

dnaCellCycle

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dApop	<i>Generate a density function for a location and scale adjusted log-normal distribution</i>
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Description

Generate a density function for a location and scale adjusted log-normal distribution

Usage

```
dApop(x, xscale, offset, sdlog)
```

Arguments

x	a vector of x-values
xscale	scale factor of distribution
offset	starting x-value for log-normal distribution
sdlog	shape parameter of log-normal distribution

Value

y vector of density values

Author(s)

Jason Waddell

diffFun	<i>Computes sums of squared error for dnaCellCycle curves with no apoptosis</i>
---------	---

Description

Computes sums of squared error for dnaCellCycle curves with no apoptosis

Usage

```
diffFun(par, sPhaseType = "uniform", n = 512, fitX = NULL, fitY = NULL,
        scale = NULL)
```

Arguments

par	List of parameters (mu1, sigma1, mu2, ...) that parameterize cell cycle function
sPhaseType	shape of the S-Phase curve
n	number of points to compute the density at
fitX	x values at which to fit the density function
fitY	y values from data kernel density estimate
scale	vector of scaling factors associated with 'par'

Value

score sum squared error between kernel density estimate and fit

Author(s)

Jason Waddell

diffFunApop	<i>Computes sums of squared error for dnaCellCycle curves with an apoptosis peak</i>
-------------	--

Description

Computes sums of squared error for dnaCellCycle curves with an apoptosis peak

Usage

```
diffFunApop(par = NULL, sPhaseType = "uniform", n = 512, fitX = NULL,
            fitY = NULL, scale = NULL)
```

Arguments

par	List of parameters (mu1, sigma1, mu2, ...) that parameterize cell cycle function
sPhaseType	shape of the S-Phase curve
n	number of points to compute the density at
fitX	x values at which to fit the density function
fitY	y values from data kernel density estimate
scale	vector of scaling factors associated with 'par'

Value

score sum squared error between kernel density estimate and fit

Author(s)

Jason Waddell

diffFunApopExp	<i>Computes sums of squared error for dnaCellCycle curves with no apoptosis</i>
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Description

Computes sums of squared error for dnaCellCycle curves with no apoptosis

Usage

```
diffFunApopExp(par = NULL, sPhaseType = "uniform", n = 512, fitX = NULL,
              fitY = NULL, scale = NULL)
```

Arguments

par	List of parameters (mu1, sigma1, mu2, ...) that parameterize cell cycle function
sPhaseType	shape of the S-Phase curve
n	number of points to compute the density at
fitX	x values at which to fit the density function
fitY	y values from data kernel density estimate
scale	vector of scaling factors associated with 'par'

Value

score sum squared error between kernel density estimate and fit

Author(s)

Jason Waddell

dnaCellCycle	<i>Function to find the G1, G2, S-Phase and Apoptosis of DNA Cell Cycle data. Values are found using the non-linear optimizer DEoptim package.</i>
--------------	--

Description

dnaCellCycle's 'control' parameters takes values as function calls to [DEoptim.control](#) . Example syntax is given below.

Usage

```
dnaCellCycle(data = NULL, sPhaseType = "firstOrder",
  includeApoptosis = FALSE, mu1 = NULL, sigma1 = NULL, mu2 = NULL,
  sigma2 = NULL, muApoptosis = NULL, sigmaApoptosis = NULL,
  lowerCutoff = NULL, upperCutoff = NULL, control = NULL, a1 = NULL,
  a2 = NULL, aApop = NULL, optimizer = "optimx", method = "L-BFGS-B",
  nbins = NULL)
```

