‘FFS’, the time series is corrected for non-stationary mean and variance, whereas if `purpose` is ‘FCS’, the time series is corrected for non-stationary mean only. `purpose` is not required for Robin Hood detrending.

**Value**

If no detrend is necessary, this function returns `NA`. If a detrend is required, this function returns a natural number which is the ideal polynomial degree for polynomial detrending. If there are multiple channels, the function returns a vector, one degree parameter for each channel.

**References**

## Not run:
## These examples are not run on CRAN because they take too long.
## You can still try them for yourself.

```r
img <- ijtiff::read_tif(system.file("extdata", "bleached.tif", 
    package = "detrendr")
)
best_degree(img, parallel = 2) 
## End(Not run)
```

---

**Usage**

```r
best_l(img, parallel = FALSE, purpose = c("FCS", "FFS"))
```

### Arguments

- **img**: A 4-dimensional array in the style of an `ijtiff_img` (indexed by `img[y,x,channel,frame]`) or a 3-dimensional array which is a single channel of an `ijtiff_img` (indexed by `img[y,x,frame]`).
- **parallel**: Would you like to use multiple cores to speed up this function? If so, set the number of cores here, or to use all available cores, use `parallel = TRUE`.
- **purpose**: What type of calculation do you intend to perform on the detrended image? If it is an FFS (fluorescence fluctuation spectroscopy) calculation (like number and brightness), choose 'FFS'. If it is an FCS (fluorescence correlation spectroscopy) calculation (like cross-correlated number and brightness or autocorrelation), choose 'FCS'. The difference is that if `purpose` is 'FFS', the time series is corrected for non-stationary mean and variance, whereas if `purpose` is 'FCS', the time series is corrected for non-stationary mean only. `purpose` is not required for Robin Hood detrending.

**Value**

If no detrend is necessary, this function returns `NA`. If a detrend is required, this function returns a natural number which is the ideal length parameter for boxcar detrending. If there are multiple channels, the function returns a vector, one 1 parameter for each channel.

**Description**

Use Nolan’s algorithm to find the ideal length parameter for boxcar detrending. Boxcar detrending is also referred to as 'running average'.

**Examples**

```r
best_l(img, parallel = 2)
```

Find the best length parameter for boxcar detrending.
References


Examples

```r
## Not run:
## These examples are not run on CRAN because they take too long.
## You can still try them for yourself.
img <- ijtiff::read_tif(system.file("extdata", "bleached.tif",
package = "detrendr")
best_l(img, parallel = 2, purpose = "FFS")
## End(Not run)

---

`best_swaps()`  
*Find the best swaps parameter for Robin Hood detrending.*

Description

Use Nolan’s algorithm to find the ideal swaps parameter for Robin Hood detrending.

Usage

```r
best_swaps(img, quick = FALSE)
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>img</code></td>
<td>A 4-dimensional array in the style of an <code>ijtiff_img</code> (indexed by <code>img[y,x,channel,frame]</code>) or a 3-dimensional array which is a single channel of an <code>ijtiff_img</code> (indexed by <code>img[y,x,frame]</code>).</td>
</tr>
<tr>
<td><code>quick</code></td>
<td>If <code>FALSE</code> (the default), the swap finding routine is run several times to get a consensus for the best parameter. If <code>TRUE</code>, the swap finding routine is run only once.</td>
</tr>
</tbody>
</table>

Value

A natural number. The ideal swaps parameter for boxcar detrending. If there are multiple channels, the function returns a vector, one swaps parameter for each channel.
Examples

```r
## Not run:
## These examples are not run on CRAN because they take too long.
## You can still try them for yourself.
img <- ijtiff::read_tif(system.file("extdata", "bleached.tif",
    package = "detrendr"
))
best_swaps(img)

## End(Not run)
```

---

**best_tau**  
*R Find the best tau parameter for exponential smoothing detrending.*

**Description**

Use Nolan’s algorithm to find the ideal tau parameter for exponential smoothing detrending.

