432 Class 10 Slides

github.com/THOMASELOVE/432-2018

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Setup

```
library(skimr)
library(broom)
library(Hmisc)
library(rms)
library(pROC)
library(ROCR)
library(simputation)
library(tidyverse)
```

Today's Materials

- A new logistic regression example
  - Modeling 10-year risk of coronary heart disease
  - based on a sample from the Framingham Heart Study

```
fram <- read.csv("data/fram_new.csv") %>% tbl_df
```

The Framingham Heart Study data (`fram_new.csv`)

Codebook (4,240 subjects, 17 variables)

Variable	Interpretation (at baseline)	NAs
`subj`	subject ID code	0
`sex`	F or M	0
`age`	in years	0
`smoker`	current smoker?	0
`cigs_day`	mean cigarettes smoked per day	29
`bp_meds`	on at least one BP medication?	53
`hx_stroke`	history of stroke?	0
`hx_htn`	history of hypertension?	0
`hx_dm`	history of diabetes?	0
`educ`	4 ordered levels (1-4)	105

- variables with ? in Interpretation are 1 = yes, 0 = no
- educ: 1 = some HS, 2 = HS diploma, 3 = some college, 4 = college grad

Codebook (4,240 subjects, 17 variables)

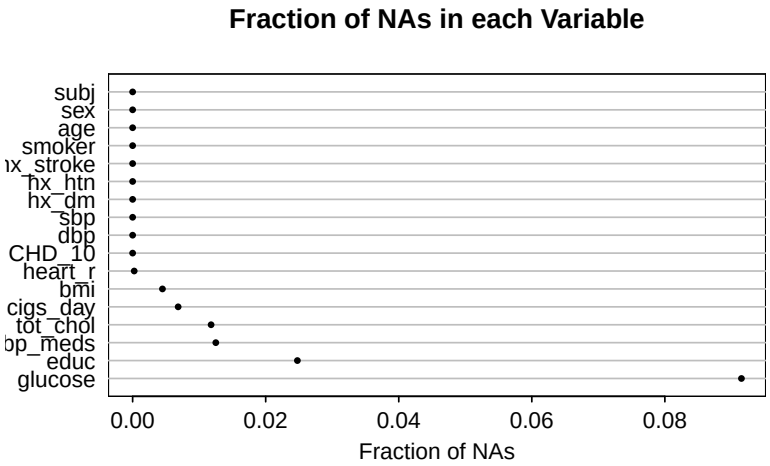
Variable	Interpretation	NAs
tot_chol	baseline total cholesterol, mg/dl	50
sbp	baseline mean systolic BP, mm Hg	0
dbp	baseline mean diastolic BP, mm Hg	0
bmi	baseline body mass index, kg/m^2	19
heart_r	baseline heart rate, beats/min	1
glucose	baseline glucose level, mg/dl	388
CHD_10	CHD in 10 years after baseline?	0

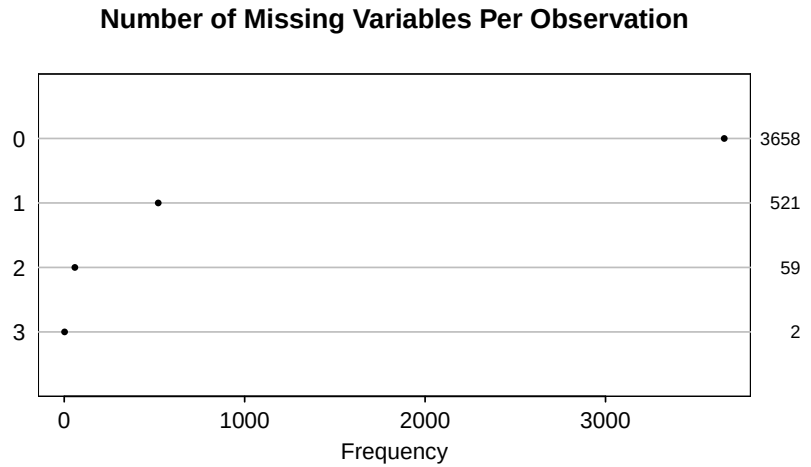
1. Goal 1. Predict CHD_10 using hx_htn
2. Goal 2. Predict CHD_10 using tot_chol and hx_htn
3. Goal 3. Predict CHD_10 using kitchen sink
4. Goal 4. Fit a smaller model almost as good as the KS.

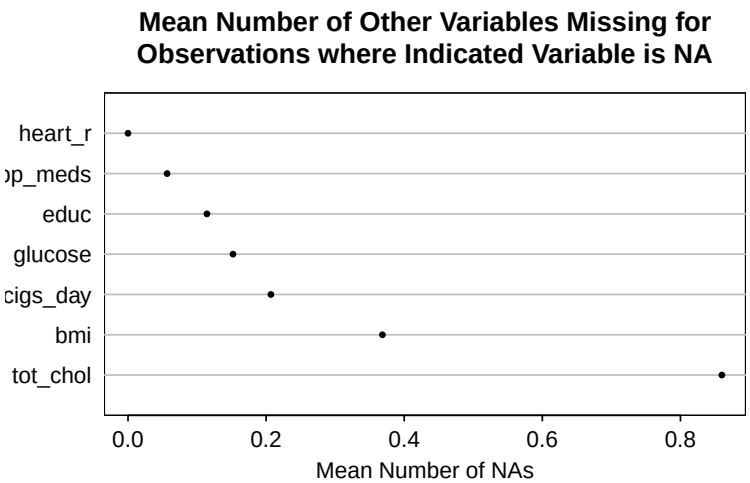
Skimming the Data, before Cleanup or Imputation

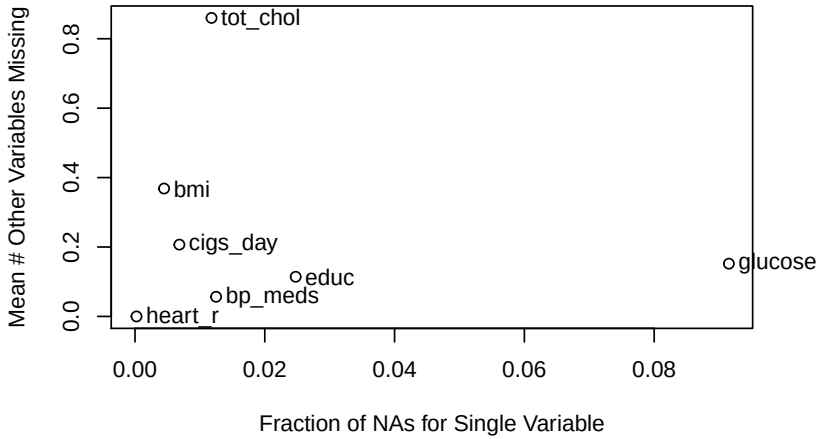
```
> fram %>% select(-subj) %>% skim
Skim summary statistics
 n obs: 4240
 n variables: 16

Variable type: factor
 variable missing complete    n n_unique             top_counts ordered
      sex       0     4240 4240        2 F: 2420, M: 1820, NA: 0   FALSE

Variable type: integer
  variable missing complete    n      mean     sd  p0 p25 median p75 p100     hist
       age       0     4240 4240  49.58    8.57   32  42     49  56   70 ▂▆▇▆▃▂▁▁
    bp_meds      53     4187 4240   0.03    0.17    0   0      0   0    1 ▇▁▁▁▁▁▁▁
     CHD_10       0     4240 4240   0.15    0.36    0   0      0   0    1 ▇▁▁▁▁▁▁▂
   cigs_day      29     4211 4240   9.01   11.92    0   0      0  20   70 ▇▂▁▁▁▁▁▁
       educ     105     4135 4240   1.98    1.02    1   1      2   3    4 ▇▃▂▃▁▂▁▂
    glucose     388     3852 4240  81.96   23.95   40  71     78  87  394 ▇▂▁▁▁▁▁▁
    heart_r       1     4239 4240  75.88   12.03   44  68     75  83  143 ▁▅▇▂▁▁▁▁
      hx_dm       0     4240 4240   0.026   0.16    0   0      0   0    1 ▇▁▁▁▁▁▁▁
     hx_htn       0     4240 4240   0.31    0.46    0   0      0   1    1 ▇▁▁▁▁▁▁▂
  hx_stroke       0     4240 4240   0.0059  0.077   0   0      0   0    1 ▇▁▁▁▁▁▁▁
     smoker       0     4240 4240   0.49    0.5     0   0      0   1    1 ▇▁▁▁▁▁▁▇
   tot_chol      50     4190 4240 236.7    44.59  107 206    234 263  696 ▁▆▂▁▁▁▁▁

Variable type: numeric
 variable missing complete    n   mean    sd    p0   p25 median   p75  p100     hist
      bmi      19     4221 4240  25.8   4.08 15.54 23.07   25.4 28.04  56.8 ▃▇▂▁▁▁▁▁
      dbp       0     4240 4240  82.9  11.91 48     75     82    90   142.5 ▂▇▅▂▁▁▁▁
      sbp       0     4240 4240 132.35 22.03 83.5  117    128   144   295  ▃▇▂▁▁▁▁▁
```

Plotting Missingness (with `Hmisc`)









Simple Imputation into `fram1`

```
set.seed(432001)

fram1 <- fram %>%
    impute_pmm(educ + cigs_day + heart_r ~ age + smoker) %>%
    impute_rlm(bmi + tot_chol ~ sex + age + sbp + heart_r) %>%
    impute_pmm(bp_meds ~ hx_htn + bmi + tot_chol) %>%
    impute_rlm(glucose ~ hx_dm + bmi + tot_chol + age)
```

Turn educ into ed_f, a factor.

```
fram1 <- fram1 %>%
    mutate(ed_f = fct_recode(factor(educ),
                    "1_Some_HS" = "1", "2_HS_grad" = "2",
                    "3_Some_Col" = "3", "4_Col_grad" = "4"))

fram1 %>% count(educ, ed_f)
```

```
# A tibble: 4 x 3
   educ ed_f           n
  <int> <fct>      <int>
1     1 1_Some_HS   1720
2     2 2_HS_grad   1358
3     3 3_Some_Col   689
4     4 4_Col_grad   473
```

Final Data Set?

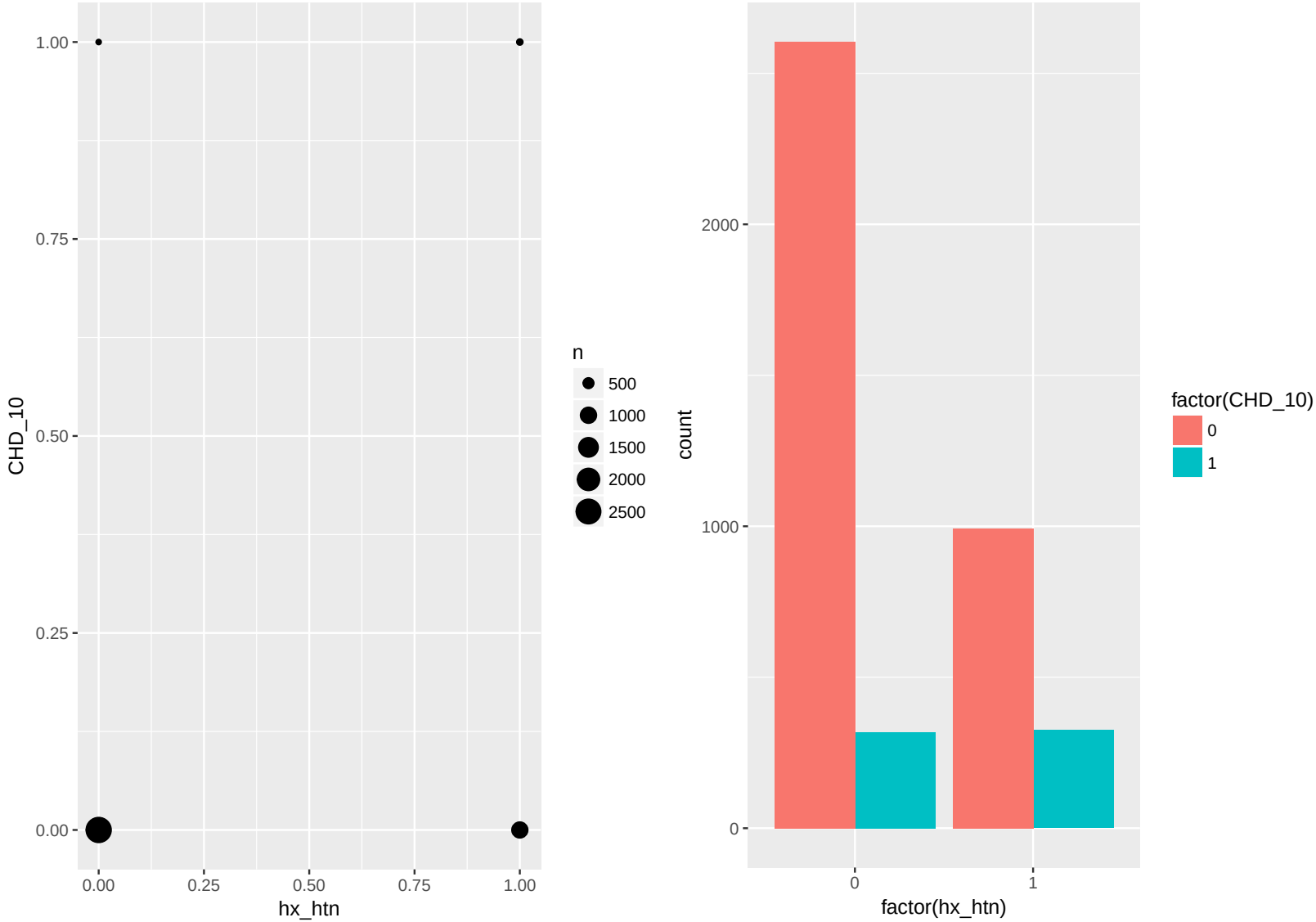
```
fram2 <- fram1 %>%
    select(subj, sex, age, smoker, cigs_day, bp_meds,
           hx_stroke, hx_htn, hx_dm, ed_f, tot_chol,
           sbp, dbp, bmi, heart_r, glucose, CHD_10)
```

fram2 %>% select(-subj) %>% skim

```
> fram2 %>% select(-subj) %>% skim
Skim summary statistics
 n obs: 4240
 n variables: 16

Variable type: factor
 variable missing complete    n n_unique                                top_counts ordered
     ed_f       0     4240 4240        4 1_S: 1720, 2_H: 1358, 3_S: 689, 4_C: 473   FALSE
      sex       0     4240 4240        2                  F: 2420, M: 1820, NA: 0   FALSE

Variable type: integer
  variable missing complete    n    mean     sd p0 p25 median p75 p100     hist
       age       0     4240 4240 49.58    8.57  32  42     49  56   70 ▂▆▇▆▃▂▂▁
   bp_meds       0     4240 4240  0.029   0.17   0   0      0   0    1 ▇▁▁▁▁▁▁▁
    CHD_10       0     4240 4240  0.15    0.36   0   0      0   0    1 ▇▁▁▁▁▁▁▂
  cigs_day       0     4240 4240  9.07   11.91   0   0      0  20   70 ▇▂▁▁▁▁▁▁
   heart_r       0     4240 4240 75.88   12.02  44  68     75  83  143 ▁▆▇▂▁▁▁▁
     hx_dm       0     4240 4240  0.026   0.16   0   0      0   0    1 ▇▁▁▁▁▁▁▁
    hx_htn       0     4240 4240  0.31    0.46   0   0      0   1    1 ▇▁▁▁▁▁▁▃
 hx_stroke       0     4240 4240  0.0059  0.077  0   0      0   0    1 ▇▁▁▁▁▁▁▁
    smoker       0     4240 4240  0.49    0.5    0   0      0   1    1 ▇▁▁▁▁▁▁▇

Variable type: numeric
 variable missing complete    n   mean    sd     p0    p25 median    p75  p100     hist
      bmi       0     4240 4240  25.8   4.07  15.54  23.08  25.38  28.04  56.8 ▃▇▂▁▁▁▁▁
      dbp       0     4240 4240  82.9  11.91  48     75     82     90    142.5 ▂▇▃▁▁▁▁▁
  glucose       0     4240 4240  81.7  22.94  40     72     78     85    394   ▇▁▁▁▁▁▁▁
      sbp       0     4240 4240 132.35 22.03  83.5  117    128    144    295   ▃▇▂▁▁▁▁▁
 tot_chol       0     4240 4240 236.73 44.36 107    206    234    263    696   ▂▇▃▁▁▁▁▁
```

Goal 1. Predict `CHD_10` using `hx_htn`

Predict CHD_10 using hx_htn



Predict CHD_10 using hx_htn

```
fram2 %>% count(hx_htn, CHD_10)
```

```
# A tibble: 4 x 3
  hx_htn CHD_10     n
   <int>  <int> <int>
1      0      0  2604
2      0      1   319
3      1      0   992
4      1      1   325
```

```
table(fram2$hx_htn, fram2$CHD_10)
```

```
     0    1
  0 2604  319
  1  992  325
```

