

Validação - Somente COVID-19

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Variáveis selecionadas

```
## Rows: 76,666
## Columns: 9
## $ EVOLUCAO    <fct> 2, 1, 1, 1, 2, 1, 2, 2, 1, 2, 1, 2, 2, 2, 1, 1, 1, 1, 1, 1,~
## $ RENAL       <fct> 2, 2, 2, 1, 2, 1, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,~
## $ DIABETES    <fct> 2, 1, 2, 1, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 2, 2, 2, 2,~
## $ OBESIDADE   <fct> 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 2, 2, 2, 1, 2, 2, 9, 2,~
## $ PNEUMOPATI <fct> 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,~
## $ UTI         <fct> 1, 1, 2, 1, 2, 2, 1, 2, 2, 2, 2, 2, 1, 1, 2, 2, 1, 2, 2, 2,~
## $ CARDIOPATI <fct> 2, 2, 2, 1, 1, 2, 2, 1, 1, 1, 1, 1, 1, 1, 2, 2, 1, 1, 1, 1,~
## $ SUPORT_VEN <fct> 2, 2, 2, 9, 3, 3, 2, 2, 3, 2, 2, 3, 1, 1, 3, 3, 2, 3, 9, 3,~
## $ ANTIVIRAL  <fct> 2, 2, 2, 9, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2,~
```

Imposição de estrutura com arcos que fazem sentido clínico (*White list*)

```
s1 <- sample_frac(ddf, .9, FALSE)
cat(nrow(ddf) - nrow(s1))

## 7667

wl = matrix(c("OBESIDADE", "DIABETES",
              #"IDADE", "DIABETES",
              #"IDADE", "SUPORT_VEN",
              #"IDADE", "NEUROLOGIC",
              "DIABETES", "RENAL",
              "DIABETES", "CARDIOPATI",
              "UTI", "EVOLUCAO"),
            ncol = 2, byrow = TRUE, dimnames = list(NULL, c("from", "to")))

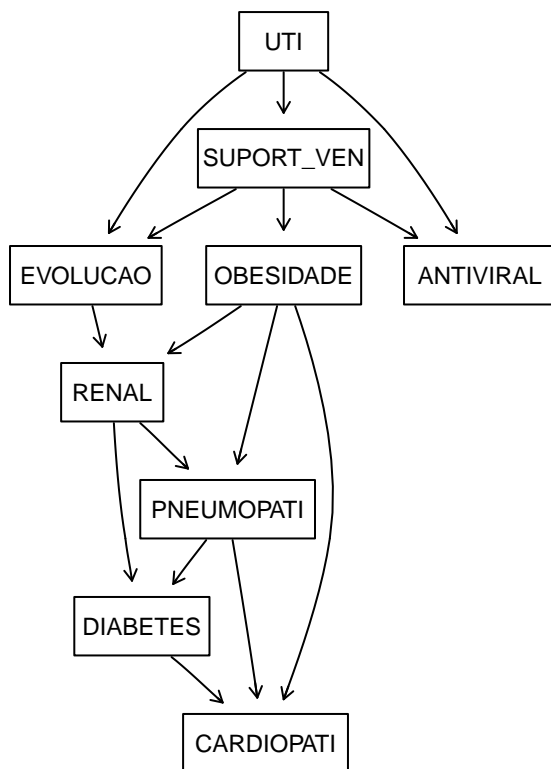
bn1 <- mmhc(s1, whitelist = wl)

#sem WL
bn2 <- mmhc(s1, whitelist = NULL)
```

