

# Package ‘EGAnet’

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**Title** Exploratory Graph Analysis - A Framework for Estimating the Number of Dimensions in Multivariate Data Using Network Psychometrics

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**Description** Implements the Exploratory Graph Analysis (EGA) framework for dimensionality and psychometric assessment. EGA is part of a new area called network psychometrics that uses undirected network models for the assessment of psychometric properties. EGA estimates the number of dimensions (or factors) using graphical lasso or Triangulated Maximally Filtered Graph (TMFG) and a weighted network community detection algorithm. A bootstrap method for verifying the stability of the dimensions and items in those dimensions is available. The fit of the structure suggested by EGA can be verified using Entropy Fit Indices. A novel approach called Unique Variable Analysis (UVA) can be used to identify and reduce redundant variables in multivariate data. Network loadings, which are roughly equivalent to factor loadings when the data generating model is a factor model, are available. Network scores can also be computed using the network loadings. Dynamic EGA (dynEGA) will estimate dimensions from time series data for individual, group, and sample levels. Golino, H., & Epskamp, S. (2017) <doi:10.1371/journal.pone.0174035>. Golino, H., Shi, D., Christensen, A. P., Garrido, L. E., Nieto, M. D., Sadana, R., & Thiyagarajan, J. A. (2020) <doi:10.1037/met0000255>. Christensen, A. P., & Golino, H. (under review) <doi:10.31234/osf.io/hz89e>. Golino, H., Moulder, R. G., Shi, D., Christensen, A. P., Garrido, L. E., Nieto, M. D., Nesselroade, J., Sadana, R., Thiyagarajan, J. A., & Boker, S. M. (2020) <doi:10.31234/osf.io/mtka2>. Christensen, A. P. & Golino, H. (2019) <doi:10.31234/osf.io/9deay>. Christensen, A. P., Garrido, L. E., & Golino, H. (under review) <doi:10.31234/osf.io/4kra2>. Golino, H., Christensen, A. P., Moulder, R. G., Kim, S., & Boker, S. M. (under review) <doi:10.31234/osf.io/tfs7c>.

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 EGAnet-package

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 EGAnet-package
 

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## Description

Implements the Exploratory Graph Analysis (EGA; Golino & Epskamp, 2017; Golino, Shi, et al., 2020) framework for dimensionality and psychometric assessment. EGA is part of a new area called *network psychometrics* that uses undirected network models for the assessment of psychometric properties. EGA estimates the number of dimensions (or factors) using graphical lasso [EBICglasso](#) or Triangulated Maximally Filtered Graph (TMFG) and a weighted network community detection algorithm (Christensen & Golino, under review). A bootstrap method for verifying the stability of the dimensions and items in those dimensions is available ([bootEGA](#); Christensen & Golino, 2019). The fit of the structure suggested by EGA can be verified using Entropy Fit Indices ([entropyFit](#), [tefi](#); Golino, Moulder, et al., 2020). A novel approach called Unique Variable Analysis (UVA) can be used to identify and reduce redundant variables in multivariate data (Christensen, Garrido, & Golino, under review). Network loadings ([net.loads](#)), which are roughly equivalent to factor loadings when the data generating model is a factor model, are available (Christensen & Golino, 2021). Network scores ([net.scores](#)) can also be computed using the network loadings. Finally, dynamic EGA ([dynEGA](#)) will estimate dimensions from time series data for individual, group, and sample levels (Golino, Christensen, et al., under review).

## Author(s)

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## References

- Christensen, A. P., Garrido, L. E., & Golino, H. (under review). Unique Variable Analysis: A novel approach to detect redundant variables in multivariate data. *PsyArXiv*. doi: [10.31234/osf.io/4kra2](https://doi.org/10.31234/osf.io/4kra2)  
# Related functions: [UVA](#)
- Christensen, A. P., & Golino, H. (under review). Estimating factors with psychometric networks: A Monte Carlo simulation comparing community detection algorithms. *PsyArXiv*. doi: [10.31234/osf.io/hz89e](https://doi.org/10.31234/osf.io/hz89e)  
# Related functions: [EGA](#)
- Christensen, A. P., & Golino, H. (2019). Estimating the stability of the number of factors via Bootstrap Exploratory Graph Analysis: A tutorial. *PsyArXiv*. doi: [10.31234/osf.io/9deay](https://doi.org/10.31234/osf.io/9deay)  
# Related functions: [bootEGA](#)
- Christensen, A. P., & Golino, H. (2021). On the equivalency of factor and network loadings. *Behavior Research Methods*. doi: [10.3758/s13428020015006](https://doi.org/10.3758/s13428020015006)  
# Related functions: [LCT](#) and [net.loads](#)
- Christensen, A. P., & Golino, H. (under review). Random, factor, or network model? Predictions from neural networks. *PsyArXiv*. doi: [10.31234/osf.io/awkcb](https://doi.org/10.31234/osf.io/awkcb)  
# Related functions: [LCT](#)
- Christensen, A. P., Golino, H., & Silvia, P. J. (2020). A psychometric network perspective on the validity and validation of personality trait questionnaires. *European Journal of Personality*, *34*, 1095-1108. doi: [10.1002/per.2265](https://doi.org/10.1002/per.2265)  
# Related functions: [bootEGA](#), [dimStability](#), # [EGA](#), [itemStability](#), and [UVA](#)
- Golino, H., Christensen, A. P., Moulder, R. G., Kim, S., & Boker, S. M. (under review). Modeling latent topics in social media using Dynamic Exploratory Graph Analysis: The case of the right-wing and left-wing trolls in the 2016 US elections. *PsyArXiv*. doi: [10.31234/osf.io/tfs7c](https://doi.org/10.31234/osf.io/tfs7c)  
# Related functions: [dynEGA](#) and [simDFM](#)
- Golino, H., & Demetriou, A. (2017). Estimating the dimensionality of intelligence like data using Exploratory Graph Analysis. *Intelligence*, *62*, 54-70. doi: [10.1016/j.intell.2017.02.007](https://doi.org/10.1016/j.intell.2017.02.007)  
# Related functions: [EGA](#)
- Golino, H., & Epskamp, S. (2017). Exploratory graph analysis: A new approach for estimating the number of dimensions in psychological research. *PLoS ONE*, *12*, e0174035. doi: [10.1371/journal.pone.0174035](https://doi.org/10.1371/journal.pone.0174035)  
# Related functions: [EGA](#)
- Golino, H., Moulder, R. G., Shi, D., Christensen, A. P., Garrido, L. E., Nieto, M. D., Nesselroade, J., Sadana, R., Thiyagarajan, J. A., & Boker, S. M. (2020). Entropy fit indices: New fit measures for assessing the structure and dimensionality of multiple latent variables. *Multivariate Behavioral Research*. doi: [10.31234/osf.io/mtka2](https://doi.org/10.31234/osf.io/mtka2)  
# Related functions: [entropyFit](#), [tefi](#), and [vn.entropy](#)
- Golino, H., Shi, D., Christensen, A. P., Garrido, L. E., Nieto, M. D., Sadana, R., Thiyagarajan, J. A., & Martinez-Molina, A. (2020). Investigating the performance of exploratory graph analysis and traditional techniques to identify the number of latent factors: A simulation and tutorial. *Psychological Methods*, *25*, 292-320. doi: [10.1037/met0000255](https://doi.org/10.1037/met0000255)  
# Related functions: [EGA](#)
- Golino, H., Thiyagarajan, J. A., Sadana, M., Teles, M., Christensen, A. P., & Boker, S. M. (under review). Investigating the broad domains of intrinsic capacity, functional ability, and environment: An

exploratory graph analysis approach for improving analytical methodologies for measuring healthy aging. *PsyArXiv*. doi: [10.31234/osf.io/hj5mc](https://doi.org/10.31234/osf.io/hj5mc)  
 # Related functions: [EGA.fit](#) and [tefi](#)

---

 boot.ergoInfo

---

*Bootstrap Test for the Ergodicity Information Index*


---

## Description

Computes a parametric Bootstrap Test for the Ergodicity Information Index, comparing the empirical Ergodicity Information index to values obtained in data generated using  $N$  parametric bootstraps of the correlation matrix estimated using the [dynEGA](#) function, for the population structure. The p-values in the bootstrap test can be calculated as  $(\text{sum}(\text{EII} \geq \text{boot.EII}) + 1) / (\text{iter} + 1)$  and as  $(\text{sum}(\text{EII} \leq \text{boot.EII}) + 1) / (\text{iter} + 1)$ , where EII is the empirical Ergodicity Information Index, boot.EII is the values of the Ergodicity Information Index obtained in the bootstrapped samples, and iter is the number of random samples generated in the simulation. The two-sided p-value is computed as two times the lowest p-value. In the bootstrap Test for the Ergodicity Information Index, the null hypothesis is that the empirical value of EII is equal to the values of EII obtained in multiple individuals with the same structure as the population structure estimated via [dynEGA](#). Small values of p indicate that is very unlikely to obtain an EII as large as the one obtained in the empirical sample if the null hypothesis is true (i.e. all individuals have the same structure as the population structure), thus there is convincing evidence that the empirical Ergodicity Information Index is different than it could be expected if all individuals had a similar latent structure.

## Usage

```
boot.ergoInfo(
  dynEGA.pop,
  iter,
  EII,
  use,
  embed,
  tau,
  delta,
  derivatives,
  model,
  model.args = list(),
  algorithm = c("walktrap", "louvain"),
  algorithm.args = list(),
  corr,
  ncores,
  ...
)
```

## Arguments

dynEGA.pop      A dynEGA or a dynEGA.pop.ind object.

iter	Numeric integer. Number of random samples to generate in the Monte-Carlo simulation. At least 500 is recommended
EII	Numeric. Empirical Ergodicity Information Index obtained via the <a href="#">ergoInfo</a> function.
use	Character. A string indicating what network element will be used to compute the algorithm complexity in the <a href="#">ergoInfo</a> function, the list of edges or the weights of the network. Defaults to use = "edge.list". Current options are: <ul style="list-style-type: none"> <li>• edge.list Calculates the algorithm complexity using the list of edges.</li> <li>• weights Calculates the algorithm complexity using the weights of the network.</li> </ul>
embed	Integer. Number of embedded dimensions (the number of observations to be used in the <a href="#">Embed</a> function). For example, an "embed = 5" will use five consecutive observations to estimate a single derivative. Default is "embed = 5".
tau	Integer. Number of observations to offset successive embeddings in the <a href="#">Embed</a> function. A tau of one uses adjacent observations. Default is "tau = 1".
delta	Integer. The time between successive observations in the time series. Default is "delta = 1".
derivatives	Integer. The order of the derivative to be used in the EGA procedure. Default to 1.
model	Character. A string indicating the method to use. Defaults to glasso. Current options are: <ul style="list-style-type: none"> <li>• glasso Estimates the Gaussian graphical model using graphical LASSO with extended Bayesian information criterion to select optimal regularization parameter. This is the default method</li> <li>• TMFG Estimates a Triangulated Maximally Filtered Graph</li> </ul>
model.args	List. A list of additional arguments for <a href="#">EBICglasso.qgraph</a> or <a href="#">TMFG</a>
algorithm	A string indicating the algorithm to use or a function from <a href="#">igraph</a> Current options are: <ul style="list-style-type: none"> <li>• walktrap Computes the Walktrap algorithm using <a href="#">cluster_walktrap</a></li> <li>• louvain Computes the Walktrap algorithm using <a href="#">cluster_louvain</a></li> </ul>
algorithm.args	List. A list of additional arguments for <a href="#">cluster_walktrap</a> , <a href="#">cluster_louvain</a> , or some other community detection algorithm function (see examples)
corr	Type of correlation matrix to compute. The default uses <a href="#">cor_auto</a> . Current options are: <ul style="list-style-type: none"> <li>• cor_auto Computes the correlation matrix using the <a href="#">cor_auto</a> function from <a href="#">qgraph</a>.</li> <li>• pearson Computes Pearson's correlation coefficient using the pairwise complete observations via the <a href="#">cor</a> function.</li> <li>• spearman Computes Spearman's correlation coefficient using the pairwise complete observations via the <a href="#">cor</a> function.</li> </ul>

ncores            Numeric. Number of cores to use in computing results. Defaults to `parallel::detectCores() / 2` or half of your computer's processing power. Set to 1 to not use parallel computing. Recommended to use maximum number of cores minus one  
 If you're unsure how many cores your computer has, then use the following code: `parallel::detectCores()`

...                Additional arguments. Used for deprecated arguments from previous versions of [EGA](#)

## Value

Returns a list containing:

boot.ergoInfo    The values of the Ergodicity Information Index obtained in the Monte-Carlo Simulation

p.value.twosided    The p-value of the Monte-Carlo test for the Ergodicity Information Index. The null hypothesis is that the empirical Ergodicity Information index is equal to the expected value of the EII if the all individuals had similar latent structures.

effect            Indicates wheter the empirical EII is greater or less then the Monte-Carlo obtained EII.

plot.dist         Histogram of the bootstrapped ergodicity information index

## Author(s)

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## Examples

```
## Not run:
\donttest{
dyn1 <- dynEGA.ind.pop(data = sim.dynEGA[,-c(22)], n.embed = 5, tau = 1,
                      delta = 1, id = 21, use.derivatives = 1,
                      model = "glasso", ncores = 2, corr = "pearson")

eii1 <- ergoInfo(data = dyn1)$EII

testing.ergoInfo <- boot.ergoInfo(dynEGA.pop = dyn1, iter = 10,EII = eii1,
embed = 5, tau = 1, delta = 1, derivatives = 1,
model = "glasso", ncores = 2, corr = "pearson")
}
## End(Not run)
```

---

`boot.wmt`*bootEGA Results of wmt2Data*

---

### Description

`bootEGA` results using the "glasso" model and 500 iterations of the Wiener Matrizen-Test 2 (WMT-2)

`bootEGA` Results of `wmt2Data`

### Usage

```
data(boot.wmt)
```

```
data(boot.wmt)
```

### Format

A list with 9 objects (see `bootEGA`)

A list with 8 objects (see `bootEGA`)

### Details

`bootEGA` results using the "glasso" model and 500 iterations of the Wiener Matrizen-Test 2 (WMT-2)

### Examples

```
data("boot.wmt")
```

```
data("boot.wmt")
```

---

`bootEGA`*Dimension Stability Analysis of EGA*

---

### Description

`bootEGA` Estimates the number of dimensions of  $n$  bootstraps using the empirical (partial) correlation matrix (parametric) or resampling from the empirical dataset (non-parametric). It also estimates a typical median network structure, which is formed by the median or mean pairwise (partial) correlations over the  $n$  bootstraps.



