

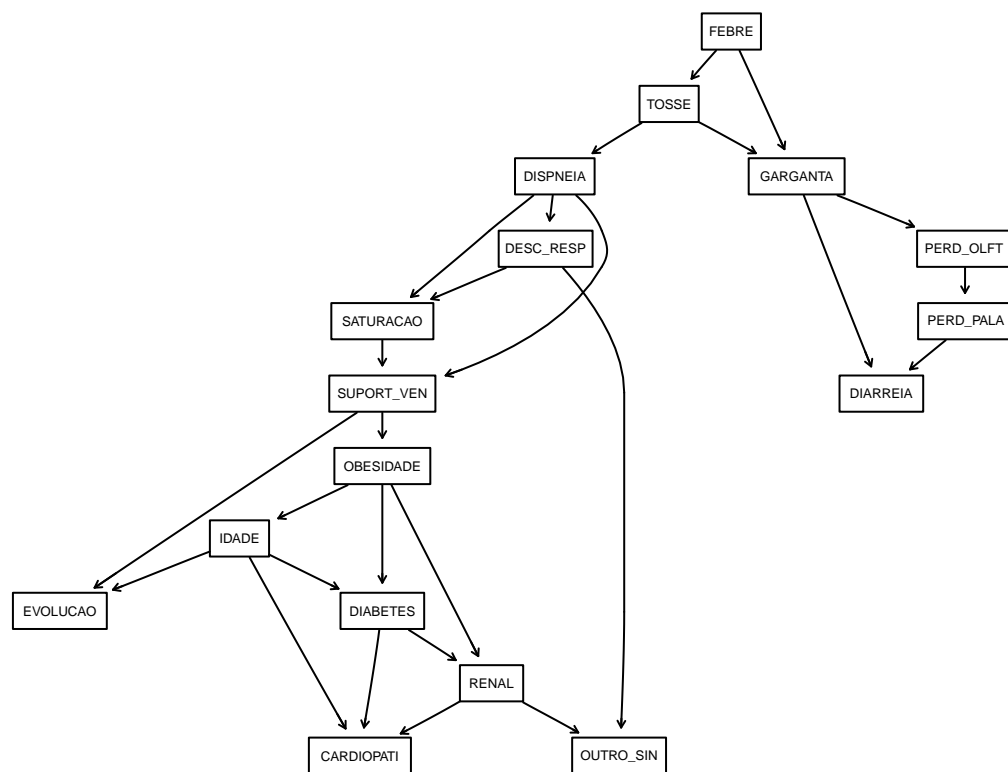
# Teste Melhor Impressão de Barcharts

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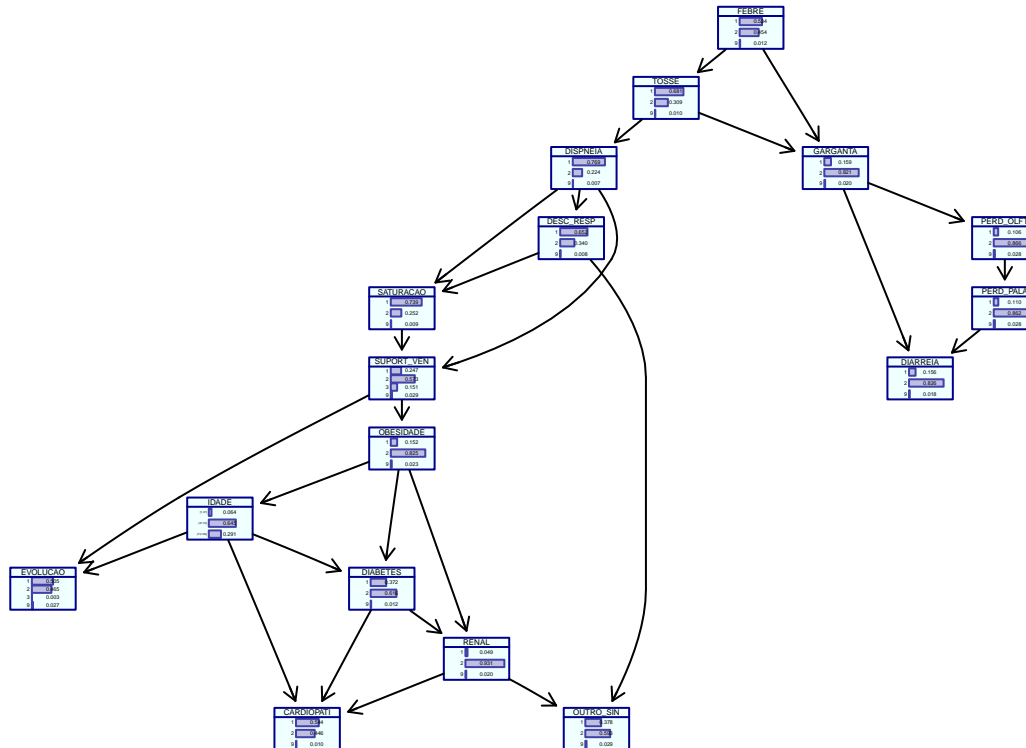
```
## Rows: 76,344
## Columns: 19
## $ IDADE      <fct> "(73,109]", "(37,73]", "(37,73]", "(73,109]", "(37,73]", "(~
## $ FEBRE      <fct> 2, 2, 2, 2, 1, 2, 1, 1, 1, 1, 2, 1, 2, 1, 2, 2, 1, 1, 2,~
## $ TOSSE      <fct> 1, 2, 2, 2, 2, 2, 2, 1, 2, 1, 1, 2, 1, 1, 2, 2, 1, 2, 2,~
## $ GARGANTA   <fct> 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 2, 1, 2, 2, 2, 1, 2, 2,~
## $ DISPNEIA   <fct> 1, 1, 2, 2, 1, 2, 2, 2, 2, 1, 1, 1, 1, 2, 1, 2, 1, 2, 1,~
## $ DESC_RESP  <fct> 1, 1, 2, 2, 2, 2, 2, 2, 1, 1, 1, 2, 1, 1, 2, 2, 1, 2, 1,~
## $ SATURACAO  <fct> 1, 1, 1, 2, 2, 2, 2, 2, 1, 2, 2, 1, 1, 1, 1, 2, 2, 2, 2,~
## $ DIARREIA   <fct> 2, 2, 1, 2, 2, 2, 2, 1, 2, 2, 2, 2, 1, 1, 2, 2, 1, 1, 2,~
## $ OUTRO_SIN  <fct> 2, 2, 1, 1, 2, 1, 2, 1, 2, 2, 2, 1, 2, 1, 1, 1, 2, 1, 2,~
## $ EVOLUCAO   <fct> 1, 2, 1, 1, 1, 2, 1, 2, 2, 1, 2, 1, 2, 2, 2, 1, 1, 1, 2,~
## $ RENAL      <fct> 2, 2, 2, 2, 1, 2, 1, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2,~
## $ DIABETES   <fct> 1, 2, 1, 2, 1, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 2, 2,~
## $ OBESIDADE  <fct> 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 2, 2, 2, 1, 2, 2,~
## $ PERD_OLFT  <fct> 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 2, 2,~
## $ PERD_PALA  <fct> 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,~
## $ CARDIOPATI <fct> 2, 2, 2, 2, 1, 1, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 2, 2, 1,~
## $ SUPORT_VEN <fct> 2, 2, 2, 2, 9, 3, 3, 2, 2, 3, 2, 2, 3, 1, 1, 3, 3, 2, 1,~
## $ HEMATOLOGI <fct> 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,~
## $ ASMA       <fct> 2, 2, 2, 2, 2, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,~

##      from      to
## [1,] "OBESIDADE" "DIABETES"
## [2,] "IDADE"     "DIABETES"
## [3,] "IDADE"     "CARDIOPATI"
## [4,] "DIABETES"  "RENAL"
## [5,] "DIABETES"  "CARDIOPATI"
## [6,] "RENAL"     "CARDIOPATI"
```



## Warning in from.bn.fit.to.grain(x): NaN conditional probabilities in CARDIOPATI,  
## replaced with a uniform distribution.

