Package 'DeMixT'

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Title Cell type-specific deconvolution of heterogeneous tumor samples with two or three components using expression data from RNAseq or microarray platforms		
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Description DeMixT is a software package that performs deconvolution on transcriptome data from a mixture of two or three components.		
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Description

Batch effect correction for multiple batches of tumor samples using ComBat

Usage

batch_correction(count.matrix, batch_labels)

Arguments

A matrix of raw expression count with G by (My), where G is the number count.matrix of genes, My is the number of mixed tumor samples. Row names are genes column names are tumor sample ids. Factor of tumor samples from different batches

batch_labels

Value

Batch effect corrected count matrix for tumor samples

DeMixT	Deconvolution of heterogeneous tumor samples with two or three com-
	ponents using expression data from RNAseq or microarray platforms

Description

DeMixT is a software that performs deconvolution on transcriptome data from a mixture of two or three components.

Usage

```
DeMixT(
  data.Y,
  data.N1,
  data.N2 = NULL
  niter = 10,
  nbin = 50,
  if.filter = TRUE,
  filter.sd = 0.5,
  ngene.selected.for.pi = NA,
  mean.diff.in.CM = 0.25,
  nspikein = min(200, ceiling(ncol(data.Y) * 0.3)),
  gene.selection.method = "GS",
  ngene.Profile.selected = NA,
  tol = 10^{(-5)}
  output.more.info = FALSE,
  pi01 = NULL,
  pi02 = NULL,
  nthread = parallel::detectCores() - 1
)
```

Arguments

data.Y

A SummarizedExperiment object of expression data from mixed tumor samples. It is a G by My matrix where G is the number of genes and My is the number of mixed samples. Samples with the same tissue type should be placed together in columns.

data.N1

A SummarizedExperiment object of expression data from reference component 1 (e.g., normal). It is a G by M1 matrix where G is the number of genes and M1 is the number of samples for component 1.

data.N2

A SummarizedExperiment object of expression data from additional reference samples. It is a G by M2 matrix where G is the number of genes and M2 is the number of samples for component 2. Component 2 is needed only for running a three-component model.

niter

The maximum number of iterations used in the algorithm of iterated conditional modes. A larger value better guarantees the convergence in estimation but increases the running time. The default is 10.

nbin

The number of bins used in numerical integration for computing complete likelihood. A larger value increases accuracy in estimation but increases the running time, especially in a three-component deconvolution problem. The default is 50.

if.filter

The logical flag indicating whether a predetermined filter rule is used to select genes for proportion estimation. The default is TRUE.

filter.sd

The cut-off for the standard deviation of lognormal distribution. Genes whose log transferred standard deviation smaller than the cut-off will be selected into the model. The default is 0.5.

ngene.selected.for.pi

The percentage or the number of genes used for proportion estimation. The difference between the expression levels from mixed tumor samples and the known component(s) are evaluated, and the most differential expressed genes are selected, which is called DE. It is enabled when if filter = TRUE. The default

is min(1500, 0.3*G), where G is the number of genes. Users can also try using more genes, ranging from 0.3*G to 0.5*G, and evaluate the outcome.

mean.diff.in.CM

Threshold of expression difference for selecting genes in the component merging strategy. We merge three-component to two-component by selecting genes with similar expressions for the two known components. Genes with the mean differences less than the threshold will be selected for component merging. It is used in the three-component setting, and is enabled when if filter = TRUE. The default is 0.25.

nspikein

The number of spikes in normal reference used for proportion estimation. The default value is min(200, 0.3*My), where My the number of mixed samples. If it is set to 0, proportion estimation is performed without any spike in normal reference.

gene.selection.method

The method of gene selection used for proportion estimation. The default method is 'GS', which applies a profile likelihood based method for gene selection. If it is set to 'DE', the most differential expressed genes are selected.

ngene.Profile.selected

The number of genes used for proportion estimation ranked by profile likelihood. The default is min(1500, 0.1 * G), where G is the number of genes. This is enabled only when gene.selection.method is set to 'GS'.

tol The convergence criterion. The default is 10^{-5} .

output.more.info

The logical flag indicating whether to show the estimated proportions in each iteration in the output.

pi01 Initialized proportion for first kown component. The default is Null and pi01 will be generated randomly from uniform distribution

will be generated randomly from uniform distribution.

Initialized proportion for second kown component. pi02 is needed only for running a three-component model. The default is Null and pi02 will be generated

randomly from uniform distribution.

nthread The number of threads used for deconvolution when OpenMP is available in the system. The default is the number of whole threads minus one. In our no-

OpenMP version, it is set to 1.

Value

pi02

pi A matrix of estimated proportion. First row and second row corresponds to the

proportion estimate for the known components and unkown component respectively for two or three component settings, and each column corresponds to one

sample.

pi.iter Estimated proportions in each iteration. It is a niter * My * p array, where p

is the number of components. This is enabled only when output.more.info =

TRUE.

ExprT A matrix of deconvolved expression profiles corresponding to T-component in

mixed samples for a given subset of genes. Each row corresponds to one gene

and each column corresponds to one sample.

ExprN1 A matrix of deconvolved expression profiles corresponding to N1-component in

mixed samples for a given subset of genes. Each row corresponds to one gene

and each column corresponds to one sample.