**Usage**

```r
best_tau(img, cutoff = 0.05, parallel = FALSE, purpose = c("FCS", "FFS"))
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>img</td>
<td>A 4-dimensional array in the style of an <em>ijtiff_img</em> (indexed by <code>img[y,x,channel,frame]</code>) or a 3-dimensional array which is a single channel of an <em>ijtiff_img</em> (indexed by <code>img[y,x,frame]</code>).</td>
</tr>
<tr>
<td>cutoff</td>
<td>In exponential filtering detrending, for the weighted average, every point gets a weight. This can slow down the computation massively. However, many of the weights will be approximately zero. With cutoff, we say that any point with weight less than or equal to cutoff times the maximum weight may be ignored; so with cutoff = 0.05, any weight less than 5% value of this parameter is sensible and its value should not be set to anything else without good reason.</td>
</tr>
<tr>
<td>parallel</td>
<td>Would you like to use multiple cores to speed up this function? If so, set the number of cores here, or to use all available cores, use <code>parallel = TRUE</code>.</td>
</tr>
<tr>
<td>purpose</td>
<td>What type of calculation do you intend to perform on the detrended image? If it is an FFS (fluorescence fluctuation spectroscopy) calculation (like number and brightness), choose 'FFS'. If it is an FCS (fluorescence correlation spectroscopy) calculation (like cross-correlated number and brightness or autocorrelation), choose 'FCS'. The difference is that if purpose is 'FFS', the time series is corrected for non-stationary mean and variance, whereas if purpose is 'FCS', the time series is corrected for non-stationary mean only. purpose is not required for Robin Hood detrending.</td>
</tr>
</tbody>
</table>
If no detrend is necessary, this function returns NA. If a detrend is required, this function returns a natural number which is the ideal tau parameter for exponential smoothing detrending. If there are multiple channels, the function returns a vector, one tau parameter for each channel.

References


Examples

```r
## Not run:
## These examples are not run on CRAN because they take too long.
## You can still try them for yourself.
img <- ijtiff::read_tif(system.file("extdata", "bleached.tif", 
   package = "detrendr" ))[, , 1, ]
best_tau(img, parallel = 2)
## End(Not run)
```

---

**brightness_pillars**

Get the brightness of pillars of a 3d array.

**Description**

For an ijtiff_img-style array `img` (indexed as `img[y,x,channel,frame]`), 3-dimensional array `mat3d`, pillar `xy` of channel `ch` is defined as `img[y,x,ch,]`. This function computes the brightness of each pillar.

**Usage**

```
brightness_pillars(img, parallel = FALSE)
```

**Arguments**

- `img`: A 4-dimensional array in the style of an ijtiff_img (indexed by `img[y,x,channel,frame]`) or a 3-dimensional array which is a single channel of an ijtiff_img (indexed by `img[y,x,frame]`).
- `parallel`: Would you like to use multiple cores to speed up this function? If so, set the number of cores here, or to use all available cores, use `parallel = TRUE`.

**Value**

An ijtiff_img-style array `arr` with one frame. `arr[y,x,ch,1]` is equal to `var(img[y,x,ch,]) / mean(img[y,x,ch,])`. 

Examples

```r
aaa <- array(1:16, dim = c(2, 2, 4))
brightness_pillars(aaa)
```

---

**detrend-directory**  
*Detrend all TIFF images in an entire folder.*

---

**Description**

Batch processing. Apply any of the available detrending routines to detrend all of the TIFF images in a folder, saving the detrended images as TIFF files in the same folder.

**Usage**

```r
dir_detrend_robinhood(
  folder_path = ".".,
  swaps = "auto",
  thresh = NULL,
  quick = FALSE,
  msg = TRUE
)

dir_detrend_rh(
  folder_path = ".".,
  swaps = "auto",
  thresh = NULL,
  quick = FALSE,
  msg = TRUE
)

dir_detrend_boxcar(
  folder_path = ".".,
  l,
  purpose = c("FCS", "FFS"),
  thresh = NULL,
  parallel = FALSE,
  msg = TRUE
)

