

# Package ‘nempi’

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**Type** Package

**Title** Inferring unobserved perturbations from gene expression data

**Version** 1.6.0

**Depends** R (>= 4.1), mnem

**Description** Takes as input an incomplete perturbation profile and differential gene expression in log odds and infers unobserved perturbations and augments observed ones. The inference is done by iteratively inferring a network from the perturbations and inferring perturbations from the network. The network inference is done by Nested Effects Models.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**biocViews** Software, GeneExpression, DifferentialExpression, DifferentialMethylation, GeneSignaling, Pathways, Network, Classification, NeuralNetwork, NetworkInference, ATACSeq, DNaseq, RNASeq, PooledScreens, CRISPR, SingleCell, SystemsBiology

**Imports** e1071, nnet, randomForest, naturalsort, graphics, stats, utils, matrixStats, epiNEM

**VignetteBuilder** knitr

**Suggests** knitr, BiocGenerics, rmarkdown, RUnit

**BugReports** <https://github.com/cbg-ethz/nempi/issues>

**URL** <https://github.com/cbg-ethz/nempi/>

**RoxygenNote** 7.1.1

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## R topics documented:

|                                 |          |
|---------------------------------|----------|
| classpi . . . . .               | 2        |
| nempi . . . . .                 | 3        |
| nempibs . . . . .               | 5        |
| pifit . . . . .                 | 6        |
| plot.nempi . . . . .            | 7        |
| plotConvergence.nempi . . . . . | 8        |
| <b>Index</b>                    | <b>9</b> |

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|         |                       |
|---------|-----------------------|
| classpi | <i>Classification</i> |
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## Description

Builds and uses different classifiers to infer perturbation profiles

## Usage

```
classpi(
  D,
  unknown = "",
  full = TRUE,
  method = "svm",
  size = NULL,
  MaxNWts = 10000,
  ...
)
```

## Arguments

|         |  |
|---------|--|
| D       | either a binary effects matrix or log odds matrix as for Nested Effects Models (see package 'nem') |
| unknown | colname of samples without mutation data, E.g. ""  |
| full    | if FALSE, does not change the known profiles   |
| method  | either one of svm, nn, rf  |
| size    | parameter for neural network (see package 'nnet')  |
| MaxNWts | parameters for neural network (see package 'nnet')   |
| ...     | additional parameters for mnem::nem  |

**Value**

plot

**Author(s)**

Martin Pirkl

**Examples**

```
D <- matrix(rnorm(1000*100), 1000, 100)
colnames(D) <- sample(seq_len(5), 100, replace = TRUE)
Gamma <- matrix(sample(c(0,1), 5*100, replace = TRUE, p = c(0.9, 0.1)), 5,
100)
Gamma <- apply(Gamma, 2, function(x) return(x/sum(x)))
Gamma[is.na(Gamma)] <- 0
rownames(Gamma) <- seq_len(5)
result <- classpi(D)
```

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nempi

*Main function for NEM based perturbation imputation.*

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**Description**

Infers perturbations profiles based on a sparse perturbation matrix and differential gene expression as log odds

**Usage**

```
nempi(
  D,
  unknown = "",
  Gamma = NULL,
  type = "null",
  full = TRUE,
  verbose = FALSE,
  logtype = 2,
  null = TRUE,
  soft = TRUE,
  combi = 1,
  converged = 0.1,
  complete = TRUE,
  mw = NULL,
  max_iter = 100,
  keepphi = TRUE,
  start = NULL,
  phi = NULL,
  ...
)
```

**Arguments**

|           |  |
|-----------|--|
| D         | either a binary effects matrix or log odds matrix as for Nested Effects Models (see package 'nem')                             |
| unknown   | colname of samples without mutation data, E.g. ""  |
| Gamma     | matrix with expectations of perturbations, e.g. if you have a binary mutation matrix, just normalize the columns to have sum 1 |
| type      | "null": does not use the unknown samples for inference at the start, "random" uses them in a random fashion (not recommended)  |
| full      | if FALSE, does not change the known profiles   |
| verbose   | if TRUE gives more output during inference   |
| logtype   | log type for the log odds  |
| null      | if FALSE does not use a NULL node for uninformative samples  |
| soft      | if FALSE discretizes Gamma during the inference  |
| combi     | if combi > 1, uses a more complex algorithm to infer combinatorial perturbations (experimental)                                |
| converged | the absolute difference of log likelihood till convergence   |
| complete  | if TRUE uses the complete-data loglikelihood (recommended for many E-genes)  |
| mw        | if NULL infers mixture weights, otherwise keeps them fixed   |
| max_iter  | maximum iterations of the EM algorithm   |
| keepphi   | if TRUE, uses the previous phi for the next inference, if FALSE always starts with start network (and empty and full)          |
| start     | starting network as adjacency matrix   |
| phi       | if not NULL uses only this phi and does not infer a new one  |
| ...       | additional parameters for the nem function (see package mnem, function nem or mnem::nem)                                       |

**Value**

nempi object

**Author(s)**

Martin Pirkl

**Examples**

```
D <- matrix(rnorm(1000*100), 1000, 100)
colnames(D) <- sample(seq_len(5), 100, replace = TRUE)
Gamma <- matrix(sample(c(0,1), 5*100, replace = TRUE, p = c(0.9, 0.1)), 5,
100)
Gamma <- apply(Gamma, 2, function(x) return(x/sum(x)))
Gamma[is.na(Gamma)] <- 0
rownames(Gamma) <- seq_len(5)
result <- nempi(D, Gamma = Gamma)
```

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|         |                               |
|---------|-------------------------------|
| nempibs | <i>Bootstrapping function</i> |
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**Description**

Bootstrap algorithm to get a more stable result.

