

Package ‘ttScreening’

February 20, 2015

Type Package

Title Genome-wide DNA methylation sites screening by use of training and testing samples.

Version 1.5

Date 2014-11-14

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Description This package utilizes training and testing samples to filter out uninformative DNA methylation sites. Surrogate variables (SVs) of DNA methylation are included in the filtering process to explain unknown factor effects.

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Depends sva, limma, matrixStats, corpcor, stats, MASS

NeedsCompilation no

Repository CRAN

Date/Publication 2014-11-14 18:18:24

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ttScreening-package *Genome-wide DNA methylation sites screening by use of training and testing samples.*

Description

A screening process to filter out non-informative DNA methylation sites by applying (ordinary or robust) linear regressions to training data, and the results are further examined using testing samples. Surrogate variables are included to account for unknown factors.

Details

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Author(s)

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References

Meredith Ray, Xin Tong, Hongmei Zhang, and Wilfred Karmaus. (2014) "DNA methylation sites screening with surrogate variables", unpublished manuscript.

Leek JT and Storey JD. (2007) "Capturing heterogeneity in gene expression studies by 'Surrogate Variable Analysis'." PLoS Genetics, 3: e161.

See Also

[sva](#)

irwsva.build2	<i>Adjusted irwsva.build which builds surrogate variables from gene expression data</i>
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Description

This function is directly modified from the original `irwsva.build()` in the SVA package. It was noticed that under certain circumstances a subscript out of bounds error would occur while running the SVA function. Therefore, this modified code has a single line altered that conditionally uses the generic singular decomposition, `svd()`, instead of fast singular decomposition, `fast.svd()`.

Usage

```
irwsva.build2(dat, mod, mod0 = NULL, n.sv, B = 5)
```

Arguments

<code>dat</code>	A m CpG sites by n subjects matrix of methylation data.
<code>mod</code>	A n by k model matrix corresponding to the primary model fit (see <code>model.matrix</code>)
<code>mod0</code>	A n by k_0 model matrix corresponding to the null model to be compared to <code>mod</code> .
<code>n.sv</code>	The number of surrogate variables to construct.
<code>B</code>	The number of iterations of the algorithm to perform.

Details

See <http://www.bioconductor.org/packages/release/bioc/manuals/sva/man/sva.pdf>

Value

<code>sv</code>	A n by $n.sv$ matrix where each column is a distinct surrogate variable.
<code>pprob.gam</code>	A vector with the posterior probability estimates that each row is affected by dependence.
<code>pprob.b</code>	A vector with the posterior probability estimates that each row is affected by the variables in <code>mod</code> , but not in <code>mod0</code> .
<code>n.sv</code>	The number of surrogate variables estimated.

Note

sva Vignette <http://www.biostat.jhsph.edu/~jleek/sva/>

Author(s)

Original `irwsva.build`: Jeffrey T. Leek <jleek@jhsph.edu>, John Storey jstorey@princeton.edu

References

Original sva: Leek JT and Storey JD. (2008) A general framework for multiple testing dependence. Proceedings of the National Academy of Sciences, 105: 18718-18723.

Leek JT and Storey JD. (2007) Capturing heterogeneity in gene expression studies by surrogate variable analysis. PLoS Genetics, 3: e161.

num.sv2	<i>Adjusted num.sv which estimates the number of important surrogate variables from a gene expression data set.</i>
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Description

This function is directly modified from the original num.sv() in the **sva** package. This function has the tolerance level in the fast.svd() function set back to its original default instead of 0.

Usage

```
num.sv2(dat, mod, method = c("be", "leek"), vfilter = NULL,
        B = 20, sv.sig = 0.1, seed = NULL)
```

Arguments

dat	A m genes by n arrays matrix of expression data.
mod	A n by k model matrix corresponding to the primary model fit (see model.matrix).
method	The method to use for estimating surrogate variables, for now there is only one option (based on Buja and Eyuboglu 1992).
vfilter	The number of most variable genes to use when building SVs, must be between 100 and m.
B	The number of null iterations to perform. Only used when method="be".
sv.sig	The significance cutoff for eigengenes. Only used when method="be".
seed	A numeric seed for reproducible results. Optional, only used when method="be".

Details

See <http://www.bioconductor.org/packages/release/bioc/manuals/sva/man/sva.pdf>

Value

n.sv	The number of significant surrogate variables
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Note

sva Vignette <http://www.biostat.jhsph.edu/~jleek/sva/>

Author(s)

Original num.sv: Jeffrey T. Leek <jleek@jhspsh.edu>, John Storey jstorey@princeton.edu

References

Original sva: Leek JT and Storey JD. (2008) A general framework for multiple testing dependence. *Proceedings of the National Academy of Sciences*, 105: 18718-18723.

Leek JT and Storey JD. (2007) Capturing heterogeneity in gene expression studies by surrogate variable analysis. *PLoS Genetics*, 3: e161.

 sva2

The adjusted sva code using irwsva.build2

Description

This function is the modified SVA function in which it uses the `irwsva.build2` function rather than the `irwsva.build` function to build the surrogate variables. Thus, only a single line has been altered from the original `SVA()` function.

