

# Package ‘imageHTS’

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**Title** Analysis of high-throughput microscopy-based screens

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**Description** imageHTS is an R package dedicated to the analysis of high-throughput microscopy-based screens. The package provides a modular and extensible framework to segment cells, extract quantitative cell features, predict cell types and browse screen data through web interfaces. Designed to operate in distributed environments, imageHTS provides a standardized access to remote data and facilitates the dissemination of high-throughput microscopy-based datasets.

**License** LGPL-2.1

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## R topics documented:

collectCellFeatures . . . . .	2
countObjects . . . . .	3
extractFeatures . . . . .	4
fileHTS . . . . .	5
getImageConf . . . . .	7

getUnames . . . . .	8
getWellFeatures . . . . .	9
highlightSegmentation . . . . .	10
imageHTS . . . . .	11
installCellPicker . . . . .	13
makeCellHTS . . . . .	14
parseDCF . . . . .	15
parseImageConf . . . . .	16
popCellPicker . . . . .	18
prw2uname . . . . .	19
readLearnTS . . . . .	20
segmentATH . . . . .	22
segmentWells . . . . .	23
segmentYeastBF . . . . .	24
summarizeWells . . . . .	26
zprime . . . . .	27

<b>Index</b>	<b>30</b>
--------------	-----------

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collectCellFeatures	<i>Collect cell features.</i>
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---

## Description

Collect cell features from a given set of cells.

## Usage

```
collectCellFeatures(x, uname, spot=NULL, id=NULL, access='cache')
```

## Arguments

x	An imageHTS object.
uname	a character vector, containing the well names from where to collect the cell features. See getUnames for details.
spot	An optional numeric vector indicating the spots from where to collect the cell features. If missing, all spots are considered. The length of the vector must be the same as uname.
id	An optional numeric vector indicating the cell ids. If missing, all cells are considered. The length of the vector must be the same as uname.
access	A character string indicating how to access the data. Valid values are local, server and cache, the default. See fileHTS for details.

## Details

Contrary to readHTS, collectCellFeatures collects cell features through multiple wells. Output data frame contains the columns uname, spot and id.

**Value**

A data frame containing the cell features.

**Author(s)**

Gregoire Pau, <gregoire.pau@embl.de>, 2010

**See Also**

[extractFeatures](#)

**Examples**

```
## see extractFeatures for an example of collectCellFeatures
## example(extractFeatures)
```

---

countObjects	<i>Count the number of objects in a segmented image</i>
--------------	---

---

**Description**

Count the number of objects in a segmented image.

**Usage**

```
countObjects(cseg)
```

**Arguments**

cseg            An image containing the objects.

**Value**

An integer indicating the number of objects in the cell mask.

**Author(s)**

Gregoire Pau, <gregoire.pau@embl.de>, 2010

**See Also**

[segmentWells](#)

## Examples

```
## initialize imageHTS object using the local submorph screen
local = tempdir()
server = system.file('submorph', package='imageHTS')
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)
x = configure(x, 'conf/description.txt', 'conf/plateconf.txt', 'conf/screenlog.txt')

## segment one well
uname = getUnames(x, content='rluc')[1]
z = segmentWells(x, uname=uname, segmentationPar='conf/segmentationpar.txt', writeData=FALSE)
n = countObjects(z$cseg)
cat('number of cells=', n, '\n')
```

---

extractFeatures	<i>Extract features from segmented images.</i>
-----------------	--

---

## Description

Extract features from segmented images.

## Usage

```
extractFeatures(x, uname, featurePar, access='cache')
```

## Arguments

x	An imageHTS object.
uname	a character vector, containing the well names to segment. See getUnames for details.
featurePar	a character string, indicating the filename containing the feature extraction parameters.
access	A character string indicating how to access the data. Valid values are local, server and cache, the default. See fileHTS for details.

## Details

extractFeatures reads the DCF segmentation parameters file pointed by featurePar. The file must contain the field extractFeatures.method that indicates which core feature extraction function to use. The function takes two arguments: cal, the calibrated image to extract the features from, and seg, a list of two images, cseg and nseg, which contains the cell and nucleus segmentation masks, respectively. The function returns a matrix of features. See getCellFtrsATH for example.

For each well, extractFeatures writes a ftrs segmentation data file that contains the cell features. Use readHTS or collectCellFeatures to get the cell features after extraction.

**Value**

None.

**Author(s)**

Gregoire Pau, <gregoire.pau@embl.de>, 2010

**See Also**

[getCellFtrsATH](#), [fileHTS](#), [collectCellFeatures](#)

**Examples**

```
## initialize imageHTS object using the local submorph screen
local = tempdir()
server = system.file('submorph', package='imageHTS')
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)
x = configure(x, 'conf/description.txt', 'conf/plateconf.txt', 'conf/screenlog.txt')

## segment one well
uname = getUnames(x, content='rluc')[1]
segmentWells(x, uname=uname, segmentationPar='conf/segmentationpar.txt')

## extract features from the well
extractFeatures(x, uname=uname, 'conf/featurepar.txt')

## read the feature file using readHTS
y = readHTS(x, type='ftrs', uname=uname)

## get features using collectCellFeatures
y = collectCellFeatures(x, uname=uname)
```

---

fileHTS

*Get access to screen data files*

---

**Description**

fileHTS builds the path or URL pointing to a screen data file. readHTS reads the file pointed by fileHTS.