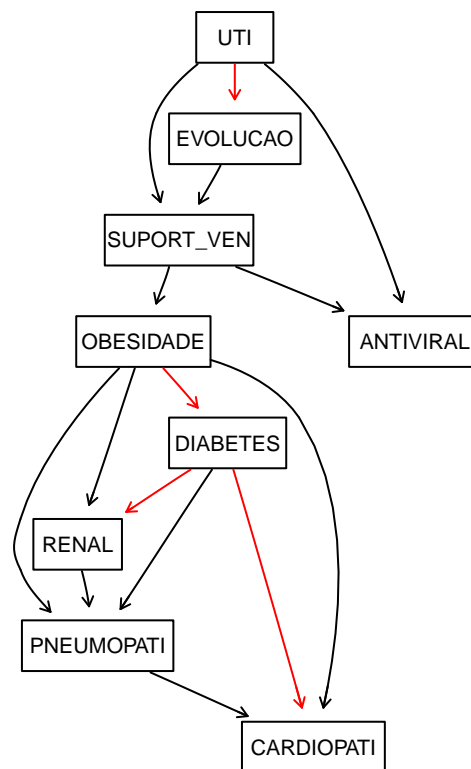
DAG (*Directed Acyclic Graph*) usando ou não *whitelisting* no algoritmo de aprendizado da estrutura da rede causal

```
par(mfrow = c(1, 2))
graphviz.plot(bn2,
              shape='rectangle',
              highlight = NULL,
              main = 'DAG sem WL')
graphviz.plot(bn1,
              shape='rectangle',
              highlight = list(arcs = wl),
              main = 'DAG com imposição de uma WL')
```

DAG sem WL



DAG com imposição de uma WL



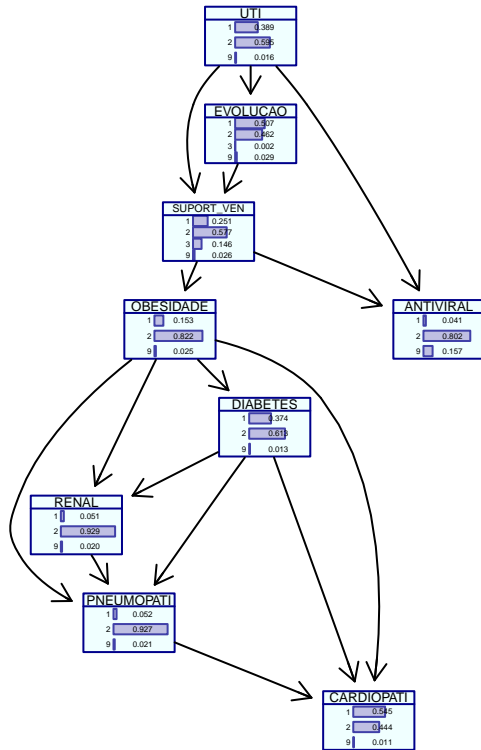
```
fitted.1 <- bn.fit(bn1, s1)
fitted.2 <- bn.fit(bn2, s1)
```

```
par(mfrow=c(1,2))
graphviz.chart(fitted.1,
               type = "barprob",
               col = "darkblue",
               bg = "azure",
               bar.col = "darkblue",
               main = "DAG sem WL")
```

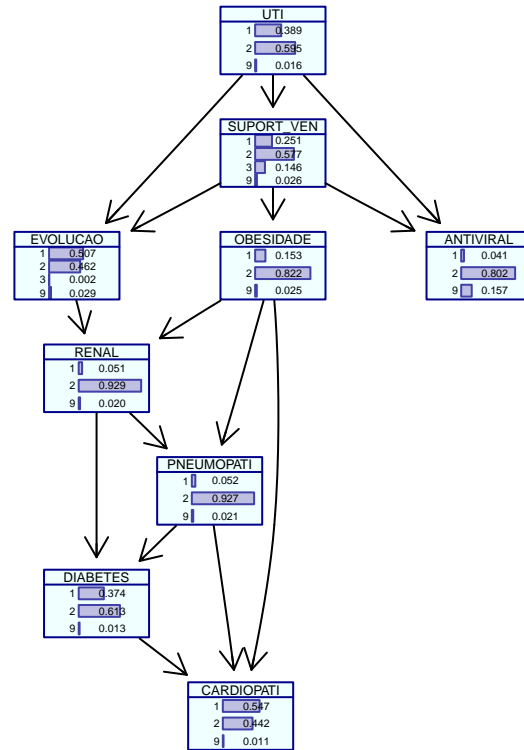
```
graphviz.chart(fitted.2,
               type = "barprob",
```

```
col = "darkblue",
bg = "azure",
bar.col = "darkblue",
main = "DAG com WL")
```

