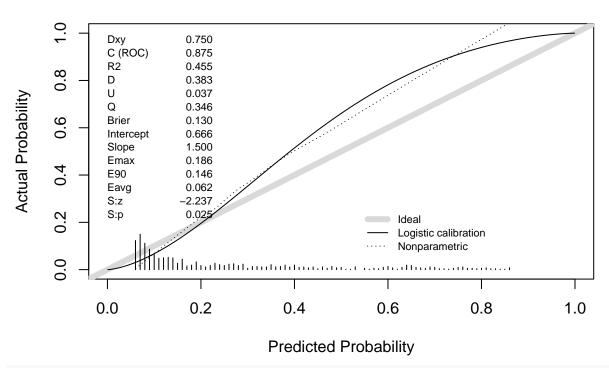
Chapter 4 Code Snippets

Calibration by isotonic regression can be performed by the following script. Note how the calibration chart improves.

```
library(CORElearn)
library(rms)
rawpreds<-1-(predict(ens,dataC,type='prob'))</pre>
## Warning in predict.ranger.forest(forest, data, predict.all, num.trees, type, :
## Forest grown in ranger version <0.11.5, converting ...
cab<-CORElearn::calibrate(dataC$EarlyRec,rawpreds,class1=2,method='isoReg')</pre>
calibratedpreds<-CORElearn::applyCalibration(rawpreds,cab)</pre>
calibratedpreds[calibratedpreds==0]<-0.00000000001
val.prob(rawpreds,as.numeric(dataC$EarlyRec)-1)
                                                          D:Chi-sq
##
                    C (ROC)
                                                   D
           Dxy
##
   7.502207e-01 8.751103e-01 4.554701e-01 3.830063e-01
                                                     3.120011e+02
##
                          U
                                U:Chi-sq
           D:p
                                                 U:p
##
                3.735025e-02 3.232840e+01
                                         9.549424e-08 3.456560e-01
##
                                                              E90
         Brier
                   Intercept
                                   Slope
                                                Emax
   1.297590e-01 6.664174e-01 1.500472e+00 1.860607e-01 1.458758e-01
##
##
                        S:z
                                     S:p
   6.189257e-02 -2.237270e+00 2.526873e-02
title('Pre-Calibration')
```

Pre-Calibration

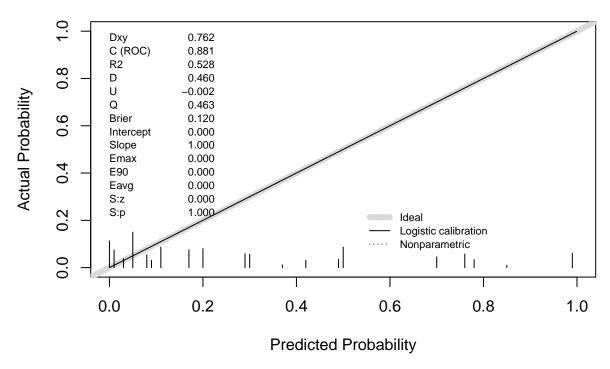


val.prob(calibratedpreds,as.numeric(dataC\$EarlyRec)-1)

```
C (ROC)
##
             Dxy
                                           R2
                                                          D
                                                                 D:Chi-sq
                  8.811867e-01
##
    7.623735e-01
                                5.276450e-01
                                               4.601452e-01
                                                             3.746379e+02
##
             D:p
                                    U:Chi-sq
                                                        U:p
              NA -2.463054e-03 -1.364242e-12
##
                                               1.000000e+00
                                                             4.626083e-01
                     Intercept
##
           Brier
                                        Slope
                                                       Emax
    1.195667e-01 1.317081e-10
                                1.000000e+00
##
                                               5.884293e-12
                                                             4.522368e-12
            Eavg
                           S:z
                                          S:p
    1.786421e-12 -2.302171e-10
                               1.000000e+00
```

title('Post-Calibration')

Post-Calibration



The raw shapley score is calculated using the iml library. It is illustrated below for two example cases. Factors that increase risk produce bars to the right of the midline in 'Yes' graph and to the left of the midline in the 'No' graph. In the first example it can be seen the chance of early recurrence is reduced most markedly by vascular invasion being negative and total lymph nodes positive being zero.

In the second example of a high risk case, vascular invasion and ypT4 produce the biggest increase in risk, with number of positive lymph nodes actually relatively less important.

```
library(iml)
predictor<-Predictor$new(model=ens,data=dataC[,-11])

data1<-dataC[100,-11]
1-predict(ens,data1,type='prob')

## Warning in predict.ranger.forest(forest, data, predict.all, num.trees, type, :
## Forest grown in ranger version <0.11.5, converting ...

## [1] 0.06579376

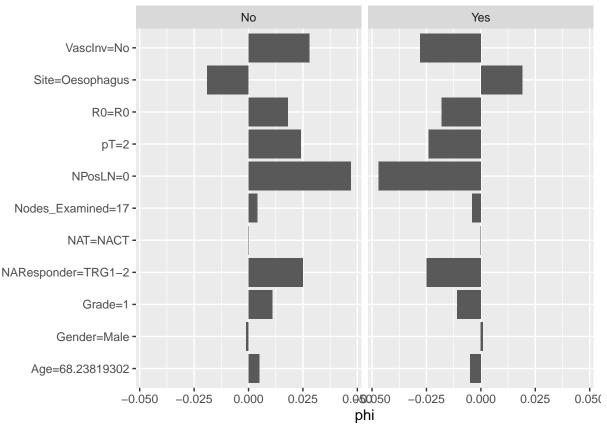
shapley<-Shapley$new(predictor,x.interest=data1,sample.size = 1000)

## Warning in predict.ranger.forest(forest, data, predict.all, num.trees, type, :
## Forest grown in ranger version <0.11.5, converting ...

## Warning in predict.ranger.forest(forest, data, predict.all, num.trees, type, :
## Forest grown in ranger version <0.11.5, converting ...

## Warning in predict.ranger.forest(forest, data, predict.all, num.trees, type, :
## Forest grown in ranger version <0.11.5, converting ...

plot(shapley)</pre>
```



```
data2<-dataC[200,-11]
1-predict(ens,data2,type='prob')

## Warning in predict.ranger.forest(forest, data, predict.all, num.trees, type, :
## Forest grown in ranger version <0.11.5, converting ...

## [1] 0.6943481

shapley2<-Shapley$new(predictor,x.interest=data2,sample.size = 1000)

## Warning in predict.ranger.forest(forest, data, predict.all, num.trees, type, :
## Forest grown in ranger version <0.11.5, converting ...

## Warning in predict.ranger.forest(forest, data, predict.all, num.trees, type, :
## Forest grown in ranger version <0.11.5, converting ...

## Warning in predict.ranger.forest(forest, data, predict.all, num.trees, type, :
## Forest grown in ranger version <0.11.5, converting ...

plot(shapley2)</pre>
```

