

Análise Bayesiana para Inferência Causal na COVID-19

José Elvano Moraes

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Dataset = <https://dados.gov.br/dataset/bd-srag-2019>

SRAG 2019 - Banco de Dados de Síndrome Respiratória Aguda Grave Vigilância de Síndrome Respiratória Aguda Grave (SRAG) O Ministério da Saúde, por meio da Secretaria de Vigilância em Saúde (SVS), desenvolve a vigilância da Síndrome Respiratória Aguda Grave (SRAG) no Brasil, desde 2009, devido a pandemia de Influenza A(H1N1)pdm09. A partir disso, a vigilância de SRAG foi implantada na rede de vigilância de Influenza e outros vírus respiratórios, que anteriormente atuava apenas com a vigilância sentinela de Síndrome Gripal (SG).

Recentemente (2020), a vigilância da COVID-19, a infecção humana causada pelo novo Coronavírus, que vem causando uma pandemia, foi incorporada na rede de vigilância da Influenza e outros vírus respiratórios.

Esta página tem como finalidade disponibilizar o legado dos banco de dados (BD) epidemiológicos de SRAG, da rede de vigilância da Influenza e outros vírus respiratórios, desde o início da sua implantação (2009) até os dias atuais (2020), com a incorporação da vigilância da COVID-19.

Para mais informações, acessar:

Gripe/Influenza - <https://saude.gov.br/saude-de-a-z/gripe>

COVID-19 - <https://coronavirus.saude.gov.br/>

```
suppressPackageStartupMessages(expr = library(tidyverse))
suppressPackageStartupMessages(expr = library(bnlearn))
suppressPackageStartupMessages(expr = library(bnstruct))
suppressPackageStartupMessages(expr = library(readr))
suppressPackageStartupMessages(expr = library(Rgraphviz))
suppressPackageStartupMessages(expr = library(Rmpfr))
```

```
dados <- read_csv("x_to_be_factors.csv",
  col_types = cols(
    FEBRE = col_factor(levels = c("1", "2", "9")),
    TOSSE = col_factor(levels = c("1", "2", "9")),
    GARGANTA = col_factor(levels = c("1", "2", "9")),
    DISPNEIA = col_factor(levels = c("1", "2", "9")),
    DESC_RESP = col_factor(levels = c("1", "2", "9")),
    SATURACAO = col_factor(levels = c("1", "2", "9")),
    DIARREIA = col_factor(levels = c("1", "2", "9")),
    VOMITO = col_factor(levels = c("1", "2", "9")),
    OUTRO_SIN = col_factor(levels = c("1", "2", "9")),
    HOSPITAL = col_factor(levels = c("1", "2", "9")),
    EVOLUCAO = col_factor(levels = c("1", "2", "3", "9")),
```

```

    RENAL = col_factor(levels = c("1", "2", "9")),
    DIABETES = col_factor(levels = c("1", "2", "9")),
    OBESIDADE = col_factor(levels = c("1", "2", "9")),
    CLASSI_OUT = col_character(),
    PERD_OLFT = col_factor(levels = c("1", "2", "9")),
    PERD_PALA = col_factor(levels = c("1", "2", "9")),
    VACINA = col_factor(levels = c("1", "2", "9")),
    CLASSI_FIN = col_factor(levels = c("1", "2", "3", "4", "5"))))

## Warning: Missing column names filled in: 'X1' [1]

#View(dados)