DAG sem WL



DAG com WL



Fase de Bootstrap

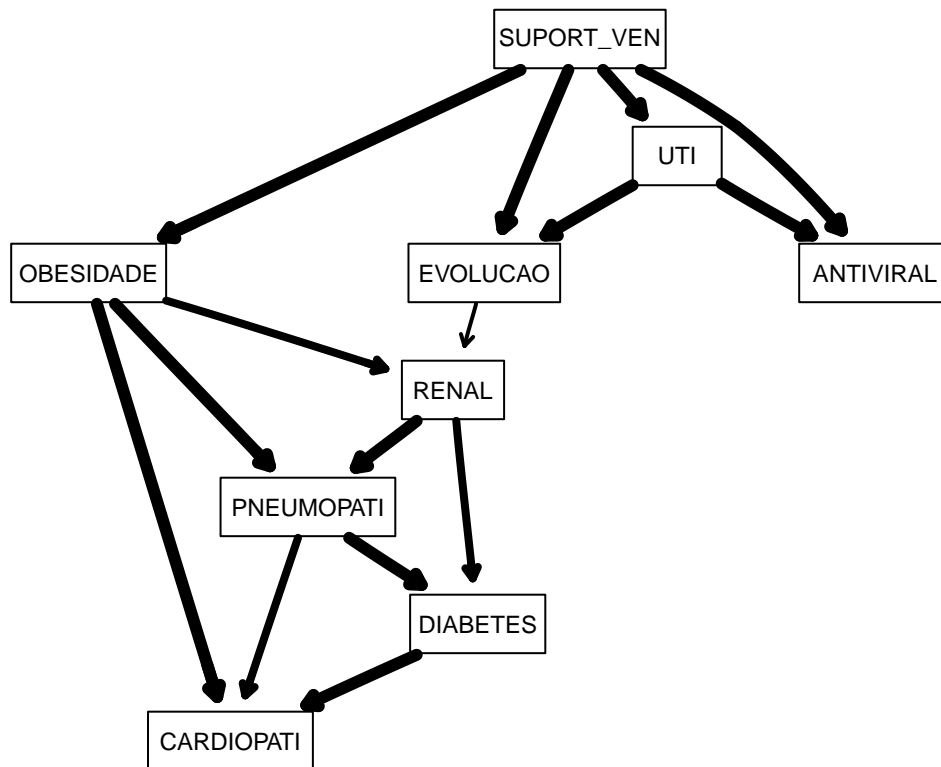
```
boots.trap <- 300

str.diff = boot.strength(s1,
                        R = boots.trap,
                        algorithm = "mmhc")

avg.diff = averaged.network(str.diff)
thr <- paste('Thr: ', attr(str.diff, "threshold"))

strength.plot(avg.diff,
             str.diff,
             shape = "rectangle",
             main = paste("Iter = ", boots.trap, thr))
```