**Usage**

```
bootEGA(
  data,
  uni = TRUE,
  iter,
  type = c("parametric", "resampling"),
  corr = c("cor_auto", "pearson", "spearman"),
  model = c("glasso", "TMFG"),
  model.args = list(),
  algorithm = c("walktrap", "louvain"),
  algorithm.args = list(),
  typicalStructure = TRUE,
  plot.typicalStructure = TRUE,
  plot.type = c("GGally", "qgraph"),
  plot.args = list(),
  ncores,
  ...
)
```

**Arguments**

<code>data</code>	Matrix or data frame. Includes the variables to be used in the bootEGA analysis
<code>uni</code>	Boolean. Should unidimensionality be checked? Defaults to TRUE. Set to FALSE to check for multidimensionality only. If TRUE, then the same number of variables as the original data (i.e., from argument <code>data</code> ) are generated from a factor model with one factor and loadings of .70. These data are then appended to the original data and dimensionality is checked. If the number of dimensions is one or two, then the original data are unidimensional; otherwise, the data are multidimensional (see Golino, Shi, et al., 2020 for more details)
<code>iter</code>	Numeric integer. Number of replica samples to generate from the bootstrap analysis. At least 500 is recommended
<code>type</code>	Character. A string indicating the type of bootstrap to use. Current options are: <ul style="list-style-type: none"> <li>• "parametric" Generates n new datasets (multivariate normal random distributions) based on the original dataset, via the <code>mvrnorm</code> function</li> <li>• "resampling" Generates n random subsamples of the original data</li> </ul>
<code>corr</code>	Type of correlation matrix to compute. The default uses <code>cor_auto</code> . Current options are: <ul style="list-style-type: none"> <li>• <code>cor_auto</code> Computes the correlation matrix using the <code>cor_auto</code> function from <code>qgraph</code>.</li> <li>• <code>pearson</code> Computes Pearson's correlation coefficient using the pairwise complete observations via the <code>cor</code> function.</li> <li>• <code>spearman</code> Computes Spearman's correlation coefficient using the pairwise complete observations via the <code>cor</code> function.</li> </ul>
<code>model</code>	Character. A string indicating the method to use. Current options are:

	<ul style="list-style-type: none"> <li>• <code>glasso</code> Estimates the Gaussian graphical model using graphical LASSO with extended Bayesian information criterion to select optimal regularization parameter. This is the default method</li> <li>• <code>TMFG</code> Estimates a Triangulated Maximally Filtered Graph</li> </ul>
<code>model.args</code>	List. A list of additional arguments for <code>EBICglasso.qgraph</code> or <code>TMFG</code>
<code>algorithm</code>	A string indicating the algorithm to use or a function from <code>igraph</code> Current options are: <ul style="list-style-type: none"> <li>• <code>walktrap</code> Computes the Walktrap algorithm using <code>cluster_walktrap</code></li> <li>• <code>louvain</code> Computes the Walktrap algorithm using <code>cluster_louvain</code></li> </ul>
<code>algorithm.args</code>	List. A list of additional arguments for <code>cluster_walktrap</code> , <code>cluster_louvain</code> , or some other community detection algorithm function (see examples)
<code>typicalStructure</code>	Boolean. If <code>TRUE</code> , returns the typical network of partial correlations (estimated via graphical lasso or via <code>TMFG</code> ) and estimates its dimensions. The "typical network" is the median of all pairwise correlations over the $n$ bootstraps. Defaults to <code>TRUE</code>
<code>plot.typicalStructure</code>	Boolean. If <code>TRUE</code> , returns a plot of the typical network (partial correlations), which is the median of all pairwise correlations over the $n$ bootstraps, and its estimated dimensions. Defaults to <code>TRUE</code>
<code>plot.type</code>	Character. Plot system to use. Current options are <code>qgraph</code> and <code>GGally</code> . Defaults to <code>"GGally"</code> .
<code>plot.args</code>	List. A list of additional arguments for the network plot. For <code>plot.type = "qgraph"</code> : <ul style="list-style-type: none"> <li>• <code>vsize</code> Size of the nodes. Defaults to 6.</li> </ul> For <code>plot.type = "GGally"</code> (see <code>ggnet2</code> for full list of arguments): <ul style="list-style-type: none"> <li>• <code>vsize</code> Size of the nodes. Defaults to 6.</li> <li>• <code>label.size</code> Size of the labels. Defaults to 5.</li> <li>• <code>alpha</code> The level of transparency of the nodes, which might be a single value or a vector of values. Defaults to 0.7.</li> <li>• <code>edge.alpha</code> The level of transparency of the edges, which might be a single value or a vector of values. Defaults to 0.4.</li> <li>• <code>legend.names</code> A vector with names for each dimension</li> <li>• <code>color.palette</code> The color palette for the nodes. For custom colors, enter HEX codes for each dimension in a vector. See <code>color_palette_EGA</code> for more details and examples</li> </ul>
<code>ncores</code>	Numeric. Number of cores to use in computing results. Defaults to <code>parallel::detectCores() / 2</code> or half of your computer's processing power. Set to 1 to not use parallel computing If you're unsure how many cores your computer has, then use the following code: <code>parallel::detectCores()</code>
<code>...</code>	Additional arguments. Used for deprecated arguments from previous versions of <code>EGA</code>

**Value**

Returns a list containing:

<code>iter</code>	Number of replica samples in bootstrap
<code>boot.ndim</code>	Number of dimensions identified in each replica sample
<code>boot.wc</code>	Item allocation for each replica sample
<code>bootGraphs</code>	Networks of each replica sample
<code>summary.table</code>	Summary table containing number of replica samples, median, standard deviation, standard error, 95% confidence intervals, and quantiles (lower = 2.5% and upper = 97.5%)
<code>frequency</code>	Proportion of times the number of dimensions was identified (e.g., .85 of 1,000 = 850 times that specific number of dimensions was found)
<code>EGA</code>	Output of the original <a href="#">EGA</a> results
<code>typicalGraph</code>	A list containing: <ul style="list-style-type: none"> <li>• <code>graph</code> Network matrix of the median network structure</li> <li>• <code>typical.dim.variables</code> An ordered matrix of item allocation</li> <li>• <code>wc</code> Item allocation of the median network</li> </ul>

**Author(s)**

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**References**

# Original implementation of bootEGA  
Christensen, A. P., & Golino, H. (2019). Estimating the stability of the number of factors via Bootstrap Exploratory Graph Analysis: A tutorial. *PsyArXiv*. doi: [10.31234/osf.io/9deay](https://doi.org/10.31234/osf.io/9deay)

# Structural consistency (see [dimStability](#))  
Christensen, A. P., Golino, H., & Silvia, P. J. (in press). A psychometric network perspective on the validity and validation of personality trait questionnaires. *European Journal of Personality*. doi: [10.1002/per.2265](https://doi.org/10.1002/per.2265)

**See Also**

[EGA](#) to estimate the number of dimensions of an instrument using EGA and [CFA](#) to verify the fit of the structure suggested by EGA using confirmatory factor analysis.

**Examples**

```
# Load data
wmt <- wmt2[,7:24]

# bootEGA glasso example
## plot.type = "qgraph" used for CRAN checks
## plot.type = "GGally" is the default
boot.wmt <- bootEGA(data = wmt, iter = 500, plot.type = "qgraph",
```

```

type = "parametric", ncores = 2)

# bootEGA TMFG example
boot.wmt <- bootEGA(data = wmt, iter = 500, model = "TMFG",
plot.type = "qgraph", type = "parametric", ncores = 2)

# bootEGA Louvain example
boot.wmt <- bootEGA(data = wmt, iter = 500, algorithm = "louvain",
plot.type = "qgraph", type = "parametric", ncores = 2)

# bootEGA Spinglass example
boot.wmt <- bootEGA(data = wmt, iter = 500, model = "TMFG", plot.type = "qgraph",
algorithm = igraph::cluster_spinglass, type = "parametric", ncores = 2)

# Load data
intwl <- intelligenceBattery[,8:66]

# Another bootEGA example
boot.intwl <- bootEGA(data = intwl, iter = 500,
plot.type = "qgraph", type = "parametric", ncores = 2)

```

---

CFA

*CFA Fit of EGA Structure*


---

## Description

Verifies the fit of the structure suggested by [EGA](#) using confirmatory factor analysis

## Usage

```
CFA(ega.obj, data, estimator, plot.CFA = TRUE, layout = "spring", ...)
```

## Arguments

<code>ega.obj</code>	An <a href="#">EGA</a> object
<code>data</code>	A dataframe with the variables to be used in the analysis
<code>estimator</code>	The estimator used in the confirmatory factor analysis. 'WLSMV' is the estimator of choice for ordinal variables. 'ML' or 'WLS' for interval variables. See <a href="#">lavOptions</a> for more details
<code>plot.CFA</code>	Logical. Should the CFA structure with its standardized loadings be plot? Defaults to TRUE
<code>layout</code>	Layout of plot (see <a href="#">semPaths</a> ). Defaults to "spring"
<code>...</code>	Arguments passed to <a href="#">cfa</a>

**Value**

Returns a list containing:

<code>fit</code>	Output from <code>cfa</code>
<code>summary</code>	Summary output from <code>lavaan-class</code>
<code>fit.measures</code>	Fit measures: chi-squared, degrees of freedom, p-value, CFI, RMSEA, GFI, and NFI. Additional fit measures can be applied using the <code>fitMeasures</code> function (see examples)

**Author(s)**

Hudson F. Golino <hfg9s at virginia.edu>

**References**

Christensen, A. P., Gross, G. M., Golino, H., Silvia, P. J., & Kwapil, T. R. (2019). Exploratory graph analysis of the Multidimensional Schizotypy Scale. *Schizophrenia Research*, 206, 43-51. doi: [10.1016/j.schres.2018.12.018](https://doi.org/10.1016/j.schres.2018.12.018)

Golino, H., & Epskamp, S. (2017). Exploratory graph analysis: A new approach for estimating the number of dimensions in psychological research. *PLoS ONE*, 12, e0174035. doi: [10.1371/journal.pone.0174035](https://doi.org/10.1371/journal.pone.0174035)

**See Also**

`EGA` to estimate the number of dimensions of an instrument using `EGA` and `bootEGA` to investigate the stability of `EGA`'s estimation via bootstrap.

**Examples**

```
# Load data
wmt <- wmt2[,7:24]

# Estimate EGA
ega.wmt <- EGA(data = wmt, uni = TRUE, plot.EGA = FALSE)

# Fit CFA model to EGA results
cfa.wmt <- CFA(ega.obj = ega.wmt, estimator = 'WLSMV', plot.CFA = TRUE, data = wmt)

# Additional fit measures
lavaan::fitMeasures(cfa.wmt$fit, fit.measures = "all")

# Load data
intel <- intelligenceBattery[,8:66]

# Estimate EGA
```

```
ega.intel <- EGA(data = intel, plot.EGA = FALSE)

# Fit CFA model to EGA results
cfa.intel <- CFA(ega.obj = ega.intel, estimator = 'WLSMV', plot.CFA = TRUE,
data = intel)
```

---

color\_palette\_EGA      [EGA Color Palettes](#)

---

## Description

Color palettes for plotting [ggnet2](#) EGA network plots

## Usage

```
color_palette_EGA(name, wc)
```

## Arguments

name	Character. Name of color scheme (see <a href="#">RColorBrewer</a> ). Defaults to "polychrome". <a href="#">EGA</a> palettes: <ul style="list-style-type: none"><li>• "polychrome" Default 20 color palette</li><li>• "blue.ridge1" Palette inspired by the Blue Ridge Mountains</li><li>• "blue.ridge2" Second palette inspired by the Blue Ridge Mountains</li><li>• "rainbow" Rainbow colors. Default for <a href="#">qgraph</a></li><li>• "rio" Palette inspired by Rio de Janiero, Brazil</li><li>• "itacare" Palette inspired by Itacare, Brazil</li></ul>
wc	For custom colors, enter HEX codes for each dimension in a vector Vector. A vector representing the community (dimension) membership of each node in the network. NA values mean that the node was disconnected from the network

## Value

Vector of colors for community memberships

## Author(s)

Hudson Golino <[hfg9s at virginia.edu](mailto:hfg9s@virginia.edu)>, Alexander P. Christensen <[alexpaulchristensen at gmail.com](mailto:alexpaulchristensen@gmail.com)>

**Examples**

```
# Default
color_palette_EGA(name = "polychrome", wc = ega.wmt$wc)

# Blue Ridge Moutains 1
color_palette_EGA(name = "blue.ridge1", wc = ega.wmt$wc)

# Custom
color_palette_EGA(name = "#7FD1B9", wc = ega.wmt$wc)
```

---

depression	<i>Depression Data</i>
------------	------------------------

---

**Description**

A response matrix (n = 574) of the Beck Depression Inventory, Beck Anxiety Inventory and the Athens Insomnia Scale.

A response matrix (n = 574) of the Beck Depression Inventory, Beck Anxiety Inventory and the Athens Insomnia Scale.

**Usage**

```
data(depression)
```

```
data(depression)
```

**Format**

A 574x78 response matrix

A 574x78 response matrix

**Examples**

```
data("depression")
```

```
data("depression")
```

---

dimStability                      *Dimension Stability Statistics from* [bootEGA](#)

---

### Description

Based on the [bootEGA](#) results, this function computes the stability of dimensions. This is computed by assessing the proportion of times the original dimension is exactly replicated in across bootstrap samples

### Usage

```
dimStability(bootega.obj, orig.wc, item.stability = TRUE)
```

### Arguments

<code>bootega.obj</code>	A <a href="#">bootEGA</a> object
<code>orig.wc</code>	Numeric or character. A vector with community numbers or labels for each item. Typically uses community results ( <code>wc</code> ) from <a href="#">EGA</a>
<code>item.stability</code>	Boolean. Should the item stability statistics be computed using <code>[EGAnet]{itemStability}</code> ? Defaults to TRUE

### Value

When argument `item.stability = TRUE`, returns a list containing:

<code>dimensions</code>	The dimensional stability of each dimension
<code>items</code>	The output from <a href="#">itemStability</a>

When argument `item.stability = FALSE`, returns a vector of the dimensional stability of each dimension

### Author(s)

Hudson Golino <hfg9s at virginia.edu> and Alexander P. Christensen <alexpaulchristensen@gmail.com>

### References

Christensen, A. P., & Golino, H. (2019). Estimating the stability of the number of factors via Bootstrap Exploratory Graph Analysis: A tutorial. *PsyArXiv*. doi: [10.31234/osf.io/9deay](https://doi.org/10.31234/osf.io/9deay)

Christensen, A. P., Golino, H., & Silvia, P. J. (in press). A psychometric network perspective on the validity and validation of personality trait questionnaires. *European Journal of Personality*. doi: [10.1002/per.2265](https://doi.org/10.1002/per.2265)

### See Also

[EGA](#) to estimate the number of dimensions of an instrument using EGA and [CFA](#) to verify the fit of the structure suggested by EGA using confirmatory factor analysis.



**Examples**

```

# Load data
wmt <- wmt2[,7:24]

# Estimate EGA network
## plot.type = "qgraph" used for CRAN checks
## plot.type = "GGally" is the default
ega.wmt <- EGA(data = wmt, model = "glasso", plot.type = "qgraph")

# Estimate dimension stability
boot.wmt <- bootEGA(data = wmt, uni = TRUE, iter = 500, typicalStructure = TRUE,
plot.typicalStructure = TRUE, model = "glasso", plot.type = "qgraph",
type = "parametric", ncores = 2)

# Estimate item stability statistics
res <- dimStability(boot.wmt, orig.wc = ega.wmt$wc, item.stability = TRUE)
res

# Changing plot features (ggplot2)
## Changing colors (ignore warnings)
### qgraph Defaults
res$items$plot.itemStability +
  ggplot2::scale_color_manual(values = rainbow(max(res$items$uniq.num)))

### Pastel
res$items$plot.itemStability +
  ggplot2::scale_color_brewer(palette = "Pastel1")

## Changing Legend (ignore warnings)
res$items$plot.itemStability +
  ggplot2::scale_color_discrete(labels = "Intelligence")

```

---

dnn.weights

*Loadings Comparison Test Deep Learning Neural Network Weights*


---

**Description**

A list of weights from four different neural network models: random vs. non-random model (`r_nr_weights`), low correlation factor vs. network model (`lf_n_weights`), high correlation with variables less than or equal to factors vs. network model (`hlf_n_weights`), and high correlation with variables greater than factors vs. network model (`hgf_n_weights`)

**Usage**

```
data(dnn.weights)
```

**Format**

A list of with a length of 4

**Examples**

```
data("dnn.weights")
```

---

dynEGA

*Dynamic Exploratory Graph Analysis*

---

**Description**

Estimates dynamic factors in multivariate time series (i.e. longitudinal data, panel data, intensive longitudinal data) at multiple time scales, in different levels of analysis: individuals (intraindividual structure), groups or population (structure of the population). Exploratory graph analysis is applied in the derivatives estimated using generalized local linear approximation ([glla](#)). Instead of estimating factors by modeling how variables are covarying, as in traditional EGA, dynEGA is a dynamic model that estimates the factor structure by modeling how variables are changing together. GLLA is a filtering method for estimating derivatives from data that uses time delay embedding and a variant of Savitzky-Golay filtering to accomplish the task.

