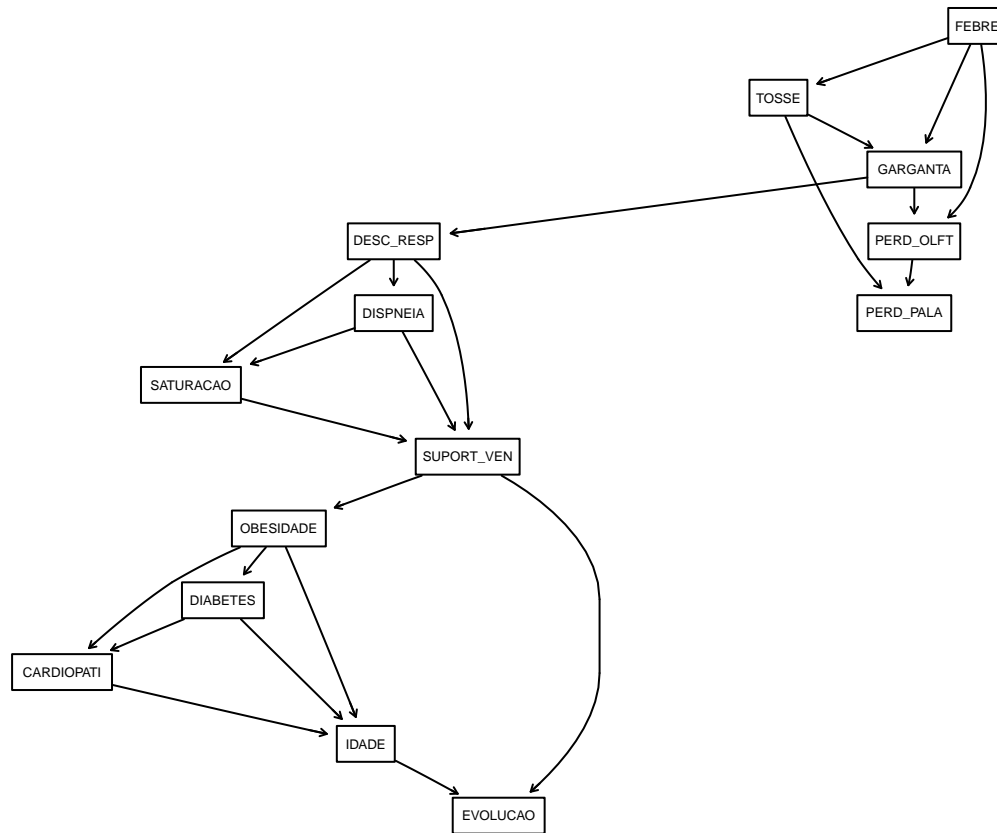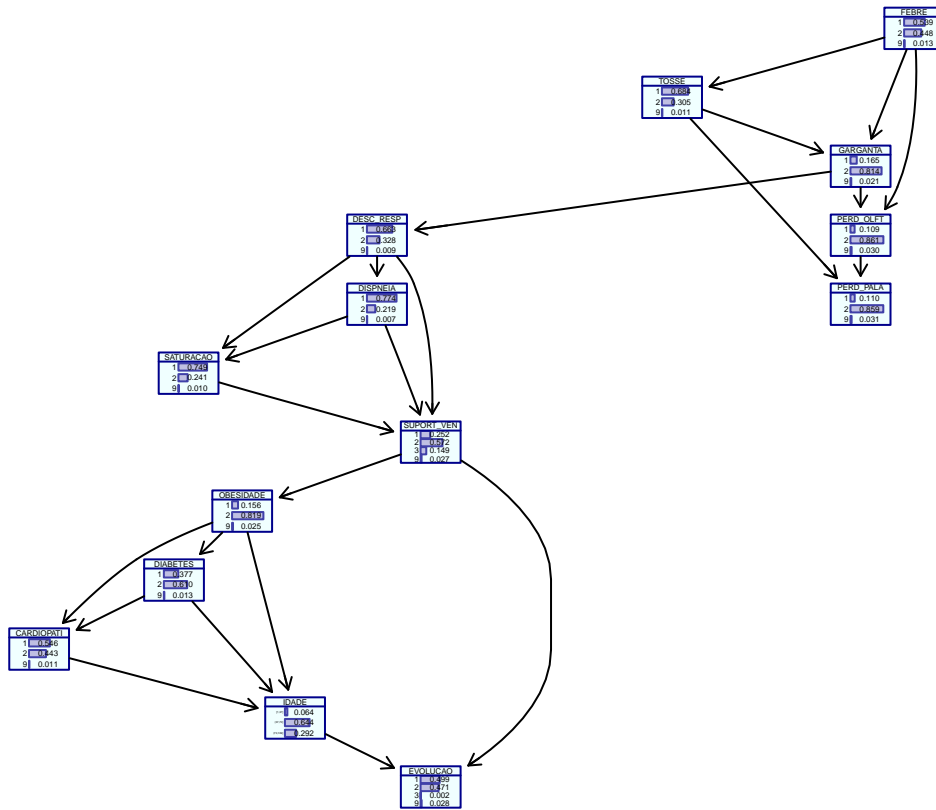# Teste Melhor Impressão de Barcharts

