

# Package ‘MInt’

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**Type** Package

**Title** Learn Direct Interaction Networks

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**Description** Learns direct microbe-microbe interaction networks using a Poisson  
multivariate-normal hierarchical model with an L1 penalized precision  
matrix. Optimization is carried out using an iterative conditional modes  
algorithm.

**License** GPL-2

**Depends** R (>= 3.1.2), glasso (>= 1.8), trust (>= 0.1-6), MASS (>=  
7.3-35), testthat (>= 0.9.1)

**Suggests** knitr

**VignetteBuilder** knitr

**NeedsCompilation** no

**Repository** CRAN

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**bootstrap***Bootstrap*

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**Description**

This function bootstraps a model learned by estimate to obtain confidence intervals on each parameter.

**Usage**

```
bootstrap(mfit, nboot = 10, seed = 1)
```

**Arguments**

|       |                                      |
|-------|--------------------------------------|
| mfit  | A MInt model object.                 |
| nboot | The number of bootstraps to perform. |
| seed  | Random number generator seed.        |

**Value**

A MInt object.

We should export this at some point.

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**estimate***Estimate parameters*

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**Description**

This function performs iterative conditional modes to obtain maximum *a posteriori* estimates for  $\beta$  (covariate coefficients),  $w$  (latent abundances), and  $P$  (the precision matrix).

**Usage**

```
estimate(mfit)
```

**Arguments**

|      |                        |
|------|------------------------|
| mfit | - a MInt model object. |
|------|------------------------|

**Value**

A MInt model object with the following attributes:

|                |  |
|----------------|--|
| optim          | List containing optimization details                                 |
| optim\$lambda  | Value of the L1 penalty used during optimization                     |
| data           | List containing the raw data   |
| data\$design   | File path of the design matrix                                       |
| data\$response | File path of the response matrix                                     |
| data\$fmla     | Formula used to model each response in terms of the design variables |
| data\$y        | Raw numerical data for the response matrix                           |
| data\$xd       | Design matrix in categorical form                                    |
| data\$x        | Design matrix in numerical form                                      |
| param          | List containing parameter estimates                                  |
| param\$beta    | p-covariates x o-responses matrix of regression coefficients         |
| param\$w       | n-samples x o-responses matrix of latent abundances                  |
| param\$P       | o-responses x o-responses precision matrix                           |

**Examples**

```
x <- system.file("extdata", "x.txt", package="MInt");
y <- system.file("extdata", "y.txt", package="MInt");
m <- mint(y,x,fmla = ~feature1 + feature2)
m <- estimate(m)
```

mint

*Construct MInt object***Description**

Constructs a MInt object that maintains the data and parameter estimates for the underlying Poisson-multivariate normal hierarchical model.

**Usage**

```
mint(y, x, fmla = ~1)
```

**Arguments**

|      |  |
|------|--|
| y    | A file path to the response matrix.  |
| x    | A file path to the design matrix.  |
| fmla | An object of class “ <a href="#">formula</a> ” (or one that can be coerced to that class): a symbolic description of the model to be fitted. |

**Value**

*mint* A MInt object.

**Examples**

```
x <- system.file("extdata", "x.txt", package="MInt");
y <- system.file("extdata", "y.txt", package="MInt");
m <- mint(y,x,fmla = ~feature1 + feature2)
```

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