**Usage**

```
nempibs(D, bsruns = 100, bssize = 0.5, replace = TRUE, ...)
```

**Arguments**

|         |  |
|---------|--|
| D       | either a binary effects matrix or log odds matrix as |
| bsruns  | number of bootstraps                                 |
| bssize  | number of E-genes for each bootstrap                 |
| replace | if TRUE, actual bootstrap, if False sub-sampling     |
| ...     | additional parameters for the function nempi         |

**Value**

list with aggregate Gamma and aggregate causal network phi

**Author(s)**

Martin Pirkl

**Examples**

```
D <- matrix(rnorm(1000*100), 1000, 100)
colnames(D) <- sample(seq_len(5), 100, replace = TRUE)
Gamma <- matrix(sample(c(0,1), 5*100, replace = TRUE, p = c(0.9, 0.1)), 5,
100)
Gamma <- apply(Gamma, 2, function(x) return(x/sum(x)))
Gamma[is.na(Gamma)] <- 0
rownames(Gamma) <- seq_len(5)
result <- nempibs(D, bsruns = 3, Gamma = Gamma)
```

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pifit

*Accuracy computation*

---

### Description

Compares the ground truth of a perturbation profile with the inferred profile

### Usage

```
pifit(x, y, D, unknown = "", balanced = FALSE, propagate = TRUE, knowns = NULL)
```

### Arguments

|           |  |
|-----------|--|
| x         | object of class nempi  |
| y         | object of class mnemsim  |
| D         | data matrix  |
| unknown   | label for the unlabelled samples   |
| balanced  | if TRUE, computes balanced accuracy  |
| propagate | if TRUE, propagates the perturbation through the network                   |
| knowns    | subset of P-genes that are known to be perturbed (the other are neglected) |

### Value

list of different accuracy measures: true/false positives/negatives, correlation, area under the precision recall curve, (balanced) accuracy

### Author(s)

Martin Pirkl

### Examples

```
library(mnem)
seed <- 42
Pgenes <- 10
Egenes <- 10
samples <- 100
uniform <- floor((Pgenes*Egenes)*0.1)
Nems <- mw <- 1
noise <- 1
multi <- c(0.2, 0.1)
set.seed(seed)
simmini <- simData(Sgenes = Pgenes, Egenes = Egenes,
Nems = Nems, mw = mw, nCells = samples,
uniform = uniform, multi = multi,
badCells = floor(samples*0.1))
data <- simmini$data
```

```
ones <- which(data == 1)
zeros <- which(data == 0)
data[ones] <- rnorm(length(ones), 1, noise)
data[zeros] <- rnorm(length(zeros), -1, noise)
lost <- sample(1:ncol(data), floor(ncol(data)*0.5))
colnames(data)[lost] <- ""
res <- nempi(data)
fit <- pifit(res, simmini, data)
```

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plot.nempi

*Plotting nempi*

---

## Description

Plot function for an object of class 'nempi'.

## Usage

```
## S3 method for class 'nempi'
plot(x, barlist = list(), heatlist = list(), ...)
```

## Arguments

|          |   |
|----------|---|
| x        | object of class 'nempi'   |
| barlist  | additional arguments for function 'barplot' from package 'graphics' |
| heatlist | additional arguments for function 'HeatmapOP' from package 'epiNEM' |
| ...      | additional arguments for function 'plotDnf' from package 'mnem'     |

## Value

Plots of the optimal network phi and perturbation matrix.

## Author(s)

Martin Pirkl

## Examples

```
D <- matrix(rnorm(1000*100), 1000, 100)
colnames(D) <- sample(seq_len(5), 100, replace = TRUE)
result <- nempi(D)
plot(result)
```

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plotConvergence.nempi *Plot convergence of EM*

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**Description**

Produces different convergence plots based on a nempi object

**Usage**

```
## S3 method for class 'nempi'  
plotConvergence(x, type = "b", ...)
```

**Arguments**

|      |                                |
|------|--------------------------------|
| x    | nempi object                   |
| type | see ?plot.default              |
| ...  | additional parameters for plot |

**Value**

plot

**Author(s)**

Martin Pirkel

**Examples**

```
D <- matrix(rnorm(1000*100), 1000, 100)  
colnames(D) <- sample(seq_len(5), 100, replace = TRUE)  
Gamma <- matrix(sample(c(0,1), 5*100, replace = TRUE, p = c(0.9, 0.1)), 5,  
100)  
Gamma <- apply(Gamma, 2, function(x) return(x/sum(x)))  
Gamma[is.na(Gamma)] <- 0  
rownames(Gamma) <- seq_len(5)  
result <- nempi(D, Gamma = Gamma)  
par(mfrow=c(2,3))  
plotConvergence(result)
```



# Index

`classpi`, [2](#)

`nempi`, [3](#)

`nempibs`, [5](#)

`pifit`, [6](#)

`plot.nempi`, [7](#)

`plotConvergence.nempi`, [8](#)