```

Inferência da estrutura da Rede Causal usando o algoritmo mmhc

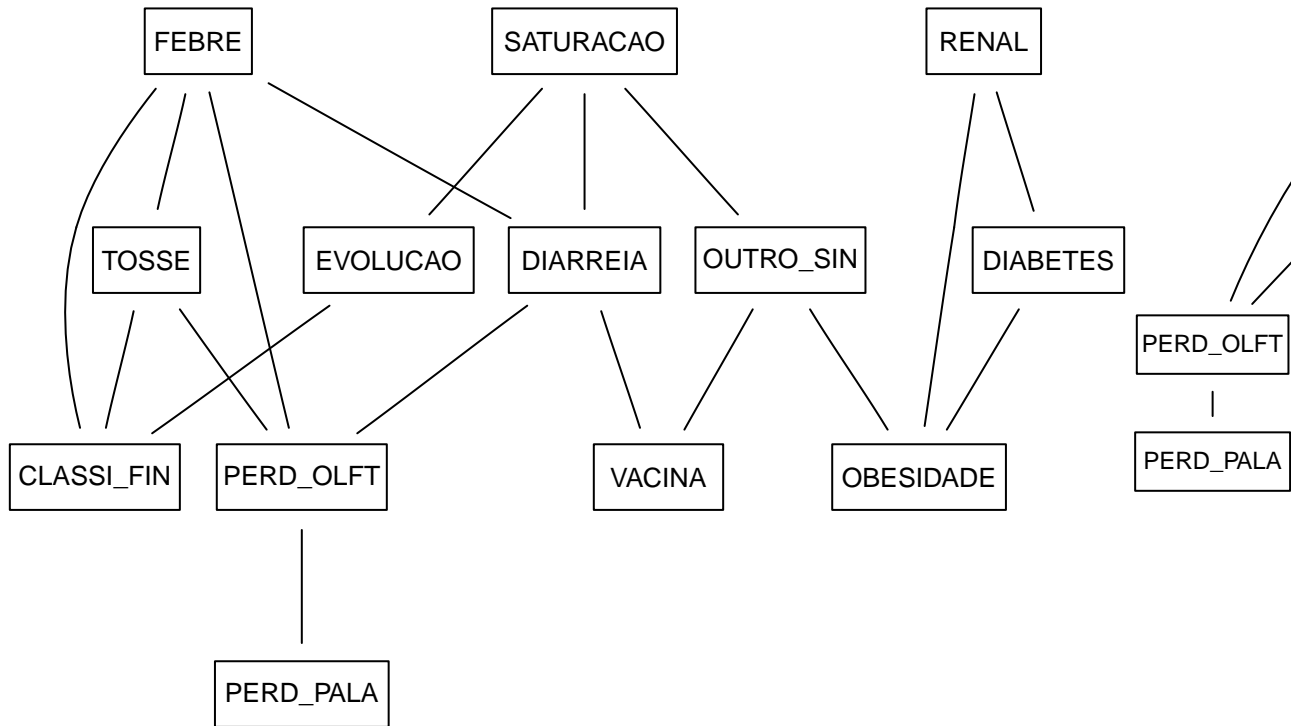
```

#reselecionar retira a variavel automatica X1
xx <- select(dados,
  FEBRE,
  TOSSE,
  #GARGANTA,
  #DISPNEIA,
  #DESC_RESP,
  SATURACAO,
  DIARREIA,
  #VOMITO,
  OUTRO_SIN,
  #HOSPITAL,
  EVOLUCAO,
  RENAL,
  DIABETES,
  OBESIDADE,
  #CLASSI_OUT,
  PERD_OLFT,
  PERD_PALA,
  VACINA,
  CLASSI_FIN)
# dado não pode ser `tibble` nas funções de *bnlearn*
x = as.data.frame(xx)

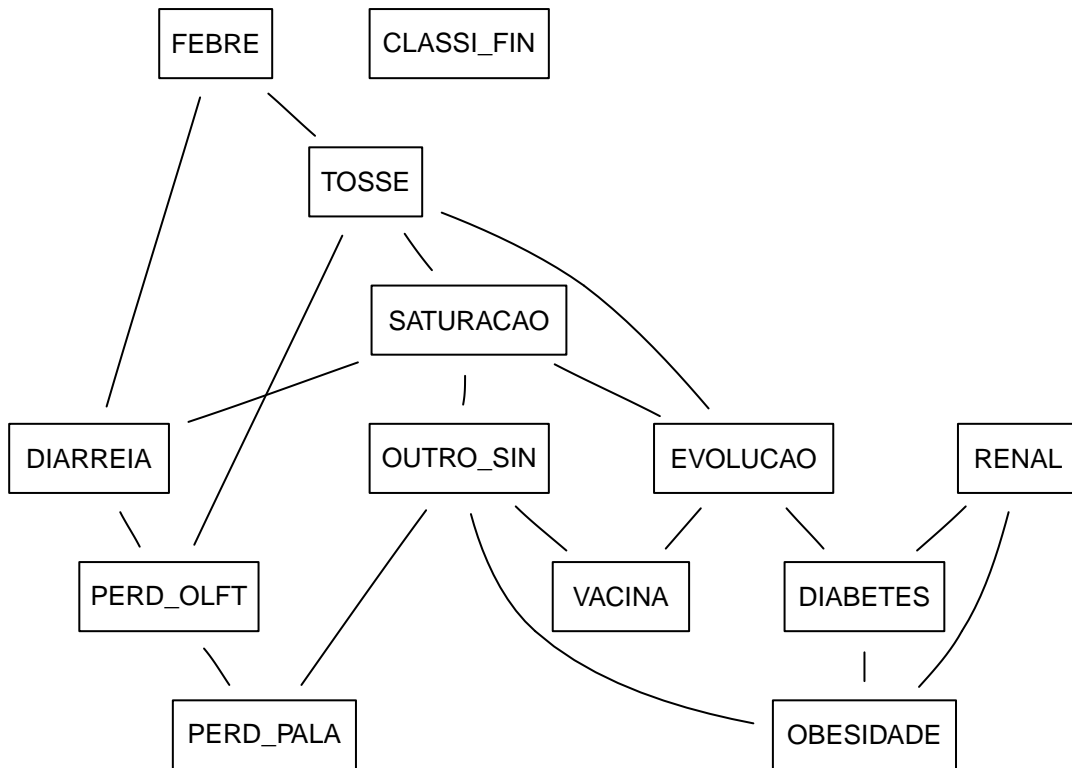
# mmhc e mmhc não admitem NA
x_no_na <- na.omit(x)

