

Package ‘TimerQuant’

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Author Joseph Barry

Maintainer Joseph Barry <joseph.barry@embl.de>

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VignetteBuilder knitr

Description Supplementary Data package for tandem timer methods paper by Barry et al. (2015) including TimerQuant shiny applications.

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License Artistic-2.0

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Contents

| | |
|-----------------------------|---|
| analyticSolutions | 2 |
| fitCV | 3 |
| FRETdata | 4 |

| | |
|-------------------------------------|----|
| genRatioHeatmap | 4 |
| genTimeSteadyStateHeatmap | 5 |
| getBreaks10 | 6 |
| getSpacedSeq | 6 |
| maturationData | 7 |
| plotPrimordiumProfile | 7 |
| profileGradients | 8 |
| ratioSteadyState | 8 |
| ratioTimeDependent | 9 |
| runShinyApps | 10 |
| signal | 11 |
| simulatedSignal | 11 |

| | |
|--------------|-----------|
| Index | 13 |
|--------------|-----------|

| | |
|-------------------|--|
| analyticSolutions | <i>Analytic model solutions for fluorescence intensity</i> |
|-------------------|--|

Description

Time-dependent and steady-state analytic solution to one-step model for number of mature fluorophores. Where f is given as a parameter the returned value is transformed from a molecular population into a fluorescence intensity. For the function names, 0 refers to the dark population of non-mature fluorophores, and 1 to the mature, fluorescent population. 'ss' indicates steady-state solutions. t_{ss} is the time required to reach steady-state.

Usage

```
tss(m, k)
x0ss(p, m, k)
x1(p, m, k, t, f=1)
x1ss(p, m, k, f=1)
x1fretFP1(p, m1, m2, k, t, E=0, f=1)
x1fretFP1ss(p, m1, m2, k, E=0, f=1)
```

Arguments

| | |
|------|---|
| p | Protein production rate (molecules produced per unit time). |
| m | Maturation rate of fluorophore, which can be for either FP1 or FP2 (convert to maturation time with $\log(2)/m$). |
| $m1$ | Maturation rate of FP1. |
| $m2$ | Maturation rate of FP2. |
| k | Protein degradation rate (convert to half-life with $\log(2)/k$). |
| t | Time (must be non-negative). |
| E | FRET coefficient representing energy transfer from FP1 to FP2. |
| f | Proportionality factor relating intensity to the number of molecules. When equal to one then the readout is number of molecules directly. |

Value

A numeric specifying the model solution for the given parameters.

Author(s)

Joseph D. Barry

Examples

```
t0 <- seq(0.001, 1000, by=0.1)
plot(t0, x1(p=10, m=log(2)/5, k=log(2)/100, t=t0), type="l", col="darkgreen",
      lwd=2, xlab="Time (min)", ylab="Number of mature fluorophores", cex.lab=1.4)
```

fitCV

fitCV

Description

Fits a smoothing line to coefficient of variation profiles.

Usage

```
fitCV(x, scaleLog10)
```

Arguments

x A dataframe with columns Time (FP maturation time) and CV (coefficient of variation of timer signal).

scaleLog10 A logical indicating whether the points are spaced on the log10 scale or not.

Value

A dataframe containing fitted values and the minimum CV of the profile.

Author(s)

Joseph D. Barry

Examples

```
if (interactive()) vignette(topic="genPaperFigures", package="TimerQuant")
```

 FRETdata

FRET Data

Description

A three-dimensional array of dimensions FRET value x tFT x assay type containing FRET readouts.

Usage

FRETdata

genRatioHeatmap

generate ratio heatmap

Description

Visualize timer ratios as a function of either FP1 or FP2 maturation time, and protein half-life.