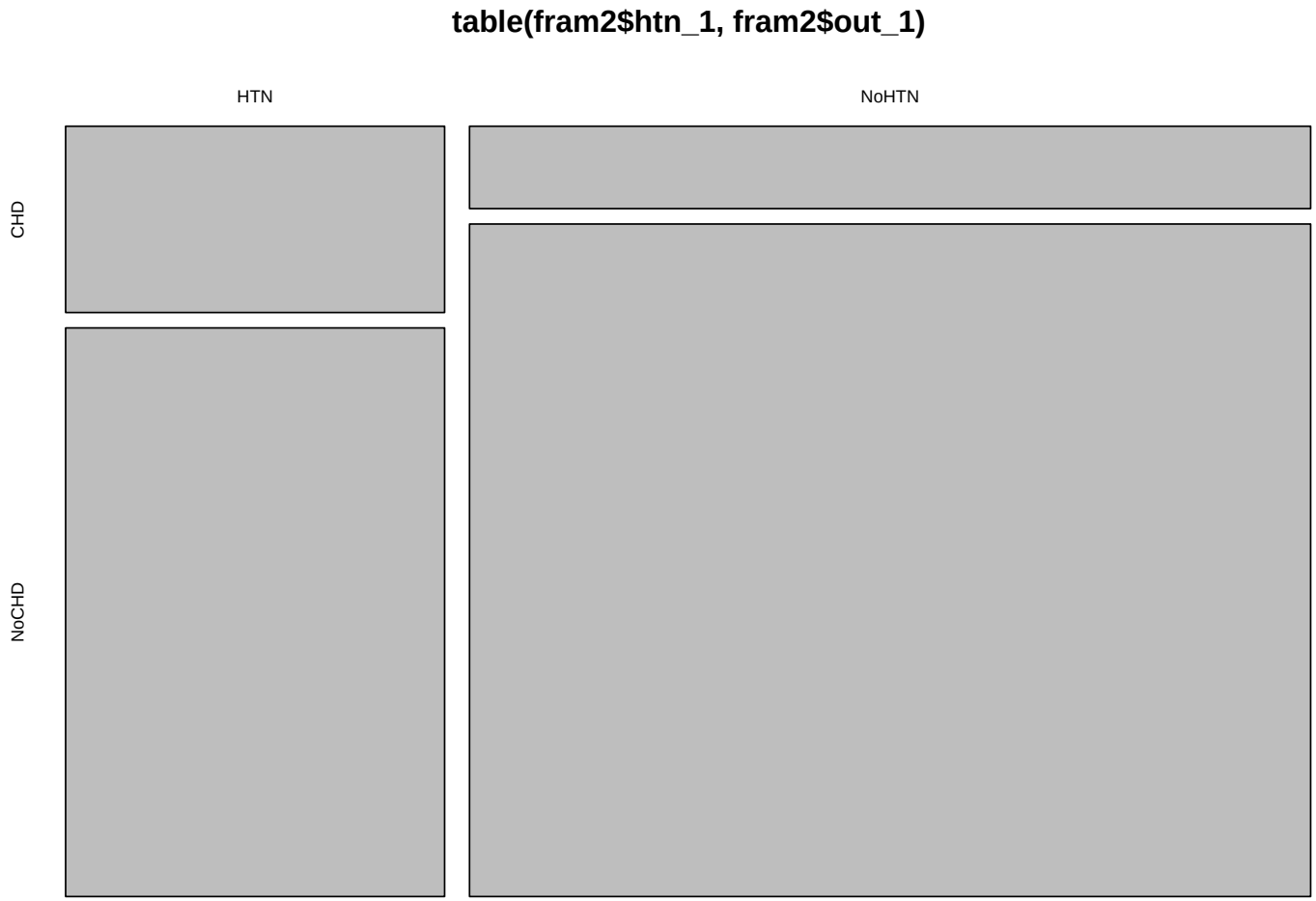
Convert to Standard Epidemiological Format

```
fram2 <- fram2 %>%
    mutate(htn_1 = fct_recode(factor(hx_htn),
                              HTN = "1", NoHTN = "0"),
           htn_1 = fct_relevel(htn_1, "HTN"),
           out_1 = fct_recode(factor(CHD_10),
                              CHD = "1", NoCHD = "0"),
           out_1 = fct_relevel(out_1, "CHD"))

fram2 %>% count(htn_1, hx_htn, out_1, CHD_10)
```

```
# A tibble: 4 x 5
  htn_1 hx_htn out_1 CHD_10     n
  <fct>  <int> <fct>  <int> <int>
1 HTN        1 CHD        1   325
2 HTN        1 NoCHD      0   992
3 NoHTN      0 CHD        1   319
4 NoHTN      0 NoCHD      0  2604
```

A mosaic plot?

```
plot(table(fram2$htn_1, fram2$out_1))
```



Two-by-Two Table Analysis (from the Epi package)

```
Epi::twoby2(table(fram2$htn_1, fram2$out_1))
```

```
2 by 2 table analysis:
------------------------------------------------------
Outcome   : CHD
Comparing : HTN vs. NoHTN

      CHD NoCHD    P(CHD) 95% conf. interval
HTN   325   992    0.2468    0.2242   0.2708
NoHTN 319  2604    0.1091    0.0983   0.1210

                                    95% conf. interval
            Relative Risk: 2.2612    1.9656   2.6013
        Sample Odds Ratio: 2.6744    2.2542   3.1728
Conditional MLE Odds Ratio: 2.6737    2.2454   3.1843
    Probability difference: 0.1376    0.1122   0.1640
```

A Logistic Regression model with glm

```
m_01 <- glm(CHD_10 ~ hx_htn, data = fram2,
            family = binomial)

m_01
```

```
Call:  glm(formula = CHD_10 ~ hx_htn, family = binomial, data

Coefficients:
(Intercept)       hx_htn
    -2.0996       0.9837

Degrees of Freedom: 4239 Total (i.e. Null);  4238 Residual
Null Deviance:      3612
Residual Deviance: 3487     AIC: 3491
```

Interpretation of the Model

```
exp(coef(m_01)); exp(confint(m_01))
```

```
(Intercept)      hx_htn
  0.1225038   2.6743730

Waiting for profiling to be done...

                 2.5 %    97.5 %
(Intercept) 0.1088612 0.1373705
hx_htn      2.2543282 3.1733406
```

Compare this to the `twoby2` result:

```
          Sample Odds Ratio: 2.6744    2.2542   3.1728
Conditional MLE Odds Ratio: 2.6737    2.2454   3.1843
```

Using broom

```
tidy(m_01)
```

```
         term  estimate  std.error statistic       p.value
1 (Intercept) -2.099613 0.05931785 -35.39597 1.969337e-274
2      hx_htn  0.983715 0.08719855  11.28132  1.622882e-29
```

```
glance(m_01)
```

```
  null.deviance df.null    logLik      AIC      BIC
1      3612.209    4239 -1743.453 3490.906 3503.611
  deviance df.residual
1 3486.906        4238
```

ROC Analysis

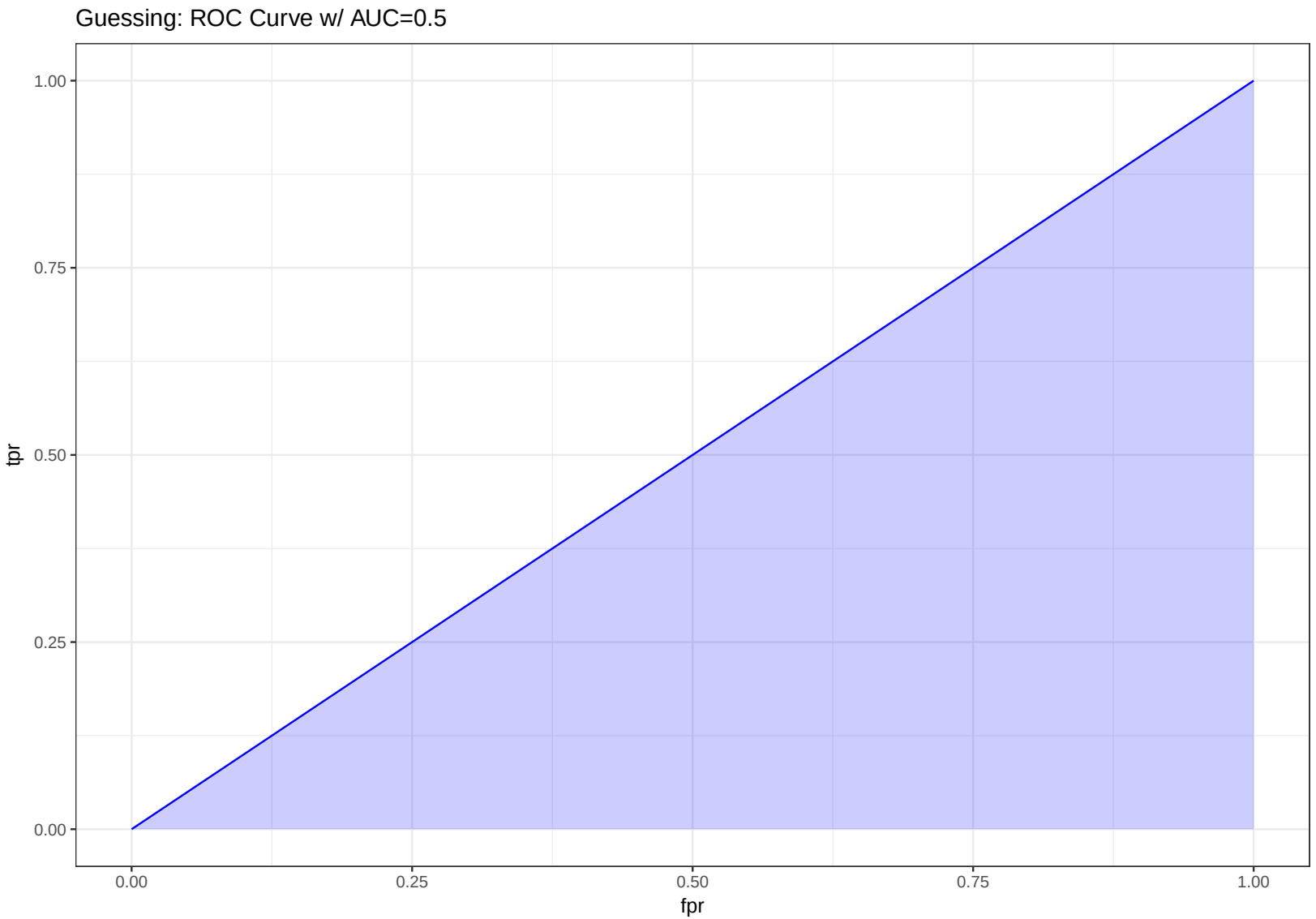
How ROC works

- If we're guessing completely at random, then we should classify a subject correctly (as CHD or no CHD) about 50% of the time.
  - In that case, the Specificity and the Sensitivity will be equal so we get a diagonal line in the plot, and AUC = 0.5.
- If we're classifying subjects perfectly, then we have a true positive rate (Sensitivity) of 1 and an false positive rate (1 - Specificity) of 0.
  - In that case, the area under the curve (AUC) will be 1.
- Values of the C statistic = AUC below 0.5 indicate models worse than guessing.
- Values of C above 0.9 indicate excellent discrimination.
- Values of C above 0.8 indicate good discrimination.

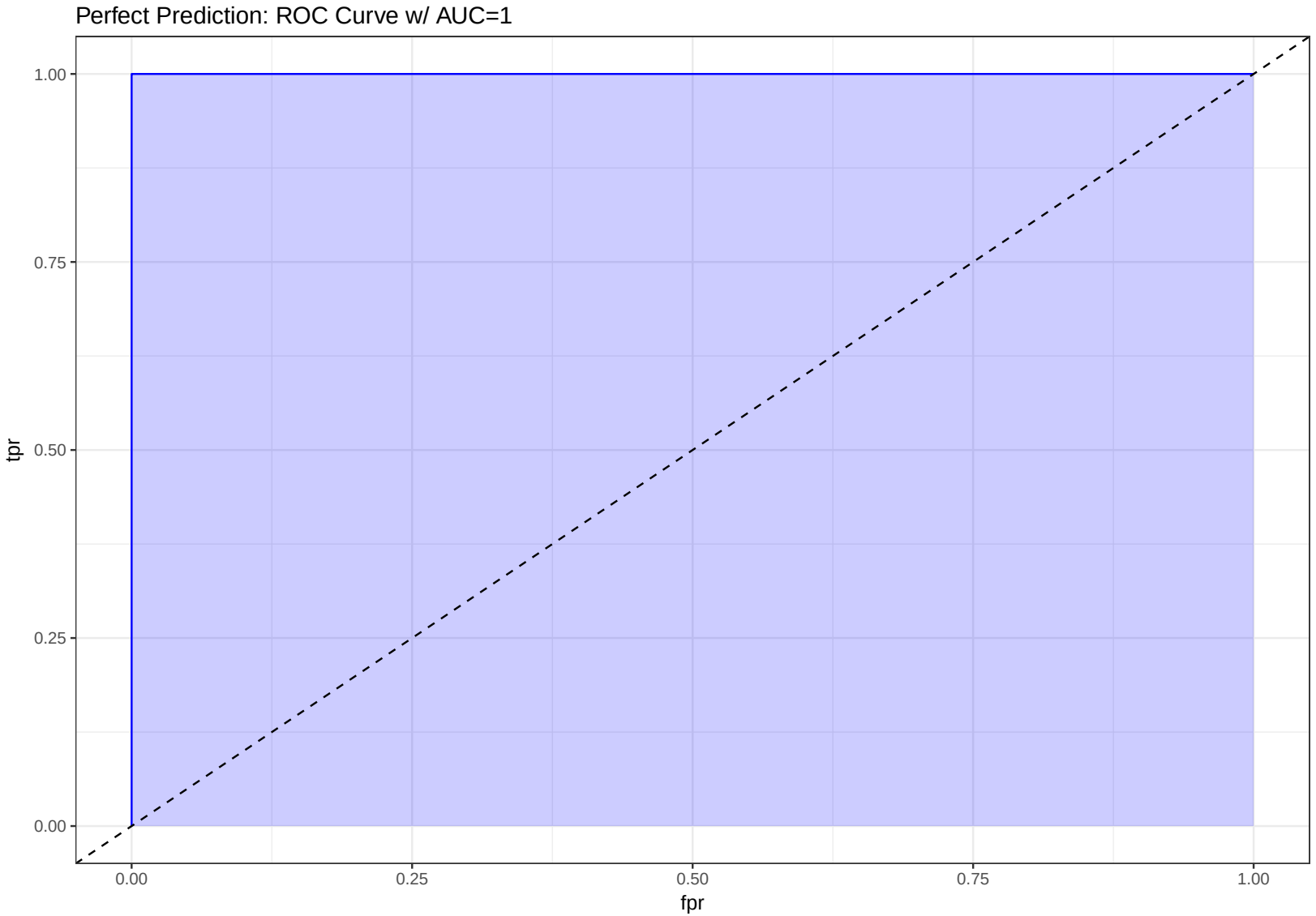
Simulation from Class 09

```
set.seed(43223)
sim.temp <- data_frame(x = rnorm(n = 200),
                       prob = exp(x)/(1 + exp(x)),
                       y = as.numeric(1 * runif(200) < prob))

sim.temp <- sim.temp %>%
    mutate(p_guess = 1,
           p_perfect = y,
           p_bad = exp(-2*x) / (1 + exp(-2*x)),
           p_ok = prob + (1-y)*runif(1, 0, 0.05),
           p_good = prob + y*runif(1, 0, 0.27))
```

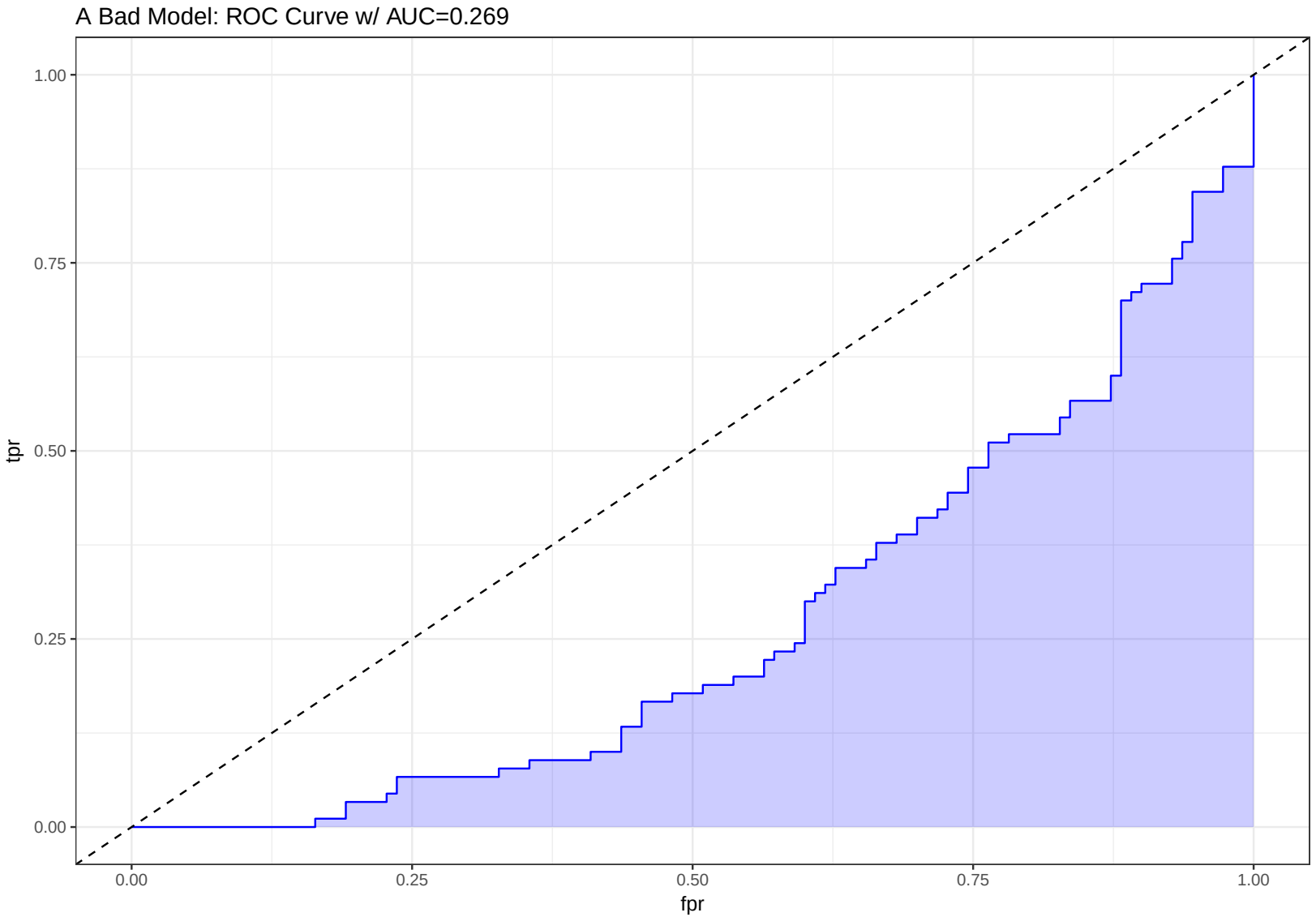
What if we are guessing?