Arguments

data	numeric input data vector
sPhaseType	shape of the S-Phase. Either "uniform" or "firstOrder"
includeApoptosis	binary value for whether to include an apoptosis peak
mu1	range of possible mu1 (G1 mean) values
sigma1	range of possible sigma1 (G1 standard deviation) values
mu2	range of possible mu2 (G2 mean) values
sigma2	range of possible sigma2 (G2 standard deviation) values
muApoptosis	range of possible apoptosis mean values
sigmaApoptosis	range of possible apoptosis standard deviation values

lowerCutoff	dnaCellCycle will ignore all data below this value
upperCutoff	dnaCellCycle will ignore all data above this value
a1	range of possible values for proportion of data in G1
a2	range of possible values for proportion of data in G2
aApop	range of possible values for proportion of data in the Apoptosis
control	control parameter to be passed to DEoptim() or optimx()
optimizer	optimizer function to be used; as of writing, either "DEoptim" or "optimx"
method	'optimx' optimizer method; defaults to "L-BFGS-B"
nbins	number of bins at which to computer the histogram. if NULL (not specified), function will set bin-widths equal to 1

Value

out 'dnaCellCycle' object with model fit

Author(s)

Jason Waddell

See Also

[DEoptim.control](#) [optimx](#)

Examples

```
## Not run:
#' basic example
exampleFile <- system.file("exampleFiles", "dna_112.001.rda", package = "dnaCellCycle")
load(exampleFile)
x <- dna
out <- dnaCellCycle(data = x, upperCutoff = 400)
plot(out, outlines = TRUE)
print(out, digits = 4)

# uniform example, custom-set ranges
out <- dnaCellCycle(data = x, upperCutoff = 400,
  sPhaseType = "uniform", mu1 = c(170, 210),
  mu2 = c(370, 390), sigma1 = c(5, 15))
plot(out)
out

# Apoptosis example
x <- c(x, rnorm(900, mean = 100, sd = 5)); plot(density(x))
out <- dnaCellCycle(data = x, upperCutoff = 400, optimizer = "DEoptim",
  includeApoptosis = TRUE, muApoptosis = c(90, 110), sigmaApoptosis = c(0, 10),
  control = DEoptim.control(itermax = 200))

#optimx
out <- dnaCellCycle(data = x, includeApoptosis = TRUE,
  muApoptosis = c(170, 180), sigmaApoptosis = c(0, 10),
  upperCutoff = 400, optimizer = "optimx", method = "L-BFGS-B",
  aApop = c(0.1, 0.2))

## End(Not run)
```

dnaCellCycleExp	<i>Function to find the G1, G2, S-Phase and Apoptosis of DNA Cell Cycle data. Values are found using the non-linear optimizer DEoptim package.</i>
-----------------	--

Description

dnaCellCycle's 'control' parameters takes values as function calls to [DEoptim.control](#). Example syntax is given below.

Usage

```
dnaCellCycleExp(data = NULL, sPhaseType = "firstOrder", mu1 = NULL,
  sigma1 = NULL, mu2 = NULL, sigma2 = NULL, lowerCutoff = NULL,
  upperCutoff = NULL, control = NULL, a1 = NULL, a2 = NULL,
  aApop = NULL, offset = NULL, xscale = NULL, sdlog = NULL,
  method = "L-BFGS-B", nbins = NULL)
```

Arguments

data	numeric input data vector
sPhaseType	shape of the S-Phase. Either "uniform" or "firstOrder"
mu1	range of possible mu1 (G1 mean) values
sigma1	range of possible sigma1 (G1 standard deviation) values
mu2	range of possible mu2 (G2 mean) values
sigma2	range of possible sigma2 (G2 standard deviation) values
lowerCutoff	dnaCellCycle will ignore all data below this value
upperCutoff	dnaCellCycle will ignore all data above this value
a1	range of possible values for proportion of data in G1
a2	range of possible values for proportion of data in G2
aApop	range of possible values for proportion of data in the Apoptosis
offset	range of the x offset range for the log-normal apoptosis distribution
xscale	range of scaling factor values for apoptosis distribution. (scale relative to regular log-normal distribution)
sdlog	range of shape parameter values for apoptosis distribution
control	control parameter to be passed to DEoptim() or optimx()
method	'optimx' optimizer method; defaults to "L-BFGS-B"
nbins	number of bins at which to computer the histogram. if NULL (not specified), function will set bin-widths equal to 1