Usage

```
genRatioHeatmap(tRangeFP, Tfixed, TA, TB, channel, E, f=1, n, ramp)
```

Arguments

| | |
|----------|---|
| tRangeFP | Vector containing two numerics specifying the range of maturation times to display for the chosen fluorescence channel. |
| Tfixed | The maturation time of the FP that will remain fixed. |
| TA | tFT half-life in location A. |
| TB | tFT half-life in location B. |
| channel | Integer specifying fluorescence channel to be varied (1 or 2). |
| E | FRET value representing transfer from FP1 to FP2. |
| f | $f=f_2/f_1$, the ratio of prefactors relating the number of molecules to the fluorescence intensity. |
| n | Integer specifying the number of data points. Choose a higher n for a higher pixel density. |
| ramp | Colour ramp, see <code>colorRampPalette</code> for more details. |

Value

Returns a ggplot2 heatmap.

Author(s)

Joseph D. Barry

Examples

```
if (interactive()) vignette(topic="genPaperFigures", package="TimerQuant")
```

genTimeSteadyStateHeatmap
Time to reach steady-state

Description

Visualize the time to reach steady-state as a function of FP2 maturation time and protein half-life.

Usage

```
genTimeSteadyStateHeatmap(tRangeFP2, tRangeHlife, n, ramp)
```

Arguments

| | |
|-------------|---|
| tRangeFP2 | Vector containing two numerics specifying the range of FP2 maturation times. |
| tRangeHlife | Vector containing two numerics specifying the range of protein half-lives. |
| n | Integer specifying the number of data points. Choose a higher n for a higher pixel density. |
| ramp | Colour ramp, see colorRampPalette for more details. |

Value

Returns a ggplot2 heatmap.

Author(s)

Joseph D. Barry

Examples

```
if (interactive()) vignette(topic="genPaperFigures", package="TimerQuant")
```

| | |
|-------------|-------------------------|
| getBreaks10 | <i>Get log10 breaks</i> |
|-------------|-------------------------|

Description

Return breaks for each half-decade on the log10 scale, e.g. 1, 5, 10, 50, ...

Usage

```
getBreaks10(x)
```

Arguments

x A vector of numbers. Breaks will be calculated across the range of x.

Value

A sequence of breaks useful for ticks or labels on the log10 scale.

Author(s)

Joseph D. Barry

Examples

```
getBreaks10(c(1, 100))
```

| | |
|--------------|----------------------------|
| getSpacedSeq | <i>Get Spaced Sequence</i> |
|--------------|----------------------------|

Description

Return points nicely spaced for on the log10 scale.

Usage

```
getSpacedSeq(x, n)
```

Arguments

x A vector of two numbers containing the minimum and maximum of the desired sequence.

n The desired length of the sequence to be returned.

Value

A sequence of numbers with appropriate spacing for the log10 scale.

Author(s)

Joseph D. Barry

Examples

```
getSpacedSeq(c(1, 1000), n=10)
```

| | |
|----------------|------------------------|
| maturationData | <i>Maturation Data</i> |
|----------------|------------------------|

Description

A five-dimensional array of dimensions time (in minutes) x data columns x sample x view x tFT (identified by the RFP since sfGFP is present for all) containing fluorescence intensity readouts for the fluorophore maturation curves.

Usage

```
maturationData
```

| | |
|-----------------------|--------------------------------|
| plotPrimordiumProfile | <i>Plot Primordium Profile</i> |
|-----------------------|--------------------------------|

Description

Visualizes primordium signal as a function of position with median and median absolute deviation across samples.

Usage

```
plotPrimordiumProfile(x, add, ylab, lwd, cex.lab, cex.axis, xlim, ylim, main,
  col, lty, alpha)
```

Arguments

| | |
|----------|---|
| x | A matrix of data where rows are samples and columns are sequential positions. |
| add | A logical indicating whether or not to add to the existing plot. |
| ylab | The y-axis label. |
| lwd | Integer specifying width of lines. |
| cex.lab | Integer specifying size of labels. |
| cex.axis | Integer specifying size of axis labels. |
| xlim | An optional vector of length 2 specifying the limits for the x-axis. |
| ylim | An optional vector of length 2 specifying the limits for the y-axis. |

| | |
|-------|--|
| main | Plot title. |
| col | Line colour. |
| lty | Style of line |
| alpha | A numeric between zero and one specifying the level of transparency for the shaded region. |

Value

Produces a plot of signal vs position summarizing across multiple primordium samples.