**Usage**

```
dynEGA(  
  data,  
  n.embed,  
  tau = 1,  
  delta = 1,  
  level = c("individual", "group", "population"),  
  id = NULL,  
  group = NULL,  
  use.derivatives = 1,  
  model = c("glasso", "TMFG"),  
  model.args = list(),  
  algorithm = c("walktrap", "louvain"),  
  algorithm.args = list(),  
  corr = c("cor_auto", "pearson", "spearman"),  
  ncores,  
  ...  
)
```

**Arguments**

**data** A dataframe with the variables to be used in the analysis. The dataframe should be in a long format (i.e. observations for the same individual (for example, individual 1) are placed in order, from time 1 to time t, followed by the observations from individual 2, also ordered from time 1 to time t.)

n.embed	Integer. Number of embedded dimensions (the number of observations to be used in the <a href="#">Embed</a> function). For example, an "n.embed = 5" will use five consecutive observations to estimate a single derivative.
tau	Integer. Number of observations to offset successive embeddings in the <a href="#">Embed</a> function. A tau of one uses adjacent observations. Default is "tau = 1".
delta	Integer. The time between successive observations in the time series. Default is "delta = 1".
level	Character. A string indicating the level of analysis. If the interest is in modeling the intraindividual structure only (one dimensionality structure per individual), then level should be set to "individual". If the interest is in the structure of a group of individuals, then level should be set to "group". Finally, if the interest is in the population structure, then level should be set to "population". Current options are: <ul style="list-style-type: none"> <li>• individual Estimates the dynamic factors per individual. This should be the preferred method if one is interested in the factor structure of individuals. An additional parameter ("id") needs to be provided identifying each individual.</li> <li>• group Estimates the dynamic factors for each group. An additional parameter ("group") needs to be provided identifying the group membership.</li> <li>• population Estimates the dynamic factors of the population</li> </ul>
id	Numeric. Number of the column identifying each individual.
group	Numeric or character. Number of the column identifying group membership. Must be specified only if level = "group".
use.derivatives	Integer. The order of the derivative to be used in the EGA procedure. Default to 1.
model	Character. A string indicating the method to use. Current options are: <ul style="list-style-type: none"> <li>• glasso Estimates the Gaussian graphical model using graphical LASSO with extended Bayesian information criterion to select optimal regularization parameter. This is the default method</li> <li>• TMFG Estimates a Triangulated Maximally Filtered Graph</li> </ul>
model.args	List. A list of additional arguments for <a href="#">EBICglasso.qgraph</a> or <a href="#">TMFG</a>
algorithm	A string indicating the algorithm to use or a function from <a href="#">igraph</a> Current options are: <ul style="list-style-type: none"> <li>• walktrap Computes the Walktrap algorithm using <a href="#">cluster_walktrap</a></li> <li>• louvain Computes the Walktrap algorithm using <a href="#">cluster_louvain</a></li> </ul>
algorithm.args	List. A list of additional arguments for <a href="#">cluster_walktrap</a> , <a href="#">cluster_louvain</a> , or some other community detection algorithm function (see examples)
corr	Type of correlation matrix to compute. The default uses <a href="#">cor_auto</a> . Current options are: <ul style="list-style-type: none"> <li>• cor_auto Computes the correlation matrix using the <a href="#">cor_auto</a> function from <a href="#">qgraph</a>.</li> </ul>

- `pearson` Computes Pearson's correlation coefficient using the pairwise complete observations via the `cor` function.
  - `spearman` Computes Spearman's correlation coefficient using the pairwise complete observations via the `cor` function.
- `ncores` Numeric. Number of cores to use in computing results. Defaults to `parallel::detectCores() / 2` or half of your computer's processing power. Set to 1 to not use parallel computing. Recommended to use maximum number of cores minus one  
If you're unsure how many cores your computer has, then use the following code: `parallel::detectCores()`
- `...` Additional arguments. Used for deprecated arguments from previous versions of EGA

### Author(s)

Hudson Golino <hfg9s at virginia.edu>

### References

- Boker, S. M., Deboeck, P. R., Edler, C., & Keel, P. K. (2010) Generalized local linear approximation of derivatives from time series. In S.-M. Chow, E. Ferrer, & F. Hsieh (Eds.), *The Notre Dame series on quantitative methodology. Statistical methods for modeling human dynamics: An interdisciplinary dialogue*, (p. 161-178). *Routledge/Taylor & Francis Group*. doi: [10.1037/a0016622](https://doi.org/10.1037/a0016622)
- Deboeck, P. R., Montpetit, M. A., Bergeman, C. S., & Boker, S. M. (2009) Using derivative estimates to describe intraindividual variability at multiple time scales. *Psychological Methods*, *14*(4), 367-386. doi: [10.1037/a0016622](https://doi.org/10.1037/a0016622)
- Golino, H., Christensen, A. P., Moulder, R. G., Kim, S., & Boker, S. M. (under review). Modeling latent topics in social media using Dynamic Exploratory Graph Analysis: The case of the right-wing and left-wing trolls in the 2016 US elections. *PsyArXiv*. doi: [10.31234/osf.io/tfs7c](https://doi.org/10.31234/osf.io/tfs7c)
- Savitzky, A., & Golay, M. J. (1964). Smoothing and differentiation of data by simplified least squares procedures. *Analytical Chemistry*, *36*(8), 1627-1639. doi: [10.1021/ac60214a047](https://doi.org/10.1021/ac60214a047)

### Examples

```
# Population structure:
## plot.type = "qgraph" used for CRAN checks
## plot.type = "GGally" is the default
dyn.random <- dynEGA(data = sim.dynEGA, n.embed = 5, tau = 1,
delta = 1, id = 21, group = 22, use.derivatives = 1,
level = "population", model = "glasso", ncores = 2)

plot(dyn.random, plot.type = "qgraph")

# Group structure:
dyn.group <- dynEGA(data = sim.dynEGA, n.embed = 5, tau = 1,
delta = 1, id = 21, group = 22, use.derivatives = 1,
level = "group", model = "glasso", ncores = 2)

plot(dyn.group, ncol = 2, nrow = 1, plot.type = "qgraph")
```

```
# Intraindividual structure (commented out for CRAN tests):
# dyn.individual <- dynEGA(data = sim.dynEGA, n.embed = 5, tau = 1,
# delta = 1, id = 21, group = 22, use.derivatives = 1,
# level = "individual", model = "glasso", ncores = 2)
```

---

dynEGA.ind.pop

*Dynamic EGA used in the mctest.ergoInfo function*


---

## Description

Dynamic EGA used in the `mctest.ergoInfo` function. DynEGA estimates dynamic factors in multivariate time series (i.e. longitudinal data, panel data, intensive longitudinal data) at multiple time scales, in different levels of analysis: individuals (intraindividual structure) and population (structure of the population). Exploratory graph analysis is applied in the derivatives estimated using generalized local linear approximation ([glla](#)). Instead of estimating factors by modeling how variables are covarying, as in traditional EGA, dynEGA is a dynamic model that estimates the factor structure by modeling how variables are changing together. GLLA is a filtering method for estimating derivatives from data that uses time delay embedding and a variant of Savitzky-Golay filtering to accomplish the task.

## Usage

```
dynEGA.ind.pop(
  data,
  n.embed,
  tau = 1,
  delta = 1,
  id = NULL,
  use.derivatives = 1,
  model = c("glasso", "TMFG"),
  model.args = list(),
  algorithm = c("walktrap", "louvain"),
  algorithm.args = list(),
  corr = c("cor_auto", "pearson", "spearman"),
  ncores,
  ...
)
```

## Arguments

<code>data</code>	A dataframe with the variables to be used in the analysis. The dataframe should be in a long format (i.e. observations for the same individual (for example, individual 1) are placed in order, from time 1 to time t, followed by the observations from individual 2, also ordered from time 1 to time t.)
-------------------	---

n.embed	Integer. Number of embedded dimensions (the number of observations to be used in the <a href="#">Embed</a> function). For example, an "n.embed = 5" will use five consecutive observations to estimate a single derivative.
tau	Integer. Number of observations to offset successive embeddings in the <a href="#">Embed</a> function. A tau of one uses adjacent observations. Default is "tau = 1".
delta	Integer. The time between successive observations in the time series. Default is "delta = 1".
id	Numeric. Number of the column identifying each individual.
use.derivatives	Integer. The order of the derivative to be used in the EGA procedure. Default to 1.
model	Character. A string indicating the method to use. Defaults to <code>glasso</code> . Current options are: <ul style="list-style-type: none"> <li>• <code>glasso</code> Estimates the Gaussian graphical model using graphical LASSO with extended Bayesian information criterion to select optimal regularization parameter. This is the default method</li> <li>• <code>TMFG</code> Estimates a Triangulated Maximally Filtered Graph</li> </ul>
model.args	List. A list of additional arguments for <a href="#">EBICglasso.qgraph</a> or <a href="#">TMFG</a>
algorithm	A string indicating the algorithm to use or a function from <a href="#">igraph</a> Current options are: <ul style="list-style-type: none"> <li>• <code>walktrap</code> Computes the Walktrap algorithm using <a href="#">cluster_walktrap</a></li> <li>• <code>louvain</code> Computes the Walktrap algorithm using <a href="#">cluster_louvain</a></li> </ul>
algorithm.args	List. A list of additional arguments for <a href="#">cluster_walktrap</a> , <a href="#">cluster_louvain</a> , or some other community detection algorithm function (see examples)
corr	Type of correlation matrix to compute. The default uses <code>cor_auto</code> . Current options are: <ul style="list-style-type: none"> <li>• <code>cor_auto</code> Computes the correlation matrix using the <code>cor_auto</code> function from <a href="#">qgraph</a>.</li> <li>• <code>pearson</code> Computes Pearson's correlation coefficient using the pairwise complete observations via the <code>cor</code> function.</li> <li>• <code>spearman</code> Computes Spearman's correlation coefficient using the pairwise complete observations via the <code>cor</code> function.</li> </ul>
ncores	Numeric. Number of cores to use in computing results. Defaults to <code>parallel::detectCores() / 2</code> or half of your computer's processing power. Set to 1 to not use parallel computing. Recommended to use maximum number of cores minus one If you're unsure how many cores your computer has, then use the following code: <code>parallel::detectCores()</code>
...	Additional arguments. Used for deprecated arguments from previous versions of <a href="#">EGA</a>

**Author(s)**

Hudson Golino &lt;hfg9s at virginia.edu&gt;

**Examples**

```
## Not run:
\donttest{# Population structure:
dyn.ega1 <- dynEGA.ind.pop(data = sim.dynEGA, n.embed = 5, tau = 1,
delta = 1, id = 21, use.derivatives = 1, model = "glasso", ncores = 2,
cor = "pearson")
}

## End(Not run)
```

---

EBICglasso.qgraph      [EBICglasso from qgraph 1.4.4](#)

---

**Description**

This function uses the [glasso](#) package (Friedman, Hastie and Tibshirani, 2011) to compute a sparse gaussian graphical model with the graphical lasso (Friedman, Hastie & Tibshirani, 2008). The tuning parameter is chosen using the Extended Bayesian Information criterium (EBIC) described by Foygel & Drton (2010).

**Usage**

```
EBICglasso.qgraph(
  data,
  n = NULL,
  gamma = 0.5,
  penalize.diagonal = FALSE,
  nlambda = 100,
  lambda.min.ratio = 0.01,
  returnAllResults = FALSE,
  penalizeMatrix,
  countDiagonal = FALSE,
  refit = FALSE,
  ...
)
```

**Arguments**

<code>data</code>	Data matrix
<code>n</code>	Number of participants
<code>gamma</code>	EBIC tuning parameter. 0.5 is generally a good choice. Setting to zero will cause regular BIC to be used.
<code>penalize.diagonal</code>	Should the diagonal be penalized?
<code>nlambda</code>	Number of lambda values to test.

<code>lambda.min.ratio</code>	Ratio of lowest lambda value compared to maximal lambda
<code>returnAllResults</code>	If TRUE this function does not return a network but the results of the entire glasso path.
<code>penalizeMatrix</code>	Optional logical matrix to indicate which elements are penalized
<code>countDiagonal</code>	Should diagonal be counted in EBIC computation? Defaults to FALSE. Set to TRUE to mimic qgraph < 1.3 behavior (not recommended!).
<code>refit</code>	Logical, should the optimal graph be refitted without LASSO regularization? Defaults to FALSE.
<code>...</code>	Arguments sent to <code>glasso</code>

### Details

The glasso is run for 100 values of the tuning parameter logarithmically spaced between the maximal value of the tuning parameter at which all edges are zero, `lambda_max`, and `lambda_max/100`. For each of these graphs the EBIC is computed and the graph with the best EBIC is selected. The partial correlation matrix is computed using `wi2net` and returned.

### Value

A partial correlation matrix

### Author(s)

Sacha Epskamp <mail@sachaepskamp.com>

### References

- Friedman, J., Hastie, T., & Tibshirani, R. (2008). Sparse inverse covariance estimation with the graphical lasso. *Biostatistics*, 9, 432-441. doi: [10.1093/biostatistics/kxm045](https://doi.org/10.1093/biostatistics/kxm045)
- #glasso package Jerome Friedman, Trevor Hastie and Rob Tibshirani (2011). glasso: Graphical lasso-estimation of Gaussian graphical models. R package version 1.7. <https://CRAN.R-project.org/package=glasso>
- Foygel, R., & Drton, M. (2010). Extended Bayesian information criteria for Gaussian graphical models. In *Advances in neural information processing systems* (pp. 604-612). <https://papers.nips.cc/paper/4087-extended-bayesian-information-criteria-for-gaussian-graphical-models>
- #psych package Revelle, W. (2014) psych: Procedures for Personality and Psychological Research, Northwestern University, Evanston, Illinois, USA. R package version 1.4.4. <https://CRAN.R-project.org/package=psych>
- #Matrix package Douglas Bates and Martin Maechler (2014). Matrix: Sparse and Dense Matrix Classes and Methods. R package version 1.1-3. <https://CRAN.R-project.org/package=Matrix>



## Examples

```
### Using wmt2 dataset from EGAnet ###
data(wmt2)

# Compute correlations:
CorMat <- qgraph::cor_auto(wmt2[,7:24])

# Compute graph with tuning = 0 (BIC):
BICgraph <- EBICglasso.qgraph(CorMat, n = nrow(wmt2), gamma = 0)

# Compute graph with tuning = 0.5 (EBIC)
EBICgraph <- EBICglasso.qgraph(CorMat, n = nrow(wmt2), gamma = 0.5)
```

---

 EGA

*Applies the Exploratory Graph Analysis technique*


---

## Description

Estimates the number of dimensions of a given dataset or correlation matrix using the graphical lasso ([EBICglasso.qgraph](#)) or the Triangulated Maximally Filtered Graph ([TMFG](#)) network estimation methods.

