Package ‘sva’

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Title Surrogate Variable Analysis

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Description The sva package contains functions for removing batch
effects and other unwanted variation in high-throughput
experiment. Specifically, the sva package contains functions
for the identifying and building surrogate variables for
high-dimensional data sets. Surrogate variables are covariates
constructed directly from high-dimensional data (like gene
expression/RNA sequencing/methylation/brain imaging data) that
can be used in subsequent analyses to adjust for unknown,
unmodeled, or latent sources of noise. The sva package can be
used to remove artifacts in three ways: (1) identifying and
estimating surrogate variables for unknown sources of variation
in high-throughput experiments (Leek and Storey 2007 PLoS
Genetics, 2008 PNAS), (2) directly removing known batch
effects using ComBat (Johnson et al. 2007 Biostatistics) and (3) removing
batch effects with known control probes (Leek 2014 biorXiv).
Removing batch effects and using surrogate variables in
differential expression analysis have been shown to reduce
dependence, stabilize error rate estimates, and improve
reproducibility, see (Leek and Storey 2007 PLoS Genetics, 2008
PNAS or Leek et al. 2011 Nat. Reviews Genetics).

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Depends R (>= 3.2), mgcv, genefilter, BiocParallel

Imports matrixStats, stats, graphics, utils, limma, edgeR

Suggests pamr, bladderbatch, BiocStyle, zebrafishRNASeq, testthat

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ComBat

Adjust for batch effects using an empirical Bayes framework

Description

ComBat allows users to adjust for batch effects in datasets where the batch covariate is known, using methodology described in Johnson et al. 2007. It uses either parametric or non-parametric empirical Bayes frameworks for adjusting data for batch effects. Users are returned an expression matrix that has been corrected for batch effects. The input data are assumed to be cleaned and normalized before batch effect removal.
ComBat

Usage

ComBat(
  dat,
  batch,
  mod = NULL,
  par.prior = TRUE,
  prior.plots = FALSE,
  mean.only = FALSE,
  ref.batch = NULL,
  BPPARAM = bpparam("SerialParam")
)

Arguments

dat Genomic measure matrix (dimensions probe x sample) - for example, expression matrix

batch Batch covariate (only one batch allowed)

mod Model matrix for outcome of interest and other covariates besides batch

par.prior (Optional) TRUE indicates parametric adjustments will be used, FALSE indicates non-parametric adjustments will be used

prior.plots (Optional) TRUE give prior plots with black as a kernel estimate of the empirical batch effect density and red as the parametric

mean.only (Optional) FALSE If TRUE ComBat only corrects the mean of the batch effect (no scale adjustment)

ref.batch (Optional) NULL If given, will use the selected batch as a reference for batch adjustment.

BPPARAM (Optional) BiocParallelParam for parallel operation

Value
da A probe x sample genomic measure matrix, adjusted for batch effects.

Examples

library(bladderbatch)
data(bladderdata)
dat <- bladderEset[1:50,]

pheno = pData(dat)
edata = exprs(dat)
batch = pheno$batch
mod = model.matrix(~as.factor(cancer), data=pheno)

# parametric adjustment
combat_edata1 = ComBat(dat=data, batch=batch, mod=NULL, par.prior=TRUE, prior.plots=FALSE)

# non-parametric adjustment, mean-only version
combat_edata2 = ComBat(dat=data, batch=batch, mod=NULL, par.prior=FALSE, mean.only=TRUE)
# reference-batch version, with covariates
combat_edata3 = ComBat(dat=edata, batch=batch, mod=mod, par.prior=TRUE, ref.batch=3)

ComBat_seq

Adjust for batch effects using an empirical Bayes framework in RNA-seq raw counts

Description

ComBat_seq is an improved model from ComBat using negative binomial regression, which specifically targets RNA-Seq count data.

