Package ‘rGammaGamma’

February 20, 2015

Type Package

Title Gamma convolutions for methylation array background correction.

Depends gsl

Version 1.0.12

Date 2013-11-10

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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

Date/Publication 2013-11-11 08:22:46

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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

```r
## not run

## foo <- methylumIDAT(barcode, parallel=T)
## foo.bg <- methylum.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..

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

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

---

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

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