**Usage**

```
fileHTS(x, type, ..., createPath=FALSE, access='cache')
readHTS(x, type, ..., access='cache', format=NULL)
```

### Arguments

x	An imageHTS object.
type	A character vector, indicating the requested file type. See Details.
...	Optional arguments. See Details.
createPath	A logical value specifying if the directories along the path should be created. Default is FALSE.
access	A character string indicating how to access the data. Valid values are cache (the default), local and server. See Details.
format	An optional character string indicating the format of the designated file. Valid formats are tab, a tab-separated file with headers; rda, a R data file; dcf, an imageHTS DCF configuration file.

### Details

In imageHTS, all screen data files are accessed through the function fileHTS. Screen data can be accessed at two locations: the localPath, which is local writable directory, and serverURL, which is a server URL. localPath and serverURL are set during the instantiation of the imageHTS object with parseImageConf.

If access equals local, fileHTS returns a local path pointing to the requested file. If server, fileHTS returns a server URL pointing to the requested file. If cache (the default), fileHTS tests if the file is present at the local path. If not, fileHTS tries to download the file from the server and copies it in the local path. fileHTS always returns a local path if access equals cache.

A file is designated by its type and optional arguments. Known file types are:

- file: general-purpose file. The character string filename indicates its path, relative to the project directory. File format is unspecified.
- source: source image, designated by the character string uname and the numeric channel. File format is unspecified.
- cal: calibrated image, designated by the character string uname. The file is a R data file which contains an EBImage image object.
- seg: segmentation data, designated by the character string uname. The file is a R data file which contains a list of two EBImage image objects: cseg containing the cell mask and nseg the nucleus mask.
- ftrs: cell features, designated by the character string uname. The file is a tab-separated file which contains the cell features.
- clabels: cell labels, designated by the character string uname. The file is a tab-separated file which contains the cell labels.
- viewfull: calibrated JPEG image, designated by the character string uname. The file is a JPEG image.
- viewunmonted: spot-untiled calibrated JPEG image, designated by the character string uname and the spot number spot. The file is a JPEG image.
- viewseg: segmented JPEG image, designated by the character string uname. The file is a JPEG image.

- viewthumb: thumbnail JPEG image, designated by the character string uname. The file is a JPEG image.

readHTS reads and returns the corresponding file. format must be specified if type is file or source.

### Value

fileHTS returns a character vector containing the path or URL of the requested file. readHTS returns the content of the requested file.

### Author(s)

Gregoire Pau, <gregoire.pau@embl.de>, 2010

### See Also

[parseImageConf](#), [getUnames](#)

### Examples

```
## initialize imageHTS object using the local submorph screen
local = tempdir()
server = system.file('submorph', package='imageHTS')
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)

## fileHTS and readHTS examples
fileHTS(x, 'file', filename='conf/imageconf.txt')
fileHTS(x, 'source', uname='001-01-C05', channel=1)
readHTS(x, 'file', filename='conf/featurepar.txt', format='dcf')

## initialize imageHTS object using the remote kimorph screen
local = tempdir()
server = 'http://www.ebi.ac.uk/huber-srv/cellmorph/kimorph/'
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)

## get cell features for well '002-02-D06'
f = readHTS(x, 'ftrs', uname='002-02-D06')
cat('nb cells=', nrow(f), '\n')
```

---

getImageConf

*Get the imageHTS configuration*

---

### Description

Get the imageHTS configuration from an imageHTS object.

### Usage

```
getImageConf(x)
```

**Arguments**

x                    An imageHTS object.

**Details**

See the documentation of [parseImageConf](#) for details.

**Value**

A list containing the imageHTS configuration attributes.

**Author(s)**

Gregoire Pau, <gregoire.pau@embl.de>, 2010

**See Also**

[parseImageConf](#)

**Examples**

```
local = tempdir()
server = system.file('submorph', package='imageHTS')
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)
getImageConf(x)
```

---

getUnames

*Get well unique names*

---

**Description**

Build valid well unique names, according to the screen layout and to input filter arguments. Each well in the screen has an unique name, based on its plate, replicate, row and column indices.

**Usage**

```
getUnames(x, plate, replicate, row, col, content)
```

**Arguments**

x                    An imageHTS object.

plate                An optional numeric vector indicating the plate indices to keep.

replicate           An optional numeric vector indicating the replicate indices to keep.

row                  An optional numeric vector indicating the row indices to keep.

col                  An optional numeric vector indicating the column indices to keep.

content             An optional character string indicating the well content type to keep.



**Details**

Well content types are defined in the `plateconf.txt` configuration file. See `getWellFeatures` for details.

Well unique names can be also built and manipulated using `prw2uname` and `uname2prw`.

**Value**

A character vector containing a set of well unique names that are compatible with the input filter arguments.

**Author(s)**

Gregoire Pau, <gregoire.pau@embl.de>, 2010

**See Also**

[prw2uname](#), [uname2prw](#), [getWellFeatures](#)

**Examples**

```
## initialize imageHTS object using the local submorph screen
local = tempdir()
server = system.file('submorph', package='imageHTS')
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)
x = configure(x, 'conf/description.txt', 'conf/plateconf.txt',
'conf/screenlog.txt')

getUnames(x, col=2)
getUnames(x, replicate=1, col=3)
getUnames(x, content='sample') ## get 'sample' wells
setdiff(getUnames(x), getUnames(x, content='empty')) ## get non-empty wells
```

---

getWellFeatures

*Get well metadata, features and annotation information*

---

**Description**

Get well metadata, features and annotation information.