## Usage

```
EGA(
  data,
  n = NULL,
  uni = TRUE,
  corr = c("cor_auto", "pearson", "spearman"),
  model = c("glasso", "TMFG"),
  model.args = list(),
  algorithm = c("walktrap", "louvain"),
  algorithm.args = list(),
  plot.EGA = TRUE,
  plot.type = c("GGally", "qgraph"),
  plot.args = list(),
  verbose = TRUE,
  ...
)
```

## Arguments

<code>data</code>	Matrix or data frame. Variables (down columns) or correlation matrix. If the input is a correlation matrix, then argument <code>n</code> (number of cases) is <b>required</b>
<code>n</code>	Integer. Sample size if data provided is a correlation matrix

uni	Boolean. Should unidimensionality be checked? Defaults to TRUE. Set to FALSE to check for multidimensionality only. If TRUE, then the same number of variables as the original data (i.e., from argument data) up to 12 are generated from a factor model with one factor and loadings of .70. These data are then appended to the original data and dimensionality is checked. If the number of dimensions is one or two, then the original data are unidimensional; otherwise, the data are multidimensional (see Golino, Shi, et al., 2020 for more details)
corr	Type of correlation matrix to compute. The default uses <code>cor_auto</code> . Current options are: <ul style="list-style-type: none"> <li>• <code>cor_auto</code> Computes the correlation matrix using the <code>cor_auto</code> function from <code>qgraph</code>.</li> <li>• <code>pearson</code> Computes Pearson's correlation coefficient using the pairwise complete observations via the <code>cor</code> function.</li> <li>• <code>spearman</code> Computes Spearman's correlation coefficient using the pairwise complete observations via the <code>cor</code> function.</li> </ul>
model	Character. A string indicating the method to use. Current options are: <ul style="list-style-type: none"> <li>• <code>glasso</code> Estimates the Gaussian graphical model using graphical LASSO with extended Bayesian information criterion to select optimal regularization parameter. This is the default method</li> <li>• <code>TMFG</code> Estimates a Triangulated Maximally Filtered Graph</li> </ul>
model.args	List. A list of additional arguments for <code>EBICglasso.qgraph</code> or <code>TMFG</code>
algorithm	A string indicating the algorithm to use or a function from <code>igraph</code> Current options are: <ul style="list-style-type: none"> <li>• <code>walktrap</code> Computes the Walktrap algorithm using <code>cluster_walktrap</code></li> <li>• <code>louvain</code> Computes the Walktrap algorithm using <code>cluster_louvain</code></li> </ul>
algorithm.args	List. A list of additional arguments for <code>cluster_walktrap</code> , <code>cluster_louvain</code> , or some other community detection algorithm function (see examples)
plot.EGA	Boolean. If TRUE, returns a plot of the network and its estimated dimensions. Defaults to TRUE
plot.type	Character. Plot system to use. Current options are <code>qgraph</code> and <code>GGally</code> . Defaults to "GGally"
plot.args	List. A list of additional arguments for the network plot. For <code>plot.type = "qgraph"</code> : <ul style="list-style-type: none"> <li>• <code>vsize</code> Size of the nodes. Defaults to 6.</li> </ul> For <code>plot.type = "GGally"</code> (see <code>ggnet2</code> for full list of arguments): <ul style="list-style-type: none"> <li>• <code>vsize</code> Size of the nodes. Defaults to 6.</li> <li>• <code>label.size</code> Size of the labels. Defaults to 5.</li> <li>• <code>alpha</code> The level of transparency of the nodes, which might be a single value or a vector of values. Defaults to 0.7.</li> <li>• <code>edge.alpha</code> The level of transparency of the edges, which might be a single value or a vector of values. Defaults to 0.4.</li> <li>• <code>legend.names</code> A vector with names for each dimension</li> </ul>

- `color.palette` The color palette for the nodes. For custom colors, enter HEX codes for each dimension in a vector. See [color\\_palette\\_EGA](#) for more details and examples

<code>verbose</code>	Boolean. Should network estimation parameters be printed? Defaults to TRUE. Set to FALSE for no print out
<code>...</code>	Additional arguments. Used for deprecated arguments from previous versions of <a href="#">EGA</a>

## Details

Two community detection algorithms, Walktrap (Pons & Latapy, 2006) and Louvain (Blondel et al., 2008), are pre-programmed because of their superior performance in simulation studies on psychological data generated from factor models (Christensen & Golino; 2020; Golino et al., 2020). Notably, any community detection algorithm from the [igraph](#) can be used to estimate the number of communities (see examples).

## Value

Returns a list containing:

<code>network</code>	A symmetric network estimated using either the <a href="#">EBICglasso.qgraph</a> or <a href="#">TMFG</a>
<code>wc</code>	A vector representing the community (dimension) membership of each node in the network. NA values mean that the node was disconnected from the network
<code>n.dim</code>	A scalar of how many total dimensions were identified in the network
<code>cor.data</code>	The zero-order correlation matrix

## Author(s)

Hudson Golino <hfg9s at virginia.edu>, Alexander P. Christensen <alexpaulchristensen at gmail.com>, Maria Dolores Nieto <acinodam at gmail.com> and Luis E. Garrido <garrido.luiseduardo at gmail.com>

## References

- # Louvain algorithm  
 Blondel, V. D., Guillaume, J.-L., Lambiotte, R., & Lefebvre, E. (2008). Fast unfolding of communities in large networks. *Journal of Statistical Mechanics: Theory and Experiment*, 2008, P10008.
- # Compared all *igraph* community detections algorithms, introduced Louvain algorithm, simulation with continuous and polytomous data  
 Christensen, A. P., & Golino, H. (under review). Estimating factors with psychometric networks: A Monte Carlo simulation comparing community detection algorithms. *PsyArXiv*. doi: [10.31234/osf.io/hz89e](https://doi.org/10.31234/osf.io/hz89e)
- # Original simulation and implementation of EGA  
 Golino, H. F., & Epskamp, S. (2017). Exploratory graph analysis: A new approach for estimating the number of dimensions in psychological research. *PLoS ONE*, 12, e0174035. doi: [10.1371/journal.pone.0174035](https://doi.org/10.1371/journal.pone.0174035)
- Golino, H. F., & Demetriou, A. (2017). Estimating the dimensionality of intelligence like data using Exploratory Graph Analysis. *Intelligence*, 62, 54-70. doi: [10.1016/j.intell.2017.02.007](https://doi.org/10.1016/j.intell.2017.02.007)

# Current implementation of EGA, introduced unidimensional checks, continuous and dichotomous data

Golino, H., Shi, D., Christensen, A. P., Garrido, L. E., Nieto, M. D., Sadana, R., & Thiyagarajan, J. A. (2020). Investigating the performance of Exploratory Graph Analysis and traditional techniques to identify the number of latent factors: A simulation and tutorial. *Psychological Methods*, 25, 292-320. doi: [10.1037/met0000255](https://doi.org/10.1037/met0000255)

# Walktrap algorithm

Pons, P., & Latapy, M. (2006). Computing communities in large networks using random walks. *Journal of Graph Algorithms and Applications*, 10, 191-218. doi: [10.7155/jgaa.00185](https://doi.org/10.7155/jgaa.00185)

### See Also

[bootEGA](#) to investigate the stability of EGA's estimation via bootstrap and [CFA](#) to verify the fit of the structure suggested by EGA using confirmatory factor analysis.

### Examples

```
# Estimate EGA
## plot.type = "qgraph" used for CRAN checks
## plot.type = "GGally" is the default
ega.wmt <- EGA(data = wmt2[,7:24], plot.type = "qgraph")

# Summary statistics
summary(ega.wmt)

# Estimate EGAtmfg
ega.wmt <- EGA(data = wmt2[,7:24], model = "TMFG", plot.type = "qgraph")

# Estimate EGA with Louvain algorithm
ega.wmt <- EGA(data = wmt2[,7:24], algorithm = "louvain", plot.type = "qgraph")

# Estimate EGA with Spinglass algorithm
ega.wmt <- EGA(data = wmt2[,7:24],
algorithm = igraph::cluster_spinglass, plot.type = "qgraph")

# Estimate EGA
ega.intel <- EGA(data = intelligenceBattery[,8:66], model = "glasso", plot.EGA = FALSE)

# Summary statistics
summary(ega.intel)
```

## Description

Estimates the number of dimensions of a given dataset or correlation matrix using the graphical lasso ([EBICglasso.qgraph](#)) or the Triangulated Maximally Filtered Graph ([TMFG](#)) network estimation methods.

## Usage

```
EGA.estimate(
  data,
  n = NULL,
  model = c("glasso", "TMFG"),
  model.args = list(),
  algorithm = c("walktrap", "louvain"),
  algorithm.args = list(),
  corr = c("cor_auto", "pearson", "spearman"),
  verbose = TRUE,
  ...
)
```

## Arguments

data	Matrix or data frame. Variables (down columns) or correlation matrix. If the input is a correlation matrix, then argument n (number of cases) is <b>required</b>
n	Integer. Sample size if data provided is a correlation matrix
model	Character. A string indicating the method to use. Current options are: <ul style="list-style-type: none"> <li>• glasso Estimates the Gaussian graphical model using graphical LASSO with extended Bayesian information criterion to select optimal regularization parameter. This is the default method</li> <li>• TMFG Estimates a Triangulated Maximally Filtered Graph</li> </ul>
model.args	List. A list of additional arguments for <a href="#">EBICglasso.qgraph</a> or <a href="#">TMFG</a>
algorithm	A string indicating the algorithm to use or a function from <a href="#">igraph</a> Current options are: <ul style="list-style-type: none"> <li>• walktrap Computes the Walktrap algorithm using <a href="#">cluster_walktrap</a></li> <li>• louvain Computes the Walktrap algorithm using <a href="#">cluster_louvain</a></li> </ul>
algorithm.args	List. A list of additional arguments for <a href="#">cluster_walktrap</a> , <a href="#">cluster_louvain</a> , or some other community detection algorithm function (see examples)
corr	Type of correlation matrix to compute. The default uses <a href="#">cor_auto</a> . Current options are: <ul style="list-style-type: none"> <li>• cor_auto Computes the correlation matrix using the <a href="#">cor_auto</a> function from <a href="#">qgraph</a>.</li> <li>• pearson Computes Pearson's correlation coefficient using the pairwise complete observations via the <a href="#">cor</a> function.</li> <li>• spearman Computes Spearman's correlation coefficient using the pairwise complete observations via the <a href="#">cor</a> function.</li> </ul>

verbose	Boolean. Should network estimation parameters be printed? Defaults to TRUE. Set to FALSE for no print out
...	Additional arguments. Used for deprecated arguments from previous versions of EGA

### Details

Two community detection algorithms, Walktrap (Pons & Latapy, 2006) and Louvain (Blondel et al., 2008), are pre-programmed because of their superior performance in simulation studies on psychological data generated from factor models (Christensen & Golino; 2020; Golino et al., 2020). Notably, any community detection algorithm from the [igraph](#) can be used to estimate the number of communities (see examples).

### Value

Returns a list containing:

estimated.network	A symmetric network estimated using either the <a href="#">EBICglasso.qgraph</a> or <a href="#">TMFG</a>
wc	A vector representing the community (dimension) membership of each node in the network. NA values mean that the node was disconnected from the network
n.dim	A scalar of how many total dimensions were identified in the network
cor.data	The zero-order correlation matrix

### Author(s)

Alexander P. Christensen <alexpaulchristensen at gmail.com> and Hudson Golino <hfg9s at virginia.edu>

### References

- # Louvain algorithm  
Blondel, V. D., Guillaume, J.-L., Lambiotte, R., & Lefebvre, E. (2008). Fast unfolding of communities in large networks. *Journal of Statistical Mechanics: Theory and Experiment*, 2008, P10008.
- # Compared all *igraph* community detections algorithms, introduced Louvain algorithm, simulation with continuous and polytomous data  
Christensen, A. P., & Golino, H. (under review). Estimating factors with psychometric networks: A Monte Carlo simulation comparing community detection algorithms. *PsyArXiv*. doi: [10.31234/osf.io/hz89e](https://doi.org/10.31234/osf.io/hz89e)
- # Original simulation and implementation of EGA  
Golino, H. F., & Epskamp, S. (2017). Exploratory graph analysis: A new approach for estimating the number of dimensions in psychological research. *PLoS ONE*, 12, e0174035. doi: [10.1371/journal.pone.0174035](https://doi.org/10.1371/journal.pone.0174035)
- Golino, H. F., & Demetriou, A. (2017). Estimating the dimensionality of intelligence like data using Exploratory Graph Analysis. *Intelligence*, 62, 54-70. doi: [10.1016/j.intell.2017.02.007](https://doi.org/10.1016/j.intell.2017.02.007)
- # Current implementation of EGA, introduced unidimensional checks, continuous and dichotomous data

Golino, H., Shi, D., Christensen, A. P., Garrido, L. E., Nieto, M. D., Sadana, R., & Thiagarajan, J. A. (2020). Investigating the performance of Exploratory Graph Analysis and traditional techniques to identify the number of latent factors: A simulation and tutorial. *Psychological Methods*, 25, 292-320. doi: [10.1037/met0000255](https://doi.org/10.1037/met0000255)

# Walktrap algorithm

Pons, P., & Latapy, M. (2006). Computing communities in large networks using random walks. *Journal of Graph Algorithms and Applications*, 10, 191-218. doi: [10.7155/jgaa.00185](https://doi.org/10.7155/jgaa.00185)

### See Also

[bootEGA](#) to investigate the stability of EGA's estimation via bootstrap and [CFA](#) to verify the fit of the structure suggested by EGA using confirmatory factor analysis.

### Examples

```
# Estimate EGA
ega.wmt <- EGA.estimate(data = wmt2[,7:24], model = "glasso")

# Estimate EGAtmfg
ega.wmt <- EGA.estimate(data = wmt2[,7:24], model = "TMFG")

# Estimate EGA with Spinglass
ega.wmt <- EGA.estimate(data = wmt2[,7:24], model = "glasso",
algorithm = igraph::cluster_spinglass)
```

---

EGA.fit

[EGA Optimal Model Fit using the Total Entropy Fit Index \(tefi\)](#)

---

### Description

Estimates the best fitting model using [EGA](#). The number of steps in the [cluster\\_walktrap](#) detection algorithm is varied and unique community solutions are compared using [tefi](#).

### Usage

```
EGA.fit(
  data,
  model = c("glasso", "TMFG"),
  steps = c(3, 4, 5, 6, 7, 8),
  n = NULL
)
```

**Arguments**

data	Matrix or data frame. Dataset or correlation matrix
model	Character. A string indicating the method to use. Defaults to "glasso" Current options are: <ul style="list-style-type: none"> <li>• "glasso" Estimates the Gaussian graphical model using graphical LASSO with extended Bayesian information criterion to select optimal regularization parameter. See <a href="#">EBICglasso.qgraph</a></li> <li>• "TMFG" Estimates a Triangulated Maximally Filtered Graph. See <a href="#">TMFG</a></li> </ul>
steps	Numeric vector. Range of steps to be used in the model selection. Defaults from 3 to 8 steps (based on Pons & Latapy, 2006)
n	Integer. Sample size (if the data provided is a correlation matrix)

**Value**

Returns a list containing:

EGA	The <a href="#">EGA</a> output for the best fitting model
steps	The number of steps used in the best fitting model from the <a href="#">cluster_walktrap</a> algorithm
EntropyFit	The <a href="#">tefi</a> Index for the unique solutions given the range of steps (vector names represent the number of steps)
Lowest.EntropyFit	The lowest value for the <a href="#">tefi</a> Index

**Author(s)**

Hudson Golino <hfg9s at virginia.edu> and Alexander P. Christensen <alexpaulchristensen@gmail.com>

**References**

# Entropy fit measures

Golino, H., Moulder, R. G., Shi, D., Christensen, A. P., Garrido, L. E., Neito, M. D., Nesselroade, J., Sadana, R., Thiyagarajan, J. A., & Boker, S. M. (in press). Entropy fit indices: New fit measures for assessing the structure and dimensionality of multiple latent variables. *Multivariate Behavioral Research*. doi: [10.31234/osf.io/mtka2](https://doi.org/10.31234/osf.io/mtka2)

# Original implementation of EGA.fit

Golino, H., Thiyagarajan, J. A., Sadana, M., Teles, M., Christensen, A. P., & Boker, S. M. (under review). Investigating the broad domains of intrinsic capacity, functional ability, and environment: An exploratory graph analysis approach for improving analytical methodologies for measuring healthy aging. *PsyArXiv*. doi: [10.31234/osf.io/hj5mc](https://doi.org/10.31234/osf.io/hj5mc)

# Walktrap algorithm

Pons, P., & Latapy, M. (2006). Computing communities in large networks using random walks. *Journal of Graph Algorithms and Applications*, *10*, 191-218. doi: [10.7155/jgaa.00185](https://doi.org/10.7155/jgaa.00185)



**See Also**

[bootEGA](#) to investigate the stability of EGA's estimation via bootstrap, [EGA](#) to estimate the number of dimensions of an instrument using EGA, and [CFA](#) to verify the fit of the structure suggested by EGA using confirmatory factor analysis.