Usage

ComBat_seq(
  counts,
  batch,
  group = NULL,
  covar_mod = NULL,
  full_mod = TRUE,
  shrink = FALSE,
  shrink.disp = FALSE,
  gene.subset.n = NULL
)

Arguments

counts Raw count matrix from genomic studies (dimensions gene x sample)
batch Vector / factor for batch
group Vector / factor for biological condition of interest
covar_mod Model matrix for multiple covariates to include in linear model (signals from these variables are kept in data after adjustment)
full_mod Boolean, if TRUE include condition of interest in model
shrink Boolean, whether to apply shrinkage on parameter estimation
shrink.disp Boolean, whether to apply shrinkage on dispersion
gene.subset.n Number of genes to use in empirical Bayes estimation, only useful when shrink = TRUE

Value

data A gene x sample count matrix, adjusted for batch effects.
Examples

```r
count_matrix <- matrix(rnbinom(400, size=10, prob=0.1), nrow=50, ncol=8)
batch <- c(rep(1, 4), rep(2, 4))
group <- rep(c(0,1), 4)

# include condition (group variable)
adjusted_counts <- ComBat_seq(count_matrix, batch=batch, group=group, full_mod=TRUE)

# do not include condition
adjusted_counts <- ComBat_seq(count_matrix, batch=batch, group=NULL, full_mod=FALSE)
```

empirical.controls

A function for estimating the probability that each gene is an empirical control.

Description

This function uses the iteratively reweighted surrogate variable analysis approach to estimate the probability that each gene is an empirical control.

Usage

```r
empirical.controls(
  dat,
  mod,
  mod0 = NULL,
  n.sv,
  B = 5,
  type = c("norm", "counts")
)
```

Arguments

dat The transformed data matrix with the variables in rows and samples in columns
mod The model matrix being used to fit the data
mod0 The null model being compared when fitting the data
n.sv The number of surrogate variables to estimate
B The number of iterations of the irwsva algorithm to perform
type If type is norm then standard irwsva is applied, if type is counts, then the moderated log transform is applied first

Value

pcontrol A vector of probabilities that each gene is a control.
Examples

```r
library(bladderbatch)
data(bladderdata)
dat <- bladderEset[1:5000,]

pheno = pData(dat)
edata = exprs(dat)
mod = model.matrix(~as.factor(cancer), data=pheno)

n.sv = num.sv(edata,mod,method="leek")
pcontrol <- empirical.controls(edata,mod,mod0=NULL,n.sv=n.sv,type="norm")
```

---

f.pvalue  

A function for quickly calculating f statistic p-values for use in sva

Description

This function does simple linear algebra to calculate f-statistics for each row of a data matrix comparing the nested models defined by the design matrices for the alternative (mod) and null (mod0) cases. The columns of mod0 must be a subset of the columns of mod.

Usage

```r
f.pvalue(dat, mod, mod0)
```

Arguments

- **dat**: The transformed data matrix with the variables in rows and samples in columns
- **mod**: The model matrix being used to fit the data
- **mod0**: The null model being compared when fitting the data

Value

- **p**: A vector of F-statistic p-values one for each row of dat.

Examples

```r
library(bladderbatch)
data(bladderdata)
dat <- bladderEset[1:50,]

pheno = pData(dat)
edata = exprs(dat)
mod = model.matrix(~as.factor(cancer), data=pheno)
mod0 = model.matrix(~1,data=pheno)

pValues = f.pvalue(edata,mod,mod0)
qValues = p.adjust(pValues,method="BH")
```
**fstats**

*A function for quickly calculating f statistics for use in sva*

**Description**

This function does simple linear algebra to calculate f-statistics for each row of a data matrix comparing the nested models defined by the design matrices for the alternative (mod) and null (mod0) cases. The columns of mod0 must be a subset of the columns of mod.

**Usage**

```r
fstats(dat, mod, mod0)
```

**Arguments**

- `dat`: The transformed data matrix with the variables in rows and samples in columns
- `mod`: The model matrix being used to fit the data
- `mod0`: The null model being compared when fitting the data

**Value**

A vector of F-statistics one for each row of dat.

**Examples**

```r
library(bladderbatch)
data(bladderdata)
dat <- bladderEset[1:50,]

pheno = pData(dat)
edata = exprs(dat)
mod = model.matrix(~as.factor(cancer), data=pheno)
mod0 = model.matrix(~1,data=pheno)

fs <- fstats(edata, mod, mod0)
```

---

**fsva**

*A function for performing frozen surrogate variable analysis as proposed in Parker, Corrada Bravo and Leek 2013*

**Description**

This function performs frozen surrogate variable analysis as described in Parker, Corrada Bravo and Leek 2013. The approach uses a training database to create surrogate variables which are then used to remove batch effects both from the training database and a new data set for prediction purposes. For inferential analysis see `sva`, `svaseq`, with low level functionality available through `irwsva.build` and `ssva`.
Usage

fsva(dbdat, mod, sv, newdat = NULL, method = c("fast", "exact"))