ExprN2	A matrix of deconvolved expression profiles corresponding to N2-component in mixed samples for a given subset of genes in a three-component setting. Each row corresponds to one gene and each column corresponds to one sample.
Mu	A matrix of estimated Mu of log2-normal distribution for both known ($MuN1, MuN2$) and unknown component (MuT). Each row corresponds to one gene.
Sigma	Estimated $Sigma$ of log2-normal distribution for both known ($SigmaN1, SigmaN2$) and unknown component ($SigmaT$). Each row corresponds to one gene.
gene.name	The names of genes used in estimating the proportions. If no gene names are provided in the original data set, the genes will be automatically indexed.
pi	A matrix of estimated proportion. First row and second row corresponds to the proportion estimate for the known components and unkown component respectively for two or three component settings, and each column corresponds to one sample.
pi.iter	Estimated proportions in each iteration. It is a $niter*My*p$ array, where p is the number of components. This is enabled only when output.more.info = TRUE.
ExprT	A matrix of deconvolved expression profiles corresponding to T-component in mixed samples for a given subset of genes. Each row corresponds to one gene and each column corresponds to one sample.
ExprN1	A matrix of deconvolved expression profiles corresponding to N1-component in mixed samples for a given subset of genes. Each row corresponds to one gene and each column corresponds to one sample.
ExprN2	A matrix of deconvolved expression profiles corresponding to N2-component in mixed samples for a given subset of genes in a three-component setting. Each row corresponds to one gene and each column corresponds to one sample.
Mu	A matrix of estimated Mu of log2-normal distribution for both known ($MuN1, MuN2$) and unknown component (MuT). Each row corresponds to one gene.
Sigma	Estimated $Sigma$ of log2-normal distribution for both known ($SigmaN1, SigmaN2$) and unknown component ($SigmaT$). Each row corresponds to one gene.
gene.name	The names of genes used in estimating the proportions. If no gene names are provided in the original data set, the genes will be automatically indexed.

Author(s)

Zeya Wang, Wenyi Wang Zeya Wang, Wenyi Wang

References

Wang Z, Cao S, Morris J S, et al. Transcriptome Deconvolution of Heterogeneous Tumor Samples with Immune Infiltration. iScience, 2018, 9: 451-460.

Wang Z, Cao S, Morris J S, et al. Transcriptome Deconvolution of Heterogeneous Tumor Samples with Immune Infiltration. iScience, 2018, 9: 451-460.

See Also

http://bioinformatics.mdanderson.org/main/DeMixT http://bioinformatics.mdanderson.org/main/DeMixT

Examples

```
# Example 1: simulated two-component data by using GS(gene selection method)
  data(test.data.2comp)
# res <- DeMixT(data.Y = test.data.2comp$data.Y,</pre>
                data.N1 = test.data.2comp$data.N1,
                data.N2 = NULL, nspikein = 50,
#
                gene.selection.method = 'GS',
#
                niter = 10, nbin = 50, if.filter = TRUE,
                ngene.selected.for.pi = 150,
#
                mean.diff.in.CM = 0.25, tol = 10^{(-5)}
# res$pi
# head(res$ExprT, 3)
# head(res$ExprN1, 3)
# head(res$Mu, 3)
# head(res$Sigma, 3)
# Example 2: simulated two-component data by using DE(gene selection method)
# data(test.data.2comp)
# res <- DeMixT(data.Y = test.data.2comp$data.Y,</pre>
                data.N1 = test.data.2comp$data.N1,
#
                data.N2 = NULL, nspikein = 50, g
                ene.selection.method = 'DE',
                niter = 10, nbin = 50, if.filter = TRUE,
                ngene.selected.for.pi = 150,
#
                mean.diff.in.CM = 0.25, tol = 10^{(-5)}
# Example 3: three-component mixed cell line data applying
# component merging strategy
# data(test.data.3comp)
# res <- DeMixT(data.Y = test.data.3comp$data.Y,</pre>
                data.N1 = test.data.3comp$data.N1,
                data.N2 = test.data.3comp$data.N2,
                if.filter = TRUE)
# Example: convert a matrix into the SummarizedExperiment format
# library(SummarizedExperiment)
# example <- matrix(c(1, 2, 3, 4, 5, 6), nrow = 2, ncol = 3, byrow = TRUE)
# example.se <- SummarizedExperiment(assays = list(counts = example))</pre>
# Example 1: simulated two-component data by using GS(gene selection method)
  data(test.data.2comp)
# res <- DeMixT(data.Y = test.data.2comp$data.Y,</pre>
                data.N1 = test.data.2comp$data.N1,
#
                data.N2 = NULL, nspikein = 50,
#
                gene.selection.method = 'GS',
                niter = 10, nbin = 50, if.filter = TRUE,
#
#
                ngene.selected.for.pi = 150,
                mean.diff.in.CM = 0.25, tol = 10^{(-5)}
# res$pi
# head(res$ExprT, 3)
# head(res$ExprN1, 3)
# head(res$Mu, 3)
# head(res$Sigma, 3)
# Example 2: simulated two-component data by using DE(gene selection method)
```

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```
# data(test.data.2comp)
# res <- DeMixT(data.Y = test.data.2comp$data.Y,</pre>
                data.N1 = test.data.2comp$data.N1,
#
                data.N2 = NULL, nspikein = 50, g
#
                ene.selection.method = 'DE',
                niter = 10, nbin = 50, if.filter = TRUE,
                ngene.selected.for.pi = 150,
                mean.diff.in.CM = 0.25, tol = 10^{(-5)}
# Example 3: three-component mixed cell line data applying
# component merging strategy
# data(test.data.3comp)
# res <- DeMixT(data.Y = test.data.3comp$data.Y,</pre>
                data.N1 = test.data.3comp$data.N1,
                data.N2 = test.data.3comp$data.N2,
#
                if.filter = TRUE)
#
# Example: convert a matrix into the SummarizedExperiment format
# library(SummarizedExperiment)
# example <- matrix(c(1, 2, 3, 4, 5, 6), nrow = 2, ncol = 3, byrow = TRUE)
# example.se <- SummarizedExperiment(assays = list(counts = example))</pre>
```

DeMixT_DE

Estimates the proportions of mixed samples for each mixing component

Description

This function is designed to estimate the deconvolved expressions of individual mixed tumor samples for unknown component for each gene.

Usage