```

Algo = mmpc. DATA = full



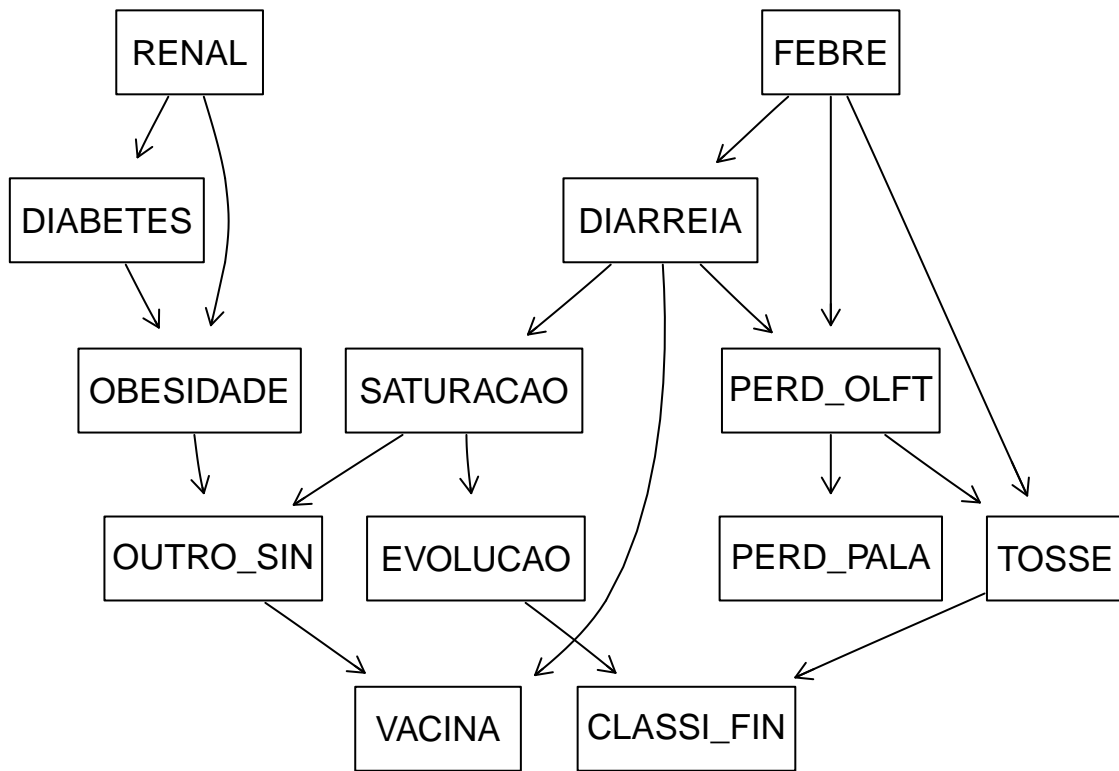
Algo = mmpc. DATA = Outras



Inferência da estrutura da Rede Causal usando o algoritmo mmhc

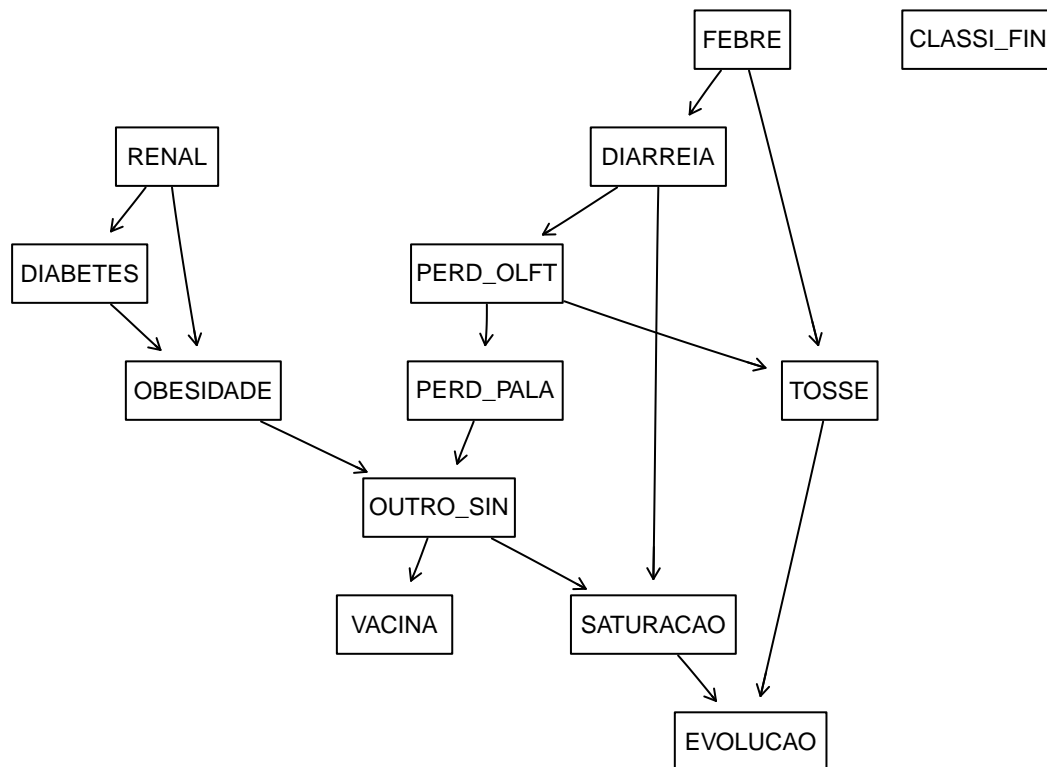
```
suppressWarnings(bn_mmhc <- mmhc(x_no_na))
suppressWarnings(bn_mmhc_outras <- mmhc(srag_outras))
suppressWarnings(bn_mmhc_covid <- mmhc(srag_covid))
graphviz.plot(bn_mmhc, shape = 'rectangle', main = "Data = full, ALGO = mmhc")
```

Data = full, ALGO = mmhc



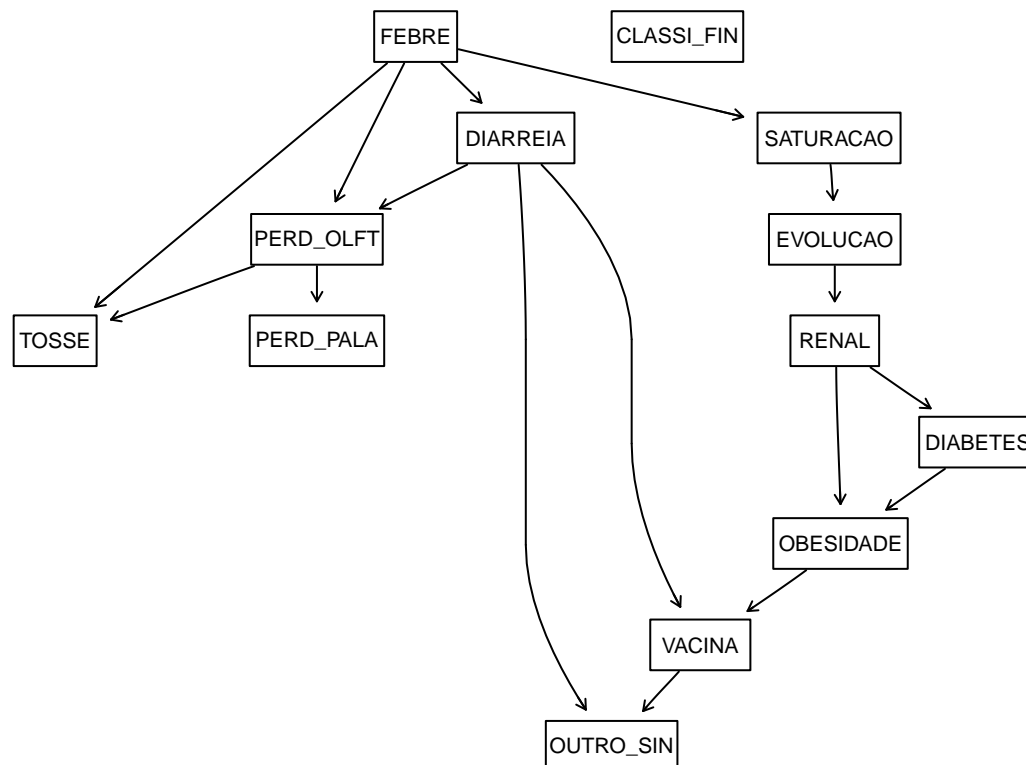
```
graphviz.plot(bn_mmhc_outras, shape = 'rectangle', main = "Data = outras, ALGO = mmhc")
```