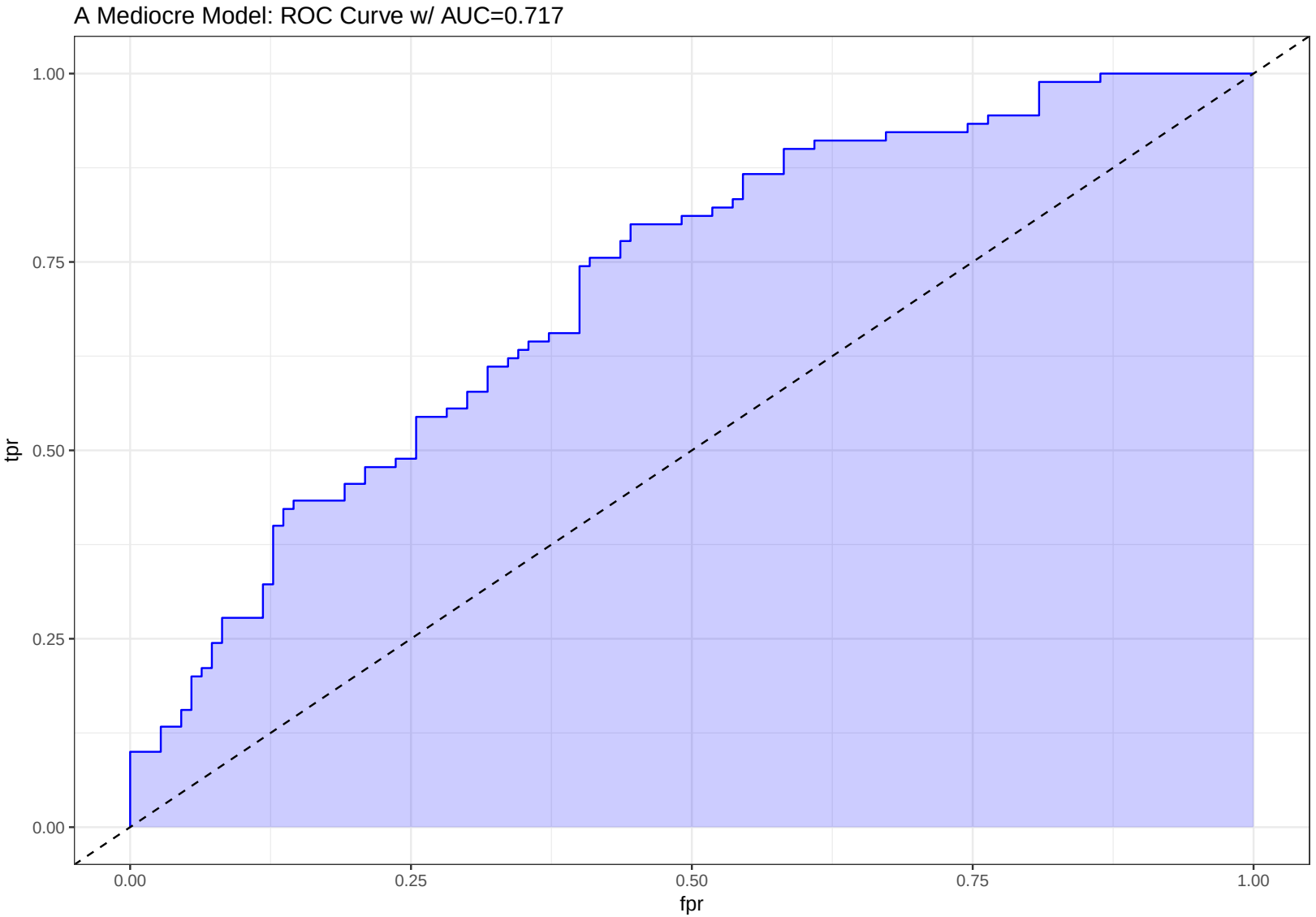
What if our model classifies things perfectly?



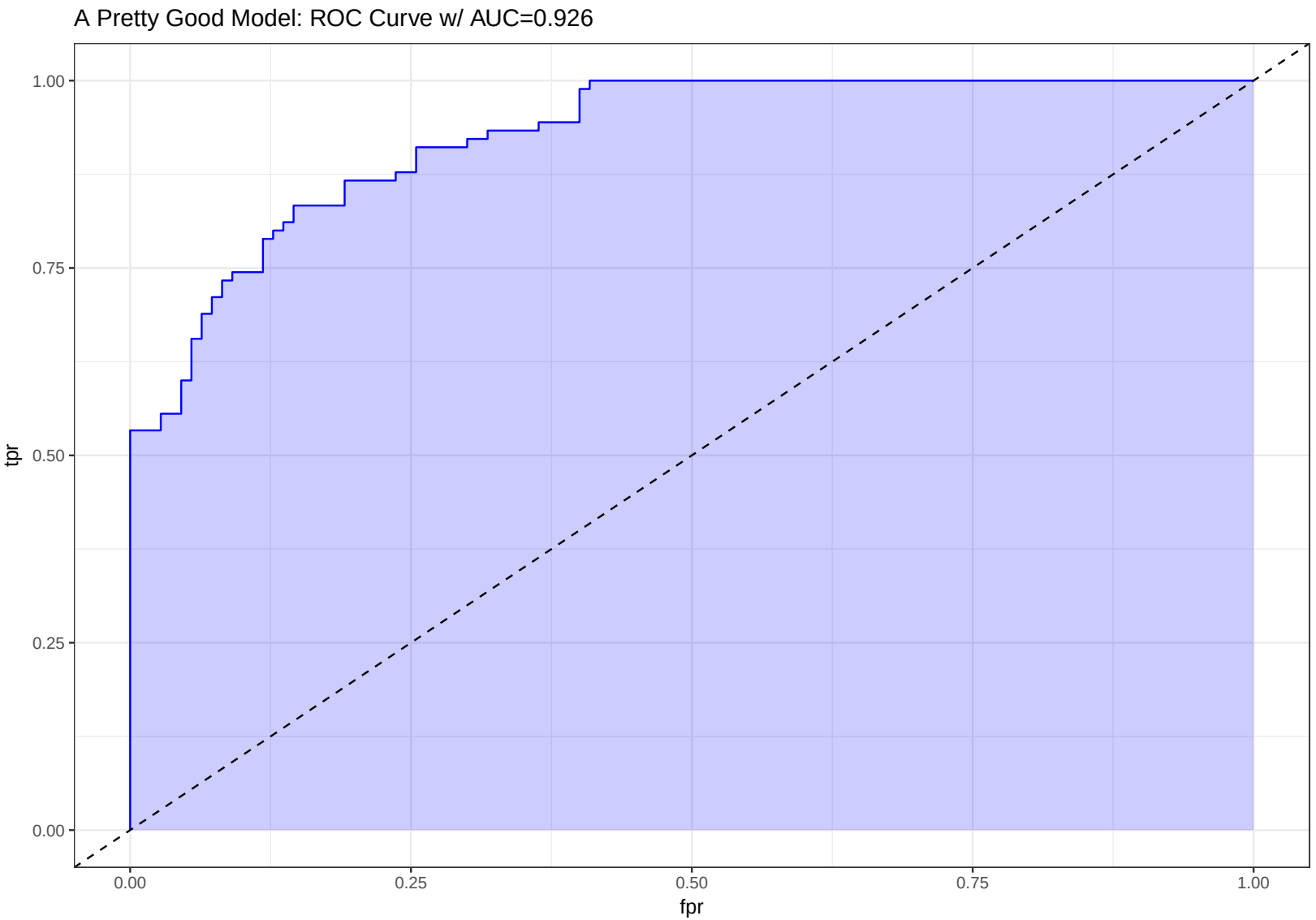
What does "worse than guessing" look like?



What does "better than guessing" look like? (C = 0.72)



What does "excellent" look like? (C = 0.93)



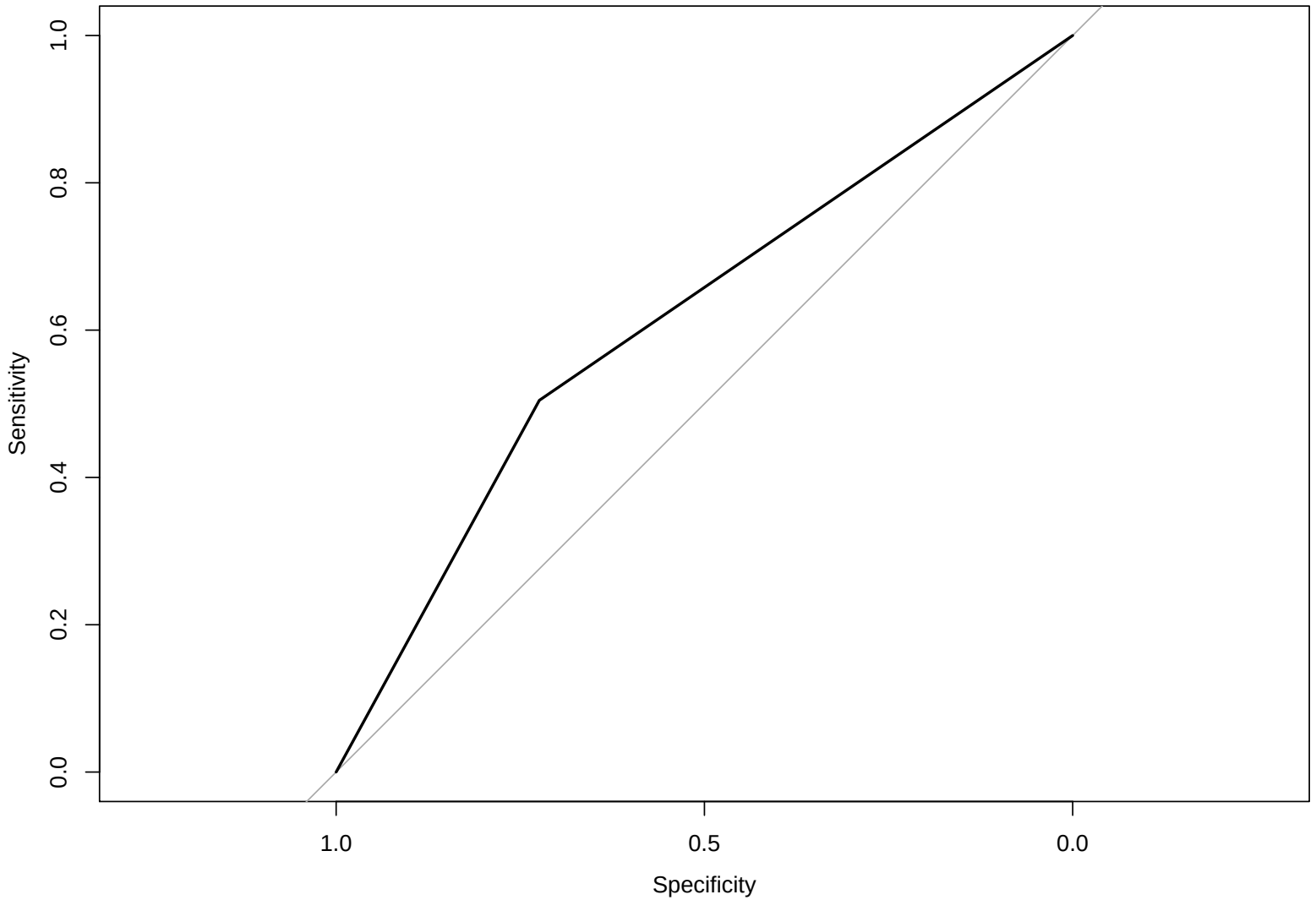
Plotting the ROC Curve for m_01

```
# requires pROC package
roc_m_01 <-
    roc(fram2$CHD_10 ~ predict(m_01, type = "response"),
        ci = TRUE)
```

```
> roc_m_01

Call:
roc.formula(formula = fram2$CHD_10 ~ predict(m_01, type = "response"),     ci = TRUE)

Data: predict(m_01, type = "response") in 3596 controls (fram2$CHD_10 0) < 644 cases (fram2$CHD_10 1).
Area under the curve: 0.6144
95% CI: 0.5937-0.6351 (DeLong)
```

ROC Curve for m_01 via pROC (C = 0.6143982)

```
plot(roc_m_01)
```



Interpreting the C statistic (0.614) for `m_01`

C statistic	Interpretation
0.90 to 1.00	model does an excellent job at discriminating "CHD" from "no" (A)
0.80 to 0.90	model does a good job (B)
0.70 to 0.80	model does a fair job (C)
0.60 to 0.70	model does a poor job (D)
0.50 to 0.60	model fails (F)
below 0.50	model is worse than random guessing

C statistic isn't a "one stop" measure of accuracy

The C statistic tells you about *discrimination* but nothing about *calibration*.

- The poor C statistic indicates that `m_01` has poor discrimination.
  - If `m_01` predicts Harry has a higher Pr(CHD) than Sally, we cannot really trust that will be an accurate ordering.
- But this isn't any indication of `m_01`'s calibration.
  - Even a large C statistic (near 1) doesn't tell you anything about whether a group of people with Pr(CHD) = 0.20 would actually have anything close to a 20% chance of CHD.
  - A large C statistic indicates that the model puts subjects in the correct order (low risk of CHD to high risk,) but we can still get the actual risks wrong if the calibration is poor.

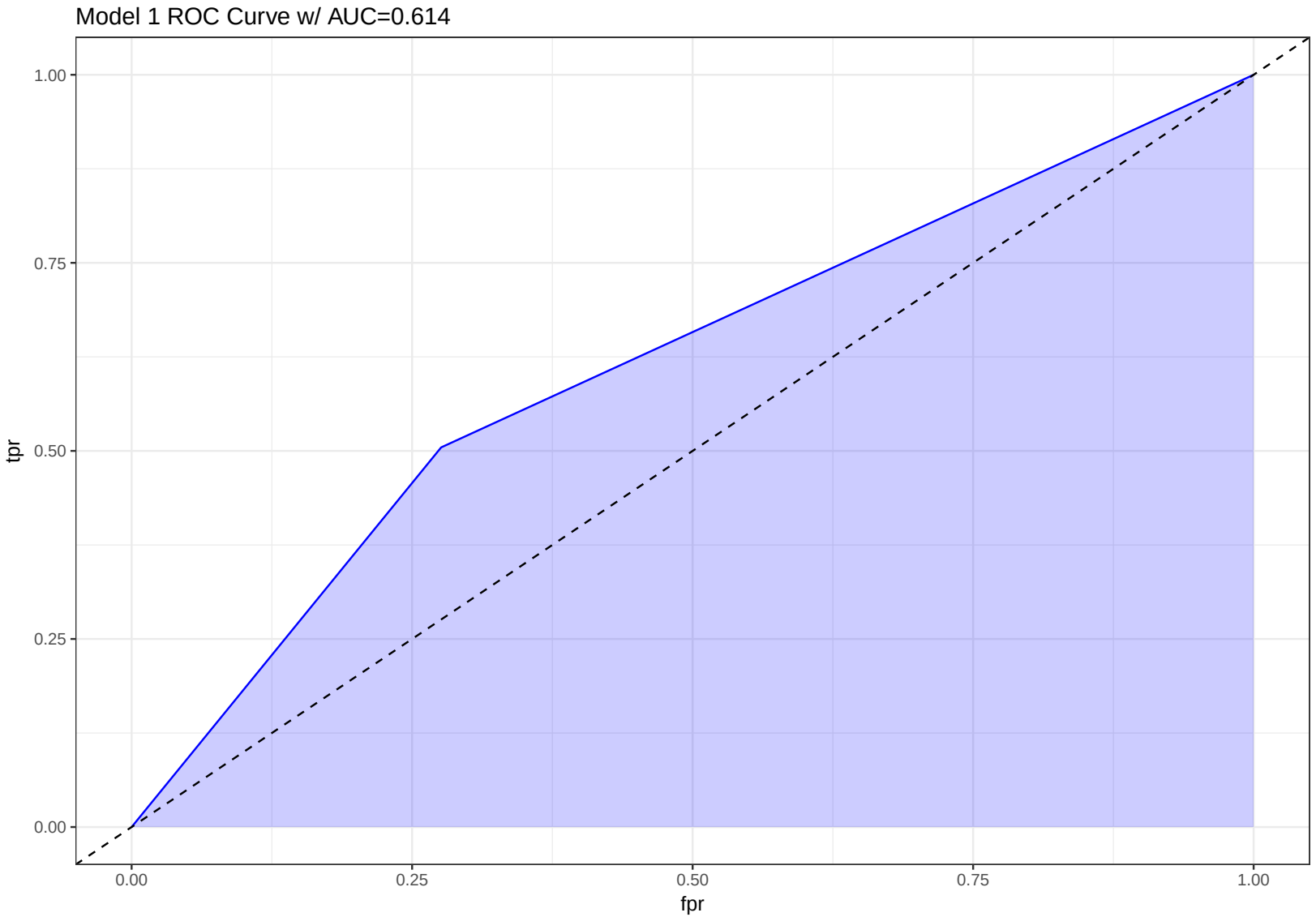
Building the ROC Curve with ROCR

```
# requires ROCR package
prob <- predict(m_01, fram2, type = "response")
pred <- prediction(prob, fram2$CHD_10)
perf <- performance(pred, measure = "tpr",
                    x.measure = "fpr")
auc <- performance(pred, measure = "auc")
auc <- round(auc@y.values[[1]], 3)
roc.dat <- data.frame(fpr = unlist(perf@x.values),
                      tpr = unlist(perf@y.values),
                      model = "GLM")
```

ROC Plot with ROCR and ggplot2 (code)

```
ggplot(roc.dat, aes(x = fpr, ymin = 0, ymax = tpr)) +
    geom_ribbon(alpha=0.2, fill = "blue") +
    geom_line(aes(y=tpr), col = "blue") +
    geom_abline(intercept = 0, slope = 1, lty = "dashed") +
    labs(title = paste0("Model 1 ROC Curve w/ AUC=", auc)) +
    theme_bw()
```

The Very Pretty Result



Using `lrm` from the `rms` package to fit Logistic Regression Models

A Logistic Regression model with `lrm`

```
d <- datadist(fram2)
options(datadist = "d")

m_01_lrm <- lrm(CHD_10 ~ hx_htn, data = fram2, x = T, y = T)
```

```
> m_01_lrm
Logistic Regression Model

 lrm(formula = CHD_10 ~ hx_htn, data = fram2, x = T, y = T)

                       Model Likelihood     Discrimination    Rank Discrim.
                          Ratio Test           Indexes           Indexes
 Obs            4240    LR chi2     125.30    R2        0.051   C         0.614
  0             3596    d.f.             1    g         0.421   Dxy       0.229
  1              644    Pr(> chi2) <0.0001    gr        1.524   gamma     0.456
 max |deriv| 1e-09                           gp        0.059   tau-a     0.059
                                             Brier     0.125

           Coef    S.E.   Wald Z Pr(>|Z|)
 Intercept -2.0996 0.0593 -35.39 <0.0001
 hx_htn     0.9837 0.0872  11.28 <0.0001
```

`lrm` output Piece by Piece

```
                      Model Likelihood
                         Ratio Test
Obs            4240    LR chi2     125.30
 0             3596    d.f.             1
 1              644    Pr(> chi2) <0.0001
```

- Likelihood-ratio test = drop in deviance test
  - How much does a goodness-of-fit statistic move as a result of this model?
  - Deviance = -2 log(likelihood function)

`lrm` output Piece by Piece, 2

Discrimination Indexes		Rank Discrim. Indexes	
R2	0.051	C	0.614
gr	1.524	Dxy	0.229
gp	0.059	gamma	0.456
Brier	0.125	tau-a	0.059

Nagelkerke pseudo-R^2 statistic = 1 if the model predicts the outcome perfectly and the likelihood function is 1.

- an adjusted version (to a 0-1 scale) of the Cox-Snell pseudo-R^2
- compares the log likelihood of our model to the log likelihood for a null model.
- so it's similar to the R^2 for a linear model in terms of improvement from a null model to a fitted model
- neither a percentage of explained variability nor the square of any correlation

`lrm` output Piece by Piece, 3

```
Discrimination    Rank Discrim.
       Indexes          Indexes
R2       0.051    C       0.614
gr       1.524    Dxy     0.229
gp       0.059    gamma   0.456
Brier    0.125    tau-a   0.059
```

- gp = Gini's index on the probability scale, which we want to be as large as possible
  - Gini's mean difference is the mean absolute difference between any two distinct predictions.
  - This measures the average "purity" in the predictions, essentially.
- R also presents g and gr, which are the same thing on the log odds, and odds scale.
- The **lower** the Brier score, the better the predictions are calibrated.
  - This is a nice measure of the accuracy of probabilistic predictions.

lrm output Piece by Piece, 4

```
Discrimination    Rank Discrim.
       Indexes          Indexes
R2       0.051    C         0.614
gr       1.524    Dxy       0.229
gp       0.059    gamma     0.456
Brier    0.125    tau-a     0.059
```

- C = C statistic = area under the ROC curve
- Dxy = Somers' d, and C = 0.5 + Dxy/2
- gamma = Goodman and Kruskal's Γ, which is a measure of the rank correlation between the observed and predicted values of CHD = 1.
  - Values range from -1 (perfect negative association) to +1 (perfect agreement.)
- tau-a = Kendall's τ, is another measure of such an association.