```
DeMixT_DE(
  data.Y,
  data.N1,
  data.N2 = NULL,
  niter = 10,
  nbin = 50,
  if.filter = TRUE,
  filter.sd = 0.5,
  ngene.selected.for.pi = NA,
  nspikein = min(200, ceiling(ncol(data.Y) * 0.3)),
  mean.diff.in.CM = 0.25,
  tol = 10^(-5),
  pi01 = NULL,
  pi02 = NULL,
  nthread = parallel::detectCores() - 1
```

DeMixT_DE

Arguments

data.Y A SummarizedExperiment object of expression data from mixed tumor samples. It is a G by My matrix where G is the number of genes and My is the number of mixed samples. Samples with the same tissue type should be placed together

in columns.

data.N1 A SummarizedExperiment object of expression data from reference component

1 (e.g., normal). It is a G by M1 matrix where G is the number of genes and

M1 is the number of samples for component 1.

data.N2 A SummarizedExperiment object of expression data from additional reference

samples. It is a G by M2 matrix where G is the number of genes and M2 is the number of samples for component 2. Component 2 is needed only for running a

three-component model.

niter The maximum number of iterations used in the algorithm of iterated conditional

modes. A larger value better guarantees the convergence in estimation but in-

creases the running time. The default is 10.

nbin The number of bins used in numerical integration for computing complete like-

lihood. A larger value increases accuracy in estimation but increases the running time, especially in a three-component deconvolution problem. The default is 50.

if.filter The logical flag indicating whether a predetermined filter rule is used to select

genes for proportion estimation. The default is TRUE.

filter.sd The cut-off for the standard deviation of lognormal distribution. Genes whose

log transferred standard deviation smaller than the cut-off will be selected into

the model. The default is 0.5.

ngene.selected.for.pi

The percentage or the number of genes used for proportion estimation. The difference between the expression levels from mixed tumor samples and the known component(s) are evaluated, and the most differential expressed genes are selected, which is called DE. It is enabled when if filter = TRUE. The default is min(1500, 0.3*G), where G is the number of genes. Users can also try using

more genes, ranging from 0.3 * G to 0.5 * G, and evaluate the outcome.

The number of spikes in normal reference used for proportion estimation. The

default value is min(200, 0.3*My), where My the number of mixed samples. If it is set to 0, proportion estimation is performed without any spike in normal

reference.

mean.diff.in.CM

Threshold of expression difference for selecting genes in the component merging strategy. We merge three-component to two-component by selecting genes with similar expressions for the two known components. Genes with the mean differences less than the threshold will be selected for component merging. It is used in the three-component setting, and is enabled when if filter = TRUE. The

default is 0.25.

tol The convergence criterion. The default is 10^{-5} .

pi01 Initialized proportion for first kown component. The default is Null and pi01

will be generated randomly from uniform distribution.

pi02 Initialized proportion for second kown component. pi02 is needed only for run-

ning a three-component model. The default is $Null\ \mathrm{and}\ \mathrm{pi}02$ will be generated

randomly from uniform distribution.

nthread The number of threads used for deconvolution when OpenMP is available in the system. The default is the number of whole threads minus one. In our no-

OpenMP version, it is set to 1.

DeMixT_DE

Value

pi	A matrix of estimated proportion. First row and second row corresponds to the proportion estimate for the known components and unkown component respectively for two or three component settings, and each column corresponds to one sample.
pi.iter	Estimated proportions in each iteration. It is a $niter*Ny*p$ array, where p is the number of components. This is enabled only when output.more.info = TRUE.
gene.name	The names of genes used in estimating the proportions. If no gene names are provided in the original data set, the genes will be automatically indexed.

Author(s)

Zeya Wang, Wenyi Wang

References

Wang Z, Cao S, Morris J S, et al. Transcriptome Deconvolution of Heterogeneous Tumor Samples with Immune Infiltration. iScience, 2018, 9: 451-460.

See Also

http://bioinformatics.mdanderson.org/main/DeMixT

Examples

```
# Example 1: estimate proportions for simulated two-component data
# with spike-in normal reference
  data(test.data.2comp)
# res.DE = DeMixT_DE(data.Y = test.data.2comp$data.Y,
                     data.N1 = test.data.2comp$data.N1,
                     niter = 10, nbin = 50, nspikein = 50,
                     if.filter = TRUE,
#
                     mean.diff.in.CM = 0.25, ngene.selected.for.pi = 150,
                     tol = 10^{(-5)}
# Example 2: estimate proportions for simulated two-component data
# without spike-in normal reference
# data(test.data.2comp)
# res.DE = DeMixT_DE(data.Y = test.data.2comp$data.Y,
                     data.N1 = test.data.2comp$data.N1,
                     niter = 10, nbin = 50, nspikein = 0,
                     if.filter = TRUE,
                     mean.diff.in.CM = 0.25, ngene.selected.for.pi = 150,
                     tol = 10^{(-5)}
# Example 3: estimate proportions for simulated three-component
# mixed cell line data
# data(test.data.3comp)
# res.DE <- DeMixT_DE(data.Y = test.data.3comp$data.Y,</pre>
                      data.N1 = test.data.3comp$data.N1,
                      data.N2 = test.data.3comp$data.N2,
#
                      if.filter = TRUE)
```

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DeMixT_GS

Estimates the proportions of mixed samples for each mixing component using profile likelihood gene selection

Description

This function is designed to estimate the proportions of all mixed samples for each mixing component with a new proposed profile likelihood based gene selection, which can select most identifiable genes as reference gene sets to achieve better model fitting quality. We first calculated the Hessian matrix of the parameter spaces and then derive the confidence interval of the profile likelihood of each gene. We then utilized the length of confidence interval as a metric to rank the identifiability of genes. As a result, the proposed gene selection approach can improve the tumor-specific transcripts proportion estimation.

Usage