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4/15/2021

```r
boots.trap  <- 50
str.diff = suppressMessages(boot.strength(s1, R = boots.trap, algorithm = "mmhc"))
cat(paste('Threshold: ', attr(str.diff, "threshold")))
```

```
## Threshold:  0.88
```

```r
avg.diff = averaged.network(str.diff)
```

```
## Warning in averaged.network.backend(strength = strength, nodes = nodes, : arc
## IDADE -> DIABETES would introduce cycles in the graph, ignoring.
```

```
## Warning in averaged.network.backend(strength = strength, nodes = nodes, : arc
## IDADE -> CARDIOPATI would introduce cycles in the graph, ignoring.
```

```r
strength.plot(avg.diff, str.diff, shape = "rectangle", main = "Iterações = 50")
```

Iterações = 50
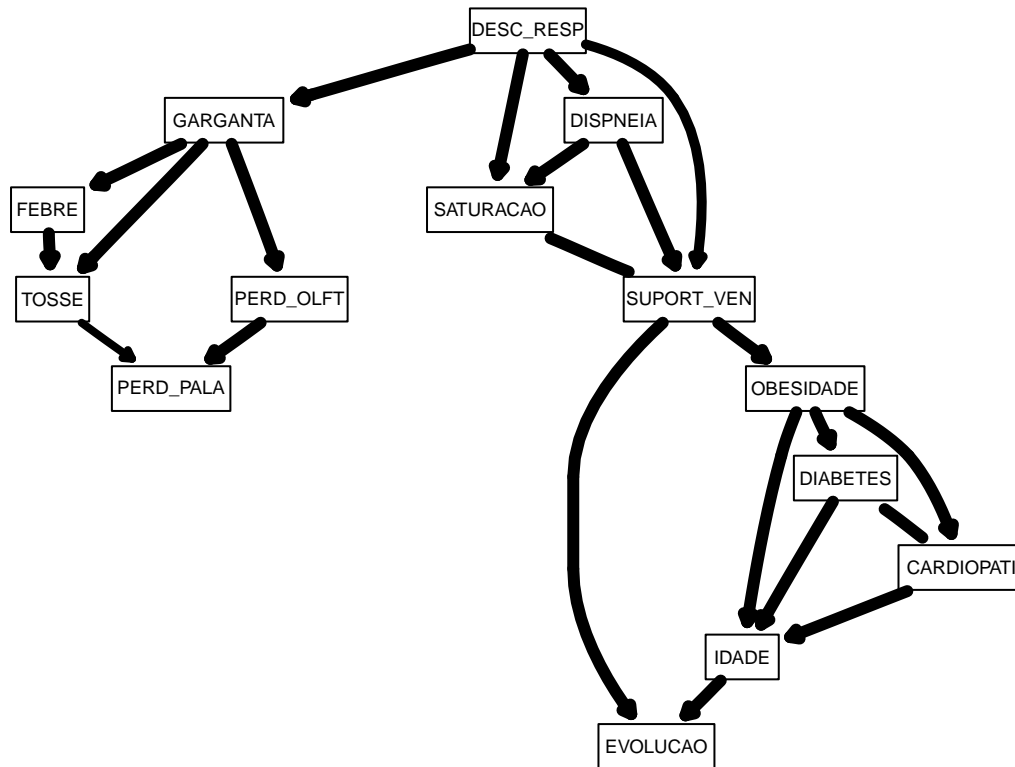