**Examples**

```
# Load data
wmt <- wmt2[,7:24]

# Estimate EGA
## plot.type = "qgraph" used for CRAN checks
## plot.type = "GGally" is the default
ega.wmt <- EGA(data = wmt, plot.type = "qgraph")

# Estimate optimal EGA
fit.wmt <- EGA.fit(data = wmt)

# Plot optimal fit
plot(fit.wmt$EGA, plot.type = "qgraph")

# Compare with CFA
cfa.ega <- CFA(ega.wmt, estimator = "WLSMV", data = wmt)
cfa.fit <- CFA(fit.wmt$EGA, estimator = "WLSMV", data = wmt)

lavaan::lavTestLRT(cfa.ega$fit, cfa.fit$fit, method = "satorra.bentler.2001")
```

---

 ega.wmt

*EGA WMT-2 Data*


---

**Description**

[EGA](#) Network of [wmt2Data](#)

An [EGA](#) using the "glasso" model of the Wiener Matrizen-Test 2 (WMT-2)

**Usage**

```
data(ega.wmt)
```

```
data(ega.wmt)
```

**Format**

A 17 x 17 adjacency matrix

A 17 x 17 adjacency matrix

**Details**

An [EGA](#) using the "glasso" model of the Wiener Matrizen-Test 2 (WMT-2)

**Examples**

```
data("ega.wmt")
```

```
data("ega.wmt")
```

---

Embed

*Time-delay Embedding*

---

**Description**

Reorganizes an individual's observed time series into an embedded matrix. The embedded matrix is constructed with replicates of an individual time series that are offset from each other in time. The function requires two parameters, one that specifies the number of observations to be used (i.e. the number of embedded dimensions) and the other that specifies the number of observations to offset successive embeddings.

**Usage**

```
Embed(x, E, tau)
```

**Arguments**

x	Vector. An observed time series to be reorganized into a time-delayed embedded matrix.
E	Integer. Number of embedded dimensions or the number of observations to be used. For example, an "E = 5" will generate a matrix with five columns, meaning that five consecutive observations are used to create each row of the embedded matrix.
tau	Integer. Number of observations to offset successive embeddings. A tau of one uses adjacent observations. Default is "tau = 1".

**Value**

Returns a matrix containing the embedded matrix.

**Author(s)**

Pascal Deboeck <pascal.deboeck@psych.utah.edu>

## References

Deboeck, P. R., Montpetit, M. A., Bergeman, C. S., & Boker, S. M. (2009) Using derivative estimates to describe intraindividual variability at multiple time scales. *Psychological Methods, 14*, 367-386. doi: [10.1037/a0016622](https://doi.org/10.1037/a0016622)

## Examples

```
# A time series with 8 time points
tseries <- 49:56
embed.tseries <- Embed(tseries, E = 4, tau = 1)
```

---

entropyFit	<i>Entropy Fit Index</i>
------------	--------------------------

---

## Description

Computes the fit of a dimensionality structure using empirical entropy. Lower values suggest better fit of a structure to the data.

## Usage

```
entropyFit(data, structure)
```

## Arguments

data	Matrix or data frame. Contains variables to be used in the analysis
structure	A vector representing the structure (numbers or labels for each item). Can be theoretical factors or the structure detected by <a href="#">EGA</a>

## Value

Returns a list containing:

Total.Correlation	The total correlation of the dataset
Total.Correlation.MM	Miller-Madow correction for the total correlation of the dataset
Entropy.Fit	The Entropy Fit Index
Entropy.Fit.MM	Miller-Madow correction for the Entropy Fit Index
Average.Entropy	The average entropy of the dataset

**Author(s)**

Hudson F. Golino <hfg9s at virginia.edu>, Alexander P. Christensen <alexpaulchristensen@gmail.com> and Robert Moulder <rgm4fd@virginia.edu>

**References**

Golino, H., Moulder, R. G., Shi, D., Christensen, A. P., Garrido, L. E., Neito, M. D., Nesselroade, J., Sadana, R., Thiyagarajan, J. A., & Boker, S. M. (2020). Entropy fit indices: New fit measures for assessing the structure and dimensionality of multiple latent variables. *Multivariate Behavioral Research*. doi: [10.31234/osf.io/mtka2](https://doi.org/10.31234/osf.io/mtka2)

**See Also**

[EGA](#) to estimate the number of dimensions of an instrument using EGA and [CFA](#) to verify the fit of the structure suggested by EGA using confirmatory factor analysis.

**Examples**

```
# Load data
wmt <- wmt2[,7:24]

# Estimate EGA model
ega.wmt <- EGA(data = wmt, model = "glasso", plot.EGA = FALSE)

# Compute entropy indices
entropyFit(data = wmt, structure = ega.wmt$wc)
```

---

ergoInfo

*Ergodicity Information Index*

---

**Description**

Computes the Ergodicity Information Index

**Usage**

```
ergoInfo(data, use = c("edge.list", "weights"))
```

**Arguments**

data	A dynEGA.ind.pop object
use	Character. A string indicating what network element will be used to compute the algorithm complexity, the list of edges or the weights of the network. Defaults to use = "edge.list". Current options are: <ul style="list-style-type: none"> <li>• edge.list Calculates the algorithm complexity using the list of edges.</li> <li>• weights Calculates the algorithm complexity using the weights of the network.</li> </ul>

**Value**

Returns a list containing:

PrimeWeight	The prime-weight encoding of the individual networks
PrimeWeight.pop	The prime-weight encoding of the population network
Kcomp	The Kolmogorov complexity of the prime-weight encoded individual networks
Kcomp.pop	The Kolmogorov complexity of the prime-weight encoded population network
EII	The Ergodicity Information Index

**Author(s)**

Hudson Golino <hfg9s at virginia.edu>

---

glla

*Generalized Local Linear Approximation*


---

**Description**

Estimates the derivatives of a time series using generalized local linear approximation (GLLA). GLLA is a filtering method for estimating derivatives from data that uses time delay embedding and a variant of Savitzky-Golay filtering to accomplish the task.

**Usage**

```
glla(x, n.embed, tau, delta, order)
```

**Arguments**

x	Vector. An observed time series.
n.embed	Integer. Number of embedded dimensions (the number of observations to be used in the <a href="#">Embed</a> function).
tau	Integer. Number of observations to offset successive embeddings in the <a href="#">Embed</a> function. A tau of one uses adjacent observations. Default is "tau = 1".

delta	Integer. The time between successive observations in the time series. Default is "delta = 1".
order	Integer. The maximum order of the derivative to be estimated. For example, "order = 2" will return a matrix with three columns with the estimates of the observed scores and the first and second derivative for each row of the embedded matrix (i.e. the reorganization of the time series implemented via the <a href="#">Embed</a> function).

**Value**

Returns a matrix containing n columns, in which n is one plus the maximum order of the derivatives to be estimated via generalized local linear approximation.

**Author(s)**

Hudson Golino <hfg9s at virginia.edu>

**References**

- Boker, S. M., Deboeck, P. R., Edler, C., & Keel, P. K. (2010) Generalized local linear approximation of derivatives from time series. In S.-M. Chow, E. Ferrer, & F. Hsieh (Eds.), *The Notre Dame series on quantitative methodology. Statistical methods for modeling human dynamics: An interdisciplinary dialogue*, (p. 161-178). *Routledge/Taylor & Francis Group*. doi: [10.1037/a0016622](https://doi.org/10.1037/a0016622)
- Deboeck, P. R., Montpetit, M. A., Bergeman, C. S., & Boker, S. M. (2009) Using derivative estimates to describe intraindividual variability at multiple time scales. *Psychological Methods*, *14*(4), 367-386. doi: [10.1037/a0016622](https://doi.org/10.1037/a0016622)
- Savitzky, A., & Golay, M. J. (1964). Smoothing and differentiation of data by simplified least squares procedures. *Analytical Chemistry*, *36*(8), 1627-1639. doi: [10.1021/ac60214a047](https://doi.org/10.1021/ac60214a047)

**Examples**

```
# A time series with 8 time points
tseries <- 49:56
deriv.tseries <- glla(tseries, n.embed = 4, tau = 1, delta = 1, order = 2)
```

---

intelligenceBattery    *Intelligence Data*

---

**Description**

A response matrix (n = 1152) of the International Cognitive Ability Resource (ICAR) intelligence battery developed by Condon and Revelle (2016).

A response matrix (n = 1152) of the International Cognitive Ability Resource (ICAR) intelligence battery developed by Condon and Revelle (2016).

**Usage**

```
data(intelligenceBattery)
```

```
data(intelligenceBattery)
```

**Format**

A 1185x125 response matrix

A 1185x125 response matrix

**Examples**

```
data("intelligenceBattery")
```

```
data("intelligenceBattery")
```

---

```
itemStability
```

*Item Stability Statistics from [bootEGA](#)*

---

**Description**

Based on the [bootEGA](#) results, this function computes and plots the number of times an item (variable) is estimated in the same factor/dimension as originally estimated by [EGA](#) (`item.replication`). The output also contains each item's replication frequency (i.e., proportion of bootstraps that an item appeared in each dimension; `item.dim.rep`) as well as the average network loading for each item in each dimension (`item.loadings`).

**Usage**

```
itemStability(bootega.obj, orig.wc, item.freq = 0.1, plot.item.rep = TRUE)
```

**Arguments**

<code>bootega.obj</code>	A <a href="#">bootEGA</a> object
<code>orig.wc</code>	Numeric or character. A vector with community numbers or labels for each item. Typically uses community results ( <code>wc</code> ) from <a href="#">EGA</a>
<code>item.freq</code>	A value for lowest frequency allowed in <code>item.dim.rep</code> output. Removes noise from table to allow for easier interpretation. Defaults to <code>.10</code>
<code>plot.item.rep</code>	Should the plot be produced for <code>item.replication</code> ? If <code>TRUE</code> , then a plot for the <code>item.replication</code> output will be produced. Defaults to <code>TRUE</code>

**Value**

Returns a list containing:

<code>item.replication</code>	The proportion of times each item replicated within the defined dimension
<code>mean.dim.rep</code>	The average replication proportion of items replicating in each dimension. More simply, the average of the <code>item.replication</code> output for each dimension
<code>item.dim.rep</code>	The proportion of times each item replicated within each possible dimension. Dimensions greater than the maximum number used in the <code>orig.wc</code> argument are labeled based on the largest remaining components after the dimensions used to <code>orig.wc</code>
<code>item.loadings</code>	Matrix of the average standardized network loading (computed using <code>net.loads</code> ) for each item in each dimension
<code>wc</code>	A matrix containing the community membership values for each bootstrapped sample. The values correspond to the values input for the <code>orig.wc</code> argument
<code>plot.itemStability</code>	A plot of the number of times each item replicates in its original community membership ( <code>orig.wc</code> )

**Author(s)**

Hudson Golino <hfg9s at virginia.edu> and Alexander P. Christensen <alexpaulchristensen@gmail.com>

**References**

Christensen, A. P., & Golino, H. (2019). Estimating the stability of the number of factors via Bootstrap Exploratory Graph Analysis: A tutorial. *PsyArXiv*. doi: [10.31234/osf.io/9deay](https://doi.org/10.31234/osf.io/9deay)

Christensen, A. P., Golino, H., & Silvia, P. J. (2020). A psychometric network perspective on the validity and validation of personality trait questionnaires. *European Journal of Personality*. doi: [10.1002/per.2265](https://doi.org/10.1002/per.2265)

**See Also**

[EGA](#) to estimate the number of dimensions of an instrument using EGA and [CFA](#) to verify the fit of the structure suggested by EGA using confirmatory factor analysis.

**Examples**

```
# Load data
wmt <- wmt2[,7:24]

# Estimate EGA network
## plot.type = "qqgraph" used for CRAN checks
## plot.type = "GGally" is the default
ega.wmt <- EGA(data = wmt, model = "glasso", plot.type = "qqgraph")

# Estimate dimension stability
```



```

boot.wmt <- bootEGA(data = wmt, iter = 100, typicalStructure = TRUE,
plot.typicalStructure = TRUE, model = "glasso", plot.type = "qgraph",
type = "parametric", ncores = 2)

# Estimate item stability statistics
res <- itemStability(boot.wmt, orig.wc = ega.wmt$wc)

# Changing plot features (ggplot2)
## Changing colors (ignore warnings)
### qgraph Defaults
res$plot.itemStability +
  ggplot2::scale_color_manual(values = rainbow(max(res$uniq.num)))

### Pastel
res$plot.itemStability +
  ggplot2::scale_color_brewer(palette = "Pastel1")

## Changing Legend (ignore warnings)
res$plot.itemStability +
  ggplot2::scale_color_discrete(labels = "Intelligence")

```

---

LCT

*Loadings Comparison Test*


---

## Description

An algorithm to identify whether data were generated from a random, factor, or network model using factor and network loadings. The algorithm uses heuristics based on theory and simulation. These heuristics were then submitted to several deep learning neural networks with 240,000 samples per model with varying parameters.

## Usage

```
LCT(data, n, iter = 100)
```

## Arguments

data	Matrix or data frame. A dataframe with the variables to be used in the test or a correlation matrix. If the data used is a correlation matrix, the argument n will need to be specified
n	Integer. Sample size (if the data provided is a correlation matrix)
iter	Integer. Number of replicate samples to be drawn from a multivariate normal distribution (uses <code>mvtnorm::mvrnorm</code> ). Defaults to 100

**Value**

Returns a list containing:

empirical	Prediction of model based on empirical dataset only
bootstrap	Prediction of model based on means of the loadings across the bootstrap replicate samples
proportion	Proportions of models suggested across bootstraps

**Author(s)**

Hudson F. Golino <hfg9s at virginia.edu> and Alexander P. Christensen <alexpaulchristensen at gmail.com>

**References**

# Original implementation of LCT

Christensen, A. P., & Golino, H. (in press). On the equivalency of factor and network loadings. *Behavior Research Methods*. doi: [10.31234/osf.io/xakez](https://doi.org/10.31234/osf.io/xakez)

# Current implementation of LCT

Christensen, A. P., & Golino, H. (under review). Random, factor, or network model? Predictions from neural networks. *PsyArXiv*. doi: [10.31234/osf.io/awkcb](https://doi.org/10.31234/osf.io/awkcb)

**Examples**

```
# Compute LCT
## Network model
LCT(data = wmt2[,7:24])

## Factor model
LCT(data = NetworkToolbox::neoOpen)
```

---

mctest.ergoInfo

*Monte-Carlo Test for the Ergodicity Information Index*

---

**Description**

Computes a Monte-Carlo Test for the Ergodicity Information Index, comparing the empirical Ergodicity Information index to values obtained in a Monte-Carlo simulation in which all individuals have a similar latent structure. The p-values in the Monte-Carlo test can be calculated as  $(\text{sum}(\text{EII} \geq \text{MC.EII}) + 1) / (\text{iter} + 1)$  and as  $(\text{sum}(\text{EII} \leq \text{MC.EII}) + 1) / (\text{iter} + 1)$ , where EII is the empirical Ergodicity Information Index, MC.EII is the values of the Ergodicity Information Index obtained in the simulation, and *iter* is the number of random samples generated in the simulation. The two-sided p-value is computed as two times the lowest p-value. In the Monte-Carlo Test for the Ergodicity Information Index, the null hypothesis is that the empirical value of EII is equal to the Monte-Carlo value of EII obtained in multiple individuals with a similar latent structure. Small

values of  $p$  indicate that is very unlikely to obtain an EII as large as the one obtained in the empirical sample if the null hypothesis is true, thus there is convincing evidence that the empirical Ergodicity Information Index is different than it could be expected if all individuals had a similar latent structure, conditioned on the parameters used to simulate the data.

