432 Class 9 Slides

github.com/THOMASELOVE/432-2018

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Setup

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

Today's Materials

- Logistic Regression and the Low Birth Weight data
- How well does the model classify subjects?
- Receiver Operating Characteristic Curve Analysis
    - The C statistic (Area under the curve)
- Assessing Residual Plots for a Logistic Regression
- A "Kitchen Sink" Logistic Regression Model
    - Comparing Models
    - Interpreting Models with Multiple Predictors
- Fitting a Logistic Model with `lrm`
    - Nagelkerke R^2, Somers' d etc.
    - Validating Summary Statistics
    - Summaries of Effects
    - Plotting In-Sample Predictions
    - Influence
    - Calibration
    - Nomograms

The Low Birth Weight data, again

```
lbw1 <- read.csv("data/lbw.csv") %>% tbl_df

lbw1 <- lbw1 %>%
    mutate(race_f = fct_recode(factor(race), white = "1",
                               black = "2", other = "3"),
           race_f = fct_relevel(race_f, "white", "black")) %>%
    mutate(preterm = fct_recode(factor(ptl > 0),
                                yes = "TRUE",
                                no = "FALSE")) %>%
    select(subject, low, lwt, age, ftv, ht, race_f,
           preterm, smoke, ui)
```

The `lbw1` data (n = 189 infants)

Variable	Description
`subject`	id code
`low`	indicator of low birth weight ($<$ 2500 g)
`lwt`	mom's weight at last menstrual period (lbs.)
`age`	age of mother in years
`ftv`	count of physician visits in first trimester (0 to 6)
`ht`	history of hypertension: 1 = yes, 0 = no
`race_f`	race of mom: white, black, other
`preterm`	prior premature labor: 1 = yes, 0 = no
`smoke`	1 = smoked during pregnancy, 0 = did not
`ui`	presence of uterine irritability: 1 = yes, 0 = no

Source: Hosmer, Lemeshow and Sturdivant, *Applied Logistic Regression* 3rd edition. Data from Baystate Medical Center, Springfield MA in 1986.