**Usage**

```
getWellFeatures(x, uname, feature=TRUE)
```

**Arguments**

x	An imageHTS object.
uname	a character vector, containing well names. See <code>getUnames</code> for details.
feature	A character vectors containing the requested features. Default is TRUE, returning all well features.

**Details**

getWellFeatures return fData, the well features loaded during the configure and annotate steps. Features include: controlStatus, the well content status derived from \plateconf.txt\.

**Value**

Returns a data frame containing well features.

**Author(s)**

Gregoire Pau, <gregoire.pau@embl.de>, 2010

**See Also**

[fData](#), [configure](#), [annotate](#)

**Examples**

```
## initialize imageHTS object using the local submorph screen
local = tempdir()
server = system.file('submorph', package='imageHTS')
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)
x = configure(x, 'conf/description.txt', 'conf/plateconf.txt', 'conf/screenlog.txt')
x = annotate(x, 'conf/annotation.txt')

## select non-empty wells
unames = setdiff(getUnames(x), getUnames(x, content='empty'))
getWellFeatures(x, unames)
```

---

highlightSegmentation *Highlight segmented objects in an image*

---

**Description**

Highlight segmented objects in an image.

**Usage**

```
highlightSegmentation(cal, nseg=NULL, cseg=NULL, thick=FALSE, opac=1, col=c('#ffff00', '#ff00ff'), b
```

**Arguments**

cal	An EBImage Image object containing the original image.
nseg	An optional EBImage Image object containing the nucleus mask.
cseg	An optional EBImage Image object containing the cell mask.
thick	A logical indicating whether to use thick borders (useful for print). Default is FALSE.

opac	A numeric of the opacity value for drawing object contours; can be either a single numeric value or a numeric vector containing two opacity values, the first one for nuclei and the second one for cell bodies. Opacity ranges from 0 to 1, with 0 being fully transparent and 1 fully opaque
col	A character vector of two R colors for drawing contours of nuclei and cell bodies. By default, nuclei are highlighted in yellow and cells are highlighted in magenta.
border	A logical indicating whether contours should be closed at borders or not. Default is FALSE.
toRGB	A logical indicating whether Grayscale images should be promoted to Color ones or not. Default is TRUE.

### Details

Highlights nuclei and cells by drawing contours of their boundaries. The colors, opacity, and border thickness can be customized via the `col`, `opacity`, and `thick` arguments, respectively.

### Value

An `EImage` image containing the annotated image.

### Author(s)

Gregoire Pau, <gregoire.pau@embl.de>, 2010

### See Also

[segmentWells](#)

### Examples

```
## see segmentWells for an example of highlightSegmentation
## example(segmentWells)
```

### Description

imageHTS is an R package dedicated to the analysis of high-throughput microscopy-based screens. The package provides a modular and extensible framework to segment cells, extract quantitative cell features, predict cell types and browse screen data through web interfaces. Designed to operate in distributed environments, imageHTS provides a standardized access to remote screen data, facilitating the dissemination of high-throughput microscopy-based screens.

## Package content

The following function instantiates the imageHTS object.

- `parseImageConf`: instantiate an imageHTS object from a local or remote screen data repository

The following functions process, segment, quantify, summarize the well images.

- `segmentWells`: segment cells in well images
- `extractFeatures`: extract cell features from segmented images
- `readLearnTS`: train a cell classifier
- `predictCellLabels`: predict cell labels
- `summarizeWells`: summarize cell populations

The following functions provides means to display and inspect the screen data.

- `installWebQuery`: install the webQuery module
- `popWebQuery`: pop the webQuery module
- `installCellPicker`: install the cellPicker module
- `popCellPicker`: pop the cellPicker module
- `segmentATH`: segment cells stained for DNA, actin and tubulin
- `getCellFtrsATH`: extract features from cells stained for DNA, actin and tubulin

The following functions give access to the screen data.

- `fileHTS`: build the path to a screen data file
- `readHTS`: read a screen data file
- `parseDCF`: read a DCF configuration file
- `collectCellFeatures`: collect cell features
- `getWellFeatures`: get well metadata, features and annotation information

The following manipulate well unique names.

- `getUnames`: get well unique names
- `prw2uname`: convert a (plate, replicate, well) data frame in well unique names
- `uname2prw`: convert well unique names in a (plate, replicate, well) data frame
- `rowcol2well`: convert a (row, col) data frame in well names
- `well2rowcol`: convert well names in a (row, col) data frame
- `well2wellid`: convert well coordinates in numerical well identifiers

Miscellaneous functions.

- `zprime`: compute the  $Z'$ -factor quality score
- `highlightSegmentation`: highlight segmented objects in an image
- `countObjects`: count the number of objects in a segmented image
- `getImageConf`: get the imageHTS configuration

## Authors

Gregoire Pau, <gregoire.pau@embl.de>, 2010

---

installCellPicker	<i>Set up imageHTS web modules</i>
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---

### Description

installCellPicker and installWebQuery install the cellPicker and webQuery modules in the local project directory.

cellPicker is a web application that allows the interactive selection/annotation of cells within images using a point-and-click web interface.

webQuery is a web application that allows to query information from the screen by well and well annotation. The webQuery module requires a web server and PHP to be installed.