Validating our Summary Statistics

```
validate(m_01_lrm)
```

```
          index.orig training    test optimism
Dxy           0.2288   0.2309  0.2288   0.0021
R2            0.0508   0.0524  0.0508   0.0016
Intercept     0.0000   0.0000 -0.0182   0.0182
Slope         1.0000   1.0000  0.9960   0.0040
Emax          0.0000   0.0000  0.0048   0.0048
D             0.0293   0.0304  0.0293   0.0010
U            -0.0005  -0.0005  0.0000  -0.0005
Q             0.0298   0.0308  0.0293   0.0015
B             0.1248   0.1255  0.1248   0.0007
g             0.4214   0.4250  0.4214   0.0036
gp            0.0590   0.0599  0.0590   0.0010
          index.corrected  n
Dxy                0.2267 40
R2                 0.0492 40
```

Coefficients Summary from `m_01_lrm`

	Coef	S.E.	Wald Z	Pr(>|Z|)
Intercept	-2.0996	0.0593	-35.39	<0.0001
hx_htn	0.9837	0.0872	11.28	<0.0001

Conclusions?

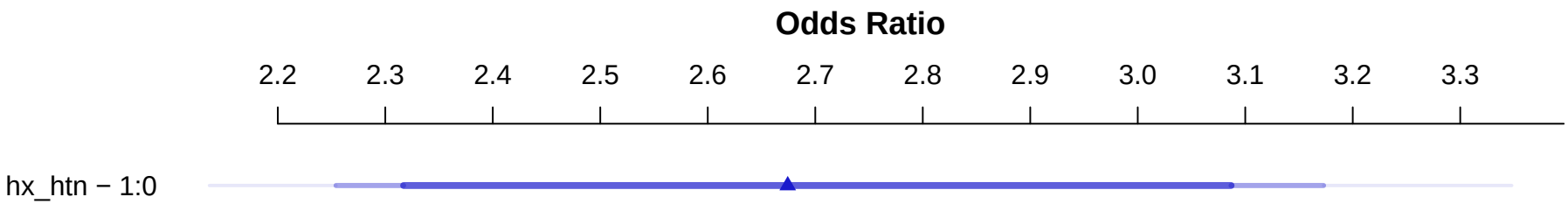
Assessing Effect Sizes

```
summary(m_01_lrm)
```

```
                Effects                   Response : CHD_10

 Factor        Low High Diff. Effect  S.E.    Lower 0.95
 hx_htn        0   1    1     0.98371 0.0872  0.81281
  Odds Ratio   0   1    1     2.67440      NA 2.25420
 Upper 0.95
 1.1546
 3.1728
```

Plotting the Effect Sizes

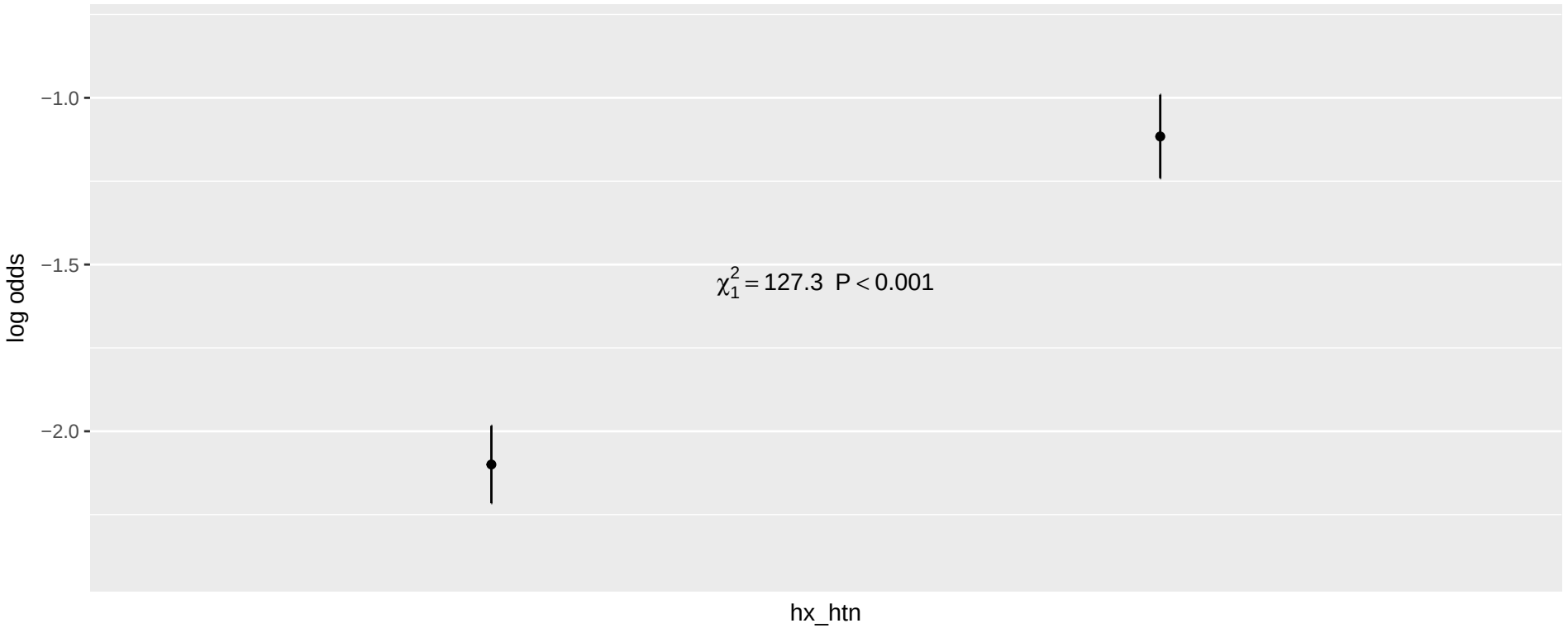
```
plot(summary(m_01_lrm))
```



The plot shows 90%, 95% and 99% confidence intervals.

Can we see the prediction results?

```
ggplot(Predict(m_01_lrm),
       anova = anova(m_01_lrm), pval = TRUE)
```

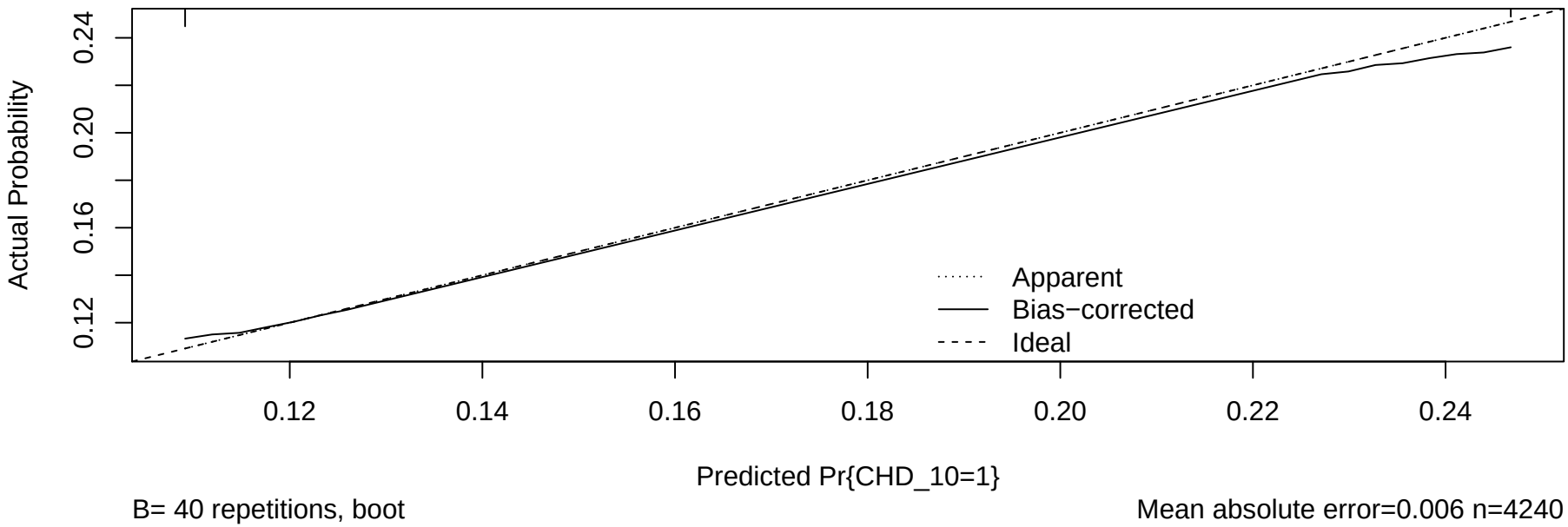


What about on a better scale?

```
ggplot(Predict(m_01_lrm, fun = plogis))
```

Is this m_01_lrm well calibrated?

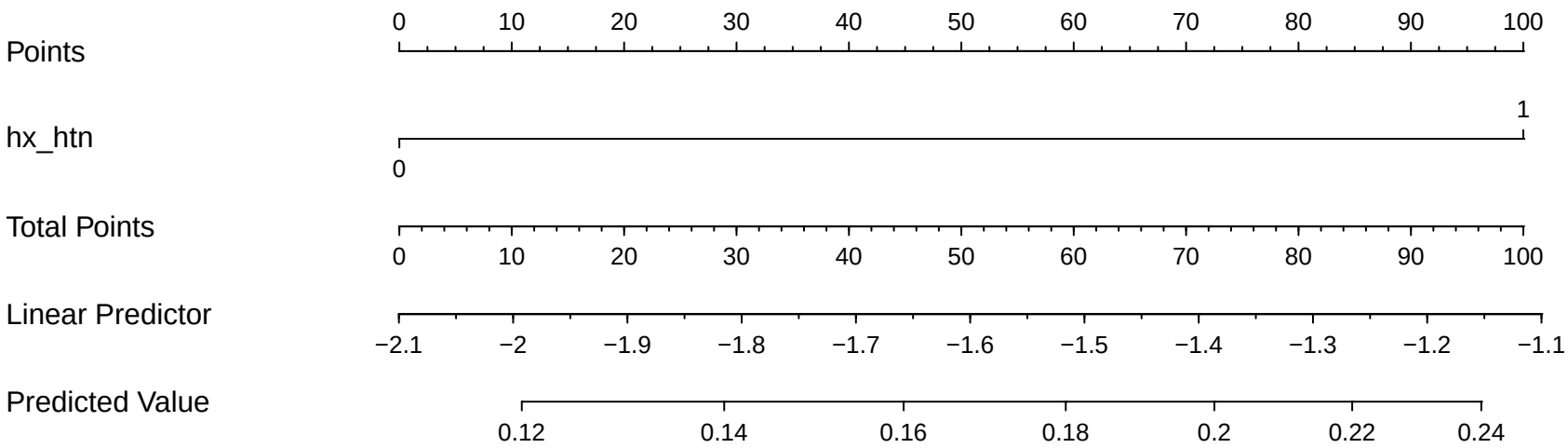
```
plot(calibrate(m_01_lrm))
```




```
n=4240   Mean absolute error=0.006   Mean squared error=5e-05
0.9 Quantile of absolute error=0.011
```

Nomogram for `m_01_lrm`

```
plot(nomogram(m_01_lrm, fun = plogis))
```



Goal 2. Predict `CHD_10` using `hx_htn` and `tot_chol`

glm fit (Don't forget family = binomial!)

```
m_02 <- glm(CHD_10 ~ hx_htn + tot_chol,
            data = fram2, family = binomial)

m_02
```

```
Call:  glm(formula = CHD_10 ~ hx_htn + tot_chol, family = bino
    data = fram2)

Coefficients:
(Intercept)       hx_htn     tot_chol
  -2.855553     0.934387     0.003229

Degrees of Freedom: 4239 Total (i.e. Null);  4237 Residual
Null Deviance:      3612
Residual Deviance: 3475     AIC: 3481
```

Does m_02 improve on m_01 by ANOVA?

```
anova(m_01, m_02)
```

```
Analysis of Deviance Table

Model 1: CHD_10 ~ hx_htn
Model 2: CHD_10 ~ hx_htn + tot_chol
  Resid. Df Resid. Dev Df Deviance
1      4238     3486.9
2      4237     3475.5  1   11.411
```

```
pchisq(11.41, 1, lower.tail = FALSE)
```

```
[1] 0.0007304983
```

Does m_02 improve on m_01 by AIC/BIC?

```
glance(m_01)
```

```
  null.deviance df.null    logLik      AIC      BIC
1      3612.209    4239 -1743.453 3490.906 3503.611
  deviance df.residual
1 3486.906        4238
```

```
glance(m_02)
```

```
  null.deviance df.null    logLik      AIC      BIC
1      3612.209    4239 -1737.748 3481.495 3500.552
  deviance df.residual
1 3475.495        4237
```

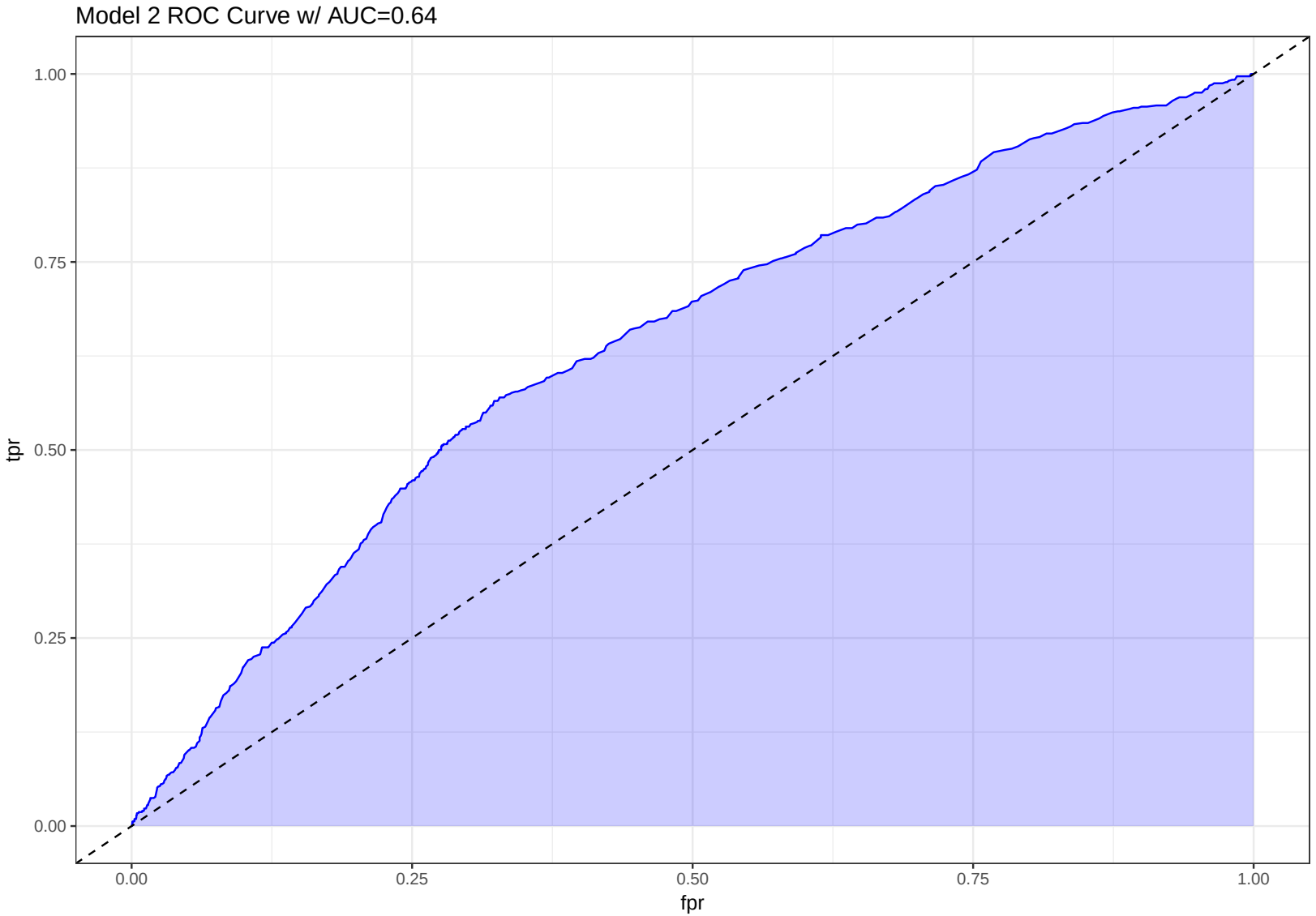
anova(m_02)

```
Analysis of Deviance Table

Model: binomial, link: logit

Response: CHD_10

Terms added sequentially (first to last)

         Df Deviance Resid. Df Resid. Dev
NULL                      4239     3612.2
hx_htn    1  125.302       4238     3486.9
tot_chol  1   11.411       4237     3475.5
```

summary(m_02)

```
> summary(m_02)

Call:
glm(formula = CHD_10 ~ hx_htn + tot_chol, family = binomial,
    data = fram2)

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.3188  -0.5493  -0.4814  -0.4494   2.2276

Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.855553   0.232476 -12.283  < 2e-16 ***
hx_htn       0.934387   0.088454  10.564  < 2e-16 ***
tot_chol     0.003229   0.000951   3.396 0.000684 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 3612.2  on 4239  degrees of freedom
Residual deviance: 3475.5  on 4237  degrees of freedom
AIC: 3481.5

Number of Fisher Scoring iterations: 4
```

ROC plot for `m_02`



Fitting with lrm

```
d <- datadist(fram2)
options(datadist = "d")
m_02_lrm <- lrm(CHD_10 ~ hx_htn + tot_chol, data = fram2,
                x = TRUE, y = TRUE)
```

```
> m_02_lrm
Logistic Regression Model

 lrm(formula = CHD_10 ~ hx_htn + tot_chol, data = fram2, x = TRUE,
     y = TRUE)

                       Model Likelihood     Discrimination    Rank Discrim.
                          Ratio Test            Indexes          Indexes
 Obs           4240    LR chi2     136.71    R2        0.055    C         0.640
  0            3596    d.f.             2    g         0.510    Dxy       0.281
  1             644    Pr(> chi2) <0.0001    gr        1.665    gamma     0.282
 max |deriv| 4e-07                          gp        0.069    tau-a     0.072
                                            Brier     0.125

           Coef    S.E.   Wald Z Pr(>|Z|)
 Intercept -2.8556 0.2325 -12.28 <0.0001
 hx_htn     0.9344 0.0885  10.56 <0.0001
 tot_chol   0.0032 0.0010   3.40 0.0007
```