Arguments

dbdat A m genes by n arrays matrix of expression data from the database/training data
mod The model matrix for the terms included in the analysis for the training data
sv The surrogate variable object created by running sva on dbdat using mod.
newdat (optional) A set of test samples to be adjusted using the training database
method If method = "fast" then the SVD is calculated using an online approach, this may introduce slight bias. If method = "exact" the exact SVD is calculated, but will be slower

Value

db An adjusted version of the training database where the effect of batch/expression heterogeneity has been removed
new An adjusted version of the new samples, adjusted one at a time using the fsva methodology.
newsv Surrogate variables for the new samples

Examples

library(bladderbatch)
library(pamr)
data(bladderdata)
dat <- bladderEset[1:50,]
pheno = pData(dat)
edata = exprs(dat)

set.seed(1234)
trainIndicator = sample(1:57, size=30, replace=FALSE)
testIndicator = (1:57)[-trainIndicator]
trainData = edata[,trainIndicator]
testData = edata[,testIndicator]
trainPheno = pheno[trainIndicator,]
testPheno = pheno[testIndicator,]

mydata = list(x=trainData, y=trainPheno$cancer)
mytrain = pamr.train(mydata)
table(pamr.predict(mytrain, testData, threshold=2), testPheno$cancer)

trainMod = model.matrix(~cancer, data=trainPheno)
trainMod0 = model.matrix(~1, data=trainPheno)
trainSv = sva(trainData, trainMod, trainMod0)

fsvaobj = fsva(trainData, trainMod, trainSv, testData)
mydataSv = list(x=fsvaobj$db, y=trainPheno$cancer)
mytrainSv = pamr.train(mydataSv)
**Description**

This function is the implementation of the iteratively re-weighted least squares approach for estimating surrogate variables. As a buy product, this function produces estimates of the probability of being an empirical control. See the function `empirical.controls` for a direct estimate of the empirical controls.

**Usage**

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

**Arguments**

- `dat` The transformed data matrix with the variables in rows and samples in columns
- `mod` The model matrix being used to fit the data
- `mod0` The null model being compared when fitting the data
- `n.sv` The number of surrogate variables to estimate
- `B` The number of iterations of the irwsva algorithm to perform

**Value**

- `sv` The estimated surrogate variables, one in each column
- `pprob.gam` A vector of the posterior probabilities each gene is affected by heterogeneity
- `pprob.b` A vector of the posterior probabilities each gene is affected by `mod`
- `n.sv` The number of significant surrogate variables

**Examples**

```r
library(bladderbatch)
data(bladderbatch)
dat <- bladderEset[1:5000,]

pheno = pData(dat)
edata = exprs(dat)
mod = model.matrix(~as.factor(cancer), data=pheno)
n.sv = num.sv(edata,mod,method="leek")
res <- irwsva.build(edata, mod, mod0 = NULL,n.sv,B=5)
```
**num.sv**

*A function for calculating the number of surrogate variables to estimate in a model*

**Description**

This function estimates the number of surrogate variables that should be included in a differential expression model. The default approach is based on a permutation procedure originally proposed by Buja and Eyuboglu 1992. The function also provides an interface to the asymptotic approach proposed by Leek 2011 Biometrics.

**Usage**

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

**Arguments**

- `dat`: The transformed data matrix with the variables in rows and samples in columns
- `mod`: The model matrix being used to fit the data
- `method`: One of "be" or "leek" as described in the details section
- `vfilter`: You may choose to filter to the vfilter most variable rows before performing the analysis
- `B`: The number of permutations to use if method = "be"
- `seed`: Set a seed when using the permutation approach

**Value**

`n.sv` The number of surrogate variables to use in the sva software

**Examples**

```r
library(bladderbatch)
data(bladderdata)
dat <- bladderEset[1:5000,]
pheno = pData(dat)
edata = exprs(dat)
mod = model.matrix(~as.factor(cancer), data=pheno)
n.sv = num.sv(edata,mod,method="leek")
```
A function for estimating surrogate variables with the two step approach of Leek and Storey 2007

Description

This function is the implementation of the two step approach for estimating surrogate variables proposed by Leek and Storey 2007 PLoS Genetics. This function is primarily included for backwards compatibility. Newer versions of the sva algorithm are available through sva, svaseq, with low level functionality available through irwsva.build and ssva.

Usage

psva(dat, batch, ...)