## Rede de probabilidades



## Bootstraping

```

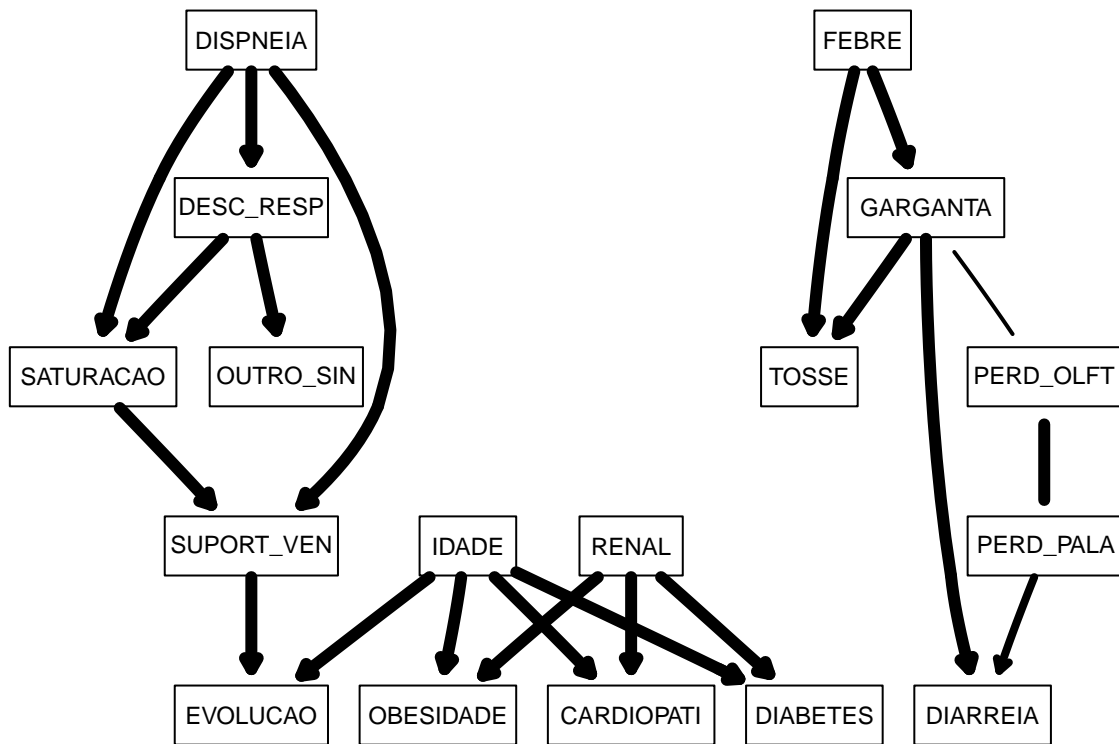
boots.trap <- 50
str.diff = suppressMessages(boot.strength(s1, R = boots.trap, algorithm = "mmhc"))
cat(paste('Threshold: ', attr(str.diff, "threshold")))

## Threshold: 0.6

avg.diff = averaged.network(str.diff)
strength.plot(avg.diff, str.diff, shape = "rectangle", main = paste("Iterações = ", boots.trap))

```

Iterações = 50



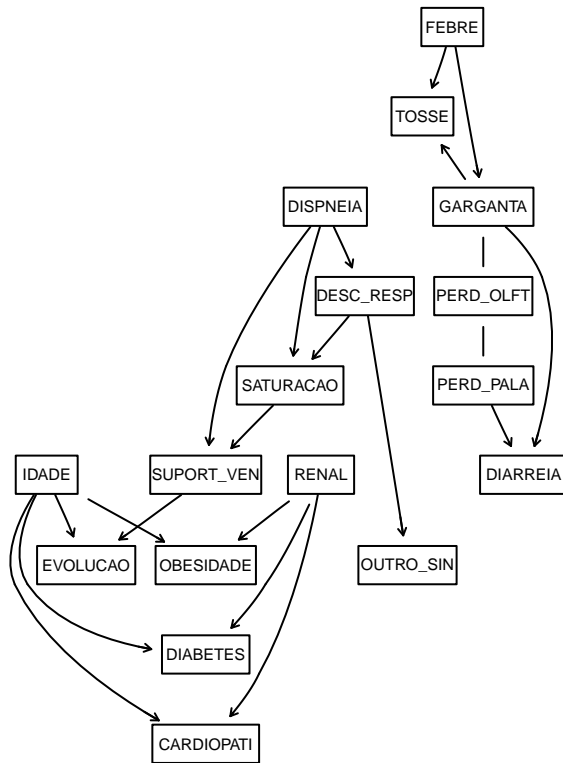
How can we compare the averaged network (avg.diff) with the network we originally learned in from all the data? The most qualitative way is to plot the two networks side by side, with the nodes in the same positions, and highlight the arcs that appear in one network and not in the other, or that appear with different directions.

```

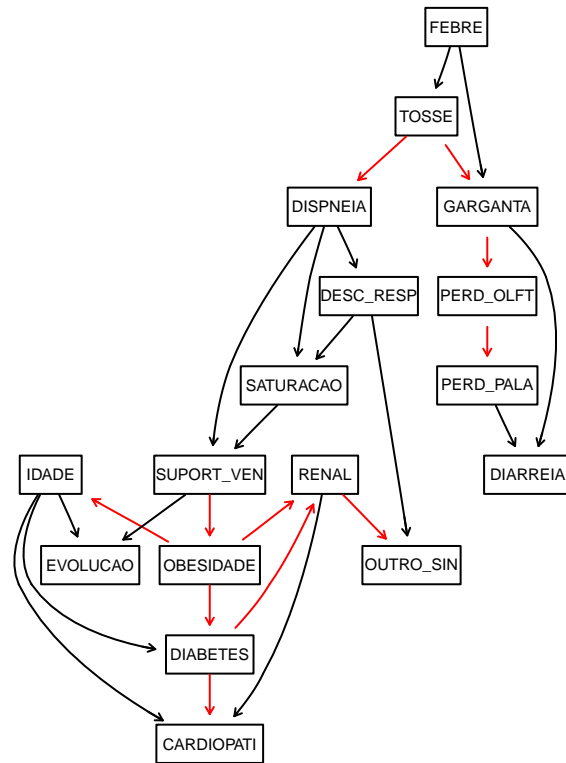
par(mfrow = c(1, 2))
graphviz.compare(avg.diff, bn1, shape = "rectangle", main = c("DAG médio", "DAG único"))