Data = outras, ALGO = mmhc



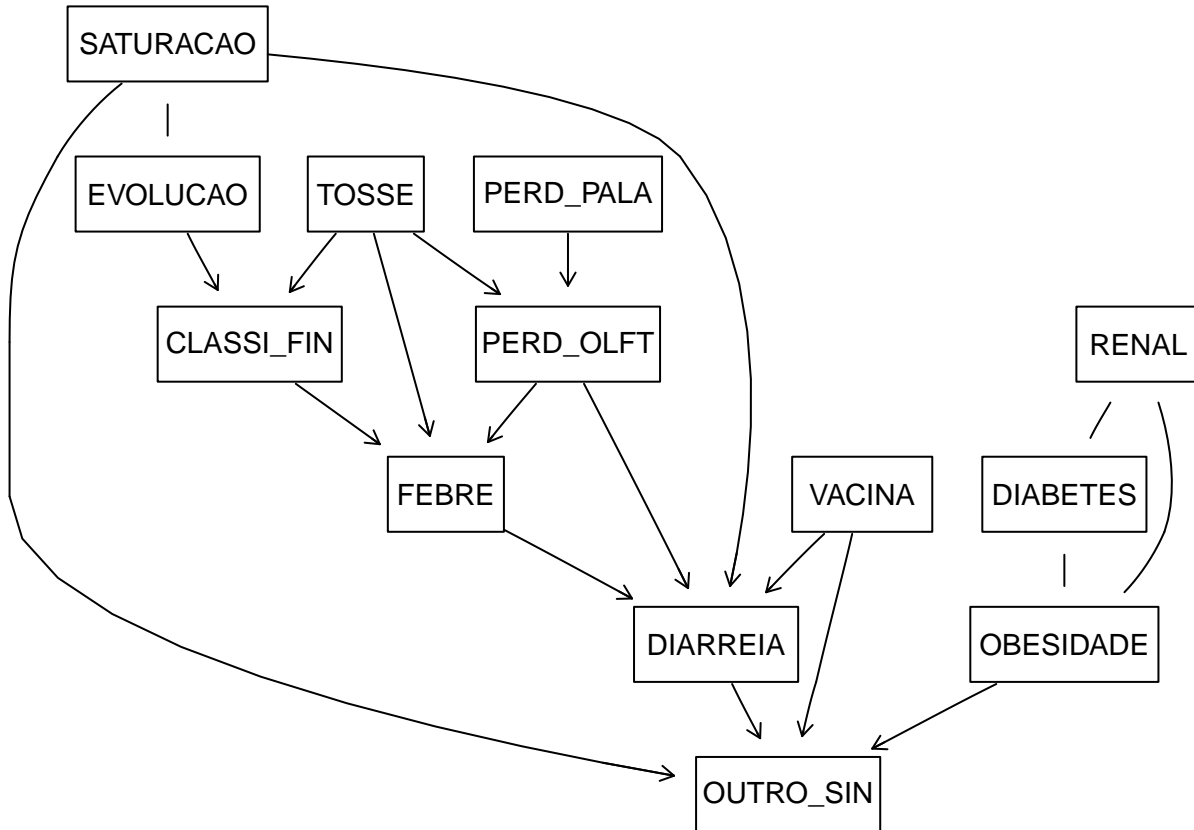
```
graphviz.plot(bn_mmhc_covid, shape = 'rectangle', main = "Data = COVID, ALGO = mmhc")
```

Data = COVID, ALGO = mmhc



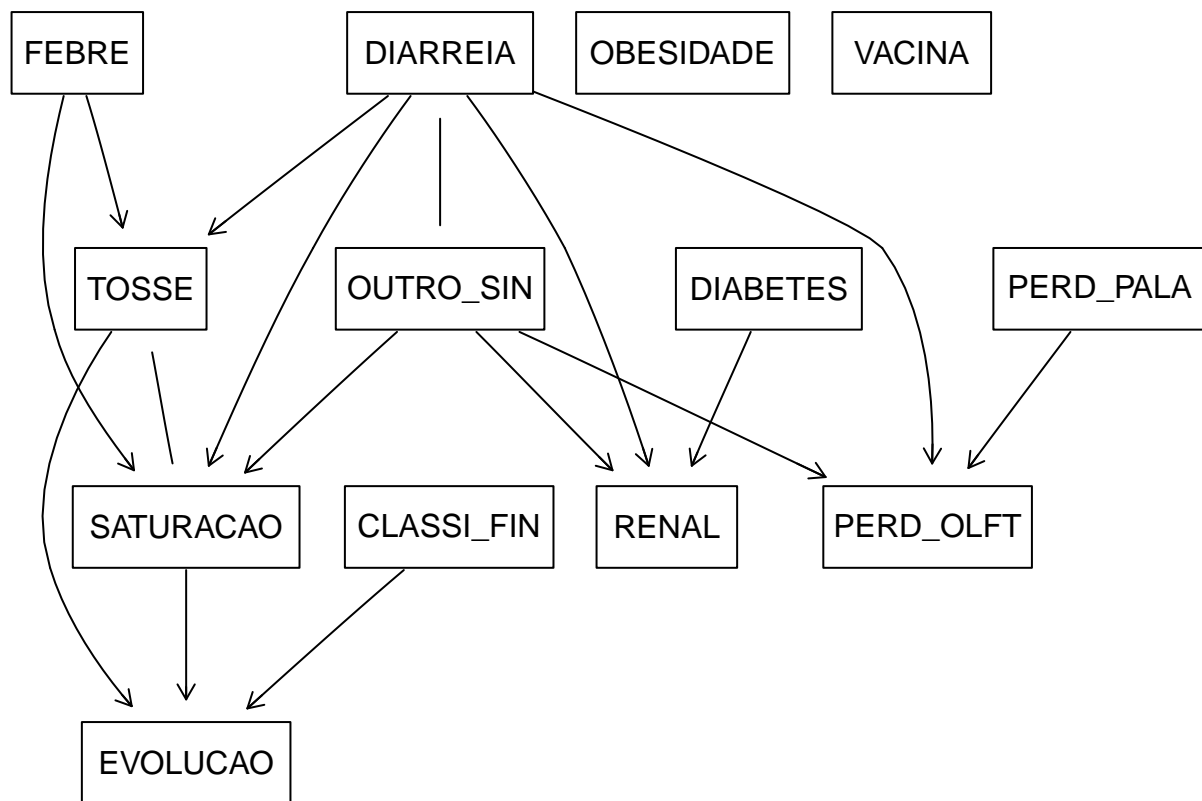
Inferência da estrutura da Rede Causal usando o algoritmo iamb

```
suppressWarnings(bn_iamb <- iamb(x_no_na))  
graphviz.plot(bn_iamb, shape = 'rectangle')
```



Inferência da estrutura da Rede Causal usando o algoritmo gs

```
suppressWarnings(bn_gs <- gs(x_no_na))  
graphviz.plot(bn_gs, shape = 'rectangle')
```



