metaArray

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em.draw Plot of transformed expression produced by EM algorithm

Description

Given a numeric vector, a plot of four panels is drawn: 1) fitted mixture distribution 2) transformed expression against original expression 3) histogram of original expression 4) progression of log-likelihood during the fit

Usage

em.draw(vec, cl, threshold=0.0001)
#em.draw(vec, cl=1-metastasis, threshold=0.0001)

Arguments

vec A numeric vector, especially a particular row of expression matrix
cl A vector of 0s and 1s. Use 1 for normal phenotype and 0 for non-normal phenotype. If left blank, all samples will be labeled as normal phenotype. Normal component of mixture is estimated using samples with normal phenotype only. POE for samples with non-normal phenotype will be calculated after EM algorithm finishes ML estimation.
threshold Criterion for convergence in likelihood.
find.init  \hspace{1cm} \textit{Initialization of EM algorithm}

\textbf{Description}

This function is an automated initialization of $'z'$ in EM algorithm.

\textbf{Usage}

\begin{verbatim}
find.init(z, width = 1)
\end{verbatim}

\textbf{Arguments}

- \texttt{z} \hspace{1cm} Unobserved probability of membership to uniform component of the mixture.
- \texttt{width} \hspace{1cm} Constant factor used when assigning 0/1 labels to samples. Larger width will result in more samples initialized at 0.

\textbf{Value}

- \texttt{z} \hspace{1cm} A vector of 0/1, initial values of the EM algorithm

\textbf{Author(s)}

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\textbf{fit.em} \hspace{1cm} \textit{Probability of expression from mixture distribution for a single gene.}

\textbf{Description}

This core function fits two-component normal-uniform mixture distribution, and extracts probability of over/under expression for all samples in all genes.

\textbf{Usage}

\begin{verbatim}
fit.em(x, cl, threshold=1e-06)
\end{verbatim}
Arguments

x A numeric vector, especially expression values for a particular gene.
cl A vector of 0s and 1s. Use 1 for normal phenotype and 0 for non-normal phenotype. Note that this is the opposite of POE MCMC. If all samples are of unknown phenotype or of the same one, give vector of zeros. When class information is provided, conditional estimation of the mixture is applied.

threshold Criterion for convergence in likelihood

Value

expr Estimated POE
a Minimum (adjusted) of Raw Expression
b Maximum (adjusted) of Raw Expression
sigmasq Estimated variance of normal component
mu Estimated mean of normal component
Pi Probability that the gene is over/under expressed on average across the samples
lik.rec Trajectory of likelihood during EM

Author(s)

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intcor

**Integrative Correlation Analysis**

Description

This function calculates gene-specific reproducibility score based on Parmigiani et al. R implementation in MergeMaid (pairwise.cor) is a very efficient function in that it calculates the correlation matrix only once and collect appropriate elements for calculation of scores for each gene. However, in case there are more than thousands of common genes across datasets, the correlation matrix may overflow memory cells allotted to a session of R. Therefore, a replacement to the function that remedies the storage problem by brute force but fast computation in C is provided here.

Usage

intcor(merged)

Arguments

merged mergeExprSet object that contains gene expression and class label with all datasets.

Value

avg.cor A vector of gene-specific integrative correlation score
pair.cor A matrix of correlations for each gene in every pair of two studies
Author(s)
Debashis Ghosh <ghoshd@umich.edu>, Hyungwon Choi <hwchoi@umich.edu>

References
Clinical Cancer Research, Parmigiani et al. 10(9):2922-2927, 2004

Examples
#intcor(merged)

logit

Description
Calculates logit of a number

Usage
logit(p)

Arguments
p Success probability

Author(s)
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mdata

metaArray sample dataset

Description
Three datasets from liver, lung, and prostate cancer microarrays. Please refer to the bibliography in the vignette. Chen (30 primary, 9 metastatic), Garber (30 primary, 6 metastatic), Lapointe (30 primary, 9 metastatic)

Usage
data(mdata)
**poe.em**

*Probability of Expression from mixture distribution for multiple genes.*

**Description**

This function applies fit.em function to all rows of a gene expression data matrix.