### Usage

```
installCellPicker(x)
installWebQuery(x)
```

### Arguments

x                    An imageHTS object.

### Details

After installation, the cellPicker module can be used with the function popCellPicker.

x must be annotated using annotate before using installWebQuery. After installation, the webQuery module can be used with the function popWebQuery.

### Value

None.

### Author(s)

Gregoire Pau, <gregoire.pau@embl.de>, 2010

### See Also

[popCellPicker](#), [popWebQuery](#)

### Examples

```
## initialize imageHTS object using the local submorph screen
local = tempdir()
server = system.file('submorph', package='imageHTS')
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)
x = annotate(x, 'conf/annotation.txt')
```

```
installCellPicker(x)  
installWebQuery(x)
```

---

**makeCellHTS***Segmentation of yeast cells and ring-shaped objects.*

---

### Description

makeCellHTS creates a cellHTS2 object.

### Usage

```
makeCellHTS(x, profiles, measurementNames, name)
```

### Arguments

x	An imageHTS object.
profiles	A data frame containing the phenotypic profiles. See Details.
measurementNames	An optional character vector containing the measurement names. If missing, column names of profiles are used.
name	An optional character string containing the name of the assay.

### Details

profiles is a data frame containing the phenotypic profiles, usually returned by summarizeWells or readHTS. Since cellHTS2 cannot handle large report, the dimension of the profiles must be lower than 10. This is usually done by subsetting columns or by dimension reduction.

### Value

Returns a cellHTS2 object.

### Author(s)

Gregoire Pau, <gregoire.pau@embl.de>, 2010

### See Also

[summarizeWells](#), [installWebQuery](#)

**Examples**

```

## Not run:
## initialize kimorph object
localPath = file.path(tempdir(), 'kimorph')
serverURL = 'http://www.ebi.ac.uk/huber-srv/cellmorph/kimorph/'
x = parseImageConf('conf/imageconf.txt', localPath=localPath, serverURL=serverURL)
x = configure(x, 'conf/description.txt', 'conf/plateconf.txt', 'conf/screenlog.txt')
x = annotate(x, 'conf/annotation.txt')

## get profiles
profiles = readHTS(x, type='file', filename='data/profiles.tab', format='tab')

## prepare cellHTS2 report
ft = c('med.c.t.m.int', 'med.c.g.ss', 'med.c.g.ec', 'med.n.h.m.int', 'med.c.a.m.int')
measurementNames = c('tubulin intensity', 'cell size', 'cell eccentricity', 'dna intensity', 'actin intensity')
y = makeCellHTS(x, profiles[,c('uname', 'ft')], measurementNames=measurementNames, name='kimorph')
pathConf = file.path(localPath, 'conf')
y = configure(y, 'description.txt', 'plateconf.txt', 'screenlog.txt', path=pathConf)
y = annotate(y, 'annotation.txt', path=pathConf)
yn = normalizePlates(y, scale='multiplicative', log=FALSE,
method='median', varianceAdjust='none')

## write cellHTS2 report
se = getSettings()
se$plateList$intensities$include = TRUE
setSettings(se)
writeReport(raw=y, normalized=yn, outdir='report-cellHTS2', force=TRUE)

## End(Not run)

```

---

parseDCF

*Parse a DCF file*

---

**Description**

Parse a DCF file.

**Usage**

```
parseDCF(filename)
```

**Arguments**

filename      A character string containing the path to a DCF file.

**Details**

The DCF format is a simple text format where each line is a field of the form `'a: a_0, a_1, ..., a_n'`: `a` is the field name and `ak` the `k`-th value of `a`. Field name is separated from values by a colon `':'`. Field values are separated from each other by a comma `','`.

`readHTS` with format `dcf` is a higher-level function that parses a specific DCF file from a given `imageHTS` project.

**Value**

A list of character vector, containing the DCF read fields.

**Author(s)**

Gregoire Pau, <gregoire.pau@embl.de>, 2010

**See Also**

[readHTS](#)

**Examples**

```
imageconf = system.file('submorph/conf/imageconf.txt', package='imageHTS')
parseDCF(imageconf)
```

---

<code>parseImageConf</code>	<i>Instantiate an imageHTS object</i>
-----------------------------	---------------------------------------

---

**Description**

Instantiate an `imageHTS` object from a local or remote screen data repository.

**Usage**

```
parseImageConf(filename, localPath='myscreen', serverURL, access='cache')
```

**Arguments**

<code>filename</code>	A character string containing the name of the <code>imageHTS</code> configuration file. See <a href="#">Details</a> .
<code>localPath</code>	A character string indicating the path to the project directory that contains (or will contain) the screen data. The directory must be writable and will be created if missing. All intermediate files created by <code>imageHTS</code> will be stored in this directory. Default is <code>myscreen</code> .
<code>serverURL</code>	An optional character string indicating the URL or path to the server from where to download the data, if not available in the local path.
<code>access</code>	A character string indicating how to access the data. Valid values are <code>cache</code> (the default), <code>local</code> and <code>server</code> . See <a href="#">fileHTS</a> for details.



