

# Package: efast (via r-universe)

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**Type** Package

**Title** Exploratory Factor Analysis with Structured Residuals

**Version** 0.6.3

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**Description** Create and estimate EFA and EFA with structured residuals (EFAST) models using structural equation modeling.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Imports** stringr, stats, MASS, corrplot

**RoxygenNote** 7.1.1

**Suggests** testthat (>= 2.1.0), knitr, rmarkdown

**Depends** lavaan (>= 0.6.4), R (>= 3.5.0)

**VignetteBuilder** knitr

**Repository** <https://lifebrain.r-universe.dev>

**RemoteUrl** <https://github.com/vankesteren/efast>

**RemoteRef** HEAD

**RemoteSha** 4c3bf819d0131f5655045a2bab514bd5da84d61

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cplot	<i>Create a clean correlation plot</i>
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## Description

This function is a thin wrapper around corrplot

## Usage

```
cplot(
  mat,
  tl.pos = "n",
  cl.pos = "n",
  method = "square",
  addgrid.col = NA,
  ...
)
```

## Arguments

mat	<matrix> or <list<matrix>> the matrix or list of matrices to be displayed.
tl.pos	<string> text label position, see corrplot::corrplot()
cl.pos	<string> color label position, see corrplot::corrplot()
method	<string> drawing method, see corrplot::corrplot()
addgrid.col	<string> grid colour see corrplot::corrplot()
...	other arguments passed to corrplot::corrplot()

## See Also

[corrplot](#)

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decomposition	<i>Get correlation matrix decomposition</i>
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**Description**

Get correlation matrix decomposition

**Usage**

```
decomposition(fit)
```

**Arguments**

fit                    an efast model

**Value**

The decomposition returns four components: the observed correlation matrix, the factor-implied covariance, the residual variance, and the structural covariance matrix. You can plot these matrices using `corrplot`.

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efast	<i>Estimate an EFAST model</i>
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**Description**

This function estimates efa models with residual covariance.

**Usage**

```
efast(  
  data,  
  M,  
  rstruct,  
  sample.nobs = NULL,  
  auto.fix.first = FALSE,  
  auto.var = TRUE,  
  auto.efa = TRUE,  
  information = "observed",  
  std.ov = TRUE,  
  ...  
)
```

**Arguments**

data	<data.frame> the dataset or <matrix> covariance matrix
M	<numeric> How many factors, minimum 2
rstruct	<list> residual structure (see details)
sample.nobs	<numeric> sample size (if data = covmat, see lavaan)
auto.fix.first	<bool> see lavaan
auto.var	<bool> see lavaan
auto.efa	<bool> see lavaan
information	<character> see lavaan
std.ov	<bool> see lavaan
...	other arguments passed to lavaan

**Details**

Residual structure (in the form of residual covariances) can be added to the EFA through a list of pairs of variable names. See the example for more information.

**Examples**

```
## Not run:
# Use a lavaan test dataset
test_data <- lavaan::HolzingerSwineford1939[,7:15]

# create an EFA model
test_efa <- efast(test_data, 3)

# create a (simple) residual structure
res_struct <- list(
  c("x4", "x7"),
  c("x5", "x9")
)

# create an efast model
test_efast <- efast(test_data, 3, res_struct)

compare the models
lavaan::lavTestLRT(test_efa, test_efast)

## End(Not run)
```

---

 efast\_efa

*Estimate an EFA model in lavaan*


---

## Description

This function estimates efa models in the same way that efast models are estimated: using lavaan.

## Usage

```
efast_efa(
  data,
  M,
  sample.nobs = NULL,
  auto.fix.first = FALSE,
  auto.var = TRUE,
  auto.efa = TRUE,
  information = "observed",
  std.ov = TRUE,
  ...
)
```

## Arguments

data	<data.frame> the dataset or <matrix> covariance matrix
M	<numeric> How many factors, minimum 2
sample.nobs	<numeric> sample size (if data = covmat, see lavaan)
auto.fix.first	<bool> see lavaan
auto.var	<bool> see lavaan
auto.efa	<bool> see lavaan
information	<character> see lavaan
std.ov	<bool> see lavaan
...	other arguments passed to lavaan

## Details

The constrained model constrains the residual covariance to be equal across the different ROIs.