```
DeMixT_GS(
  data.Y,
  data.N1,
  data.N2 = NULL,
  niter = 10,
  nbin = 50,
  if.filter = TRUE,
  filter.sd = 0.5,
  ngene.Profile.selected = NA,
  ngene.selected.for.pi = NA,
  mean.diff.in.CM = 0.25,
  nspikein = min(200, ceiling(ncol(data.Y) * 0.3)),
  tol = 10^{(-5)},
  pi01 = NULL,
  pi02 = NULL,
  nthread = parallel::detectCores() - 1
```

Arguments

data.N2

niter

data.Y	A SummarizedExperiment object of expression data from mixed tumor samples.
	It is a G by My matrix where G is the number of genes and My is the number
	of mixed samples. Samples with the same tissue type should be placed together
	in columns.

data.N1 A SummarizedExperiment object of expression data from reference component 1 (e.g., normal). It is a G by M1 matrix where G is the number of genes and M1 is the number of samples for component 1.

A SummarizedExperiment object of expression data from additional reference samples. It is a G by M2 matrix where G is the number of genes and M2 is the number of samples for component 2. Component 2 is needed only for running a three-component model.

The maximum number of iterations used in the algorithm of iterated conditional modes. A larger value better guarantees the convergence in estimation but increases the running time. The default is 10.

DeMixT_GS

nbin The number of bins used in numerical integration for computing complete likelihood. A larger value increases accuracy in estimation but increases the running

time, especially in a three-component deconvolution problem. The default is 50.

if.filter The logical flag indicating whether a predetermined filter rule is used to select

genes for proportion estimation. The default is TRUE.

filter.sd The cut-off for the standard deviation of lognormal distribution. Genes whose

log transferred standard deviation smaller than the cut-off will be selected into

the model. The default is TRUE.

ngene.Profile.selected

The number of genes used for proportion estimation ranked by profile likelihood. The default is min(1500, 0.1 * G), where G is the number of genes.

ngene.selected.for.pi

The percentage or the number of genes used for proportion estimation. The difference between the expression levels from mixed tumor samples and the known component(s) are evaluated, and the most differential expressed genes are selected, which is called DE. It is enabled when if filter = TRUE. The default is min(1500, 0.3*G), where G is the number of genes. Users can also try using more genes, ranging from 0.3*G to 0.5*G, and evaluate the outcome.

mean.diff.in.CM

Threshold of expression difference for selecting genes in the component merging strategy. We merge three-component to two-component by selecting genes with similar expressions for the two known components. Genes with the mean differences less than the threshold will be selected for component merging. It is used in the three-component setting, and is enabled when if filter = TRUE. The

default is 0.25.

nspikein The number of spikes in normal reference used for proportion estimation. The

default value is min(200, 0.3 * My), where My the number of mixed samples. If it is set to 0, proportion estimation is performed without any spike in normal

reference.

tol The convergence criterion. The default is 10^(-5).

pi01 Initialized proportion for first kown component. The default is Null and pi01

will be generated randomly from uniform distribution.

pi02 Initialized proportion for second kown component. pi02 is needed only for run-

ning a three-component model. The default is Null and pi02 will be generated

randomly from uniform distribution.

nthread The number of threads used for deconvolution when OpenMP is available in

the system. The default is the number of whole threads minus one. In our no-

OpenMP version, it is set to 1.

Value

pi A matrix of estimated proportion. First row and second row corresponds to the

proportion estimate for the known components and unkown component respectively for two or three component settings, and each column corresponds to one

sample.

pi.iter Estimated proportions in each iteration. It is a niter * My * p array, where p

is the number of components. This is enabled only when output.more.info =

TRUE.

gene.name The names of genes used in estimating the proportions. If no gene names are

provided in the original data set, the genes will be automatically indexed.

Note

A Hessian matrix file will be created in the working directory and the corresponding Hessian matrix with an encoded name from the mixed tumor sample data will be saved under this file. If a user reruns this function with the same dataset, this Hessian matrix will be loaded to in place of running the profile likelihood method and reduce running time.

Author(s)

Shaolong Cao, Zeya Wang, Wenyi Wang

References

Gene Selection and Identifiability Analysis of RNA Deconvolution Models using Profile Likelihood. Manuscript in preparation.

See Also

http://bioinformatics.mdanderson.org/main/DeMixT

Examples

```
# Example 1: estimate proportions for simulated two-component data
# with spike-in normal reference
  data(test.data.2comp)
# res.GS = DeMixT_GS(data.Y = test.data.2comp$data.Y,
                     data.N1 = test.data.2comp$data.N1,
#
                     niter = 10, nbin = 50, nspikein = 50,
#
                     if.filter = TRUE, ngene.Profile.selected = 150,
                     mean.diff.in.CM = 0.25, ngene.selected.for.pi = 150,
                     tol = 10^{(-5)}
# Example 2: estimate proportions for simulated two-component data
# without spike-in normal reference
# data(test.dtat.2comp)
# res.GS = DeMixT_GS(data.Y = test.data.2comp$data.Y,
                     data.N1 = test.data.2comp$data.N1,
                     niter = 10, nbin = 50, nspikein = 0,
                     if.filter = TRUE, ngene.Profile.selected = 150,
                     mean.diff.in.CM = 0.25, ngene.selected.for.pi = 150,
                     tol = 10^{(-5)}
```

Description

DeMixT preprocessing in one go

 $DeMixT_S2$

Usage

