Predição. Dados de 22 abril 2021

Efeito do tempo de internação até entrada na UTI versus desfecho

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02/junho/2021

SRAG 12/04/2021

URL: https://s3-sa-east-1.amazonaws.com/ckan.saude.gov.br/SRAG/2021/INFLUD21-12-04-2021.csv

Do resumo do conjunto de dados Vigilância de Síndrome Respiratória Aguda Grave (SRAG) O Ministério da Saúde (MS), por meio da Secretaria de Vigilância em Saúde (SVS), desenvolve a vigilância da Síndrome Respiratória... Fonte: SRAG 2021 - Banco de Dados de Síndrome Respiratória Aguda Grave - incluindo dados da COVID-19

Dicionário de Dados

URL: https://opendatasus.saude.gov.br/dataset/9f76e80f-a2f1-4662-9e37-71084eae23e3/resource/b3321e55-24e9-49ab-8651-29cf5c8f3179/download/dicionario-de-dados-srag-hospitalizado-27.07.2020-final.pdf

Do resumo do conjunto de dados

Vigilância de Síndrome Respiratória Aguda Grave (SRAG) O Ministério da Saúde (MS), por meio da Secretaria de Vigilância em Saúde (SVS), desenvolve a vigilância da Síndrome Respiratória... Fonte: SRAG 2021 - Banco de Dados de Síndrome Respiratória Aguda Grave - incluindo dados da COVID-19

Variaveis disponíveis e números de valores faltantes para cada uma

```
## DT_NOTIFIC    0
## SEM_NOT   0
## DT_SIN_PRI    0
## SEM_PRI   0
## SG_UF_NOT     0
## ID_REGIONA    51139
## CO_REGIONA    51139
## ID_MUNICIP    0
## CO_MUN_NOT    0
## ID_UNIDADE    0
## CO_UNI_NOT    0
## CS_SEXO   0
## DT_NASC   467
## NU_IDADE_N    0
```

```
## TP_IDADE      0
## COD_IDADE     5
## CS_GESTANT    0
## CS_RACA   0
## CS_ETINIA     543745
## CS_ESCOL_N    195124
## ID_PAIS   0
## CO_PAIS   0
## SG_UF     67
## ID_RG_RESI    49762
## CO_RG_RESI    49762
## ID_MN_RESI    67
## CO_MUN_RES    67
## CS_ZONA   65852
## SURTO_SG      303974
## NOSOCOMIAL    131465
## AVE_SUINO     122475
## FEBRE     94804
## TOSSE     76941
## GARGANTA      167574
## DISPNEIA      69599
## DESC_RESP     104682
## SATURACAO     88992
## DIARREIA      171927
## VOMITO    178962
## OUTRO_SIN     170807
## OUTRO_DES     379866
## PUERPERA      351948
## FATOR_RISC    0
## CARDIOPATI    290068
## HEMATOLOGI    351142
## SIND_DOWN     351721
## HEPATICA      351612
## ASMA      348156
## DIABETES      308477
## NEUROLOGIC    346821
## PNEUMOPATI    346942
## IMUNODEPRE    349463
## RENAL     348253
## OBESIDADE     340105
## OBES_IMC      537264
## OUT_MORBI     310984
## MORB_DESC     413692
## VACINA    144773
## DT_UT_DOSE    515312
## MAE_VAC   539340
## DT_VAC_MAE    543745
## M_AMAMENTA    540399
## DT_DOSEUNI    543745
## DT_1_DOSE     543745
## DT_2_DOSE     543745
## ANTIVIRAL     99762
## TP_ANTIVIR    528180
## OUT_ANTIV     541639
```

```
## DT_ANTIVIR    530185
## HOSPITAL      19704
## DT_INTERNA    42426
## SG_UF_INTE    2
## ID_RG_INTE    121033
## CO_RG_INTE    121033
## ID_MN_INTE    31118
## CO_MU_INTE    31118
## UTI   83155
## DT_ENTUTI     402818
## DT_SAIDUTI    480078
## SUPORT_VEN    81011
## RAIOX_RES     244069
## RAIOX_OUT     528680
## DT_RAIOX      448344
## AMOSTRA   38895
## DT_COLETA     68379
## TP_AMOSTRA    77497
## OUT_AMOST     496533
## PCR_RESUL     75631
## DT_PCR    215118
## POS_PCRFLU    409681
## TP_FLU_PCR    543721
## PCR_FLUASU    543736
## FLUASU_OUT    543745
## PCR_FLUBLI    543745
## FLUBLI_OUT    543745
## POS_PCROUT    320869
## PCR_VSR   541871
## PCR_PARA1     543709
## PCR_PARA2     543726
## PCR_PARA3     543731
## PCR_PARA4     543737
## PCR_ADENO     543670
## PCR_METAP     543744
## PCR_BOCA      543729
## PCR_RINO      543073
## PCR_OUTRO     543498
## DS_PCR_OUT    543745
## CLASSI_FIN    103974
## CLASSI_OUT    543233
## CRITERIO      132247
## EVOLUCAO      193581
## DT_EVOLUCA    223453
## DT_ENCERRA    193851
## DT_DIGITA     0
## HISTO_VGM     0
## PAIS_VGM      543745
## CO_PS_VGM     543690
## LO_PS_VGM     543745
## DT_VGM    543745
## DT_RT_VGM     543745
## PCR_SARS2     324649
## PAC_COCBO     526233
```

```
## PAC_DSCBO     526233
## OUT_ANIM      543745
## DOR_ABD   187846
## FADIGA    166485
## PERD_OLFT     181929
## PERD_PALA     182275
## TOMO_RES      208995
## TOMO_OUT      530868
## DT_TOMO   345333
## TP_TES_AN     474946
## DT_RES_AN     475975
## RES_AN    94744
## POS_AN_FLU    509408
## TP_FLU_AN     543700
## POS_AN_OUT    495760
## AN_SARS2      496986
## AN_VSR    543265
## AN_PARA1      543742
## AN_PARA2      543743
## AN_PARA3      543744
## AN_ADENO      543744
## AN_OUTRO      543591
## DS_AN_OUT     543745
## TP_AM_SOR     497310
## SOR_OUT   538877
## DT_CO_SOR     503913
## TP_SOR    498300
## OUT_SOR   540607
## DT_RES    497374
## RES_IGG   480084
## RES_IGM   478770
## RES_IGA   500128
```

