Package 'mitoODEdata'

April 4, 2014

Version 0.99.6

Date 9 Dec 2012

Title Experimental data associated to the paper ``Dynamical modelling of phenotypes in a genome-wide RNAi live-cell imaging assay" (submitted).

Author Gregoire Pau

Maintainer Gregoire Pau <pau.gregoire@gene.com>

SystemRequirements <not required>

Depends R (>= 2.14.0)

Description This package contains the experimental data (assay annotation, siRNA annotation, time-lapse cell counts) associated to the paper ``Dynamical modelling of phenotypes in a genome-wide RNAi live-cell imaging assay" (submitted). The data ultimately come from the Mitocheck assay reported in ``Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes" (Neumann, Walter et al, Nature 2010).

License LGPL

LazyLoad yes

biocViews ExperimentData, TimeCourse, CellBasedAssays, Preprocessing

R topics documented:

getspot *Mitocheck annotation*

Description

Functions to access Mitocheck screen annotation.

Usage

```
getanno(spot=NULL, sirna=NULL, field="hgnc")
getspot(sirna=NULL, ann=NULL, field="hgnc")
getsirna(spot=NULL, ann=NULL, field="hgnc")
```

Arguments

spot	A numeric indicating a spot ID, synchronised with the global Mitocheck tab object.
sirna	A character string indicating a Mitocheck siRNA ID, as referenced in http://www.mitocheck.org.
ann	A character string indicating an annoated value of a siRNA ID, from the field value of the global Mitocheck anno object.
field	A character vector indicating siRNA annotation field values. Possible values include: ensembl, entrez, hgnc and getname. Default is hgnc.

Value

A numeric or character vector.

Author(s)

Gregoire Pau, <pau.gregoire@gene.com>, 2012

See Also

readspot, plotspot

Examples

```
## which siRNAs are targeting the gene CDH1?
getsirna(ann="CDH1")

## which spots contains the siRNA MCO_0026105?
getspot(sirna="MCO_0026105")

## which spots target the gene VIM?
getspot(ann="VIM")

## which gene is targeted by spot 12345?
getanno(spot=12345)
getanno(spot=12345, field=c("hgnc", "entrez", "genename"))
```

`mitoODEdata` *Access to the Mitocheck assay data*

Description

The Mitocheck screen *mitocheck* is a time-lapse imaging assay that employed small-interfering RNAs (siRNAs) to test the implication of human genes in transient biological processes such as cell division or migration genome-wide. In this experiment, HeLa cells stably expressing core histone 2B tagged with green fluorescent protein (GFP) were seeded on siRNA-spotted slides, incubated for 18 h and imaged with automated fluorescence microscopy for 48~h. Video sequences of cell populations on each siRNA-spot were analysed by image segmentation, and at each frame, each individual cell was categorised into one of 16 morphological classes mostly related to cell division.

The `mitoODE` package implements a modelling by differential equations of cellular populations *mitoODE*, to quantify the phenotypic effect induced by siRNA treatments in the Mitocheck screen. The package includes the code to fit any time course data to the model and the scripts used to generate the figures and results presented in the paper.

The `mitoODEdata` package, the experimental companion package of `mitoODE`, contains the screen data and methods to access the Mitocheck assay layout, siRNA annotation, time-lapse cell counts and the fitted phenotypes for each spot. Four cell types are considered: interphase (referred in the Mitocheck paper as: Interphase, Large, Elongated, Folded, Hole, SmallIrregular or Undefined-Condensed), mitotic (Metaphase, Anaphase, MetaphaseAlignment, Prometaphase or ADCCM), polynucleated (Shape1, Shape3, Grape) and apoptotic (Apoptosis).

Usage

```
readspot(spot)
plotspot(spot)
```

Arguments

`spot`	A numeric indicating a spot ID, synchronised with the global Mitocheck `tab` object.

Details

Loading the package `mitoODEdata` loads the Mitocheck screen annotation variables `tab` and `anno` in the global environement. The object `tab` is a data.frame containing spot metadata, including: `plate` (plate number), `replicate` (replicate number), `spot` (spot number within the plate), `qc` (original quality control from the paper), `type` (spot type) and `sirna` (spot siRNA ID). The object `anno` is a data.frame containing the siRNA to gene mapping, including: `sirna` (siRNA ID), `ensembl` (target Ensembl gene ID), `hgnc` (target HGNC gene symbol), `entrez` (target Entrez gene ID), `genename` (target HGNC gene name).

Value

The function `readspot` returns a matrix containing the number of cells of a given type (interphase "i", mitotic "m", polynucleated "s" and apoptotic "a") per frame. The first frame (e.g. row) was acquired 18 h after cell seeding and following frames were acquired every 30 minutes.

Author(s)

Gregoire Pau, <pau.gregoire@gene.com>, 2012

References

Pau G, Walter T, Neumann B, Heriche JK, Ellenberg J, and Huber W (2013) Dynamical modelling of phenotypes in a genome-wide RNAi live-cell imaging assay. Submitted.\

Neumann B, Walter T, Heriche JK, Bulkescher J, Erfle H, et~al. (2010) Phenotypic profiling of the human genome by time-lapse microscopy reveals cell division genes. Nature Nature 464: 721–727.

See Also

`getspot`, `getsirna`, `getanno`

Examples

```
## read spot
spotid <- getspot(ann="FGFR2")[1]
y <- readspot(spotid)
y[1:10,]

## plot spot
plotspot(spotid)
```

Index