```
DeMixT_preprocessing(
   count.matrix,
   normal.id,
   tumor.id,
   cutoff_normal_range = c(0.1, 1),
   cutoff_tumor_range = c(0, 2.5),
   cutoff_step = 0.2
)
```

Arguments

count.matrix

A matrix of raw expression count with G by (My+M1), where G is the number of genes, My is the number of mixed samples and M1 is the number of normal samples. Row names are genes column names are sample ids.

normal.id

A vector of normal sample ids

tumor.id

A vector of tumor sample ids

cutoff_normal_range

A vector of two numeric values, indicating the lower and upper bounds of standard deviation of log2 count matrix from the normal samples to subset. Default is c(0.2, 0.6)

cutoff_tumor_range

A vector of two numeric values, indicating the lower and upper bounds to search standard deviation of log2 count matrix from the normal samples to subset. Default is c(0.2, 0.6)

cutoff_step

A scatter value indicating the step size of changing cutoff_normal_range and cutoff_tumor_range to find a suitable subset of count matrix for downstream analysis

Value

processed count matrix

DeMixT_S2

Deconvolves expressions of each individual sample for unknown component

Description

This function is designed to estimate the deconvolved expressions of individual mixed tumor samples for unknown component for each gene.

Usage

```
DeMixT_S2(
  data.Y,
  data.N1,
  data.N2 = NULL,
  givenpi,
  nbin = 50,
  nthread = parallel::detectCores() - 1
)
```

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Arguments

data.Y A SummarizedExperiment object of expression data from mixed tumor samples. It is a G by My matrix where G is the number of genes and My is the number of mixed samples. Samples with the same tissue type should be placed together in columns. data.N1 A SummarizedExperiment object of expression data from reference component 1 (e.g., normal). It is a G by M1 matrix where G is the number of genes and M1 is the number of samples for component 1. data.N2 A SummarizedExperiment object of expression data from additional reference samples. It is a G by M2 matrix where G is the number of genes and M2 is the number of samples for component 2. Component 2 is needed only for running a three-component model. A vector of proportions for all mixed tumor samples. In two-component analygivenpi sis, it gives the proportions of the unknown reference component, and in threecomponent analysis, it gives the proportions for the two known components. nbin Number of bins used in numerical integration for computing complete likelihood. A larger value increases accuracy in estimation but increases the running time, especially in a three-component deconvolution problem. The default is 50. nthread The number of threads used for deconvolution when OpenMP is available in the system. The default is the number of whole threads minus one. In our no-OpenMP version, it is set to 1.

Value

decovExprT	A matrix of deconvolved expression profiles corresponding to T-component in mixed samples for a given subset of genes. Each row corresponds to one gene and each column corresponds to one sample.
decovExprN1	A matrix of deconvolved expression profiles corresponding to N1-component in mixed samples for a given subset of genes. Each row corresponds to one gene and each column corresponds to one sample.
decovExprN2	A matrix of deconvolved expression profiles corresponding to N2-component in mixed samples for a given subset of genes in a three-component setting. Each row corresponds to one gene and each column corresponds to one sample.
decovMu	A matrix of estimated Mu of log2-normal distribution for both known ($MuN1, MuN2$) and unknown component (MuT). Each row corresponds to one gene.
decovSigma	Estimated $Sigma$ of log2-normal distribution for both known ($SigmaN1, SigmaN2$) and unknown component ($SigmaT$). Each row corresponds to one gene.

Author(s)

Zeya Wang, Wenyi Wang

References

Wang Z, Cao S, Morris J S, et al. Transcriptome Deconvolution of Heterogeneous Tumor Samples with Immune Infiltration. iScience, 2018, 9: 451-460.

See Also

http://bioinformatics.mdanderson.org/main/DeMixT

Examples

```
# Example 1: two-component deconvolution given proportions
  data(test.data.2comp)
  givenpi <- c(t(as.matrix(test.data.2comp$pi[-2,])))</pre>
  res.S2 <- DeMixT_S2(data.Y = test.data.2comp$data.Y,
                       data.N1 = test.data.2comp$data.N1,
                       data.N2 = NULL,
                       givenpi = givenpi,
                       nbin = 50)
#
# Example 2: three-component deconvolution given proportions
# data(test.data.3comp)
# givenpi = c(t(test.data.3comp$pi[-3,]))
# res <- DeMixT_S2(data.Y = test.data.3comp$data.Y,</pre>
                   data.N1 = test.data.3comp$data.N1,
#
                   data.N2 = test.data.3comp$data.N2,
#
                   givenpi = givenpi,
#
                   nbin = 50)
```

Description

Detect suspicious samples by a hierarchical clustering

This function is designed to evaluate the separation of tumor samples and normal samples in a PCA space. If some normal samples appear in the tumor-sample dominated cluster, these normal samples are likely to be tumor samples and they are supposed to be filtered out before downstream analysis. But for those tumor samples appearing in the normal-sample dominated cluster, we do not remove them since they may be the ones with low tumor purity.

Plot the standard deviation of log2 raw expression

Plot the distribution of tumor and normal samples in a 2D PCA space based on their expressions

Usage