variáveis usadas

dados contendo NA´s

```
## Rows: 543,745
## Columns: 14
## $ CLASSI_FIN <dbl> 4, 5, 4, 4, 4, 4, 5, 5, 5, 5, 4, NA, 5, 5, 5, 4, 5, 4, 5, 4~
## $ DT_SIN_PRI <chr> "04/01/2021", "04/01/2021", "03/01/2021", "03/01/2021", "05~
## $ DT_EVOLUCA <chr> "04/01/2021", NA, NA, "05/01/2021", "13/01/2021", "12/01/20~
## $ EVOLUCAO   <dbl> 1, 1, NA, 1, 1, 1, 1, 1, 2, 1, 1, 1, 1, 2, NA, NA, 1, 1, 1,~
## $ TP_IDADE   <dbl> 2, 3, 3, 3, 2, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 2,~
## $ SG_UF_NOT  <chr> "SP", "BA", "SP", "SP", "MG", "PR", "SP", "SP", "SP", "SP",~
## $ NU_IDADE_N <dbl> 3, 46, 65, 84, 10, 16, 70, 55, 81, 44, 3, 2, 58, 51, 40, 15~
## $ SATURACAO  <dbl> 2, 2, 1, 1, 2, 1, NA, 2, 2, 1, 1, 2, 1, 1, NA, 2, 2, 2, 1, ~
## $ DIABETES   <dbl> NA, 1, NA, 1, NA, 2, 1, 1, 2, NA, 2, NA, 1, NA, NA, 2, NA, ~
## $ OBESIDADE  <dbl> NA, 2, NA, 2, NA, 2, NA, 2, 2, NA, 2, NA, 2, NA, NA, 2, NA,~
## $ UTI        <dbl> 2, 1, NA, 2, 2, 2, 2, 1, 2, 1, 1, 2, 2, 1, NA, 2, 2, 1, 1, ~
## $ DT_ENTUTI  <chr> NA, "04/01/2021", NA, NA, NA, NA, NA, "09/01/2021", NA, "11~
## $ CARDIOPATI <dbl> NA, 1, NA, 1, NA, 2, NA, 1, 1, NA, 2, NA, 1, NA, NA, 2, NA,~
## $ SUPORT_VEN <dbl> 3, NA, NA, 2, 3, 2, 2, 9, 3, 2, 2, 3, 2, 1, 3, 3, 3, 3, 2, ~
```

```
## Rows: 42,924
## Columns: 14
## $ CLASSI_FIN <dbl> 5, 4, 4, 5, 5, 5, 5, 5, 5, 5, 4, 5, 4, 5, 4, 4, 5, 5, 5, 5,~
## $ DT_SIN_PRI <chr> "05/01/2021", "10/01/2021", "05/01/2021", "03/01/2021", "05~
## $ DT_EVOLUCA <chr> "21/01/2021", "15/02/2021", "25/01/2021", "22/01/2021", "29~
## $ EVOLUCAO   <dbl> 1, 1, 1, 1, 1, 2, 2, 2, 2, 1, 2, 2, 1, 1, 2, 1, 2, 1, 2, 2,~
## $ TP_IDADE   <dbl> 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3,~
## $ SG_UF_NOT  <chr> "SP", "MG", "BA", "PR", "SP", "GO", "SP", "SP", "SP", "BA",~
## $ NU_IDADE_N <dbl> 55, 3, 68, 57, 80, 43, 88, 57, 73, 53, 71, 81, 62, 52, 77, ~
## $ SATURACAO  <dbl> 2, 1, 2, 1, 2, 1, 1, 2, 2, 2, 2, 1, 2, 1, 1, 1, 1, 1, 1, 1,~
## $ DIABETES   <dbl> 1, 2, 1, 1, 1, 1, 2, 2, 2, 2, 2, 1, 2, 2, 2, 1, 1, 1, 1, 1,~
## $ OBESIDADE  <dbl> 2, 2, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 2, 2, 2,~
## $ UTI        <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,~
## $ DT_ENTUTI  <chr> "09/01/2021", "11/01/2021", "09/01/2021", "09/01/2021", "11~
## $ CARDIOPATI <dbl> 1, 2, 1, 2, 1, 1, 1, 2, 2, 1, 1, 2, 1, 2, 1, 1, 2, 1, 1, 1,~
## $ SUPORT_VEN <dbl> 9, 2, 3, 2, 9, 1, 2, 2, 1, 2, 1, 1, 1, 2, 2, 2, 2, 2, 1, 2,~
```

Dados com NA´s omitidos

```
## Rows: 42,924
## Columns: 14
## $ CLASSI_FIN <dbl> 5, 4, 4, 5, 5, 5, 5, 5, 5, 5, 4, 5, 4, 5, 4, 4, 5, 5, 5, 5,~
## $ DT_SIN_PRI <dttm> 2021-01-05, 2021-01-10, 2021-01-05, 2021-01-03, 2021-01-05~
## $ DT_EVOLUCA <dttm> 2021-01-21, 2021-02-15, 2021-01-25, 2021-01-22, 2021-01-29~
## $ EVOLUCAO   <dbl> 1, 1, 1, 1, 1, 2, 2, 2, 2, 1, 2, 2, 1, 1, 2, 1, 2, 1, 2, 2,~
## $ TP_IDADE   <dbl> 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3,~
## $ SG_UF_NOT  <chr> "SP", "MG", "BA", "PR", "SP", "GO", "SP", "SP", "SP", "BA",~
## $ NU_IDADE_N <dbl> 55, 3, 68, 57, 80, 43, 88, 57, 73, 53, 71, 81, 62, 52, 77, ~
## $ SATURACAO  <dbl> 2, 1, 2, 1, 2, 1, 1, 2, 2, 2, 2, 1, 2, 1, 1, 1, 1, 1, 1, 1,~
## $ DIABETES   <dbl> 1, 2, 1, 1, 1, 1, 2, 2, 2, 2, 2, 1, 2, 2, 2, 1, 1, 1, 1, 1,~
## $ OBESIDADE  <dbl> 2, 2, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 2, 2, 2,~
## $ UTI        <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,~
## $ DT_ENTUTI  <dttm> 2021-01-09, 2021-01-11, 2021-01-09, 2021-01-09, 2021-01-11~
## $ CARDIOPATI <dbl> 1, 2, 1, 2, 1, 1, 1, 2, 2, 1, 1, 2, 1, 2, 1, 1, 2, 1, 1, 1,~
## $ SUPORT_VEN <dbl> 9, 2, 3, 2, 9, 1, 2, 2, 1, 2, 1, 1, 1, 2, 2, 2, 2, 2, 1, 2,~
```

