

# Package: gadjid (via r-universe)

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**Title** Graph Adjustment Identification Distances for Causal Graphs

**Version** 0.1.0

**Description** Make efficient Rust implementations of graph adjustment identification distances available in R. These distances (based on ancestor, optimal, and parent adjustment) count how often the respective adjustment identification strategy leads to causal inferences that are incorrect relative to a ground-truth graph when applied to a candidate graph instead. See also Henckel, Würtzen, Weichwald (2024)  [<doi:10.48550/arXiv.2402.08616>](https://doi.org/10.48550/arXiv.2402.08616).

**License** MPL

**Encoding** UTF-8

**RoxygenNote** 7.3.2

**Config/rextendr/version** 0.4.1

**SystemRequirements** Cargo (Rust's package manager), rustc

**Depends** R (>= 4.2)

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**URL** <https://github.com/CausalDisco/gadjid>

**BugReports** <https://github.com/CausalDisco/gadjid/issues>

**NeedsCompilation** yes

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**Config/pak/sysreqs** libclang-dev

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

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ancestor_aid	<i>Ancestor Adjustment Identification Distance between two DAG / CPDAG adjacency matrices</i>
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### Description

Computes the ancestor adjustment intervention distance between the true `g_true` DAG or CPDAG and an estimated `g_guess` DAG or CPDAG.

### Usage

```
ancestor_aid(g_true, g_guess, edge_direction)
```

### Arguments

<code>g_true</code>	Adjacency matrix of the true graph
<code>g_guess</code>	Adjacency matrix of the guess graph
<code>edge_direction</code>	either "from row to column" or "from column to row"

### Details

For details see Henckel, Würtzen, Weichwald (2024) [doi:10.48550/arXiv.2402.08616](https://doi.org/10.48550/arXiv.2402.08616)  
 The source code is available at [github.com/CausalDisco/gadjid](https://github.com/CausalDisco/gadjid)

Graph inputs are accepted as adjacency matrices of type double. An adjacency matrix for a DAG may only contain 0s and 1s. An adjacency matrix for a CPDAG may only contain 0s, 1s and 2s. DAG and CPDAG inputs are validated for acyclicity. However, for CPDAG inputs, **the user needs to ensure the adjacency matrix indeed codes a valid CPDAG (instead of just a PDAG)**.

If `edge_direction="from row to column"`, then a 1 in row `r` and column `c` codes a directed edge '`r → c`'; if `edge_direction="from column to row"`, then a 1 in row `r` and column `c` codes a directed edge '`c → r`'; for either setting of `edge_direction`, a 2 in row `r` and column `c` codes an undirected edge '`r - c`' (an additional 2 in row `c` and column `r` is ignored; one of the two entries is sufficient to code an undirected edge).

### Value

2-element vector of type double  
`c`(normalized error in  $[0,1]$ , total number of errors)

## References

L Henckel, T Würtzen, S Weichwald. "Adjustment Identification Distance: A gadjid for Causal Structure Learning." Proceedings of the 40th Conference on Uncertainty in Artificial Intelligence (UAI), 2024. doi:10.48550/arXiv.2402.08616

## Examples

```
full <- rbind(c(0, 1, 1, 1),
             c(0, 0, 1, 1),
             c(0, 0, 0, 1),
             c(0, 0, 0, 0))
chain <- rbind(c(0, 1, 0, 0),
              c(0, 0, 1, 0),
              c(0, 0, 0, 1),
              c(0, 0, 0, 0))
identical(ancestor_aid(full, chain, "from row to column"), c(0/12, 0))
```

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oset_aid	<i>Optimal Adjustment Identification Distance between two DAG / CPDAG adjacency matrices</i>
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## Description

Computes the optimal adjustment intervention distance between the true `g_true` DAG or CPDAG and an estimated `g_guess` DAG or CPDAG.

## Usage

```
oset_aid(g_true, g_guess, edge_direction)
```

## Arguments

<code>g_true</code>	Adjacency matrix of the true graph
<code>g_guess</code>	Adjacency matrix of the guess graph
<code>edge_direction</code>	either "from row to column" or "from column to row"

## Details

For details see Henckel, Würtzen, Weichwald (2024) doi:10.48550/arXiv.2402.08616  
The source code is available at [github.com/CausalDisco/gadjid](https://github.com/CausalDisco/gadjid)

Graph inputs are accepted as adjacency matrices of type double. An adjacency matrix for a DAG may only contain 0s and 1s. An adjacency matrix for a CPDAG may only contain 0s, 1s and 2s. DAG and CPDAG inputs are validated for acyclicity. However, for CPDAG inputs, **the user needs to ensure the adjacency matrix indeed codes a valid CPDAG (instead of just a PDAG)**.