dir_detrend_exp(
  folder_path = ".".,
  tau,
  purpose = c("FCS", "FFS"),
  thresh = NULL,
  parallel = FALSE,
  msg = TRUE
)
```
def detrend_directory
    folder_path = ".",
    degree,
    purpose = c("FCS", "FFS"),
    thresh = NULL,
    parallel = FALSE,
    msg = TRUE
)  

Arguments

folder_path: The path (relative or absolute) to the folder you wish to process.

swaps: The number of swaps (giving of one count from rich to poor) to perform during the Robin Hood detrending. Set this to "auto" (the default) to use Nolan’s algorithm to automatically find a suitable value for this parameter (recommended). For multi-channel images, it is possible to have a different swaps for each channel by specifying swaps as a vector or list.

thresh: The threshold or thresholding method (see autothresholdr::mean_stack_thresh()) to use on the image prior to detrending.

quick: If FALSE (the default), the swap finding routine is run several times to get a consensus for the best parameter. If TRUE, the swap finding routine is run only once.

msg: Receive messages to tell you how the processing of the directory is going? Default is yes.

l: The length parameter for boxcar detrending. The size of the sliding window will be 2 * l + 1. This must be a positive integer. Set this to "auto" to use Nolan’s algorithm to automatically find a suitable value for this parameter (recommended). For multi-channel images, it is possible to have a different l for each channel by specifying l as a vector or list.

purpose: What type of calculation do you intend to perform on the detrended image? If it is an FFS (fluorescence fluctuation spectroscopy) calculation (like number and brightness), choose 'FFS'. If it is an FCS (fluorescence correlation spectroscopy) calculation (like cross-correlated number and brightness or autocorrelation), choose 'FCS'. The difference is that if purpose is 'FFS', the time series is corrected for non-stationary mean and variance, whereas if purpose is 'FCS', the time series is corrected for non-stationary mean only. purpose is not required for Robin Hood detrending.

parallel: Would you like to use multiple cores to speed up this function? If so, set the number of cores here, or to use all available cores, use parallel = TRUE.

tau: The tau parameter for exponential filtering detrending. This must be a positive number. Set this to "auto" to use Nolan’s algorithm to automatically find a suitable value for this parameter (recommended). For multi-channel images, it is possible to have a different tau for each channel by specifying tau as a vector or list.
**detrended_img**

**degree**

The degree of the polynomial to use for the polynomial detrending. This must be a positive integer. Set this to "auto" to use Nolan’s algorithm to automatically find a suitable value for this parameter (recommended). For multi-channel images, it is possible to have a different degree for each channel by specifying degree as a vector or list.

**Details**

These functions include a thresholding option, unlike their non-batch processing counterparts which they wrap (i.e. img_detrend_boxcar, img_detrend_exp and img_detrend_polynom). This is because, when working interactively, it’s easy to threshold and then detrend, but for batch processing, it’s not so easy to efficiently do one after the other, so it’s nice to have that taken care of should you want it.

**Value**

Silently, a character vector of the paths to the detrended images.

**Examples**

