Aprendizagem Estatística em Altas Dimensões [MAE0501/MAE5904/IBI5904]

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Sumário

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Leitura dos Dados

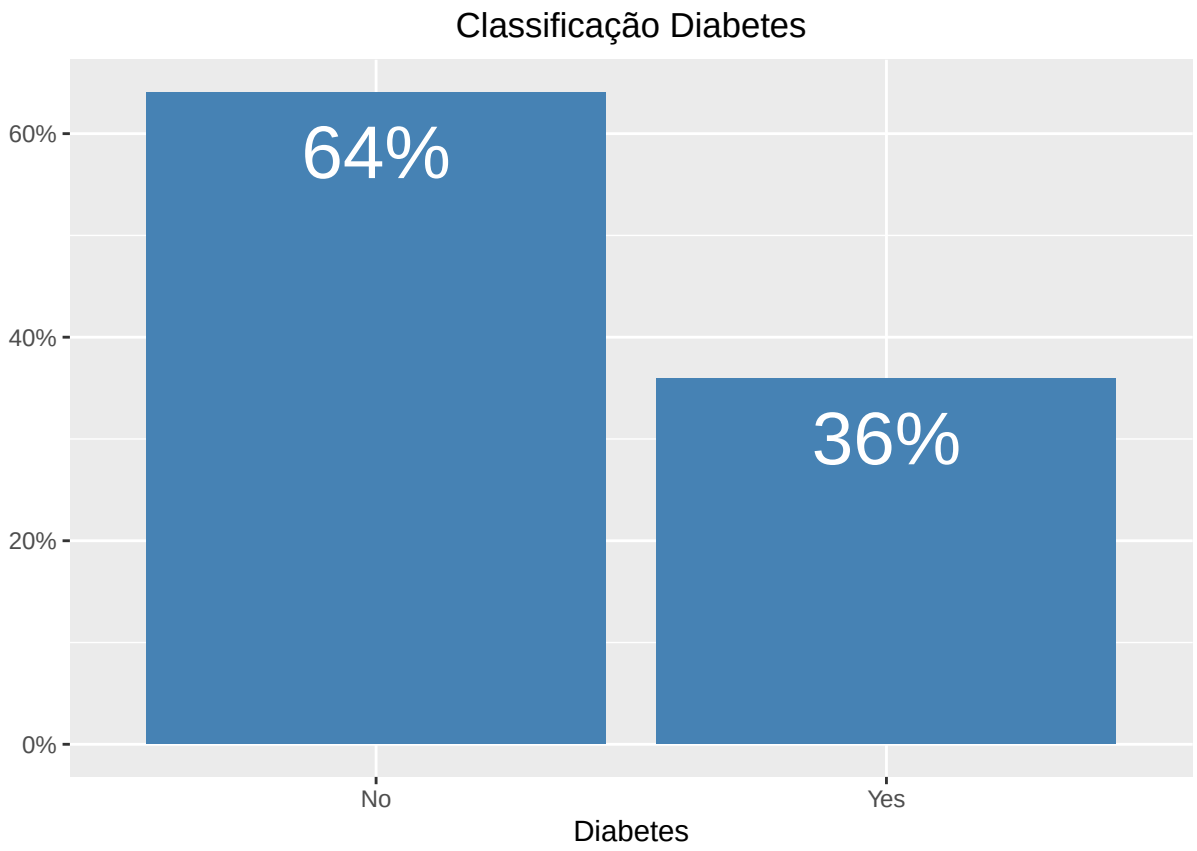
```
diabetes <- read_csv("diabetes.csv")

colnames(diabetes)[9] <- "diabetes"
diabetes$diabetes <- as.factor(diabetes$diabetes)
levels(diabetes$diabetes) <- c("No","Yes")

diabetes[, 2:6][diabetes[, 2:6] == 0] <- NA

head(diabetes) %>% kable(caption="Dados.")
```

Tabela 1: Dados.

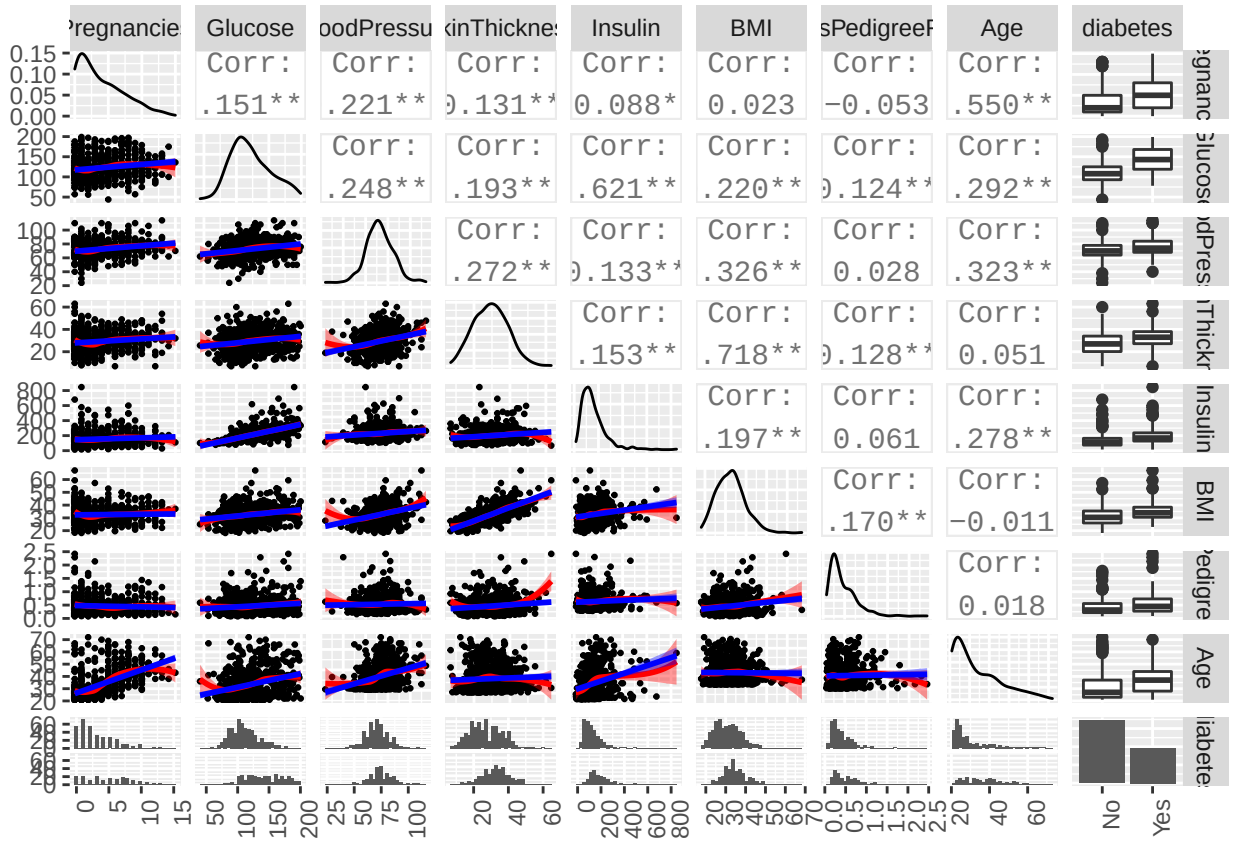
Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	diabetes
6	148	72	35	NA	33,6	0,63	50	Yes
1	85	66	29	NA	26,6	0,35	31	No
8	183	64	NA	NA	23,3	0,67	32	Yes
1	89	66	23	94	28,1	0,17	21	No
0	137	40	35	168	43,1	2,29	33	Yes
5	116	74	NA	NA	25,6	0,20	30	No

Análise Descritiva

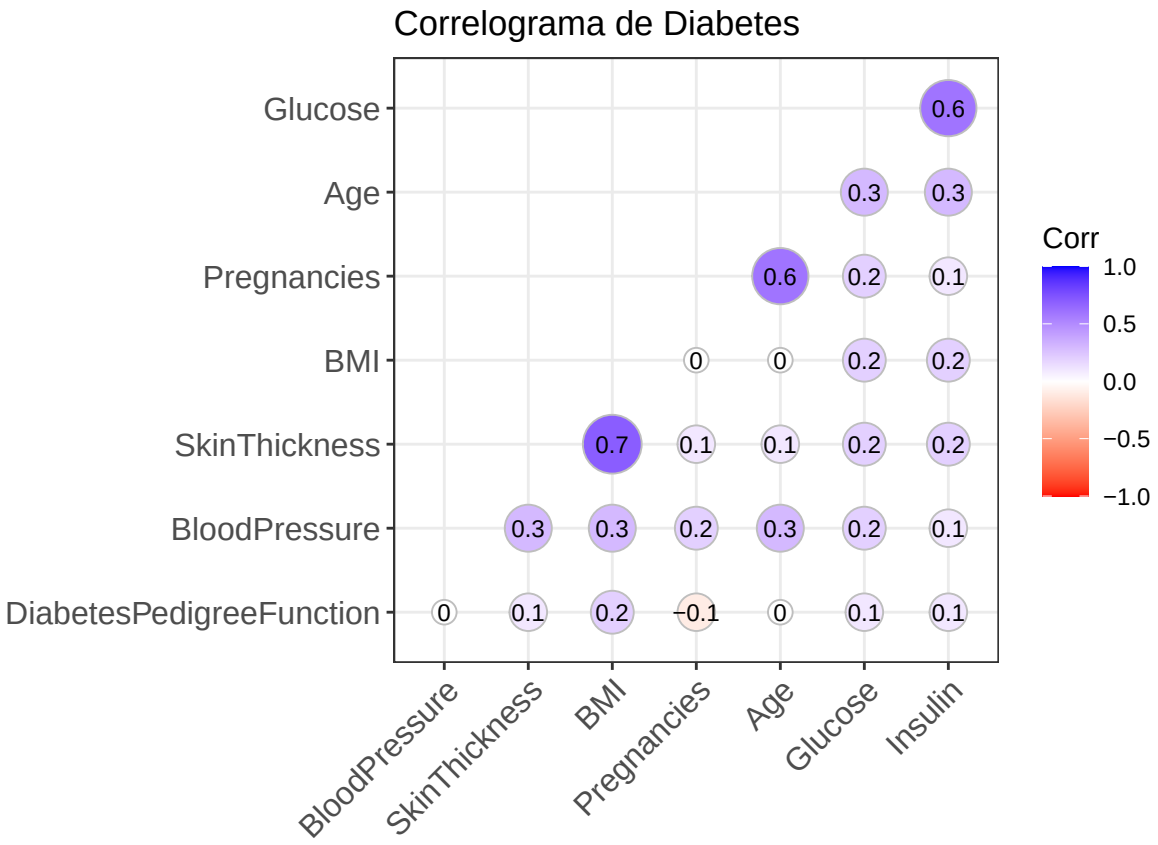
```
# OBS: análise descritiva com base no conjunto de treinamento para evitar data snooping

# Distribuição da variável resposta

train %>% count(Diabetes = factor(diabetes)) %>% mutate(pct = prop.table(n)) %>%
  ggplot(aes(x = Diabetes, y = pct, fill = pct, label = scales::percent(pct))) +
  geom_col(position = 'dodge', fill="steelblue") +
  labs(title = "Classificação Diabetes", x = "Diabetes", y = "") +
  geom_text(aes(label=scales::percent(pct) ), vjust=1.6, color="white", size=10) +
  scale_y_continuous(labels = scales::percent) +
  theme(plot.title = element_text(hjust = 0.5), legend.title = element_blank())
```



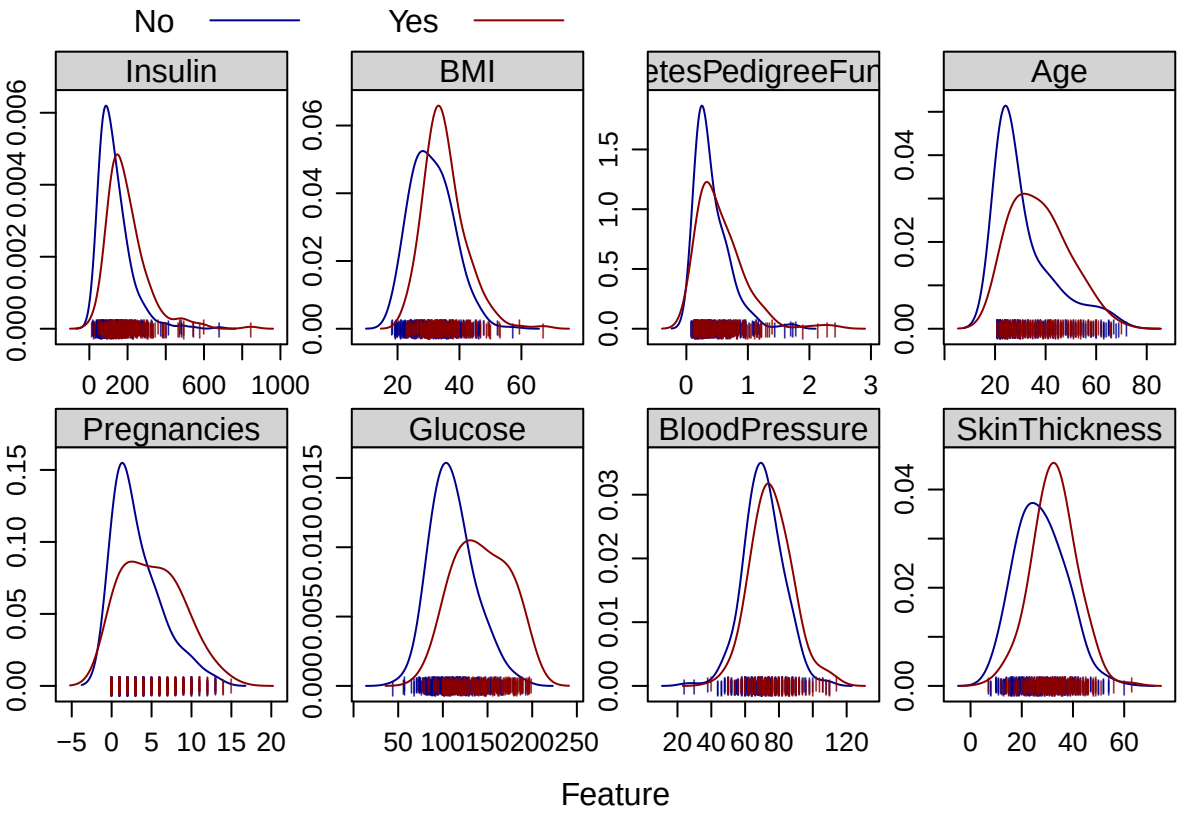

```
# Matriz completa com dispersão, densidades, correlações, retas de regressão (com IC) e LOESS (com IC)

      # Função auxiliar para curvas de regressão linear e LOESS nos gráficos abaixo
      curvas <- function(data, mapping, ...){
        p <- ggplot(data = data, mapping = mapping) +
          geom_point(size = 0.5) +
          geom_smooth(method = loess, fill = "red", color = "red", ...) +
          geom_smooth(method = lm, fill = "blue", color = "blue", ...)
        p
      }

ggpairs(train, columns = 1:9, lower = list(continuous = curvas)) + # Obs: pode demorar para montar o gr
    theme(axis.text.x = element_text(angle = 90, hjust = 1))
```



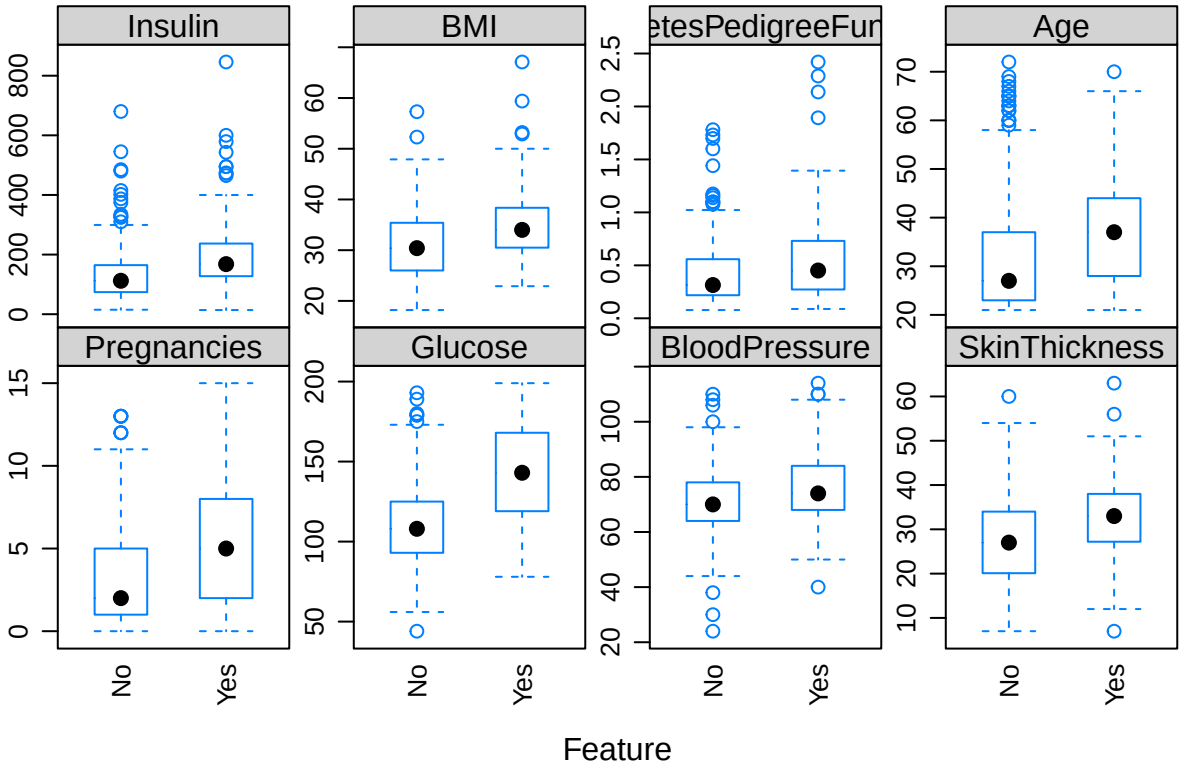

```
# Correlações/Correlograma
corr<-round(cor(train[,-9]),1)
ggcorrplot(corr, hc.order = TRUE,
           type = "lower",
           lab = TRUE,
           lab_size = 3,
           method="circle",
           colors = c("red", "white", "blue"),
           title="Correlograma de Diabetes",
           ggtheme=theme_bw)
```




```
# Distribuição da diabetes Yes/No por feature

featurePlot(x = train[, 1:8], # Densidades alisadas
            y = train$diabetes,
            plot = "density",
            scales = list(x = list(relation="free"), y = list(relation="free")),
            adjust = 1.5,
            pch = "|",
            layout = c(4, 2),
            auto.key = list(columns = 4),
            par.settings = list(strip.background=list(col="lightgrey"),
            superpose.line = list(col = c("darkblue","darkred")),
            superpose.symbol = list(col = c("darkblue","darkred")) ))
```




```
featurePlot(x = train[, 1:8], # Boxplots
            y = train$diabetes,
            plot = "box",
            scales = list(y = list(relation="free"), x = list(rot = 90)),
            layout = c(4,2 ),
            auto.key = list(columns = 4),
            par.settings = list(strip.background=list(col="lightgrey")))
```



Funções auxiliares

```
library(dplyr)
library(ggraph)
library(igraph)
```

```
plotaroc <- function(rocobj, titulo = "Curva ROC"){
  # Função que plota as curvas roc para os modelos ajustados
  b <- which.max(rocobj$sensitivities + rocobj$specificities)
  best <- round(c(rocobj$thresholds[b],rocobj$specificities[b],rocobj$sensitivities[b]), 3)

  pROC::ggroc(rocobj, col = "red", alpha = 0.5, size = 0.5) +
    theme_gray() +
    ggtitle(titulo) +
    geom_abline(intercept = 1, slope=1, linetype = "dashed") +
    labs(x="Especificidade", y = "Sensibilidade")  +
    geom_point(data = tibble(Sensibilidade = best[2],
                             Especificidade = best[3]),
               mapping = aes(x=Sensibilidade, y=Especificidade),
               col = "black") +
    geom_text(mapping =  aes(x = best[2] - 0.15,
                             y = best[3] - 0.05),
              label = paste( best[1], "(", best[2], ",", best[3], ")")) +
    geom_text(mapping = aes(x = 0.5,
                            y = 0.01),
              label = paste("AUC: ", round(rocobj$auc,3)))
```

```
}

tree_func <- function(final_model,
                      tree_num) {

  # get tree by index
  tree <- randomForest::getTree(final_model,
                                k = tree_num,
                                labelVar = TRUE) %>%
    tibble::rownames_to_column() %>%
    # make leaf split points to NA, so the 0s won't get plotted
    mutate(`split point` = ifelse(is.na(prediction), `split point`, NA))

  # prepare data frame for graph
  graph_frame <- data.frame(from = rep(tree$rowname, 2),
                            to = c(tree$`left daughter`, tree$`right daughter`))

  # convert to graph and delete the last node that we don't want to plot
  graph <- graph_from_data_frame(graph_frame) %>%
    delete_vertices("0")

  # set node labels
  V(graph)$node_label <- gsub("_", " ", as.character(tree$`split var`))
  V(graph)$leaf_label <- as.character(tree$prediction)
  V(graph)$split <- as.character(round(tree$`split point`, digits = 2))

  # plot
  plot <- ggraph(graph, 'dendrogram') +
    theme_bw() +
    geom_edge_link() +
    geom_node_point() +
    geom_node_text(aes(label = node_label), na.rm = TRUE, repel = TRUE) +
    geom_node_label(aes(label = split), vjust = 2, na.rm = TRUE, fill = "white") +
    geom_node_label(aes(label = leaf_label, fill = leaf_label), na.rm = TRUE,
                    repel = TRUE, colour = "white", fontface = "bold", show.legend = FALSE) +
    theme(panel.grid.minor = element_blank(),
          panel.grid.major = element_blank(),
          panel.background = element_blank(),
          plot.background = element_rect(fill = "white"),
          panel.border = element_blank(),
          axis.line = element_blank(),
          axis.text.x = element_blank(),
          axis.text.y = element_blank(),
          axis.ticks = element_blank(),
          axis.title.x = element_blank(),
          axis.title.y = element_blank(),
          plot.title = element_text(size = 14))

  return(plot)
}
```

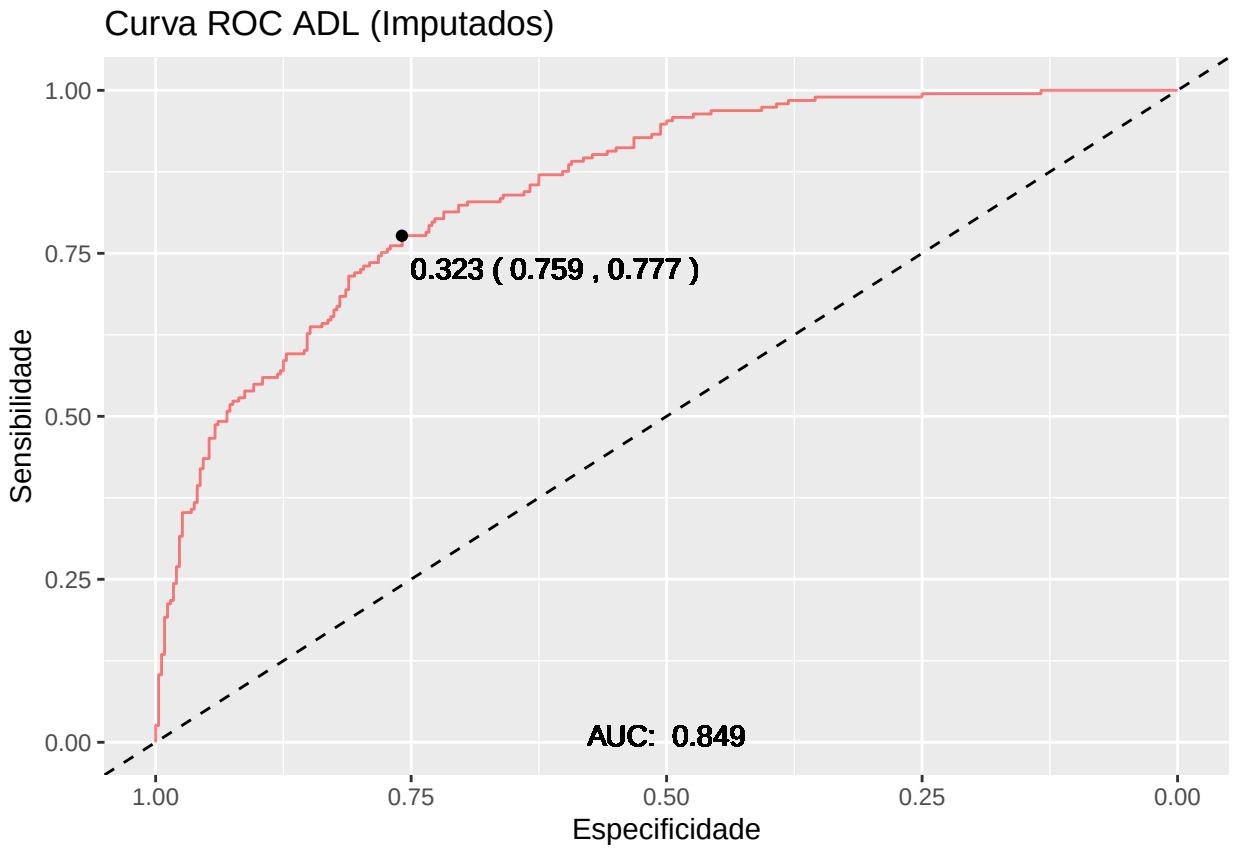
Análise Discriminante

Modelagem

```
# Obs: possibilidades de modelos de AD: rda, lda, pda (acurácias iguais) e qda (pior)

train.control <- caret::trainControl(method = "cv", number = 15, classProbs =  TRUE) # Cross-validation

## ADL com dados imputados
set.seed(23)
modeloAD1 <- caret::train(diabetes ~ ., data = train, trControl = train.control, method = "lda")
print(modeloAD1)
```

```
## Linear Discriminant Analysis
##
## 537 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (15 fold)
## Summary of sample sizes: 501, 501, 501, 501, 501, 501, ...
## Resampling results:
##
##   Accuracy   Kappa
##   0.7636508  0.4650271
```