### Usage

```
mctest.ergoInfo(
  iter,
  N,
  EII,
  use,
  variab,
  timep,
  nfact,
  error,
  dfm,
  loadings,
  autoreg,
  crossreg,
  var.shock,
  cov.shock,
  embed,
  tau,
  delta,
  derivatives,
  model,
  model.args = list(),
  algorithm = c("walktrap", "louvain"),
  algorithm.args = list(),
  corr,
  ncores,
  ...
)
```

### Arguments

<code>iter</code>	Numeric integer. Number of random samples to generate in the Monte-Carlo simulation. At least 500 is recommended
<code>N</code>	Numeric integer. Number of individuals to simulate data from, using the <a href="#">simDFM</a> function.
<code>EII</code>	Numeric. Empirical Ergodicity Information Index obtained via the <a href="#">ergoInfo</a> function.
<code>use</code>	Character. A string indicating what network element will be used to compute the algorithm complexity in the <a href="#">ergoInfo</a> function, the list of edges or the weights of the network. Defaults to <code>use = "edge.list"</code> . Current options are: <ul style="list-style-type: none"> <li><code>edge.list</code> Calculates the algorithm complexity using the list of edges.</li> </ul>

	<ul style="list-style-type: none"> <li>• <code>weights</code> Calculates the algorithm complexity using the weights of the network.</li> </ul>
<code>variab</code>	Number of variables per factor.
<code>timep</code>	Number of time points.
<code>nfact</code>	Number of factors.
<code>error</code>	Value to be used to construct a diagonal matrix $Q$ . This matrix is $p \times p$ covariance matrix $Q$ that will generate random errors following a multivariate normal distribution with mean zeros. The value provided is squared before constructing $Q$ .
<code>dfm</code>	<p>A string indicating the dynamical factor model to use. Defaults to "DAFS". Current options are:</p> <ul style="list-style-type: none"> <li>• <code>DAFS</code> Simulates data using the direct autoregressive factor score model. This is the default method</li> <li>• <code>RandomWalk</code> Simulates data using a dynamic factor model with random walk factor scores.</li> </ul>
<code>loadings</code>	Magnitude of the loadings.
<code>autoreg</code>	Magnitude of the autoregression coefficients. Default is " <code>autoreg = 0.8</code> ".
<code>crossreg</code>	Magnitude of the cross-regression coefficients. Default is " <code>crossreg = 0.1</code> ".
<code>var.shock</code>	Magnitude of the random shock variance. Default is " <code>var.shock = 0.18</code> ".
<code>cov.shock</code>	Magnitude of the random shock covariance Default is " <code>cov.shock = 0.36</code> ".
<code>embed</code>	Integer. Number of embedded dimensions (the number of observations to be used in the <code>Embed</code> function). For example, an " <code>embed = 5</code> " will use five observations to estimate a single derivative. Defaults to <code>embed = 5</code> .
<code>tau</code>	Integer. Number of observations to offset successive embeddings in the <code>Embed</code> function. A tau of one uses adjacent observations. Default is " <code>tau = 1</code> ".
<code>delta</code>	Integer. The time between successive observations in the time series. Default is " <code>delta = 1</code> ".
<code>derivatives</code>	Integer. The order of the derivative to be used in the EGA procedure. Default to 1.
<code>model</code>	<p>Character. A string indicating the method to use. Defaults to <code>glasso</code>. Current options are:</p> <ul style="list-style-type: none"> <li>• <code>glasso</code> Estimates the Gaussian graphical model using graphical LASSO with extended Bayesian information criterion to select optimal regularization parameter. This is the default method</li> <li>• <code>TMFG</code> Estimates a Triangulated Maximally Filtered Graph</li> </ul>
<code>model.args</code>	List. A list of additional arguments for <code>EBICglasso.qgraph</code> or <code>TMFG</code>
<code>algorithm</code>	<p>A string indicating the algorithm to use or a function from <code>igraph</code></p> <p>Current options are:</p> <ul style="list-style-type: none"> <li>• <code>walktrap</code> Computes the Walktrap algorithm using <code>cluster_walktrap</code></li> <li>• <code>louvain</code> Computes the Walktrap algorithm using <code>cluster_louvain</code></li> </ul>

algorithm.args	List. A list of additional arguments for <code>cluster_walktrap</code> , <code>cluster_louvain</code> , or some other community detection algorithm function (see examples)
corr	Type of correlation matrix to compute. The default uses <code>cor_auto</code> . Current options are: <ul style="list-style-type: none"> <li>• <code>cor_auto</code> Computes the correlation matrix using the <code>cor_auto</code> function from <code>qgraph</code>.</li> <li>• <code>pearson</code> Computes Pearson's correlation coefficient using the pairwise complete observations via the <code>cor</code> function.</li> <li>• <code>spearman</code> Computes Spearman's correlation coefficient using the pairwise complete observations via the <code>cor</code> function.</li> </ul>
ncores	Numeric. Number of cores to use in computing results. Defaults to <code>parallel::detectCores() / 2</code> or half of your computer's processing power. Set to 1 to not use parallel computing. Recommended to use maximum number of cores minus one If you're unsure how many cores your computer has, then use the following code: <code>parallel::detectCores()</code>
...	Additional arguments. Used for deprecated arguments from previous versions of <a href="#">EGA</a>

**Value**

Returns a list containing:

mc.ergoInfo	The values of the Ergodicity Information Index obtained in the Monte-Carlo Simulation
p.value.twosided	The p-value of the Monte-Carlo test for the Ergodicity Information Index. The null hypothesis is that the empirical Ergodicity Information index is equal to the expected value of the EII if the all individuals had similar latent structures.
effect	Indicates wheter the empirical EII is greater or less then the Monte-Carlo obtained EII.
plot.dist	Histogram of the bootstrapped ergodicity information index

**Author(s)**

Hudson Golino <hfg9s at virginia.edu>

**Examples**

```
## Not run:
\donttest{
dyn1 <- dynEGA.ind.pop(data = sim.dynEGA, n.embed = 5, tau = 1,
                      delta = 1, id = 21, group = 22, use.derivatives = 1,
                      model = "lasso", ncores = 2, corr = "pearson")

eii1 <- ergoInfo(data = dyn1)$EII

dist.ergoinfo <- mctest.ergoInfo(iter = 10, N = 10, EII = eii1,
```

```

variab = 4,
timep = 100, nfact = 2, error = 0.05, dfm = "DAFS", loadings = 0.55, autoreg = 0.8,
crossreg = 0.1, var.shock = 0.18, cov.shock = 0.36, embed = 5, tau=1, delta=1, derivatives=1,
model = "glasso", ncores = 2, corr = "pearson")
}
## End(Not run)

```

---

methods.section

*Automated Methods Section for [EGAnet](#) Objects*

---

## Description

This function accepts [EGA](#) objects and generates a Methods section for your analysis. The output is an HTML page containing the descriptions of the methods and parameters as well as a Reference section for appropriate citation.

## Usage

```

methods.section(
  ...,
  stats = c("net.loads", "net.scores", "dimStability", "itemStability")
)

```

## Arguments

- |       |   |
|-------|---|
| ...   | <p><a href="#">EGAnet</a> objects. Available methods (more methods will be added soon!):</p> <ul style="list-style-type: none"> <li>• <a href="#">EGA</a> Exploratory graph analysis</li> <li>• <a href="#">bootEGA</a> Bootstrap exploratory graph analysis</li> </ul>   |
| stats | <p>Methods section for statistics in <a href="#">EGAnet</a>. Multiple statistics can be input. Available statistics:</p> <ul style="list-style-type: none"> <li>• <a href="#">net.loads</a> Network loadings. Requires <a href="#">EGA</a> object to be input</li> <li>• <a href="#">net.scores</a> Network scores. Requires <a href="#">EGA</a> object to be input</li> <li>• <a href="#">dimStability</a> Structural consistency. Requires <a href="#">bootEGA</a> object to be input</li> <li>• <a href="#">itemStability</a> Item stability. Requires <a href="#">bootEGA</a> object to be input</li> </ul> |

## Value

Automated HTML Methods section in your default browser

**Examples**

```

# Estimate EGA
## plot.type = "qgraph" used for CRAN checks
## plot.type = "GGally" is the default
ega.wmt <- EGA(data = wmt2[,7:24], plot.type = "qgraph")

# EGA Methods section
if(interactive()){
  methods.section(ega.wmt)
}

# Estimate standardized network loadings
wmt.loads <- net.loads(ega.wmt)$std

# EGA Methods section with network loadings
if(interactive()){
  methods.section(ega.wmt, stats = "net.loads")
}

# bootEGA example
## plot.type = "qgraph" used for CRAN checks
## plot.type = "GGally" is the default
boot.wmt <- bootEGA(data = wmt2[,7:24], iter = 500, plot.type = "qgraph",
  type = "parametric", ncores = 2)

# EGA and bootEGA Methods section
if(interactive()){
  methods.section(ega.wmt, boot.wmt)
}

# Estimate structural consistency
sc.wmt <- dimStability(boot.wmt, orig.wc = ega.wmt$wc, item.stability = TRUE)

# EGA and bootEGA Methods section with structural consistency and item stability
if(interactive()){
  methods.section(boot.wmt, stats = c("dimStability", "itemStability"))
}

# EGA with network loadings and
# bootEGA Methods section with structural consistency and item stability
if(interactive()){
  methods.section(ega.wmt, boot.wmt, stats = c("net.loads", "dimStability", "itemStability"))
}

```

## Description

Computes the between- and within-community [strength](#) of each item for each community. This function uses the [comcat](#) and [stable](#) functions to calculate the between- and within-community strength of each item, respectively.

## Usage

```
net.loads(A, wc, pos.manifold = FALSE, min.load = 0, plot.NL = FALSE)
```

## Arguments

A	Matrix, data frame, or <a href="#">EGA</a> object. An adjacency matrix of network data
wc	Numeric or character vector. A vector of community assignments. If input into A is an <a href="#">EGA</a> object, then wc is automatically detected
pos.manifold	Boolean. Should a positive manifold be applied (i.e., should all dimensions be positively correlated)? Defaults to FALSE. Set to TRUE for a positive manifold
min.load	Numeric. Sets the minimum loading allowed in the standardized network loading matrix. Values equal or greater than the minimum loading are kept in the output. Values less than the minimum loading are removed. This matrix can be viewed using <code>print()</code> or <code>summary()</code> Defaults to 0
plot.NL	Boolean. Should proportional loadings be plotted? Defaults to FALSE. Set to TRUE for plot with pie charts visualizing the proportion of loading associated with each dimension

## Details

Simulation studies have demonstrated that a node's strength centrality is roughly equivalent to factor loadings (Christensen, Golino, & Silvia, 2019; Hallquist, Wright, & Molenaar, in press). Hallquist and colleagues (in press) found that node strength represented a combination of dominant and cross-factor loadings. This function computes each node's strength within each specified dimension, providing a rough equivalent to factor loadings (including cross-loadings).

For more details, type `vignette("Network_Scores")`

## Value

Returns a list containing:

unstd	A matrix of the unstandardized within- and between-community strength values for each node
std	A matrix of the standardized within- and between-community strength values for each node
minLoad	The minimum loading to appear in summary of network loadings. Use <code>print()</code> or <code>summary()</code> to view
plot	A <a href="#">qgraph</a> plot of the network loadings. Use <code>plot</code> to view



**Author(s)**

Alexander P. Christensen <alexpaulchristensen@gmail.com> and Hudson Golino <hfg9s at virginia.edu>

**References**

Christensen, A. P., & Golino, H. (2021). On the equivalency of factor and network loadings. *Behavior Research Methods*. doi: [10.3758/s13428020015006](https://doi.org/10.3758/s13428020015006)

Christensen, A. P., Golino, H., & Silvia, P. J. (in press). A psychometric network perspective on the validity and validation of personality trait questionnaires. *European Journal of Personality*. doi: [10.1002/per.2265](https://doi.org/10.1002/per.2265)

Hallquist, M., Wright, A. C. G., & Molenaar, P. C. M. (2019). Problems with centrality measures in psychopathology symptom networks: Why network psychometrics cannot escape psychometric theory. *Multivariate Behavioral Research*, 1-25. doi: [10.1080/00273171.2019.1640103](https://doi.org/10.1080/00273171.2019.1640103)

**Examples**

```
# Load data
wmt <- wmt2[,7:24]

## Not run:
# Estimate EGA
ega.wmt <- EGA(wmt)

## End(Not run)

# Network loadings
net.loads(ega.wmt)
```

---

 net.scores

*Network Scores*


---

**Description**

This function computes network scores computed based on each node's *strength* within each community (i.e., factor) in the network (see [net.loads](#)). These values are used as network "factor loadings" for the weights of each item. Notably, network analysis allows nodes to contribute to more than one community. These loadings are considered in the network scores. In addition, if the construct is a hierarchy (e.g., personality questionnaire; items in facet scales in a trait domain), then an overall score can be computed (see argument `global`). An important difference is that the network scores account for cross-loadings in their estimation of scores

**Usage**

```
net.scores(data, A, wc, global = FALSE, impute, ...)
```

**Arguments**

data	Matrix or data frame. Must be a dataset
A	Matrix, data frame, or <a href="#">EGA</a> object. An adjacency matrix of network data
wc	Numeric. A vector of community assignments. Not necessary if an <a href="#">EGA</a> object is input for argument A
global	Boolean. Should general network loadings be computed in scores? Defaults to FALSE. If there is more than one dimension and there is theoretically one global dimension, then general loadings of the dimensions onto the global dimension can be included in the weighted scores
impute	Character. In the presence of missing data, imputation can be implemented. Currently, three options are available: <ul style="list-style-type: none"> <li>• none No imputation is performed. This is the default.</li> <li>• mean The "mean" value of the columns are used to replace the missing data.</li> <li>• median The "median" value of the columns are used to replace the missing data.</li> </ul>
...	Additional arguments for <a href="#">EGA</a>

**Details**

For more details, type `vignette("Network_Scores")`

**Value**

Returns a list containing:

unstd.scores	The unstandardized network scores for each participant and community (including the overall score)
std.scores	The standardized network scores for each participant and community (including the overall score)
commCor	Partial correlations between the specified or identified communities
loads	Standardized network loadings for each item in each dimension (computed using <a href="#">net.loads</a> )

**Author(s)**

Alexander P. Christensen <[alexpaulchristensen@gmail.com](mailto:alexpaulchristensen@gmail.com)> and Hudson F. Golino <[hfg9s@virginia.edu](mailto:hfg9s@virginia.edu)>

**References**

- Christensen, A. P., & Golino, H. (2021). On the equivalency of factor and network loadings. *Behavior Research Methods*. doi: [10.3758/s13428020015006](https://doi.org/10.3758/s13428020015006)
- Christensen, A. P., Golino, H., & Silvia, P. J. (in press). A psychometric network perspective on the measurement and assessment of personality traits. *European Journal of Personality*. doi: [10.1002/per.2265](https://doi.org/10.1002/per.2265)

Golino, H., Christensen, A. P., Moulder, R., Kim, S., & Boker, S. M. (under review). Modeling latent topics in social media using Dynamic Exploratory Graph Analysis: The case of the right-wing and left-wing trolls in the 2016 US elections. *PsyArXiv*. doi: [10.31234/osf.io/tfs7c](https://doi.org/10.31234/osf.io/tfs7c)

### Examples

```
# Load data
wmt <- wmt2[,7:24]

## Not run:
# Estimate EGA
ega.wmt <- EGA(wmt)

## End(Not run)

# Network scores
net.scores(data = wmt, A = ega.wmt)
```

---

node.redundant	<i>Detects Redundant Nodes in a Network</i>
----------------	---

---

### Description

Identifies redundant nodes in the network based on several measures. Computes the weighted topological overlap between each node and every other node in the network. The weighted topological overlap is implemented using the method from Nowick et al. (2009; see references) and the function [wTO](#) from the [wTO](#) package.

