

Package ‘fmt’

February 19, 2015

Type Package

Title Variance estimation of FMT method (Fully Moderated t-statistic)

Version 1.0

Date 2012-08-30

Author Lianbo Yu, The Ohio State University

Maintainer Lianbo Yu <Lianbo.Yu@osumc.edu>

Description This package computes posterior residual variances to be used in the denominator of a moderated t-statistic from a linear model analysis of microarray data. It is an extension of the moderated t-statistic original proposed by Smyth (2004). LOESS local regression and empirical Bayesian method are used to estimate gene specific prior degrees of freedom and prior variance based on average gene intensity level. The posterior residual variance in the denominator is a weighted average of prior and residual variance and the weights are prior degrees of freedom and residual variance degrees of freedom. The degrees of freedom of the moderated t-statistic is simply the sum of prior and residual variance degrees of freedom.

Suggests limma

License GPL-2

Repository CRAN

Date/Publication 2012-08-30 19:46:07

NeedsCompilation no

R topics documented:

fmt 2

Index 4

Description

This function computes posterior residual variances to be used in the denominator of a moderated t-statistic from a linear model analysis of microarray data. It is an extension of the moderated t-statistic original proposed by Smyth (2004). LOESS local regression and empirical Bayesian method are used to estimate gene specific prior degrees of freedom and prior variance based on average gene intensity level. The posterior residual variance in the denominator is a weighted average of prior and residual variance and the weights are prior degrees of freedom and residual variance degrees of freedom. The degrees of freedom of the moderated t-statistic is simply the sum of prior and residual variance degrees of freedom.

Usage

```
fmt(Amean, sigmasq, df, ...)  
  
## Default S3 method:  
fmt(Amean, sigmasq, df, span1 = 0.5, span2 = 0.95, iter1 = 4, iter2 = 4, b = 20, ...)  
## S3 method for class 'fmt'  
plot(x, type, ...)
```

Arguments

Amean	vector of average log intensity levels of all genes.
sigmasq	vector of residual variances of all genes.
df	degrees of freedom for sigmasq.
span1	span parameter in LOESS smoothing function.
span2	span parameter in LOESS smoothing function.
iter1	iteration number in LOESS smoothing function.
iter2	iteration number in LOESS smoothing function.
b	number of genes on either side of moving average window when calculating variance of log residual variances.
x	object of class "fmt".
type	type of plot.
...	not used.

Value

df.prior	estimated prior degrees of freedom.
df.post	estimated posterior degrees of freedom.
s2.prior	estimated prior variance.

<code>s2.post</code>	estimated posterior variance.
<code>Ameansort</code>	intermediate result for plotting.
<code>eg</code>	intermediate result for plotting.
<code>egpred</code>	intermediate result for plotting.
<code>MAvar</code>	intermediate result for plotting.
<code>tri.d0</code>	intermediate result for plotting.

Author(s)

Lianbo Yu

References

Yu L, Gulati P, Fernandez S, Pennell M, Kirschner L, Jarjoura D. Fully moderated t-statistic for small sample size gene expression arrays. *Statistical Applications in Genetics and Molecular Biology*, 2011; 10:article 42.

Index

*Topic **fully moderated t-statistic**

fmt, 2

*Topic **variance smoothing**

fmt, 2

fmt, 2

plot.fmt (fmt), 2