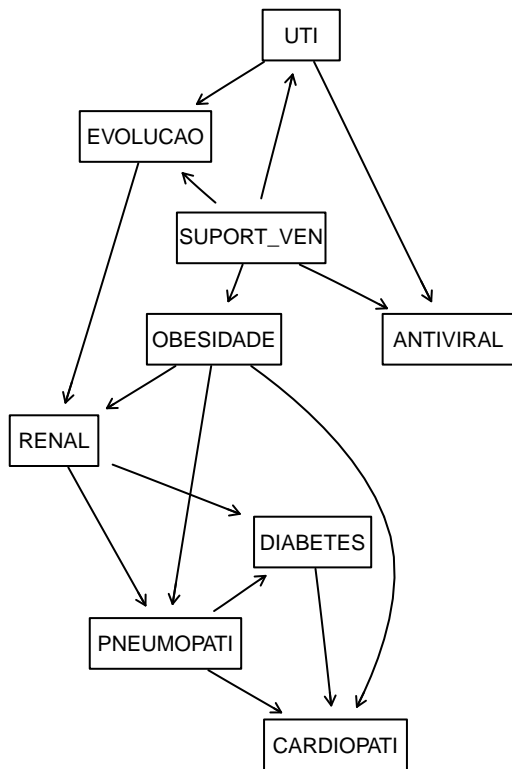
Iter = 300 Thr: 0.5066666666666667



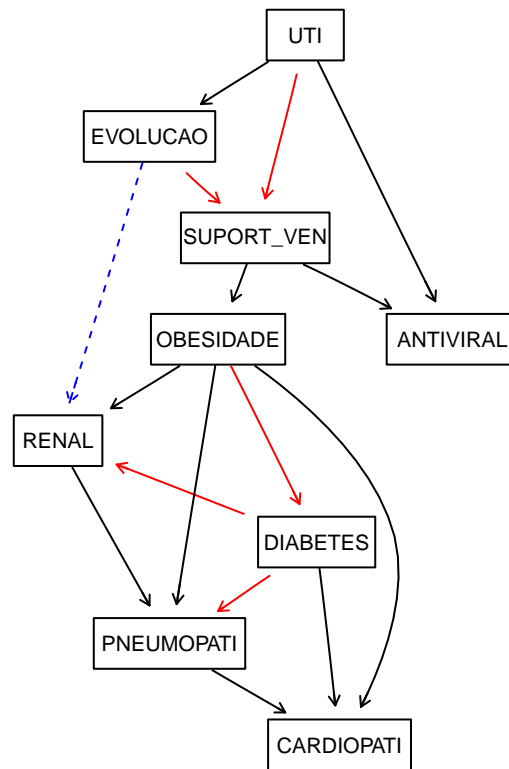
How can we compare the averaged network (avg.diff) with the network we originally learned in from all the data? The most qualitative way is to plot the two networks side by side, with the nodes in the same positions, and highlight the arcs that appear in one network and not in the other, or that appear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

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

DAG médio sem WL



DAG médio com WL

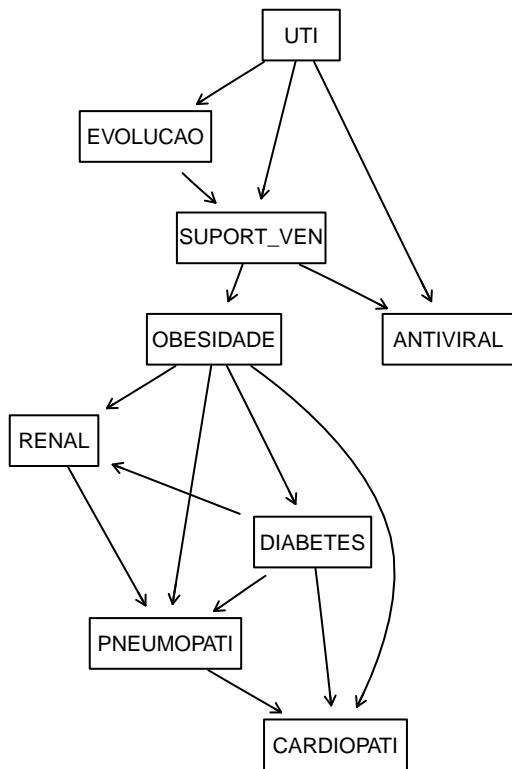


```

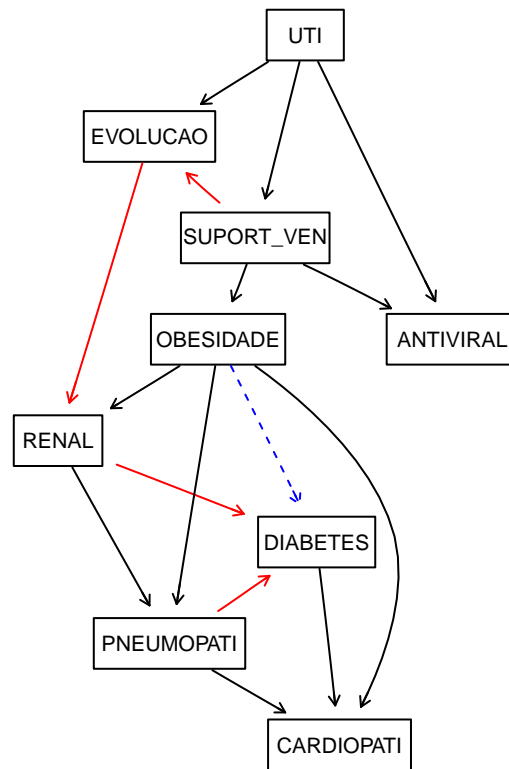
par(mfrow = c(1, 2))
graphviz.compare(bn1,
                 bn2,
                 shape = "rectangle",
                 main = c("DAG único sem WL", "DAG único com WL"))