cria colunas com intervalos de tempo

```
## Rows: 42,656
## Columns: 12
## $ CLASSI_FIN       <fct> 5, 4, 4, 5, 5, 5, 5, 5, 5, 5, 4, 5, 4, 5, 4, 4, 5, 5,~
## $ EVOLUCAO         <fct> 1, 1, 1, 1, 1, 2, 2, 2, 2, 1, 2, 2, 1, 1, 2, 1, 2, 1,~
## $ SG_UF_NOT        <fct> SP, MG, BA, PR, SP, GO, SP, SP, SP, BA, SP, RS, RS, P~
## $ IDADE            <fct> "(16,71]", "[1,16]", "(16,71]", "(16,71]", "(71,80]",~
## $ SATURACAO        <fct> 2, 1, 2, 1, 2, 1, 1, 2, 2, 2, 2, 1, 2, 1, 1, 1, 1, 1,~
## $ DIABETES         <fct> 1, 2, 1, 1, 1, 1, 2, 2, 2, 2, 2, 1, 2, 2, 2, 1, 1, 1,~
## $ OBESIDADE        <fct> 2, 2, 2, 2, 2, 1, 2, 2, 2, 2, 2, 2, 2, 2, 2, 2, 1, 2,~
## $ UTI              <fct> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,~
## $ CARDIOPATI       <fct> 1, 2, 1, 2, 1, 1, 1, 2, 2, 1, 1, 2, 1, 2, 1, 1, 2, 1,~
## $ SUPORT_VEN       <fct> 9, 2, 3, 2, 9, 1, 2, 2, 1, 2, 1, 1, 1, 2, 2, 2, 2, 2,~
## $ INTER_P_SIN_EVOL <fct> "(13,55]", "(13,55]", "(13,55]", "(13,55]", "(13,55]"~
## $ INTER_P_SIN_UTI  <fct> "(3,7]", "(-266,3]", "(3,7]", "(3,7]", "(3,7]", "(7,1~
```

```
##
##     L     T
## 37656  5000
```