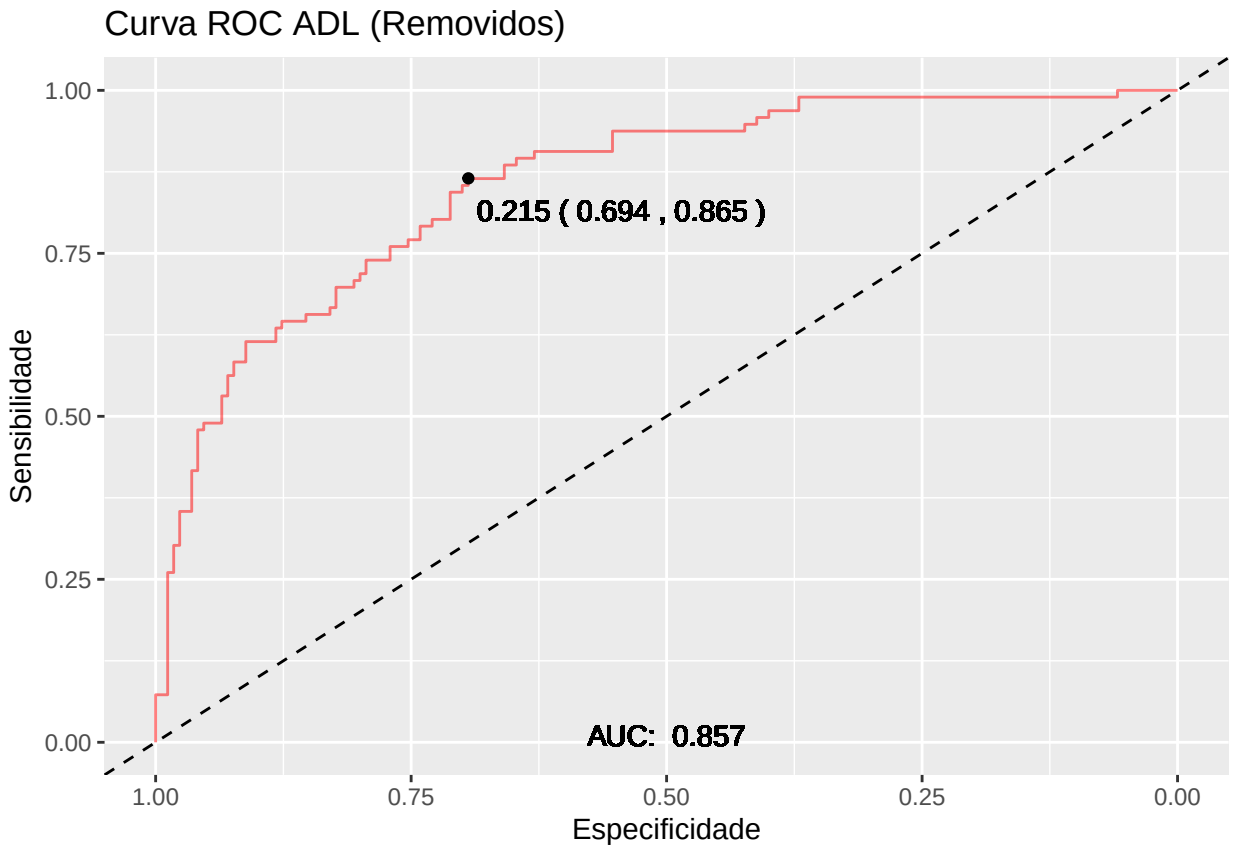
```
rocAD1 <- roc(response = train$diabetes, predictor = predict(modeloAD1, train, type = "prob")[,2])
plotaroc(rocAD1, titulo = "Curva ROC ADL (Imputados)")
```




```
## ADL sem missing
set.seed(23)
modeloAD2 <- caret::train(diabetes ~ ., data = train_without_NAs, trControl = train.control, method = "
print(modeloAD2)
```

```
## Linear Discriminant Analysis
##
## 266 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (15 fold)
## Summary of sample sizes: 248, 248, 249, 248, 247, 249, ...
## Resampling results:
##
##   Accuracy   Kappa
##   0.7784199  0.5053595
```

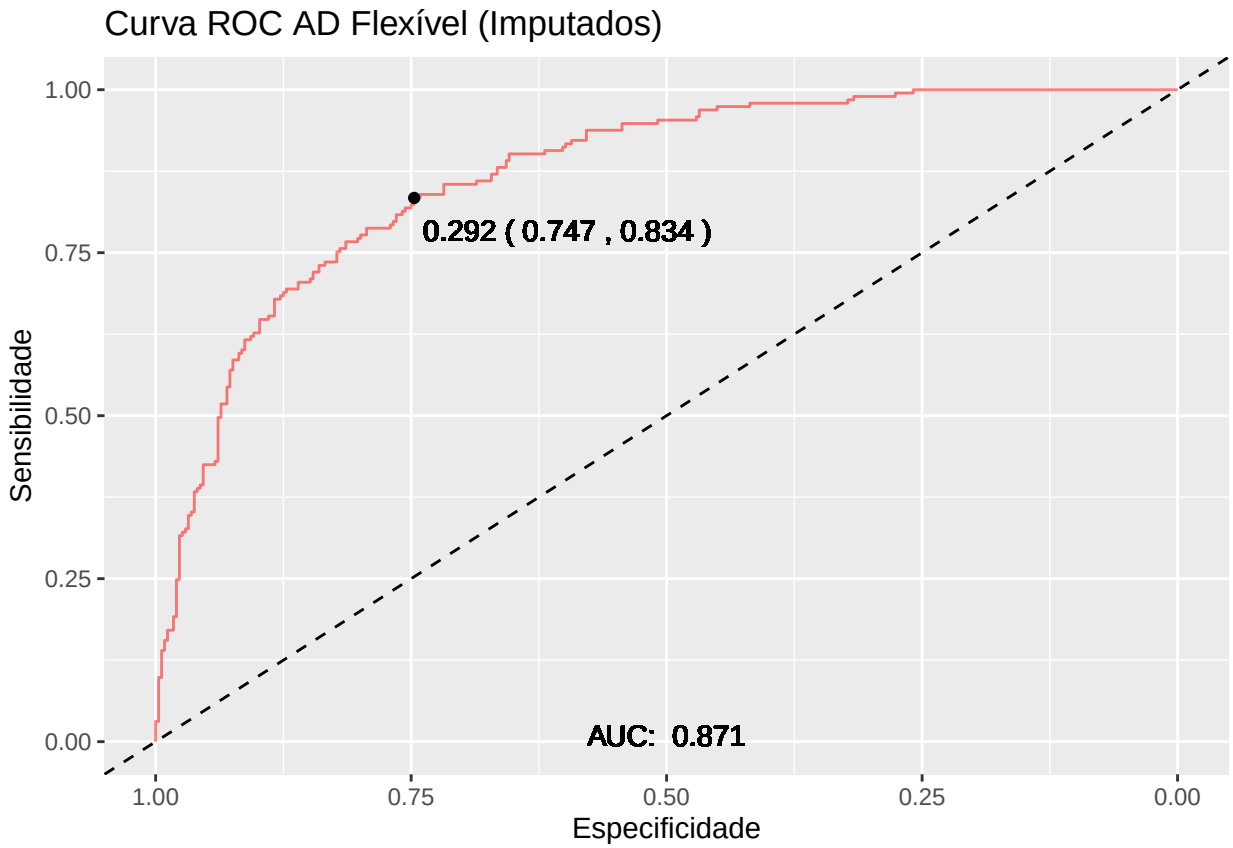
```
rocAD2 <- roc(response = train_without_NAs$diabetes, predictor = predict(modeloAD2, train_without_NAs, 
plotaroc(rocAD2, titulo = "Curva ROC ADL (Removidos)")
```




```
## AD Flexível com dados imputados
set.seed(23)
modeloAD3 <- caret::train(diabetes ~ ., data = train, trControl = train.control, method = "fda")
print(modeloAD3)
```

```
## Flexible Discriminant Analysis
##
## 537 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (15 fold)
## Summary of sample sizes: 501, 501, 501, 501, 501, 501, ...
## Resampling results across tuning parameters:
##
##   nprune  Accuracy   Kappa
##    2      0.7450794  0.4129759
##    8      0.7823280  0.5204850
##   15      0.7823280  0.5192155
##
## Tuning parameter 'degree' was held constant at a value of 1
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were degree = 1 and nprune = 8.
```

```r
rocAD3 <- roc(response = train$diabetes, predictor = predict(modeloAD3, train, type = "prob")[,2])
plotaroc(rocAD3, titulo = "Curva ROC AD Flexível (Imputados)")
```

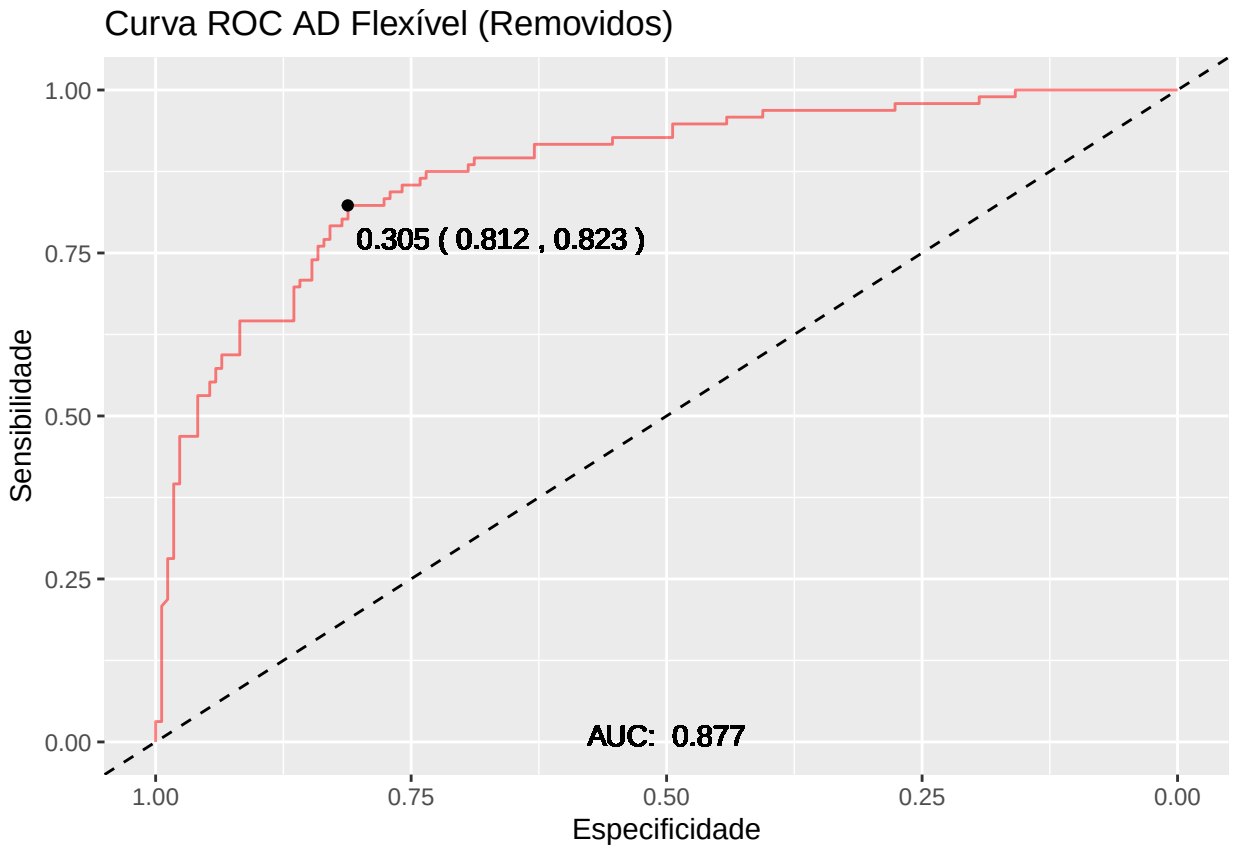



```r
## AD Flexível sem missing
set.seed(23)
modeloAD4 <- caret::train(diabetes ~ ., data = train_without_NAs, trControl = train.control, method = "
print(modeloAD4)
```

```
## Flexible Discriminant Analysis
##
## 266 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (15 fold)
## Summary of sample sizes: 248, 248, 249, 248, 247, 249, ...
## Resampling results across tuning parameters:
##
##   nprune  Accuracy   Kappa
##    2      0.7481137  0.4233678
##    8      0.7516455  0.4422724
##   15      0.7446279  0.4240573
##
```

```
## Tuning parameter 'degree' was held constant at a value of 1
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were degree = 1 and nprune = 8.
```

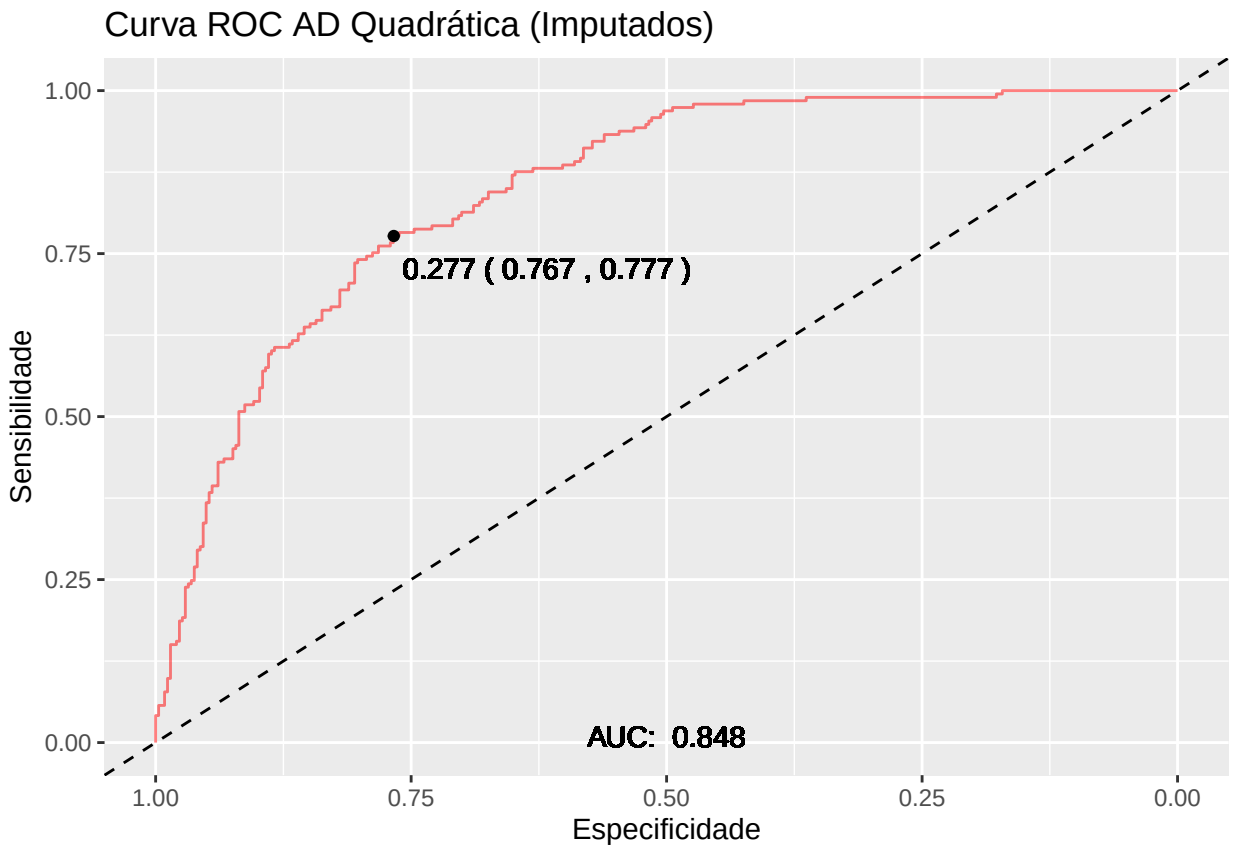
```
rocAD4 <- roc(response = train_without_NAs$diabetes, predictor = predict(modeloAD4, train_without_NAs,
plotaroc(rocAD4, titulo = "Curva ROC AD Flexível (Removidos)")
```




```
## AD Quadrática com dados imputados
set.seed(23)
modeloAD5 <- caret::train(diabetes ~ ., data = train, trControl = train.control, method = "qda")
print(modeloAD5)
```

```
## Quadratic Discriminant Analysis
##
## 537 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (15 fold)
## Summary of sample sizes: 501, 501, 501, 501, 501, 501, ...
## Resampling results:
##
##   Accuracy   Kappa
##   0.7431217  0.4201363
```

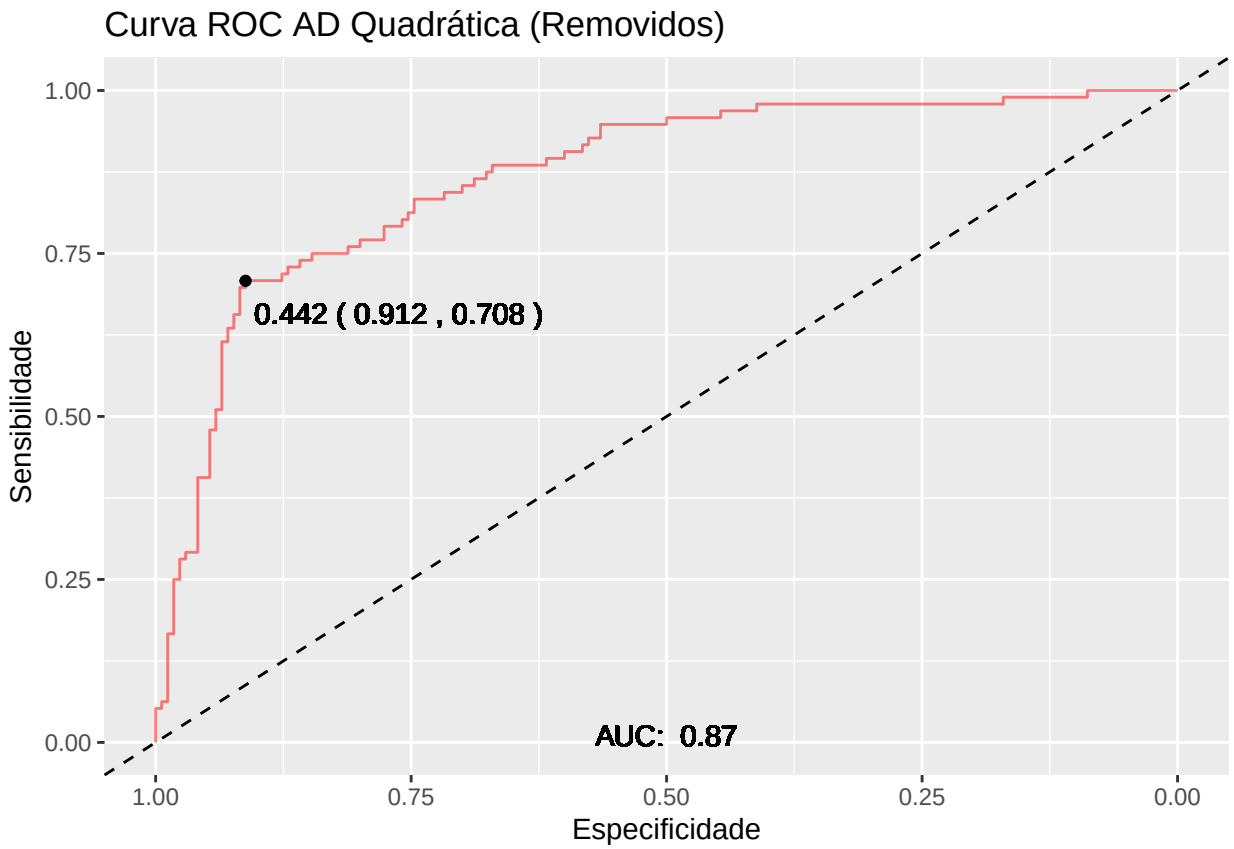
```r
rocAD5 <- roc(response = train$diabetes, predictor = predict(modeloAD5, train, type = "prob")[,2])
plotaroc(rocAD5, titulo = "Curva ROC AD Quadrática (Imputados)")
```




```r
## AD Quadrática sem missing
set.seed(23)
modeloAD6 <- caret::train(diabetes ~ ., data = train_without_NAs, trControl = train.control, method = "
print(modeloAD6)
```

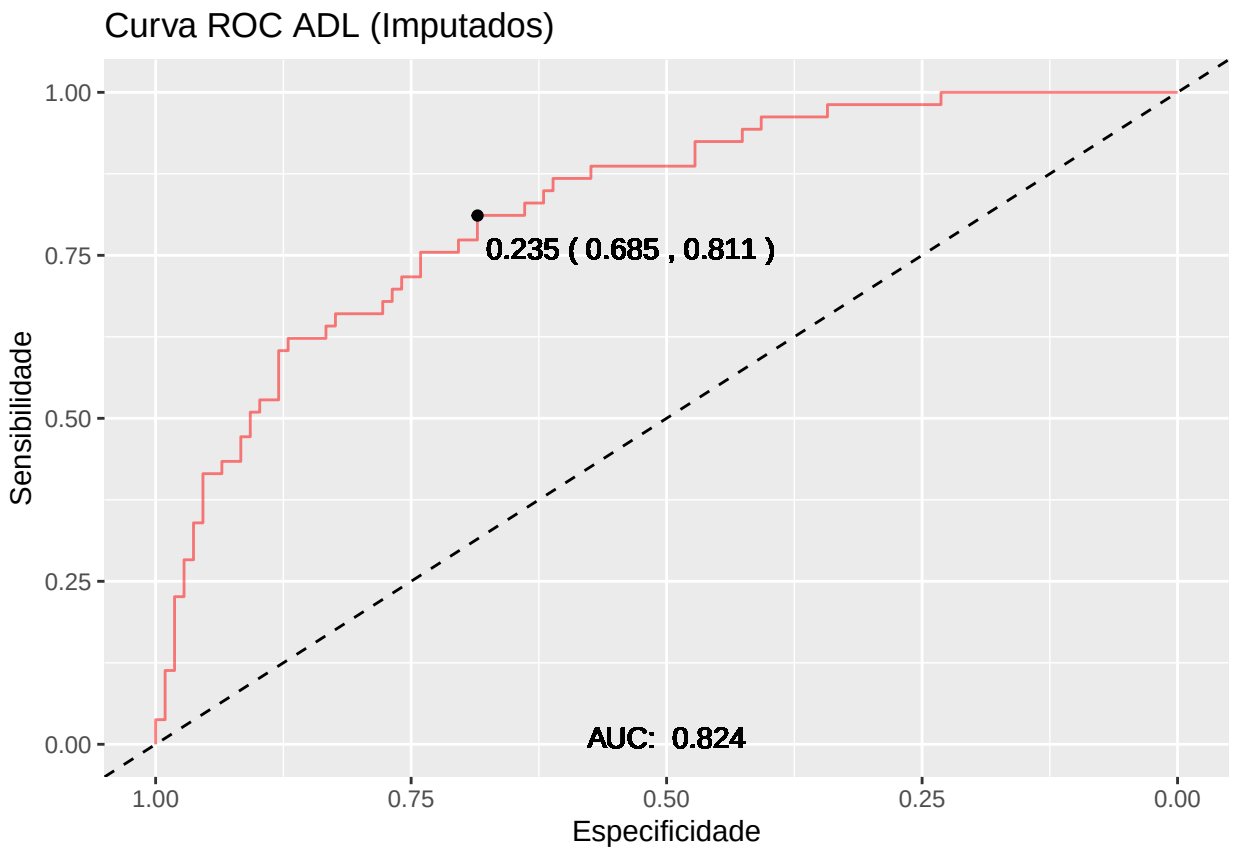
```
## Quadratic Discriminant Analysis
##
## 266 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (15 fold)
## Summary of sample sizes: 248, 248, 249, 248, 247, 249, ...
## Resampling results:
##
##   Accuracy   Kappa
##   0.7860681  0.5158632
```

```
rocAD6 <- roc(response = train_without_NAs$diabetes, predictor = predict(modeloAD6, train_without_NAs,
plotaroc(rocAD6, titulo = "Curva ROC AD Quadrática (Removidos)")
```



Validação

```
## ADL com dados imputados
rocAD1 <- roc(response = validacao$diabetes, predictor = predict(modeloAD1, validacao, type = "prob")[,
plotaroc(rocAD1, titulo = "Curva ROC ADL (Imputados)")
```