## Examples

```
## Not run:
# create a test dataset
test_data <- simulate_efast()
fit_efa <- efast_efa(simdat, M = 4)
summary(fit_efa)

## End(Not run)
```

---

 efast\_hemi

*Estimate an EFAST-hemi model*


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### Description

This function estimates efast models with covariance due to hemispheric symmetry.

### Usage

```
efast_hemi(
  data,
  M,
  lh_idx,
  rh_idx,
  roi_names,
  constrain = FALSE,
  sample.nobs = NULL,
  auto.fix.first = FALSE,
  auto.var = TRUE,
  auto.efa = TRUE,
  information = "observed",
  std.ov = TRUE,
  ...
)
```

### Arguments

data	<data.frame> the dataset or <matrix> covariance matrix
M	<numeric> How many factors, minimum 2
lh_idx	<numeric> column numbers of left hemisphere variables
rh_idx	<numeric> column numbers of right hemisphere variables
roi_names	<character> optional names of rois
constrain	<bool> whether to constrain the symmetry (see details)
sample.nobs	<numeric> sample size (if data = covmat, see lavaan)
auto.fix.first	<bool> see lavaan
auto.var	<bool> see lavaan
auto.efa	<bool> see lavaan
information	<character> see lavaan
std.ov	<bool> see lavaan
...	other arguments passed to lavaan

### Details

The constrained model constrains the residual covariance to be equal across the different ROIs.

**Examples**

```
## Not run:  
# create a test dataset  
test_data <- simulate_efast()  
fit_efast <- efast_hemi(test_data, M = 4, 1:17, 18:34)  
summary(fit_efast)  
  
## End(Not run)
```

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efast_loadings	<i>Get loadings</i>
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**Description**

Get loadings

**Usage**

```
efast_loadings(fit, symmetry = FALSE)
```

**Arguments**

fit	efa or efast model
symmetry	whether to display the left and right hemisphere loadings side-by-side

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is_efast	<i>Check whether an object is an efast model</i>
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**Description**

Check whether an object is an efast model

**Usage**

```
is_efast(x)
```

**Arguments**

x	any object
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is_efast_efa	<i>Check whether an object is an efast-efa model</i>
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**Description**

Check whether an object is an efast-efa model

**Usage**

```
is_efast_efa(x)
```

**Arguments**

x	any object
---	------------

---

is_efast_hemi	<i>Check whether an object is an efast-hemi model</i>
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---

**Description**

Check whether an object is an efast-hemi model

**Usage**

```
is_efast_hemi(x)
```

**Arguments**

x	any object
---	------------

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lateralization	<i>Get lateralization per ROI</i>
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**Description**

The lateralization index (LI) is calculated as (sum of the uniquenesses for the contralateral homologues) / (total residual variance after accounting for the exploratory factors). Thus, if there is no symmetry at all, the LI is 1, and if all the residual variance is explained by symmetry, the LI is 0.

**Usage**

```
lateralization(fit)
```



**Arguments**

fit                    an efast model

**Value**

parameter estimates table of lateralization per ROI

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roi_volume	<i>Synthesised volume data for DKT-atlas ROIs.</i>
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**Description**

This data has been synthesised on the basis of real-world data from the Cam-CAN cohort. It contains 68 grey matter volume measurements (34 LH and 34 RH ROIs) for 647 participants.

**Usage**

```
data(roi_volume)
```

**Format**

A data frame with 647 rows and 68 columns

**References**

[cam-can.org](http://cam-can.org)

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simulate_efast	<i>Simulate data from an efast matrix</i>
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**Description**

Simulate a dataset as in the simulations of Van Kesteren & Kievit (2019). There are 17 regions of interest, measured in both the left and right hemisphere. These ROIs have a predefined amount of correlation over and above that expected by only the underlying factors.

**Usage**

```
simulate_efast(
  N = 650L,
  lam_lat = 0.595,
  lam_bil = 0.7,
  psi_cov = 0.5,
  cor_uniq = 0.4
)
```

**Arguments**

N	<int> Sample size
lam_lat	<numeric> factor loading for the lateralised factor
lam_bil	<numeric> factor loading for the bilateral factors
psi_cov	<numeric> covariances of latent variables in (0, 1)
cor_uniq	<numeric> residual correlation

**Value**

data frame with 17 regions of interest, bilaterally measured with 4 underlying factors and contralateral homology.

**References**

Van Kesteren, E. J., & Kievit, R. K. (2019) Exploratory factor analysis with structured residuals applied to brain morphology.

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