## Details

parseImageConf gets access to the configuration file depending on the value of the access argument. If local, the file is loaded from the local path; if server, from the server and if cache parseImageConf tries to first load the file from the local path, and if not present, downloads it from the server. This dual repository feature is useful when screen images are stored in a different location from where they are analysed. See fileHTS for details.

The imageHTS configuration file is a DCF file which contains the following fields:

- AssayName: a character string containing the name of the assay
- SourceFilenamePattern: a character string containing the source image pattern path, relative to the local path. Special fields: {plate}, {replicate}, {row}, {col} and {channel} will be replaced by elements of the corresponding fields PlateNames, ReplicateNames, RowNames, ColNames and ChannelNames.
- PlateNames: a comma-separated character vector, containing the plate names, to be replaced in the field {plate} of SourceFilenamePattern.
- ReplicateNames: same as PlateNames for the field {replicate}.
- RowNames: same as PlateNames for the field {row}.
- ColNames: same as PlateNames for the field {col}.
- ChannelNames: same as PlateNames for the field {channel}.
- Montage: an optional comma-separated vector of two integers. If source images contain assembled different spot images of the well, this vector contains the dimension of the montage.

Use the command getImageConf to retrieve the configuration file from an imageHTS object.

## Value

An imageHTS object.

## Author(s)

Gregoire Pau, <gregoire.pau@embl.de>, 2010

## See Also

[imageHTS](#), [fileHTS](#), [configure](#), [getImageConf](#)

## Examples

```
local = tempdir()
server = system.file('submorph', package='imageHTS')
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)
getImageConf(x)
```

---

`popCellPicker`*Pop up imageHTS web modules*

---

**Description**

Pop up the imageHTS web modules cellPicker and webQuery, using the web browser.

**Usage**

```
popCellPicker(x, uname, spot, id.highlight, access='server', browse=TRUE)
popWebQuery(x, access='server', browse=TRUE)
```

**Arguments**

<code>x</code>	An imageHTS object.
<code>uname</code>	A character vector, containing the well names to annotate. See <code>getUnames</code> for details.
<code>spot</code>	An optional numeric vector, containing the spot indexes of the wells to annotate. If missing, only the first spot is used.
<code>id.highlight</code>	An optional numeric vector, containing the object indexes to highlight. If missing, no object is highlighted.
<code>access</code>	A character string indicating how to access the data. Valid values are <code>local</code> , <code>cache</code> and <code>server</code> , the default. See <code>fileHTS</code> for details.
<code>browse</code>	A logical indicating whether the web browser should be loaded. Default is <code>TRUE</code> .

**Details**

`cellPicker` must be installed using `installCellPicker` before using `popCellPicker` on the local project directory. If present, the numeric vector `spot` must have the same length as `uname`.

`webQuery` must be installed using `installWebQuery` before using `popWebQuery` on the local project directory.

**Value**

A character string containing the URL to access the cellPicker or the webQuery web module.

**Author(s)**

Gregoire Pau, <gregoire.pau@embl.de>, 2010

**See Also**

[installCellPicker](#), [installWebQuery](#), [getUnames](#)

**Examples**

```
## initialize imageHTS object using the remote kimorph screen
local = tempdir()
server = 'http://www.ebi.ac.uk/huber-srv/cellmorph/kimorph/'
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)

if (interactive()) {
  popCellPicker(x, uname=c('002-02-A11', '001-01-C17'))
  popWebQuery(x)
}
```

prw2uname

*Convert and parse well unique names***Description**

Functions to convert and parse well unique names.

**Usage**

```
prw2uname(plate, replicate, row, col, well)
uname2prw(uname)
rowcol2well(row, col)
well2rowcol(well)
well2wellid(row, col, direction='row', dim)
```

**Arguments**

plate	An numeric vector of plate indices or a list containing the numeric vectors plate, replicate, row and col.
replicate	A numeric vector of replicate indices.
row	A numeric vector of row indices.
col	A numeric vector of column indices
well	A character vector of well names.
uname	A character vector of well unique names.
direction	A character string containing the direction of the mapping. Valid values are row and col. Default is row, where the well identifier 2 points is mapped to well (1, 2).
dim	A numeric vector of length two, containing the dimensions (number of rows, number of columns) of a plate.

**Details**

In prw2uname, wells can be specified using the arguments row and col or using the argument well.

**Value**

prw2uname returns a character vector of well unique names. unname2prw returns a data frame containing the columns plate, replicate, row and col. rowcol2well returns a character vector of well names. well2rowcol returns a data.frame containing the numeric vectors row and col. well2wellid returns a numeric vector containing the well identifiers.

**Author(s)**

Gregoire Pau, <gregoire.pau@embl.de>, 2010

**See Also**

[getWellFeatures](#)

**Examples**

```
## prw2uname and unname2prw
u = prw2uname(plate=1:2, replicate=1, row=2, col=3:4)
print(u)
prw = unname2prw(u)
print(prw)
prw2uname(prw)

## rowcol2well and well2rowcol
w = rowcol2well(row=1:3, col=5:7)
print(w)
rc = well2rowcol(w)
print(rc)
```

---

readLearnTS

*Learn, classify and predict cell labels.*

---

**Description**

readLearnTS trains an SVM classifier using cell features and a training cell set. predictCellLabels predicts cell labels.