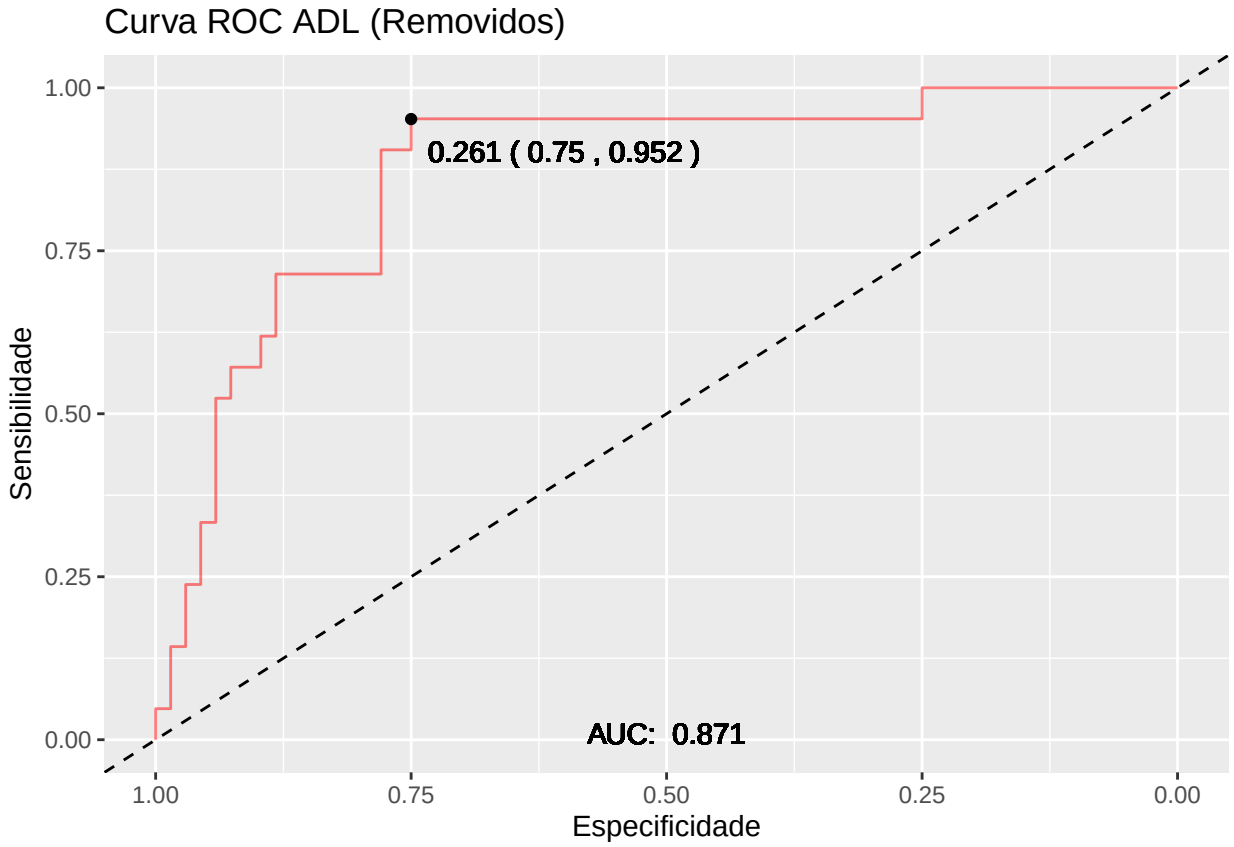



```
predictAD1 <- predict(modeloAD1, newdata = validacao)
confusionMatrix(predictAD1, validacao$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  99  28
##        Yes  9  25
##
##                Accuracy : 0.7702
##                  95% CI : (0.6974, 0.8327)
##     No Information Rate : 0.6708
##     P-Value [Acc > NIR] : 0.003815
##
##                   Kappa : 0.4274
##
##  Mcnemar's Test P-Value : 0.003085
##
##             Sensitivity : 0.9167
##             Specificity : 0.4717
##          Pos Pred Value : 0.7795
##          Neg Pred Value : 0.7353
##              Prevalence : 0.6708
##          Detection Rate : 0.6149
```

```
##    Detection Prevalence : 0.7888
##       Balanced Accuracy : 0.6942
##
##        'Positive' Class : No
##
```

```
## ADL sem missing
rocAD2 <- roc(response = validacao_without_NAs$diabetes, predictor = predict(modeloAD2, validacao_withou
plotaroc(rocAD2, titulo = "Curva ROC ADL (Removidos)")
```

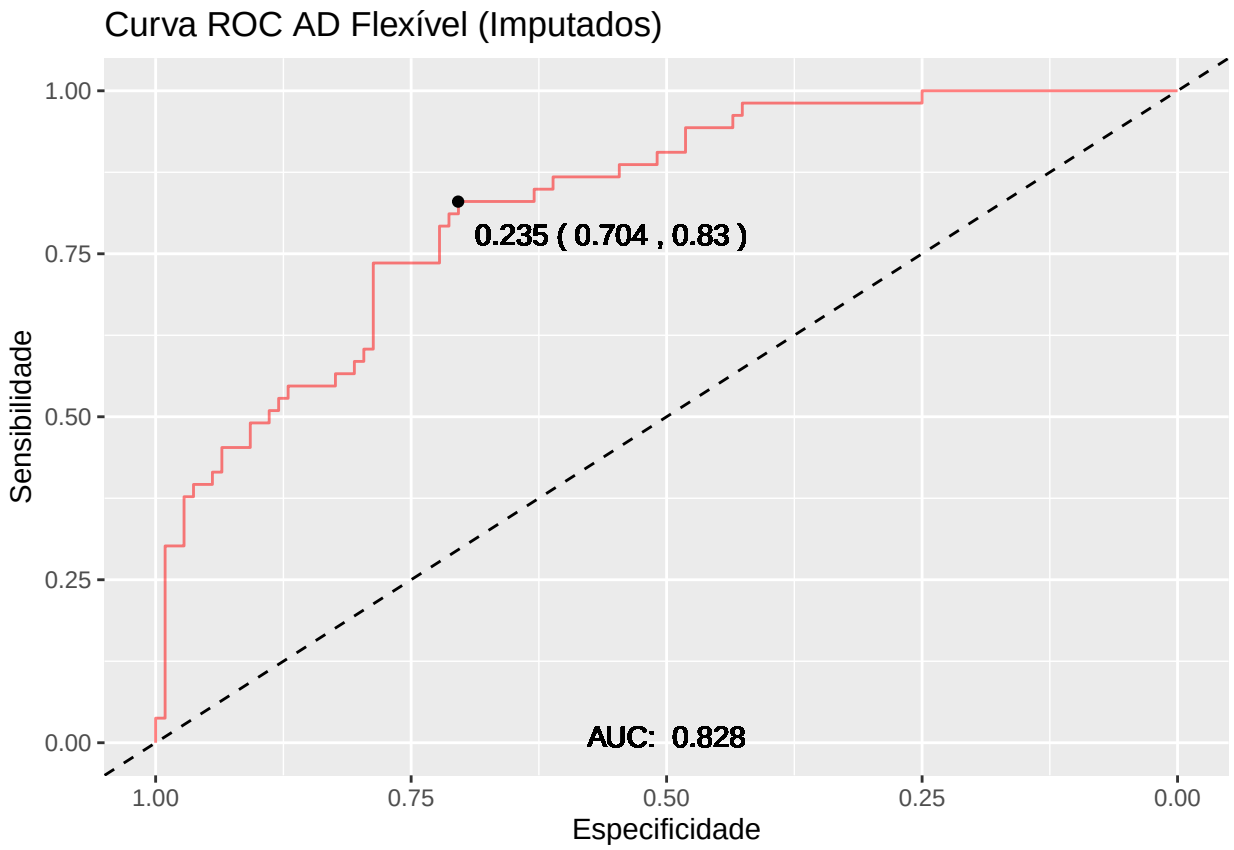



```
predictAD2 <- predict(modeloAD2, newdata = validacao_without_NAs)
confusionMatrix(predictAD2, validacao_without_NAs$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  64  12
##        Yes  4   9
##
##                Accuracy : 0.8202
##                  95% CI : (0.7245, 0.8936)
##     No Information Rate : 0.764
##     P-Value [Acc > NIR] : 0.12910
```

```
##
##                   Kappa : 0.4258
##
##  Mcnemar's Test P-Value : 0.08012
##
##             Sensitivity : 0.9412
##             Specificity : 0.4286
##          Pos Pred Value : 0.8421
##          Neg Pred Value : 0.6923
##              Prevalence : 0.7640
##          Detection Rate : 0.7191
##    Detection Prevalence : 0.8539
##       Balanced Accuracy : 0.6849
##
##        'Positive' Class : No
##
```

```
## ADL Flexível com dados imputados
rocAD3 <- roc(response = validacao$diabetes, predictor = predict(modeloAD3, validacao, type = "prob")[,
plotaroc(rocAD3, titulo = "Curva ROC AD Flexível (Imputados)")
```

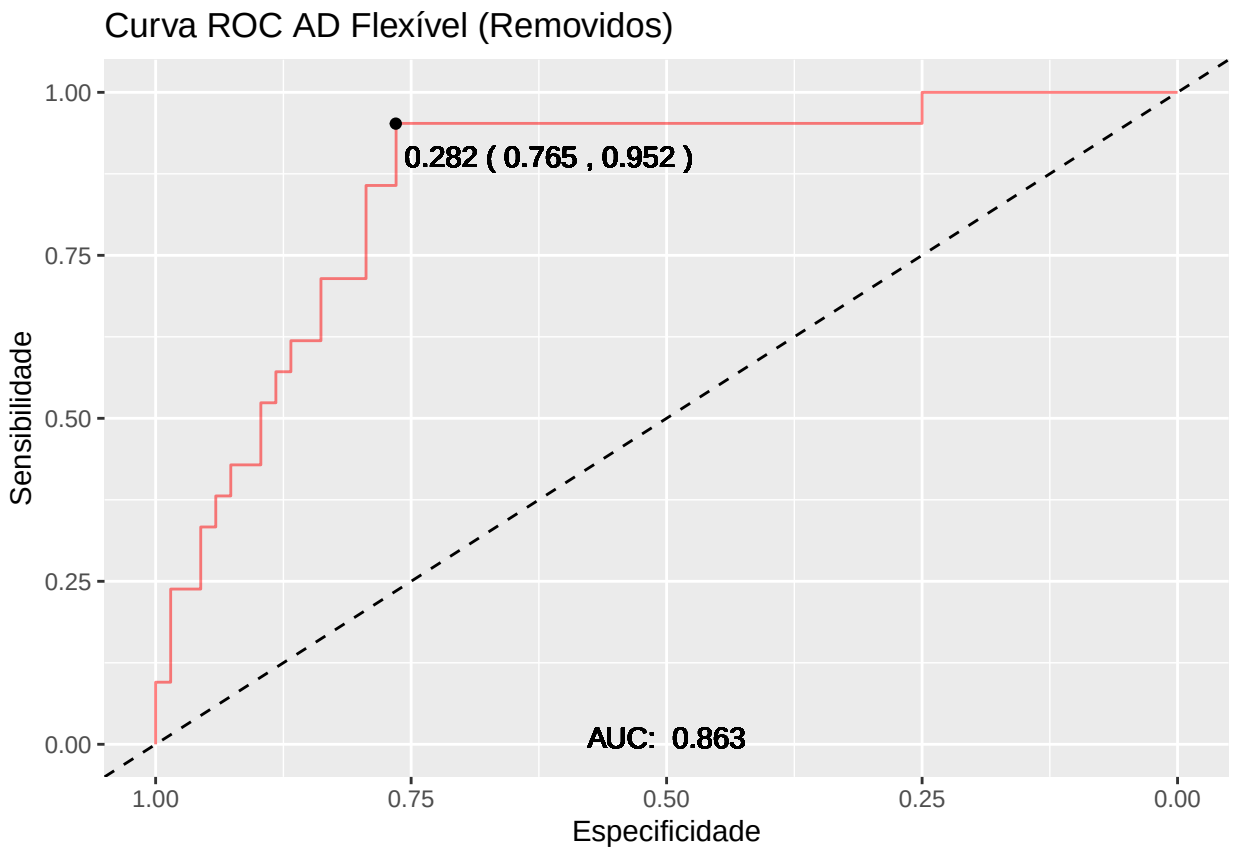



```
predictAD3 <- predict(modeloAD3, newdata = validacao)
confusionMatrix(predictAD3, validacao$diabetes)
```

```
## Confusion Matrix and Statistics
```

```
##
##           Reference
## Prediction No Yes
##        No  95  26
##        Yes 13  27
##
##                Accuracy : 0.7578
##                  95% CI : (0.6841, 0.8217)
##     No Information Rate : 0.6708
##     P-Value [Acc > NIR] : 0.01039
##
##                   Kappa : 0.415
##
##  Mcnemar's Test P-Value : 0.05466
##
##             Sensitivity : 0.8796
##             Specificity : 0.5094
##          Pos Pred Value : 0.7851
##          Neg Pred Value : 0.6750
##              Prevalence : 0.6708
##          Detection Rate : 0.5901
##    Detection Prevalence : 0.7516
##       Balanced Accuracy : 0.6945
##
##        'Positive' Class : No
##
```

```
## ADL Flexível sem missing
rocAD4 <- roc(response = validacao_without_NAs$diabetes, predictor = predict(modeloAD4, validacao_withou
plotaroc(rocAD4, titulo = "Curva ROC AD Flexível (Removidos)")
```

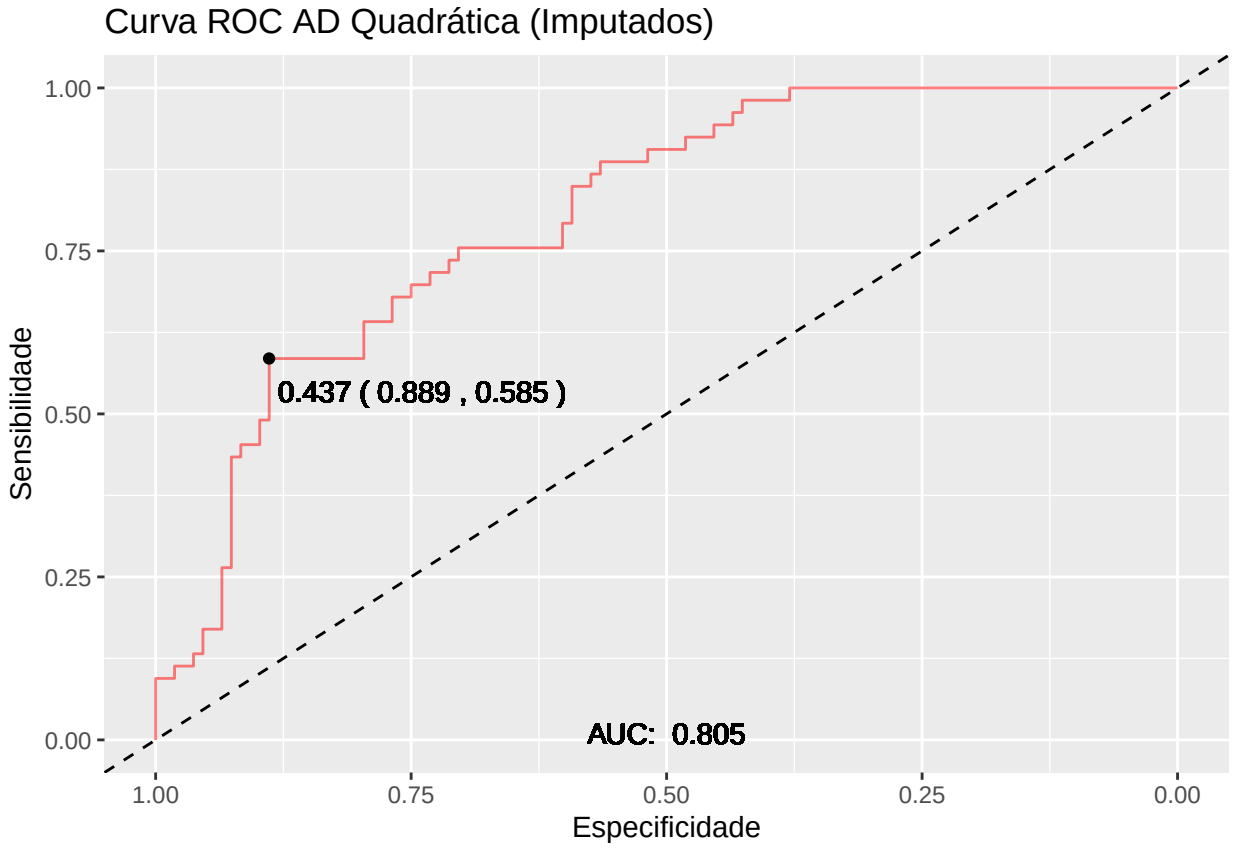



```
predictAD4 <- predict(modeloAD4, newdata = validacao_without_NAs)
confusionMatrix(predictAD4, validacao_without_NAs$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  61  11
##        Yes  7  10
##
##                Accuracy : 0.7978
##                  95% CI : (0.6993, 0.8755)
##     No Information Rate : 0.764
##     P-Value [Acc > NIR] : 0.2709
##
##                   Kappa : 0.3996
##
##  Mcnemar's Test P-Value : 0.4795
##
##             Sensitivity : 0.8971
##             Specificity : 0.4762
##          Pos Pred Value : 0.8472
##          Neg Pred Value : 0.5882
##              Prevalence : 0.7640
##          Detection Rate : 0.6854
```

```
##    Detection Prevalence : 0.8090
##       Balanced Accuracy : 0.6866
##
##        'Positive' Class : No
##
```

```
## AD Quadrática com dados imputados
rocAD5 <- roc(response = validacao$diabetes, predictor = predict(modeloAD5, validacao, type = "prob")[,1
plotaroc(rocAD5, titulo = "Curva ROC AD Quadrática (Imputados)")
```

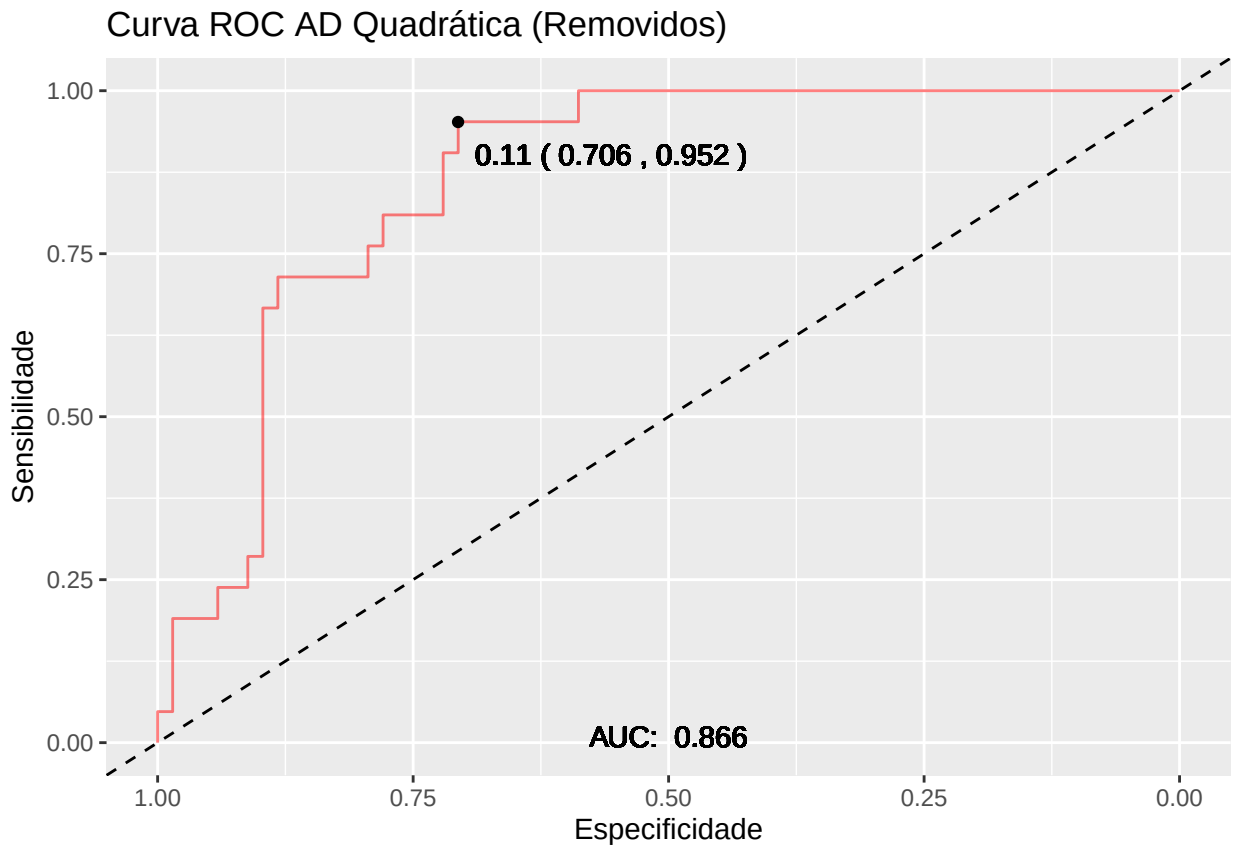



```
predictAD5 <- predict(modeloAD5, newdata = validacao)
confusionMatrix(predictAD5, validacao$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  96  25
##        Yes 12  28
##
##                Accuracy : 0.7702
##                  95% CI : (0.6974, 0.8327)
##     No Information Rate : 0.6708
##     P-Value [Acc > NIR] : 0.003815
```

```
##
##                   Kappa : 0.445
##
##  Mcnemar's Test P-Value : 0.048520
##
##             Sensitivity : 0.8889
##             Specificity : 0.5283
##          Pos Pred Value : 0.7934
##          Neg Pred Value : 0.7000
##              Prevalence : 0.6708
##          Detection Rate : 0.5963
##    Detection Prevalence : 0.7516
##       Balanced Accuracy : 0.7086
##
##        'Positive' Class : No
##
```

```
## AD Quadrática sem missing
rocAD6 <- roc(response = validacao_without_NAs$diabetes, predictor = predict(modeloAD6, validacao_withou
plotaroc(rocAD6, titulo = "Curva ROC AD Quadrática (Removidos)")
```




```
predictAD6 <- predict(modeloAD6, newdata = validacao_without_NAs)
confusionMatrix(predictAD6, validacao_without_NAs$diabetes)
```

```
## Confusion Matrix and Statistics
```

```
##
##           Reference
## Prediction No Yes
##        No  60   6
##        Yes  8  15
##
##                Accuracy : 0.8427
##                  95% CI : (0.7502, 0.9112)
##     No Information Rate : 0.764
##     P-Value [Acc > NIR] : 0.04778
##
##                   Kappa : 0.5776
##
##  Mcnemar's Test P-Value : 0.78927
##
##             Sensitivity : 0.8824
##             Specificity : 0.7143
##          Pos Pred Value : 0.9091
##          Neg Pred Value : 0.6522
##              Prevalence : 0.7640
##          Detection Rate : 0.6742
##    Detection Prevalence : 0.7416
##       Balanced Accuracy : 0.7983
##
##        'Positive' Class : No
##
```

Regressão Logística

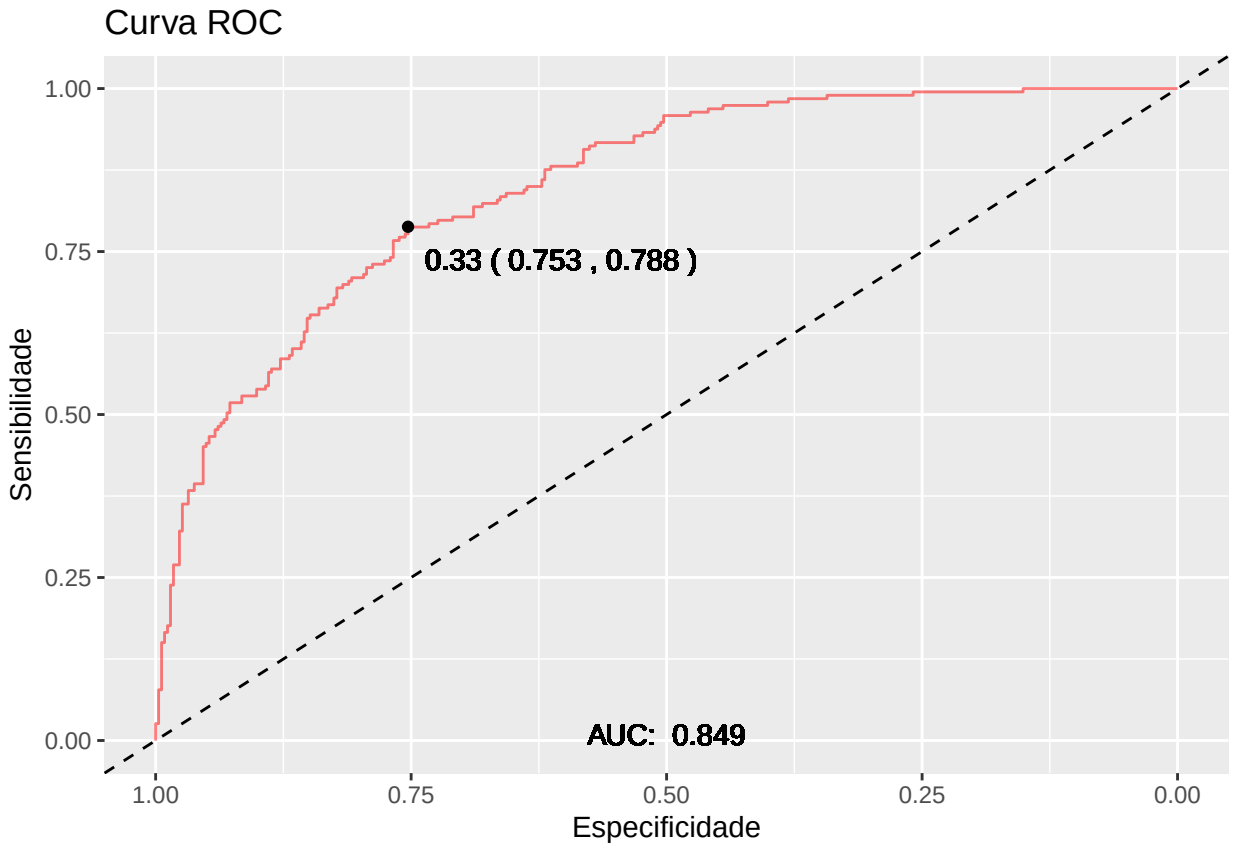
Modelagem

```
library(caret)

train.control <- caret::trainControl(method = "cv", number = 10) # Cross-validation com k=10

## Logística simples com ligação logit / dados imputados
set.seed(23)
modeloRL1 <- caret::train(diabetes ~ ., data = train, trControl = train.control, method = "glm", family=
print(modeloRL1)
```

```
## Generalized Linear Model
##
## 537 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 483, 483, 484, 483, 482, 484, ...
```

```
## Resampling results:
##
##   Accuracy   Kappa
##   0.7595623  0.4586088
```

```
rocRL1 <- roc(response = train$diabetes, predictor = predict(modeloRL1, train, type = "prob")[,2])
plotaroc(rocRL1)
```