Arguments

dat  The transformed data matrix with the variables in rows and samples in columns
batch  A factor variable giving the known batch levels
...  Other arguments to the sva function.

Value

psva.D Data with batch effect removed but biological heterogeneity preserved

Author(s)

Elana J. Fertig

Examples

library(bladderbatch)
library(limma)
data(bladderdata)
dat <- bladderEset[1:50,]
pheno = pData(dat)
edata = exprs(dat)
batch = pheno$batch
batch.fac = as.factor(batch)

psva_data <- psva(edata,batch.fac)
**qsva**

*A function for computing quality surrogate variables (qSVs)*

**Description**

This function computes quality surrogate variables (qSVs) from the library-size- and read-length-normalized degradation matrix for subsequent RNA quality correction.

**Usage**

```r
qsva(
  degradationMatrix,
  mod = matrix(1, ncol = 1, nrow = ncol(degradationMatrix))
)
```

**Arguments**

- **degradationMatrix**
  the normalized degradation matrix, region by sample

- **mod**
  (Optional) statistical model used in DE analysis

**Value**

the qSV adjustment variables

**Examples**

```r
## Find files
bwPath <- system.file('extdata', 'bwtool', package = 'sva')

## Read the data
degCovAdj = read.degradation.matrix(
  covFiles = list.files(bwPath,full.names=TRUE),
  sampleNames = list.files(bwPath), readLength = 76,
  totalMapped = rep(100e6,5),type="bwtool")

## Input data
head(degCovAdj)

## Results
qsva(degCovAdj)
```
read.degradation.matrix

A function for reading in coverage data from degradation-susceptible regions

Description

This function reads in degradation regions to form a library-size- and read-length-normalized degradation matrix for subsequent RNA quality correction.

Usage

read.degradation.matrix(
  covFiles, 
  sampleNames, 
  totalMapped, 
  readLength = 100, 
  normFactor = 8e+07, 
  type = c("bwtool", "region_matrix_single", "region_matrix_all"), 
  BPPARAM = bpparam()
)

Arguments

covFiles coverage file(s) for degradation regions
sampleNames sample names; creates column names of degradation matrix
totalMapped how many reads per sample (library size normalization)
readLength read length in base pairs (read length normalization)
normFactor common library size to normalize to; 80M reads as default
type whether input are individual ‘bwtool’ output, ‘region_matrix’ run on individual samples, or ‘region_matrix’ run on all samples together
BPPARAM (Optional) BiocParallelParam for parallel operation

Value

the normalized degradation matrix, region by sample

Examples

# bwtool
bwPath = system.file('extdata', 'bwtool', package = 'sva')
degCovAdj = read.degradation.matrix(
  covFiles = list.files(bwPath,full.names=TRUE), 
  sampleNames = list.files(bwPath), readLength = 76, 
  totalMapped = rep(100e6,5), type="bwtool")
head(degCovAdj)
# region_matrix: each sample
r1Path = system.file('extdata', 'region_matrix_one', package = 'sva')
degCovAdj1 = read.degradation.matrix(
  covFiles = list.files(r1Path, full.names=TRUE),
  sampleNames = list.files(r1Path), readLength = 76,
  totalMapped = rep(100e6, 5), type="region_matrix_single")
head(degCovAdj1)

r2Path = system.file('extdata', 'region_matrix_all', package = 'sva')
degCovAdj2 = read.degradation.matrix(
  covFiles = list.files(r2Path, full.names=TRUE),
  sampleNames = list.files(r1Path), readLength = 76,
  totalMapped = rep(100e6, 5), type="region_matrix_all")
head(degCovAdj2)

ssva

A function for estimating surrogate variables using a supervised approach

Description

This function implements a supervised surrogate variable analysis approach where genes/probes known to be affected by artifacts but not by the biological variables of interest are assumed to be known in advance. This supervised sva approach can be called through the sva and svaseq functions by specifying controls.