Validating our Summary Statistics

```
validate(m_02_lrm)
```

```
          index.orig training    test optimism
Dxy           0.2805   0.2849  0.2805   0.0044
R2            0.0553   0.0567  0.0549   0.0018
Intercept     0.0000   0.0000 -0.0112   0.0112
Slope         1.0000   1.0000  0.9907   0.0093
Emax          0.0000   0.0000  0.0041   0.0041
D             0.0320   0.0328  0.0317   0.0011
U            -0.0005  -0.0005  0.0000  -0.0004
Q             0.0325   0.0333  0.0318   0.0015
B             0.1245   0.1241  0.1246  -0.0005
g             0.5098   0.5137  0.5063   0.0074
gp            0.0690   0.0693  0.0685   0.0008
          index.corrected  n
Dxy                0.2761 40
R2                 0.0535 40
```

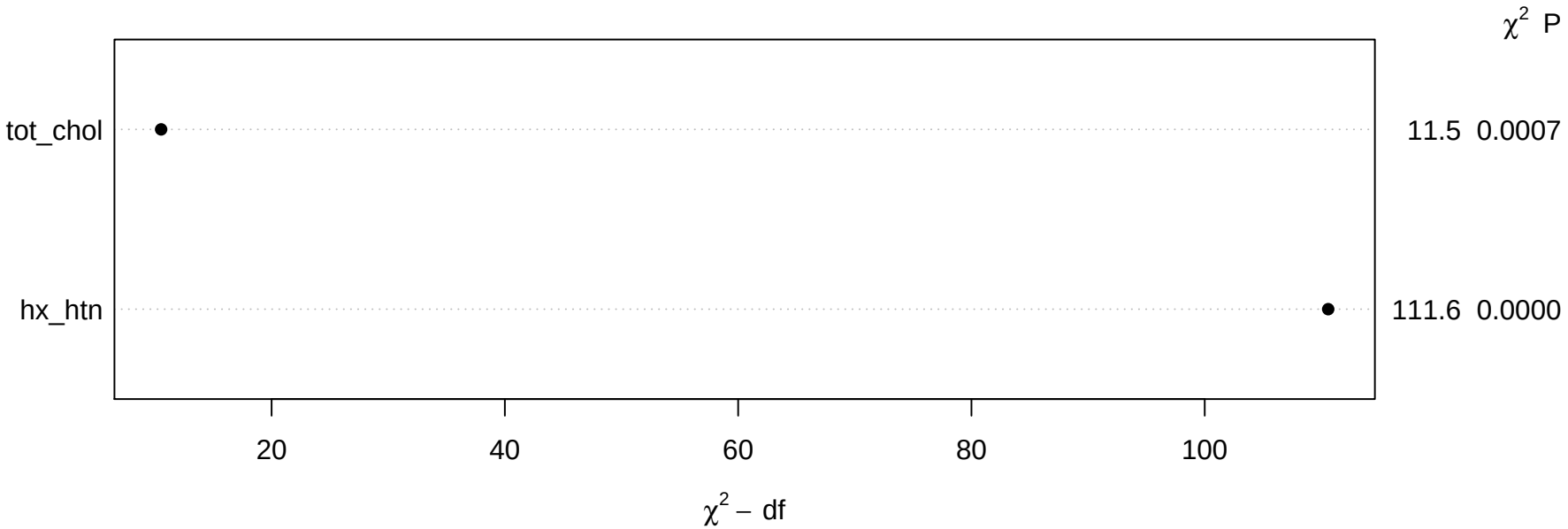
ANOVA with `lrm`

```
anova(m_02_lrm)
```

```
                Wald Statistics          Response: CHD_10

 Factor     Chi-Square d.f. P
 hx_htn     111.59     1    <.0001
 tot_chol    11.53     1    7e-04
 TOTAL      137.85     2    <.0001
```

ANOVA plot in `lrm`

```
plot(anova(m_02_lrm))
```



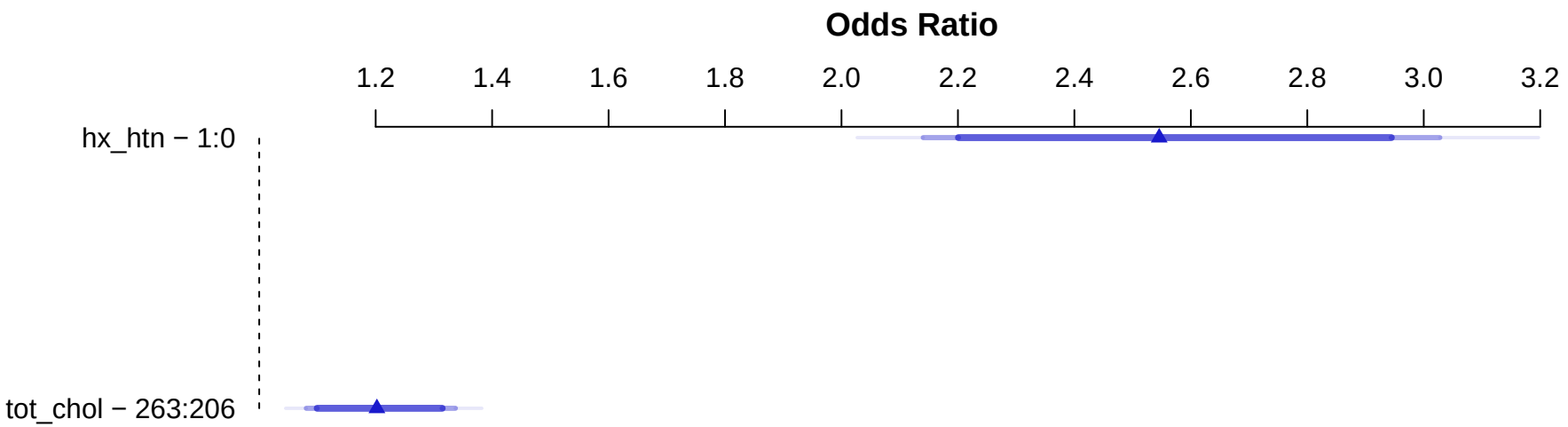
Estimated Effect Sizes

```
summary(m_02_lrm)
```

```
                Effects                   Response : CHD_10

 Factor        Low High Diff. Effect  S.E.      Lower 0.95
 hx_htn          0    1    1     0.93439 0.088455 0.761020
  Odds Ratio     0    1    1     2.54570       NA 2.140500
 tot_chol      206 263   57     0.18407 0.054208 0.077827
  Odds Ratio   206 263   57     1.20210       NA 1.080900
 Upper 0.95
 1.10780
 3.02760
 0.29032
 1.33690
```

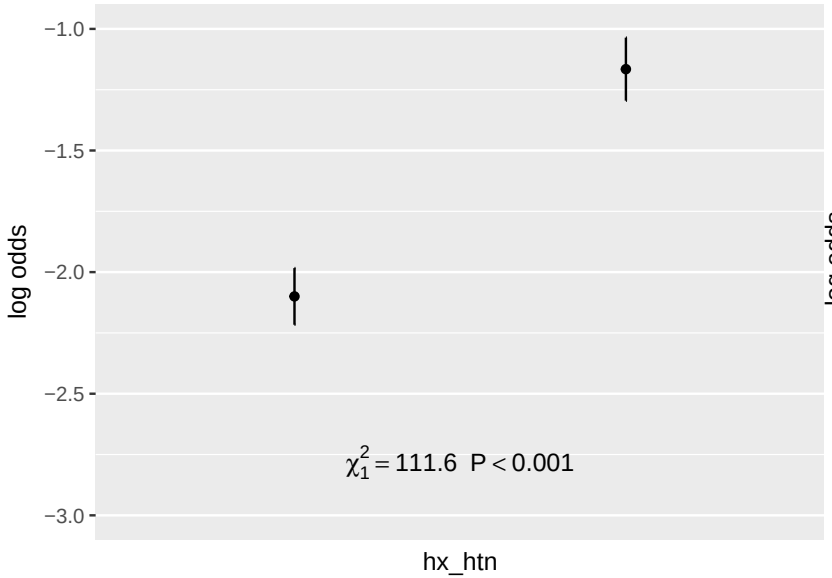
Plotting the Effect Sizes

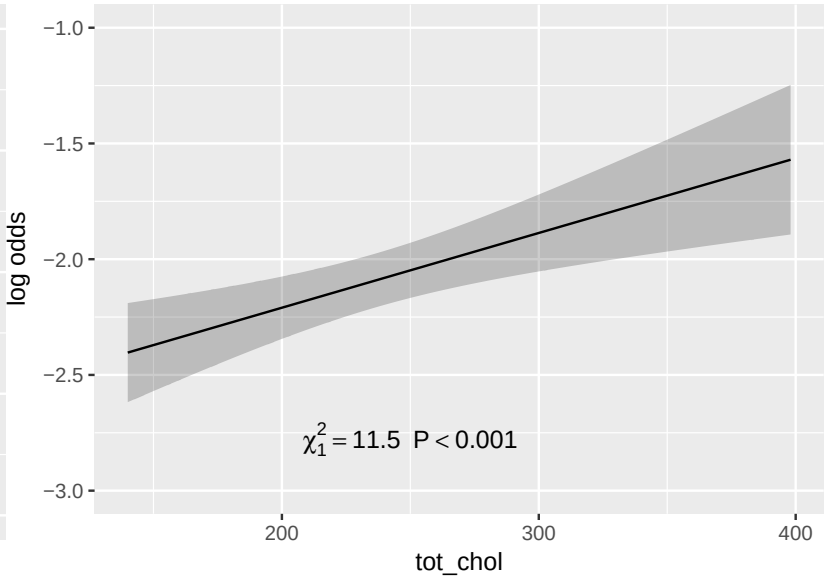
```
plot(summary(m_02_lrm))
```



Can we see the prediction results?

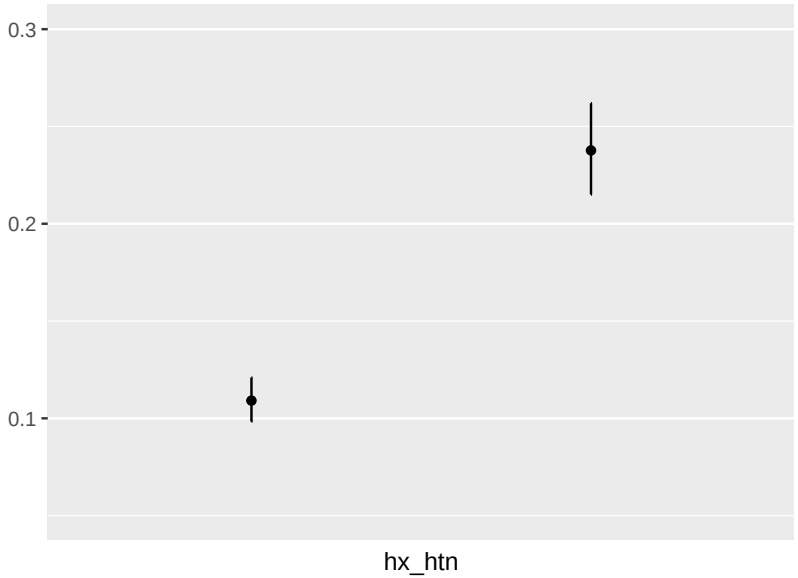
```
ggplot(Predict(m_02_lrm),
       anova = anova(m_02_lrm), pval = TRUE)
```

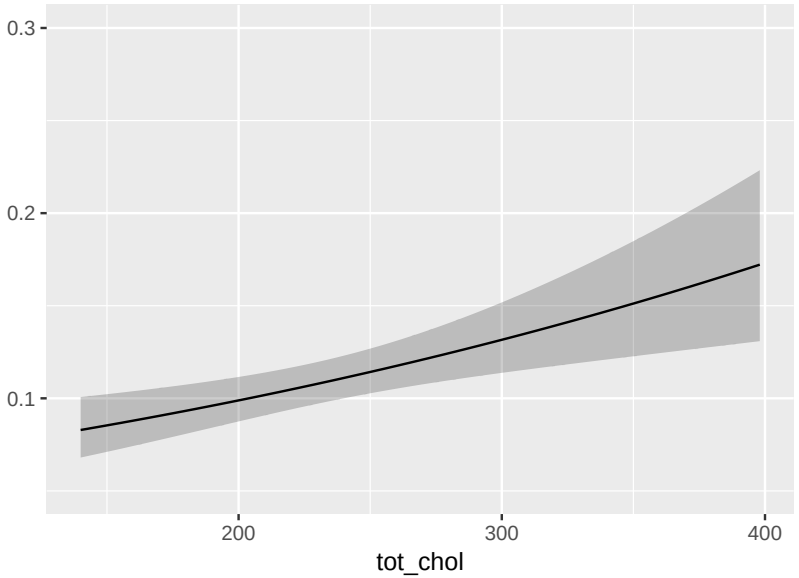




What about on a better scale?

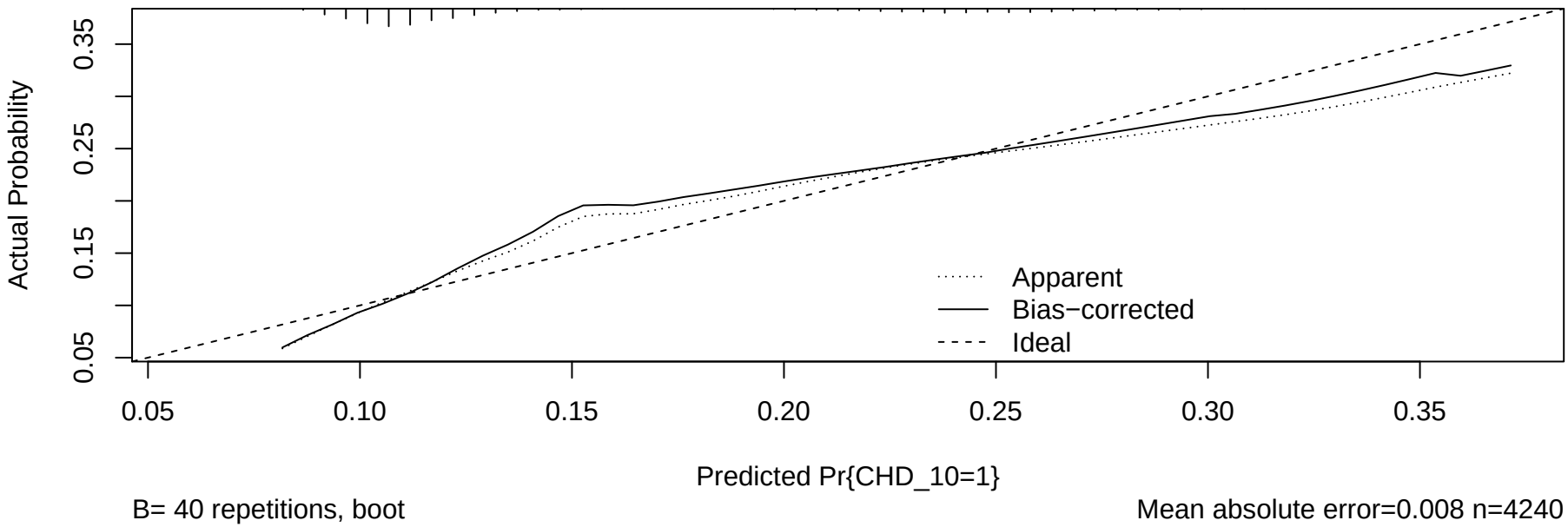
```
ggplot(Predict(m_02_lrm, fun = plogis))
```





Calibration of mod_02_lrm

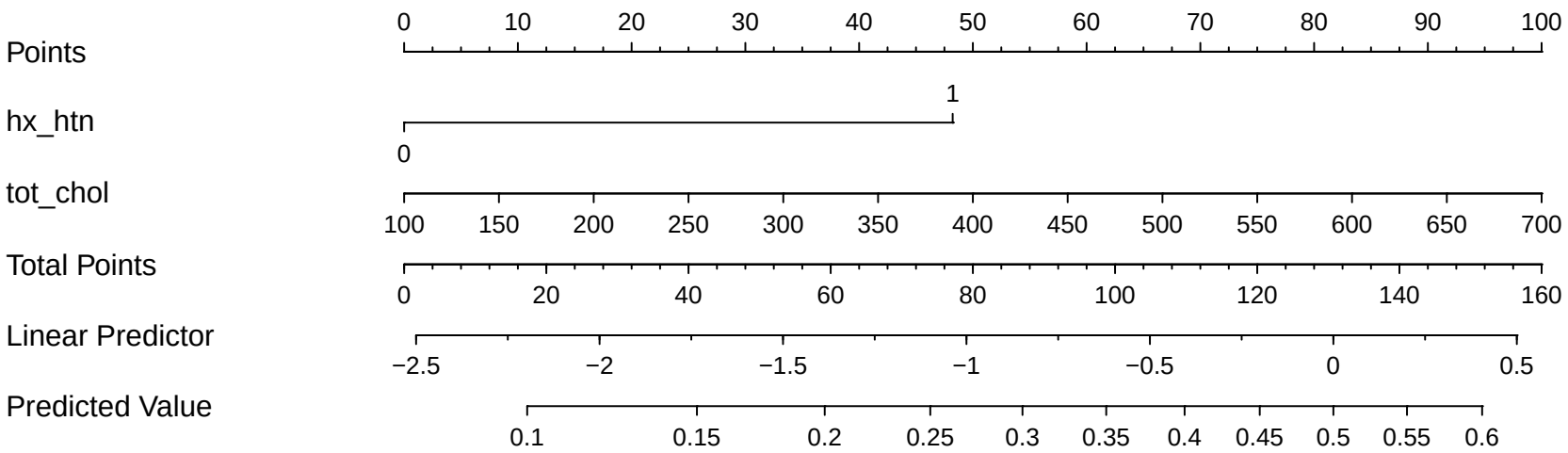
```
plot(calibrate(m_02_lrm))
```




```
n=4240   Mean absolute error=0.008   Mean squared error=0.0001
0.9 Quantile of absolute error=0.017
```