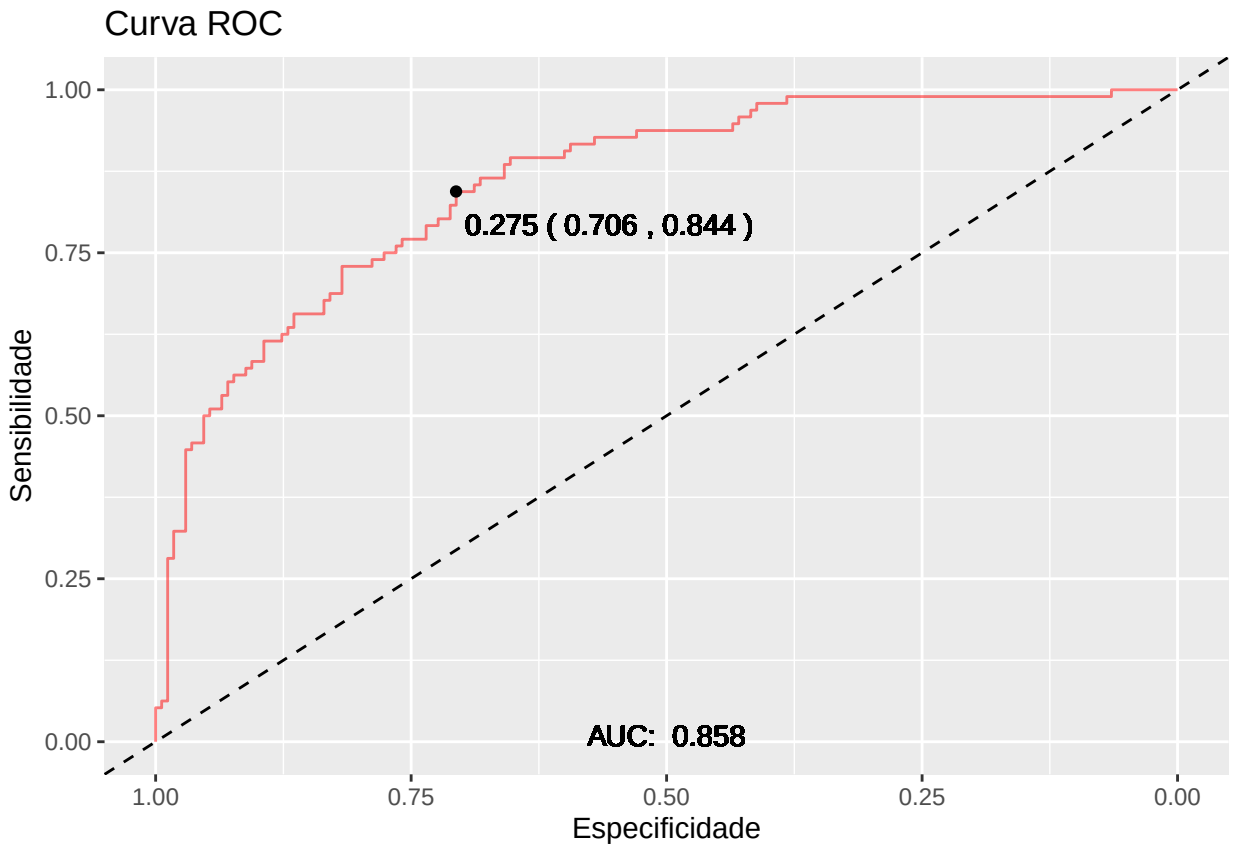



```
## Logística simples com ligação logit / dados sem missing
set.seed(23)
modeloRL2 <- caret::train(diabetes ~ ., data = train_without_NAs, trControl = train.control, method = "
print(modeloRL2)
```

```
## Generalized Linear Model
##
## 266 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 240, 240, 239, 239, 239, 239, ...
## Resampling results:
##
```

```
##   Accuracy   Kappa
##   0.7673789  0.4828079
```

```
rocRL2 <- roc(response = train_without_NAs$diabetes, predictor = predict(modeloRL2, train_without_NAs,
plotaroc(rocRL2)
```

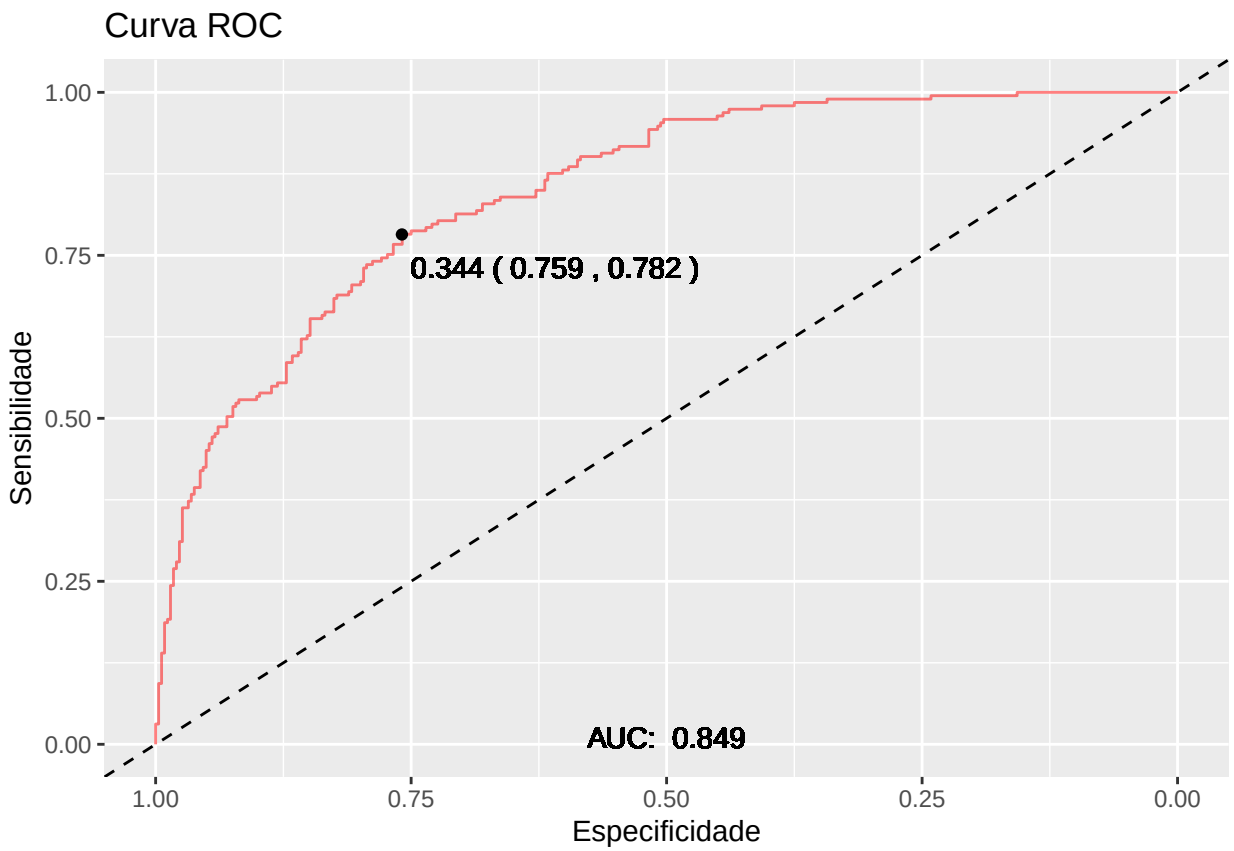



```
## Logística regularizada / dados imputados
set.seed(23)
modeloRL3 <- caret::train(diabetes ~ ., data = train, trControl = train.control, method = "regLogistic"
print(modeloRL3)
```

```
## Regularized Logistic Regression
##
## 537 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 483, 483, 484, 483, 482, 484, ...
## Resampling results across tuning parameters:
##
##   cost  loss       epsilon  Accuracy   Kappa
##   0.5   L1         0.001    0.7482765  0.4294592
```

```
##   0.5   L1         0.010    0.7426847  0.4156713
##   0.5   L1         0.100    0.7482053  0.4254680
##   0.5   L2_dual    0.001    0.6961737  0.2507155
##   0.5   L2_dual    0.010    0.6813925  0.2298081
##   0.5   L2_dual    0.100    0.6217813  0.1749702
##   0.5   L2_primal  0.001    0.7445715  0.4210244
##   0.5   L2_primal  0.010    0.6998126  0.3193385
##   0.5   L2_primal  0.100    0.6964195  0.3018360
##   1.0   L1         0.001    0.7558236  0.4469887
##   1.0   L1         0.010    0.7539369  0.4431172
##   1.0   L1         0.100    0.7426161  0.4055951
##   1.0   L2_dual    0.001    0.6039839  0.1296527
##   1.0   L2_dual    0.010    0.6144038  0.2065002
##   1.0   L2_dual    0.100    0.6311416  0.1155712
##   1.0   L2_primal  0.001    0.7464583  0.4229977
##   1.0   L2_primal  0.010    0.6998126  0.3193385
##   1.0   L2_primal  0.100    0.6964195  0.3018360
##   2.0   L1         0.001    0.7595623  0.4554919
##   2.0   L1         0.010    0.7558236  0.4468964
##   2.0   L1         0.100    0.7538670  0.4388071
##   2.0   L2_dual    0.001    0.6149863  0.1897020
##   2.0   L2_dual    0.010    0.5702999  0.1900379
##   2.0   L2_dual    0.100    0.5902649  0.1230814
##   2.0   L2_primal  0.001    0.7500934  0.4318992
##   2.0   L2_primal  0.010    0.7070802  0.3426133
##   2.0   L2_primal  0.100    0.6964195  0.3018360
##
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were cost = 2, loss = L1 and epsilon
##  = 0.001.
```

```
rocRL3 <- roc(response = train$diabetes, predictor = predict(modeloRL3, train, type = "prob")[,2])
plotaroc(rocRL3)
```

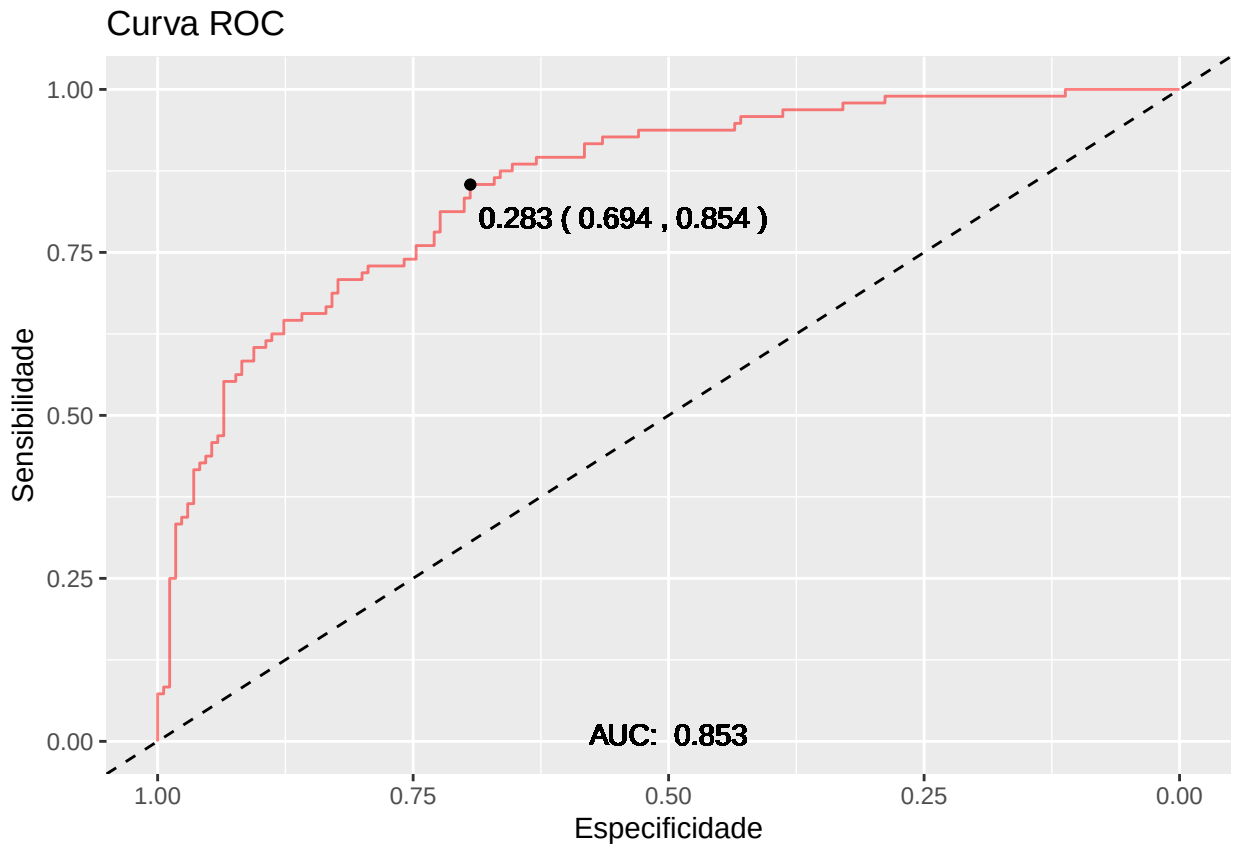



```
## Logística regularizada / dados sem missing
set.seed(23)
modeloRL4 <- caret::train(diabetes ~ ., data = train_without_NAs, trControl = train.control, method = "
print(modeloRL4)
```

```
## Regularized Logistic Regression
##
## 266 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 240, 240, 239, 239, 239, 239, ...
## Resampling results across tuning parameters:
##
##   cost  loss       epsilon  Accuracy   Kappa
##   0.5   L1         0.001    0.7598291  0.4596795
##   0.5   L1         0.010    0.7636752  0.4669602
##   0.5   L1         0.100    0.7488604  0.4299137
##   0.5   L2_dual    0.001    0.6394587  0.1554546
##   0.5   L2_dual    0.010    0.6065527  0.1369186
##   0.5   L2_dual    0.100    0.6501425  0.1759711
##   0.5   L2_primal  0.001    0.7263533  0.3848223
##   0.5   L2_primal  0.010    0.7149573  0.3616567
```

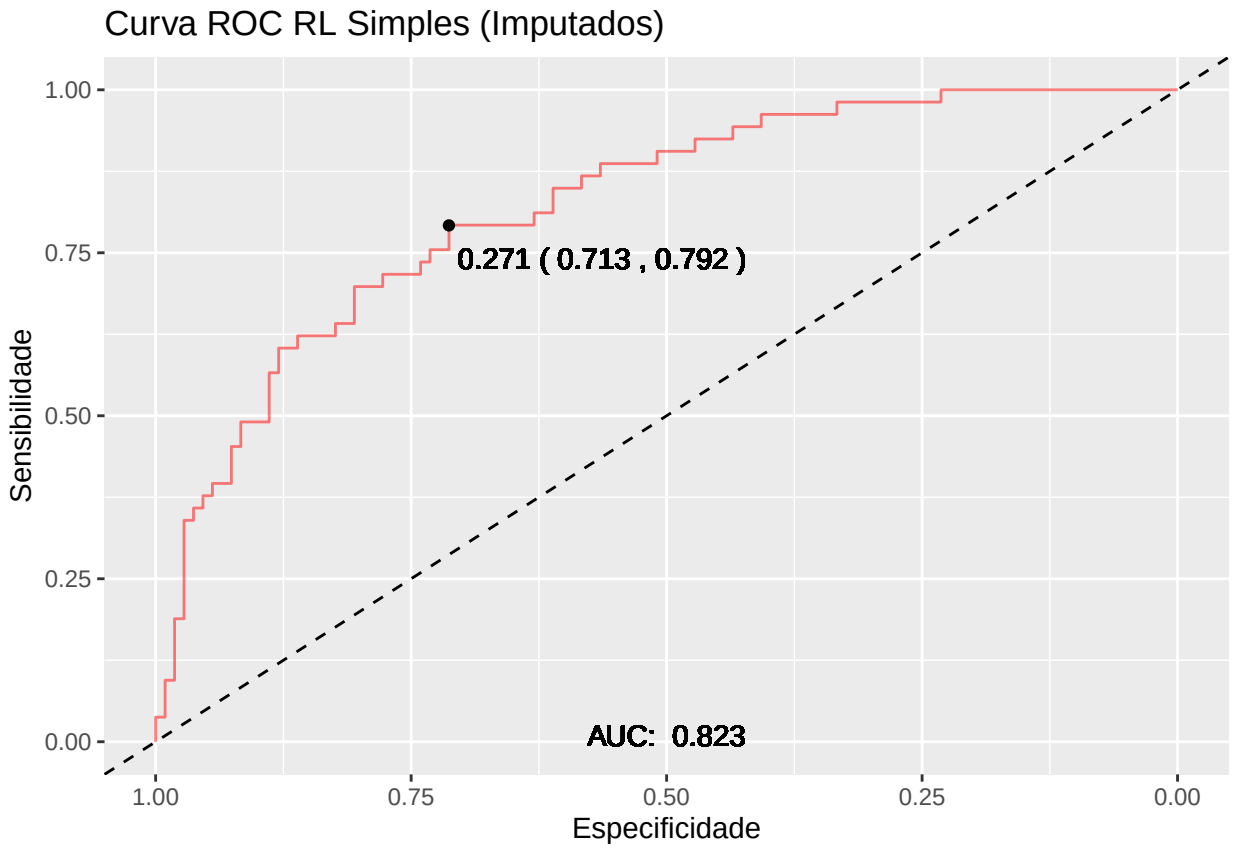
```
##   0.5   L2_primal  0.100    0.6807692  0.2740010
##   1.0   L1         0.001    0.7709402  0.4834174
##   1.0   L1         0.010    0.7747863  0.4903988
##   1.0   L1         0.100    0.7522792  0.4352616
##   1.0   L2_dual    0.001    0.6249288  0.1842344
##   1.0   L2_dual    0.010    0.5915954  0.1786622
##   1.0   L2_dual    0.100    0.6173789  0.1770171
##   1.0   L2_primal  0.001    0.7565527  0.4527102
##   1.0   L2_primal  0.010    0.7339031  0.4037206
##   1.0   L2_primal  0.100    0.6807692  0.2740010
##   2.0   L1         0.001    0.7710826  0.4902196
##   2.0   L1         0.010    0.7747863  0.4970394
##   2.0   L1         0.100    0.7712251  0.4816945
##   2.0   L2_dual    0.001    0.5992877  0.1660801
##   2.0   L2_dual    0.010    0.6019943  0.2116899
##   2.0   L2_dual    0.100    0.6427350  0.1862283
##   2.0   L2_primal  0.001    0.7601140  0.4623563
##   2.0   L2_primal  0.010    0.7487179  0.4343284
##   2.0   L2_primal  0.100    0.6807692  0.2740010
##
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were cost = 1, loss = L1 and epsilon = 0.01.
```

```
rocRL4 <- roc(response = train_without_NAs$diabetes, predictor = predict(modeloRL4, train_without_NAs,
plotaroc(rocRL4)
```



Validação

```
## Regressão Logística Simples com dados imputados
rocRL1 <- roc(response = validacao$diabetes, predictor = predict(modeloRL1, validacao, type = "prob")[,1
plotaroc(rocRL1, titulo = "Curva ROC RL Simples (Imputados)")
```

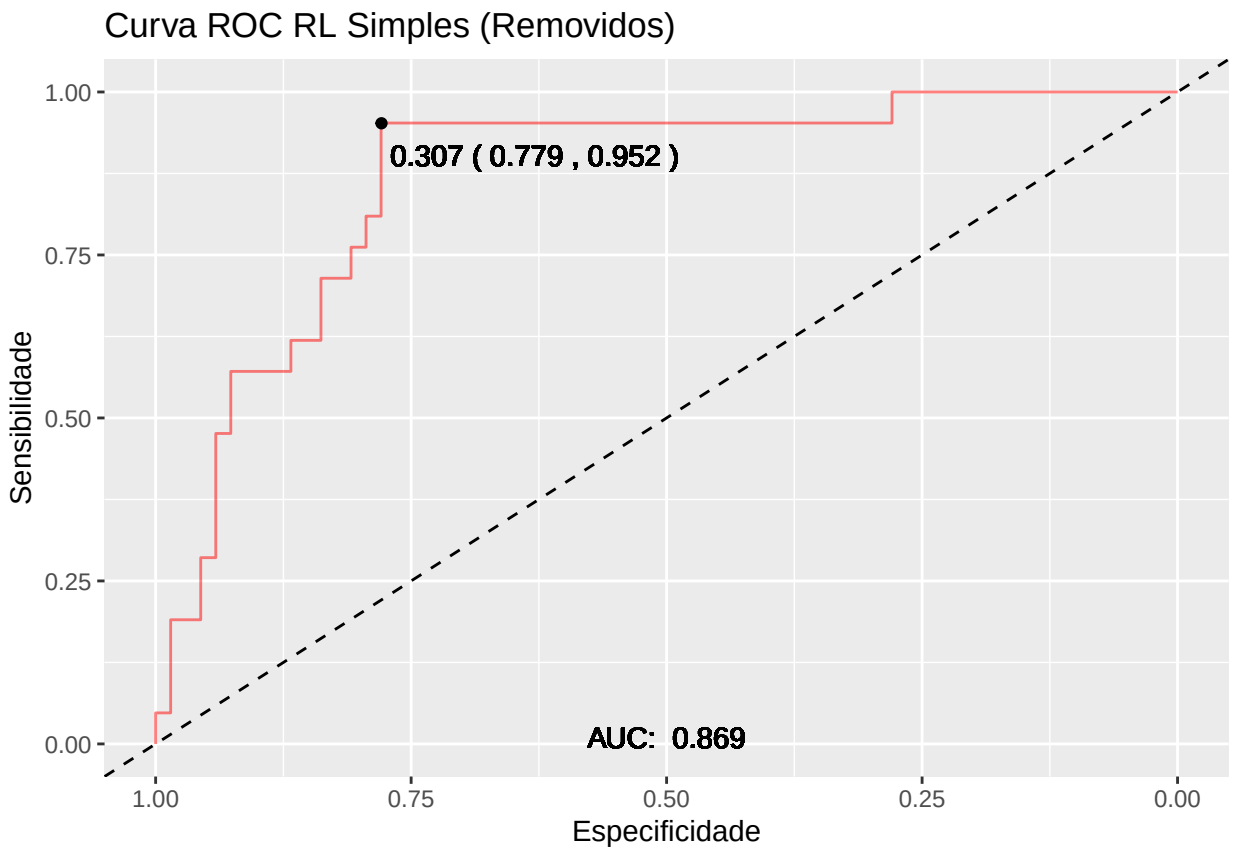



```
predictRL1 <- predict(modeloRL1, newdata = validacao)
confusionMatrix(predictRL1, validacao$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  99  27
##        Yes  9  26
##
##                Accuracy : 0.7764
##                  95% CI : (0.7041, 0.8382)
##     No Information Rate : 0.6708
##     P-Value [Acc > NIR] : 0.002203
##
##                   Kappa : 0.4458
##
```

```
##  Mcnemar's Test P-Value : 0.004607
##
##             Sensitivity : 0.9167
##             Specificity : 0.4906
##          Pos Pred Value : 0.7857
##          Neg Pred Value : 0.7429
##              Prevalence : 0.6708
##          Detection Rate : 0.6149
##    Detection Prevalence : 0.7826
##       Balanced Accuracy : 0.7036
##
##        'Positive' Class : No
##
```

```
## Regressão Logística Simples sem missing
rocRL2 <- roc(response = validacao_without_NAs$diabetes, predictor = predict(modeloRL2, validacao_withou
plotaroc(rocRL2, titulo = "Curva ROC RL Simples (Removidos)")
```