Value

out 'dnaCellCycleExp' object with model fit

Author(s)

Jason Waddell

dSphase	<i>Function for computing the density of the sPhase at given x values</i>
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Description

Function for computing the density of the sPhase at given x values

Usage

```
dSphase(x = NULL, lower = NULL, upper = NULL, sd1 = NULL, sd2 = NULL,
        a = NULL, sPhaseType = NULL, shape = NULL)
```

Arguments

x	A vector of numeric values
lower	lower cutoff: function removes all x values below this point
upper	upper cutoff: function removes all x values above this point
sd1	standard deviation value of the left tail
sd2	standard deviation of the right tail
a	proportion of total distribution the s-phase takes
sPhaseType	shape of the S-Phase: "uniform", or "firstOrder"
shape	shape parameter

Value

a vector of density values for each element of x

Author(s)

Jason Waddell

findCombinedCurve	<i>Function for fitting G1, G2, Sphase and Apoptosis peaks to cell cycle data</i>
-------------------	---

Description

Function for fitting G1, G2, Sphase and Apoptosis peaks to cell cycle data

Usage

```
findCombinedCurve(mu1 = NULL, sigma1 = NULL, mu2 = NULL, sigma2 = NULL,
                  a1 = NULL, a2 = NULL, aApop = NULL, x = NULL, shape = NULL,
                  sPhaseType = sPhaseType, muApoptosis = NULL, sigmaApoptosis = NULL)
```

Arguments

mu1	G1 mean
sigma1	G1 standard deviation
mu2	G2 mean
sigma2	G2 standard deviation
a1	proportion of data in G1
a2	proportion of data in G2
aApop	proportion of data in Apoptosis
x	data vector
shape	shape parameter for S-Phase
sPhaseType	shape type for S-Phase
muApoptosis	apoptosis mean
sigmaApoptosis	apoptosis standard deviation

Value

vector of density estimates for cell cycle function

Author(s)

Jason Waddell

findCombinedCurveExp *Function for fitting G1, G2, Sphase and Apoptosis peaks to cell cycle data*

Description

Function for fitting G1, G2, Sphase and Apoptosis peaks to cell cycle data

Usage

```
findCombinedCurveExp(x = NULL, mu1 = NULL, sigma1 = NULL, mu2 = NULL,
  sigma2 = NULL, a1 = NULL, a2 = NULL, aApop = NULL, offset = NULL,
  xscale = NULL, sdlog = NULL, shape = NULL, sPhaseType = sPhaseType)
```

Arguments

mu1	G1 mean
sigma1	G1 standard deviation
mu2	G2 mean
sigma2	G2 standard deviation
a1	proportion of data in G1
a2	proportion of data in G2
aApop	proportion of data in Apoptosis
x	data vector

shape	shape parameter for S-Phase
sPhaseType	shape type for S-Phase
offset	the x offset range for the log-normal apoptosis distribution
xscale	scaling factor values for apoptosis distribution
sdlog	shape parameter values for apoptosis distribution

Value

vector of density estimates for cell cycle function

Author(s)

Jason Waddell

`plot.dnaCellCycle` *Plot a dnaCellCycle object*

Description

Plot a dnaCellCycle object

Usage

```
## S3 method for class 'dnaCellCycle'  
plot(x, outlines = FALSE, ylim = NULL, ...)
```

Arguments

x	output object from dnaCellCycle
outlines	binary parameter indicating whether to plot density curve outlines
ylim	y limits for plot (vector of length 2)
...	further arguments; currently none used

Value

none

Author(s)

Jason Waddell

plot.dnaCellCycleExp *Plot a dnaCellCycle object*

Description

Plot a dnaCellCycle object

Usage

```
## S3 method for class 'dnaCellCycleExp'
plot(x, outlines = FALSE, ylim = NULL, ...)
```