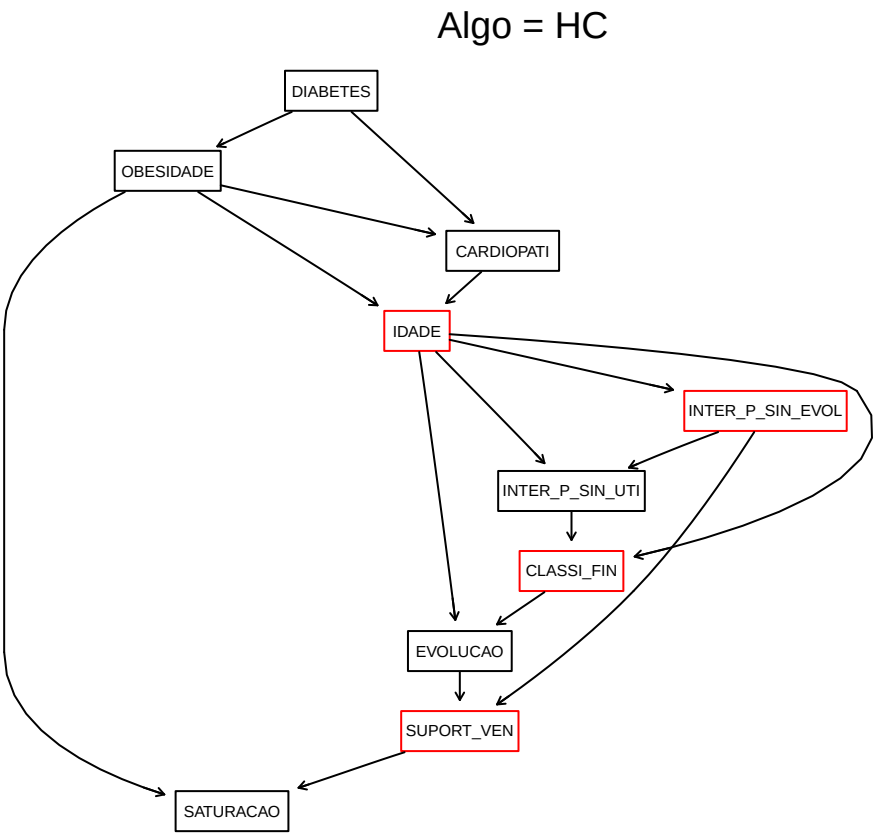
```
train <- s1
test <- s2
```

Aprendizagem da estrutura da rede

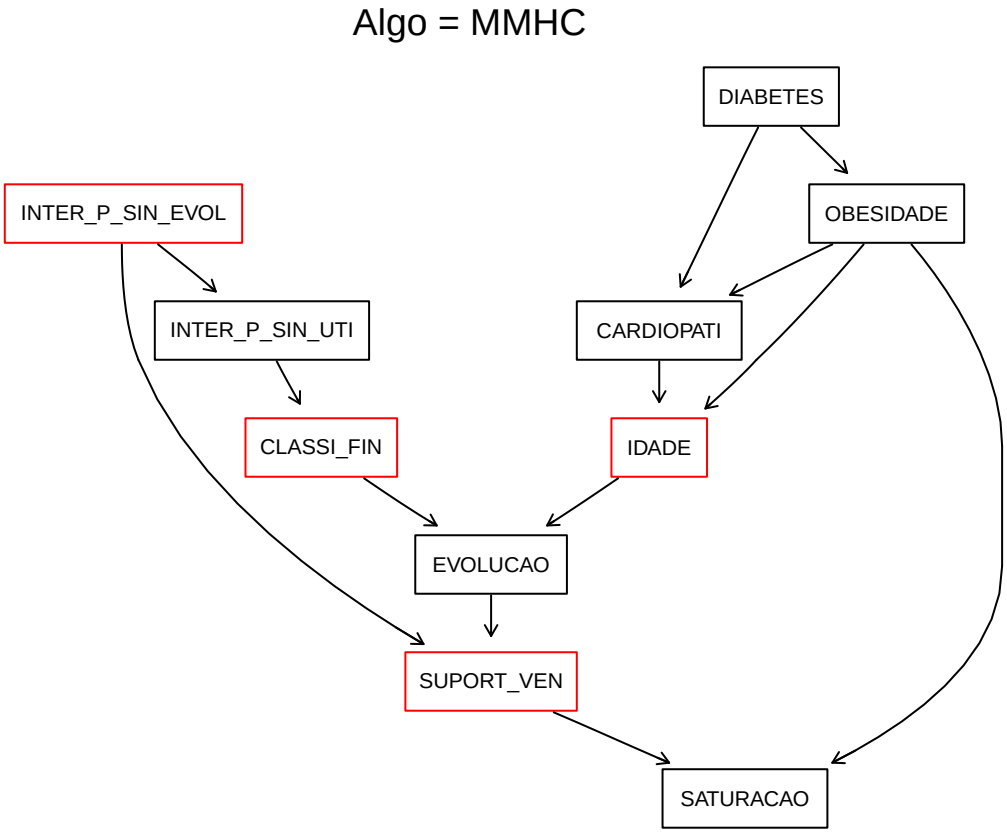
Diferentes algortimos de prendizagem

-HC -GS -IAMB -MMHC

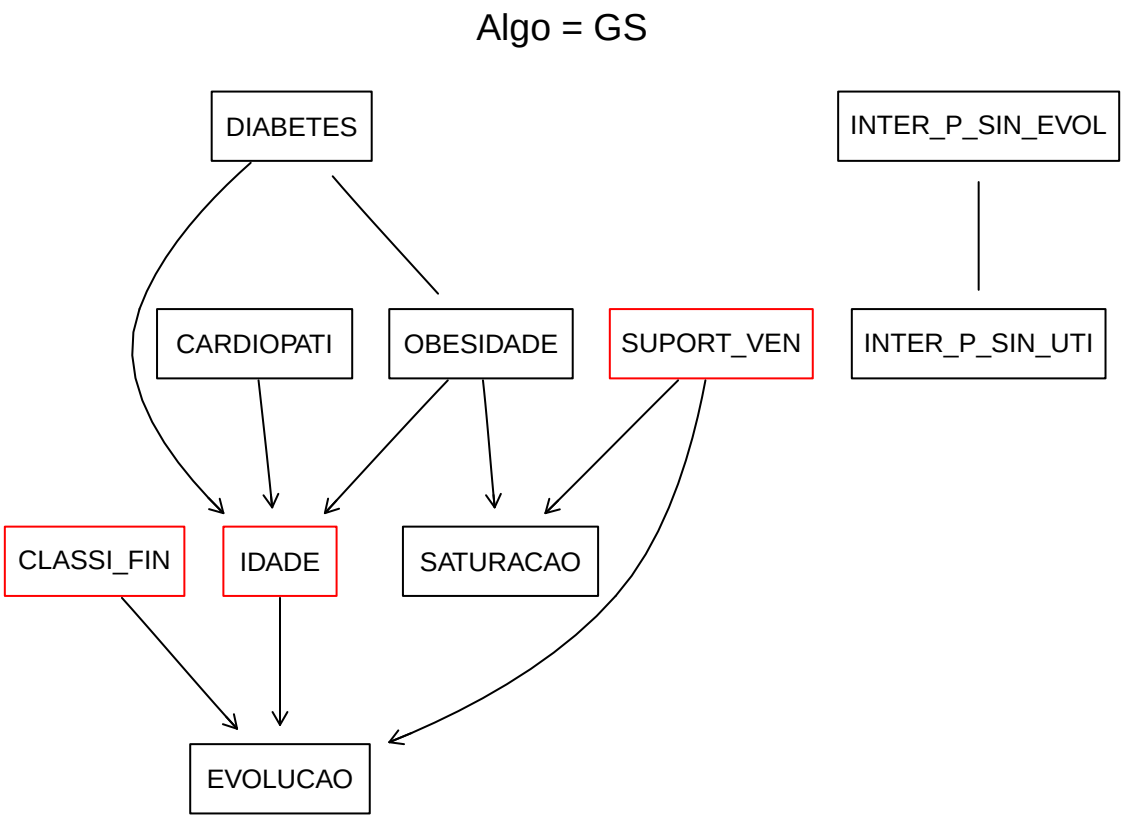
Algo = HC



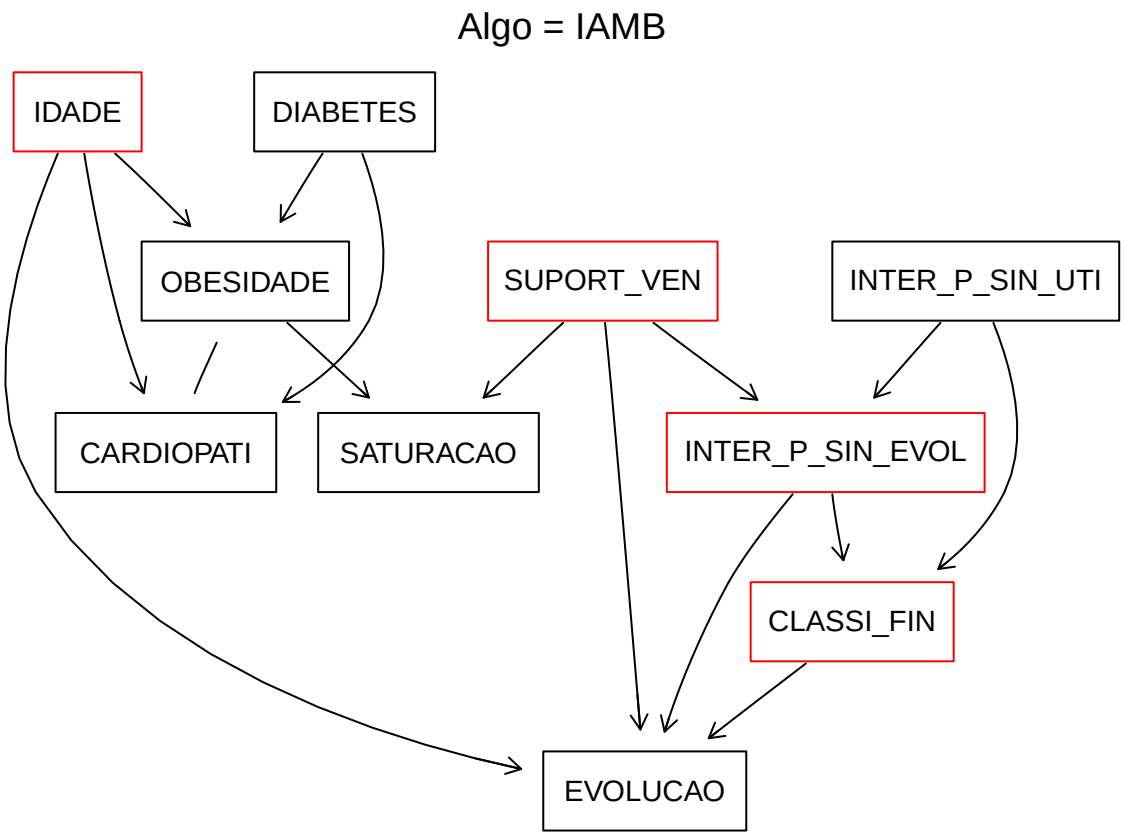
Algo = MMHC


Algo = MMHC
DIABETES
INTER_P_SIN_EVOL
OBESIDADE
INTER_P_SIN_UTI
CARDIOPATI
CLASSI_FIN
IDADE
EVOLUCAO
SUPORT_VEN
SATURACAO