Author(s)

Joseph D. Barry

Examples

```
if (interactive()) vignette(topic="genPaperFigures", package="TimerQuant")
```

profileGradients *Profile Gradients*

Description

A three-dimensional array of dimensions tFT x sample x position containing ratio readouts for migrating posterior lateral line primordia.

Usage

```
profileGradients
```

ratioSteadyState *analytic function ratioSteadyState*

Description

Steady-state analytic solution to one-step model for the ratio of mature to non-mature fluorophores.

Usage

```
ratioSteadyState(T1, T2, halfLife, E=0, f=1)
```


Arguments

| | |
|----------|---|
| T1 | Maturation time of fluorescent protein 1 (FP1, fast maturing). |
| T2 | Maturation time of fluorescent protein 2 (FP2, slow maturing). |
| halfLife | Protein half-life. |
| E | FRET value representing transfer from FP1 to FP2. |
| f | $f=f_2/f_1$, the ratio of prefactors relating the number of molecules to fluorescence intensity for each fluorescence channel. |

Value

A numeric specifying the model steady-state solution for the given parameters.

Author(s)

Joseph D. Barry

Examples

```
halfLifeSeq <- seq(1, 2000, by=0.1)
plot(halfLifeSeq, ratioSteadyState(T1=5, T2=100, halfLife=halfLifeSeq),
     type="l", lwd=2, ylim=c(0, 1), xlab="tFT half-life (min)",
     ylab="Steady-state ratio", cex.lab=1.4, log="x", col="red")
```

ratioTimeDependent *analytic function ratioTimeDependent*

Description

Steady-state analytic solution to one-step model for the ratio of mature to non-mature fluorophores.

Usage

```
ratioTimeDependent(T1, T2, halfLife, t, E=0, f=1)
```

Arguments

| | |
|----------|---|
| T1 | Maturation time of fluorescent protein 1 (FP1, fast maturing). |
| T2 | Maturation time of fluorescent protein 2 (FP2, slow maturing). |
| halfLife | Protein half-life. |
| t | Time, which must be non-negative. |
| E | FRET value representing energy transfer from FP1 to FP2. |
| f | $f=f_2/f_1$, the ratio of prefactors relating the number of molecules to fluorescence intensity. |

Value

A numeric specifying the model time-dependent solution for the given parameters.

Author(s)

Joseph D. Barry

Examples

```
tSeq <- seq(0.1, 300, by=0.1)
plot(tSeq, ratioTimeDependent(T1=5, T2=100, halfLife=30, t=tSeq, E=0, f=1), type="l", lwd=2,
     xlab="time (min)", ylab="ratio", cex.lab=1.4, col="black", ylim=c(0, 0.3))
points(tSeq, ratioTimeDependent(T1=5, T2=100, halfLife=30, t=tSeq, E=0.4, f=1), type="l", lwd=2,
      col="red")
abline(h=ratioSteadyState(T1=5, T2=100, halfLife=30, E=0, f=1), lty=2, col="black")
abline(h=ratioSteadyState(T1=5, T2=100, halfLife=30, E=0.4, f=1), lty=2, col="red")
```

runShinyApps

Run R-shiny applications

Description

Wrapper functions that run shiny apps located in extdata subdirectory of R package.

Usage

```
runChooseFP2App()
runTimerModellingApp()
```

Author(s)

Joseph D. Barry

Examples

```
runChooseFP2App()

runTimerModellingApp()
```

| | |
|--------|---------------|
| signal | <i>Signal</i> |
|--------|---------------|

Description

Computes timer signal (without additive noise) for a set of model parameters.