```
detect_suspicious_sample_by_hierarchical_clustering_2comp(
   count.matrix,
   normal.id,
   tumor.id
)

plot_sd(count.matrix, normal.id, tumor.id)

plot_dim(
   count.matrix,
   labels,
   legend.position = "bottomleft",
   legend.cex = 1.2
)
```

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Arguments

 ${\tt count.matrix} \qquad {\tt A \ matrix \ of \ raw \ expression \ count \ with \ } G \ {\tt by} \ (My+M1), \ {\tt where} \ G \ {\tt is \ the \ number}$

of genes, My is the number of mixed samples and M1 is the number of normal

samples. Row names are genes column names are sample ids.

normal.id A vector of normal sample ids

tumor.id A vector of tumor sample ids

legend.position

Position of legend in the plot. Default is bottomleft.

legend.cex Character expansion factor relative to current par("cex"). Default = 1.2

Value

list object

Optimum_KernelC

Kernel function for optimizing parameters and hidden variables in DeMixT

Description

This function is invoked by DeMixT_GS or DeMixT_DE and DeMixT_S2 to finish parameter estimation by iterated conditional mode algorithm and reconstitute gene expression profile of all components.

Usage

```
Optimum_KernelC(
  inputdata,
 groupid,
 nspikein,
 setting.pi,
 givenpi,
 givenpiT,
 niter,
 ninteg,
  tol,
  sg0 = 0.5^2,
 mu0 = 0,
 pi01 = NULL,
 pi02 = NULL,
 nthread = 1
)
```

Arguments

inputdata

A matrix of expression data (e.g gene expressions) from reference (e.g. normal) and mixed samples (e.g. mixed tumor samples). It is a G*M matrix where G is the number of genes and M is the number of samples including reference and mixed samples. Samples with the same tissue type should be placed together in columns (e.g. cbind(normal amples, mixed tumor samples).

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groupid

A vector of indicators to denote if the corresponding samples are reference samples or mixed tumor samples. DeMixT is able to deconvolve mixed tumor samples with at most three components. We use 1 and 2 to denote the samples referencing the first and the second known component in mixed tumor samples. We use 3 to indicate mixed tumor samples prepared to be deconvolved. For example, in two-component deconvolution, we have c(1,1,...,3,3) and in threecomponent deconvolution, we have c(1,1,...,2,2,...,3,3).

nspikein

The number of spikes in normal reference used for proportion estimation. The default value is min(200, 0.3 * My), where My the number of mixed tumor samples. If it is set to 0, proportion estimation is performed without any spike in normal reference.

setting.pi

If it is set to 0, then deconvolution is performed without any given proportions; if set to 1, deconvolution with given proportions for the first and the second known component is run; if set to 2, deconvolution is run with given tumor proportions. This option helps to perform deconvolution in different settings. In estimation of component-specific proportions, we use a subset of genes; so when it is required to deconvolve another subset of genes, we just easily plug back our estimated proportions by setting this option to 1. In our two-step estimation strategy in a three-component setting, this option is set to 2 to implement the second step.

givenpi

ST-Vector of proportions. Given the number of mixed tumor samples is My(My <M), ST is set to 2 * My in a three-component setting and My in a twocomponent setting. When setting.pi is 1, it is fixed with the given proportions for the first and the second known component of mixed tumor samples, or for one unknown component when there is just one type of reference tissues. It has the form of Vector PiN1-1, PiN1-2, ..., PiN1-My, PiN2-1, PiN2-2, ..., PiN2 - My.

givenpiT

ST-Vector of proportions. When setting pi is set to 2, givenpiT is fixed with given proportions for unknown component of mixed tumor samples. This option is used when we adopt a two-step estimation strategy in deconvolution. It has the form of Vector PiT - 1, PiT - 2, ..., PiT - My. If option is not 2, this vector can be given with any element.

niter

The number of iterations used in the algorithm of iterated conditional modes. A larger value can better guarantee the convergence in estimation but increase the computation time.

ninteg

The number of bins used in numerical integration for computing complete likelihood. A larger value can increase accuracy in estimation but also increase the running time. Especially in three-component deconvolution, the increase of number of bins can greatly lengthen the running time.

tol The convergence criterion. The default is 10^{-5} .

Initial value for σ^2 . The default is 0.5². sg0

Initial value for μ . The default is 0. mu0

Initialized proportion for first kown component. The default is Null and pi01 pi01 will be generated randomly from uniform distribution.

Initialized proportion for second kown component. pi02 is needed only for runpi02 ning a three-component model. The default is Null and pi02 will be generated randomly from uniform distribution.

nthread

The number of threads used for deconvolution when OpenMP is available in the system. The default is the number of whole threads minus one. In our no-OpenMP version, it is set to 1.

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Value

pi	Matrix of estimated proportions for each known component. The first row corresponds to the proportion estimate of each sample for the first known component (groupid = 1) and the second row corresponds to that for the second known component (groupid = 2).
decovExpr	A matrix of deconvolved expression profiles corresponding to unknown (e.g tumor) component in mixed samples for a given subset of genes. Each row corresponds to one gene and each column corresponds to one sample.
decovMu	Estimated Mu of log2-normal distribution for tumor component.
decovSigma	Estimated $Sigma$ of log2-normal distribution for tumor component.
pi1	An $My*I$ matrix of estimated proportions for each iteration, where I is the number of iteration, for the first known component.
pi2	An $My*I$ matrix of estimated proportions for each iteration, where I is the number of iteration, for the second known component.

Author(s)

Zeya Wang, Wenyi Wang

References

Wang Z, Cao S, Morris J S, et al. Transcriptome Deconvolution of Heterogeneous Tumor Samples with Immune Infiltration. iScience, 2018, 9: 451-460.

See Also

http://bioinformatics.mdanderson.org/main/DeMixT

Examples

Description

Quantile normalization for the raw count matrix of tumor and normal reference using the 0.75 quantile scale normalization

Usage