Algo = GS


Algo = GS
DIABETES
INTER_P_SIN_EVOL
CARDIOPATI
OBESIDADE
SUPORT_VEN
INTER_P_SIN_UTI
CLASSI_FIN
IDADE
SATURACAO
EVOLUCAO

Algo = IAMB

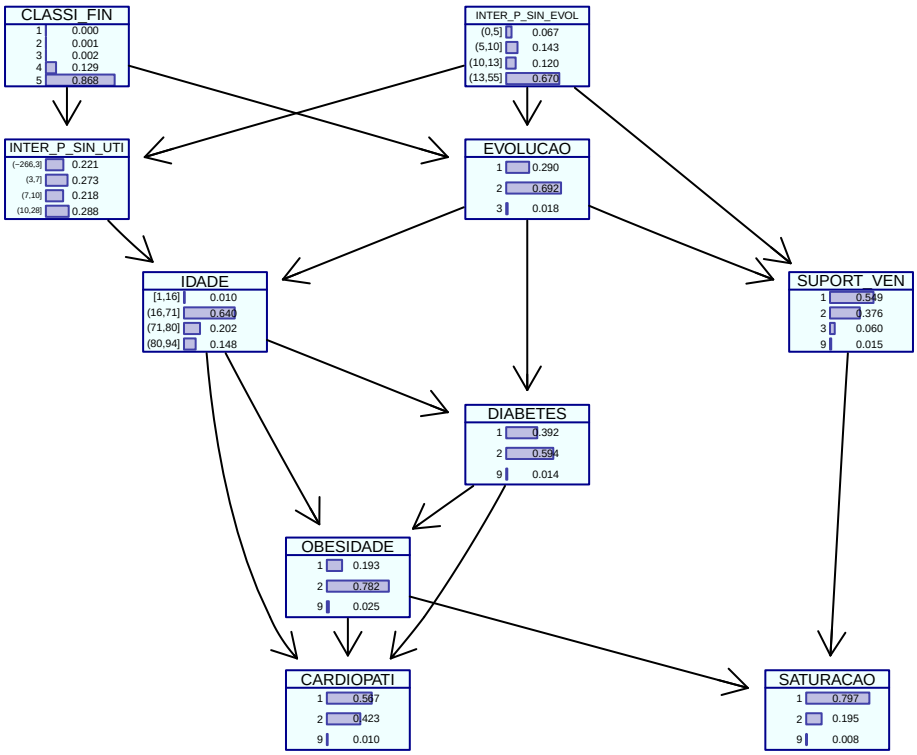


Distribuição conjunta de probabilidades entre as variáveis.

Algoritmo *HC*

```
forca.real.hc <- suppressWarnings(boot.strength(train,
                                R = boots.trap,
                                algorithm = "hc"))
rede.media.train.hc = averaged.network(forca.real.hc)

rede.media.train.dagged.hc <- pdag2dag(rede.media.train.hc,
                                       ordering = names(train))
thr.real.gs <- paste('Thr: ', attr(forca.real.hc, "threshold"))

par(mfrow = c(1, 1))
fit.bn.hc <- bn.fit(x = rede.media.train.dagged.hc, data = s1)
graphviz.chart(fit.bn.hc,
               type = "barprob",
               col = "darkblue",
               bg = "azure",
               bar.col = "darkblue",
               main = "Rede de probabilidades")
```

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



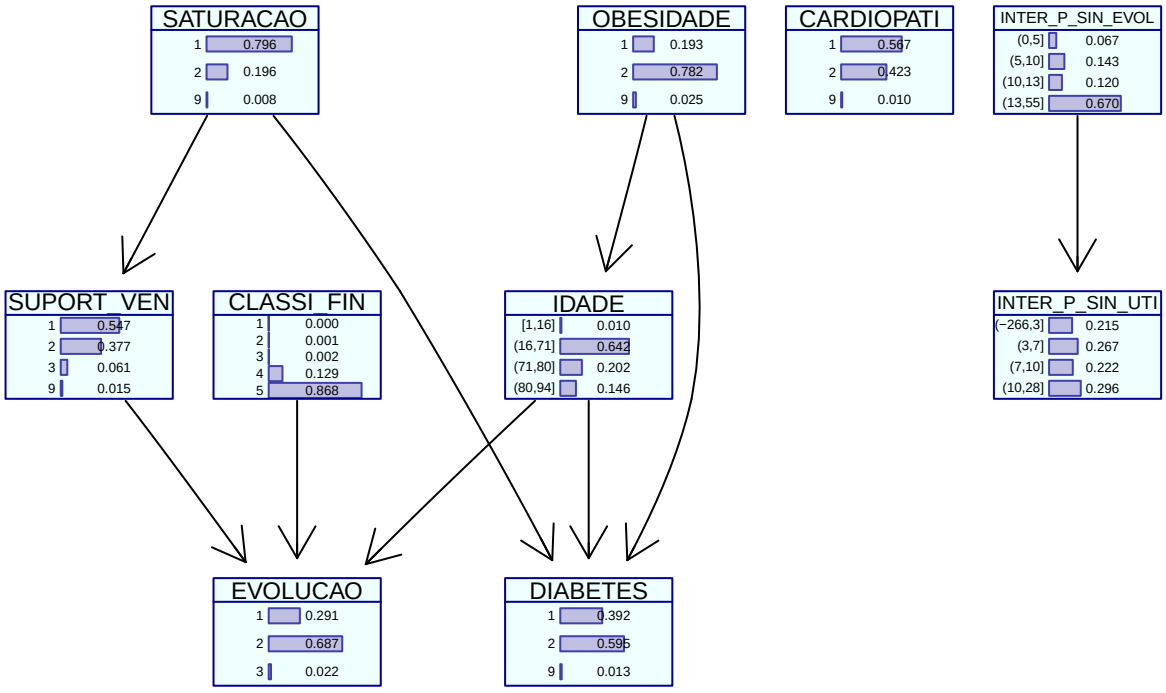
Distribuição conjunta de probabilidades entre as variáveis.

Algoritmo GS

```
forca.real.gs <- suppressWarnings(boot.strength(train,
                                R = boots.trap,
                                algorithm = "gs"))
rede.media.train.gs = averaged.network(forca.real.gs)

rede.media.train.dagged.gs <- pdag2dag(rede.media.train.gs,
                                       ordering = names(train))
thr.real.gs <- paste('Thr: ', attr(forca.real.gs, "threshold"))

par(mfrow = c(1, 1))
fit.bn.gs <- bn.fit(x = rede.media.train.dagged.gs, data = s1)
graphviz.chart(fit.bn.gs,
               type = "barprob",
               col = "darkblue",
               bg = "azure",
               bar.col = "darkblue",
               main = "Rede de probabilidades")
```