**Usage**

```
readLearnTS(x, featurePar, trainingSet, access='cache', cost, gamma)
predictCellLabels(x, unname, access='cache')
```

**Arguments**

x	An imageHTS object.
unname	A character vector, containing the well names to segment. See getUnames for details.
featurePar	A character string, indicating the filename containing the feature parameters.

trainingSet	A character string, indicating the filename containing the training cell set. See Details.
access	A character string indicating how to access the data. Valid values are local, server and cache, the default. See fileHTS for details.
cost	An optional numeric vector containing the SVM costs to be explored during the cross-validation parameter grid-search. Default is $c(0.1, 1, 10, 20)$ .
gamma	An optional numeric vector containing the radial kernel gamma parameters to be explored during the cross-validation parameter grid-search. Default is $c(0.0001, 0.001, 0.01, 0.1)$ .

## Details

readLearnTS trains an SVM classifier using cell features and a training cell set. Features enumerated in the `remove.classification.features` field of the feature parameters are not considered for classification. The training set, pointed by `trainingSet`, is a tab-separated file containing the rows `uname`, `spot`, `id` and `label`. Each row designates a cell. This file is constructed by using the output of the `cellPicker` module, see `popCellPicker`. After completion, `readLearnTS` writes the a RDA file `\data/classifier.rda` in the local project directory. This file contains the list returned by `readLearnTS`.

`predictCellLabels` uses the trained classifier located in the file `\data/classifier.rda` and cell features to predict cell labels of wells indicated by `uname`. For each well, the function writes the file `clabels`, which contains the predicted cell labels.

If present, `popCellPicker` shows the predicted cell labels. Several iterations of `readLearnTS`, `predictCellLabels` and `popCellPicker` calls are useful to build an efficient cell classifier.

## Value

Returns an invisible list which contains: `classifier`, the trained classifier obtained by `tune.svm` and `cft`, the features that were used to train the classifier.

## Author(s)

Gregoire Pau, <gregoire.pau@embl.de>, 2010

## See Also

[popCellPicker](#)

## Examples

```
## see vignette for details
```

---

segmentATH	<i>Segmentation and quantification of cells stained for DNA, actin and tubulin.</i>
------------	---

---

## Description

segmentATH and getCellFtrsATH are segmentation and feature extraction functions designed for cell images stained for DNA, actin and tubulin.

## Usage

```
segmentATH(x, uname, p, access)
getCellFtrsATH(cal, seg)
```

## Arguments

x	An imageHTS object.
uname	A character string, containing the well name to segment.
p	A list of character vectors, containing the segmentation parameters. This is the output of parseDCF, given an input segmentation configuration file.
access	A character string indicating how to access the data. Valid values are local, server and cache, the default. See fileHTS for details.
cal	An EImage image object containing the calibrated image.
seg	A list of two EImage image objects: cseg, the cell segmentation mask and nseg, the nucleus segmentation mask.

## Details

segmentATH is a segmentation function that can be specified in the seg.method field of a segmentation configuration file, called by the higher-level function segmentWells.

getCellFtrsATH is a feature extraction function that can be specified in the extractfeatures.method field of a feature configuration file, called by the higher-level function extractFeatures.

## Value

segmentATH returns a list containing three EImage images: cal, the calibrated image; nseg, the nucleus mask and cseg, the cell mask.

getCellFtrsATH returns a data frame containing the cell features.

## Author(s)

Gregoire Pau, <gregoire.pau@embl.de>, 2010

## See Also

[parseDCF](#), [segmentWells](#), [extractFeatures](#)

**Examples**

```
## see segmentWells and extractFeatures
```

---

segmentWells	<i>Segment cells in well images</i>
--------------	-------------------------------------

---

**Description**

Segment cells in well images.

**Usage**

```
segmentWells(x, unname, segmentationPar, access='cache', writeData=TRUE)
```

**Arguments**

x	An imageHTS object.
unname	A character vector, containing the well names to segment. See getUnames for details.
segmentationPar	A character string, indicating the filename containing the segmentation parameters.
access	A character string indicating how to access the data. Valid values are local, server and cache, the default. See fileHTS for details.
writeData	A boolean indicating whether the segmentation data should be written to the project directory. Default is TRUE.

**Details**

segmentWells reads the DCF segmentation parameters file pointed by segmentationPar. The file must contain the core segmentation function name indicated in the seg.method field. For each well indicated by unname, segmentWells calls the core segmentation function which returns a list containing a list of three EBImage images: cal, the calibrated image; nseg, the nucleus mask and cseg, the cell mask. See segmentATH for an example of a core segmentation function.

If writeData is TRUE, segmentWells writes for each well indicated by unname: the calibrated image data cal, the segmentation data seg, a calibrated JPEG image viewfull, untiled JPEG images viewunmonted, a calibrated JPEG image with segmentation annotation viewseg, a thumbnail JPEG image viewthumb and Javascript segmentation contour information contour. See fileHTS for details about these files.

**Value**

If unname is of length 1, returns an invisible list containing: cal, the calibrated image; nseg, the nucleus mask and cseg, the cell mask.