```
scale_normalization_75th_percentile(count.matrix)
```

Arguments

count.matrix

A matrix of raw expression count with G by (My+M1), where G is the number of genes, My is the number of mixed samples and M1 is the number of normal samples. Row names are genes column names are sample ids.

Value

the scale normalized count matrix

simulate_2comp

Function to simulate two-component test data

Description

Function to simulate two-component test data for DeMixT.

Usage

```
simulate_2comp(G = 500, My = 100, M1 = 100, output.more.info = FALSE)
```

Arguments

G Number of genes for simulation.

My Number of mixture tumor samples for simulation.

M1 Number of normal reference for simulation.

output.more.info

The logical flag indicating wheter to show True.data.T and True.data.N1 in the output. The default is FALSE.

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Value

pi	A matrix of estimated proportion. First row and second row corresponds to the proportion estimate for the known components and unkown component respectively for two or three component settings. Each column corresponds to one sample.
Mu	Simulated Mu of log2-normal distribution for both known ($MuN1$) and unknown component (MuT).
Sigma	Simulated $Sigma$ of log2-normal distribution for both known ($SigmaN1$) and unknown component ($SigmaT$).
data.Y	A SummarizedExperiment object of expression data from mixed tumor samples. It is a G by My matrix where G is the number of genes and My is the number of mixed samples. Samples with the same tissue type should be placed together in columns.
data.N1	A SummarizedExperiment object of expression data from reference component 1 (e.g., normal). It is a G by $M1$ matrix where G is the number of genes and $M1$ is the number of samples for component 1.
True.data.T	A SummarizedExperiment object of simulated tumor expression data. It is a G by My matrix, where G is the number of genes and My is the number of mixed samples. This is enabled only when output.more.info = TRUE.
True.data.N1	A SummarizedExperiment object of simulated true expression data for reference component 1 (e.g., normal). It is a G by $M1$ matrix where G is the number of genes and $M1$ is the number of samples for component 1. This is enabled only when output.more.info = TRUE.

Examples

```
test.data = simulate_2comp(G = 500, My = 100, M1 = 100)
test.data$pi
test.data$Mu
test.data$Sigma
```

simulate_3comp

Function to simulate three-component mixed cell line test data

Description

Function to simulate three-component mixed cell line test data used in DeMixT function.

Usage

```
simulate_3comp(
   G1 = 675,
   G2 = 25,
   My = 20,
   M1 = 100,
   M2 = 100,
   output.more.info = FALSE
)
```

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Arguments

G1	Number of genes, where μ_{N1} is close to μ_{N2} .
G2	Number of genes, where μ_{N1} is not close to μ_{N2} .
Му	Number of mixture tumor samples for simulation.
M1	Number of first known reference for simulation.
M2	Number of second known reference for simulation.
output more	info

output.more.info

The logical flag indicating wheter to show True.data.T, True.data.N1 and True.data.N2 in the output. The default is FALSE.

Value

11	iue		
	pi	A matrix of estimated proportion. First row and second row corresponds to the proportion estimate for the known components and unkown component respectively for two or three component settings. Each column corresponds to one sample.	
	Mu	Simulated Mu of log2-normal distribution for both known ($MuN1, MuN2$) and unknown component (MuT).	
	Sigma	Simulated $Sigma$ of log2-normal distribution for both known ($SigmaN1, SigmaN2$) and unknown component ($SigmaT$).	
	data.Y	A SummarizedExperiment object of simulated expression data from mixed tumor samples. It is a G by My matrix where G is the number of genes and My is the number of mixed samples. Samples with the same tissue type should be placed together in columns.	
	data.N1	A SummarizedExperiment object of simulated expression data from reference component 1 (e.g., normal). It is a G by $M1$ matrix where G is the number of genes and $M1$ is the number of samples for component 1.	
	data.N2	A SummarizedExperiment object of expression data from additional reference samples. It is a G by $M2$ matrix where G is the number of genes and $M2$ is the number of samples for component 2.	
	Tours data T	A Communication of Communication of simulated towns a supersisted data. It is a C	

True.data.T A SummarizedExperiment object of simulated tumor expression data. It is a Gby My matrix, where G is the number of genes and My is the number of mixed

samples. This is enabled only when output.more.info = TRUE.

True.data.N1 A SummarizedExperiment object of simulated true expression data for reference component 1 (e.g., stroma). It is a G by M1 matrix where G is the number of genes and M1 is the number of samples for component 1. This is enabled only when output.more.info = TRUE.

> A SummarizedExperiment object of simulated true expression data for reference component 2 (e.g., immue). It is a G by M2 matrix where G is the number of genes and M2 is the number of samples for component 2. This is enabled only when output.more.info = TRUE.

Examples

True.data.N2

```
test.data = simulate_3comp(G1 = 675, G2 = 25, My = 20, M1 = 100, M2 = 100)
test.data$pi
test.data$Mu
test.data$Sigma
```

 $subset_sd$

subset_sd

Description

Subset a count matrix given the the ranges of the standard deviations of the log2 expressions from the tumor and normal samples

Usage