**Usage**

```r
poe.em(mat, cl, threshold=1e-05, every = 100)
```

**Arguments**

- `mat`: Gene expression data matrix
- `cl`: A vector of 0s and 1s. Use 1 for normal phenotype and 0 for non-normal phenotype. If all samples are of unknown phenotype, give vectors of 0.
- `threshold`: Criterion of convergence in likelihood
- `every`: Progress of estimation is reported at every integer mode of the value 'every'

**Value**

A data matrix of transformed expression will result.

**Author(s)**

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**poe.mcmc**

*Probability of Expression (POE)*

**Description**

Differential expression using latent categories of up/down regulation. Three component normal-uniform mixture model under Bayesian hierarchical analysis. This is a C implementation of poe.fit function of POE package (MCMC). R portion of source code was directly adapted from POE; poe.one.iteration function was re-written in C. Some of the optional arguments available in poe.fit are suppressed here, and you cannot save the chain of samples drawn for numerical integration.

**Usage**

```r
poe.mcmc(AA, NN = NULL, id = NULL, M = 2000, kap.min=3.0,
         logdata=FALSE, stepsize=0.5,
         centersample = FALSE, centergene = FALSE, generatestarts = TRUE, start.met
         startobject = R0, collapse.to.two = FALSE, burnin=200,
         collapse.window=50, converge.threshold=0.01,
         PR = list(alpha.mm = 0, alpha.sd = 100, mu.mm = 0, mu.sd = 100,
                     pipos.mm = 0, pipos.sd = 100, pineg.mm = 0, pineg.sd = 100,
                     kap.pri.rate = 1, tausqinv.aa = 1, tausqinv.bb = 0.1))
# poe.mcmc(AA = chen, NN = 1 - chen.spl$metastasis, M=2000)
```
Zscore

**Arguments**

| AA | Matrix or `exprs` from an `ExpressionSet` object. |
| NN | Phenotypic label of arrays. If provided, all genes from arrays with label 1 are forced $e=0$ in all iterations. A gene with $e=0$ is involved in sampling of $\mu$ and $\alpha$. For arrays with label 0, $e$ is assumed to be unknown, thus sampled differently at every iteration. If this slot is left `NULL`, all arrays will be marked 0, so that the effect of the latter above applies to all arrays. |
| M | Number of MCMC iterations after burn-in. |

**Value**

| poe | Probability of over/under expression. Transformed gene expression on a fixed scale of $[-1,1]$. |

**Other values**

Posterior median estimates of parameters. Please refer to POE package for details.

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**References**

G. Parmigiani et al, JRSS, 64:717-736, 2002 or URL: http://astor.som.jhmi.edu/poe/

**Examples**

```r
# poe.mat <- poe.mcmc(AA=exprmat, NN=clvec, M=10000)
# One can also provide different hyperparameter values.
```

---

**Zscore**  
*Meta-analysis of Microarray Data from Different Platforms*

**Description**

This function calculates Z-score for each matched gene across all datasets. In each dataset, it performs local regression smoothing of mean vs variance. Z score is constructed by taking the ratio of weighted mean difference and combined standard deviation according to Box and Tiao (1992).

**Usage**

```r
Zscore(merged, pheno = NULL, permute = 0, verbose = TRUE)
```

**Arguments**

| merged | `mergeExprSet` object that contains gene expression and class label with all datasets. Class label should consist of two unique elements. If pheno is `NULL`, first columns of phenoData from each `ExpressionSet` is sought as class labels. If a vector of particular column number in each data is specified, corresponding columns of phenoData will be considered for class labels. |
Zscore

**pheno** A numeric vector specifying the location of class labels in phenoData from each `ExpressionSet`, a unit of `mergeExprSet` representing one dataset.

**permute** If `permute` is 0, weighted Z-score will be referenced to standard normal distribution for two-sided p-value. Otherwise, columns of all datasets (each dataset separately) will be shuffled at random, from which a permutation distribution of Z-scores are formed and Z-scores are referenced to this distribution.

**verbose** If `verbose` is TRUE, the progress of permutation will be reported.

**Value**
A data.frame with matched genes, Z-scores and p-values will result.

**Author(s)**
Debashis Ghosh <ghoshd@umich.edu>, Hyungwon Choi <hwchoi@umich.edu>

**References**
J.Wang et al, Bioinformatics 2004 Nov 22;20(17):3166-78

**Examples**
```
# Zscore(merged, pheno=NULL, permute=10000, verbose=FALSE)
```
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