How can we compare the averaged network (avg.diff) with the network we originally learned in from all the data (dag)? The most qualitative way is to plot the two networks side by side, with the nodes in the same positions, and highlight the arcs that appear in one network and not in the other, or that appear with different directions.
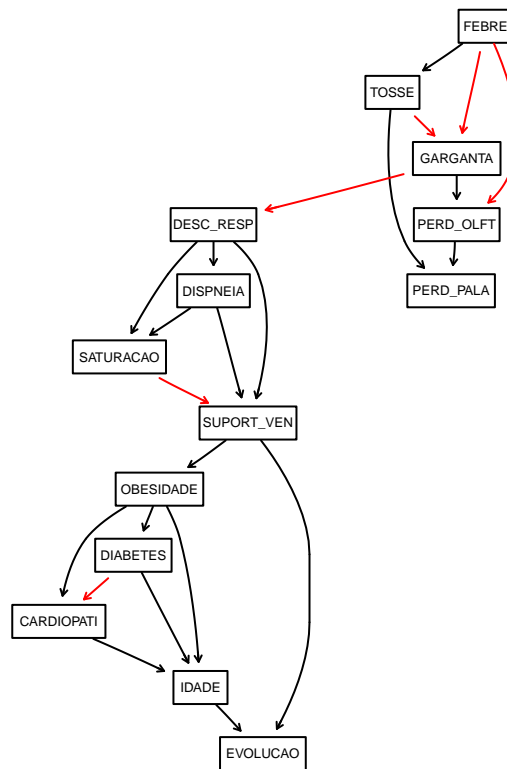
```r
par(mfrow = c(1, 2))
graphviz.compare(avg.diff, bn1, shape = "rectangle", main = c("DAG médio", "DAG único"))
```

DAG médio
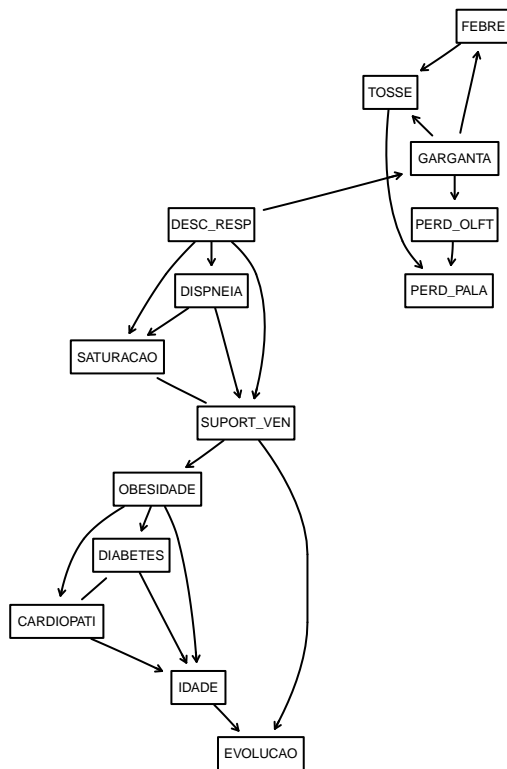
DAG único

It is also a good idea to look at the threshold with respect to the distribution of the arc strengths: the averaged network is fairly dense (17 arcs for 9 nodes) and it is difficult to read.

```
plot(str.diff)
abline(v = 0.75, col = "tomato", lty = 2, lwd = 2)
abline(v = 0.85, col = "steelblue", lty = 2, lwd = 2)
```

threshold = 0.88