If `edge_direction="from row to column"`, then a 1 in row `r` and column `c` codes a directed edge `r → c`; if `edge_direction="from column to row"`, then a 1 in row `r` and column `c` codes a directed

edge 'c → r'; for either setting of edge\_direction, a 2 in row r and column c codes an undirected edge 'r – c' (an additional 2 in row c and column r is ignored; one of the two entries is sufficient to code an undirected edge).

### Value

2-element vector of type double  
c(normalized error in [0,1], total number of errors)

### References

L Henckel, T Würtzen, S Weichwald. "Adjustment Identification Distance: A gadjid for Causal Structure Learning." Proceedings of the 40th Conference on Uncertainty in Artificial Intelligence (UAI), 2024. doi:10.48550/arXiv.2402.08616

### Examples

```
full <- rbind(c(0, 1, 1, 1),
             c(0, 0, 1, 1),
             c(0, 0, 0, 1),
             c(0, 0, 0, 0))
chain <- rbind(c(0, 1, 0, 0),
              c(0, 0, 1, 0),
              c(0, 0, 0, 1),
              c(0, 0, 0, 0))
identical(oset_aid(full, chain, "from row to column"), c(3/12, 3))
```

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parent_aid	<i>Parent Adjustment Identification Distance between two DAG / CPDAG adjacency matrices</i>
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### Description

Computes the parent adjustment intervention distance between the true g\_true DAG or CPDAG and an estimated g\_guess DAG or CPDAG.

### Usage

```
parent_aid(g_true, g_guess, edge_direction)
```

### Arguments

g_true	Adjacency matrix of the true graph
g_guess	Adjacency matrix of the guess graph
edge_direction	either "from row to column" or "from column to row"

## Details

For details see Henckel, Würtzen, Weichwald (2024) [doi:10.48550/arXiv.2402.08616](https://doi.org/10.48550/arXiv.2402.08616)  
 The source code is available at [github.com/CausalDisco/gadjid](https://github.com/CausalDisco/gadjid)

Graph inputs are accepted as adjacency matrices of type double. An adjacency matrix for a DAG may only contain 0s and 1s. An adjacency matrix for a CPDAG may only contain 0s, 1s and 2s. DAG and CPDAG inputs are validated for acyclicity. However, for CPDAG inputs, **the user needs to ensure the adjacency matrix indeed codes a valid CPDAG (instead of just a PDAG)**.

If `edge_direction="from row to column"`, then a 1 in row  $r$  and column  $c$  codes a directed edge ' $r \rightarrow c$ '; if `edge_direction="from column to row"`, then a 1 in row  $r$  and column  $c$  codes a directed edge ' $c \rightarrow r$ '; for either setting of `edge_direction`, a 2 in row  $r$  and column  $c$  codes an undirected edge ' $r - c$ ' (an additional 2 in row  $c$  and column  $r$  is ignored; one of the two entries is sufficient to code an undirected edge).

## Value

2-element vector of type double  
 $c(\text{normalized error in } [0,1], \text{total number of errors})$

## References

L Henckel, T Würtzen, S Weichwald. "Adjustment Identification Distance: A gadjid for Causal Structure Learning." Proceedings of the 40th Conference on Uncertainty in Artificial Intelligence (UAI), 2024. [doi:10.48550/arXiv.2402.08616](https://doi.org/10.48550/arXiv.2402.08616)

## Examples

```
full <- rbind(c(0, 1, 1, 1),
             c(0, 0, 1, 1),
             c(0, 0, 0, 1),
             c(0, 0, 0, 0))
chain <- rbind(c(0, 1, 0, 0),
              c(0, 0, 1, 0),
              c(0, 0, 0, 1),
              c(0, 0, 0, 0))
identical(parent_aid(full, chain, "from row to column"), c(4/12, 4))
```

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 shd

*Structural Hamming Distance between two DAG / CPDAG adjacency matrices*

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## Description

Computes the structural Hamming distance between the true `g_true` PDAG and an estimated `g_guess` PDAG.