Inferência da estrutura da Rede Causal usando o algoritmo hc

```

#suppressWarnings(bn_hc <- hc(x_no_na))
#pvalues = arc.strength(bn_hc, data = t, criterion = "x2")
#graphviz.plot(bn_hc, shape = 'rectangle')

suppressWarnings(bn_hc <- hc(x_no_na))
suppressWarnings(bn_hc_outras <- hc(srag_outras))
suppressWarnings(bn_hc_covid <- hc(srag_covid))
graphviz.plot(bn_hc, shape = 'rectangle', main = "Algo = hc DATA = full")

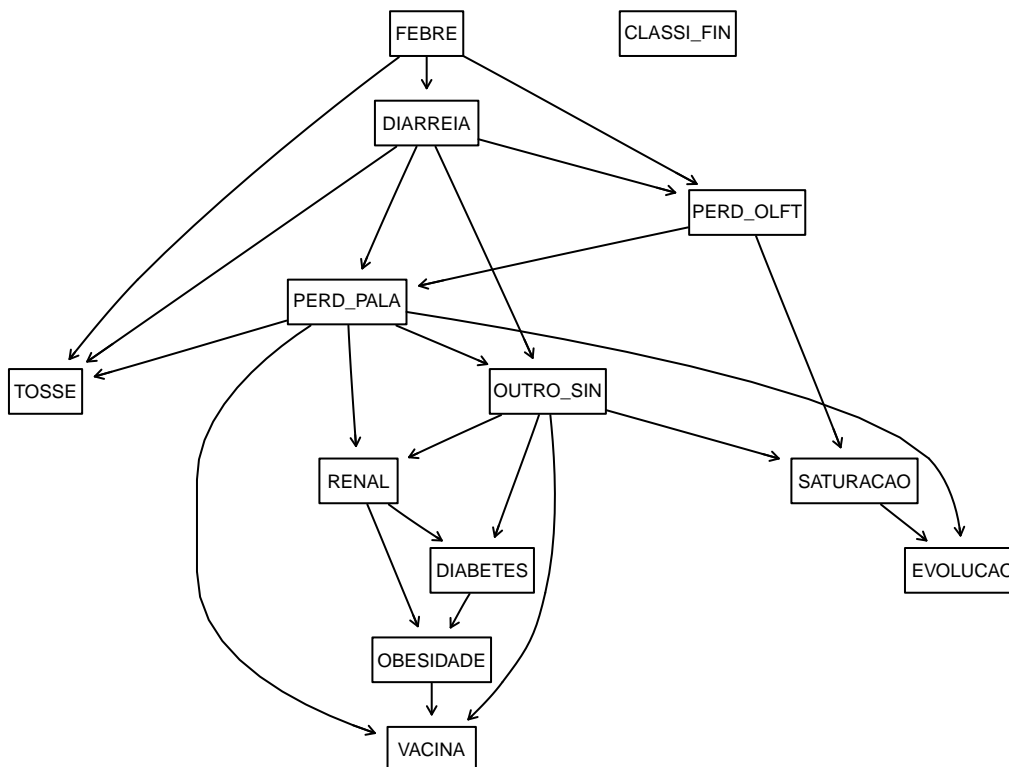
```

Algo = hc DATA = full



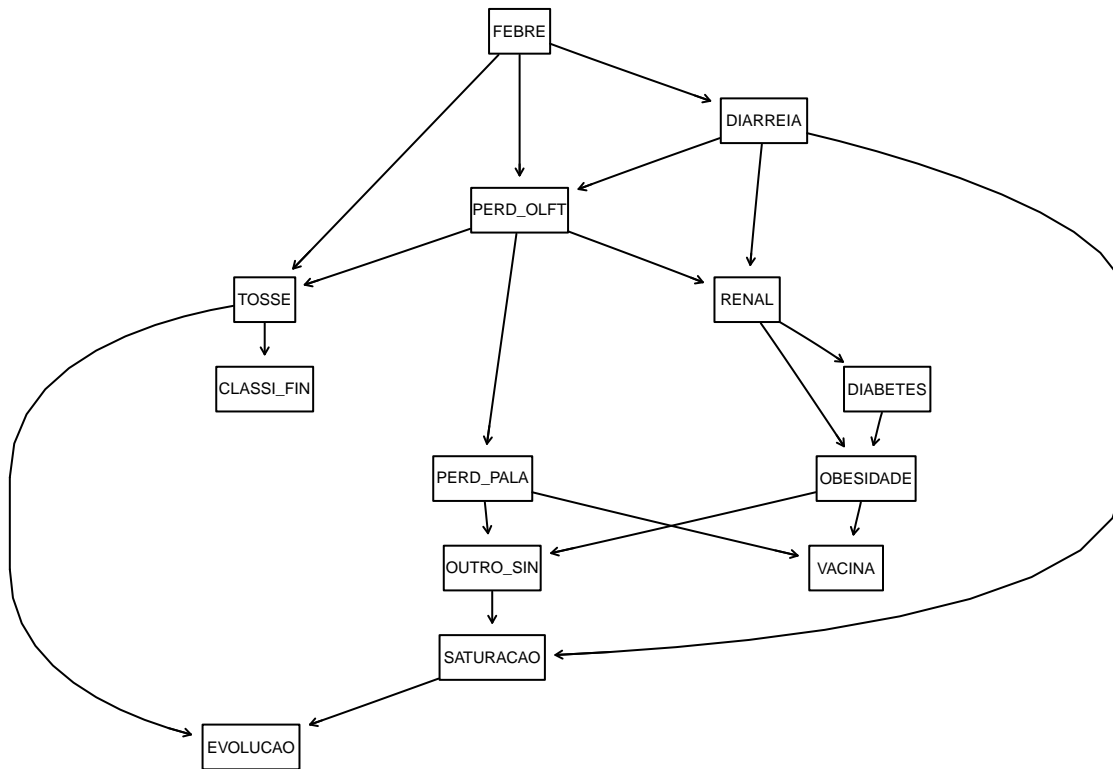
```
graphviz.plot(bn_hc_covid, shape = 'rectangle', main = "Algo = hc DATA = COVID")
```

Algo = hc DATA = COVID




```
graphviz.plot(bn_hc_outras, shape = 'rectangle', main = "Algo = hc DATA = OUTRAS")
```

Algo = hc DATA = OUTRAS



Ajustamento da estrutura do algoritmo *hc* com os dados

```
fitted_hc = bn.fit(bn_hc, x_no_na)
fitted_hc_outras = bn.fit(bn_hc_outras, srag_outras)
```

```
## Warning in check.data(data, allow.missing = TRUE): variable CLASSI_FIN has
## levels that are not observed in the data.
```

```
fitted_hc_covid = bn.fit(bn_hc_covid, srag_covid)
```

```
## Warning in check.data(data, allow.missing = TRUE): variable CLASSI_FIN has
## levels that are not observed in the data.
```

Descrição estatística da rede para a variável EVOLUCAO DATA = full

```
##
## Parameters of node EVOLUCAO (multinomial distribution)
##
## Conditional probability table:
##
## , , SATURACAO = 1
```

```

##
##          TOSSE
## EVOLUCAO      1          2          9
##      1 0.531606852 0.450254831 0.325301205
##      2 0.427839519 0.487152262 0.614457831
##      3 0.011597675 0.031269909 0.030120482
##      9 0.028955954 0.031322999 0.030120482
##
## , , SATURACAO = 2
##
##          TOSSE
## EVOLUCAO      1          2          9
##      1 0.669059068 0.642127024 0.533333333
##      2 0.292112251 0.288848053 0.333333333
##      3 0.010263403 0.030779832 0.066666667
##      9 0.028565277 0.038245090 0.066666667
##
## , , SATURACAO = 9
##
##          TOSSE
## EVOLUCAO      1          2          9
##      1 0.542579075 0.382716049 0.445086705
##      2 0.411192214 0.506172840 0.520231214
##      3 0.012165450 0.074074074 0.005780347
##      9 0.034063260 0.037037037 0.028901734