Usage

```
sva2(dat, mod, mod0 = NULL, n.sv = NULL, method = c("irw", "two-step"),
      vfilter = NULL, B = 5, numSVmethod = "be")
```

Arguments

<code>dat</code>	A m CpG sites by n subjects matrix of methylation data.
<code>mod</code>	A n by k model matrix corresponding to the primary model fit (see <code>model.matrix</code>).
<code>mod0</code>	A n by k0 model matrix corresponding to the null model to be compared to <code>mod</code> .
<code>n.sv</code>	Optional. The number of surrogate variables to estimate, can be estimated using the <code>num.sv</code> function.
<code>method</code>	Choose between the iteratively re-weighted or two-step surrogate variable estimation algorithms.
<code>vfilter</code>	The number of most variable CpG sites to use when building SVs, must be between 100 and m.
<code>B</code>	The number of iterations of the algorithm to perform.
<code>numSVmethod</code>	The method for determining the number of surrogate variables to use.

Details

See <http://www.bioconductor.org/packages/release/bioc/manuals/sva/man/sva.pdf>

Value

sv	A n by n.sv matrix where each column is a distinct surrogate variable.
pprob.gam	A vector with the posterior probability estimates that each row is affected by dependence.
pprob.b	A vector with the posterior probability estimates that each row is affected by the variables in mod, but not in mod0.
n.sv	The number of surrogate variables estimated.

Note

sva Vignette <http://www.biostat.jhsph.edu/~jleek/sva/>

Author(s)

Original sva: Jeffrey T. Leek <jleek@jhsph.edu>, John Storey jstorey@princeton.edu

References

Original sva: Leek JT and Storey JD. (2008) A general framework for multiple testing dependence. Proceedings of the National Academy of Sciences, 105: 18718-18723.

Leek JT and Storey JD. (2007) Capturing heterogeneity in gene expression studies by surrogate variable analysis. PLoS Genetics, 3: e161.

 ttScreening

A screening process built upon training and testing samples

Description

A screening process to filter out non-informative DNA methylation sites by applying (ordinary or robust) linear regressions to training data, and the results are further examined using testing samples. Surrogate variables are included to account for unknown factors.

Usage

```
ttScreening(y = y, formula, imp.var, data, iterations = 100,
  sva.method = c("two-step", "irw"), cv.cutoff = 50, n.sv = NULL,
  train.alpha = 0.05, test.alpha = 0.05, FDR.alpha = 0.05, Bon.alpha = 0.05,
  percent = (2/3), linear = c("robust", "ls"), vfilter = NULL, B = 5,
  numSVmethod = "be", rowname = NULL)
```

Arguments

y	Data matrix of logit transformed DNA methylation measures (m by n, m subjects and n CpG sites). Each row represents DNA methylation measures of all CpG sites for one subject.
formula	An object of class <code>formula</code> (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under "Details".
imp.var	A vector indicating the location of the term(s) in the formula option on which the selection of CpG sites are made. Interactions are considered a single term. For example, suppose the right-hand side of the equation is: $x + z + x:z$. If the decision of selecting a CpG site is based on one single term, e.g., the significance of interaction effect, then <code>imp.var</code> is set as the location of that term, e.g., <code>imp.var=3</code> (the third term). If the decision is desired to base on all the three terms, then <code>imp.var=c(1,2,3)</code> .
data	Data frame created from <code>model.frame</code> .
iterations	Number of loops for the training/testing (TT) procedure. The default is 100.
sva.method	Option of the two surrogate variable estimation algorithms, the iteratively re-weighted, "irw", or two-step, "two-step". The default is "two-step".
cv.cutoff	The minimum frequency required for a DNA methylation site to be treated as an informative site. After "iterations" iterations, the frequency of each DNA methylation being selected out of "iterations" iterations is recorded. The higher the frequency, the more likely the site is informative. The default is 50.
n.sv	Number of surrogate variables. If NULL, the number of surrogate variables will be determined based on the data. The default is NULL.
train.alpha	Significance level for training samples. The default is 0.05.
test.alpha	Significance level for testing samples. The default is 0.05.
FDR.alpha	False discovery rate. The default is 0.05. This is to fit the need of selecting variables based on FDR.
Bon.alpha	Overall significance level by use of the Bonferroni method for multiple testing correction. The default is 0.05. This is to fit the need of selecting variables based on the Bonferroni multiple testing correction.
percent	Proportion of the full sample to be used for training. The default is 2/3.
linear	Choice of linear regression methods, "robust" (robust regression) or "ls" (ordinary least squares). The default is "ls".
vfilter	The number of most variable CpG sites to use when building SVs, must be between 100 and the number of genes; Must be NULL or numeric (> 0), The default is NULL.
B	Number of iterations in generating surrogate variables. The default is 5.
numSVmethod	The method for determining the number of surrogate variables to use. The default is "be", the other method is "leek".
rowname	Optional, NULL or "TRUE". The default is NULL. If rownames are not already present with the data, the order in which the DNA methylation sites are listed will become the rowname. Surrogate variable estimates are formed based on the algorithms in Leek and Storey (2007).