**Author(s)**

Gregoire Pau, <gregoire.pau@embl.de>, 2010

**See Also**

[segmentATH](#), [getUnames](#), [fileHTS](#)

**Examples**

```
## initialize imageHTS object using the local submorph screen
local = tempdir()
server = system.file('submorph', package='imageHTS')
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)
x = configure(x, 'conf/description.txt', 'conf/plateconf.txt', 'conf/screenlog.txt')

## segment one well
uname = getUnames(x, content='rluc')[1]
z = segmentWells(x, uname=uname, segmentationPar='conf/segmentationpar.txt', writeData=FALSE)
if (interactive()) {
  seg = highlightSegmentation(z$cal, z$nseg, z$cseg)
  display(seg)
}
```

---

segmentYeastBF

*Segmentation of yeast cells and ring-shaped objects.*


---

**Description**

segmentYeastBF segments yeast cells from bright field microscopy images. segmentRing segments ring-shape objects in images.

**Usage**

```
segmentYeastBF(x, uname, p, access)
segmentRing(a, p)
```

**Arguments**

x	An imageHTS object.
uname	A character string, containing the well name to segment.
p	A list of character vectors, containing the segmentation parameters. This is the output of parseDCF, given an input segmentation configuration file. See details.
access	A character string indicating how to access the data. Valid values are local, server and cache, the default. See fileHTS for details.
a	An EBImage image object or a matrix containing the image to segment.



## Details

segmentYeastBF is a high-level segmentation function that can be specified in the `seg.method` field of a segmentation configuration file, called by the higher-level function `segmentWells`.

`segmentRing` is used by `segmentYeastBF` and segments an image containing ring-shaped objects. The list of parameters `p` should contain:

- `edge.threshold`: a threshold parameter giving the cell edges
- `max.membrane.thickness`: the maximum membrane thickness, in pixels
- `crown.thickness`: the membrane thickness, in pixels
- `crown.steps`: a vector of 3 values, containing the minimum cell diameter, the maximum cell diameter, and the step between all possible diameters
- `locmin.threshold.width`: the adaptive threshold window width to compute the local minima, to call cell centers
- `locmin.threshold.offset`: the adaptive threshold window offset
- `locmin.erode.size`: the size of the erode parameter cleaning up the local minima map
- `cell.max.overlap`: the maximum cell overlap size, in pixels
- `nucleus.radius.offset`: the nucleus radius negative offset
- `cell.radius.offset`: the cell radius negative offset

## Value

`segmentYeastBF` returns a list containing three `EImage` images: `cal`, the calibrated image; `nseg`, the nucleus mask and `cseg`, the cell mask.

`segmentRing` returns a list containing two `EImage` images: `nseg`, the nucleus mask and `cseg`, the cell mask.

## Author(s)

Gregoire Pau, <gregoire.pau@embl.de>, 2010

## See Also

[segmentWells](#), [segmentATH](#)

## Examples

```
filename = system.file('yeast.jpeg', package='imageHTS')
a = readImage(filename)
if (interactive()) display(a)
p = list(edge.threshold=0.05, max.membrane.thickness=5, crown.thickness=8,
        crown.steps=c(31, 61, 4), locmin.threshold.width=9, locmin.threshold.offset=0.15,
        locmin.erode.size=3, cell.max.overlap=2, nucleus.radius.offset=10,
        cell.radius.offset=4)
seg = segmentRing(a, p)
hseg = highlightSegmentation(EImage::channel(a, 'rgb'), cseg=seg$cseg, thick=TRUE)
if (interactive()) display(hseg)
```

---

summarizeWells	<i>Summarize cell features</i>
----------------	--------------------------------

---

### Description

Compute phenotypic profiles by summarizing cell population features.

### Usage

```
summarizeWells(x, uname, featurePar, profileFilename="data/profiles.tab", access='cache')
```

### Arguments

x	An imageHTS object.
uname	A character vector, containing the well names to summarize. See <code>getUnames</code> for details.
featurePar	A character string, indicating the filename containing the feature extraction parameters.
profileFilename	A character string, indicating the output filename to store the phenotypic profiles.
access	A character string indicating how to access the data. Valid values are <code>local</code> , <code>server</code> and <code>cache</code> , the default. See <code>fileHTS</code> for details.

### Details

`summarizeWells` computes for each well, summary statistics about cell features. Currently, cell number `n` and median cell feature `med.*` (for each feature) are computed.

Moreover, if the DCF segmentation parameters file pointed by `featurePar` includes the field `cell.classes`, containing a list of comma-separated cell classes, cell classes ratio are computed and included in the phenotypic profiles.

`summarizeWells` creates the file `data/profiles.tab` which contains the phenotypic profiles. Use `readHTS` to read this file.

### Value

A data frame, containing the phenotypic profiles.

### Author(s)

Gregoire Pau, <gregoire.pau@embl.de>, 2010

### See Also

[extractFeatures](#), [readHTS](#)

## Examples

```
## Not run:
## initialize imageHTS object using the local submorph screen
local = tempdir()
server = system.file('submorph', package='imageHTS')
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)
x = configure(x, 'conf/description.txt', 'conf/plateconf.txt', 'conf/screenlog.txt')

## segment non-empty wells
unames = setdiff(getUnames(x), getUnames(x, content='empty'))
segmentWells(x, unname=unames, segmentationPar='conf/segmentationpar.txt')

## extract features
extractFeatures(x, unname=unames, 'conf/featurepar.txt')

## cell classification
readLearnTS(x, 'conf/featurepar.txt', 'conf/trainingset.txt')
predictCellLabels(x, unames)

## summarize features
summarizeWells(x, unames, 'conf/featurepar.txt')

## get profiles
profiles = readHTS(x, type='file', filename='data/profiles.tab', format='tab')

## End(Not run)
```

---

zprime

*Compute the Z'-factor quality score*

---

## Description

Compute the Z'-factor quality score.