### Usage

```
node.redundant(
  data,
  n = NULL,
  sig,
  method = c("wTO", "pcor", "cor"),
  thresh = TRUE,
  type = c("alpha", "adapt"),
  plot = FALSE
)
```

### Arguments

data	Matrix or data frame. Input can either be data or a correlation matrix
n	Numeric. If input in data is a correlation matrix and method = "wTO", then sample size is required. Defaults to NULL
sig	Numeric. <i>p</i> -value for significance of overlap (defaults to .05)

method	Character. Computes weighted topological overlap ("wTO" using <a href="#">EBICglasso</a> ), partial correlations ("pcor"), and correlations ("cor"). Defaults to "wTO"
thresh	Boolean. Should a threshold be applied? Defaults to TRUE. If TRUE, then based on a certain threshold only redundancies above that value will be returned. Uses argument "sig" to input the desired threshold. Defaults for each method: <ul style="list-style-type: none"> <li>• "wTO" .20</li> <li>• "pcor" .20</li> <li>• "cor" .70</li> </ul>
type	Character. Type of significance. Computes significance using the standard $p$ -value ("alpha"), or adaptive alpha $p$ -value ( <a href="#">adapt.a</a> ). Defaults to "adapt"
plot	Boolean. Should redundancies be plotted in a network plot? Defaults to FALSE

### Value

Returns a list:

redundant	Vectors nested within the list corresponding to redundant nodes with the name of object in the list
data	Returns original data
weights	Returns weights determine by weighted topological overlap or partial correlations
network	The network compute by <a href="#">EBICglasso</a>
descriptives	<ul style="list-style-type: none"> <li>• basicA vector containing the mean, standard deviation, median, median absolute deviation (MAD), 3 times the MAD, 6 times the MAD, minimum, maximum, and critical value for the overlap measure (i.e., weighted topological overlap, partial correlation, or threshold)</li> <li>• centralTendencyA matrix for all (absolute) non-zero values and their respective standard deviation from the mean and median absolute deviation from the median</li> </ul>
distribution	Distribution that was used to determine significance

### Author(s)

Alexander Christensen <[alexpaulchristensen@gmail.com](mailto:alexpaulchristensen@gmail.com)>

### References

# Simulation using node.redundant

Christensen, A. P. (2020). Towards a network psychometrics approach to assessment: Simulations for redundancy, dimensionality, and loadings (Unpublished doctoral dissertation). University of North Carolina at Greensboro, Greensboro, NC, USA. doi: [10.31234/osf.io/84kgd](https://doi.org/10.31234/osf.io/84kgd)

# Implementation of node.redundant

Christensen, A. P., Golino, H., & Silvia, P. J. (in press). A psychometric network perspective on the validity and validation of personality trait questionnaires. *European Journal of Personality*. doi: [10.1002/per.2265](https://doi.org/10.1002/per.2265)

```
# wTO measure
Nowick, K., Gernat, T., Almaas, E., & Stubbs, L. (2009). Differences in human and chimpanzee gene expression patterns define an evolving network of transcription factors in brain. Proceedings of the National Academy of Sciences, 106, 22358-22363. doi: 10.1073/pnas.0911376106
```

## Examples

```
# obtain SAPA items
items <- psychTools::spi[,c(11:20)]

# weighted topological overlap
redund <- node.redundant(items, method = "wTO", type = "adapt", plot = TRUE)

# partial correlation
redund <- node.redundant(items, method = "pcor", type = "adapt", plot = TRUE)

# threshold
redund <- node.redundant(items, method = "pcor", thresh = TRUE, sig = .20, plot = TRUE)
```

---

node.redundant.combine

*Combines Redundant Nodes*

---

## Description

Allows user to combine redundant nodes into sum scores and latent variables to reduce the redundancy of variables in their data

## Usage

```
node.redundant.combine(
  node.redundant.obj,
  type = c("sum", "latent"),
  estimator = "WLSMV",
  auto = FALSE,
  ...
)
```

## Arguments

node.redundant.obj

A [node.redundant](#) object

type

Character. Method to use to combine redundant variables.

- "sum" Computes sum scores (i.e., means) of the variables
- "latent" Computes latent variable scores using `[lavaan]{cfa}`

Defaults to "latent"

estimator	Character. Estimator to use for latent variables. Defaults to "WLSMV". See <code>[lavaan]{cfa}</code> for more options
auto	NOT RECOMMENDED. Boolean. Should redundant nodes be automatically combined? Defaults to FALSE. If set to TRUE, then redundant nodes will be combined using the following heuristics: <ol style="list-style-type: none"> <li>1. Redundant nodes that form a 3-clique (i.e., a triangle) with the target node are automatically redundant</li> <li>2. If there are no 3-cliques, then the 2-clique with the largest regularized partial correlation is selected</li> </ol>
...	Options to be passed onto <code>[lavaan]{cfa}</code>

**Value**

Returns a list:

data	New data with redundant variables merged
merged	A matrix containing the variables that were decided to be redundant with one another

**Author(s)**

Alexander Christensen <alexpaulchristensen@gmail.com>

**References**

Christensen, A. P., Golino, H., & Silvia, P. J. (in press). A psychometric network perspective on the validity and validation of personality trait questionnaires. *European Journal of Personality*. doi: [10.1002/per.2265](https://doi.org/10.1002/per.2265)

**Examples**

```
# obtain SAPA items
items <- psychTools::spi[, -c(1:10)]

# weighted topological overlap
redund <- node.redundant(items, method = "wTO", type = "adapt")

# partial correlation
redund <- node.redundant(items, method = "pcor", type = "adapt")

# check redundancies
key.ind <- match(colnames(items), as.character(psychTools::spi.dictionary$item_id))
key <- as.character(psychTools::spi.dictionary$item[key.ind])

# change names in redundancy output to questionnaire item description
named.nr <- node.redundant.names(redund, key)

if(interactive())
```

```
{combine <- node.redundant.combine(named.nr)}
```

---

node.redundant.names *Changes Variable Names to Descriptions for node.redundant Objects*

---

### Description

Using a key, this function changes the variable names in the `node.redundant` output to descriptions

### Usage

```
node.redundant.names(node.redundant.obj, key)
```

### Arguments

node.redundant.obj	A <code>node.redundant</code> object
key	Character vector. A vector with variable descriptions that correspond to the order of variables from the data used as input into the <code>node.redundant</code> function

### Value

Returns a list:

redundant	Vectors nested within the list corresponding to redundant nodes with the name of object in the list
data	Returns original data
weights	Returns weights determine by weighted topological overlap or partial correlations
key	Returns original key

### Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

### References

Christensen, A. P., Golino, H., & Silvia, P. J. (in press). A psychometric network perspective on the validity and validation of personality trait questionnaires. *European Journal of Personality*. doi: [10.1002/per.2265](https://doi.org/10.1002/per.2265)

**Examples**

```
# obtain SAPA items
items <- psychTools::spi[,-c(1:10)]

# weighted topological overlap
redund <- node.redundant(items, method = "wTO", type = "adapt")

# partial correlation
redund <- node.redundant(items, method = "pcor", type = "adapt")

# check redundancies
key.ind <- match(colnames(items), as.character(psychTools::spi.dictionary$item_id))
key <- as.character(psychTools::spi.dictionary$item[key.ind])

# change names in redundancy output to questionnaire item description
named.nr <- node.redundant.names(redund, key)
```

---

optimism

*Optimism Data*


---

**Description**

A response matrix (n = 282) containing responses to 10 items of the Revised Life Orientation Test (LOT-R), developed by Scheier, Carver, & Bridges (1994).

A response matrix (n = 282) containing responses to 10 items of the Revised Life Orientation Test (LOT-R), developed by Scheier, Carver, & Bridges (1994).

**Usage**

```
data(optimism)
```

```
data(optimism)
```

**Format**

A 282x10 response matrix

A 282x10 response matrix

**References**

Scheier, M. F., Carver, C. S., & Bridges, M. W. (1994). Distinguishing optimism from neuroticism (and trait anxiety, self-mastery, and self-esteem): a reevaluation of the Life Orientation Test. *Journal of Personality and Social Psychology*, *67*, 1063-1078. doi: [10.1037/00223514.67.6.1063](https://doi.org/10.1037/00223514.67.6.1063)

Scheier, M. F., Carver, C. S., & Bridges, M. W. (1994). Distinguishing optimism from neuroticism (and trait anxiety, self-mastery, and self-esteem): a reevaluation of the Life Orientation Test. *Journal of Personality and Social Psychology*, *67*, 1063-1078.



**Examples**

```
data("optimism")

data("optimism")
```

plots

*S3Methods for Plotting***Description**

Plots for EGAnet objects

**Usage**

```
## S3 method for class 'bootEGA'
plot(x, plot.type = c("GGally", "qgraph"), plot.args = list(), ...)

## S3 method for class 'CFA'
plot(x, layout = "spring", vsize = 6, ...)

## S3 method for class 'dynEGA'
plot(x, title = "", plot.type = c("GGally", "qgraph"), plot.args = list(), ...)

## S3 method for class 'dynEGA.Groups'
plot(x, ncol, nrow, title = "",
      plot.type = c("GGally", "qgraph"), plot.args = list(), ...)

## S3 method for class 'dynEGA.Individuals'
plot(x, title = "", id = NULL,
      plot.type = c("GGally", "qgraph"), plot.args = list(), ...)

## S3 method for class 'EGA'
plot(x, title = "", plot.type = c("GGally", "qgraph"), plot.args = list(), ...)

## S3 method for class 'NetLoads'
plot(x, ...)
```

**Arguments**

<code>x</code>	Object from EGAnet package
<code>plot.type</code>	Character. Plot system to use. Current options are <a href="#">qgraph</a> and <a href="#">GGally</a> . Defaults to "GGally".
<code>plot.args</code>	List. A list of additional arguments for the network plot. For <code>plot.type = "qgraph"</code> : <ul style="list-style-type: none"> <li><code>vsize</code> Size of the nodes. Defaults to 6.</li> </ul>

For `plot.type = "GGally"` (see [ggnet2](#) for full list of arguments):

- `vsiz` Size of the nodes. Defaults to 6.
- `label.size` Size of the labels. Defaults to 5.
- `alpha` The level of transparency of the nodes, which might be a single value or a vector of values. Defaults to 0.7.
- `edge.alpha` The level of transparency of the edges, which might be a single value or a vector of values. Defaults to 0.4.
- `legend.names` A vector with names for each dimension
- `color.palette` The color palette for the nodes. For custom colors, enter HEX codes for each dimension in a vector. See [color\\_palette\\_EGA](#) for more details and examples

...	Arguments passed on to
	<ul style="list-style-type: none"> <li>• <a href="#">qgraph</a> Functions: <code>bootEGA</code>, <code>dynEGA</code>, <code>dynEGA.Groups</code>, <code>dynEGA.Individuals</code>, <code>EGA</code>, and <code>net.loads</code></li> <li>• <a href="#">semPaths</a> Functions: <code>CFA</code></li> </ul>
<code>vsiz</code>	Numeric. Size of vertices in <a href="#">CFA</a> plots. Defaults to 6
<code>layout</code>	Character. Layout of plot (see <a href="#">semPaths</a> ). Defaults to "spring"
<code>ncol</code>	Numeric. Number of columns
<code>nrow</code>	Numeric. Number of rows
<code>title</code>	Character. Title of the plot. Defaults to ""
<code>id</code>	Numeric. An integer or character indicating the ID of the individual to plot

### Value

Plots of EGAnet object

### Author(s)

Hudson Golino <[hfg9s@virginia.edu](mailto:hfg9s@virginia.edu)> and Alexander P. Christensen <[alexpaulchristensen@gmail.com](mailto:alexpaulchristensen@gmail.com)>

---

prints

*S3Methods for Printing*

---

### Description

Prints for EGAnet objects

**Usage**

```
## S3 method for class 'dynEGA'  
print(x, ...)  
  
## S3 method for class 'dynEGA.Groups'  
print(x, ...)  
  
## S3 method for class 'dynEGA.Individuals'  
print(x, ...)  
  
## S3 method for class 'EGA'  
print(x, ...)  
  
## S3 method for class 'NetLoads'  
print(x, ...)
```

**Arguments**

x	Object from EGAnet package
...	Additional arguments

**Value**

Prints EGAnet object

**Author(s)**

Hudson Golino <hfg9s at virginia.edu> and Alexander P. Christensen <alexpaulchristensen@gmail.com>

---

residualEGA

*Residualized* [EGA](#)

---

**Description**

residualEGA Estimates the number of dimensions after controlling for wording effects. EGA is applied in the residual of a random intercept item factor model (RIIFA) with one method factor and one substantive factor.

**Usage**

```
residualEGA(data, manifests, lat, negative.items, plot = TRUE)
```

**Arguments**

<code>data</code>	Matrix or data frame. Includes the variables to be used in the residualEGA analysis
<code>manifests</code>	Character vector. Vector indicating the names of the variables (items) to be used in the analysis.
<code>lat</code>	Numeric integer. Number of latent factors to be estimated. Only one substantive latent factor is recommended in the current version of the function.
<code>negative.items</code>	Numeric vector A numeric vector indicating the column of the negative items.
<code>plot</code>	Boolean. If TRUE, returns a plot of the residualized network and its estimated dimensions. Defaults to TRUE

**Value**

Returns a list containing:

<code>openMx.model</code>	OpenMX model
<code>openMx.result</code>	OpenMX results
<code>openMx.std.par</code>	OpenMX standardized parameters
<code>ResidualMatrix</code>	Residual matrix
<code>EGA.Residuals</code>	Results of the residualized EGA
<code>Fit</code>	Fit metrics of the network structure, calculated using the <code>ggmfit</code> function of the <a href="#">qgraph</a> package
<code>WordLoads</code>	Loadings of the wording effects

**Author(s)**

Hudson F. Golino <hfg9s at virginia.edu> and Robert Moulder <rgm4fd@virginia.edu>

**See Also**

[EGA](#) to estimate the number of dimensions of an instrument using EGA and [CFA](#) to verify the fit of the structure suggested by EGA using confirmatory factor analysis.

**Examples**

```
data <- optimism

## Not run:
# resEGA example
opt.res <- residualEGA(data = data, manifests = colnames(optimism),
  lat = 1, negative.items = c(3,7,9), plot = TRUE)

# Fit:
opt.res$Fit

## End(Not run)
```

---

shinyEGA	<i>Shiny App for EGA</i> <a href="#">net</a>
----------	--

---

**Description**

An interactive Shiny application for running [EGAnet](#) analysis

**Usage**

```
shinyEGA()
```

**Value**

A list called resultShiny containing:

data	The data imported into <a href="#">shinyEGA</a>
EGA	The output generated from <a href="#">EGA</a>

**Author(s)**

Hudson Golino <hfg9s at virginia.edu> and Alexander P. Christensen <alexpaulchristensen@gmail.com>

**Examples**

```
if(interactive())  
{shinyEGA()}
```

---

sim.dynEGA	<i>sim.dynEGA Data</i>
------------	------------------------

---

**Description**

A simulated (multivariate time series) data with 20 variables, 200 individual observations, 50 time points per individual and 2 groups of individuals.

**Usage**

```
data(sim.dynEGA)
```

**Format**

A 10000x22 multivariate time series

**Examples**

```
data("sim.dynEGA")
```

simDFM

*Simulate data following a Dynamic Factor Model***Description**

Function to simulate data following a dynamic factor model (DFM). Two DFMs are currently available: the direct autoregressive factor score model (Engle & Watson, 1981; Nesselroade, McArdle, Aggen, and Meyers, 2002) and the dynamic factor model with random walk factor scores.

**Usage**

```
simDFM(
  variab,
  timep,
  nfact,
  error,
  dfm = c("DAFS", "RandomWalk"),
  loadings,
  autoreg,
  crossreg,
  var.shock,
  cov.shock,
  burnin = 1000
)
```

**Arguments**

variab	Number of variables per factor.
timep	Number of time points.
nfact	Number of factors.
error	Value to be used to construct a diagonal matrix Q. This matrix is p x p covariance matrix Q that will generate random errors following a multivariate normal distribution with mean zeros. The value provided is squared before constructing Q.
dfm	A string indicating the dynamical factor model to use. Current options are: <ul style="list-style-type: none"> <li>• DAFS Simulates data using the direct autoregressive factor score model. This is the default method</li> <li>• RandomWalk Simulates data using a dynamic factor model with random walk factor scores.</li> </ul>
loadings	Magnitude of the loadings.
autoreg	Magnitude of the autoregression coefficients.
crossreg	Magnitude of the cross-regression coefficients.
var.shock	Magnitude of the random shock variance.
cov.shock	Magnitude of the random shock covariance
burnin	Number of n first samples to discard when computing the factor scores. Defaults to 1000.