Arguments

x	output object from dnaCellCycle
outlines	binary parameter indicating whether to plot density curve outlines
ylim	y limits for plot (vector of length 2)
...	further arguments; currently none used

Value

none

Author(s)

Jason Waddell

plotLogNormal *Plot a normal density curve of specified mean and standard deviation*

Description

Plot a normal density curve of specified mean and standard deviation

Usage

```
plotLogNormal(par = NULL, polygon = FALSE, outlines = FALSE, outlineCol,
...)
```

Arguments

par	Parameter vector from dnaCellCycle object
polygon	binary parameter indicating whether to plot curve as a polygon
outlines	binary specification of whether to plot density curve outlines
outlineCol	color of the density outline
...	optional graphics parameters to be handed to 'lines' function

Value

none

Author(s)

Jason Waddell

plotNormal	<i>Plot a normal density curve of specified mean and standard deviation</i>
------------	---

Description

Plot a normal density curve of specified mean and standard deviation

Usage

```
plotNormal(mean = NULL, sd = NULL, a = NULL, polygon = FALSE,  
           outlines = FALSE, outlineCol, ...)
```

Arguments

mean	mean of normal distribution
sd	standard deviation of normal distribution
a	cluster proportion vector
polygon	binary parameter indicating whether to plot curve as a polygon
outlines	binary specification of whether to plot density curve outlines
outlineCol	color of the density outline
...	optional graphics parameters to be handed to 'lines' function

Value

none

Author(s)

Jason Waddell

plotOptim	<i>Plots the combined</i>
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Description

Plots the combined

Usage

```
plotOptim(par, sPhaseType = NULL, includeApoptosis = FALSE, alpha = 0.65,
  outlines = NULL)
```

Arguments

par	Parameter vector from dnaCellCycle object
sPhaseType	S Phase shape type, one of "uniform", "firstOrder", or "kumaraswamy"
includeApoptosis	binary parameter for whether an apoptosis peak is included
alpha	color opacity level
outlines	binary specification of whether to plot density curve outlines

Value

none

Author(s)

Jason Waddell

plotOptimExp	<i>Plots the combined</i>
--------------	---------------------------

Description

Plots the combined

Usage

```
plotOptimExp(par, sPhaseType = NULL, includeApoptosis = FALSE,
  alpha = 0.65, outlines = NULL)
```

Arguments

par	Parameter vector from dnaCellCycle object
sPhaseType	S Phase shape type, one of "uniform", "firstOrder", or "kumaraswamy"
includeApoptosis	binary parameter for whether an apoptosis peak is included
alpha	color opacity level
outlines	binary specification of whether to plot density curve outlines

Value

none

Author(s)

Jason Waddell

plotSphase

*Plots the S-Phase line to the current plot***Description**

Plots the S-Phase line to the current plot

Usage

```
plotSphase(lower = NULL, upper = NULL, sd1 = NULL, sd2 = NULL,
  a = NULL, shape = shape, sPhaseType = sPhaseType, polygon = FALSE,
  outlines = FALSE, outlineCol, ...)
```

Arguments

lower	lower cutoff: function removes all x values below this point
upper	upper cutoff: function removes all x values above this point
sd1	standard deviation value of the left tail
sd2	standard deviation of the right tail
a	proportion of total distribution the s-phase takes
shape	shape parameter
sPhaseType	shape of the S-Phase: "uniform", "firstOrder", or "kumaraswamy"
polygon	binary parameter indicating whether to plot curve as a polygon
outlines	binary specification of whether to plot density curve outlines
outlineCol	color of the density outline
...	optional graphics parameters to be handed to 'lines' function

Value

no value returned

Author(s)

Jason Waddell

print.dnaCellCycle *Print function for objects of type 'dnaCellCycle'*

Description

Print function for objects of type 'dnaCellCycle'

Usage

```
## S3 method for class 'dnaCellCycle'  
print(x, ...)
```

Arguments

x	'dnaCellCycle' object
...	further paramaters to be passed to 'print'

Value

none

Author(s)

Jason Waddell

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