Usage

ssva(dat, controls, n.sv)

Arguments

dat
controls
n.sv

The transformed data matrix with the variables in rows and samples in columns
A vector of probabilities (between 0 and 1, inclusive) that each gene is a control. A value of 1 means the gene is certainly a control and a value of 0 means the gene is certainly not a control.
The number of surrogate variables to estimate

Value

sv The estimated surrogate variables, one in each column
pprob.gam: A vector of the posterior probabilities each gene is affected by heterogeneity (exactly equal to controls for ssva)
pprob.b A vector of the posterior probabilities each gene is affected by mod (always null for ssva)
n.sv The number of significant surrogate variables
Examples

```r
library(bladderbatch)
data(bladderdata)
dat <- bladderEset[1:5000,]

pheno = pData(dat)
edata = exprs(dat)
mod = model.matrix(~as.factor(cancer), data=pheno)
n.sv = num.sv(edata,mod,method="leek")
set.seed(1234)
controls <- runif(nrow(edata))
ssva_res <- ssva(edata,controls,n.sv)
```

Description

sva has functionality to estimate and remove artifacts from high dimensional data the **sva** function can be used to estimate artifacts from microarray data the **svaseq** function can be used to estimate artifacts from count-based RNA-sequencing (and other sequencing) data. The **ComBat** function can be used to remove known batch effects from microarray data. The **fsva** function can be used to remove batch effects for prediction problems.

This function is the implementation of the iteratively re-weighted least squares approach for estimating surrogate variables. As a by product, this function produces estimates of the probability of being an empirical control. See the function **empirical.controls** for a direct estimate of the empirical controls.

Usage

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

- **dat**: The transformed data matrix with the variables in rows and samples in columns.
- **mod**: The model matrix being used to fit the data.
- **mod0**: The null model being compared when fitting the data.
- **n.sv**: The number of surrogate variables to estimate.
- **controls**: A vector of probabilities (between 0 and 1, inclusive) that each gene is a control. A value of 1 means the gene is certainly a control and a value of 0 means the gene is certainly not a control.
- **method**: For empirical estimation of control probes use "irw". If control probes are known use "supervised".
- **vfilter**: You may choose to filter to the vfilter most variable rows before performing the analysis. vfilter must be NULL if method is "supervised".
- **B**: The number of iterations of the irwsva algorithm to perform.
- **numSVmethod**: If n.sv is NULL, sva will attempt to estimate the number of needed surrogate variables. This should not be adapted by the user unless they are an expert.

Details

A vignette is available by typing `browseVignettes("sva")` in the R prompt.

Value

- **sv**: The estimated surrogate variables, one in each column.
- **pprob.gam**: A vector of the posterior probabilities each gene is affected by heterogeneity.
- **pprob.b**: A vector of the posterior probabilities each gene is affected by mod.
- **n.sv**: The number of significant surrogate variables.

Author(s)

Jeffrey T. Leek, W. Evan Johnson, Hilary S. Parker, Andrew E. Jaffe, John D. Storey, Yuqing Zhang

References


For svaseq: Leek JT (2014) svaseq: removing batch and other artifacts from count-based sequencing data. bioRxiv doi: TBD
For fsva: Parker HS, Bravo HC, Leek JT (2013) Removing batch effects for prediction problems with frozen surrogate variable analysis arXiv:1301.3947


Examples

```r
library(bladderbatch)
data(bladderdata)
dat <- bladderEset[1:5000,]

pheno = pData(dat)
edata = exprs(dat)
mod = model.matrix(~as.factor(cancer), data=pheno)
mod0 = model.matrix(~1, data=pheno)

n.sv = num.sv(edata, mod, method="leek")
svobj = sva(edata, mod, mod0, n.sv=n.sv)
```

details

sva.check  

**A function for post-hoc checking of an sva object to check for degenerate cases.**

Description

This function is designed to check for degenerate cases in the sva fit and fix the sva object where possible.

Usage

`sva.check(svaobj, dat, mod, mod0)`

Arguments

- `svaobj`: The transformed data matrix with the variables in rows and samples in columns
- `dat`: The data set that was used to build the surrogate variables
- `mod`: The model matrix being used to fit the data
- `mod0`: The null model matrix being used to fit the data

Details

`empirical.controls` for a direct estimate of the empirical controls.
svaseq

A function for estimating surrogate variables for count based RNA-seq data.

Description

This function is the implementation of the iteratively re-weighted least squares approach for estimating surrogate variables. As a by product, this function produces estimates of the probability of being an empirical control. This function first applies a moderated log transform as described in Leek 2014 before calculating the surrogate variables. See the function `empirical.controls` for a direct estimate of the empirical controls.