**Author(s)**

Hudson F. Golino <hfg9s at virginia.edu>

**References**

A one-factor multivariate time series model of metropolitan wage rates. *Journal of the American Statistical Association*, 76(376), 774-781. ref:01621459.1981.10477720#.XmkWWy2ZMuA

Nesselroade, J. R., McArdle, J. J., Aggen, S. H., & Meyers, J. M. (2002). Dynamic factor analysis models for representing process in multivariate time-series. In D. S. Moskowitz & S. L. Hershberger (Eds.), *Multivariate applications book series. Modeling intraindividual variability with repeated measures data: Methods and applications*, 235–265. <https://psycnet.apa.org/record/2001-05300-009>

**Examples**

```
## Not run:
\donttest{
# Estimate EGA network
data1 <- simDFM(variab = 5, timep = 50, nfact = 3, error = 0.05,
dfm = "DAFS", loadings = 0.7, autoreg = 0.8,
crossreg = 0.1, var.shock = 0.18,
cov.shock = 0.36, burnin = 1000)
}

## End(Not run)
```

---

summarys

*S3Methods for Summaries*


---

**Description**

Summaries for EGAnet objects

**Usage**

```
## S3 method for class 'CFA'
summary(object, ...)

## S3 method for class 'dynEGA'
summary(object, ...)

## S3 method for class 'dynEGA.Groups'
summary(object, ...)

## S3 method for class 'dynEGA.Individuals'
```

```
summary(object, ...)

## S3 method for class 'EGA'
summary(object, ...)

## S3 method for class 'NetLoads'
summary(object, ...)
```

### Arguments

```
object      Object from EGAnet package
...         Additional arguments
```

### Value

Summarizes EGAnet object

### Author(s)

Hudson Golino <hfg9s at virginia.edu> and Alexander P. Christensen <alexpaulchristensen@gmail.com>

---

tefi	<i>Total Entropy Fit Index using Von Neumman's entropy (Quantum Information Theory) for correlation matrices</i>
------	--

---

### Description

Computes the fit (TEFI) of a dimensionality structure using Von Neumman's entropy when the input is a correlation matrix. Lower values suggest better fit of a structure to the data.

### Usage

```
tefi(data, structure)
```

### Arguments

```
data          A dataframe or correlation matrix
structure     A vector representing the structure (numbers or labels for each item). Can be
              theoretical factors or the structure detected by EGA
```

### Value

Returns a list containing:

```
VN.Entropy.Fit  The Entropy Fit Index using Von Neumman's entropy
Total.Correlation
                The total correlation of the dataset
Average.Entropy
                The average entropy of the dataset
```



**Author(s)**

Hudson Golino <hfg9s at virginia.edu>, Alexander P. Christensen <alexpaulchristensen@gmail.com>, and Robert Moulder <rgm4fd@virginia.edu>

**References**

Golino, H., Moulder, R. G., Shi, D., Christensen, A. P., Garrido, L. E., Neito, M. D., Nesselroade, J., Sadana, R., Thiyagarajan, J. A., & Boker, S. M. (2020). Entropy fit indices: New fit measures for assessing the structure and dimensionality of multiple latent variables. *Multivariate Behavioral Research*. doi: [10.31234/osf.io/mtka2](https://doi.org/10.31234/osf.io/mtka2)

**See Also**

[EGA](#) to estimate the number of dimensions of an instrument using EGA and [CFA](#) to verify the fit of the structure suggested by EGA using confirmatory factor analysis.

**Examples**

```
# Load data
wmt <- wmt2[,7:24]

## Not run:
# Estimate EGA model
ega.wmt <- EGA(data = wmt, model = "glasso")

## End(Not run)

# Compute entropy indices
tefi(data = ega.wmt$correlation, structure = ega.wmt$wc)
```

---

totalCor

*Total Correlation*

---

**Description**

Computes the total correlation of a dataset

**Usage**

```
totalCor(data)
```

**Arguments**

data                    Matrix or data frame. Variables to be used in the analysis

**Value**

Returns a list containing:

Ind.Entropies Individual entropies for each variable  
 Joint.Entropy The joint entropy of the dataset  
 Total.Cor The total correlation of the dataset

**Author(s)**

Hudson F. Golino <hfg9s at virginia.edu>

**References**

Watanabe, S. (1960). Information theoretical analysis of multivariate correlation. *IBM Journal of Research and Development* 4, 66-82.

**Examples**

```
# Compute total correlation
totalCor(wmt2[,7:24])
```

---

totalCorMat

*Total Correlation Matrix*

---

**Description**

Computes the pairwise total correlation for a dataset

**Usage**

```
totalCorMat(data)
```

**Arguments**

data Matrix or data frame. Variables to be used in the analysis

**Value**

Returns a square matrix with pairwise total correlations

**Author(s)**

Hudson F. Golino <hfg9s at virginia.edu>

**References**

Watanabe, S. (1960). Information theoretical analysis of multivariate correlation. *IBM Journal of Research and Development* 4, 66-82.

**Examples**

```
# Compute total correlation
totalCorMat(wmt2[,7:24])
```

---

toy.example

*Toy Example Data*


---

**Description**

A simulated dataset with 2 factors, three items per factor and n = 500.

**Usage**

```
data(toy.example)
```

**Format**

A 500x6 response matrix

**Examples**

```
data("toy.example")
```

---

UVA

*Unique Variable Analysis*


---

**Description**

Identifies redundant variables in a multivariate dataset using a number of different association methods and types of significance values (see Christensen, Garrido, & Golino, 2020 for more details)

**Usage**

```
UVA(
  data,
  n = NULL,
  model = c("glasso", "TMFG"),
  corr = c("cor_auto", "pearson", "spearman"),
  method = c("cor", "pcor", "wTO"),
  type = c("adapt", "alpha", "threshold"),
  sig,
  key = NULL,
  reduce = TRUE,
  reduce.method = c("latent", "remove", "sum"),
```

```

lavaan.args = list(),
adhoc = TRUE,
plot.redundancy = FALSE,
plot.args = list()
)

```

## Arguments

<code>data</code>	Matrix or data frame. Input can either be data or a correlation matrix
<code>n</code>	Numeric. If input in <code>data</code> is a correlation matrix, then sample size is required. Defaults to NULL
<code>model</code>	Character. A string indicating the method to use. Current options are: <ul style="list-style-type: none"> <li>• <code>glasso</code> Estimates the Gaussian graphical model using graphical LASSO with extended Bayesian information criterion to select optimal regularization parameter. This is the default method</li> <li>• <code>TMFG</code> Estimates a Triangulated Maximally Filtered Graph</li> </ul>
<code>corr</code>	Type of correlation matrix to compute. The default uses <code>cor_auto</code> . Current options are: <ul style="list-style-type: none"> <li>• <code>cor_auto</code> Computes the correlation matrix using the <code>cor_auto</code> function from <code>qgraph</code>.</li> <li>• <code>pearson</code> Computes Pearson's correlation coefficient using the pairwise complete observations via the <code>cor</code> function.</li> <li>• <code>spearman</code> Computes Spearman's correlation coefficient using the pairwise complete observations via the <code>cor</code> function.</li> </ul>
<code>method</code>	Character. Computes weighted topological overlap (" <code>wT0</code> " using <code>EBICglasso</code> ), partial correlations (" <code>pcor</code> "), and correlations (" <code>cor</code> "). Defaults to " <code>wT0</code> "
<code>type</code>	Character. Type of significance. Computes significance using the standard $p$ -value (" <code>alpha</code> "), adaptive alpha $p$ -value ( <code>adapt.a</code> ), or some threshold " <code>threshold</code> ". Defaults to " <code>adapt</code> "
<code>sig</code>	Numeric. $p$ -value for significance of overlap (defaults to <code>.05</code> ). Defaults for " <code>threshold</code> " for each method: <ul style="list-style-type: none"> <li>• "<code>wT0</code>" <code>.20</code></li> <li>• "<code>pcor</code>" <code>.20</code></li> <li>• "<code>cor</code>" <code>.70</code></li> </ul>
<code>key</code>	Character vector. A vector with variable descriptions that correspond to the order of variables input into <code>data</code> . Defaults to NULL or the column names of <code>data</code>
<code>reduce</code>	Boolean. Should redundancy reduction be performed? Defaults to TRUE. Set to FALSE for redundancy analysis only
<code>reduce.method</code>	Character. How should data be reduced? Defaults to " <code>latent</code> " <ul style="list-style-type: none"> <li>• "<code>latent</code>" Redundant variables will be combined into a latent variable</li> <li>• "<code>remove</code>" All but one redundant variable will be removed</li> <li>• "<code>sum</code>" Redundant variables are combined by summing across cases (rows)</li> </ul>

lavaan.args	<p>List. If <code>reduce.method = "latent"</code>, then <code>lavaan</code>'s <code>cfa</code> function will be used to create latent variables to reduce variables. Arguments should be input as a list. Some example arguments (see <a href="#">lavOptions</a> for full details):</p> <ul style="list-style-type: none"> <li>• <code>estimator</code> Estimator to use for latent variables (see <a href="#">Estimators</a>) for more details. Defaults to "MLR" for continuous data and "WLSMV" for mixed and categorical data. Data are considered continuous data if they have 6 or more categories (see Rhemtulla, Brosseau-Liard, &amp; Savalei, 2012)</li> <li>• <code>missing</code> How missing data should be handled. Defaults to "fiml"</li> <li>• <code>std.lv</code> If TRUE, the metric of each latent variable is determined by fixing their (residual) variances to 1.0. If FALSE, the metric of each latent variable is determined by fixing the factor loading of the first indicator to 1.0. If there are multiple groups, <code>std.lv = TRUE</code> and "loadings" is included in the <code>group.label</code> argument, then only the latent variances <math>i</math> of the first group will be fixed to 1.0, while the latent variances of other groups are set free. Defaults to TRUE</li> </ul>
adhoc	<p>Boolean. Should adhoc check of redundancies be performed? Defaults to TRUE. If TRUE, adhoc check will run the redundancy analysis on the reduced variable set to determine if there are any remaining redundancies. This check is performed with the arguments: <code>method = "wTO"</code>, <code>type = "threshold"</code>, and <code>sig = .20</code>. This check is based on Christensen, Garrido, and Golino's (2020) simulation where these parameters were found to be the most conservative, demonstrating few false positives and false negatives</p>
plot.redundancy	<p>Boolean. Should redundancies be plotted in a network plot? Defaults to FALSE</p>
plot.args	<p>List. Arguments to be passed onto <code>ggnet2</code>. Defaults:</p> <ul style="list-style-type: none"> <li>• <code>vsize = 6</code></li> <li>• <code>alpha = 0.4</code></li> <li>• <code>label.size = 5</code></li> <li>• <code>edge.alpha = 0.7</code></li> </ul>

## Value

Returns a list:

redundancy	<p>A list containing several objects:</p> <ul style="list-style-type: none"> <li>• <code>redudant</code> Vectors nested within the list corresponding to redundant nodes with the name of object in the list</li> <li>• <code>data</code> Original data</li> <li>• <code>correlation</code> Correlation matrix of original data</li> <li>• <code>weights</code> Weights determine by weighted topological overlap, partial correlation, or zero-order correlation</li> <li>• <code>network</code> If <code>method = "wTO"</code>, then the network computed following <a href="#">EGA</a> with <a href="#">EBICglasso</a> network estimation</li> <li>• <code>plot</code> If <code>redundancy.plot = TRUE</code>, then a plot of all redundancies found</li> <li>• <code>descriptives</code></li> </ul>
------------	---

- basic A vector containing the mean, standard deviation, median, median absolute deviation (MAD), 3 times the MAD, 6 times the MAD, minimum, maximum, and critical value for the overlap measure (i.e., weighted topological overlap, partial correlation, or threshold)
  - centralTendency A matrix for all (absolute) non-zero values and their respective standard deviation from the mean and median absolute deviation from the median
  - method Returns method argument
  - type Returns type argument
  - distribution If type != "threshold", then distribution that was used to determine significance
- reduced      If reduce = TRUE, then a list containing:
- data New data with redundant variables merged or removed
  - mergedA matrix containing the variables that were decided to be redundant with one another
  - method Method used to perform redundancy reduction
- adhoc        If adhoc = TRUE, then the adhoc check containing the same objects as in the redundancy list object in the output

### Author(s)

Alexander Christensen <alexpaulchristensen@gmail.com>

### References

# Simulation using UCA

Christensen, A. P., Garrido, L. E., & Golino, H. (2020). Unique Variable Analysis: A novel approach for detecting redundant variables in multivariate data. *PsyArXiv*. doi: [10.31234/osf.io/4kra2](https://doi.org/10.31234/osf.io/4kra2)

# Implementation of UCA (formally node .redundant)

Christensen, A. P., Golino, H., & Silvia, P. J. (2020). A psychometric network perspective on the validity and validation of personality trait questionnaires. *European Journal of Personality*, *34*, 1095-1108. doi: [10.1002/per.2265](https://doi.org/10.1002/per.2265)

# wTO measure

Nowick, K., Gernat, T., Almaas, E., & Stubbs, L. (2009). Differences in human and chimpanzee gene expression patterns define an evolving network of transcription factors in brain. *Proceedings of the National Academy of Sciences*, *106*, 22358-22363. doi: [10.1073/pnas.0911376106](https://doi.org/10.1073/pnas.0911376106)

# Selection of CFA Estimator

Rhemtulla, M., Brosseau-Liard, P. E., & Savalei, V. (2012). When can categorical variables be treated as continuous? A comparison of robust continuous and categorical SEM estimation methods under suboptimal conditions. *Psychological Methods*, *17*, 354-373. doi: [10.1037/a0029315](https://doi.org/10.1037/a0029315)

### Examples

```
# Select Five Factor Model personality items only
idx <- na.omit(match(gsub("-", ""), unlist(psychTools::spi.keys[1:5])), colnames(psychTools::spi)))
items <- psychTools::spi[,idx]
```

```

# Change names in redundancy output to each item's description
key.ind <- match(colnames(items), as.character(psychTools::spi.dictionary$item_id))
key <- as.character(psychTools::spi.dictionary$item[key.ind])

if(interactive()){
  UVA(data = items, method = "wT0", type = "adapt",
      key = key, reduce.method = "latent")
}

```

---

vn.entropy	<i>Entropy Fit Index using Von Neumman's entropy (Quantum Information Theory) for correlation matrices</i>
------------	--

---

### Description

Computes the fit of a dimensionality structure using Von Neumman's entropy when the input is a correlation matrix. Lower values suggest better fit of a structure to the data.

### Usage

```
vn.entropy(data, structure)
```

### Arguments

data	A dataframe or a correlation matrix
structure	A vector representing the structure (numbers or labels for each item). Can be theoretical factors or the structure detected by <a href="#">EGA</a>

### Value

Returns a list containing:

VN.Entropy.Fit	The Entropy Fit Index using Von Neumman's entropy
Total.Correlation	The total correlation of the dataset
Average.Entropy	The average entropy of the dataset

### Author(s)

Hudson Golino <hfg9s at virginia.edu>, Alexander P. Christensen <alexpaulchristensen@gmail.com>, and Robert Moulder <rgm4fd@virginia.edu>

## References

Golino, H., Moulder, R. G., Shi, D., Christensen, A. P., Garrido, L. E., Neito, M. D., Nesselroade, J., Sadana, R., Thiyagarajan, J. A., & Boker, S. M. (2020). Entropy fit indices: New fit measures for assessing the structure and dimensionality of multiple latent variables. *Multivariate Behavioral Research*. doi: [10.31234/osf.io/mtka2](https://doi.org/10.31234/osf.io/mtka2)

## See Also

[EGA](#) to estimate the number of dimensions of an instrument using EGA and [CFA](#) to verify the fit of the structure suggested by EGA using confirmatory factor analysis.

## Examples

```
# Load data
dep <- depression[,24:44]

# Estimate EGA
## plot.type = "qqgraph" used for CRAN checks
## plot.type = "GGally" is the default
ega.dep <- EGA(data = dep, model = "glasso", plot.type = "qgraph")

# Compute entropy indices
vn.entropy(data = ega.dep$correlation, structure = ega.dep$wc)
```

---

wmt2

*WMT-2 Data*

---

## Description

A response matrix (n = 1185) of the Wiener Matrizen-Test 2 (WMT-2).

A response matrix (n = 1185) of the Wiener Matrizen-Test 2 (WMT-2).

## Usage

```
data(wmt2)
```

```
data(wmt2)
```

## Format

A 1185x24 response matrix

A 1185x24 response matrix



**Examples**

```
data("wmt2")
```

```
data("wmt2")
```

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