```

Descrição estatística da rede para a variável EVOLUCAO DATA = COVID

```

##
## Parameters of node EVOLUCAO (multinomial distribution)
##
## Conditional probability table:
##
## , , PERD_PALA = 1
##
##          SATURACAO
## EVOLUCAO      1          2          9
##      1 0.5916789396 0.7500000000 0.5208333333
##      2 0.3854933726 0.2236238532 0.4583333333
##      3 0.0009204713 0.0000000000 0.0000000000
##      9 0.0219072165 0.0263761468 0.0208333333
##
## , , PERD_PALA = 2
##
##          SATURACAO
## EVOLUCAO      1          2          9
##      1 0.4621413129 0.6092697386 0.4000000000
##      2 0.5050117925 0.3580571275 0.5636363636
##      3 0.0026778695 0.0027620587 0.0000000000
##      9 0.0301690252 0.0299110752 0.0363636364
##

```

```

## , , PERD_PALA = 9
##
##          SATURACAO
## EVOLUCAO      1      2      9
##      1 0.3566978193 0.6111111111 0.4199584200
##      2 0.6082554517 0.3777777778 0.5488565489
##      3 0.0023364486 0.0111111111 0.0000000000
##      9 0.0327102804 0.0000000000 0.0311850312

```

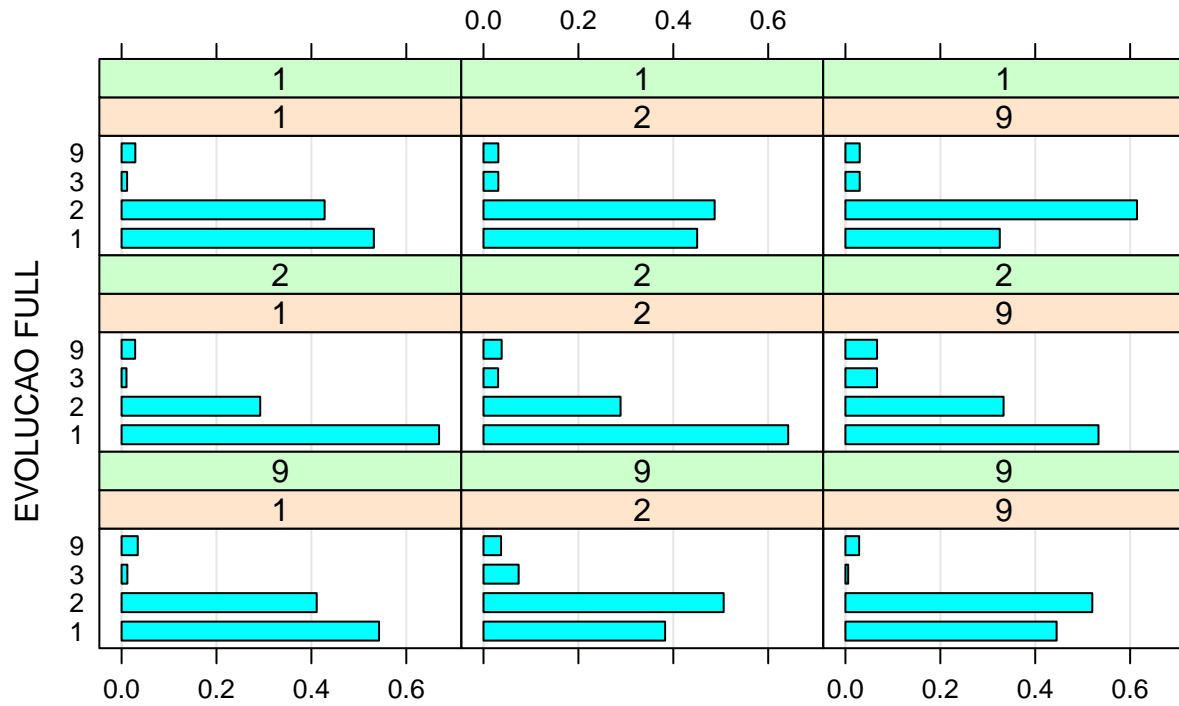
Descrição estatística da rede para a variável EVOLUCAO DATA = OUTRAS

```

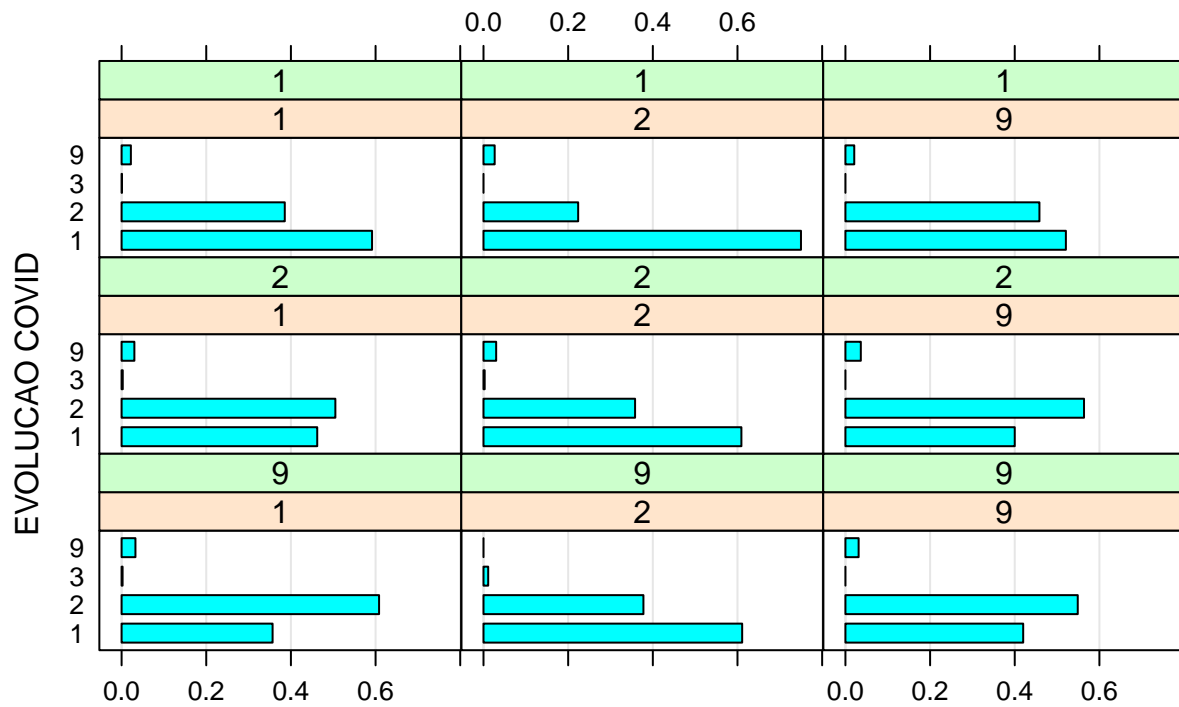
##
## Parameters of node EVOLUCAO (multinomial distribution)
##
## Conditional probability table:
##
## , , SATURACAO = 1
##
##          TOSSE
## EVOLUCAO      1      2      9
##      1 0.69520929 0.54742376 0.41666667
##      2 0.21088652 0.30851735 0.40740741
##      3 0.06302722 0.11188223 0.12962963
##      9 0.03087697 0.03217666 0.04629630
##
## , , SATURACAO = 2
##
##          TOSSE
## EVOLUCAO      1      2      9
##      1 0.78907535 0.72085890 0.25000000
##      2 0.12668641 0.15848671 0.25000000
##      3 0.04244817 0.08179959 0.25000000
##      9 0.04179006 0.03885481 0.25000000
##
## , , SATURACAO = 9
##
##          TOSSE
## EVOLUCAO      1      2      9
##      1 0.74468085 0.53846154 0.67088608
##      2 0.17021277 0.23076923 0.25316456
##      3 0.05319149 0.23076923 0.02531646
##      9 0.03191489 0.00000000 0.05063291

