

pcalg: A brief overview

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1 General Introduction

This vignette is not up to date! It will soon be updated. Please use `skeleton`, `pc`, `fci` instead of `pcAlgo`. Also use `ida`, `idaFast` instead of `beta.special`, `beta.special.pcObj`. Until the new vignette is ready, we show the old vignette for your convenience.

In this document, we will give a short overview of the R-package `pcalg`. The package can be used to analyze dependencies among random variables. The main functions are

- `pcAlgo`: (also see `?pcAlgo`) Use the PC-Algorithm to estimate the skeleton of a DAG. A DAG is a Directed Acyclic Graph and the skeleton of a DAG is the DAG without the arrowheads. In practice, the skeleton will only be a good estimate, if you have way more samples than nodes. If not, you will only get the edges, that show the most obvious “direct” dependencies (“direct” means: The dependence didn’t go away, even when conditioning on any subset of the remaining variables). Using the plot option `zvalue.lwd` you can further qualify the edges by choosing their line width according to their reliability in the statistical tests. I.e., thick lines show reliable dependencies. The value of this function is an object of S4 class “`pcAlgo`” (see `?pcAlgo-class`) on which you can use `plot`, `summary` and `show`.
- `corGraph`: (see also `?corGraph`) Each pair of variables is tested for zero correlation on a given significance level. If a test is rejected, the corresponding edge in the graph is kept. I.e., the graph shows an edge between correlated nodes.

Furthermore, there are some functions that generate random data and perform statistical tests.

2 Some examples

In this section, we will show some simple examples with the most important functions. First, we generate a data set that will be used later on:

```
> library(pcalg)
> p <- 10
> n <- 10000
> s <- 0.4
> set.seed(42)
> g <- randomDAG(p, s)
> d <- rmvDAG(n, g)
```

The DAG that was produced by `g <- randomDAG(p,s)` is shown in Figure 1.

`d` contains the datamatrix you would start from in practice. Let’s try to estimate the skeleton of the DAG and also compute the correlation graph:

```
> gSkel <- pcAlgo(d, alpha = 0.05)
```

This function is deprecated and is only kept for backward compatibility. Please use `skeleton`, `pc`,

```
> gCor <- corGraph(d, alpha = 0.05)
```

```
> plot(g)
```

