Package ‘TimerQuant’

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analyticSolutions

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

\[
\begin{align*}
tss(m, k) \\
x0ss(p, m, k) \\
x1(p, m, k, t, f=1) \\
x1ss(p, m, k, f=1) \\
x1fretFP1(p, m1, m2, k, t, E=0, f=1) \\
x1fretFP1ss(p, m1, m2, k, E=0, f=1)
\end{align*}
\]

Arguments

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

**Value**

A numeric specifying the model solution for the given parameters.

**Author(s)**

Joseph D. Barry

**Examples**

```r
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)
```

**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**

```r
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 colorRampPalette 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**

```r
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  
*Get log10 breaks*

**Description**

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

**Usage**

```r
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**

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

---

getSpacedSeq  
*Get Spaced Sequence*

**Description**

Return points nicely spaced for on the log10 scale.

**Usage**

```r
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.
**maturationData**

**Author(s)**

Joseph D. Barry

**Examples**

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

---

**maturationData**  
*Maturation Data*

**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**  
*Plot Primordium Profile*

**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.
ratioSteadyState

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**

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

**Value**

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

**Author(s)**

Joseph D. Barry

**Examples**

```r
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")
```

---

**Description**

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

**Usage**

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

**Arguments**

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

**Value**

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

**Author(s)**

Joseph D. Barry

**Examples**

```r
 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")
```

---

**Description**

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

**Usage**

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

**Author(s)**

Joseph D. Barry

**Examples**

```r
 runChooseFP2App()
 runTimerModellingApp()
```
**signal**

Signal

**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**

Simulated Timer Signal

**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)
simulatedSignal

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

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