```

DAG único sem WL



DAG único com WL



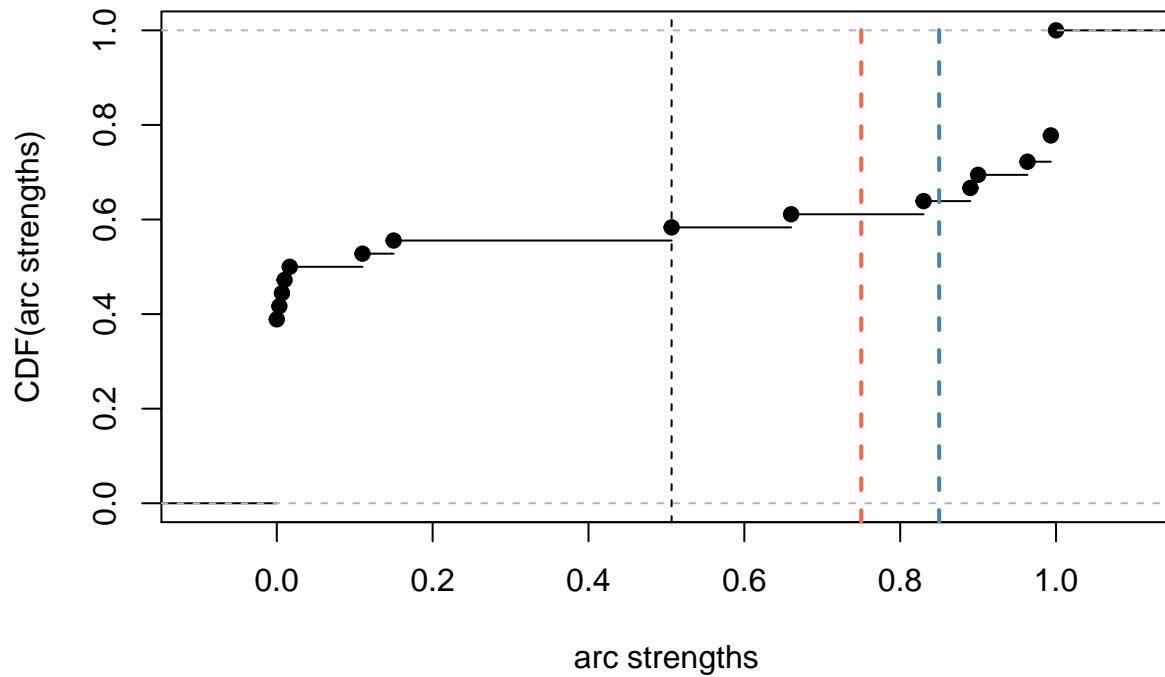
It is also a good idea to look at the threshold with respect to the distribution of the arc strengths

```

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

```

threshold = 0.507



The simpler network we obtain by setting **threshold = 0.95** in `averaged.network()` is shown below; it is certainly easier to reason with from a qualitative point of view. Na figura abaixo R é o número de iterações usadas na fase de *bootstrapping*