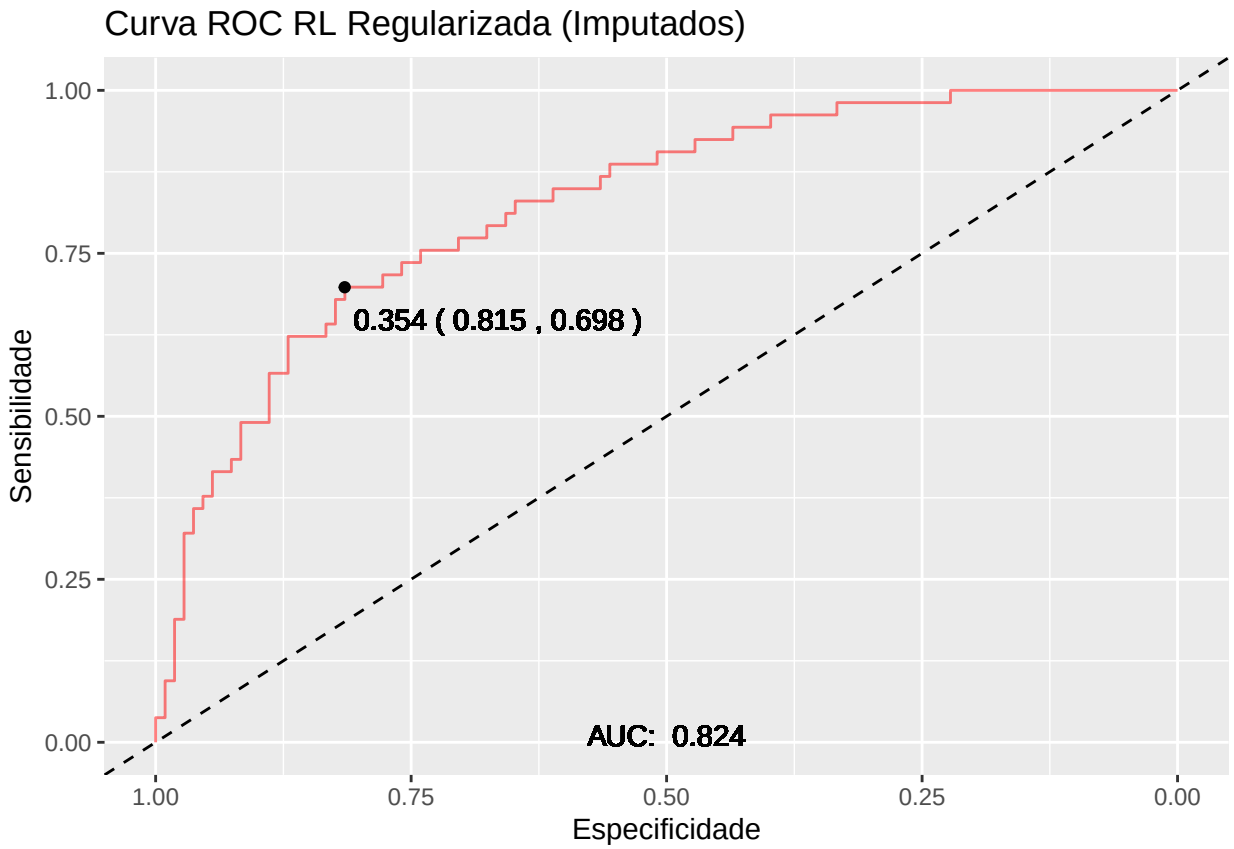



```
predictRL2 <- predict(modeloRL2, newdata = validacao_without_NAs)
confusionMatrix(predictRL2, validacao_without_NAs$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
```

```
## Prediction No Yes
##        No  64  11
##        Yes  4  10
##
##                Accuracy : 0.8315
##                  95% CI : (0.7373, 0.9025)
##     No Information Rate : 0.764
##     P-Value [Acc > NIR] : 0.08127
##
##                   Kappa : 0.4717
##
##  Mcnemar's Test P-Value : 0.12134
##
##             Sensitivity : 0.9412
##             Specificity : 0.4762
##          Pos Pred Value : 0.8533
##          Neg Pred Value : 0.7143
##              Prevalence : 0.7640
##          Detection Rate : 0.7191
##    Detection Prevalence : 0.8427
##       Balanced Accuracy : 0.7087
##
##        'Positive' Class : No
##
```

```
## Regressão Logística Regularizada com dados imputados
rocRL3 <- roc(response = validacao$diabetes, predictor = predict(modeloRL3, validacao, type = "prob")[,1
plotaroc(rocRL3, titulo = "Curva ROC RL Regularizada (Imputados)")
```

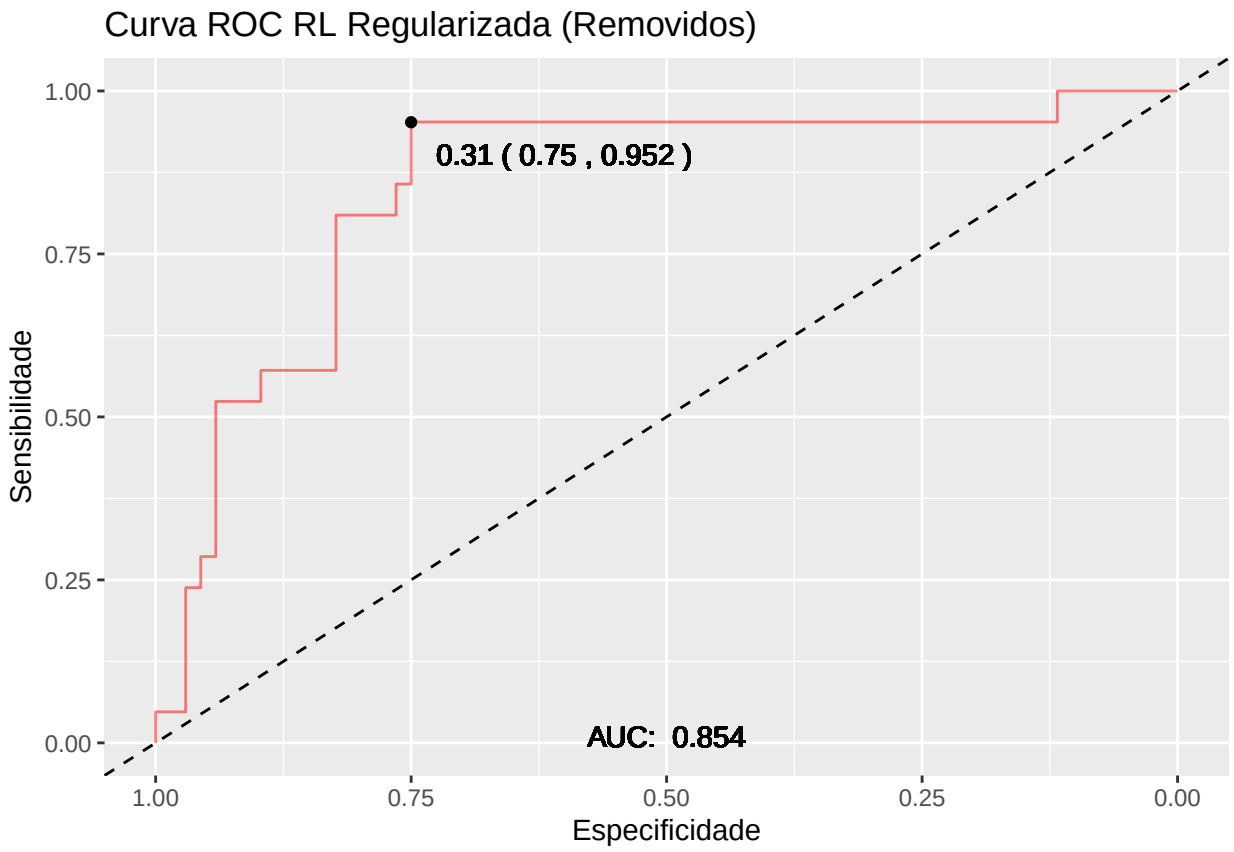



```
predictRL3 <- predict(modeloRL3, newdata = validacao)
confusionMatrix(predictRL3, validacao$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  99  28
##        Yes  9  25
##
##                Accuracy : 0.7702
##                  95% CI : (0.6974, 0.8327)
##     No Information Rate : 0.6708
##     P-Value [Acc > NIR] : 0.003815
##
##                   Kappa : 0.4274
##
##  Mcnemar's Test P-Value : 0.003085
##
##             Sensitivity : 0.9167
##             Specificity : 0.4717
##          Pos Pred Value : 0.7795
##          Neg Pred Value : 0.7353
##              Prevalence : 0.6708
##          Detection Rate : 0.6149
```

```
##    Detection Prevalence : 0.7888
##       Balanced Accuracy : 0.6942
##
##        'Positive' Class : No
##
```

```
## Regressão Logística Regularizada sem missing
rocRL4 <- roc(response = validacao_without_NAs$diabetes, predictor = predict(modeloRL4, validacao_withou
plotaroc(rocRL4, titulo = "Curva ROC RL Regularizada (Removidos)")
```




```
predictRL4 <- predict(modeloRL4, newdata = validacao_without_NAs)
confusionMatrix(predictRL4, validacao_without_NAs$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  64  11
##        Yes  4  10
##
##                Accuracy : 0.8315
##                  95% CI : (0.7373, 0.9025)
##     No Information Rate : 0.764
##     P-Value [Acc > NIR] : 0.08127
```

```
##
##                   Kappa : 0.4717
##
##  Mcnemar's Test P-Value : 0.12134
##
##             Sensitivity : 0.9412
##             Specificity : 0.4762
##          Pos Pred Value : 0.8533
##          Neg Pred Value : 0.7143
##              Prevalence : 0.7640
##          Detection Rate : 0.7191
##    Detection Prevalence : 0.8427
##       Balanced Accuracy : 0.7087
##
##        'Positive' Class : No
##
```

Random Forest

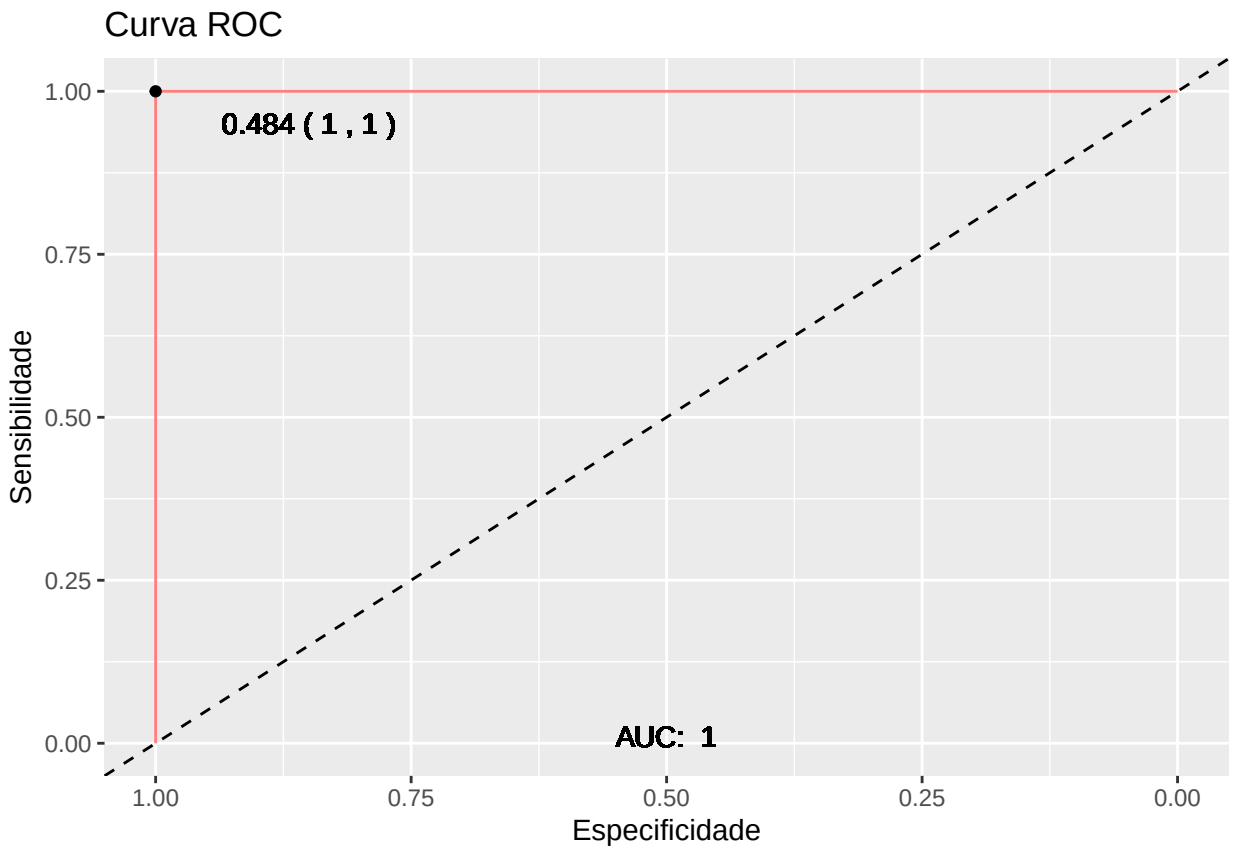
Modelagem

```
library(caret)

train.control <- caret::trainControl(method = "cv", number = 10) # Cross-validation com k=10

## Random Forest / dados imputados
set.seed(23)
tuneGrid <- expand.grid(.mtry = c(1: 10))
modeloRF1 <- train(diabetes~.,
    train,
    method = "rf",
    metric = "Accuracy",
    tuneGrid = tuneGrid,
    trControl = train.control,
    importance = TRUE,
    ntree = 1000)

print(modeloRF1)
```

```
## Random Forest
##
## 537 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 483, 483, 484, 483, 482, 484, ...
## Resampling results across tuning parameters:
```

```
##
##   mtry  Accuracy   Kappa
##    1    0.7506099  0.4361204
##    2    0.7562004  0.4559871
##    3    0.7468001  0.4344252
##    4    0.7486869  0.4382093
##    5    0.7487218  0.4409065
##    6    0.7505387  0.4457852
##    7    0.7523569  0.4506149
##    8    0.7468001  0.4377380
##    9    0.7431300  0.4295050
##   10    0.7487567  0.4392488
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 2.
```

```
rocRF1 <- roc(response = train$diabetes, predictor = predict(modeloRF1, train, type = "prob")[,2])
plotaroc(rocRF1)
```

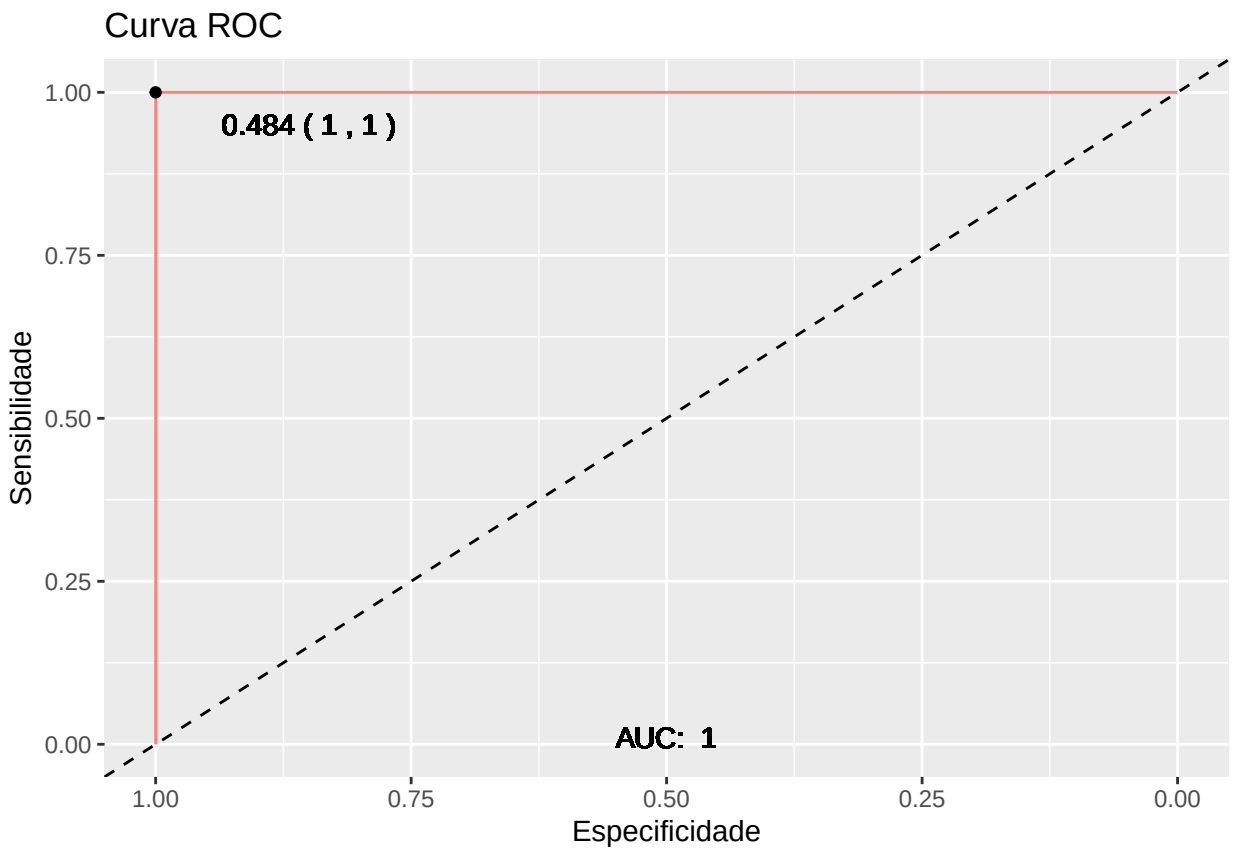



```
## Random Forest / sem missing
set.seed(23)
tuneGrid <- expand.grid(.mtry = c(1: 10))
modeloRF2 <- train(diabetes~.,
    train_without_NAs,
    method = "rf",
```

```
    metric = "Accuracy",
    tuneGrid = tuneGrid,
    trControl = train.control,
    importance = TRUE,
    ntree = 1000)

print(modeloRF2)
```

```
## Random Forest
##
## 266 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 240, 240, 239, 239, 239, 239, ...
## Resampling results across tuning parameters:
##
##   mtry  Accuracy   Kappa
##    1    0.7750712  0.4927747
##    2    0.7787749  0.5063822
##    3    0.7903134  0.5363471
##    4    0.7938746  0.5468630
##    5    0.7826211  0.5182975
##    6    0.7827635  0.5166230
##    7    0.7864672  0.5255357
##    8    0.7827635  0.5201542
##    9    0.7904558  0.5372170
##   10    0.7903134  0.5347168
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 4.
```

```
rocRF2 <- roc(response = train_without_NAs$diabetes, predictor = predict(modeloRF1, train_without_NAs,
plotaroc(rocRF2)
```

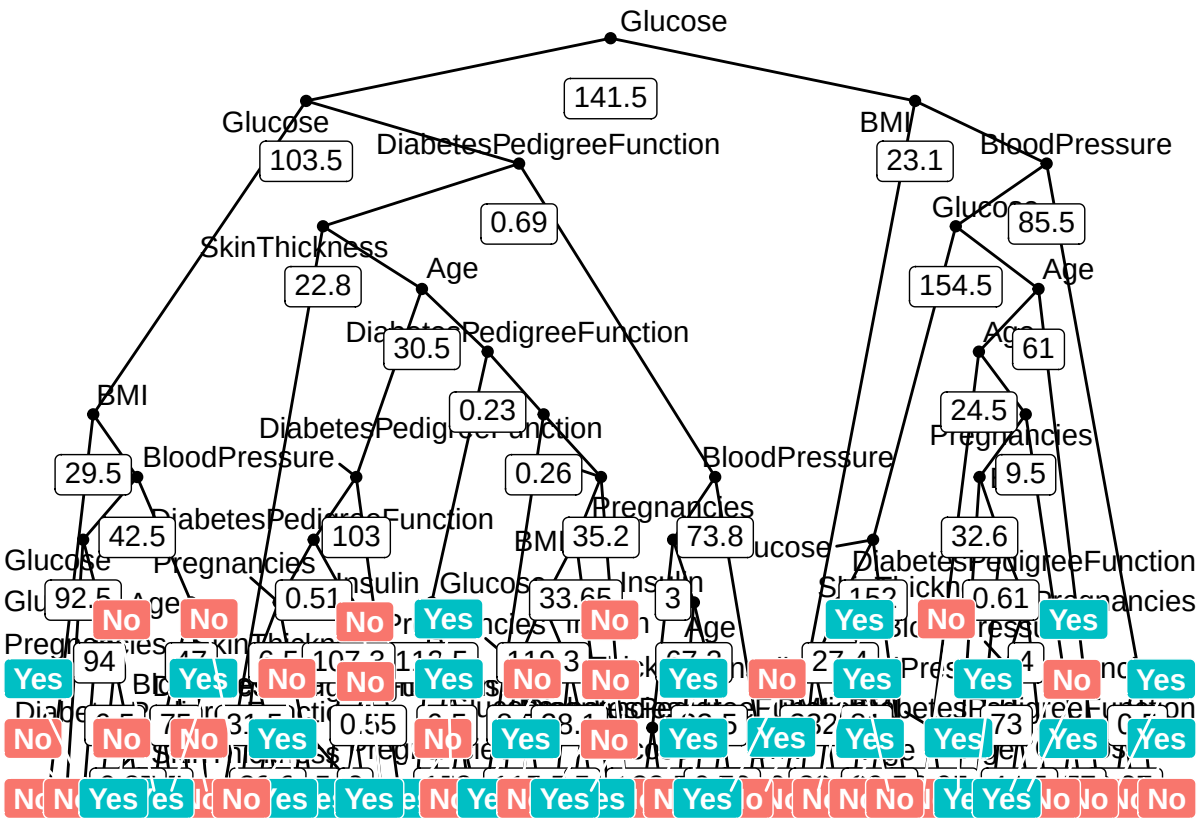


Árvores de decisão geradas

```
tree_num <- which(modeloRF1$finalModel$forest$ndbigtree == min(modeloRF1$finalModel$forest$ndbigtree))
print(paste("Menor árvore com imputação",tree_num))
```

```
## [1] "Menor árvore com imputação 876"
```

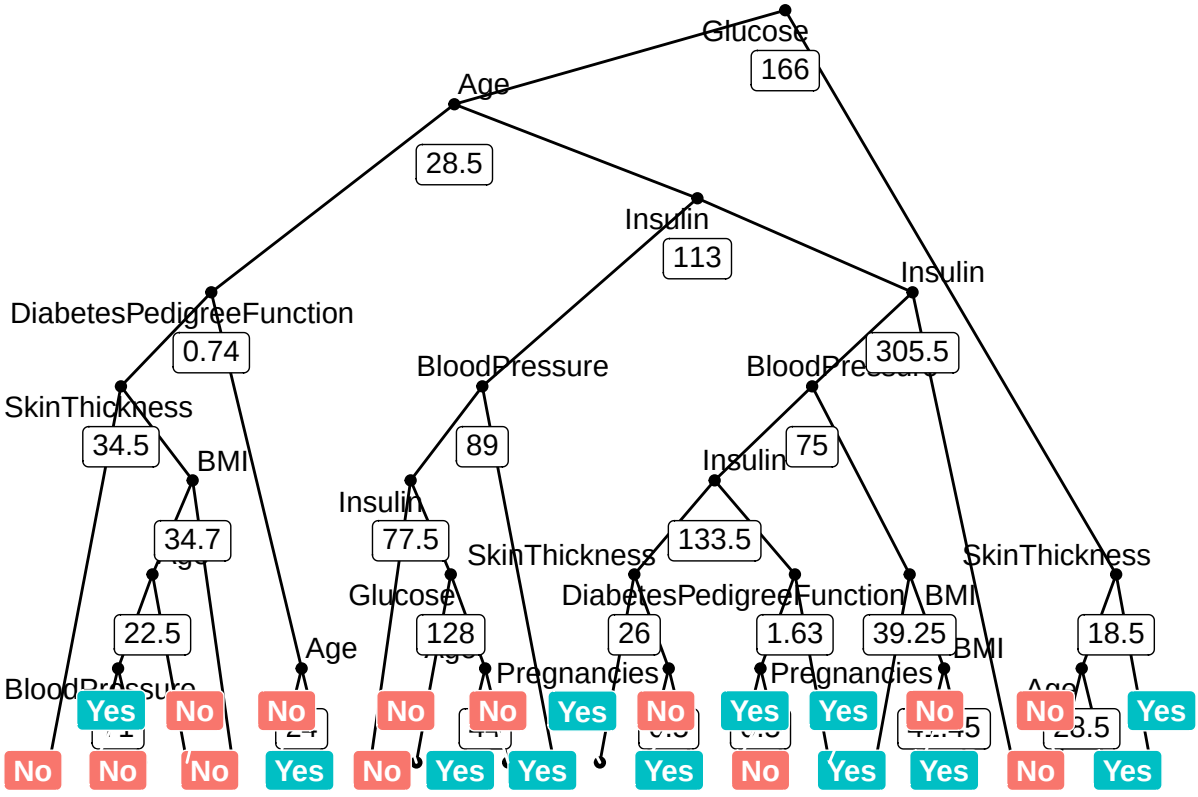
```
tree_func(final_model = modeloRF1$finalModel, tree_num[1])
```




```
tree_num <- which(modeloRF2$finalModel$forest$ndbigtree == min(modeloRF2$finalModel$forest$ndbigtree))
print(paste("Menor árvore sem imputação:",tree_num))
```