Usage

```r
svaseq(
  dat,
  mod,
  mod0 = NULL,
  n.sv = NULL,
  controls = NULL,
  method = c("irw", "two-step", "supervised"),
  vfilter = NULL,
  B = 5,
  numSVmethod = "be",
)```
constant = 1

Arguments

dat The transformed data matrix with the variables in rows and samples in columns
mod The model matrix being used to fit the data
mod0 The null model being compared when fitting the data
n.sv The number of surrogate variables to estimate
controls A vector of probabilities (between 0 and 1, inclusive) that each gene is a control. A value of 1 means the gene is certainly a control and a value of 0 means the gene is certainly not a control.
method For empirical estimation of control probes use "irw". If control probes are known use "supervised"
Vfilter You may choose to filter to the Vfilter most variable rows before performing the analysis. Vfilter must be NULL if method is "supervised"
B The number of iterations of the irwsva algorithm to perform
numSVmethod If n.sv is NULL, sva will attempt to estimate the number of needed surrogate variables. This should not be adapted by the user unless they are an expert.
constant The function takes log(dat + constant) before performing sva. By default constant = 1, all values of dat + constant should be positive.

Value

sv The estimated surrogate variables, one in each column
pprob.gam: A vector of the posterior probabilities each gene is affected by heterogeneity
pprob.b A vector of the posterior probabilities each gene is affected by mod
n.sv The number of significant surrogate variables

Examples

library(zebrafishRNASeq)
data(zfGenes)
filter = apply(zfGenes, 1, function(x) length(x[x>5])>=2)
filtered = zfGenes[filter,]
gen = rownames(filtered)[grep("ENS", rownames(filtered))]
controls = grep("ERCC", rownames(filtered))
group = as.factor(rep(c("Ctl", "Trt"), each=3))
dat0 = as.matrix(filtered)

mod1 = model.matrix(~group)
mod0 = cbind(mod1[,1])
svseq = svaseq(dat0,mod1,mod0,n.sv=1)$sv
plot(svseq,pch=19,col="blue")
sva_network 

A function to adjust gene expression data before network inference

Description

This function corrects a gene expression matrix prior to network inference by returning the residuals after regressing out the top principal components. The number of principal components to remove can be determined using a permutation-based approach using the "num.sv" function with method = "be"

Usage

sva_network(dat, n.pc)

Arguments

dat 
The uncorrected normalized gene expression data matrix with samples in rows and genes in columns

n.pc 
The number of principal components to remove

Value

dat.adjusted Cleaned gene expression data matrix with the top principal components removed

Examples

library(bladderbatch)
data(bladderdata)
dat <- bladderEset[1:5000,]

edata = exprs(dat)
mod = matrix(1, nrow = dim(dat)[2], ncol = 1)

n.pc = num.sv(edata, mod, method="be")
dat.adjusted = sva_network(t(edata), n.pc)

---

twostepsva.build 

A function for estimating surrogate variables with the two step approach of Leek and Storey 2007

Description

This function is the implementation of the two step approach for estimating surrogate variables proposed by Leek and Storey 2007 PLoS Genetics. This function is primarily included for backwards compatibility. Newer versions of the sva algorithm are available through sva, svaseq, with low level functionality available through irwsva.build and ssva.
**twostepsva.build**

**Usage**

`twostepsva.build(dat, mod, n.sv)`

**Arguments**

- **dat**: The transformed data matrix with the variables in rows and samples in columns
- **mod**: The model matrix being used to fit the data
- **n.sv**: The number of surrogate variables to estimate

**Value**

- **sv**: The estimated surrogate variables, one in each column
- **pprob.gam**: A vector of the posterior probabilities each gene is affected by heterogeneity
- **pprob.b**: A vector of the posterior probabilities each gene is affected by `mod` (this is always null for the two-step approach)
- **n.sv**: The number of significant surrogate variables

**Examples**

```r
library(bladderbatch)
library(limma)
data(bladderdata)
dat <- bladderEset
pheno = pData(dat)
edata = exprs(dat)
mod = model.matrix(~as.factor(cancer), data=pheno)
n.sv = num.sv(edata, mod, method="leek")
svatwostep <- twostepsva.build(edata, mod, n.sv)
```
Index

ComBat, 2, 15
ComBat_seq, 4

empirical.controls, 5, 9, 15, 17, 18

f.pvalue, 6
fstats, 7
fsva, 7, 15

irwsva.build, 7, 9, 11, 20

num.sv, 10

psva, 11

qsva, 12

read.degradation.matrix, 13

ssva, 7, 11, 14, 20
sva, 7, 11, 14, 15, 15, 20
sva.check, 17
sva_network, 20
svaseq, 7, 11, 14, 15, 18, 20

twostepsva.build, 20