## Usage

```
zprime(a, b, method=c('mahalanobis', 'robust', 'fixsd', 'original'))
```

## Arguments

a, b	Matrices of control features.
method	a character vector, indicating which method should be used to compute the Z'-factor. Default is mahalanobis. See Details.

## Details

The Z'-factor is a popular metric measuring the separation of control features in high-throughput screens. The original paper describing the Z'-factor is Zhang, 1999, J Biomol Screen.

Several univariate Z'-factor scores exist. The original Z'-factor from Zhang, 1999 is computed by  $Z' = 1 - 3 \cdot (\text{sd}(a) + \text{sd}(b)) / \text{abs}(\text{mean}(a) - \text{mean}(b))$ . A more rigorous definition of the score, implemented by the method `fixsd` is given by  $Z' = 1 - 3 \cdot \sqrt{\text{var}(a) + \text{var}(b)} / \text{abs}(\text{mean}(a) - \text{mean}(b))$ , where the pooled standard deviation is computed by the square root of the sum of the control variances. A robust method, less sensitive to outliers, is computed by the relation  $Z' = 1 - 3 \cdot (\text{mad}(a) + \text{mad}(b)) / \text{abs}(\text{median}(a) - \text{median}(b))$  where the control dispersions are computed with the `mad` and the control locations with the `median`.

A multivariate extension of the Z'-factor score can be designed by linearly transforming the multivariate data to one dimension and computing the standard (here, `fixsd`) Z'-factor. It can be shown that the linear transform that maximizes the score is the LDA. Moreover, one can demonstrate that the resulting Z'-factor score is equivalent of computing  $Z' = 1 - 3 / \text{dMaha}(\mu_a, \mu_b, \Sigma_a + \Sigma_b)$  where `dMaha` is the Mahalanobis distance.

## Value

The Z'-factor, a numeric ranging from -infinity to 1.

## Author(s)

Gregoire Pau, <gregoire.pau@embl.de>, 2010

## References

J. H. Zhang, T. D. Chung, K. R. Oldenburg. A Simple Statistical Parameter for Use in Evaluation and Validation of High Throughput Screening Assays. J Biomol Screening, 1999.

## See Also

[readHTS](#)

## Examples

```
## initialize imageHTS object using the local submorph screen
local = tempdir()
server = system.file('submorph', package='imageHTS')
x = parseImageConf('conf/imageconf.txt', localPath=local, serverURL=server)
x = configure(x, 'conf/description.txt', 'conf/plateconf.txt', 'conf/screenlog.txt')

## get profiles
profiles = readHTS(x, type='file', filename='data/profiles.tab', format='tab')
a = profiles[match(getUnames(x, content='rluc'), profiles$uname),]
b = profiles[match(getUnames(x, content='ubc'), profiles$uname),]

## compute Z'-factor scores on some features
ft = c('med.c.t.m.majoraxis')
cat('Z'-factor original=', zprime(a[,ft], b[,ft], 'original'), 'fixsd=', zprime(a[,ft], b[,ft], 'fixsd'), '\n')
```

```
## multivariate Z'-factor  
ft = c('med.c.t.m.majoraxis', 'med.n.h.m.majoraxis', 'med.c.h.b.mean')  
cat('Z\'-factor mahalanobis=', zprime(a[,ft], b[,ft], 'mahalanobis'), '\n')
```

# Index

## \* package

- imageHTS, 11
- annotate, 10
- collectCellFeatures, 2, 5
- configure, 10, 17
- countObjects, 3
- extractFeatures, 3, 4, 22, 26
- fData, 10
- fileHTS, 5, 5, 17, 24
- getCellFtrsATH, 5
- getCellFtrsATH (segmentATH), 22
- getImageConf, 7, 17
- getUnames, 7, 8, 18, 24
- getWellFeatures, 9, 9, 20
- highlightSegmentation, 10
- imageHTS, 11, 17
- imageHTS-class (imageHTS), 11
- installCellPicker, 13, 18
- installWebQuery, 14, 18
- installWebQuery (installCellPicker), 13
- makeCellHTS, 14
- parseDCF, 15, 22
- parseImageConf, 7, 8, 16
- popCellPicker, 13, 18, 21
- popWebQuery, 13
- popWebQuery (popCellPicker), 18
- predictCellLabels (readLearnTS), 20
- prw2uname, 9, 19
- readHTS, 16, 26, 28
- readHTS (fileHTS), 5
- readLearnTS, 20
- rowcol2well (prw2uname), 19
- segmentATH, 22, 24, 25
- segmentRing (segmentYeastBF), 24
- segmentWells, 3, 11, 22, 23, 25
- segmentYeastBF, 24
- summarizeWells, 14, 26
- uname2prw, 9
- uname2prw (prw2uname), 19
- well2rowcol (prw2uname), 19
- well2wellid (prw2uname), 19
- zprime, 27