Details

See [lm](#) or [glm](#) for details.

Value

train.cpg	Number of DNA methylation sites selected after the training step of each loop.
test.cpg	Number of DNA methylation sites selected after the testing step of each loop.
selection	Indicator matrix for the TT method after the testing step. The number of rows is the number of methylation sites, and the number of columns is the number of iterations. An entry of 1 indicates the selection of a site, and 0 otherwise.
pvalue.matrix	Matrix of p-values of the selected DNA methylation sites after the testing step. The number of rows is the number of methylation sites and the number of columns is the number of iterations. For methylation sites not selected, NA is listed.
TT.cpg	Final list of the DNA methylation sites by their original rownames selected from the TT method.
FDR.cpg	Final list of the DNA methylation sites by their original rownames selected from the FDR method.
Bon.cpg	Final list of the DNA methylation sites by their original rownames selected from the Bonferroni method.
TT.output	Dataframe containing the list of DNA methylation sites selected from the TT method and the respective coefficients and pvalues for the variables and SVs.
FDR.output	Dataframe containing the list of DNA methylation sites selected from the FDR method and the respective coefficients and pvalues for the variables and SVs.
Bon.output	Dataframe containing the list of DNA methylation sites selected from the Bonferroni method and the respective coefficients and pvalues for the variables and SVs.

References

Meredith Ray, Xin Tong, Hongmei Zhang, and Wilfred Karmaus. (2014) "DNA methylation sites screening with surrogate variables", unpublished manuscript.

Leek JT and Storey JD. (2007) "Capturing heterogeneity in gene expression studies by 'Surrogate Variable Analysis'." PLoS Genetics, 3: e161.

Examples

```
## Not run:
library(mvtnorm)
nsub=600
imp=100
num=2000

set.seed(1)
x1= rnorm(nsub,1,1)
size1<-rmultinom(1,nsub,c(0.15,0.25,0.25,0.35))
```



```

x2= matrix(sample(c(rep(0,size1[1,]),
rep(1,size1[2,]),
rep(2,size1[3,]),
rep(3,size1[4,])),replace=F),byrow=250,ncol=1)

sur1<-rnorm(nsub,0,5)
sur2<-rnorm(nsub,3,1)
sur3<-rnorm(nsub,0,1)
sur4<-rnorm(nsub,2,4)
sur5<-rnorm(nsub,0,3)

sigma1<-matrix(0,nrow=num,ncol=num)
diag(sigma1)<-1.5

beta0<-0.5
beta1<-0.3
beta2<-0.3
beta3<-0.3

sbeta1<-rnorm(1,0.5,0.01)
sbeta2<-rnorm(1,0.5,0.01)
sbeta3<-rnorm(1,0.5,0.01)
sbeta4<-rnorm(1,0.5,0.01)
sbeta5<-rnorm(1,0.5,0.01)

#beta matrix#
beta<-as.matrix(cbind(beta0,beta1,beta2,beta3,sbeta1,sbeta2,sbeta3,sbeta4,sbeta5))
beta.no2<-as.matrix(cbind(beta0,beta1,beta3,sbeta1,sbeta2,sbeta3,sbeta4,sbeta5))
beta.sur<-as.matrix(cbind(sbeta1,sbeta2,sbeta3,sbeta4,sbeta5))
#design matrix#
X<-as.matrix(cbind(rep(1,length(x1)),x1,x2,x1*x2,sur1,sur2,sur3,sur4,sur5))
X.no2<-as.matrix(cbind(rep(1,length(x1)),x1,x1*x2,sur1,sur2,sur3,sur4,sur5))
X.sur<-as.matrix(cbind(sur1,sur2,sur3,sur4,sur5))
#mu matrix#
imp1.mu<-matrix(rep(X
imp2.mu<-matrix(rep(X.no2
noimp.mu<-matrix(rep(X.sur
mu.matrix=cbind(imp1.mu, imp2.mu, noimp.mu)
error<-rmvnorm(nsub,mean=rep(0,num),sigma=sigma1,method = "chol")
y<-t(mu.matrix+error)

n<-nrow(y)

runs<-ttScreening(y=y,formula=~x1+x2+x1:x2,
data=data.frame(x1,x2), imp.var=3,sva.method="two-step", iterations=100,
cv.cutoff=50, n.sv=NULL, train.alpha=0.05,test.alpha=0.05,
FDR.alpha=0.05,Bon.alpha=0.05,percent=(2/3),linear= "ls",
vfilter = NULL,B = 5, numSVmethod = "be",rowname=NULL)

runs$TT.output
runs$FDR.output
runs$Bon.output

```

End(Not run)

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