

# Package ‘gcor’

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**Title** Generalized Correlation and Related Measures

**Version** 0.1.0

**Depends** R (>= 4.0.0)

**Description** Generalized correlation and related measures for assessing nonlinear relationships between variables, including mixed-type data. For methodological background, see <<https://r-suzuki.github.io/gcor/method.html>>.

**License** MIT + file LICENSE

**Encoding** UTF-8

**RoxygenNote** 7.3.3

**URL** <https://github.com/r-suzuki/gcor-r>

**BugReports** <https://github.com/r-suzuki/gcor-r/issues>

**NeedsCompilation** no

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**Repository** CRAN

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**Description**

Estimate generalized correlation and related measures, which includes:

- Generalized correlation measure (gcor)
- Directed generalized correlation measure (dgcov)
- Dissimilarity between variables (gdis)

**Usage**

```
gcor(  
  x,  
  y = NULL,  
  data = NULL,  
  dropNA = "none",  
  k = NULL,  
  max_levels = 100,  
  simplify = TRUE  
)
```

```
dgcov(  
  x,  
  y = NULL,  
  data = NULL,  
  dropNA = "none",  
  k = NULL,  
  max_levels = 100,  
  simplify = TRUE  
)
```

```
gdis(x, dropNA = "none", k = NULL, max_levels = 100, ...)
```

**Arguments**

x	a vector, matrix, data frame or formula. If formula, data should be specified. gdis requires a matrix or data frame.
y	NULL (default) or a vector, matrix or data frame with compatible dimensions to x.
data	NULL (default) or a data frame. Required if x is a formula.
dropNA	a character specifying how to handle missing values. It should be one of the following:

	"none" (default) Treat missing values as observations of a single categorical value, namely NA. Recommended for reflecting missing patterns in the analysis.
	"casewise" Casewise deletion; rows containing any missing value are removed. Similar to use = "complete.obs" in <a href="#">cor</a> .
	"pairwise" Pairwise deletion; for any pair of columns (x,y), the i-th row is removed if x[i] or y[i] is missing. This process is applied per pair; the same row is not removed with another pair (w,z), if both w[i] and z[i] are not missing. Similar to use = "pairwise.complete.obs" in <a href="#">cor</a> .
k	NULL (default) or an integer specifying the number of groups for discretization. Numerical data are divided into k groups using k-quantiles. If NULL, it is determined automatically.
max_levels	an integer specifying the maximum number of levels allowed when converting non-numeric variables to factors.
simplify	a logical. If TRUE, the returned value is coerced to a vector when one of its dimensions is one.
...	additional arguments (diag and upper) passed to <a href="#">as.dist</a> function. See <a href="#">as.dist</a> for details.

### Value

For `gcor` and `dgcor`, a numeric matrix is returned (or a vector if `simplify = TRUE`). For `gdis`, an object of class "dist" is returned.

### References

Suzuki, R. (2026). *Method Overview of gcor*. <https://r-suzuki.github.io/gcor/method.html>

### Examples

```
# Generalized correlation measure
gcor(iris)

# Dependency of Species on other variables
dgc <- dgcor(Species ~ ., data = iris)
dotchart(sort(dgc), main = "Dependency of Species")

# Clustering
gd <- gdis(iris)
hc <- hclust(gd, method = "ward.D2")
plot(hc)

# Multidimensional scaling
mds <- cmdscale(gd, k = 2)
plot(mds, type = "n", xlab = "", ylab = "", asp = 1, axes = FALSE,
      main = "cmdscale with gdis(iris)")
text(mds[,1], mds[,2], rownames(mds))
```

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