

pickgene

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Simulation.pickgene

Yi Lin's simulations for microarray analysis

Description

Example simulations

See Also

multipickgene

Examples

```
### Note: This uses old pickgene
#detail of the model (7-8). (first run does not include meas error \eta_i)
#par(mfrow=c(3,3))
t<-rnorm(10000,4,2)
changes1<-rep(0,10000)
changes1[1:500]<-rnorm(500)
t1<-t+changes1
changes2<-rep(0,10000)
changes2[1:500]<-rnorm(500)
t2<-t+changes2
s<-rnorm(10000,0,0.1)
cx<-3
cy<-2
t1<-t1+rnorm(10000,0,0.1)
t2<-t2+rnorm(10000,0,0.1)
x<-cx*exp(t1)
y<-cy*exp(t2)
#x<-cx*exp(t1)+rnorm(10000,0,50)
#y<-cy*exp(t2)+rnorm(10000,0,40)
xx<-qnorm(rank(x)/(10000+1))
yy<-qnorm(rank(y)/(10000+1))
#hist(x,breaks=100)
#hist(y,breaks=100)
#plot(x,y)
#hist(y[x<=0],breaks=20)
#hist(x[y<=0],breaks=20)
```

```

#plot(xx,yy)
topgenepick<-multipickgene( cbind(xx,yy),condi=0:1, geneID=1:10000, d=1,
                             npickgene=500)$pick[[1]]$probe
abchangesrank<-rank((-1)*abs(t1-t2))
count <- rep(NA,500)
for( i in 1:500 ) {
topipick <- topgenepick[1:i]
count[i] <- sum( abchangesrank[topipick] <= i )
}

## Figure 2
plot( 1:500, 1:500, type="n",
      xlab="Rank of 500 most changed genes by our procedure",
      ylab="Number similarly ranked by the 'optimal' procedure",
      xaxs="i", yaxs="i" )
lines( 1:500, count, type="s", lty=1, lwd=2 )
abline(0,1)
## Not run: dev.print( hor=F, height=6.5, width=6.5, file="rank1.ps" )

#again, but with the additive noise. (includes \eta_i)
par(mfrow=c(2,2))
t<-rnorm(10000,4,2)
changes1<-rep(0,10000)
changes1[1:500]<-rnorm(500)
t1<-t+changes1
changes2<-rep(0,10000)
changes2[1:500]<-rnorm(500)
t2<-t+changes2
s<-rnorm(10000,0,0.1)
cx<-3
cy<-2
t1<-t1+rnorm(10000,0,0.1)
t2<-t2+rnorm(10000,0,0.1)
### note that noise is very large here (50,40)
x<-cx*exp(t1)+rnorm(10000,0,50)
y<-cy*exp(t2)+rnorm(10000,0,40)
xx<-qnorm(rank(x)/(10000+1))
yy<-qnorm(rank(y)/(10000+1))
hist(x,breaks=100)
hist(y,breaks=100)
plot(x,y,cex=0.4)
#hist(y[x<=0],breaks=20)
#hist(x[y<=0],breaks=20)
plot(xx,yy,cex=0.4)
## Not run: dev.print( hor=F, height=6.5, width=6.5, file="simudata.ps" )

topgenepick<-multipickgene(cbind(xx,yy),condi=0:1, geneID=1:10000, d=1,
                             npickgene=500)$pick[[1]]$probe
abchangesrank<-rank((-1)*abs(t1-t2))
count <- rep(NA,500)
for( i in 1:500 ) {
topipick <- topgenepick[1:i]
count[i] <- sum( abchangesrank[topipick] <= i )
}
par(mfrow=c(1,1)) # figure 4
plot( 1:500, 1:500, type="n",
      xlab="Rank of 500 most changed genes by our procedure",

```

```

      ylab="Number similarly ranked by the 'optimal' procedure",
      xaxs="i", yaxs="i" )
lines( 1:500, count, type="s", lty=1, lwd=2 )
abline(0,1)
## Not run: dev.print( hor=F, height=6.5, width=6.5, file="rank2.ps" )

### Figure 5
genepick <- multipickgene( cbind(xx,yy), condi=0:1, geneID=1:10000, d=1)
## Not run: dev.print( hor=F, height=6.5, width=6.5, file="simutest.ps" )$pick[[1]]$probe
npick<-length(genepick$pickedgene)
genepick$pickedgene
npick
count[npick]

```

em.ggb

*EM calculation for Gamma-Gamma-Bernoulli Model***Description**

The function plots contours for the odds that points on microarray show differential expression between two conditions (e.g. Cy3 and Cy5 dye channels on the same microarray).