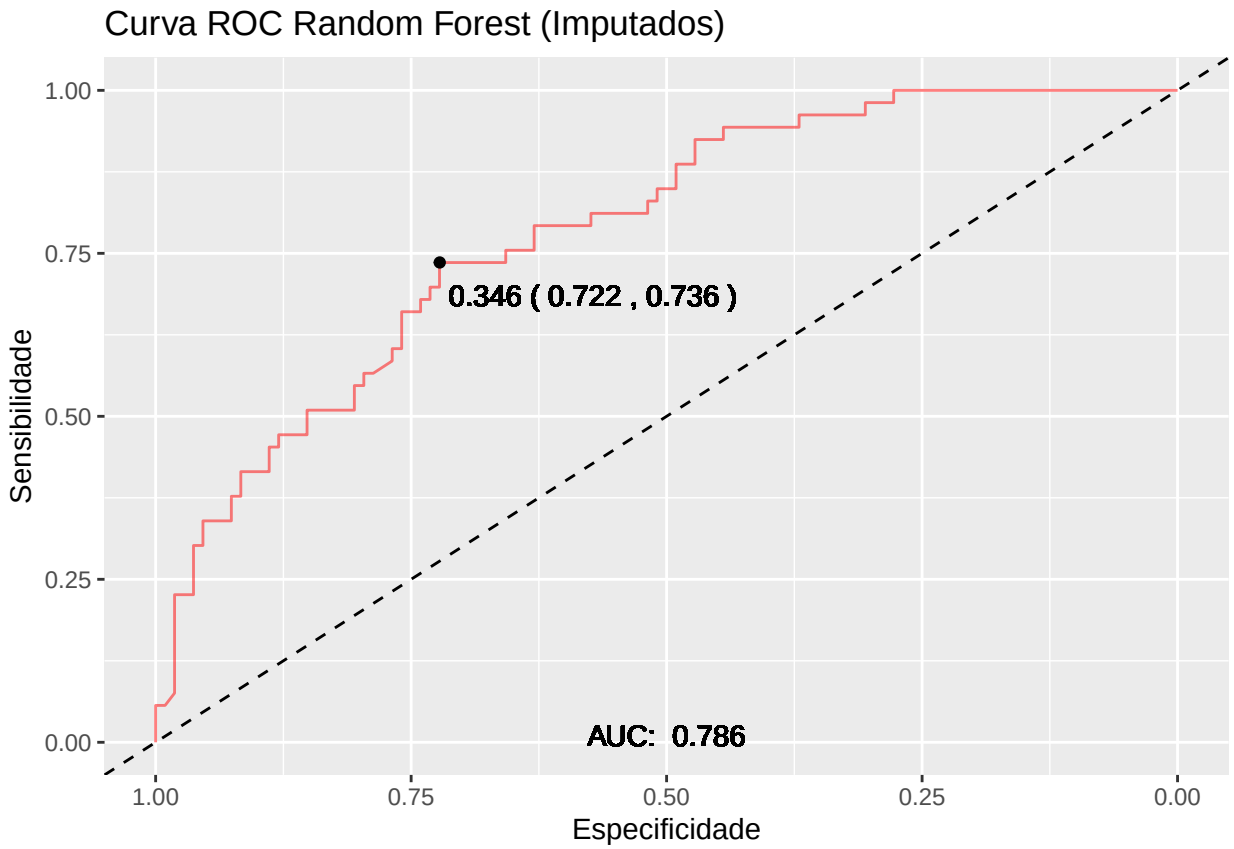
```
## [1] "Menor árvore sem imputação: 250"
```

```
tree_func(final_model = modeloRF2$finalModel, tree_num[1])
```



Validacão

```
## Random Forest com dados imputados
rocRF1 <- roc(response = validacao$diabetes, predictor = predict(modeloRF1, validacao, type = "prob")[,
plotaroc(rocRF1, titulo = "Curva ROC Random Forest (Imputados)")
```




```
predictRF1 <- predict(modeloRF1, newdata = validacao)
print("Dados imputados:")
```

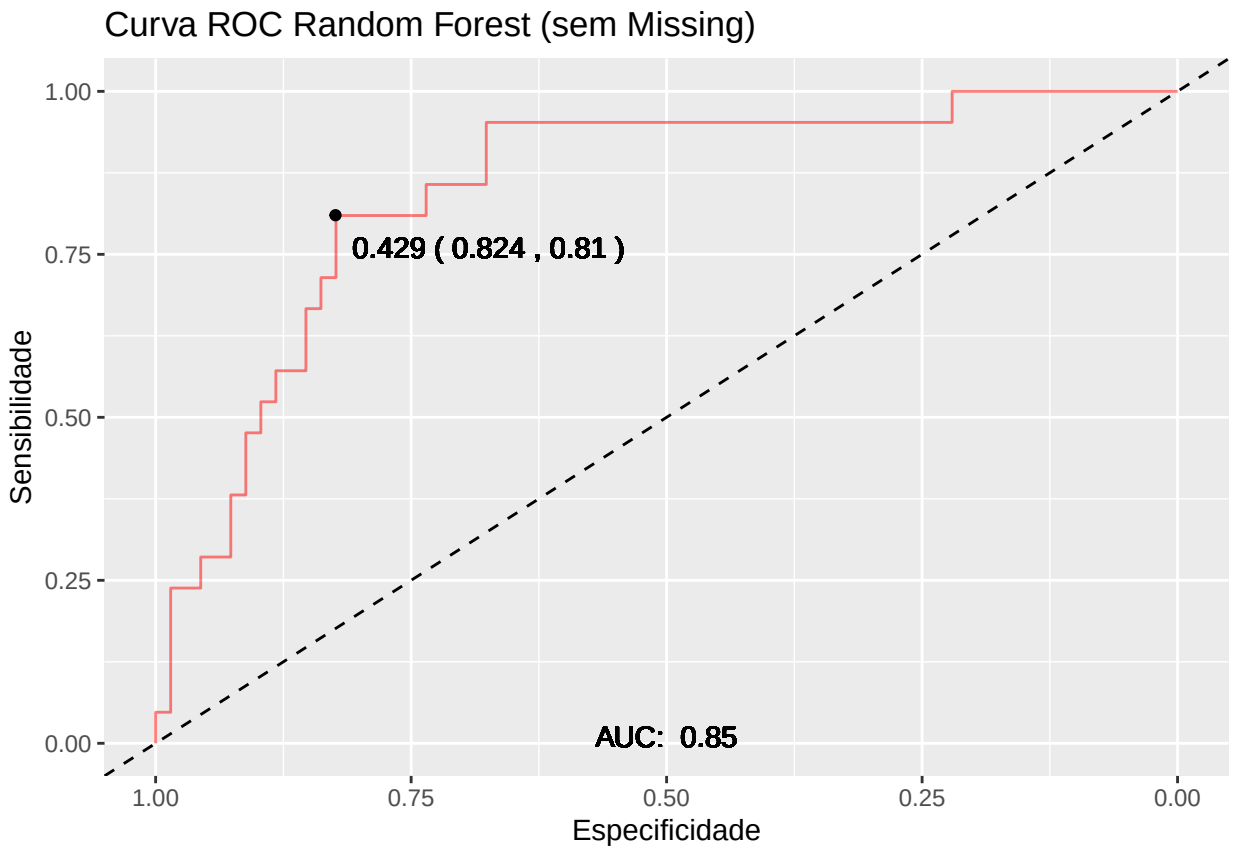
```
## [1] "Dados imputados:"
```

```
confusionMatrix(predictRF1, validacao$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  93  28
##        Yes 15  25
##
##                Accuracy : 0.7329
##                  95% CI : (0.6576, 0.7995)
##     No Information Rate : 0.6708
##     P-Value [Acc > NIR] : 0.05368
##
##                   Kappa : 0.355
##
##  Mcnemar's Test P-Value : 0.06725
##
##             Sensitivity : 0.8611
```

```
##             Specificity : 0.4717
##          Pos Pred Value : 0.7686
##          Neg Pred Value : 0.6250
##              Prevalence : 0.6708
##          Detection Rate : 0.5776
##    Detection Prevalence : 0.7516
##       Balanced Accuracy : 0.6664
##
##        'Positive' Class : No
##
```

```
## Random Forest com dados imputados
rocRF2 <- roc(response = validacao_without_NAs$diabetes, predictor = predict(modeloRF2, validacao_withou
plotaroc(rocRF2, titulo = "Curva ROC Random Forest (sem Missing)")
```




```
predictRF2 <- predict(modeloRF2, newdata = validacao_without_NAs)
print("Sem Missing:")
```

```
## [1] "Sem Missing:"
```

```
confusionMatrix(predictRF2, validacao_without_NAs$diabetes)
```

```
## Confusion Matrix and Statistics
```

```
##
##           Reference
## Prediction No Yes
##        No  59   9
##        Yes  9  12
##
##                Accuracy : 0.7978
##                  95% CI : (0.6993, 0.8755)
##     No Information Rate : 0.764
##     P-Value [Acc > NIR] : 0.2709
##
##                   Kappa : 0.4391
##
##  Mcnemar's Test P-Value : 1.0000
##
##             Sensitivity : 0.8676
##             Specificity : 0.5714
##          Pos Pred Value : 0.8676
##          Neg Pred Value : 0.5714
##              Prevalence : 0.7640
##          Detection Rate : 0.6629
##    Detection Prevalence : 0.7640
##       Balanced Accuracy : 0.7195
##
##        'Positive' Class : No
##
```

Support Vector Machine

Support Vector Machine (SVM) estabelece um limite de decisão ideal que separa os pontos de dados de diferentes classes e, em seguida, prevê a classe de novas observações com base nesse limite de separação. Os diferentes grupos podem ser separáveis por uma linha reta linear ou por uma linha limite não linear.

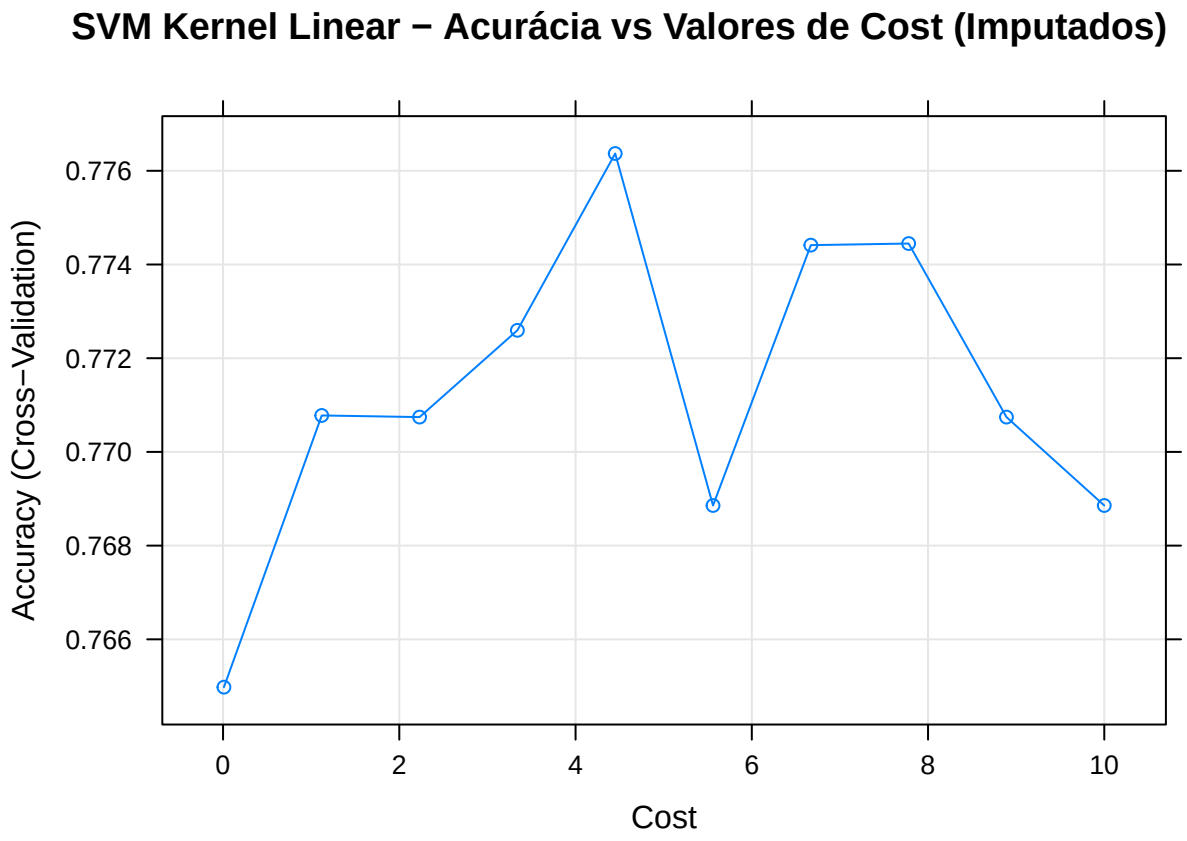
Modelagem

SVM Kernel Linear com dados imputados

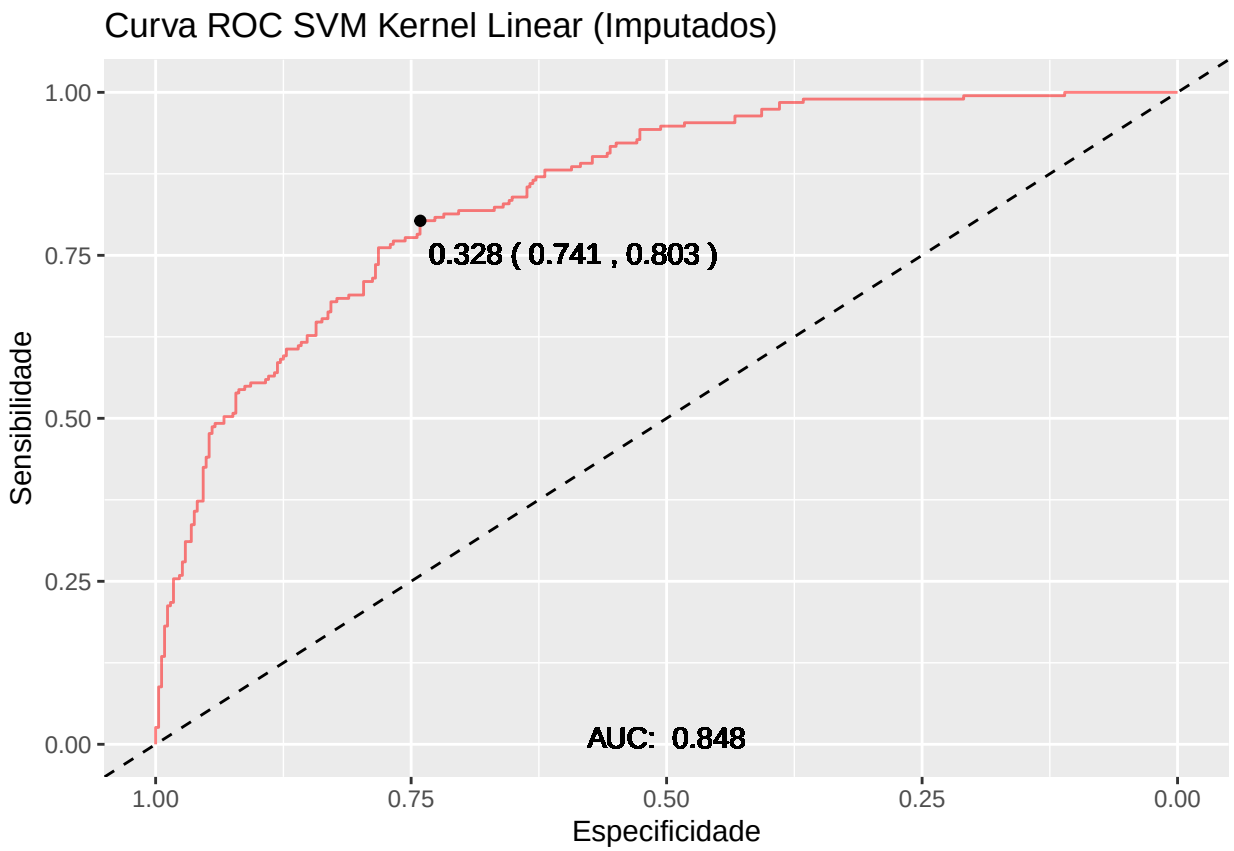
```
train.control <- caret::trainControl(method = "cv", number = 10, savePred=T, classProb=T) # Cross-valid
#library(e1071) #SVM
## SVM Kernel Linear com dados imputados
set.seed(23)
modeloSVM1 <- caret::train(
  diabetes ~., data = train, method = "svmLinear",
  probability = T,
  trControl = train.control,
  preProcess = c("center","scale"),
  tuneGrid = expand.grid(C = seq(0.01, 10, length = 10))
)
print(modeloSVM1)
```

```
## Support Vector Machines with Linear Kernel
##
## 537 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## Pre-processing: centered (8), scaled (8)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 483, 483, 484, 483, 482, 484, ...
## Resampling results across tuning parameters:
##
##   C      Accuracy   Kappa
##    0.01  0.7649794  0.4734524
##    1.12  0.7707782  0.4824355
##    2.23  0.7707433  0.4808278
##    3.34  0.7725951  0.4843473
##    4.45  0.7763687  0.4917503
##    5.56  0.7688565  0.4769505
##    6.67  0.7744133  0.4896157
##    7.78  0.7744470  0.4862920
##    8.89  0.7707433  0.4778763
##   10.00  0.7688565  0.4754528
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was C = 4.45.
```

```
plot(modeloSVM1, main="SVM Kernel Linear - Acurácia vs Valores de Cost (Imputados)")
```




```r
rocSVM1 <- roc(response = train$diabetes, predictor = predict(modeloSVM1, train, type = "prob")[,2])
plotaroc(rocSVM1, titulo = "Curva ROC SVM Kernel Linear (Imputados)")
```



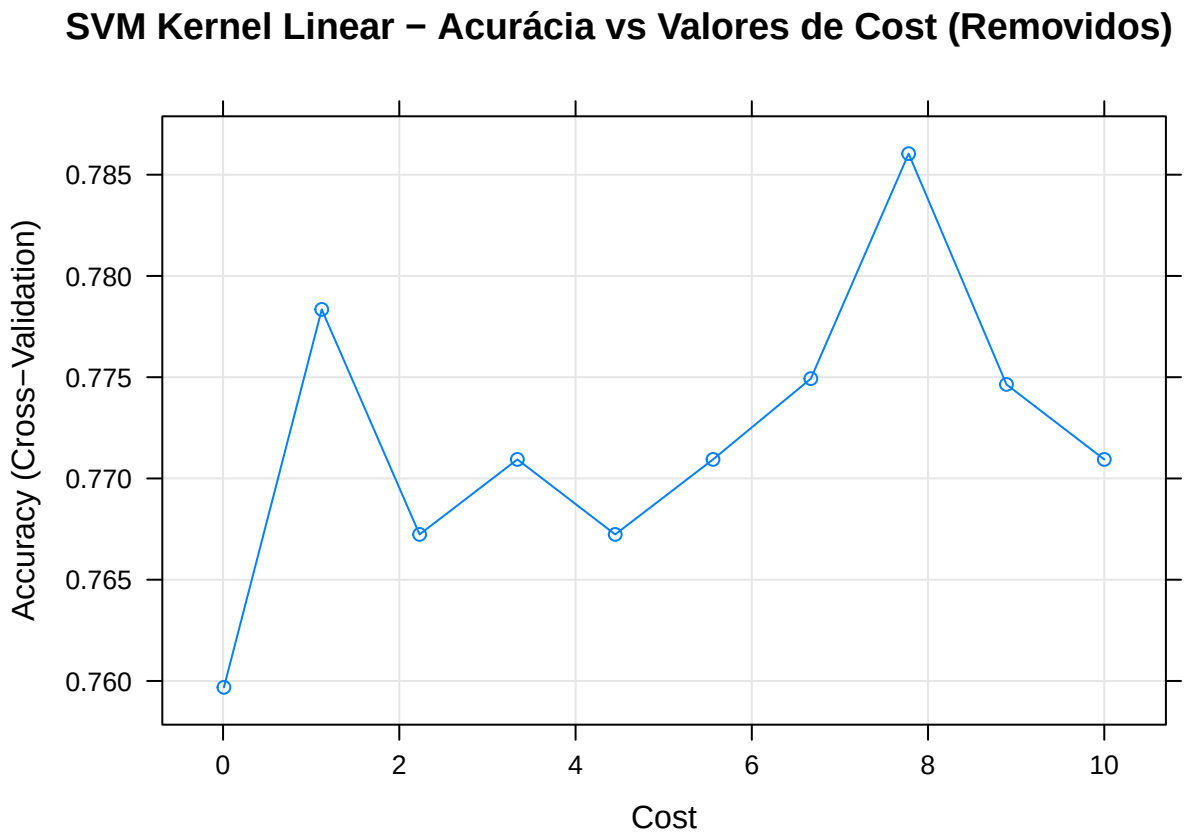
SVM Kernel Linear sem missing

```
## SVM Kernel Linear sem missing
set.seed(23)
modeloSVM2 <- caret::train(
  diabetes ~., data = train_without_NAs, method = "svmLinear",
  trControl = train.control,
  preProcess = c("center","scale"),
  tuneGrid = expand.grid(C = seq(0.01, 10, length = 10))
)
print(modeloSVM2)
```

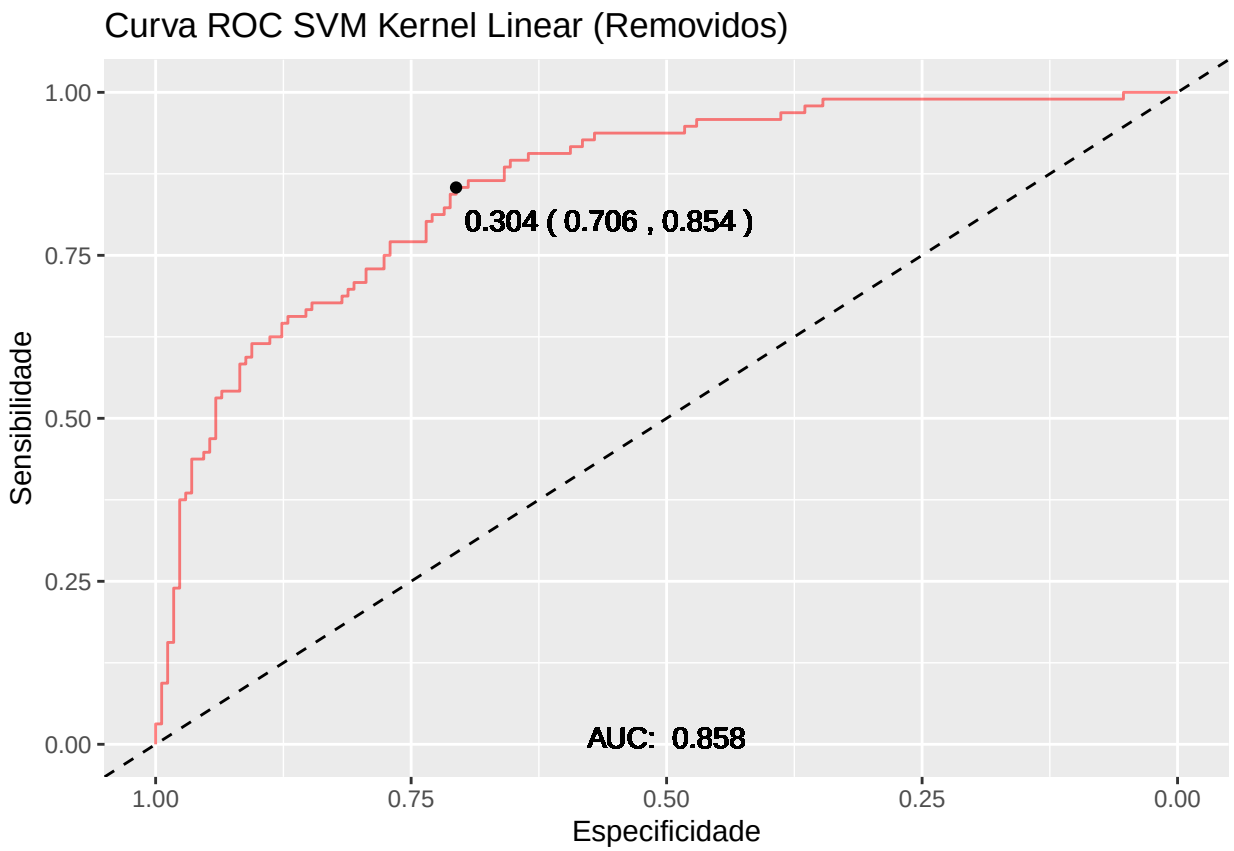
```
## Support Vector Machines with Linear Kernel
##
## 266 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## Pre-processing: centered (8), scaled (8)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 240, 240, 239, 239, 239, 239, ...
## Resampling results across tuning parameters:
##
```

```
##    C      Accuracy   Kappa
##     0.01  0.7596866  0.4629441
##     1.12  0.7783476  0.4980691
##     2.23  0.7672365  0.4744505
##     3.34  0.7709402  0.4839230
##     4.45  0.7672365  0.4774236
##     5.56  0.7709402  0.4781789
##     6.67  0.7749288  0.4893745
##     7.78  0.7860399  0.5103509
##     8.89  0.7746439  0.4906956
##    10.00  0.7709402  0.4754996
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was C = 7.78.
```

```
plot(modeloSVM2, main="SVM Kernel Linear - Acurácia vs Valores de Cost (Removidos)")
```




```
rocSVM2 <- roc(response = train_without_NAs$diabetes, predictor = predict(modeloSVM2, train_without_NAs
plotaroc(rocSVM2, titulo ="Curva ROC SVM Kernel Linear (Removidos)")
```