```

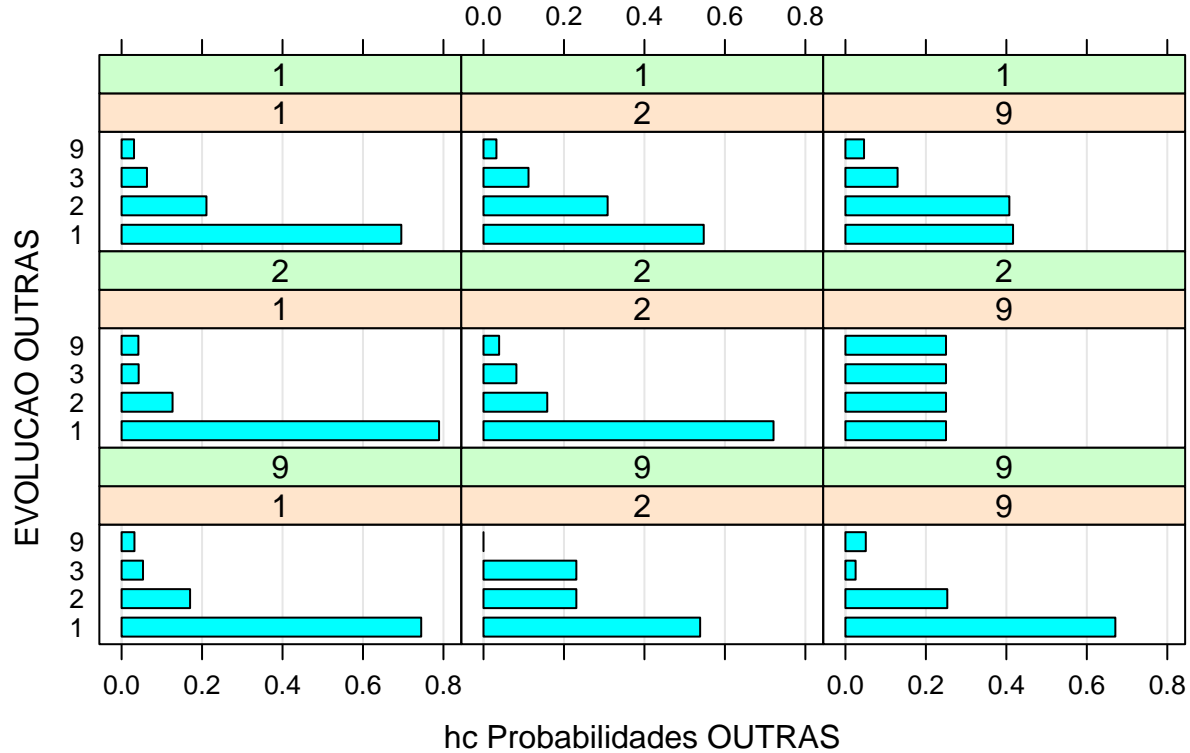
Conditional Probabilities for Node EVOLUCAO



Conditional Probabilities for Node EVOLUCAO



Conditional Probabilities for Node EVOLUCAO



Descrição estatística da rede para a variável EVOLUCAO ALGO = mmhc

```
## Warning in check.data(data, allow.missing = TRUE): variable CLASSI_FIN has
## levels that are not observed in the data.
```

```
## Warning in check.data(data, allow.missing = TRUE): variable CLASSI_FIN has
## levels that are not observed in the data.
```

```
##
## Parameters of node EVOLUCAO (multinomial distribution)
##
## Conditional probability table:
##
## SATURACAO
## EVOLUCAO      1      2      9
##      1 0.50368815 0.65861841 0.48687351
##      2 0.44850254 0.29088501 0.46539379
##      3 0.01808216 0.01818583 0.01551313
##      9 0.02972715 0.03231075 0.03221957
##
## Parameters of node EVOLUCAO (multinomial distribution)
##
```