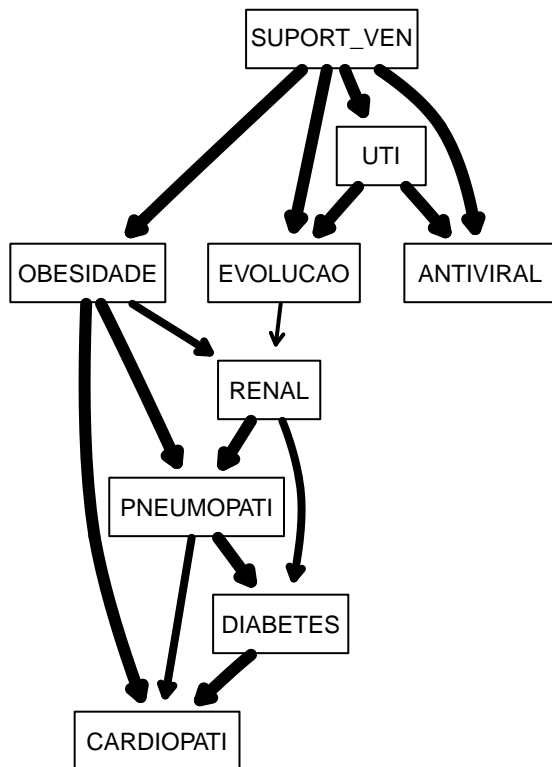
```
avg.simpler = averaged.network(str.diff, threshold = 0.95)

par(mfrow = c(1, 2))

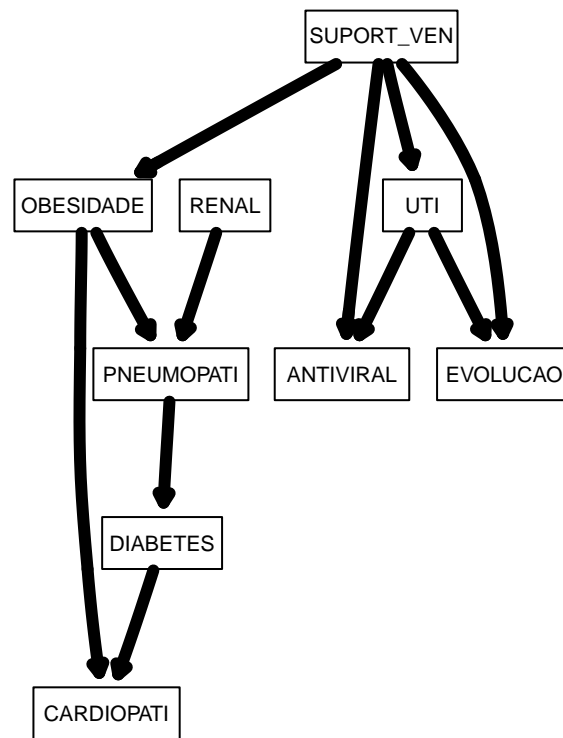
strength.plot(avg.diff,
  highlight = list((mb(avg.diff, 'EVOLUCAO'))),
  str.diff,
  shape = "rectangle",
  main = paste("R = ",
    boots.trap,
    " Thr = ",
    attr(str.diff, "threshold")))

strength.plot(avg.simpler,
  highlight = list((mb(avg.simpler, 'EVOLUCAO'))),
  str.diff,
  shape = "rectangle",
  main = paste("R = ",
    boots.trap,
    " Thr = ",
    attr(avg.simpler, "threshold")))
```

R = 300 Thr = 0.5066666666666667



R = 300 Thr =



#0.95))

Markov Blanket da variável EVOLUCAO

```
cat (mb(x = avg.diff, node = 'EVOLUCAO'))
```

```
## RENAL OBESIDADE UTI SUPOORT_VEN
```

```
##
```

```
cat (mb(x = avg.simpler, node = 'EVOLUCAO'))
```

```
## UTI SUPOORT_VEN
```

```
#par(mfrow = c(1, 2))
```

```
#save the current workspace
```

```
save(list = ls(all.names = TRUE),
      file = "kk_09_sem_neuro_sem_idade_90pc_300it.RData",
      envir = .GlobalEnv)
```