SVM Kernel Não Linear com dados imputados

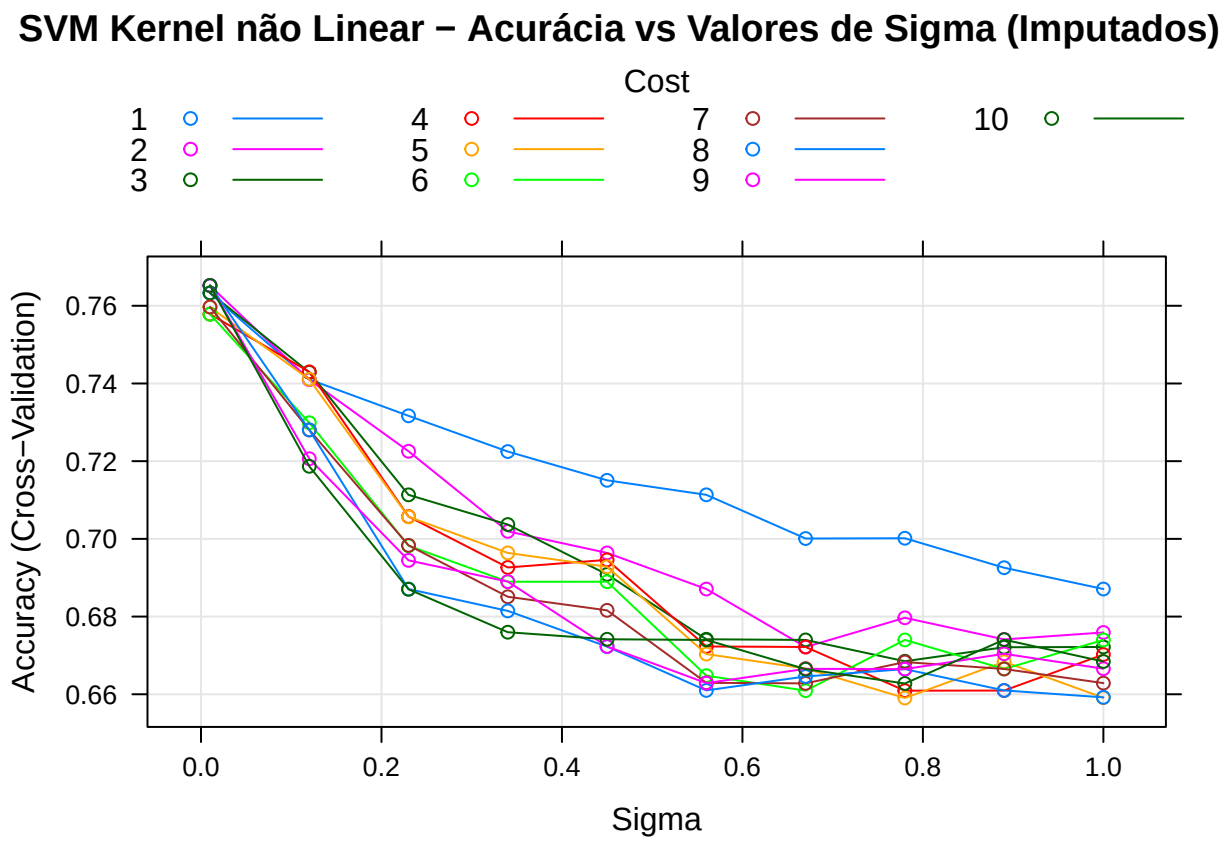
```
train.control <- caret::trainControl(method = "cv", number = 10, savePred=T, classProb=T)

## SVM Kernel Não Linear com dados imputados
set.seed(23)
modeloSVM3 <- caret::train(
  diabetes ~., data = train, method = "svmRadial",
  trControl = train.control,
  preProcess = c("center","scale"),
  tuneGrid = expand.grid(sigma = seq(0.01, 1, length = 10) , C = seq(1, 10, length = 10))
)
print(modeloSVM3)
```

```
## Support Vector Machines with Radial Basis Function Kernel
##
## 537 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## Pre-processing: centered (8), scaled (8)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 483, 483, 484, 483, 482, 484, ...
```

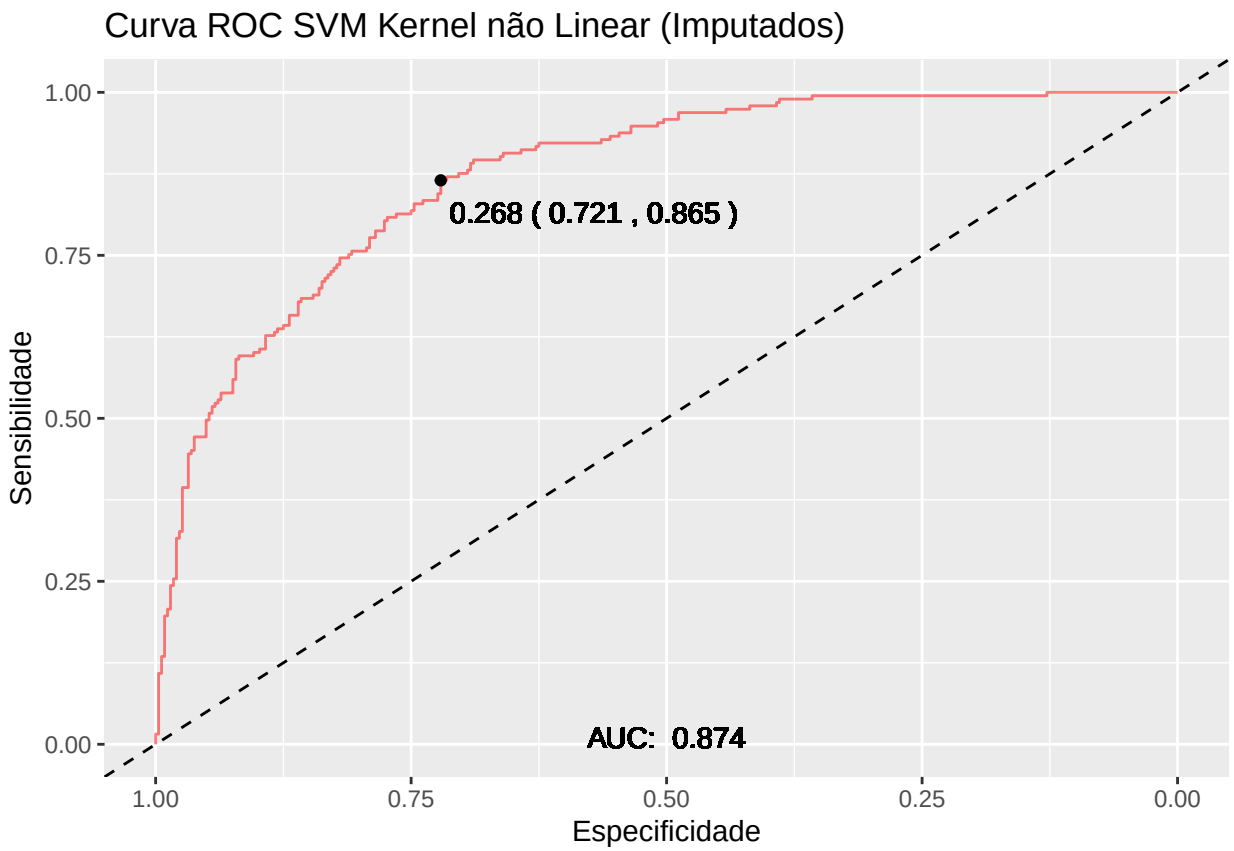
```
## Resampling results across tuning parameters:
##
##   sigma  C   Accuracy   Kappa
##   0.01    1  0.7632323  0.4654255
##   0.01    2  0.7651541  0.4686906
##   0.01    3  0.7633371  0.4652478
##   0.01    4  0.7578502  0.4499811
##   0.01    5  0.7596334  0.4565153
##   0.01    6  0.7578153  0.4521902
##   0.01    7  0.7597021  0.4544051
##   0.01    8  0.7652576  0.4649773
##   0.01    9  0.7652576  0.4667128
##   0.01   10  0.7652227  0.4665617
##   0.12    1  0.7410412  0.4172729
##   0.12    2  0.7409688  0.4130742
##   0.12    3  0.7428905  0.4189473
##   0.12    4  0.7429928  0.4173560
##   0.12    5  0.7410724  0.4173790
##   0.12    6  0.7298901  0.3891193
##   0.12    7  0.7280382  0.3836402
##   0.12    8  0.7280382  0.3865933
##   0.12    9  0.7206296  0.3666429
##   0.12   10  0.7186754  0.3627544
##   0.23    1  0.7316746  0.3933253
##   0.23    2  0.7225513  0.3738773
##   0.23    3  0.7113354  0.3457537
##   0.23    4  0.7057449  0.3323967
##   0.23    5  0.7056750  0.3313558
##   0.23    6  0.6982314  0.3163946
##   0.23    7  0.6983362  0.3096625
##   0.23    8  0.6870853  0.2825074
##   0.23    9  0.6944578  0.3009454
##   0.23   10  0.6870167  0.2782018
##   0.34    1  0.7224827  0.3714102
##   0.34    2  0.7019376  0.3273452
##   0.34    3  0.7036872  0.3239199
##   0.34    4  0.6926421  0.2970354
##   0.34    5  0.6963808  0.3111219
##   0.34    6  0.6889721  0.2906708
##   0.34    7  0.6850975  0.2810966
##   0.34    8  0.6814624  0.2675126
##   0.34    9  0.6890071  0.2828918
##   0.34   10  0.6759742  0.2551517
##   0.45    1  0.7150753  0.3509448
##   0.45    2  0.6963833  0.3062685
##   0.45    3  0.6908589  0.2926231
##   0.45    4  0.6945988  0.3106269
##   0.45    5  0.6928156  0.3041198
##   0.45    6  0.6889734  0.2984869
##   0.45    7  0.6816009  0.2875827
##   0.45    8  0.6722718  0.2590777
##   0.45    9  0.6723067  0.2552091
##   0.45   10  0.6741586  0.2616750
##   0.56    1  0.7113379  0.3428026
```

```
##   0.56    2  0.6870866  0.2825257
##   0.56    3  0.6741573  0.2575748
##   0.56    4  0.6723054  0.2584329
##   0.56    5  0.6703500  0.2495136
##   0.56    6  0.6647958  0.2365721
##   0.56    7  0.6629439  0.2385834
##   0.56    8  0.6609872  0.2203032
##   0.56    9  0.6628740  0.2280941
##   0.56   10  0.6739864  0.2501550
##   0.67    1  0.7000870  0.3084599
##   0.67    2  0.6721670  0.2416235
##   0.67    3  0.6739864  0.2500257
##   0.67    4  0.6721695  0.2490706
##   0.67    5  0.6666463  0.2338014
##   0.67    6  0.6609186  0.2177422
##   0.67    7  0.6628054  0.2275974
##   0.67    8  0.6645887  0.2323034
##   0.67    9  0.6665428  0.2321039
##   0.67   10  0.6664754  0.2375644
##   0.78    1  0.7001569  0.3088335
##   0.78    2  0.6796805  0.2585207
##   0.78    3  0.6684982  0.2323193
##   0.78    4  0.6609186  0.2142967
##   0.78    5  0.6590318  0.2111359
##   0.78    6  0.6739877  0.2470423
##   0.78    7  0.6682924  0.2377308
##   0.78    8  0.6664754  0.2266465
##   0.78    9  0.6664754  0.2258914
##   0.78   10  0.6627705  0.2125283
##   0.89    1  0.6925761  0.2908961
##   0.89    2  0.6741236  0.2431205
##   0.89    3  0.6721009  0.2334575
##   0.89    4  0.6609536  0.2093185
##   0.89    5  0.6683610  0.2275698
##   0.89    6  0.6665091  0.2235560
##   0.89    7  0.6665091  0.2188595
##   0.89    8  0.6609872  0.2072523
##   0.89    9  0.6704212  0.2236802
##   0.89   10  0.6740550  0.2476682
##   1.00    1  0.6870891  0.2753881
##   1.00    2  0.6759081  0.2379519
##   1.00    3  0.6721695  0.2306436
##   1.00    4  0.6702128  0.2300421
##   1.00    5  0.6591017  0.2023119
##   1.00    6  0.6739864  0.2383797
##   1.00    7  0.6628728  0.2097380
##   1.00    8  0.6592040  0.2043506
##   1.00    9  0.6665790  0.2159346
##   1.00   10  0.6684308  0.2258624
##
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were sigma = 0.01 and C = 9.
```

```
plot(modeloSVM3, main="SVM Kernel não Linear - Acurácia vs Valores de Sigma (Imputados)")
```




```
rocSVM3 <- roc(response = train$diabetes, predictor = predict(modeloSVM3, train, type = "prob")[,2])
plotaroc(rocSVM3, titulo ="Curva ROC SVM Kernel não Linear (Imputados)")
```



SVM Kernel Não Linear sem missing

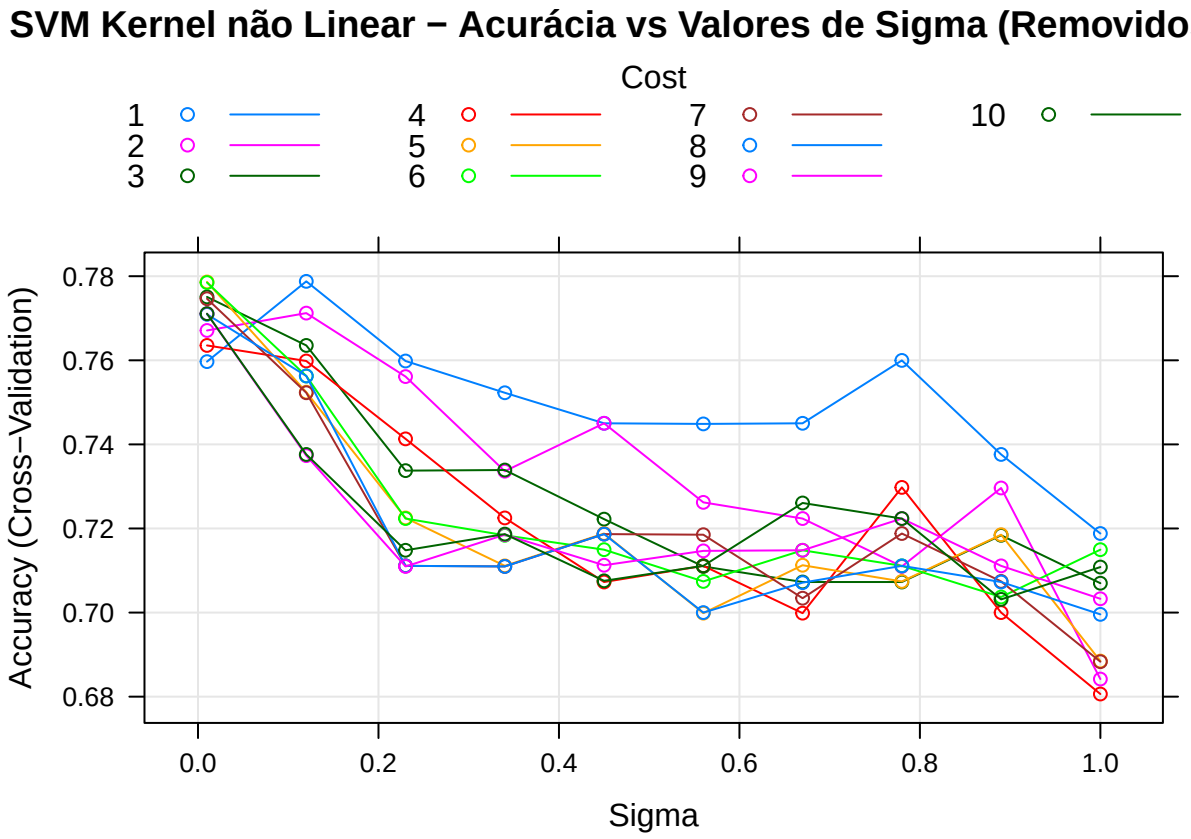
```
## SVM Kernel Não Linear sem missing
set.seed(23)
modeloSVM4 <- caret::train(
  diabetes ~., data = train_without_NAs, method = "svmRadial",
  trControl = train.control,
  preProcess = c("center","scale"),
  tuneGrid = expand.grid(sigma = seq(0.01, 1, length = 10) , C = seq(1, 10, length = 10))
)
print(modeloSVM4)
```

```
## Support Vector Machines with Radial Basis Function Kernel
##
## 266 samples
##   8 predictor
##   2 classes: 'No', 'Yes'
##
## Pre-processing: centered (8), scaled (8)
## Resampling: Cross-Validated (10 fold)
## Summary of sample sizes: 240, 240, 239, 239, 239, 239, ...
## Resampling results across tuning parameters:
##
```

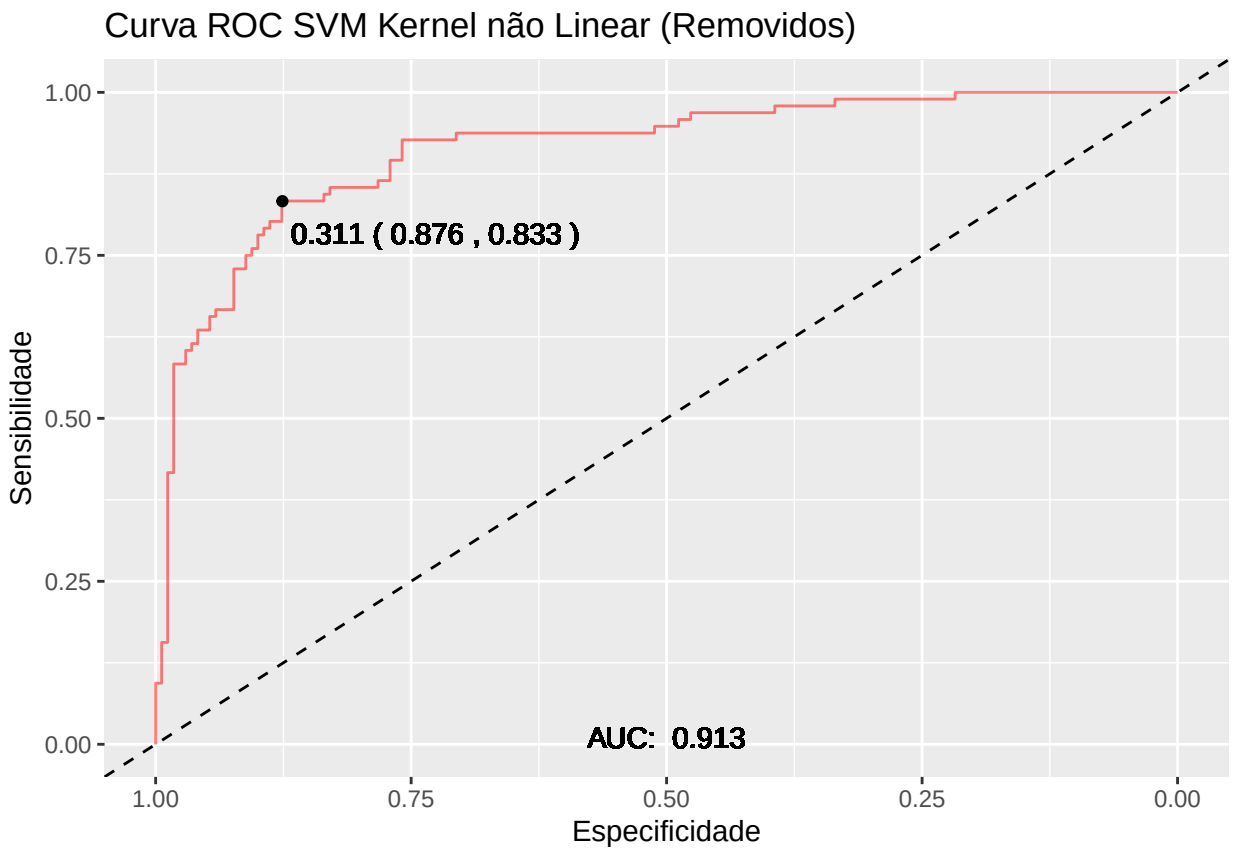
```
##   sigma  C   Accuracy   Kappa
##   0.01    1  0.7596866  0.4650398
##   0.01    2  0.7670940  0.4812458
##   0.01    3  0.7750712  0.4961683
##   0.01    4  0.7635328  0.4698621
##   0.01    5  0.7786325  0.4972411
##   0.01    6  0.7784900  0.4946139
##   0.01    7  0.7746439  0.4843767
##   0.01    8  0.7709402  0.4757028
##   0.01    9  0.7710826  0.4782618
##   0.01   10  0.7710826  0.4782618
##   0.12    1  0.7787749  0.4951781
##   0.12    2  0.7712251  0.4802989
##   0.12    3  0.7635328  0.4566007
##   0.12    4  0.7598291  0.4445875
##   0.12    5  0.7524217  0.4302310
##   0.12    6  0.7562678  0.4371691
##   0.12    7  0.7522792  0.4200541
##   0.12    8  0.7562678  0.4370246
##   0.12    9  0.7373219  0.3911532
##   0.12   10  0.7376068  0.3892707
##   0.23    1  0.7598291  0.4523565
##   0.23    2  0.7561254  0.4451085
##   0.23    3  0.7337607  0.4021808
##   0.23    4  0.7413105  0.4199586
##   0.23    5  0.7225071  0.3736789
##   0.23    6  0.7223647  0.3670588
##   0.23    7  0.7111111  0.3417905
##   0.23    8  0.7111111  0.3408347
##   0.23    9  0.7109687  0.3405406
##   0.23   10  0.7148148  0.3367158
##   0.34    1  0.7522792  0.4378279
##   0.34    2  0.7336182  0.4009842
##   0.34    3  0.7339031  0.3950800
##   0.34    4  0.7225071  0.3770402
##   0.34    5  0.7111111  0.3487114
##   0.34    6  0.7183761  0.3638857
##   0.34    7  0.7109687  0.3366912
##   0.34    8  0.7109687  0.3441970
##   0.34    9  0.7185185  0.3508626
##   0.34   10  0.7186610  0.3590489
##   0.45    1  0.7450142  0.4217840
##   0.45    2  0.7450142  0.4322630
##   0.45    3  0.7222222  0.3712480
##   0.45    4  0.7072650  0.3469918
##   0.45    5  0.7188034  0.3656221
##   0.45    6  0.7149573  0.3580174
##   0.45    7  0.7186610  0.3583701
##   0.45    8  0.7186610  0.3619806
##   0.45    9  0.7112536  0.3476623
##   0.45   10  0.7075499  0.3454457
##   0.56    1  0.7448718  0.4243368
##   0.56    2  0.7262108  0.3809057
##   0.56    3  0.7109687  0.3386173
```

```
##   0.56    4  0.7111111  0.3454171
##   0.56    5  0.6998575  0.3195248
##   0.56    6  0.7074074  0.3369069
##   0.56    7  0.7185185  0.3779832
##   0.56    8  0.7000000  0.3153407
##   0.56    9  0.7146724  0.3515126
##   0.56   10  0.7111111  0.3485484
##   0.67    1  0.7450142  0.4361749
##   0.67    2  0.7223647  0.3844141
##   0.67    3  0.7072650  0.3418878
##   0.67    4  0.6998575  0.3169579
##   0.67    5  0.7112536  0.3447735
##   0.67    6  0.7148148  0.3577632
##   0.67    7  0.7034188  0.3278498
##   0.67    8  0.7071225  0.3375983
##   0.67    9  0.7148148  0.3570661
##   0.67   10  0.7260684  0.3767459
##   0.78    1  0.7599715  0.4719043
##   0.78    2  0.7109687  0.3479731
##   0.78    3  0.7072650  0.3401029
##   0.78    4  0.7297721  0.3925998
##   0.78    5  0.7074074  0.3478802
##   0.78    6  0.7111111  0.3430724
##   0.78    7  0.7188034  0.3574965
##   0.78    8  0.7111111  0.3475439
##   0.78    9  0.7223647  0.3713868
##   0.78   10  0.7223647  0.3729232
##   0.89    1  0.7376068  0.4239749
##   0.89    2  0.7296296  0.3890878
##   0.89    3  0.7183761  0.3677189
##   0.89    4  0.7000000  0.3174928
##   0.89    5  0.7185185  0.3622729
##   0.89    6  0.7037037  0.3369286
##   0.89    7  0.7074074  0.3383008
##   0.89    8  0.7072650  0.3383578
##   0.89    9  0.7111111  0.3472359
##   0.89   10  0.7031339  0.3065973
##   1.00    1  0.7188034  0.3915682
##   1.00    2  0.6841880  0.2662962
##   1.00    3  0.7069801  0.3218391
##   1.00    4  0.6806268  0.2520008
##   1.00    5  0.6884615  0.2735769
##   1.00    6  0.7149573  0.3506383
##   1.00    7  0.6883191  0.2773509
##   1.00    8  0.6995726  0.2933212
##   1.00    9  0.7032764  0.3099552
##   1.00   10  0.7108262  0.3449889
##
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were sigma = 0.12 and C = 1.
```

```
plot(modeloSVM4, main="SVM Kernel não Linear - Acurácia vs Valores de Sigma (Removidos)")
```