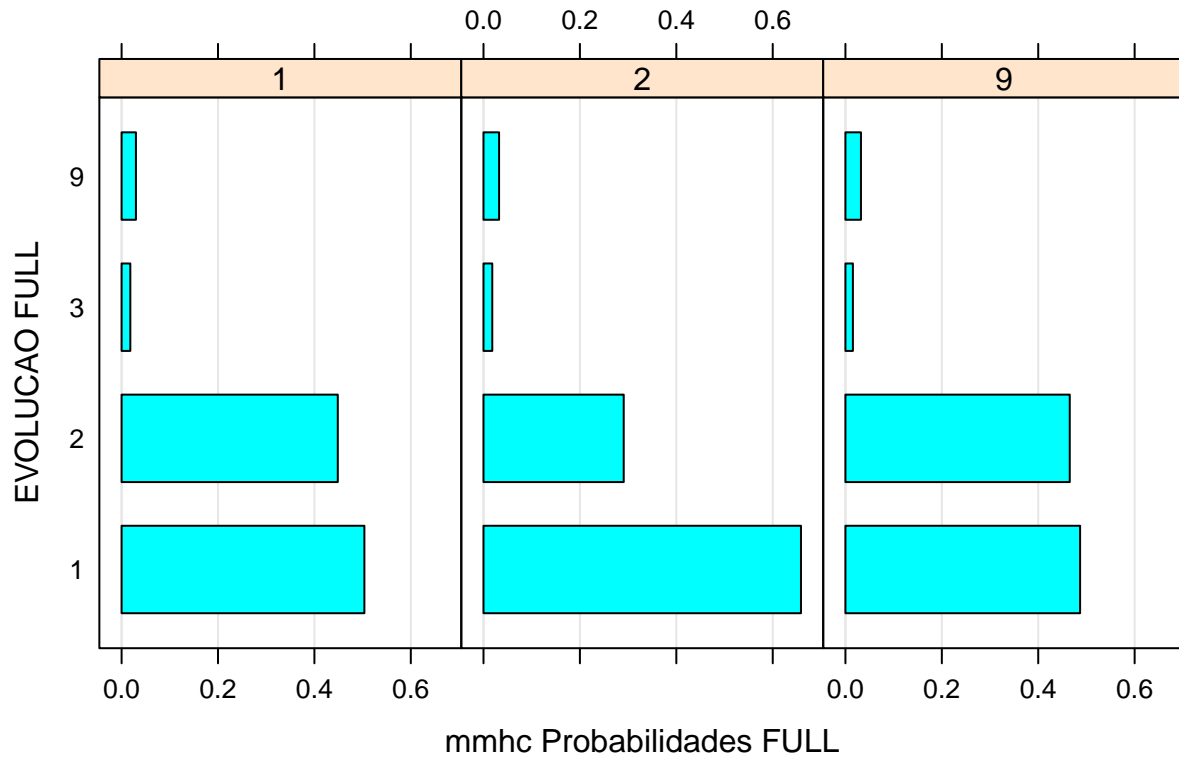
```

## Conditional probability table:
##
##          SATURACAO
## EVOLUCAO      1      2      9
##      1 0.474124842 0.623995683 0.424100156
##      2 0.494116407 0.344106008 0.544600939
##      3 0.002467313 0.002518288 0.000000000
##      9 0.029291438 0.029380022 0.031298905

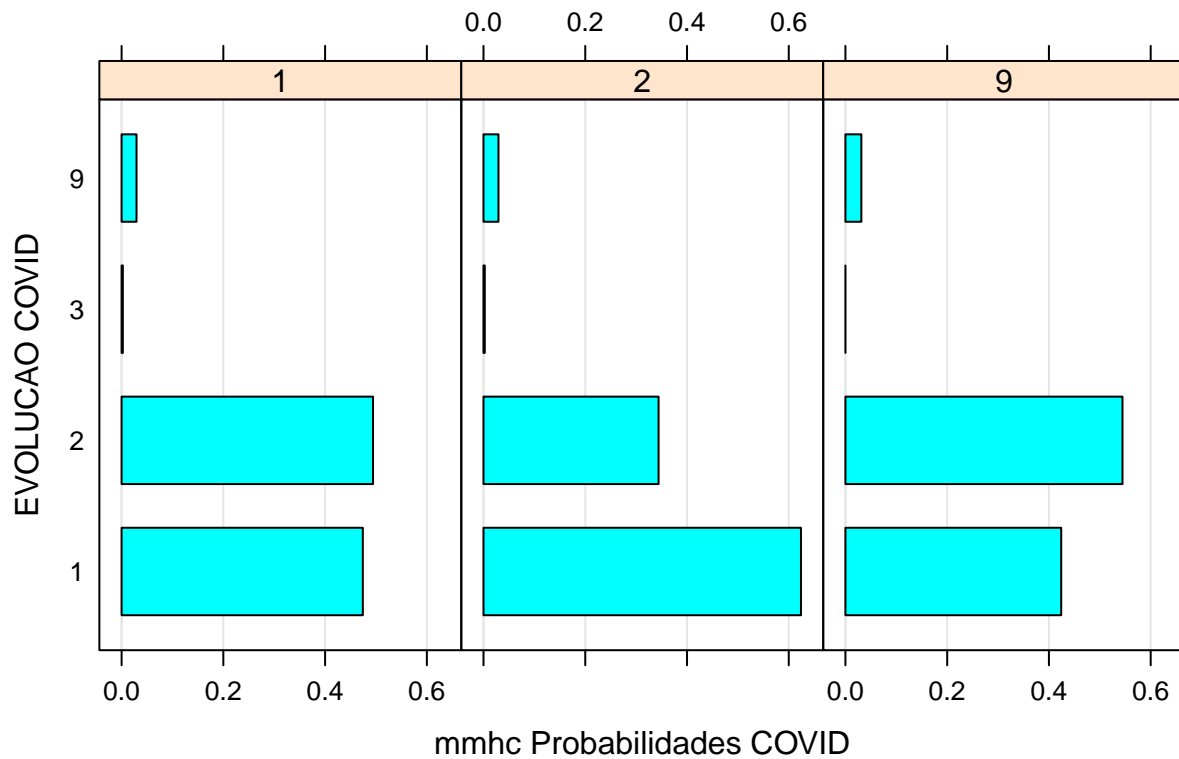
##
## Parameters of node EVOLUCAO (multinomial distribution)
##
## Conditional probability table:
##
## , , SATURACAO = 1
##
##          TOSSE
## EVOLUCAO      1      2      9
##      1 0.69520929 0.54742376 0.41666667
##      2 0.21088652 0.30851735 0.40740741
##      3 0.06302722 0.11188223 0.12962963
##      9 0.03087697 0.03217666 0.04629630
##
## , , SATURACAO = 2
##
##          TOSSE
## EVOLUCAO      1      2      9
##      1 0.78907535 0.72085890 0.25000000
##      2 0.12668641 0.15848671 0.25000000
##      3 0.04244817 0.08179959 0.25000000
##      9 0.04179006 0.03885481 0.25000000
##
## , , SATURACAO = 9
##
##          TOSSE
## EVOLUCAO      1      2      9
##      1 0.74468085 0.53846154 0.67088608
##      2 0.17021277 0.23076923 0.25316456
##      3 0.05319149 0.23076923 0.02531646
##      9 0.03191489 0.00000000 0.05063291

```

Conditional Probabilities for Node EVOLUCAO



Conditional Probabilities for Node EVOLUCAO



Conditional Probabilities for Node EVOLUCAO