**Usage**

```
shd(g_true, g_guess)
```

**Arguments**

`g_true` Adjacency matrix of the true partially directed acyclic graph  
`g_guess` Adjacency matrix of the guess partially directed acyclic graph

**Details**

For details see Henckel, Würtzen, Weichwald (2024) [doi:10.48550/arXiv.2402.08616](https://doi.org/10.48550/arXiv.2402.08616)  
 The source code is available at [github.com/CausalDisco/gadjid](https://github.com/CausalDisco/gadjid)

Graph inputs are accepted as adjacency matrices of type double. An adjacency matrix for a PDAG may only contain 0s, 1s and 2s. PDAG are validated for acyclicity.

A 1 in row  $r$  and column  $c$  codes a directed edge and a 1 in row  $c$  and column  $r$  codes a directed edge in reverse direction; a 2 in row  $r$  and column  $c$  codes an undirected edge ‘ $r - c$ ’ (an additional 2 in row  $c$  and column  $r$  is ignored; one of the two entries is sufficient to code an undirected edge).

**Value**

2-element vector of type double  
`c(normalized error in [0,1], total number of errors)`

**Examples**

```
full <- rbind(c(0, 1, 1, 1),
             c(0, 0, 1, 1),
             c(0, 0, 0, 1),
             c(0, 0, 0, 0))
chain <- rbind(c(0, 1, 0, 0),
              c(0, 0, 1, 0),
              c(0, 0, 0, 1),
              c(0, 0, 0, 0))
identical(shd(full, chain), c(3/6, 3))
```

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<code>sid</code>	<i>Structural Identification Distance between two DAG adjacency matrices</i>
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**Description**

Computes the structural intervention distance (SID), between the true `g_true` DAG and an estimated `g_guess` DAG.

**Usage**

```
sid(g_true, g_guess, edge_direction)
```

## Arguments

`g_true` Adjacency matrix of the true directed acyclic graph  
`g_guess` Adjacency matrix of the guess directed acyclic graph  
`edge_direction` either "from row to column" or "from column to row"

## Details

Since the Parent-AID reduces to the SID in the special case of DAG inputs and is efficiently implemented using reachability algorithms, it offers a faster way to calculate the SID; see also Henckel, Würtzen, Weichwald (2024) [doi:10.48550/arXiv.2402.08616](https://doi.org/10.48550/arXiv.2402.08616). The example below can be compared to

```
library("SID")
system.time(structIntervDist(random_dag(20), random_dag(20)))
```

For details see Henckel, Würtzen, Weichwald (2024) [doi:10.48550/arXiv.2402.08616](https://doi.org/10.48550/arXiv.2402.08616)  
 The source code is available at [github.com/CausalDisco/gadjid](https://github.com/CausalDisco/gadjid)

Graph inputs are accepted as adjacency matrices of type double. An adjacency matrix for a DAG may only contain 0s and 1s. DAG inputs are validated for acyclicity.

If `edge_direction="from row to column"`, then a 1 in row  $r$  and column  $c$  codes a directed edge ' $r \rightarrow c$ '; if `edge_direction="from column to row"`, then a 1 in row  $r$  and column  $c$  codes a directed edge ' $c \rightarrow r$ '.

## Value

2-element vector of type double  
 $c(\text{normalized error in } [0,1], \text{total number of errors})$

## References

L Henckel, T Würtzen, S Weichwald. "Adjustment Identification Distance: A gadjid for Causal Structure Learning." Proceedings of the 40th Conference on Uncertainty in Artificial Intelligence (UAI), 2024. [doi:10.48550/arXiv.2402.08616](https://doi.org/10.48550/arXiv.2402.08616)

J Peters, P Bühlmann. "Structural intervention distance for evaluating causal graphs." Neural Computation 27(3), 771–799, 2015. [doi:10.1162/NECO\\_a\\_00708](https://doi.org/10.1162/NECO_a_00708)

## Examples

```
random_dag <- function(n, p=0.1) {
  P <- sample(n)
  m <- matrix(0, n, n)
  m[upper.tri(m)] <- rbinom(n*(n-1)/2, 1, p)
  m[P, P]
}

system.time(sid(random_dag(400), random_dag(400), "from row to column"))
```

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