```

DAG médio



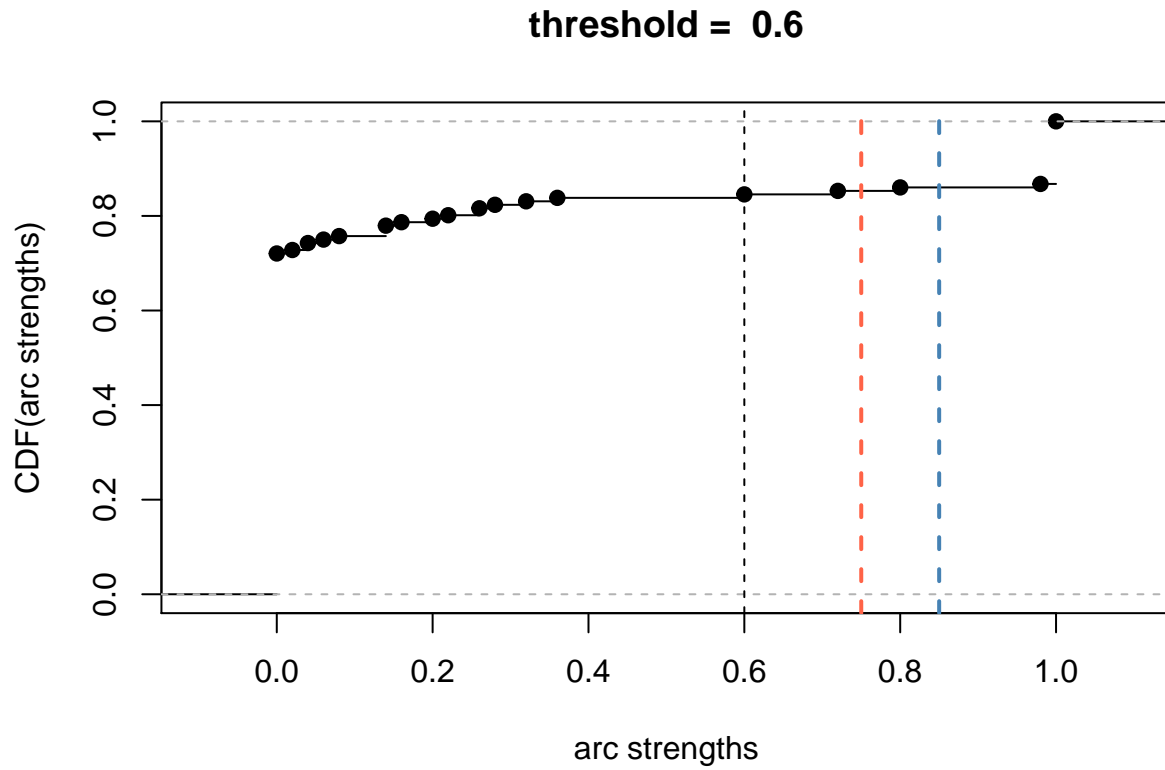
DAG único



It is also a good idea to look at the threshold with respect to the distribution of the arc strengths

```

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



The simpler network we obtain by setting `threshold = 0.8` in `averaged.network()` is shown below; it is certainly easier to reason with from a qualitative point of view.

```
par(mfrow = c(1, 2))
avg.simpler = averaged.network(str.diff, threshold = 0.8)
strength.plot(avg.diff, str.diff, shape = "rectangle", main = "Iterações = 200. Completo. Thr = ")
strength.plot(avg.simpler, str.diff, shape = "rectangle", main = "Iterações = 200. Simplificado. Thr = ")
```

Iterações = 200. Completo. Thr = Iterações = 200. Simplificado. Thr = 0.7

