Package ‘rGammaGamma’

February 20, 2015

Type Package

Title Gamma convolutions for methylation array background correction.

Depends gsl

Version 1.0.12

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Description This package implements a Gamma convolution model for background correction.

License GPL (>= 2.0)

LazyLoad yes

NeedsCompilation no

Repository CRAN

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R topics documented:

`rGammaGamma-package` *Implementation of a gamma deconvolution for background correction.*

Description

SNP and methylation microarrays exhibit a different distribution of signal and background intensities than expression microarrays. The flexibility of the gamma distribution suits the observed signal and background intensity distributions well, encompassing as a special case the normal-exponential convolution (the de facto standard for expression background correction). In addition, a signal/noise mixture model is implemented for empirical deconvolution of cross-hybridization between probe alleles.

Details

Package: rGammaGamma Type: Package Version: 1.0.11 Date: 2012-12-04 License: Artistic LazyLoad: yes

Author(s)

Tim Triche, Jr.<ttriche@usc.edu>

Examples

```
## not run

##  foo <- methylumIDAT(barcodes, parallel=T)
##  foo.bg <- methylumi.bgcorr(foo, method='goob')
```

`gammaIntegral` *gammaIntegral: get the conditional expectation of a convolved gamma RV*

Description

Conditional expectation of one (out of two) gamma RVs given their sum & params

Usage

```
gammaIntegral(total, params, offset=50, minx=1)
```

Arguments

`total`	a vector of sums (convolutions)
`params`	parameters for the signal and background distributions
`offset`	an offset to be added to the estimate
`minx`	a minimum value below which we will replace x

Details

See Triche et al., Nucleic Acids Research (submitted).

Value

The conditional expectation(s) of the signal given the total.

Author(s)

Tim Triche, Jr..

`gammaMLE` *gammaMLE: get the MLE of a gamma distribution via fast conditional likelihood*

Description

Maximum likelihood estimator for the parameters of a gamma distribution

Usage

```
gammaMLE(x, w=NULL, niter=100, tol=0.1, minx=1)
```

Arguments

`x`	A vector
`w`	Weights
`niter`	Maximum number of iterations
`tol`	Maximum difference in parameters at convergence
`minx`	Minimum permissible value for x (smaller values will be bumped to this)

Details

Not yet.

Value

The MLE of the parameters.

Author(s)

Tim Triche, Jr..

Examples

```
foo <- rgamma(100, 12, 10)
gammaMLE(foo, w=NULL, niter=100, tol=0.1, minx=1)
```

`gammaMME` *gammaMME: get the MME of a gamma distribution via fast conditional likelihood*

Description

Method of moments estimator for the parameters of a gamma distribution

Usage

```
gammaMME(x)
```

Arguments

`x`	A vector

Details

Not yet.

Value

The method of moments estimate of the parameters.

Author(s)

Tim Triche, Jr..

Examples

```
foo <- rgamma(100, 12, 10)
gammaMME(foo)
```

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