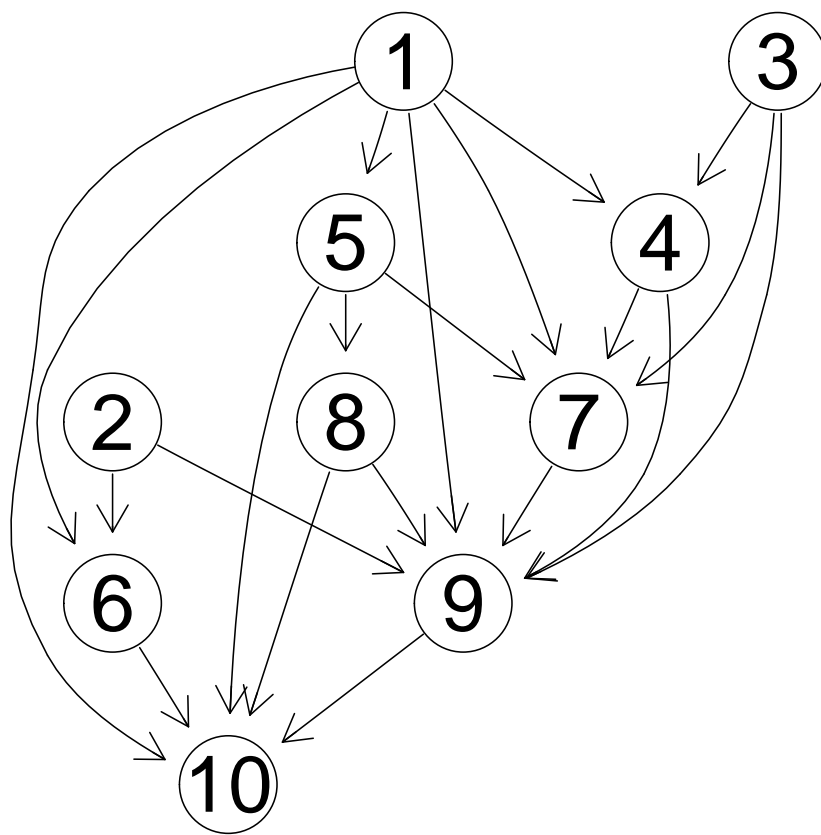


Figure 1: True DAG

```
> plot(gCor)
```

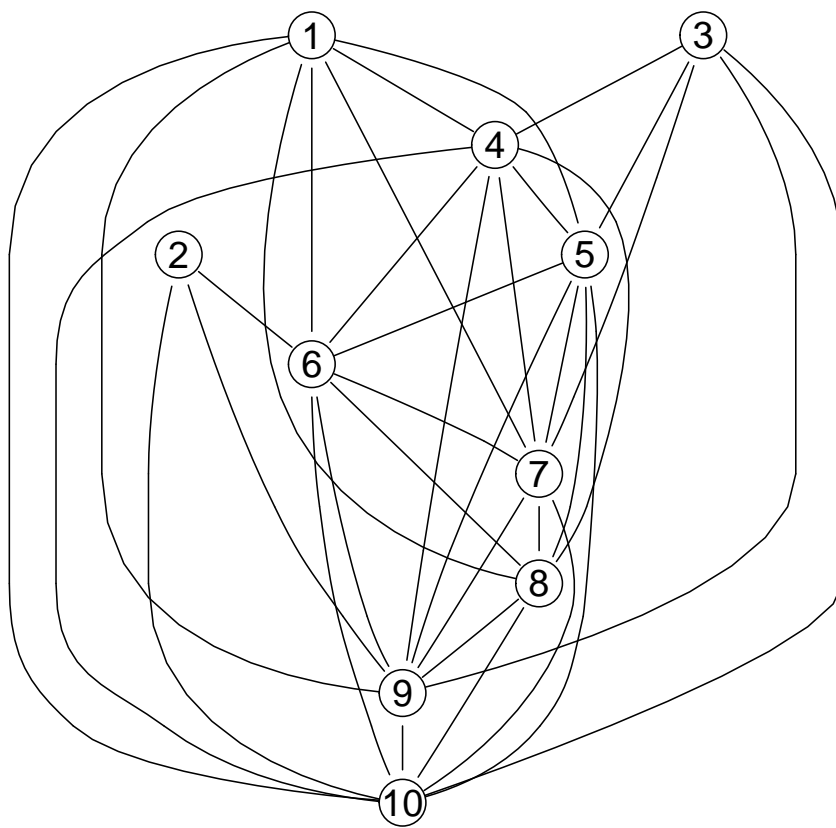


Figure 2: Correlation Graph

The result of `corGraph` is a `graph` object and can be plotted with `plot(gCor)` (see Figure 2).
The result of `pcAlgo` is a `pcAlgo` object. To get an overview, you can use the `summary` function:

```
> summary(gSkel)

Object of class 'pcAlgo', from Call:
pcAlgo(dm = d, alpha = 0.05)

Nmb. edgetests during skeleton estimation:
=====
Max. order of algorithm: 5
Number of edgetests from m = 0 up to m = 5 : 81 295 329 277 36 0

Graphical properties of skeleton:
=====
Max. number of neighbours: 5 at node(s) 9 10
Avg. number of neighbours: 3.2

> plot(gSkel)
```