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

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



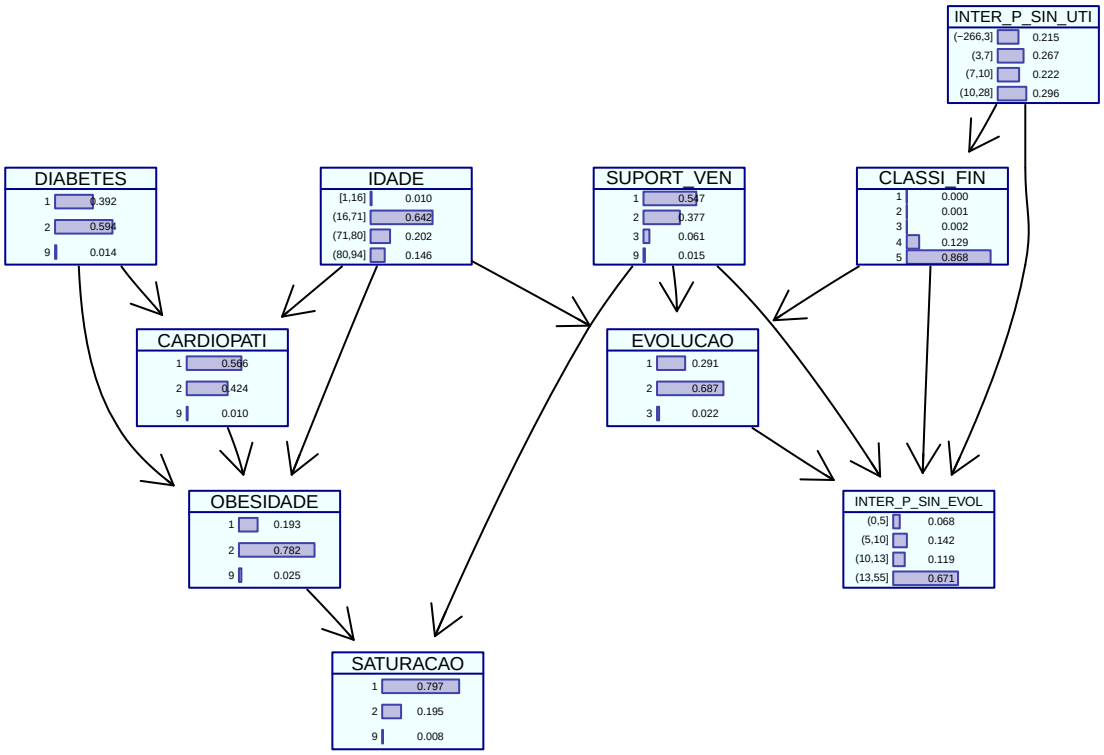
Distribuição conjunta de probabilidades entre as variáveis.

Algoritmo IAMB

```
forca.real.iamb <- suppressWarnings(boot.strength(train,
                                R = boots.trap,
                                algorithm = "iamb"))
rede.media.train.iamb = averaged.network(forca.real.iamb)

rede.media.train.dagged.iamb <- pdag2dag(rede.media.train.iamb,
                                         ordering = names(train))
thr.real.gs <- paste('Thr: ', attr(forca.real.iamb, "threshold"))
fit.bn.iamb <- bn.fit(x = rede.media.train.dagged.iamb, data = s1)
par(mfrow = c(1, 1))
graphviz.chart(fit.bn.iamb,
               type = "barprob",
               col = "darkblue",
               bg = "azure",
               bar.col = "darkblue",
               main = "Rede de probabilidades")
```

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

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

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

Rede de probabilidades



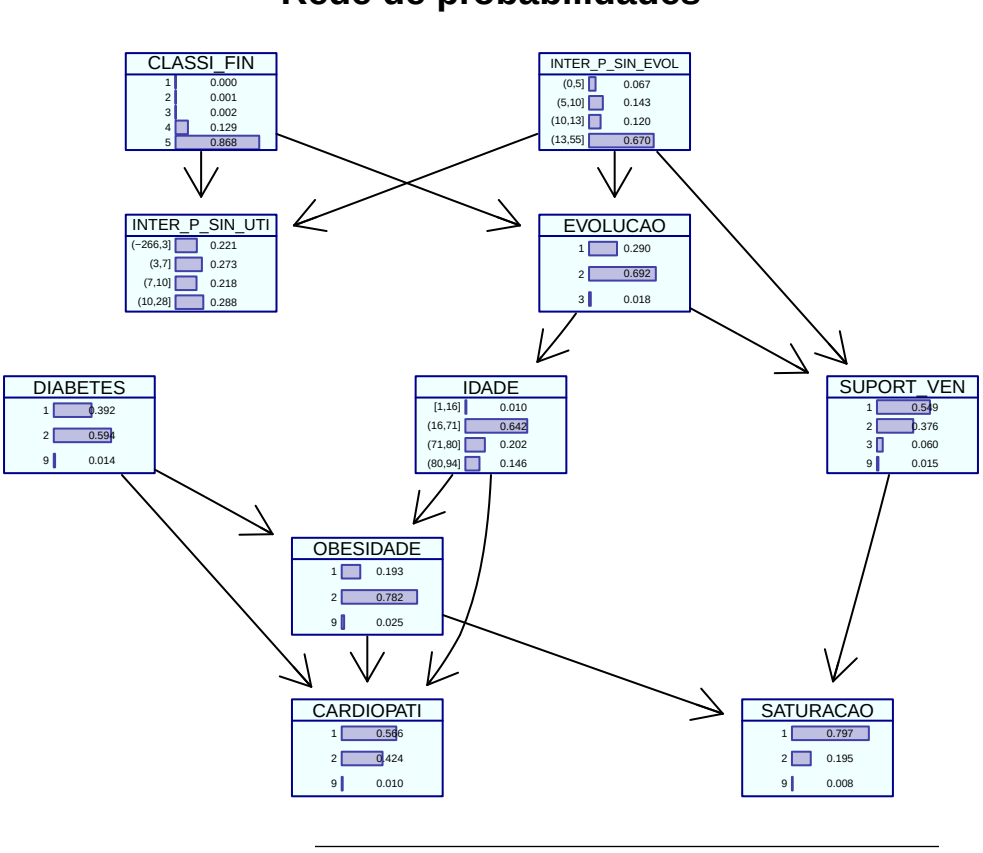
Distribuição conjunta de probabilidades entre as variáveis.