Usage

```
em.ggb(x, y, theta, start = c(2,1.2,2.7), pprior = 2,
       printit = FALSE, tol = 1e-9, offset = 0 )
```

Arguments

x	first condition expression levels
y	second condition expression levels
theta	four parameters a, a_0, ν, p
start	starting estimates for theta
pprior	Beta hyperparameter for prob p of differential expression
printit	print iterations if TRUE
tol	parameter tolerance for convergence
offset	offset added to xx and yy before taking log (can help with negative adjusted values)

Details

Fit Gamma/Gamma/Bernoulli model (equal marginal distributions) The model has spot intensities $x \sim \text{Gamma}(a,b)$; $y \sim \text{Gamma}(a,c)$. The shape parameters b and c are $\sim \text{Gamma}(a_0,\nu)$. With probability p , $b = c$; otherwise $b \neq c$. All spots are assumed to be independent.

Value

Four parameter vector `theta` after convergence.

Author(s)

Michael Newton

References

MA Newton, CM Kendzierski, CS Richmond, FR Blattner and KW Tsui (2000) "On differential variability of expression ratios: improving statistical inference about gene expression changes from microarray data," *J Computational Biology 00*: 000-000.

See Also[oddsplot](#)**Examples**

```
## Not run:
em.ggb( x, y )
## End(Not run)
```

model.pickgene

Create Model Matrix for Orthogonal Contrasts

Description

The function created a model matrix of orthogonal contrasts to be used by pickgene.

Usage

```
model.pickgene(faclevel, facnames = letters[seq(length(faclevel))],
               contrasts.fac = "contr.poly", collapse = "+", show =
               NULL, renorm = 1, modelexpr = formula(paste("~",
               paste(facnames, collapse = collapse))),
               contrasts.list = contr.list)
```

Arguments

faclevel	vector with number of levels for each factor
facnames	vector of factor names (default = "a","b",...)
contrasts.fac	vector of contrast types
collapse	"+" for additive model, "*" for full model with interactions
show	vector of contrast numbers to show (default is all)
renorm	vector to renormalize contrasts (e.g. use <code>sqrt(2)</code> to turn two-condition contrast into fold change)
modelexpr	model formula
contrasts.list	list of contrasts indexed by

Details

Creates a model matrix data frame with first column having all 1's and other columns having contrasts.

Value

Result of call to `model.matrix`

Author(s)

Brian Yandell

See Also

[model.matrix](#)

Examples

```
model.pickgene( c(2,3), c("sex", "genotype") )
```

oddsplot

Odds Plot for Differential Microarray Expression

Description

The function plots contours for the odds that points on microarray show differential expression between two conditions (e.g. Cy3 and Cy5 dye channels on the same microarray).

Usage

```
oddsplot(x, y, theta, by.level = 10, rotate = FALSE, offset =
         0, main = "", xlab = xlabs, ylab = ylabs, col = NULL,
         cex = c(0.25, 0.75), shrink = FALSE, lims =
         range(c(x, y)))
```

Arguments

<code>x</code>	first condition expression levels
<code>y</code>	second condition expression levels
<code>theta</code>	four parameters from <code>em.ggb</code>
<code>by.level</code>	odds plot contours increase by this level
<code>rotate</code>	rotate to average versus ratio if TRUE, otherwise plot conditions against each other
<code>offset</code>	offset for log transform
<code>main</code>	main title for plot
<code>xlab</code>	horizontal axis label (default if Cy3 if <code>rotate</code> is FALSE, Average Intensity otherwise)
<code>ylab</code>	vertical axis label (default if Cy5 if <code>rotate</code> is FALSE, Cy3 / Cy5 otherwise)

col	color of points (if NULL, use black for non-changing points, blue for changing points)
cex	character expansion (use <code>rep(.25, 2)</code> to have all points the same size)
shrink	use shrinkage on expression levels if TRUE (default is FALSE)
lims	limits for plot area

Details

Fit Gamma/Gamma/Bernoulli model (equal marginal distributions) The model has spot intensities $x \sim \text{Gamma}(a,b)$; $y \sim \text{Gamma}(a,c)$. The shape parameters b and c are $\sim \text{Gamma}(a_0, \nu)$. With probability p , $b = c$; otherwise $b \neq c$. All spots are assumed to be independent.

Value

Log odds for all points in original order.