Nomogram of `mod_02_lrm`

```
plot(nomogram(m_02_lrm, fun = plogis))
```



Goal 3. Kitchen Sink Model

Focus on model with `lrm` first!

```
m_03 <- glm(CHD_10 ~ hx_htn + tot_chol + sex + age +
                     smoker + cigs_day + bp_meds +
                     hx_stroke + hx_dm + ed_f + sbp + dbp +
                     bmi + heart_r + glucose,
                   data = fram2, family = binomial)

d <- datadist(fram2)
options(datadist = "d")
m_03_lrm <- lrm(CHD_10 ~ hx_htn + tot_chol + sex + age +
                     smoker + cigs_day + bp_meds +
                     hx_stroke + hx_dm + ed_f + sbp + dbp +
                     bmi + heart_r + glucose,
                   data = fram2, x = TRUE, y = TRUE)
```

m_03_lrm (first section of output)

```
> m_03_lrm
Logistic Regression Model

 lrm(formula = CHD_10 ~ hx_htn + tot_chol + sex + age + smoker +
     cigs_day + bp_meds + hx_stroke + hx_dm + ed_f + sbp + dbp +
     bmi + heart_r + glucose, data = fram2, x = TRUE, y = TRUE)

                       Model Likelihood     Discrimination    Rank Discrim.
                          Ratio Test           Indexes           Indexes
 Obs            4240    LR chi2     405.40    R2        0.159   C         0.733
  0             3596    d.f.            17    g         1.016   Dxy       0.466
  1              644    Pr(> chi2) <0.0001    gr        2.763   gamma     0.466
 max |deriv| 6e-10                           gp        0.120   tau-a     0.120
                                             Brier     0.115
```

m_03_lrm (second section of output)

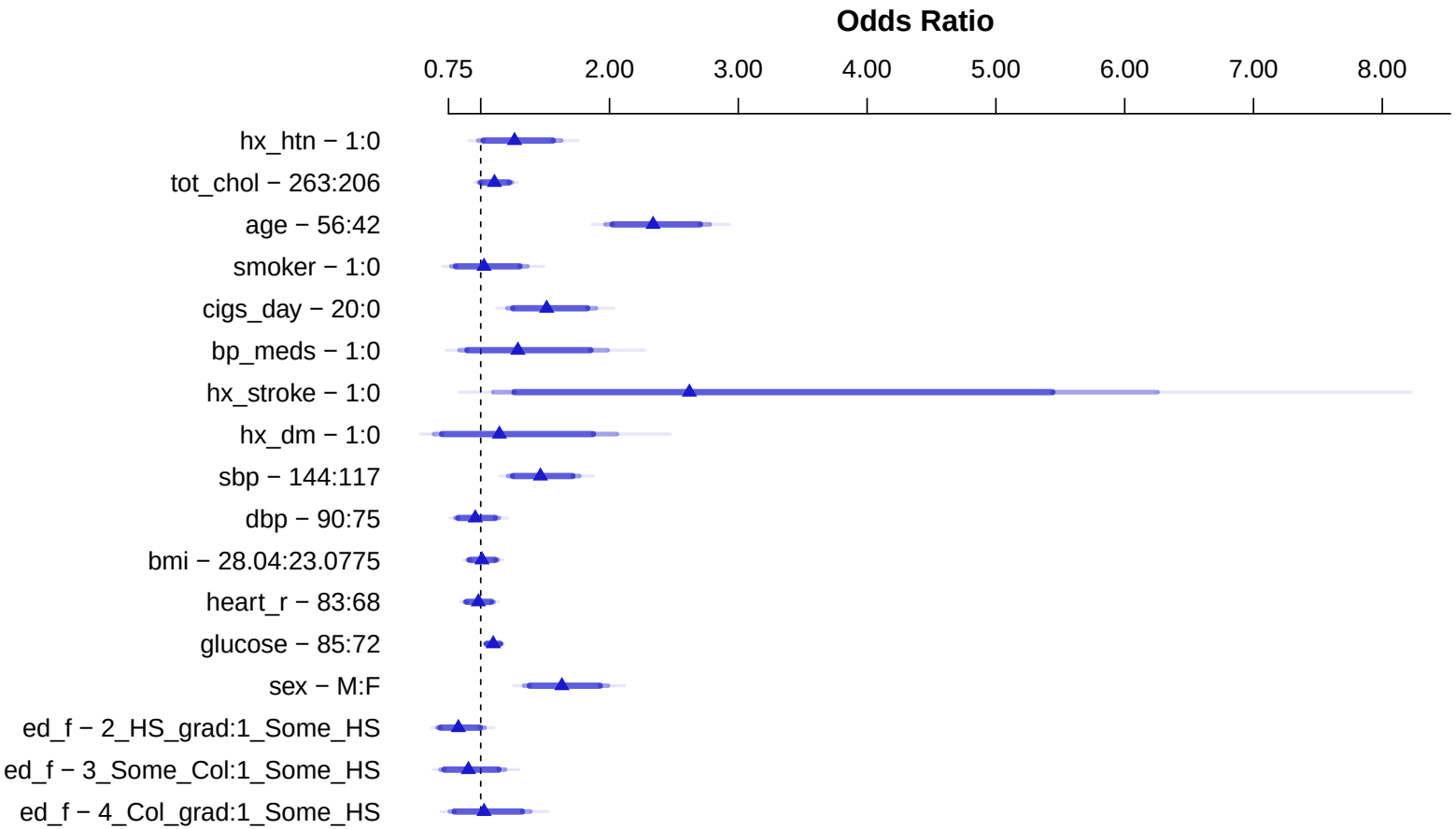
	Coef	S.E.	Wald Z	Pr(>|Z|)
Intercept	-7.9981	0.6583	-12.15	<0.0001
hx_htn	0.2331	0.1287	1.81	0.0700
tot_chol	0.0018	0.0010	1.73	0.0842
sex=M	0.4886	0.1012	4.83	<0.0001
age	0.0607	0.0063	9.67	<0.0001
smoker	0.0248	0.1451	0.17	0.8642
cigs_day	0.0207	0.0057	3.60	0.0003
bp_meds	0.2534	0.2206	1.15	0.2506
hx_stroke	0.9633	0.4439	2.17	0.0300
hx_dm	0.1353	0.2989	0.45	0.6507
ed_f=2_HS_grad	-0.1906	0.1120	-1.70	0.0889
ed_f=3_Some_Col	-0.1005	0.1397	-0.72	0.4719
ed_f=4_Col_grad	0.0255	0.1533	0.17	0.8679
sbp	0.0141	0.0035	3.98	<0.0001
dbp	-0.0029	0.0060	-0.48	0.6294
bmi	0.0019	0.0118	0.16	0.8712
heart_r	-0.0012	0.0039	-0.32	0.7524
glucose	0.0071	0.0022	3.28	0.0010

Validating our Summary Statistics

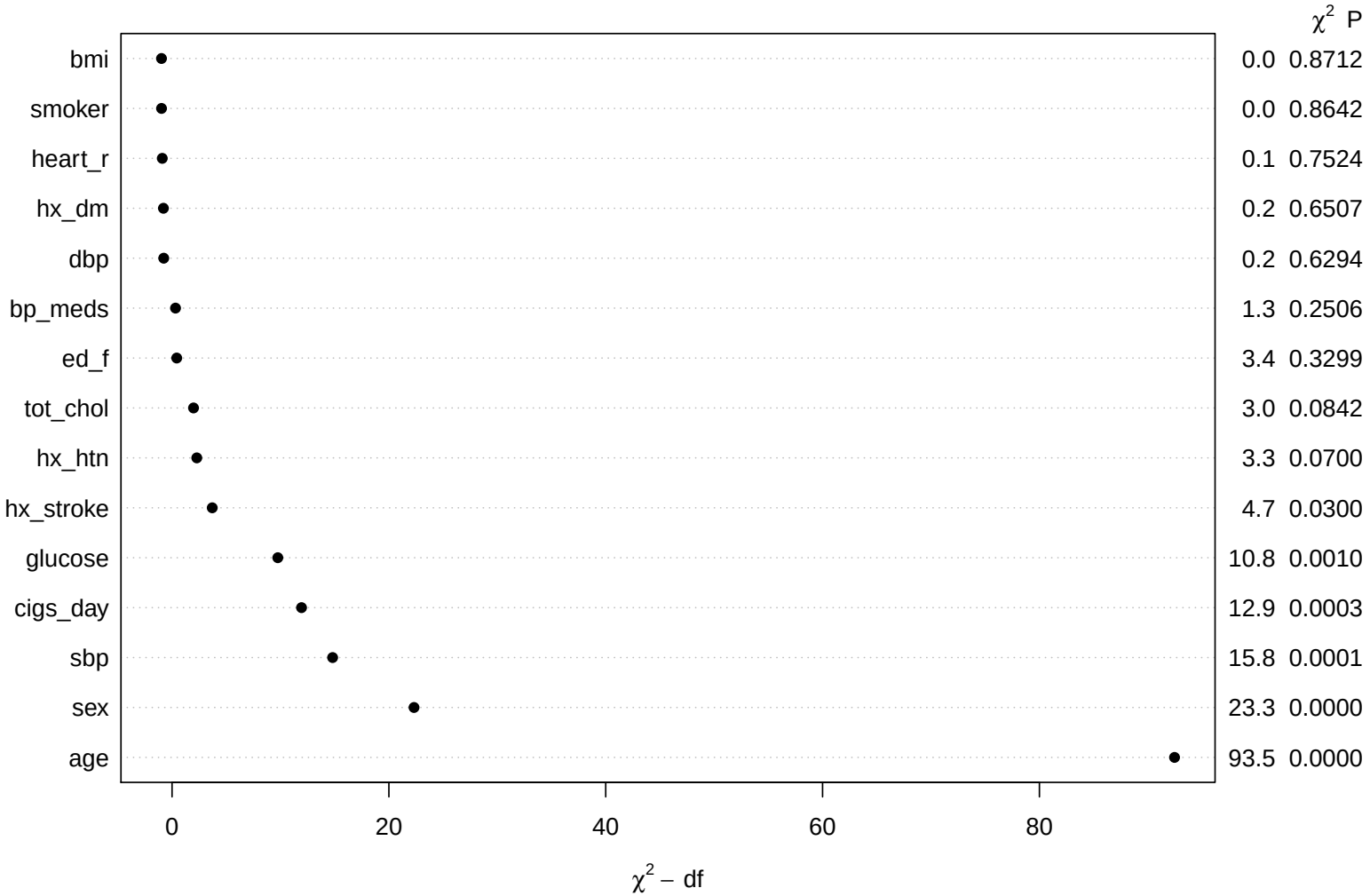
```
validate(m_03_lrm)
```

```
          index.orig training    test optimism
Dxy           0.4659   0.4746  0.4588   0.0158
R2            0.1590   0.1659  0.1532   0.0127
Intercept     0.0000   0.0000 -0.0529   0.0529
Slope         1.0000   1.0000  0.9543   0.0457
Emax          0.0000   0.0000  0.0198   0.0198
D             0.0954   0.0994  0.0917   0.0077
U            -0.0005  -0.0005  0.0002  -0.0006
Q             0.0958   0.0998  0.0915   0.0083
B             0.1152   0.1136  0.1159  -0.0023
g             1.0164   1.0417  0.9910   0.0507
gp            0.1203   0.1218  0.1180   0.0038
          index.corrected  n
Dxy                0.4500 40
R2                 0.1464 40
```

plot(summary(m_03_lrm))

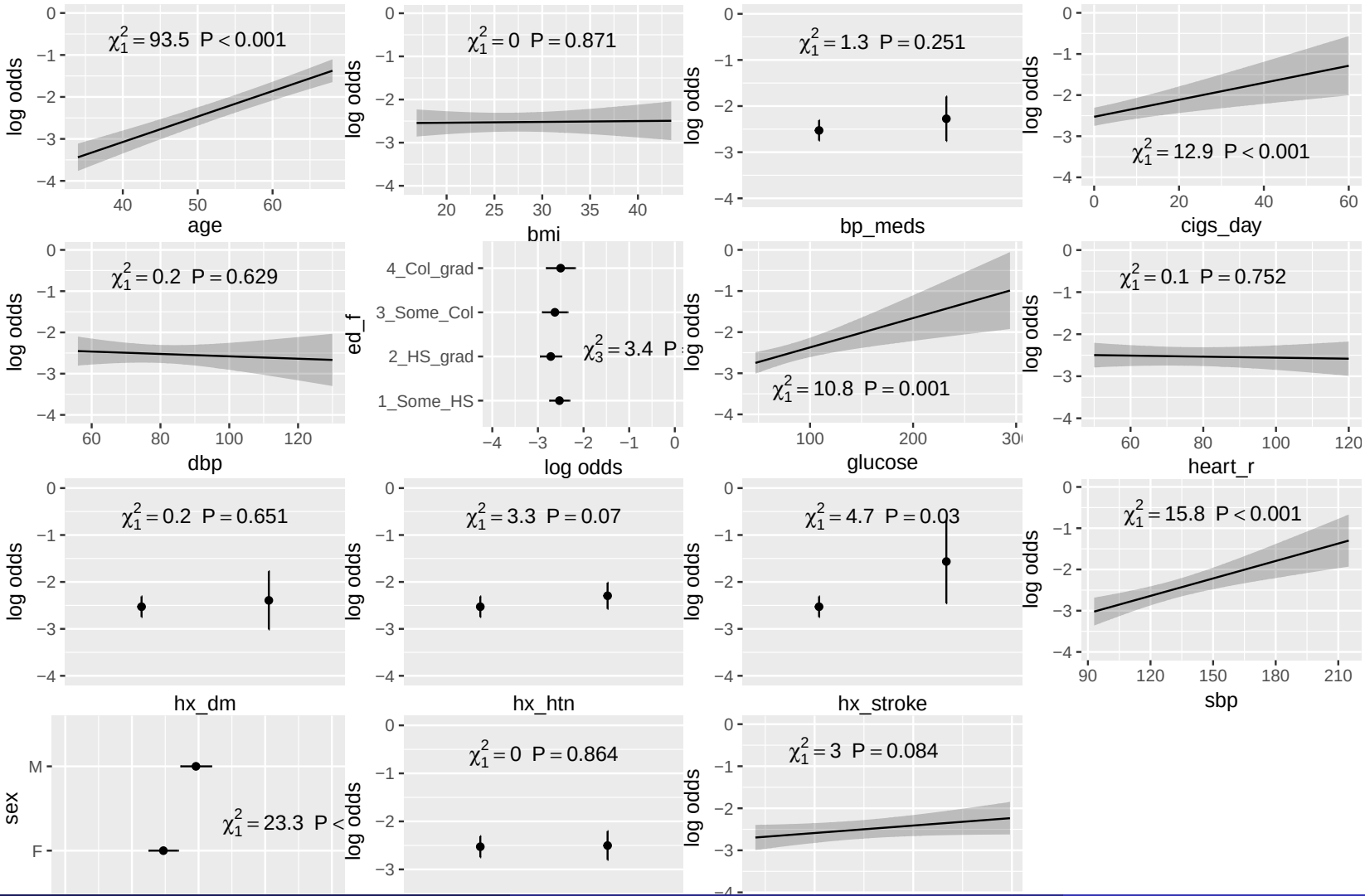


plot(anova(m_03_lrm))



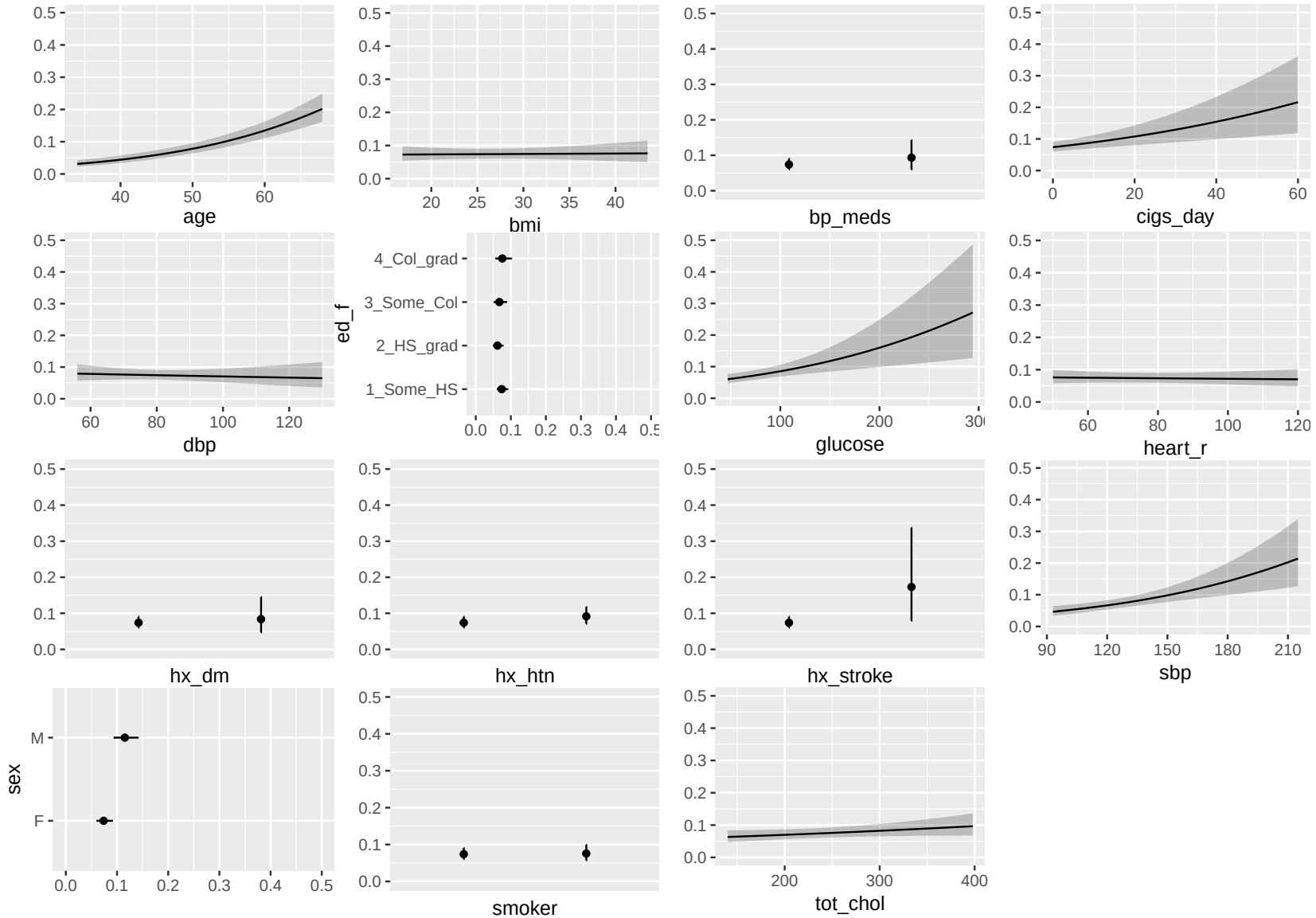
Can we see the prediction results?

```
ggplot(Predict(m_03_lrm),
       anova = anova(m_03_lrm), pval = TRUE)
```