Algoritmo MMHC

```
forca.real.mmhc <- suppressWarnings(boot.strength(train,
                                R = boots.trap,
                                algorithm = "mmhc"))
rede.media.train.mmhc = averaged.network(forca.real.mmhc)

rede.media.train.dagged.mmhc <- pdag2dag(rede.media.train.mmhc,
                                         ordering = names(train))
thr.real.gs <- paste('Thr: ', attr(forca.real.mmhc, "threshold"))
fit.bn.mmhc <- bn.fit(x = rede.media.train.dagged.mmhc, data = s1)
par(mfrow = c(1, 1))
graphviz.chart(fit.bn.mmhc,
               type = "barprob",
               col = "darkblue",
```

```
              bg = "azure",
              bar.col = "darkblue",
              main = "Rede de probabilidades")
```

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



Predição

SET.EVIDENCE + QUERYGRAIN

```
#
# [1] "CLASSI_FIN" "IDADE" "OBESIDADE"  "UTI"  "SUPORT_VEN"
#

# IDADE
# [1,36] (36,71] (71,106]

# UTI
#  1-Sim
#  2-Nao
#  9-Ignorado
```

```r
#SUPORT_VEN
# 1-Sim, invasivo
# 2-Sim, nao invasivo
# 3-Nao
# 9-Ignorado
#
prediga <- function(rede, amostras, estados){

  fitt1 <- bn.fit(rede, amostras)
  junction = compile(as.grain(fitt1))
  jedu = setEvidence(propagate = TRUE, junction,
                     node = c("CLASSI_FIN",
                              "IDADE",
                              #"UTI",
                              "INTER_P_SIN_EVOL",
                              "INTER_P_SIN_UTI",
                              "SUPORT_VEN"),
                     states =  estados)
  suppressWarnings(pred.rede <- querygrain(jedu,
                           nodes = c("EVOLUCAO"),
                           type = "marginal"))
  return(pred.rede)
}

estados <- c("5", "(71, 80]", "(13,55]", "(10,28]", "1")

pred.rede <- suppressWarnings(prediga(bn.hc, train, estados))


print(pred.rede)
```

```
## $EVOLUCAO
## EVOLUCAO
##           1           2           3
## 0.115835490 0.880964299 0.003200211
```

predição por proporção dos dados

```r
# usando dataset de test
x <- filter(test,
            CLASSI_FIN == 5,
            IDADE == "(71, 80]",
            INTER_P_SIN_EVOL == "(13,55]",
            INTER_P_SIN_UTI == "(10,28]",
            #UTI == 1,
            SUPORT_VEN == 1)
pred.proporcao <- nrow(filter(x, EVOLUCAO == 1))/nrow(x)

x2 <- filter(test,
            CLASSI_FIN == 5,
            IDADE == "(71, 80]",
            INTER_P_SIN_EVOL == "(13,55]",
```

```
            INTER_P_SIN_UTI == "(10,28]",
            #UTI == 1,
            SUPORT_VEN == 1)
pred.proporcao2 <- nrow(filter(x2, EVOLUCAO == 2))/nrow(x2)

print(pred.proporcao)
```

```
## [1] NaN
```

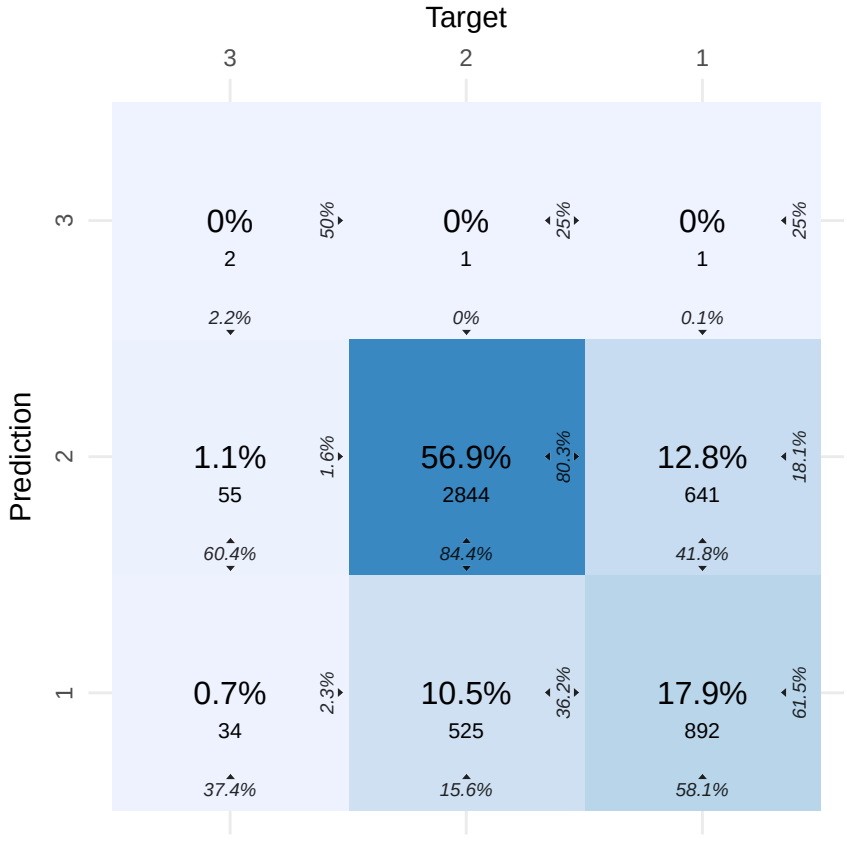
```
print(pred.proporcao2)
```

```
## [1] NaN
```

Fit dag to data and predict the value of latent variable

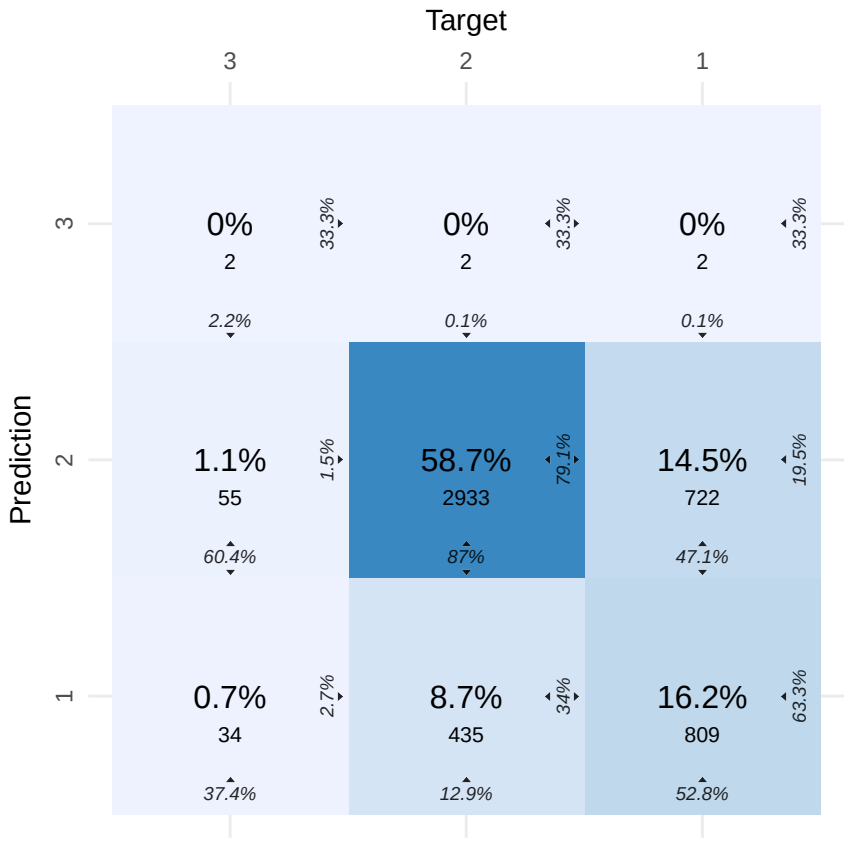
predicting a variable in the test set. EVOLUCAO

```
## Warning in map.prediction(node = node, fitted = object, data = data, n =
## extra.args$n, : dropping 1000 observations because generated samples are NAs.
```