Model 1

Our current model

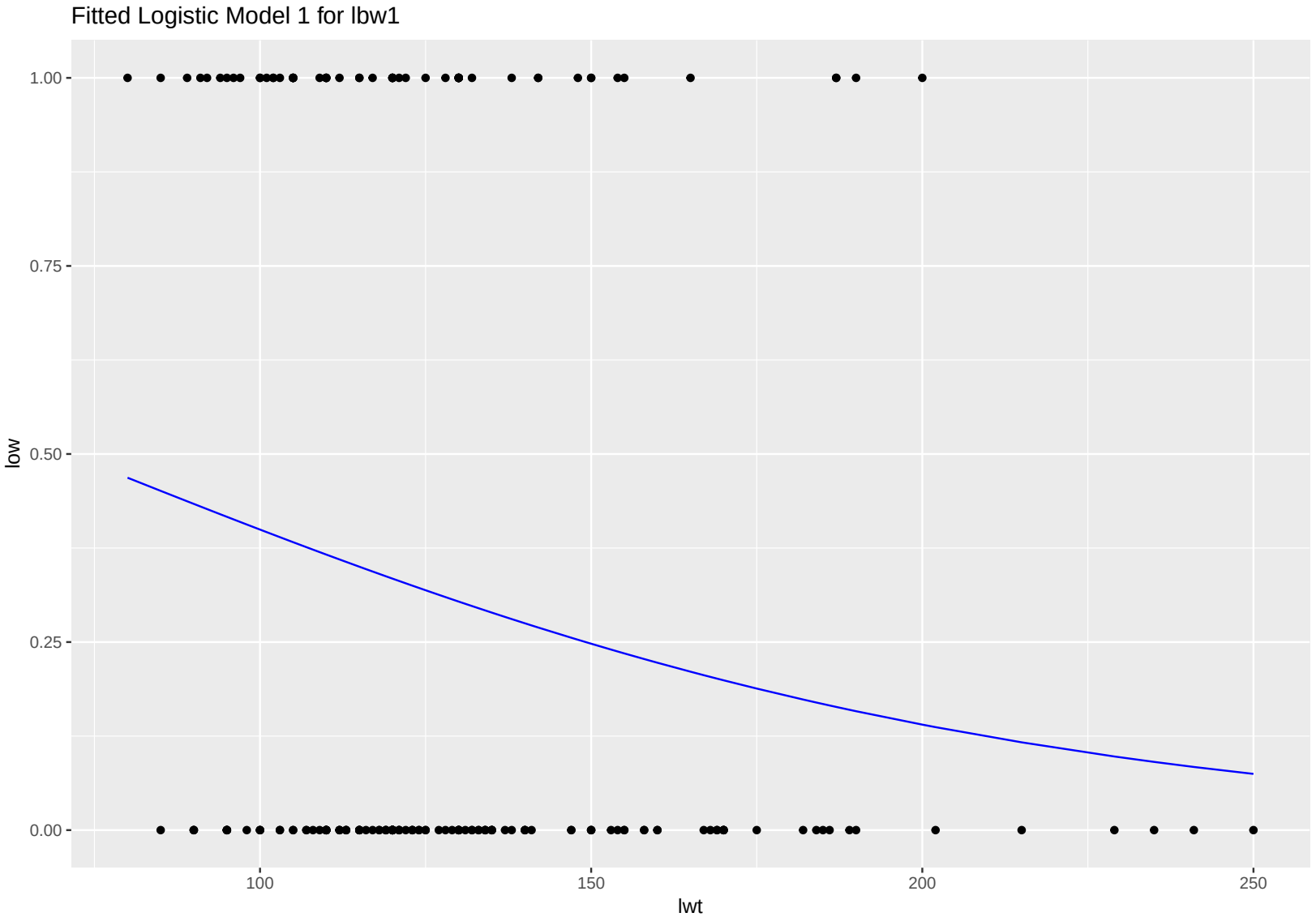
```
model.1 <- glm(low ~ lwt, data = lbw1, family = binomial)
model.1
```

```
Call:  glm(formula = low ~ lwt, family = binomial, data = lbw1

Coefficients:
(Intercept)          lwt
    0.99831     -0.01406

Degrees of Freedom: 188 Total (i.e. Null);  187 Residual
Null Deviance:      234.7
Residual Deviance: 228.7    AIC: 232.7
```

Plotting the Logistic Regression Model (as last time)

```
mod1.aug <- augment(model.1, lbw1,
                    type.predict = "response")

ggplot(mod1.aug, aes(x = lwt, y = low)) +
    geom_point() +
    geom_line(aes(x = lwt, y = .fitted), col = "blue") +
    labs(title = "Fitted Logistic Model 1 for lbw1")
```