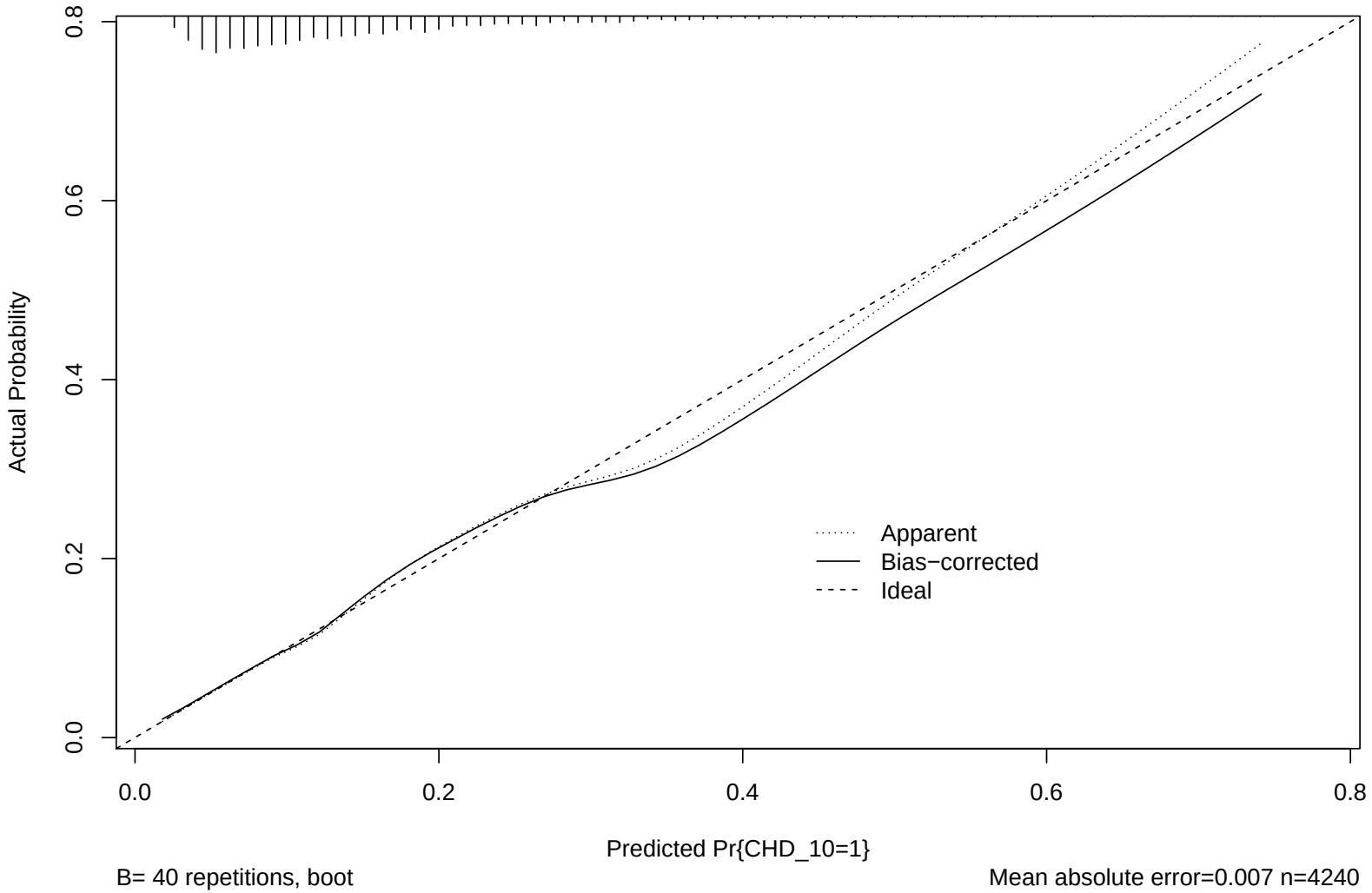
What about on a better scale?

```
ggplot(Predict(m_03_lrm, fun = plogis))
```



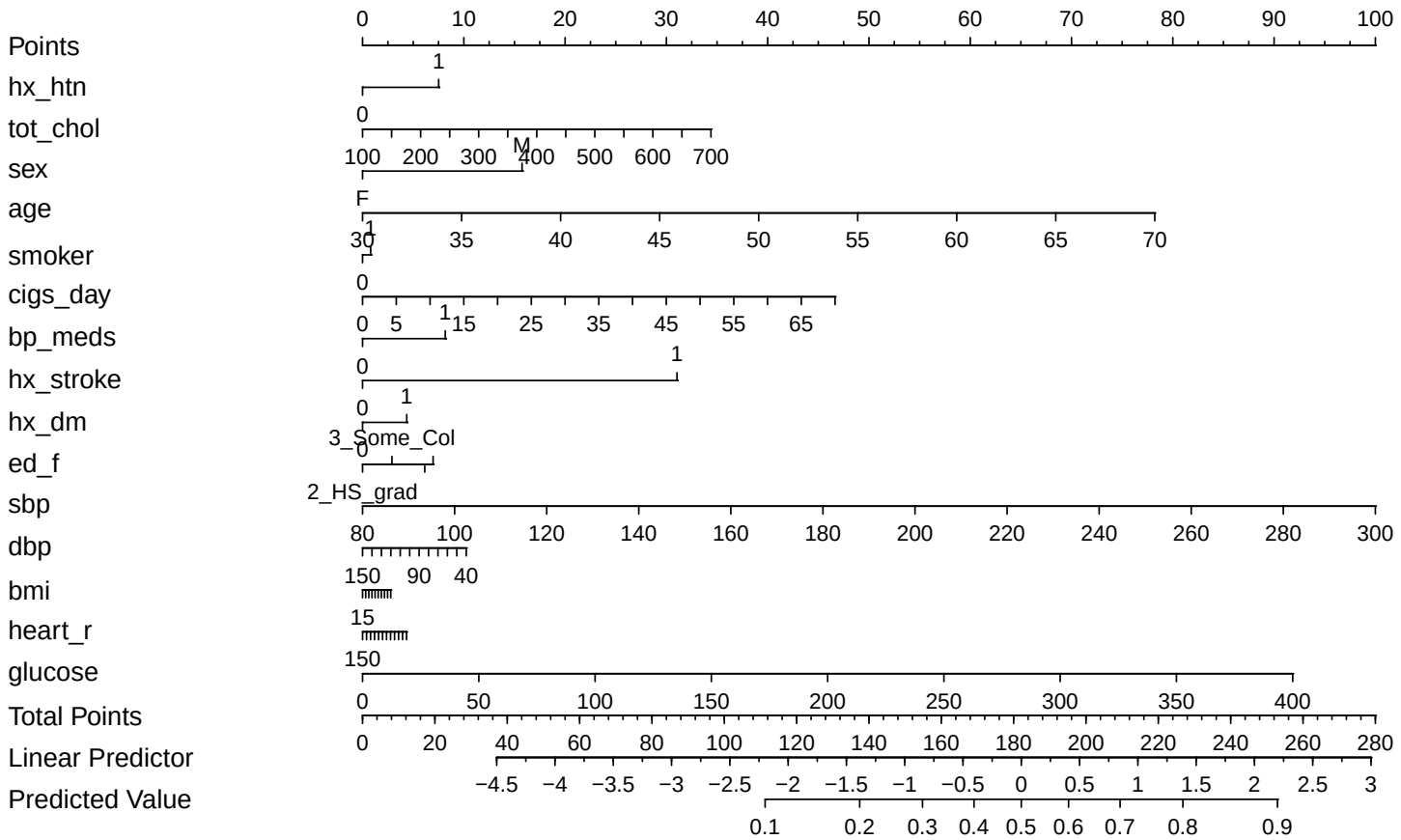
Calibration of `mod_03_lrm`

```
plot(calibrate(m_03_lrm))
```



Nomogram of `mod_03_lrm`

```
plot(nomogram(m_03_lrm, fun = plogis))
```



Comparing our Three Nested Models

```
anova(m_01, m_02, m_03)
```

```
Analysis of Deviance Table

Model 1: CHD_10 ~ hx_htn
Model 2: CHD_10 ~ hx_htn + tot_chol
Model 3: CHD_10 ~ hx_htn + tot_chol + sex + age + smoker + cig
    bp_meds + hx_stroke + hx_dm + ed_f + sbp + dbp + bmi + hea
    glucose
  Resid. Df Resid. Dev Df Deviance
1      4238     3486.9
2      4237     3475.5  1   11.411
3      4222     3206.8 15  268.682
```

Model 2 vs. Model 3 at a glance

```
glance(m_02)
```

```
  null.deviance df.null    logLik      AIC      BIC
1      3612.209    4239 -1737.748 3481.495 3500.552
  deviance df.residual
1 3475.495        4237
```

```
glance(m_03)
```

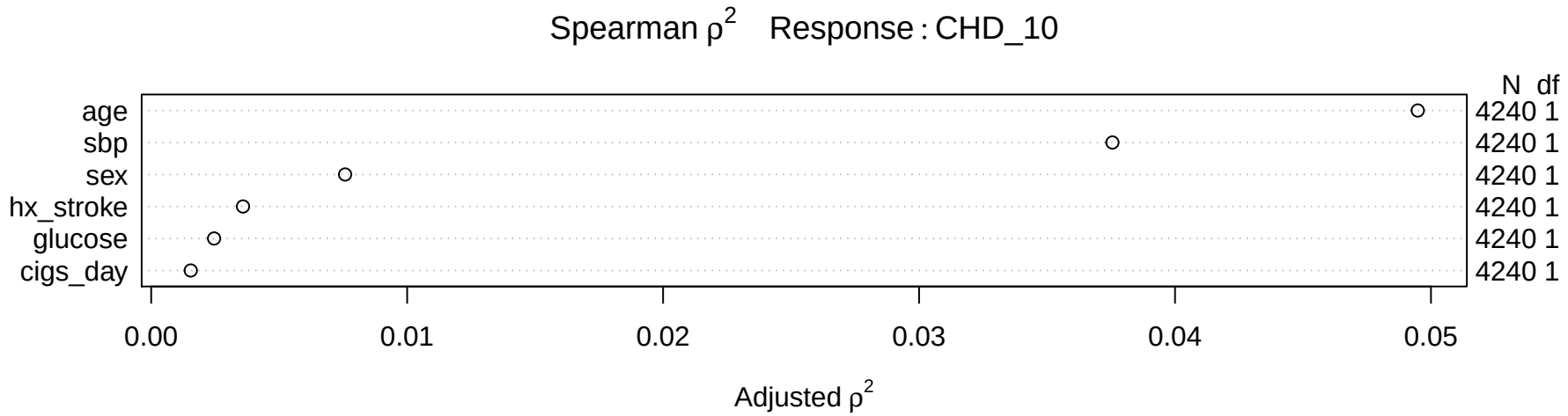
```
  null.deviance df.null    logLik      AIC      BIC
1      3612.209    4239 -1603.407 3242.813 3357.155
  deviance df.residual
1 3206.813        4222
```

Fitting a 6-predictor, but still useful model

What looks useful?

By ANOVA on `m_03_lrm` it looks like `age`, `sex`, `sbp`, `cigs_day`, `glucose`, `hx_stroke` for sure.

```
plot(spearman2(CHD_10 ~ age + sex + sbp + cigs_day +
                        glucose + hx_stroke, data = fram2))
```



New Model 4

```
m_04 <- glm(CHD_10 ~ rcs(age, 5) + rcs(sbp, 3) + sex +
                     hx_stroke + glucose + cigs_day,
                   data = fram2, family = binomial)


dd <- datadist(fram2)
options(datadist = "dd")

m_04_lrm <- lrm(CHD_10 ~ rcs(age, 5) + rcs(sbp, 3) + sex +
                     hx_stroke + glucose + cigs_day,
                   data = fram2, x = TRUE, y = TRUE)
```

m_04_lrm

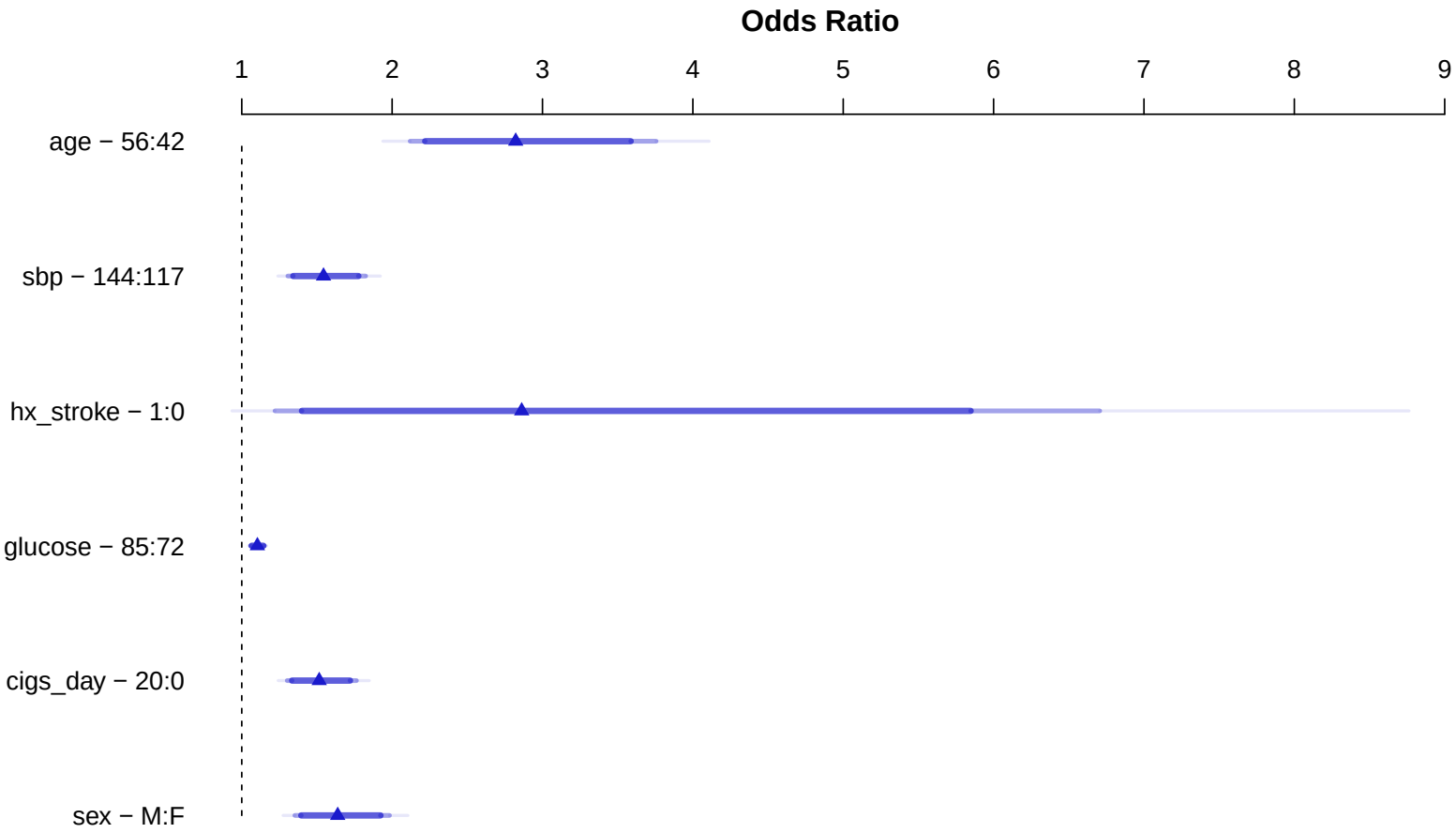
```
> m_04_lrm
Logistic Regression Model

 lrm(formula = CHD_10 ~ rcs(age, 5) + rcs(sbp, 3) + sex + hx_stroke +
     glucose + cigs_day, data = fram2, x = TRUE, y = TRUE)

                       Model Likelihood     Discrimination    Rank Discrim.
                          Ratio Test           Indexes           Indexes
 Obs           4240    LR chi2     401.44    R2        0.158    C         0.731
  0            3596    d.f.            10    g         1.041    Dxy       0.461
  1             644    Pr(> chi2) <0.0001    gr        2.833    gamma     0.461
 max |deriv| 2e-06                          gp        0.120    tau-a     0.119
                                            Brier     0.115

           Coef    S.E.   Wald Z Pr(>|Z|)
 Intercept -8.7201 2.4092 -3.62  0.0003
 age        0.0732 0.0576  1.27  0.2037
 age'       0.2871 0.3539  0.81  0.4172
 age''     -1.1057 0.9608 -1.15  0.2498
 age'''     1.4723 0.9640  1.53  0.1267
 sbp        0.0147 0.0066  2.23  0.0256
 sbp'       0.0030 0.0080  0.37  0.7080
 sex=M      0.4935 0.0973  5.07  <0.0001
 hx_stroke  1.0514 0.4345  2.42  0.0155
 glucose    0.0076 0.0016  4.69  <0.0001
 cigs_day   0.0208 0.0039  5.39  <0.0001
```

Validating our Summary Statistics

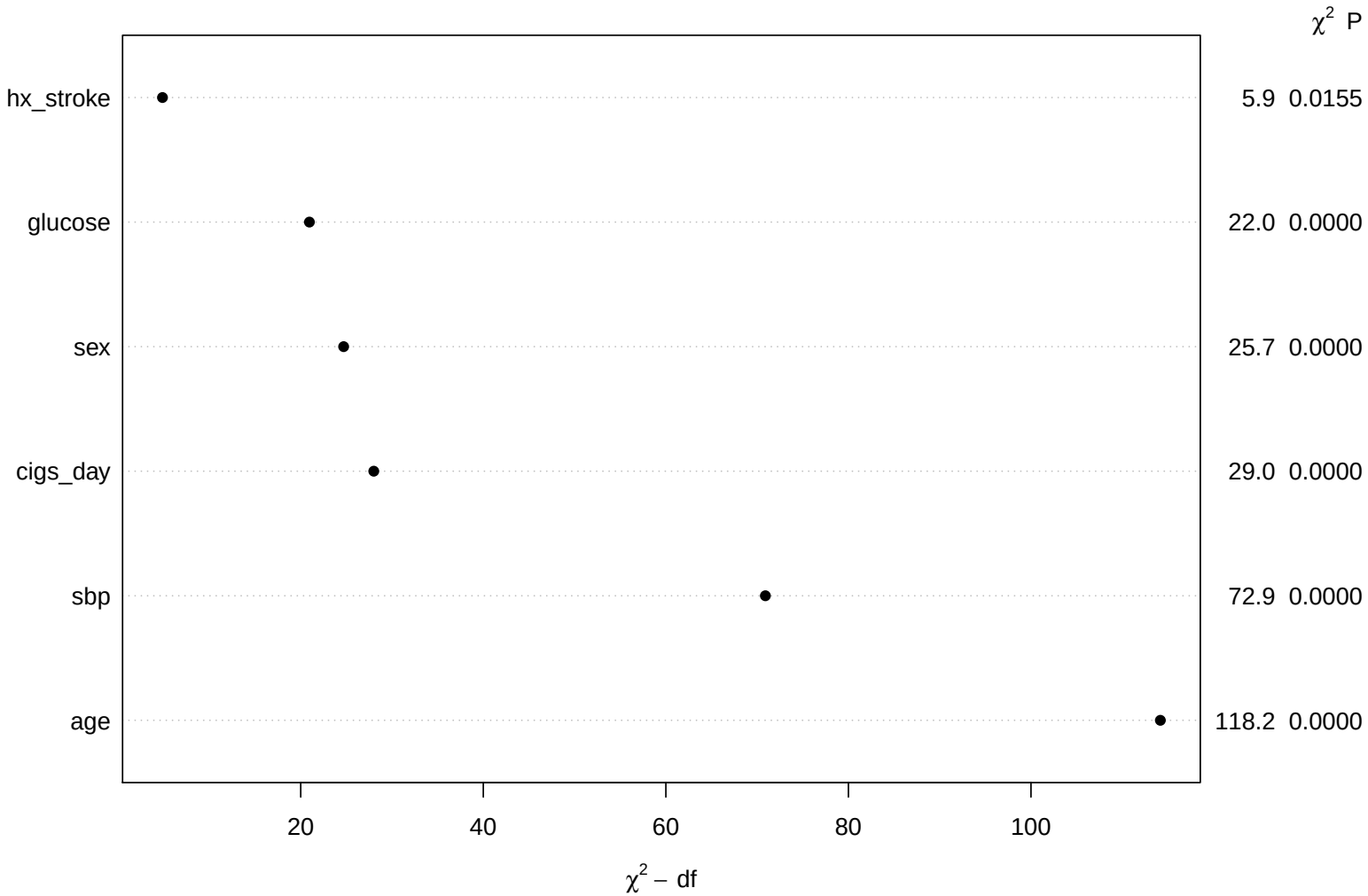
```
validate(m_04_lrm)
```

```
          index.orig training    test optimism
Dxy           0.4611   0.4604  0.4576   0.0028
R2            0.1575   0.1576  0.1544   0.0031
Intercept     0.0000   0.0000 -0.0221   0.0221
Slope         1.0000   1.0000  0.9860   0.0140
Emax          0.0000   0.0000  0.0072   0.0072
D             0.0944   0.0944  0.0925   0.0019
U            -0.0005  -0.0005  0.0002  -0.0006
Q             0.0949   0.0948  0.0923   0.0025
B             0.1152   0.1149  0.1156  -0.0008
g             1.0414   1.0419  1.0266   0.0153
gp            0.1198   0.1193  0.1184   0.0009
          index.corrected  n
Dxy                0.4583 40
R2                 0.1544 40
```

plot(summary(m_04_lrm))