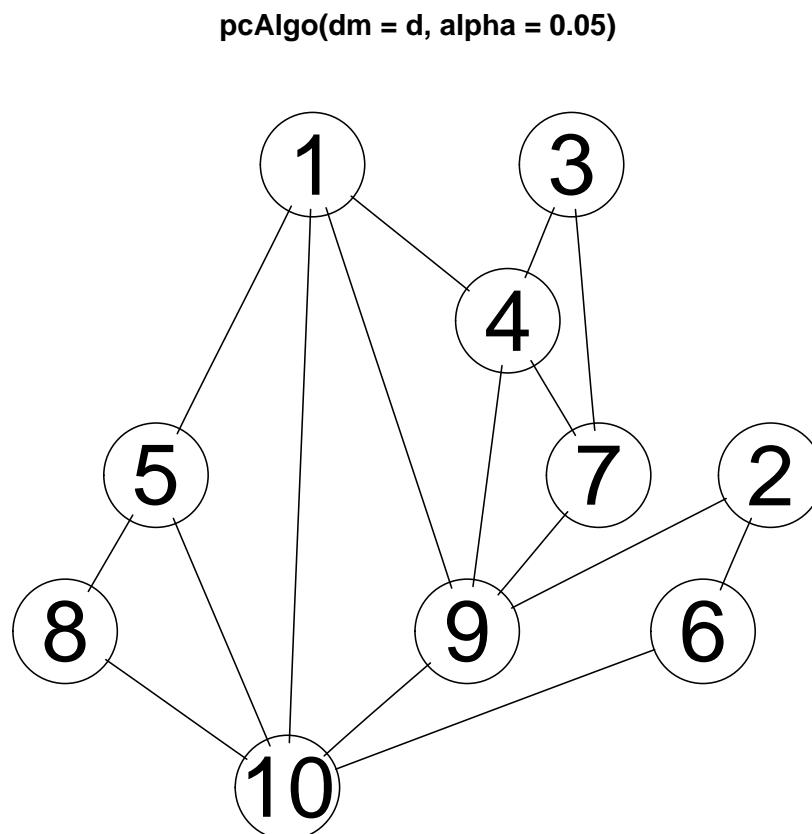


Figure 3: Estimated skeleton

When plotting the `pcAlgo` object by using `plot(gSkel)`, we obtain Figure 3; choosing the option `zvalue.lwd = TRUE`, we can adapt the line width of the graph according to the reliability of the corresponding statistical test (see Figure 4).

To compare the estimate of the skeleton with the true skeleton, use

```
> plot(gSkel, zvalue.lwd = TRUE)
```

pcAlgo(dm = d, alpha = 0.05)

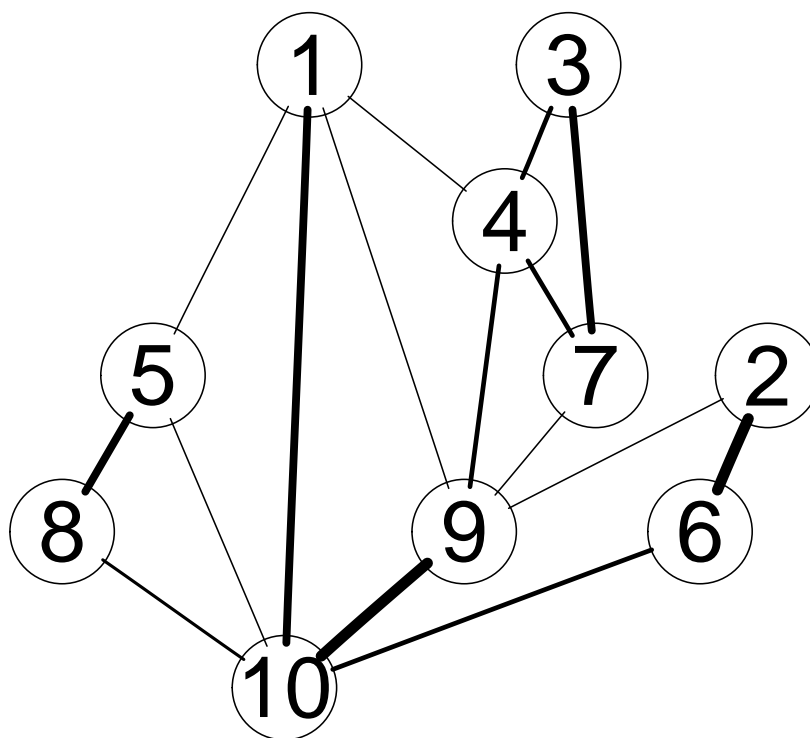


Figure 4: Estimated skeleton using variable line width

```
> compareGraphs(gSkel@graph, g)
```

tpr	fpr	tdr
0.7619048	0.0000000	1.0000000