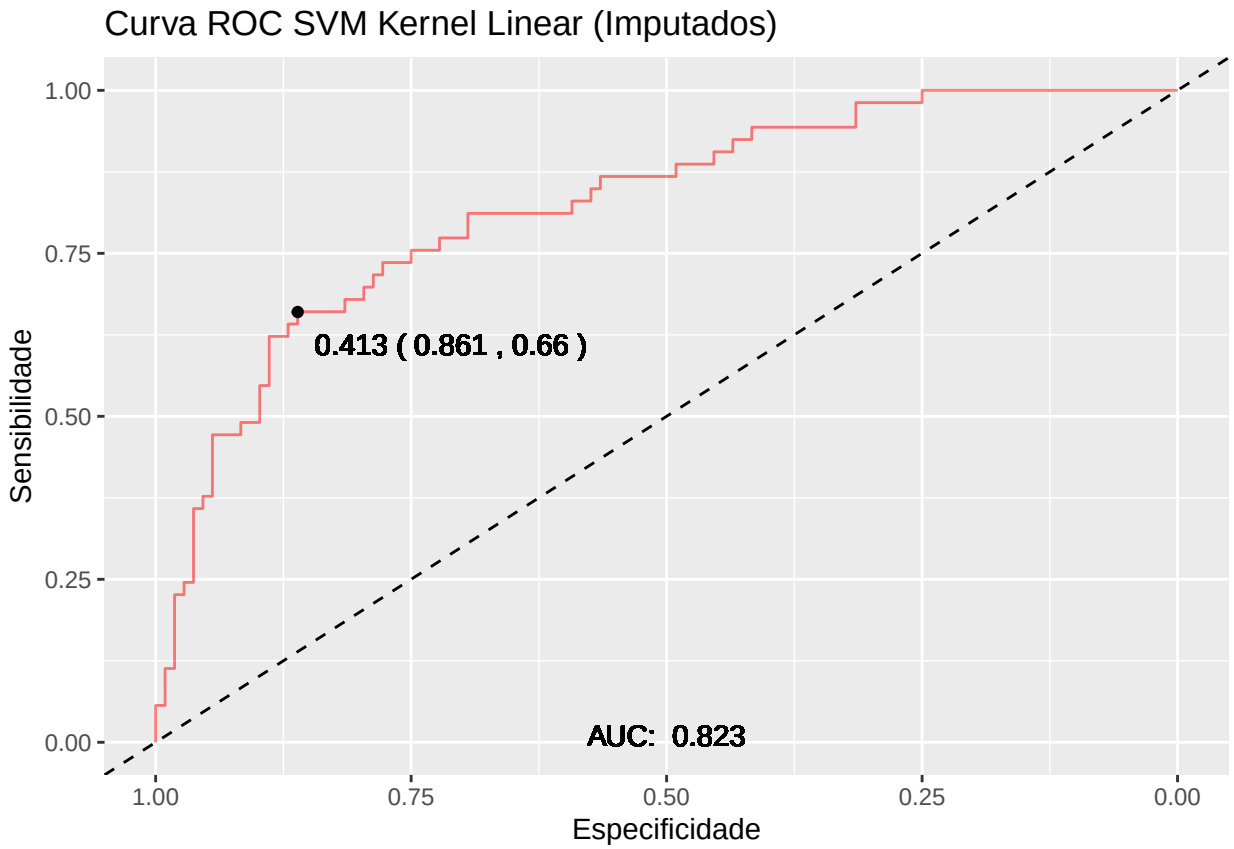



```
rocSVM4 <- roc(response = train_without_NAs$diabetes, predictor = predict(modeloSVM4, train_without_NAs
plotaroc(rocSVM4, titulo ="Curva ROC SVM Kernel não Linear (Removidos)")
```



Validação

```
## SVM Kernel Linear com dados imputados
rocSVM1 <- roc(response = validacao$diabetes, predictor = predict(modeloSVM1, validacao, type = "prob")
plotaroc(rocSVM1, titulo = "Curva ROC SVM Kernel Linear (Imputados)")
```

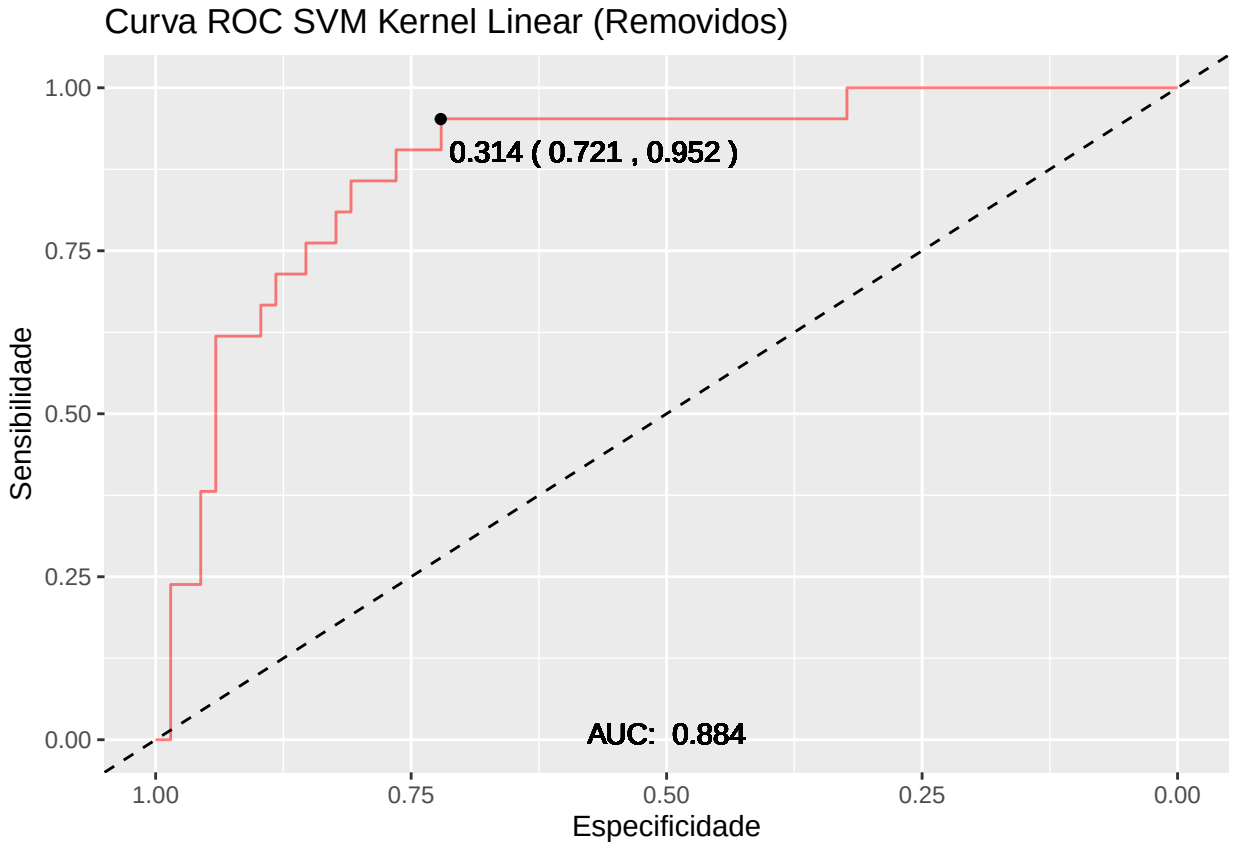



```
predictSVM1 <- predict(modeloSVM1, newdata = validacao)
confusionMatrix(predictSVM1, validacao$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  98  27
##        Yes 10  26
##
##                Accuracy : 0.7702
##                  95% CI : (0.6974, 0.8327)
##     No Information Rate : 0.6708
##     P-Value [Acc > NIR] : 0.003815
##
##                   Kappa : 0.4334
##
##  Mcnemar's Test P-Value : 0.008529
##
##             Sensitivity : 0.9074
##             Specificity : 0.4906
##          Pos Pred Value : 0.7840
##          Neg Pred Value : 0.7222
##              Prevalence : 0.6708
##          Detection Rate : 0.6087
```

```
##    Detection Prevalence : 0.7764
##       Balanced Accuracy : 0.6990
##
##        'Positive' Class : No
##
```

```
## SVM Kernel Linear sem missing
rocSVM2 <- roc(response = validacao_without_NAs$diabetes, predictor = predict(modeloSVM2, validacao_wit
plotaroc(rocSVM2, titulo = "Curva ROC SVM Kernel Linear (Removidos)")
```

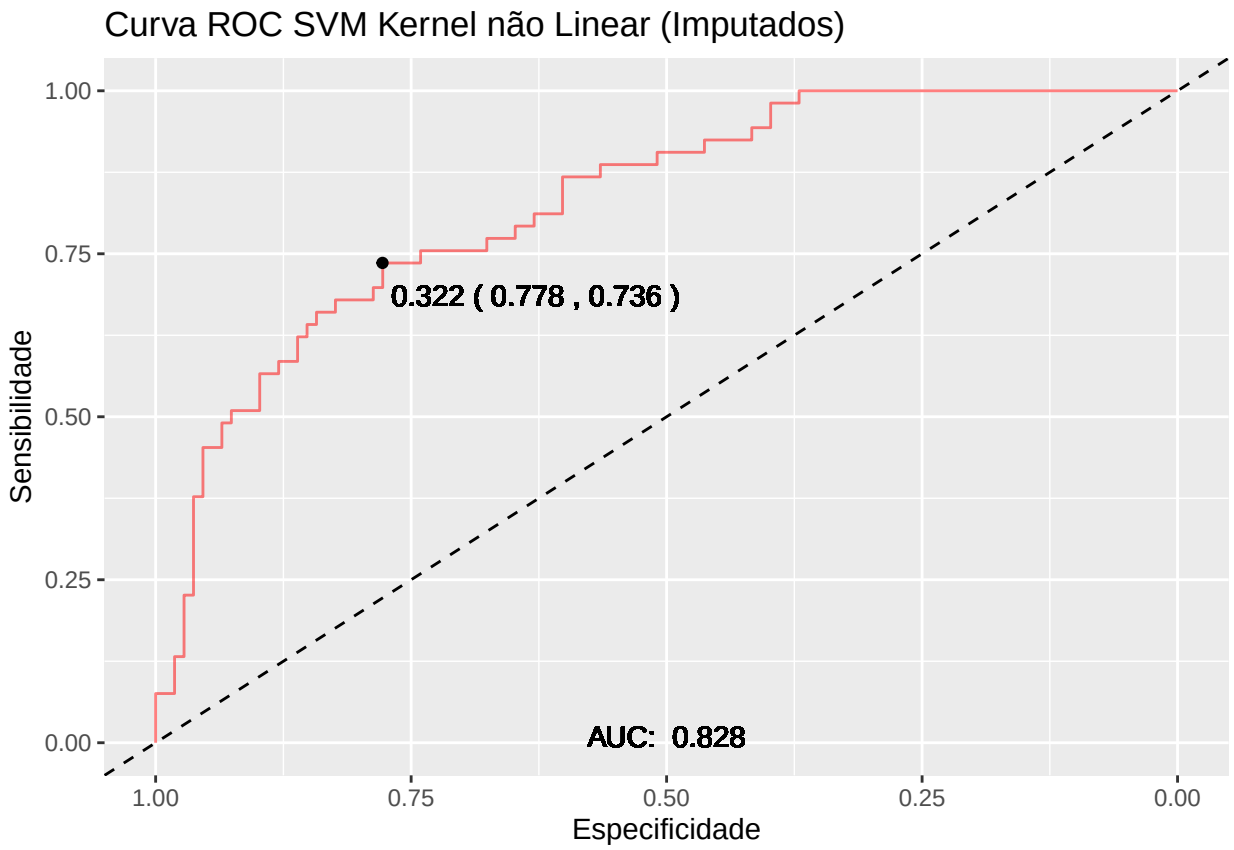



```
predictSVM2 <- predict(modeloSVM2, newdata = validacao_without_NAs)
confusionMatrix(predictSVM2, validacao_without_NAs$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  64  12
##        Yes  4   9
##
##                Accuracy : 0.8202
##                  95% CI : (0.7245, 0.8936)
##     No Information Rate : 0.764
##     P-Value [Acc > NIR] : 0.12910
```

```
##
##                   Kappa : 0.4258
##
##  Mcnemar's Test P-Value : 0.08012
##
##             Sensitivity : 0.9412
##             Specificity : 0.4286
##          Pos Pred Value : 0.8421
##          Neg Pred Value : 0.6923
##              Prevalence : 0.7640
##          Detection Rate : 0.7191
##    Detection Prevalence : 0.8539
##       Balanced Accuracy : 0.6849
##
##        'Positive' Class : No
##
```

```
## SVM Kernel não Linear com dados imputados
rocSVM3 <- roc(response = validacao$diabetes, predictor = predict(modeloSVM3, validacao, type = "prob")
plotaroc(rocSVM3, titulo = "Curva ROC SVM Kernel não Linear (Imputados)")
```

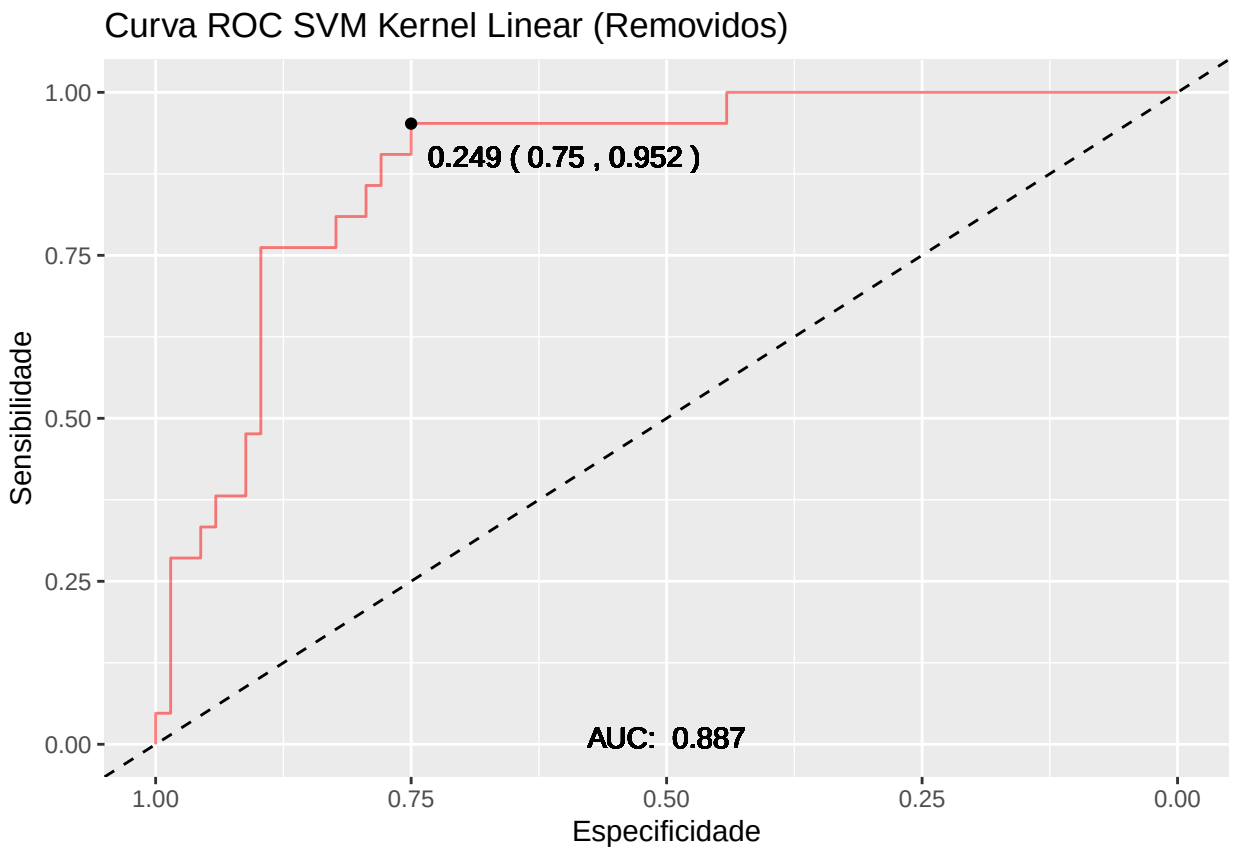



```
predictSVM3 <- predict(modeloSVM3, newdata = validacao)
confusionMatrix(predictSVM3, validacao$diabetes)
```

```
## Confusion Matrix and Statistics
```

```
##
##          Reference
## Prediction No Yes
##        No  99  26
##        Yes  9  27
##
##               Accuracy : 0.7826
##                 95% CI : (0.7109, 0.8437)
##    No Information Rate : 0.6708
##    P-Value [Acc > NIR] : 0.001230
##
##                  Kappa : 0.464
##
##  Mcnemar's Test P-Value : 0.006841
##
##             Sensitivity : 0.9167
##             Specificity : 0.5094
##          Pos Pred Value : 0.7920
##          Neg Pred Value : 0.7500
##              Prevalence : 0.6708
##          Detection Rate : 0.6149
##    Detection Prevalence : 0.7764
##       Balanced Accuracy : 0.7131
##
##        'Positive' Class : No
##
```

```
## SVM Kernel Linear sem missing
rocSVM4 <- roc(response = validacao_without_NAs$diabetes, predictor = predict(modeloSVM4, validacao_wit
plotaroc(rocSVM4, titulo = "Curva ROC SVM Kernel Linear (Removidos)")
```




```
predictSVM4 <- predict(modeloSVM4, newdata = validacao_without_NAs)
confusionMatrix(predictSVM4, validacao_without_NAs$diabetes)
```

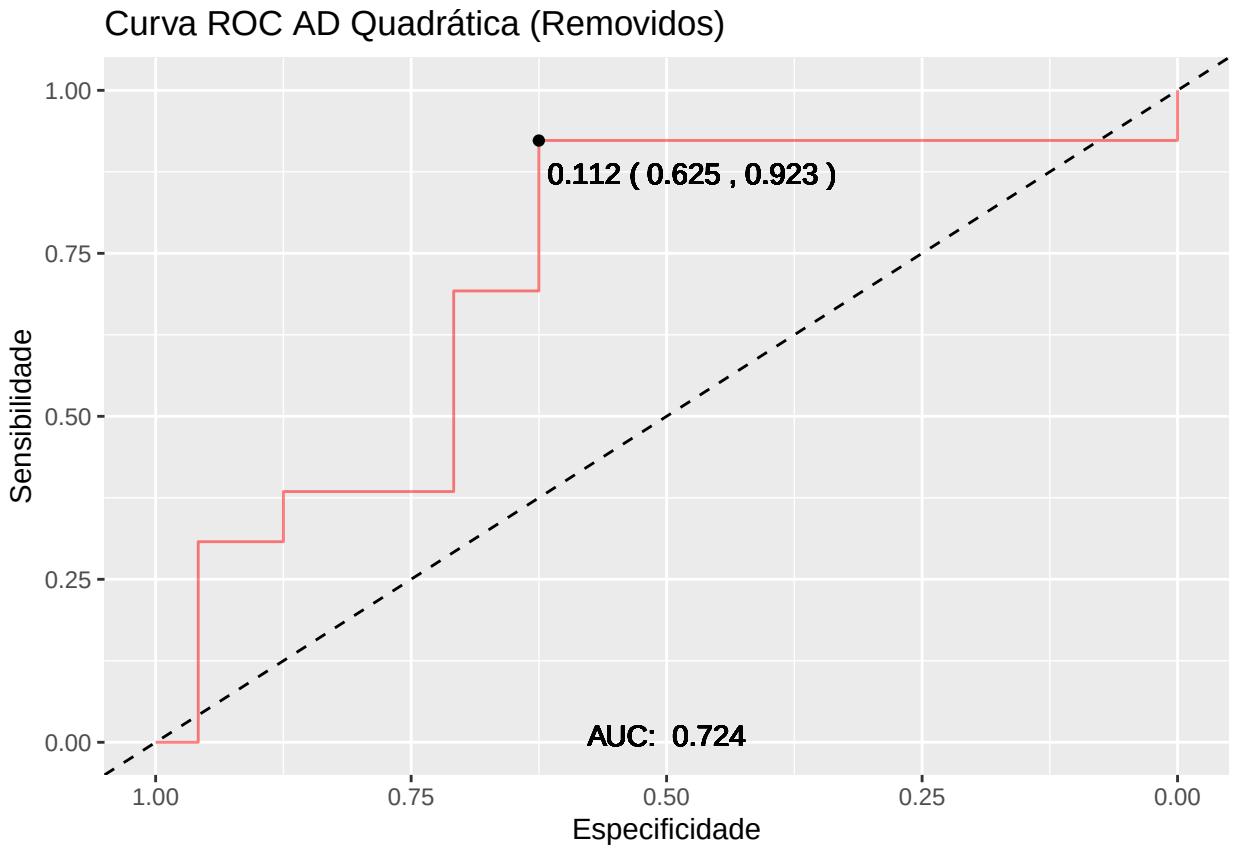
```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  63  13
##        Yes  5   8
##
##                Accuracy : 0.7978
##                  95% CI : (0.6993, 0.8755)
##     No Information Rate : 0.764
##     P-Value [Acc > NIR] : 0.27088
##
##                   Kappa : 0.354
##
##  Mcnemar's Test P-Value : 0.09896
##
##             Sensitivity : 0.9265
##             Specificity : 0.3810
##          Pos Pred Value : 0.8289
##          Neg Pred Value : 0.6154
##              Prevalence : 0.7640
##          Detection Rate : 0.7079
```

```
##    Detection Prevalence : 0.8539
##       Balanced Accuracy : 0.6537
##
##        'Positive' Class : No
##
```

Teste

AD Quadrática - Dados Removidos

```
rocAD6out <- roc(response = test_whitout_NAs$diabetes, predictor = predict(modeloAD6, test_whitout_NAs,
plotaroc(rocAD6out, titulo = "Curva ROC AD Quadrática (Removidos)")
```



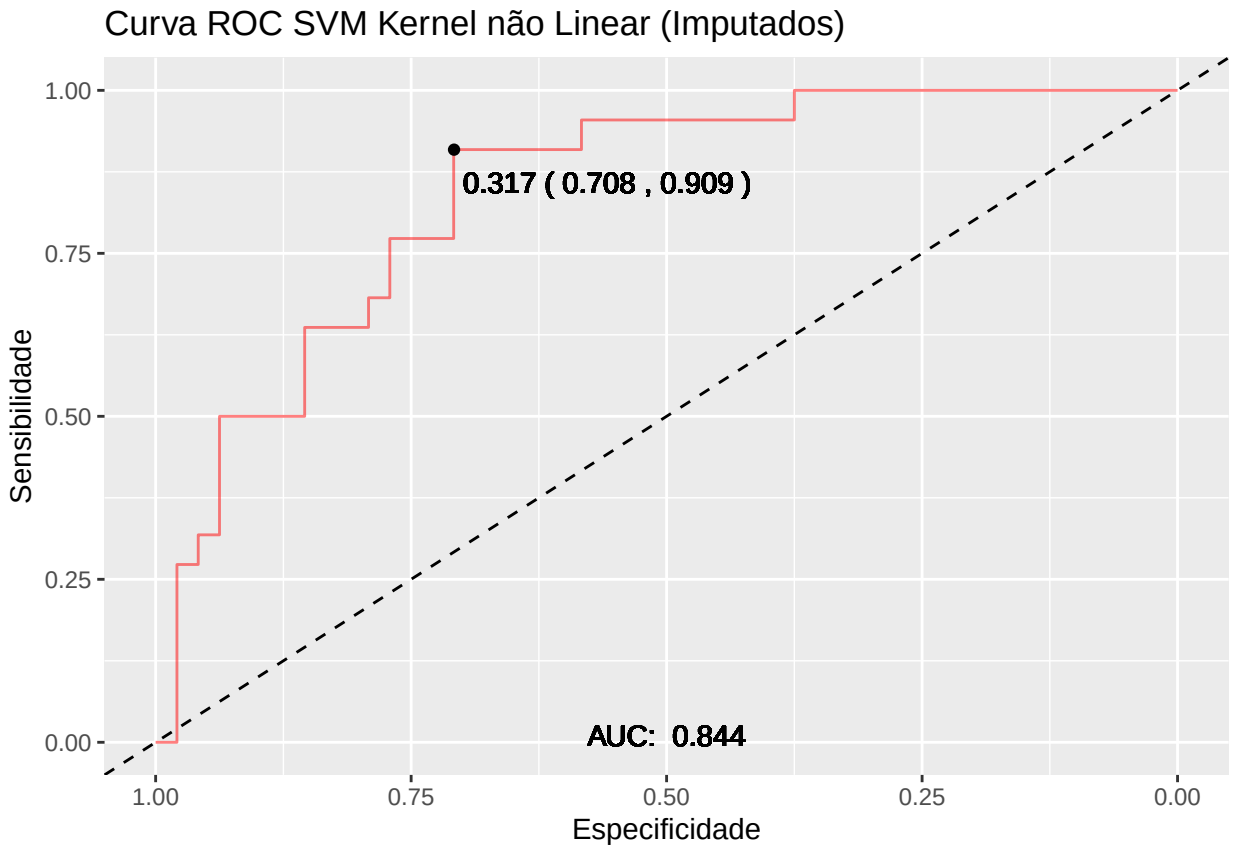

```
predictAD6out <- predict(modeloAD6, newdata = test_whitout_NAs)
confusionMatrix(predictAD6out, test_whitout_NAs$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
```

```
##        No  17   5
##        Yes  7   8
##
##                Accuracy : 0.6757
##                  95% CI : (0.5021, 0.8199)
##     No Information Rate : 0.6486
##     P-Value [Acc > NIR] : 0.4384
##
##                   Kappa : 0.3127
##
##  Mcnemar's Test P-Value : 0.7728
##
##             Sensitivity : 0.7083
##             Specificity : 0.6154
##          Pos Pred Value : 0.7727
##          Neg Pred Value : 0.5333
##              Prevalence : 0.6486
##          Detection Rate : 0.4595
##    Detection Prevalence : 0.5946
##       Balanced Accuracy : 0.6619
##
##        'Positive' Class : No
##
```

SVM Kernel Não Linear - Dados Imputados

```
## SVM Kernel não Linear com dados imputados
rocSVM3 <- roc(response = test$diabetes, predictor = predict(modeloSVM3, test, type = "prob")[,2])
plotaroc(rocSVM3, titulo = "Curva ROC SVM Kernel não Linear (Imputados)")
```




```
predictSVM3 <- predict(modeloSVM3, newdata = test)
confusionMatrix(predictSVM3, test$diabetes)
```

```
## Confusion Matrix and Statistics
##
##           Reference
## Prediction No Yes
##        No  38   8
##        Yes 10  14
##
##                Accuracy : 0.7429
##                  95% CI : (0.6244, 0.8399)
##     No Information Rate : 0.6857
##     P-Value [Acc > NIR] : 0.1846
##
##                   Kappa : 0.4177
##
##  Mcnemar's Test P-Value : 0.8137
##
##             Sensitivity : 0.7917
##             Specificity : 0.6364
##          Pos Pred Value : 0.8261
##          Neg Pred Value : 0.5833
##              Prevalence : 0.6857
##          Detection Rate : 0.5429
```

```
##    Detection Prevalence : 0.6571
##       Balanced Accuracy : 0.7140
##
##        'Positive' Class : No
##
```