```r
## Not run:
setwd(tempdir())
file.copy(
  c(
    system.file("extdata", "bleached.tif", package = "detrendr"),
    system.file("img", "2ch_ij.tif", package = "ijtiff")
  ),
  "."
)
dir_detrend_robinhood(thresh = "huang")
dir_detrend_boxcar(l = "auto", thresh = "tri", purpose = "FFS")
dir_detrend_exp(tau = "auto", thresh = "tri", purpose = "FCS")
dir_detrend_polynom(degree = "auto", thresh = "huang", purpose = "FFS")
## End(Not run)
```

---

detrended_img  

**Detrended image class.**

**Description**

A detrended_img is a 4-dimensional array of positive integers in the style of an ijtiff_img (indexed by img[y,x,channel,frame]) which is the result of a detrending routine. It has 4 attributes:

- **method** The detrending method used. This must be one of "boxcar", "exponential" or "polynomial".
- **parameter** The value of the parameter used. This will be the l, tau or degree parameter for the respective methods.
- **auto** A boolean that is TRUE if the parameter was found automatically or FALSE if it was manually selected.
purpose Either "FCS" or "FFS" to denote whether the detrending was done for the purpose of fluorescence correlation spectroscopy or fluorescence fluctuation spectroscopy calculations respectively. purpose is not required for Robin Hood detrending.

Usage

detrended_img(img, method, parameter, auto, purpose = NULL)

Arguments

- **img**: The detrended image series. A 4-dimensional array of non-negative integers in the style of an *ijiff_img*, or a 3-dimensional array of non-negative integers which represents a single channel of an *ijiff_img*-style array (indexed by `img[y,x,frame]`).
- **method**: The method used. One of "robinhood", "boxcar", "exponential" or "polynomial".
- **parameter**: A number. The detrend parameter used. One per channel.
- **auto**: Logical. Was automatic detrending used? One per channel.
- **purpose**: Either "FCS" or "FFS". Was the image detrended for the purpose of doing FCS or FFS calculations? See detrending. purpose is not required for Robin Hood detrending.

Details

Sometimes when detrending, you can get slight negative values in the detrended image. These values should really just be zero, so this constructor function sets negative values of `img` to zero.

Value

An object of class detrended_img.

---

detrending

**Detrend images.**

Description

Correct images for bleaching (or any other effect that introduces an unwanted trend) by *detrending*.

Usage

- `img_detrend_robinhood(img, swaps = "auto", quick = FALSE)`
- `img_detrend_rh(img, swaps = "auto", quick = FALSE)`
- `img_detrend_boxcar(img, l, purpose = c("FCS", "FFS"), parallel = FALSE)`
- `img_detrend_exp(img,`
```r
img_detrend_polynom(img, degree, purpose = c("FCS", "FFS"), parallel = FALSE)
```

### Arguments

**img**

A 4-dimensional array in the style of an `ijtiff_img` (indexed by `img[y,x,channel,frame]`) or a 3-dimensional array which is a single channel of an `ijtiff_img` (indexed by `img[y,x,frame]`).

**swaps**

The number of swaps (giving of one count from rich to poor) to perform during the *Robin Hood* detrending. Set this to "auto" (the default) to use Nolan's algorithm to automatically find a suitable value for this parameter (recommended). For multi-channel images, it is possible to have a different `swaps` for each channel by specifying `swaps` as a vector or list.

**quick**

If `FALSE` (the default), the swap finding routine is run several times to get a consensus for the best parameter. If `TRUE`, the swap finding routine is run only once.

**l**

The length parameter for `boxcar` detrending. The size of the sliding window will be $2 \times l + 1$. This must be a positive integer. Set this to "auto" to use Nolan's algorithm to automatically find a suitable value for this parameter (recommended). For multi-channel images, it is possible to have a different `l` for each channel by specifying `l` as a vector or list.

**purpose**

What type of calculation do you intend to perform on the detrended image? If it is an FFS (fluorescence fluctuation spectroscopy) calculation (like number and brightness), choose 'FFS'. If it is an FCS (fluorescence correlation spectroscopy) calculation (like cross-correlated number and brightness or autocorrelation), choose 'FCS'. The difference is that if `purpose` is 'FFS', the time series is corrected for non-stationary mean and variance, whereas if `purpose` is 'FCS', the time series is corrected for non-stationary mean only. `purpose` is not required for *Robin Hood* detrending.

**parallel**

Would you like to use multiple cores to speed up this function? If so, set the number of cores here, or to use all available cores, use `parallel = TRUE`.

**tau**

The `tau` parameter for `exponential filtering` detrending. This must be a positive number. Set this to "auto" to use Nolan's algorithm to automatically find a suitable value for this parameter (recommended). For multi-channel images, it is possible to have a different `tau` for each channel by specifying `tau` as a vector or list.

**cutoff**

In `exponential filtering` detrending, for the weighted average, every point gets a weight. This can slow down the computation massively. However, many of the weights will be approximately zero. With `cutoff`, we say that any point with weight less than or equal to `cutoff` times the maximum weight may be ignored; so with `cutoff = 0.05`, any weight less than 5\% value of this parameter is sensible and its value should not be set to anything else without good reason.
The degree of the polynomial to use for the polynomial detrending. This must be a positive integer. Set this to "auto" to use Nolan’s algorithm to automatically find a suitable value for this parameter (recommended). For multi-channel images, it is possible to have a different degree for each channel by specifying degree as a vector or list.

Details

There are 4 detrending methods available: Robin Hood, boxcar, exponential filtering and polynomial. Robin Hood is described in Nolan et al., 2018. The others are described in Nolan et al., 2017.

- **Robin Hood** is a method whereby counts are taken from frames with higher mean intensity and given directly to frames of lower intensity.
- **Boxcar** detrending with parameter \( l \) is a moving average detrending method using a sliding window of size \( 2l + 1 \).
- **Exponential filtering** detrending is a moving weighted average method where for parameter \( \tau \) the weights are calculated as \( \exp(-t/\tau) \) where \( t \) is the distance from the point of interest.
- **Polynomial** detrending works by fitting a polynomial line to a series of points and then correcting the series to remove the trend detailed by this polynomial fit.

Value

The detrended image, an object of class `detrended_img`.

References


Examples

```r
## Not run:
## These examples are not run on CRAN because they take too long.
## You can still try them for yourself.