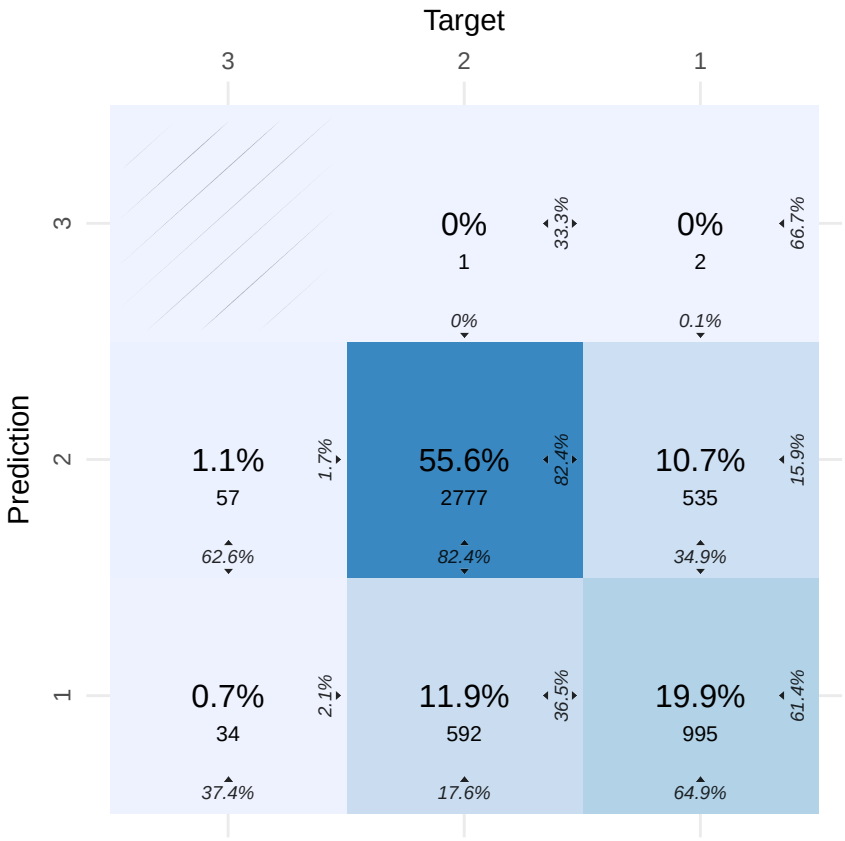


predicting a variable in the test set. EVOLUCAO rede simplificada ## *__HC__

```
## Warning in map.prediction(node = node, fitted = object, data = data, n =
## extra.args$n, : dropping 500 observations because generated samples are NAs.
```


Target
3
2
1
Prediction
3
2
1
0%
2
2.2%
33.3%
0%
2
0.1%
33.3%
0%
2
0.1%
33.3%
1.1%
55
60.4%
1.5%
58.7%
2933
87%
79.1%
14.5%
722
47.1%
19.5%
0.7%
34
37.4%
2.7%
8.7%
435
12.9%
34%
16.2%
809
52.8%
63.3%

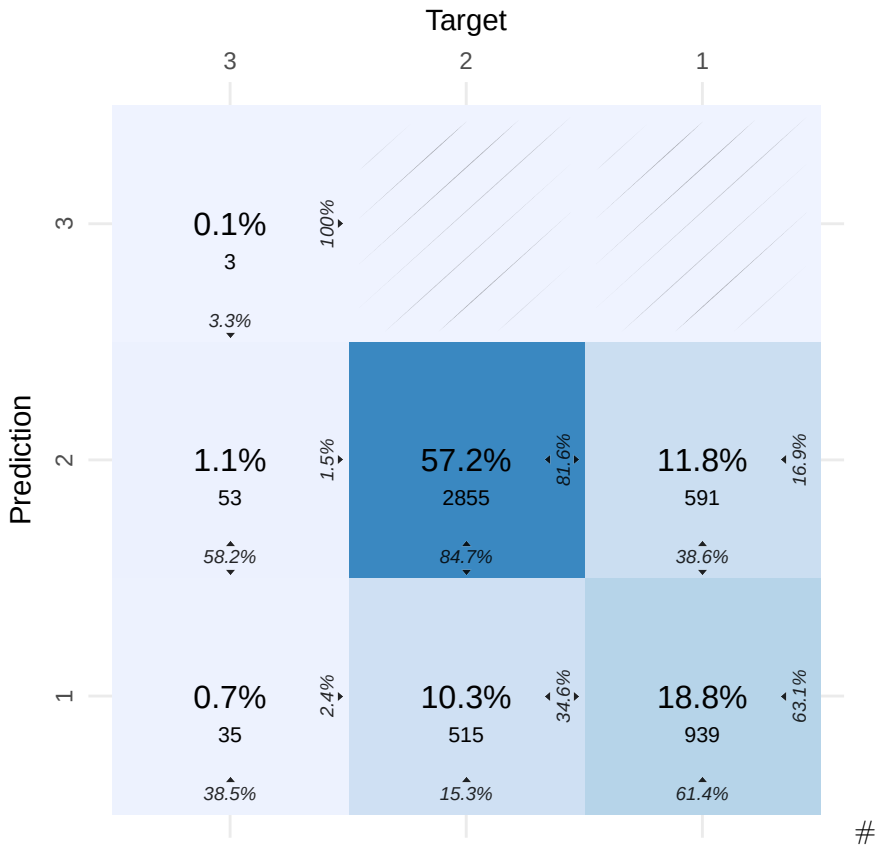
predicting a variable in the test set. EVOLUCAO rede simplificada GS



predicting a variable in the test set. EVOLUCAO rede simplificada MMHC

predicting a variable in the test set. EVOLUCAO rede simplificada IAMB

```
## Warning in map.prediction(node = node, fitted = object, data = data, n =
## extra.args$n, : dropping 284 observations because generated samples are NAs.
```


Target
3
2
1
Prediction
3
2
1
0.1%
3
3.3%
100%
1.1%
53
58.2%
1.5%
57.2%
2855
84.7%
81.6%
11.8%
591
38.6%
16.9%
0.7%
35
38.5%
2.4%
10.3%
515
15.3%
34.6%
18.8%
939
61.4%
63.1%
#