Usage

```
signal(T1, T2, TA, TB, E=0)
```

Arguments

| | |
|----|---|
| T1 | Maturation time of fluorescent protein 1 (fast maturing). |
| T2 | Maturation time of fluorescent protein 2 (slow maturing). |
| TA | Minimum protein half-life. |
| TB | Maximum protein half-life. |
| E | FRET value representing transfer from FP1 to FP2. |

Value

A numeric specifying the timer signal.

Author(s)

Joseph D. Barry

Examples

```
signal(T1=5, T2=60, TA=30, TB=180, E=0)
signal(T1=5, T2=60, TA=30, TB=180, E=0.5)
```

| | |
|-----------------|-------------------------------|
| simulatedSignal | <i>Simulated Timer Signal</i> |
|-----------------|-------------------------------|

Description

Additive error model for timer signal.

Usage

```
simulatedRatio(T1, T2, hLife, sigmaAdd, p, E)
simulatedSignal(T1, T2, TA, TB, sigmaAdd, p, E)
simulatedSignalN(T1, T2, TA, TB, sigmaAdd, N, p, E)
```

Arguments

| | |
|----------|---|
| T1 | Maturation time of fluorescent protein 1 (FP1, fast maturing). |
| T2 | Maturation time of fluorescent protein 2 (FP2, slow maturing). |
| hLife | Protein half-life. |
| TA | Minimum protein half-life. |
| TB | Maximum protein half-life. |
| sigmaAdd | Standard deviation of normal distribution from which noise terms are drawn. |
| p | Protein production rate (molecules produced per unit time). |
| E | FRET value representing energy transfer from FP1 to FP2. |
| N | Number of simulation realizations. |

Value

Returns simulated values for ratios or timer signal.

Author(s)

Joseph D. Barry

Examples

```
if (interactive()) vignette(topic="genPaperFigures", package="TimerQuant")
```

Index

- * **FRETdata**
 - FRETdata, 4
 - * **datasets**
 - maturationData, 7
 - profileGradients, 8
 - * **fitCV**
 - fitCV, 3
 - * **genRatioHeatmap**
 - genRatioHeatmap, 4
 - * **genTimeSteadyStateHeatmap**
 - genTimeSteadyStateHeatmap, 5
 - * **getBreaks10**
 - getBreaks10, 6
 - * **getSpacedSeq**
 - getSpacedSeq, 6
 - * **plotPrimordiumProfile**
 - plotPrimordiumProfile, 7
 - * **ratioSteadyState**
 - ratioSteadyState, 8
 - * **ratioTimeDependent**
 - ratioTimeDependent, 9
 - * **runShinyApps**
 - runShinyApps, 10
 - * **signal**
 - signal, 11
 - * **simulatedSignal**
 - simulatedSignal, 11
 - * **x1**
 - analyticSolutions, 2
- analyticSolutions, 2
- fitCV, 3
- FRETdata, 4
- genRatioHeatmap, 4
- genTimeSteadyStateHeatmap, 5
- getBreaks10, 6
- getSpacedSeq, 6
- maturationData, 7
- plotPrimordiumProfile, 7
- profileGradients, 8
- ratioSteadyState, 8
- ratioTimeDependent, 9
- runChooseFP2App (runShinyApps), 10
- runShinyApps, 10
- runTimerModellingApp (runShinyApps), 10
- signal, 11
- simulatedRatio (simulatedSignal), 11
- simulatedSignal, 11
- simulatedSignalN (simulatedSignal), 11
- tss (analyticSolutions), 2
- x0ss (analyticSolutions), 2
- x1 (analyticSolutions), 2
- x1fretFP1 (analyticSolutions), 2
- x1fretFP1ss (analyticSolutions), 2
- x1ss (analyticSolutions), 2