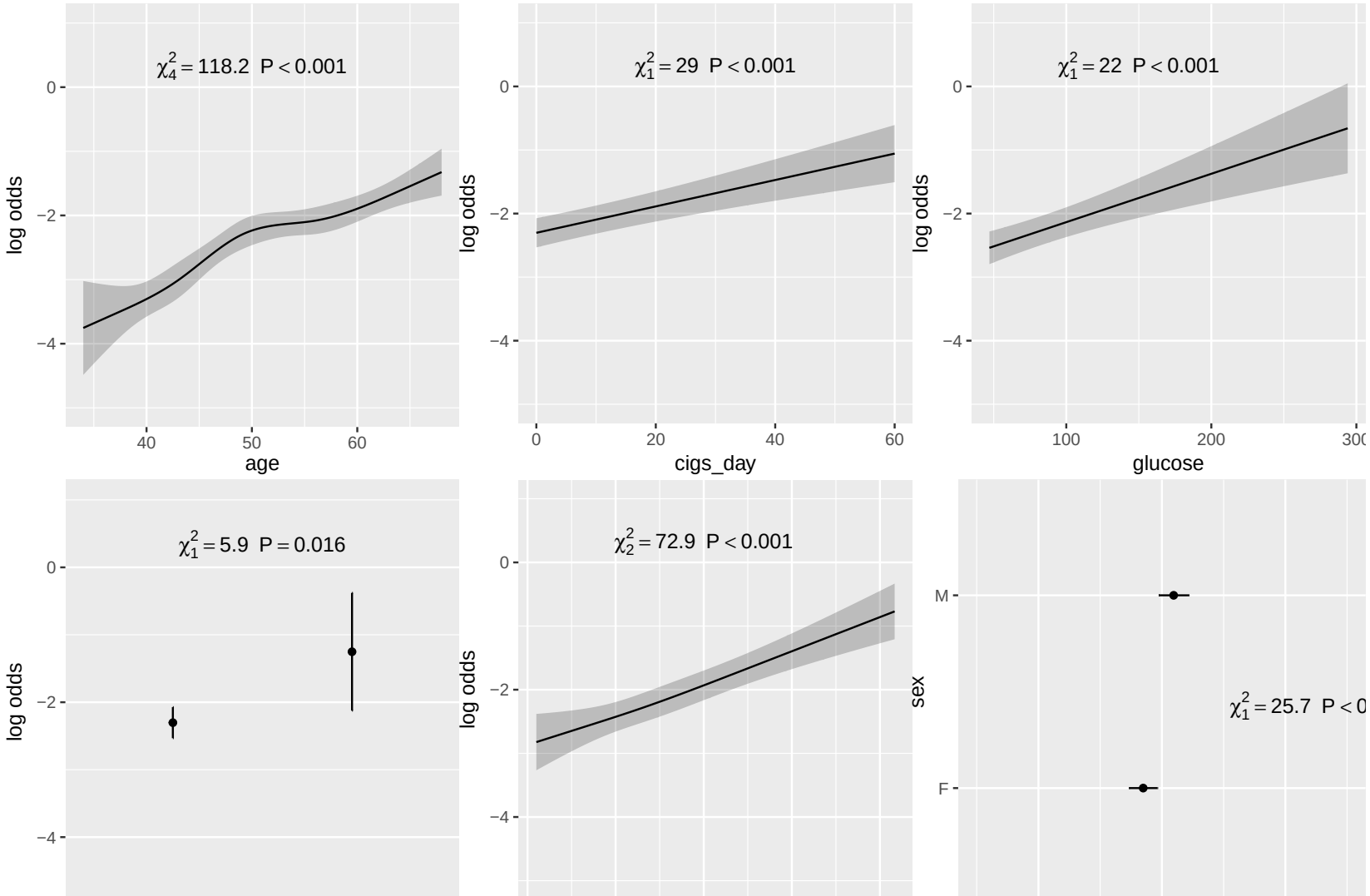


plot(anova(m_04_lrm))



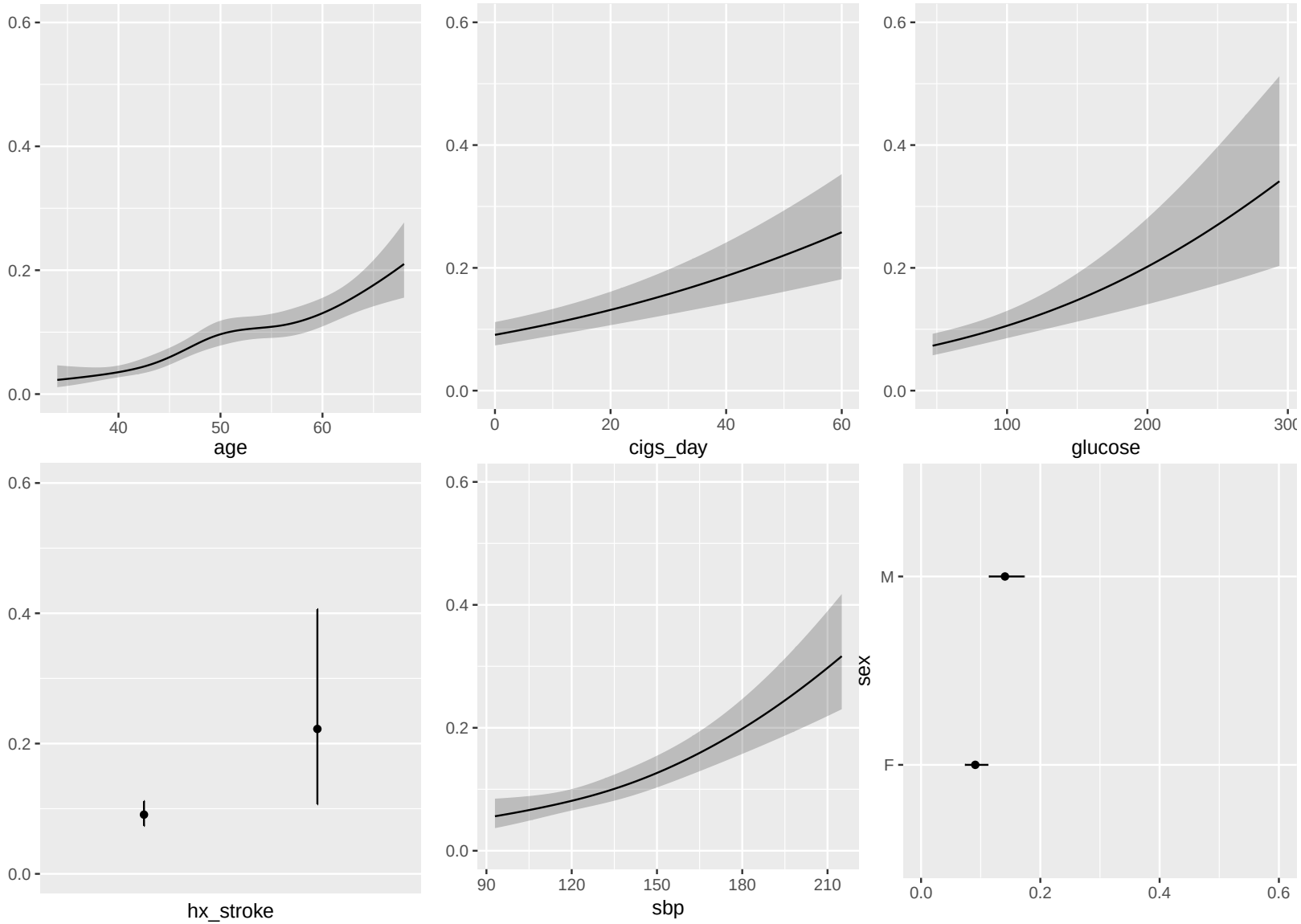
Can we see the prediction results?

```
ggplot(Predict(m_04_lrm),
       anova = anova(m_04_lrm), pval = TRUE)
```



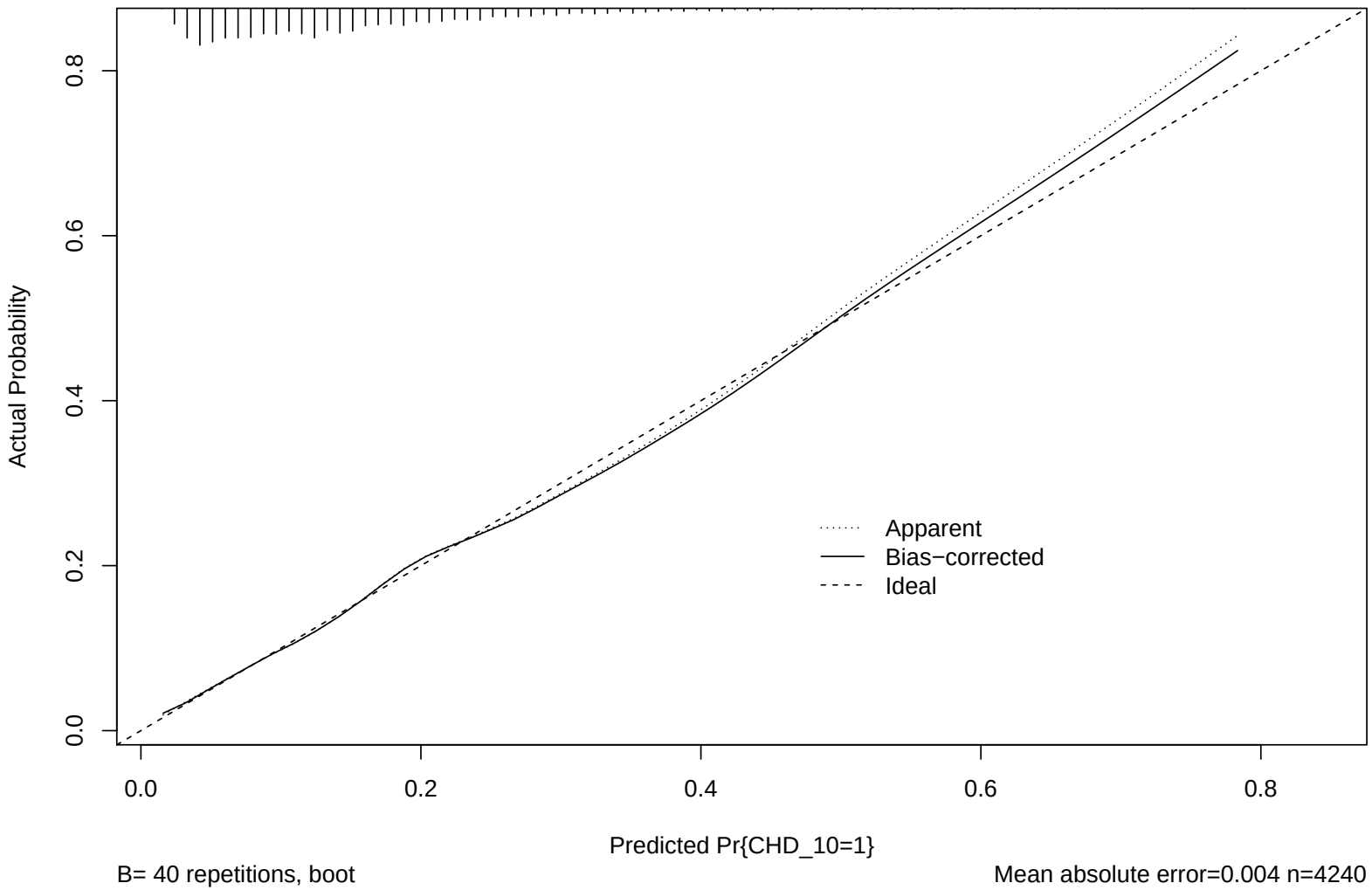
What about on a better scale?

```
ggplot(Predict(m_04_lrm, fun = plogis))
```



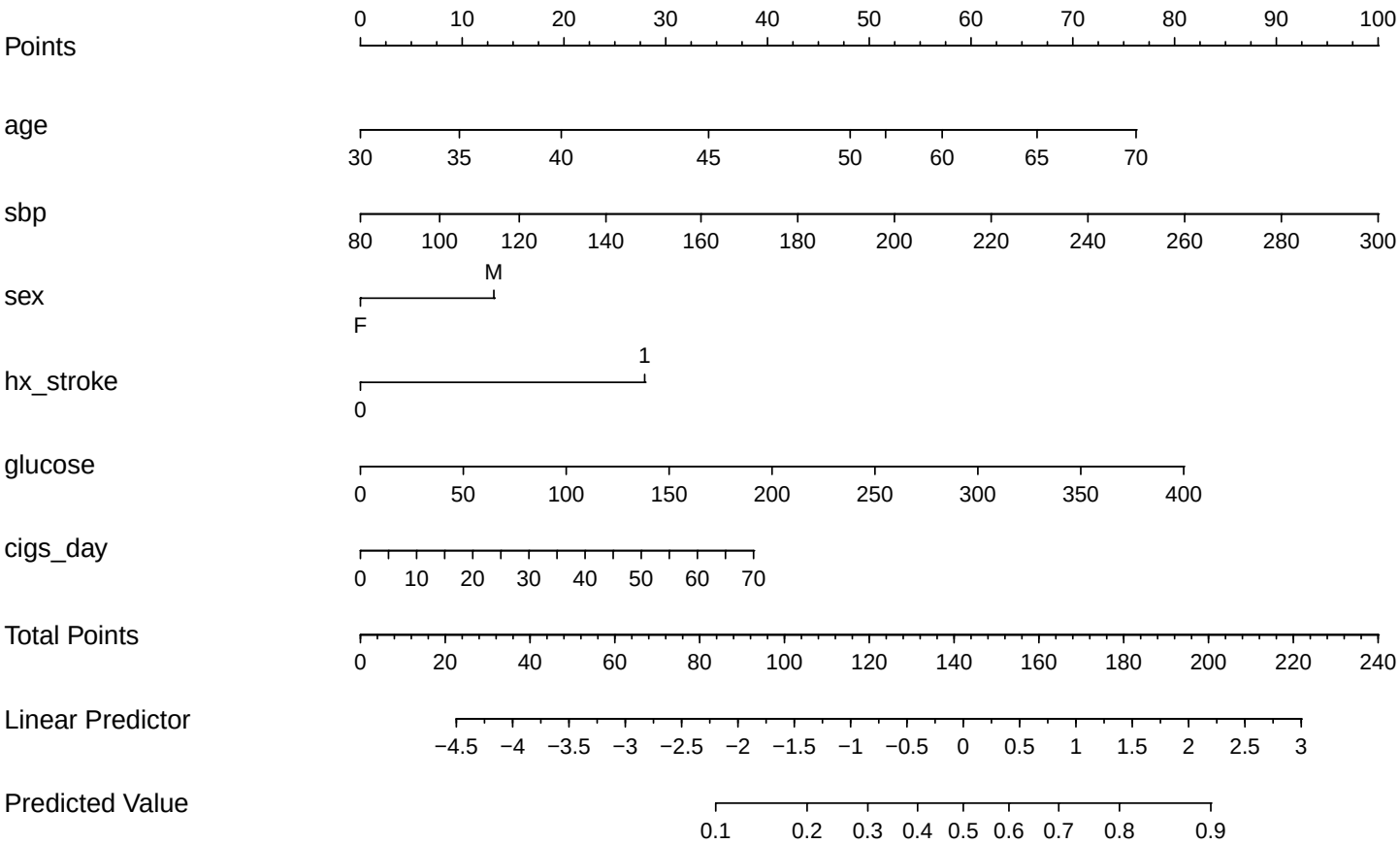
Calibration of mod_04_lrm

```
plot(calibrate(m_04_lrm))
```



Nomogram of mod_04_lrm

```
plot(nomogram(m_04_lrm, fun = plogis))
```



Comparing Models 3 and 4 (which aren't nested)

```
glance(m_03) # kitchen sink but no non-linear terms
```

```
  null.deviance df.null    logLik      AIC      BIC
1      3612.209    4239 -1603.407 3242.813 3357.155
  deviance df.residual
1 3206.813        4222
```

```
glance(m_04) # six predictors but with non-linear terms
```

```
  null.deviance df.null    logLik      AIC     BIC deviance
1      3612.209    4239 -1605.382 3232.764 3302.64 3210.764
  df.residual
1        4229
```

Checking Residuals?

- Yes/No outcomes contain less information than quantitative outcomes
- Residuals cannot be observed - predicted
    - There are several different types of residuals defined
- Assumptions of logistic regression are different
    - Model is deliberately non-linear
    - Error variance is a function of the mean, so it isn't constant
    - Errors aren't assumed to follow a Normal distribution
    - Only thing that's the same: leverage and influence

So, plot 5 (residuals/leverage/influence) can be a little useful, but that's it.

- We'll need better diagnostic tools for generalized linear models.

Any observations particularly influential on Model 4?

```
which.influence(m_04_lrm, cutoff = 0.3)
```

```
$Intercept
[1] "3896"

$glucose
[1] "1785" "3703"
```

Influence and Model 4?

```
plot(m_04, which = 5)
```