```
subset_sd(
  count.matrix,
  normal.id,
  tumor.id,
  cutoff_normal = c(0.1, 0.6),
  cutoff_tumor = c(0.2, 0.8)
)
```

Arguments

count.matrix A matrix of raw expression count with G by (My+M1), where G is the number of genes, My is the number of mixed samples and M1 is the number of normal

samples. Row names are genes column names are sample ids.

normal.id A vector of normal sample ids tumor.id A vector of tumor sample ids

cutoff_normal A vector of two numeric values, indicating the lower and upper bounds of stan-

dard deviation of log2 count matrix from the normal samples to subset. Default

is c(0.1, 0.6)

cutoff_tumor A vector of two numeric values, indicating the lower and upper bounds of stan-

dard deviation of log2 count matrix from the tumor samples to subset. Default

is c(0.2, 0.8)

Value

A subset of the count matrix

```
subset_sd_gene_remaining
subset_sd_gene_remaining
```

Description

Find the cutoffs to filter out genes with large standard deviations of log2 expressions in both normal and tumor samples

test.data.2comp 23

Usage

```
subset_sd_gene_remaining(
  count.matrix,
  normal.id,
  tumor.id,
  cutoff_normal_range = c(0.2, 0.6),
  cutoff_tumor_range = c(0.2, 0.8),
  cutoff_step = 0.2
)
```

Arguments

count.matrix

A matrix of raw expression count with G by (My+M1), where G is the number of genes, My is the number of mixed samples and M1 is the number of normal samples. Row names are genes column names are sample ids.

normal.id

A vector of normal sample ids

tumor.id

A vector of tumor sample ids

cutoff_normal_range

A vector of two numeric values, indicating the lower and upper bounds of standard deviation of log2 count matrix from the normal samples to subset. Default is c(0.2, 0.6)

cutoff_tumor_range

A vector of two numeric values, indicating the lower and upper bounds to search standard deviation of log2 count matrix from the normal samples to subset. Default is c(0.2, 0.6)

cutoff_step

A scatter value indicating the step size of changing cutoff_normal_range and cutoff_tumor_range to find a suitable subset of count matrix for downstream analysis

test.data.2comp

Simulated two-component test data

Description

A list of simulated two-component test data used in DeMixT function. Expression data with 500 genes and 100 samples are simulated.

Usage

```
test.data.2comp
```

Format

An object of class list of length 5.

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Value

Sigma

data.Y

A list with 5 elements (2 more elements when output.more.info = TRUE), which are

A matrix of estimated proportion. First row and second row corresponds to the proportion estimate for the known components and unkown component respectively for two or three component settings. Each column corresponds to one sample.

Mu Simulated Mu of log2-normal distribution for both known (MuN1) and un-

Simulated Mu of log2-normal distribution for both known (MuN1) and unknown component (MuT).

Simulated Sigma of log2-normal distribution for both known (SigmaN1) and

unknown component (SigmaT).

A SummarizedExperiment object of expression data from mixed tumor samples. It is a G by My matrix where G is the number of genes and My is the number of mixed samples. Samples with the same tissue type should be placed together

in columns.

data.N1 A SummarizedExperiment object of expression data from reference component

1 (e.g., normal). It is a G by M1 matrix where G is the number of genes and

M1 is the number of samples for component 1.

True.data.T A SummarizedExperiment object of simulated tumor expression data. It is a G

by ${\cal M}y$ matrix, where ${\cal G}$ is the number of genes and ${\cal M}y$ is the number of mixed

samples. This is shown only when output.more.info = TRUE.

True.data.N1 A SummarizedExperiment object of simulated true expression data for reference

component 1 (e.g., normal). It is a G by M1 matrix where G is the number of genes and M1 is the number of samples for component 1. This is shown only

when output.more.info = TRUE.

test.data.3comp Simulated three-component mixed cell line test data

Description

A list of simulated three-component mixed cell line test data used in DeMixT function. Expression data with 700 genes and 20 samples are simulated, where 675 genes' MuN1 is close to MuN2.

Usage

test.data.3comp

Format

An object of class list of length 6.

Value

A list with 6 elements (3 more elements when output.more.info = TRUE), which are

A matrix of estimated proportion. First row and second row corresponds to the proportion estimate for the known components and unkown component respectively for two or three component settings. Each column corresponds to one sample.

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Mu Simulated Mu of log2-normal distribution for both known (MuN1, MuN2) and unknown component (MuT). Sigma Simulated Sigma of log2-normal distribution for both known (SigmaN1, SigmaN2) and unknown component (SigmaT). data.Y A SummarizedExperiment object of simulated expression data from mixed tumor samples. It is a G by My matrix where G is the number of genes and Myis the number of mixed samples. Samples with the same tissue type should be placed together in columns. data.N1 A SummarizedExperiment object of simulated expression data from reference component 1 (e.g., normal). It is a G by M1 matrix where G is the number of genes and M1 is the number of samples for component 1. data.N2 A SummarizedExperiment object of expression data from additional reference samples. It is a G by M2 matrix where G is the number of genes and M2 is the number of samples for component 2. True.data.T A SummarizedExperiment object of simulated tumor expression data. It is a Gby My matrix, where G is the number of genes and My is the number of mixed samples. This is shown only when output.more.info = TRUE. True.data.N1 A SummarizedExperiment object of simulated true expression data for reference component 1 (e.g., stroma). It is a G by M1 matrix where G is the number of genes and M1 is the number of samples for component 1. This is shown only when output.more.info = TRUE. True.data.N2 A SummarizedExperiment object of simulated true expression data for reference component 2 (e.g., immue). It is a G by M2 matrix where G is the number of genes and M2 is the number of samples for component 2. This is shown only when output.more.info = TRUE.

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