img <- ijtiff::read_tif(system.file("extdata", "bleached.tif", package = "detrendr")
)
corrected <- img_detrend_rh(img)
corrected10 <- img_detrend_boxcar(img, "auto", purpose = "fcs", parallel = 2)
corrected50 <- img_detrend_boxcar(img, 50, purpose = "fcs", parallel = 2)
corrected <- img_detrend_exp(img, "auto", purpose = "ffs", parallel = 2)
corrected10 <- img_detrend_exp(img, 10, purpose = "ffs", parallel = 2)
corrected50 <- img_detrend_exp(img, 50, purpose = "ffs", parallel = 2)
corrected <- img_detrend_polynom(img, "auto", purpose = "ffs", parallel = 2)
corrected2 <- img_detrend_polynom(img, 2, purpose = "ffs", parallel = 2)
```
detrendr

**detrendr: Image detrending in R.**

**Description**

The `detrendr` package gives functions for detrending images, most often used for preprocessing in fluorescence fluctuation and correlation spectroscopy (FFS and FCS).

**References**


---

**mean_frames**

*Get the sums/means of frames in a 3-dimensional array.*

**Description**

Frame `i` of a 3-dimensional array `arr3d` is defined as `arr3d[, , i]`.

**Usage**

```r
mean_frames(arr3d, na_rm = FALSE)
sum_frames(arr3d, na_rm = FALSE)
```

**Arguments**

- `arr3d` A 3-dimensional numeric array.
- `na_rm` Do you want `NA` values to be excluded from calculations?

**Value**

A numeric vector.

**Examples**

```r
a <- array(seq_len(2^3), dim = rep(2, 3))
sum_frames(a)
mean_frames(a)
```
pillar-stats

Get the sums/means/medians/variances of pillars of an ijtiff_img-style array.

Description

For an ijtiff_img-style array `img` (indexed as `img[y,x,channel,frame]`), pillar `xy` of channel `ch` is defined as `img[y,x,ch,]`. These functions compute the mean, median and variance of each pillar for each channel.

Usage

```r
sum_pillars(img, parallel = FALSE)
mean_pillars(img, parallel = FALSE)
median_pillars(img, parallel = FALSE)
var_pillars(img, parallel = FALSE)
```

Arguments

- `img`: A 4-dimensional array in the style of an ijtiff_img (indexed by `img[y,x,channel,frame]`) or a 3-dimensional array which is a single channel of an ijtiff_img (indexed by `img[y,x,frame]`).
- `parallel`: Would you like to use multiple cores to speed up this function? If so, set the number of cores here, or to use all available cores, use `parallel = TRUE`.

Value

An ijtiff_img-style array `arr` with one frame. `arr[y,x,ch,1]` is equal to `mean(img[y,x,ch,])`, `median(img[y,x,ch,])`, or `var(img[y,x,ch,])`.

Examples

```r
aaa <- array(seq_len(2^4), dim = rep(2, 4)) # a 2-channel, 2-frame array
sum_pillars(aaa)
mean_pillars(aaa)
median_pillars(aaa)
var_pillars(aaa)
```
Randomly draw balls from boxes.

Description

Given a number of boxes with a specified number of balls in each, randomly draw a number of balls from these boxes, recording how many balls was drawn from each. An empty box cannot be drawn from.

Usage

rfromboxes(n, balls, weights = NULL)

Arguments

n  A natural number. The number of balls to draw.
balls  A vector of natural numbers. The number of balls in each box to begin with.
weights  A non-negative numeric vector the same length as balls. The relative probabilities of drawing a ball from each box. Default is each box is equally likely to be drawn from.

Value

A vector of natural numbers with the same length as balls. The number of balls drawn from each box.

See Also

rtoboxes

Examples

balls <- 1:10
rfromboxes(40, balls)
rfromboxes(40, balls, weights = c(rep(1, 9), 0))

Randomly place balls in boxes.

Description

Given a number of boxes, randomly distribute n balls into these boxes.

Usage

rtoboxes(n, boxes, weights = NULL, capacities = NULL)
Arguments

- **n**
  A natural number. The number of balls to put into the boxes.

- **boxes**
  A natural number. The number of boxes.

- **weights**
  A non-negative numeric vector. The relative probabilities of putting a ball in each box. Default is each box is equally likely.

- **capacities**
  A vector of natural numbers. The capacity of each box. Default is each box has infinite capacity.

Value

A vector of natural numbers with the same length as **boxes**. The number of balls placed in each box.

See Also

rfromboxes

Examples

```r
toboxes(30, 7)
toboxes(30, 7, capacities = c(rep(1, 3), rep(7, 4)))
toboxes(30, 7, 
  capacities = c(rep(1, 3), rep(70, 4)), 
  weights = c(rep(0.1, 6), 1) 
)
```
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