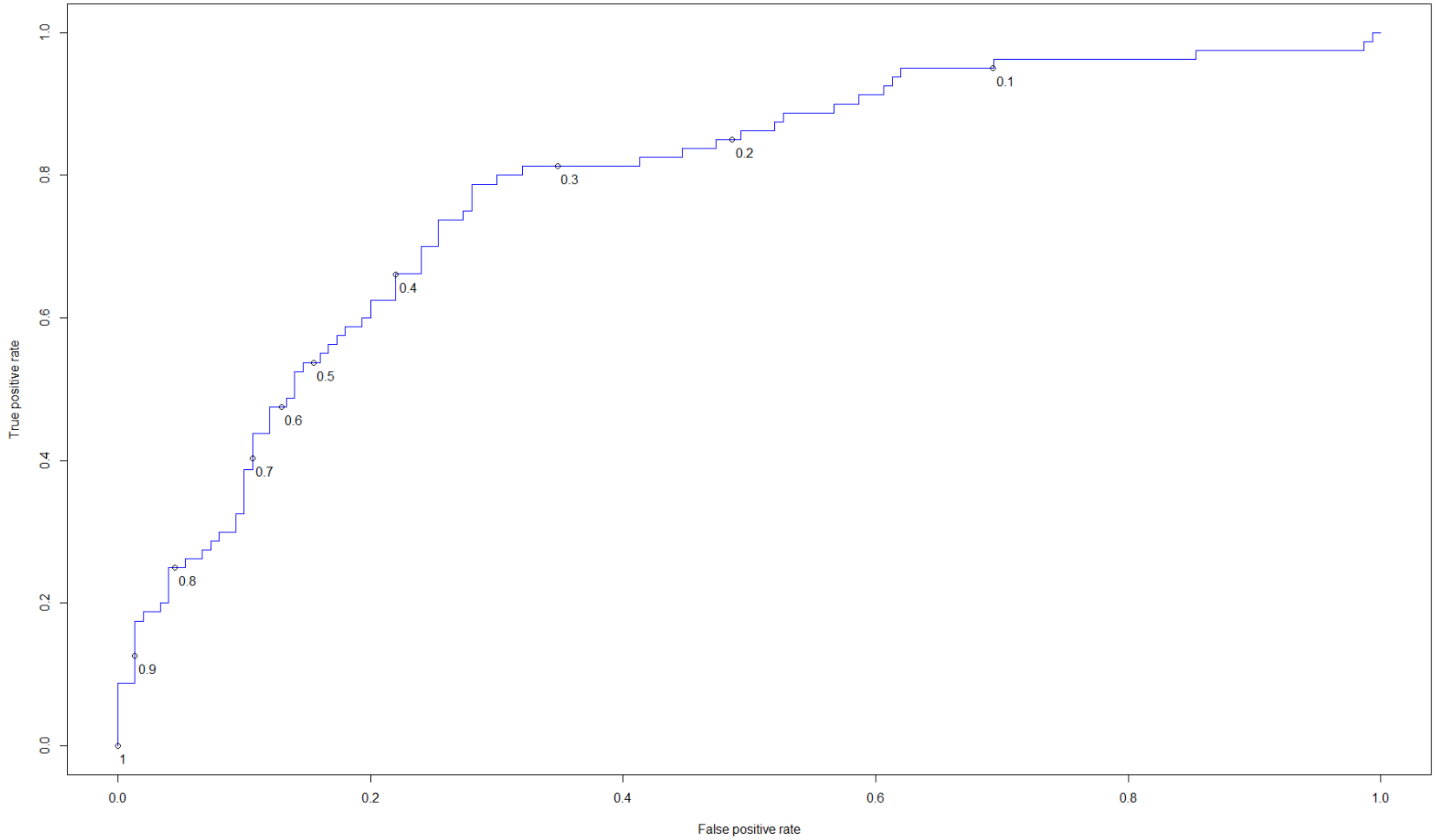
```
> training_set <- subset(diabet, di == TRUE)
> testing_set <- subset(diabet, di == FALSE)
> model2 <- glm(Is_Diabetic~.,data = training_set, family = "binomial" )
> summary(model2)

Call:
glm(formula = Is_Diabetic ~ ., family = "binomial", data = training_set)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.7124  -0.6772  -0.3820   0.6426   2.5654

Coefficients:
                       Estimate Std. Error z value Pr(>|z|)
(Intercept)          -9.256065   0.906286 -10.213  < 2e-16 ***
No.of_times_pregnant  0.102536   0.040193   2.551   0.0107 *
glucose_conc          0.044270   0.004978   8.892  < 2e-16 ***
blood_pressure       -0.014853   0.007046  -2.108   0.0350 *
skin_fold_thickness   0.007975   0.008803   0.906   0.3649
X2.Hour_serum_insulin -0.003353   0.001256  -2.669   0.0076 **
BMI                   0.089144   0.018969   4.699 2.61e-06 ***
Diabetes_pedigree_fn  0.832683   0.385883   2.158   0.0309 *
Age                   0.016337   0.011838   1.380   0.1675
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 696.28  on 537  degrees of freedom
Residual deviance: 477.81  on 529  degrees of freedom
AIC: 495.81

Number of Fisher Scoring iterations: 5

> predi <- predict(model2,newdata = testing_set,type = "response")
```

```
0.262659210 0.635927310 0.083913125 0.018291855 0.278908246 0.460242613 0.368007779
        544         547         548         549         550         555         558
0.082688838 0.971834246 0.288160295 0.737259113 0.863623819 0.079544359 0.255051067
        559         563         566         567         568         572         573
0.657040450 0.097856948 0.074336739 0.177372592 0.121184664 0.105178813 0.190143783
        577         584         585         586         592         593         594
0.197598224 0.300816391 0.128383805 0.044441626 0.218939096 0.456858889 0.115109418
        595         601         602         606         610         620         625
0.373725442 0.084169779 0.159413257 0.416381827 0.045787432 0.356585917 0.119181657
        629         630         632         633         634         639         643
0.419295213 0.056979057 0.098314291 0.115953340 0.093105281 0.370788985 0.567916205
        648         649         656         657         661         665         667
0.856621936 0.478403830 0.377892659 0.045999967 0.767874705 0.433313164 0.675953761
        680         687         691         692         693         695         696
0.041099036 0.187870158 0.193722286 0.889127510 0.450576945 0.035723663 0.184281850
        699         700         704         708         710         712         716
0.282552044 0.618358561 0.733957792 0.183154409 0.136900525 0.371756794 0.901290517
        717         718         719         720         724         730         736
0.827735361 0.178627453 0.169210407 0.264069958 0.360479892 0.069752624 0.193618557
        741         748         750         751         754         756
0.730420985 0.275248213 0.677259870 0.564626433 0.636519476 0.471662919
> table(Actualvalues = testing_set$Is_Diabetic, Predictedvalues = predi>0.5)
            Predictedvalues
Actualvalues FALSE TRUE
           0   127   23
           1    37   43
>
```


True positive rate
False positive rate
0.0
0.2
0.4
0.6
0.8
1.0
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1