Author(s)

Michael Newton

References

MA Newton, CM Kendziorski, CS Richmond, FR Blattner and KW Tsui (2000) "On differential variability of expression ratios: improving statistical inference about gene expression changes from microarray data," *J Computational Biology* 00: 000-000.

See Also

[em.ggb](#)

Examples

```
## Not run:
oddsplot( x, y )
## End(Not run)
```

pickgene

Plot and Pick Genes based on Differential Expression

Description

The function picks plots the average intensity versus linear contrasts (currently linear, quadratic up to cubic) across experimental conditions. Critical line is determine according to Bonferroni-like multiple comparisons, allowing SD to vary with intensity.

Usage

```
pickgene(data, geneID = 1:nrow(data), overalllevel = 0.05,
         npickgene = -1, marginal = FALSE, rankbased = TRUE,
         allrank = FALSE, meanrank = FALSE, offset = 0,
         modelmatrix = model.pickgene(faclevel, facnames,
         contrasts.fac, collapse, show, renorm), faclevel =
         ncol(data), facnames =
         letters[seq(length(faclevel))], contrasts.fac =
         "contr.poly", show = NULL, main = "", renorm = 1,
         drop.negative = FALSE, plotit = npickgene < 1, mfrow
         = c(nr, nc), mfcol = NULL, ylab = paste(shownames,
         "Trend"), ...)
```

Arguments

data	data matrix
geneID	gene identifier (default 1:nrow(x))
overalllevel	overall significance level (default 0.05)
npickgene	number of genes to pick (default -1 allows automatic selection)
marginal	additive model if TRUE, include interactions if FALSE
rankbased	use ranks if TRUE, log transform if FALSE
allrank	rank all chips together if true, otherwise rank separately
meanrank	show mean abundance as rank if TRUE
offset	offset for log transform
modelmatrix	model matrix with first row all 1's and other rows corresponding to design contrasts; automatically created by call to model.pickgene if omitted
faclevel	number of factor levels for each factor
facnames	factor names
contrasts.fac	type of contrasts
show	vector of contrast numbers to show (default is all)
main	vector of main titles for plots (default is none)
renorm	vector to renormalize contrasts (e.g. use sqrt(2) to turn two-condition contrast into fold change)
drop.negative	drop negative values in log transform
plotit	plot if TRUE
mfrow	par() plot arrangement by rows (default up to 6 per page; set to NULL to not change)
mfcol	par() plot arrangement by columns (default is NULL)
ylab	vertical axis labels
...	parameters for robustscale

Details

Infer genes that differentially express across conditions using a robust data-driven method. Adjusted gene expression levels A are replaced by $qnorm(rank(A))$, followed by `robustscale` estimation of center and spread. Then Bonferroni-style gene by gene tests are performed and displayed graphically.

Value

Data frame containing significant genes with the following information:

pick	data frame with picked genes
score	data frame with center and spread for plotting
probe	gene identifier
average	average gene intensity
fold1	positive fold change
fold2	negative fold change
pvalue	Bonferroni-corrected p-value
x	mean expression level (antilog scale)
y	contrast (antilog scale)
center	center for contrast
scale	scale (spread) for contrast
lower	lower test limit
upper	upper test limit

Author(s)

Yi Lin and Brian Yandell

References

Y Lin, BS Yandell and ST Nadler (2000) "Robust Data-Driven Inference for Gene Expression Microarray Experiments," Technical Report, Department of Statistics, UW-Madison.

See Also

[pickgene](#)

Examples

```
## Not run:
pickgene( data )
## End(Not run)
```

robustscale

Robust Estimation of Median (center) and MAD (scale)

Description

Smoothing spline estimate of median and mean absolute deviation (MAD).

Usage

```
robustscale(y, x, nslice=400, corcenter=TRUE, decrease=TRUE)
```


Arguments

<code>y</code>	response
<code>x</code>	predictor
<code>nslice</code>	number of slices (should be "large")
<code>corcenter</code>	correct for center
<code>decrease</code>	force MAD to decrease with <code>x</code>

Details

This divides data into roughly many `nslice` slices and computes median and mean absolute deviation (`mad`) for each slice. These are then smoothed using `smooth.spline`.

Value

Data frame containing significant genes with the following information:

<code>center</code>	estimate of center median
<code>scale</code>	MAD estimate of scale
<code>x</code>	ordered <code>x</code> values for plotting
<code>y</code>	<code>y</code> sorted by <code>x</code>

Author(s)

Yi Lin

See Also

[mad](#), [smooth.spline](#)

Examples

```
## Not run:  
robustscale(y, x)  
## End(Not run)
```

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