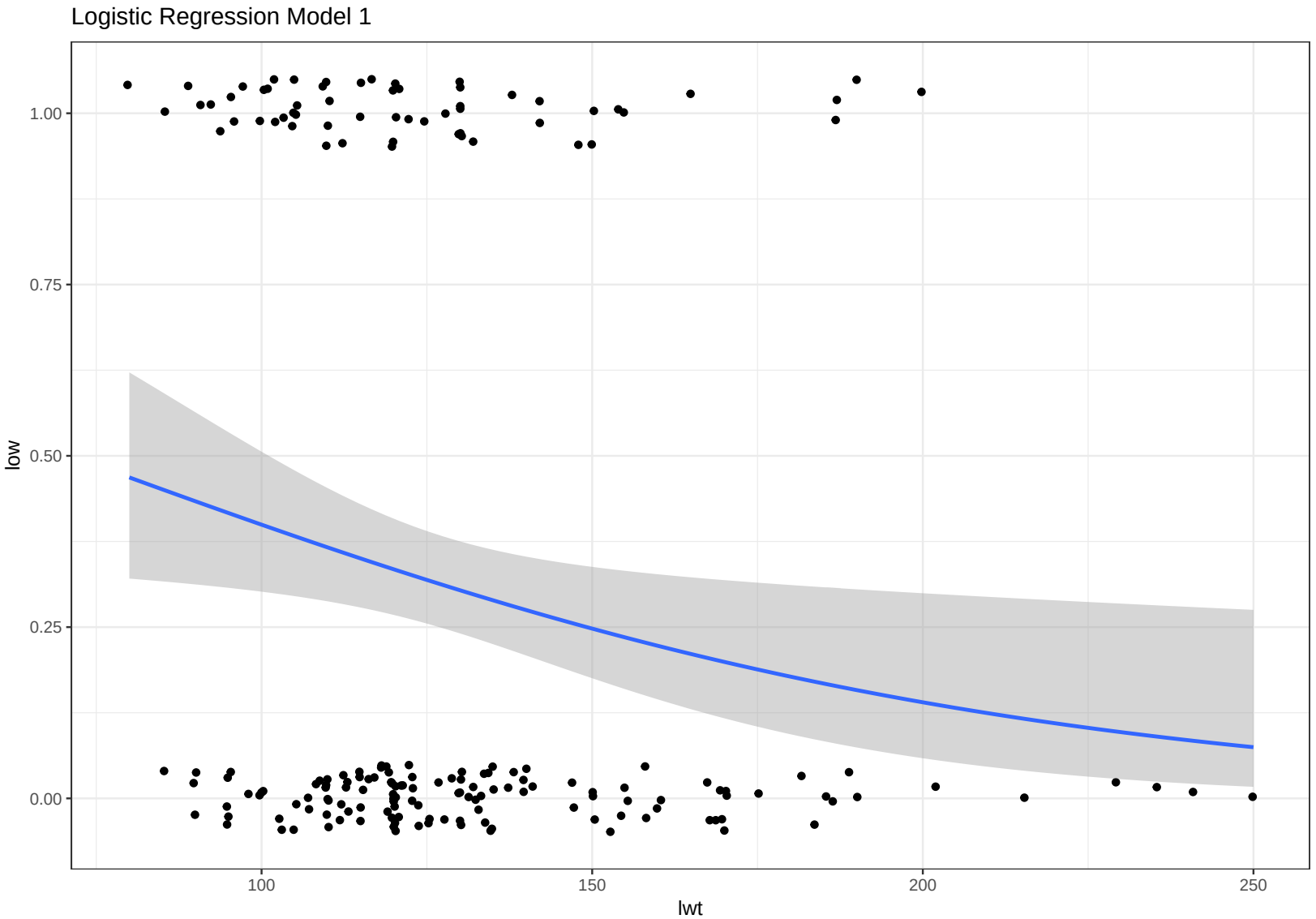
Plotting the Logistic Regression Model (as last time)



Plotting a Simple Logistic Model using `binomial_smooth`

```
binomial_smooth <- function(...) {
  geom_smooth(method = "glm",
              method.args = list(family = "binomial"), ...)
}

ggplot(lbw1, aes(x = lwt, y = low)) +
  geom_jitter(height = 0.05) +
  binomial_smooth() +
    ## ...smooth(se=FALSE) to leave out interval
  labs(title = "Logistic Regression Model 1") +
  theme_bw()
```

The Resulting Plot



glance on model.1

```
glance(model.1)
```

```
  null.deviance df.null    logLik      AIC      BIC
1       234.672     188 -114.3453 232.6907 239.1742
  deviance df.residual
1 228.6907          187
```

- Deviance $= -2 \times$ log (likelihood)
- AIC and BIC are based on the deviance, but with differing penalties for complicating the model
- AIC and BIC remain useful for comparing multiple models for the same outcome

summary of model.1

```
> round(summary(model.2)$coef,3)
             Estimate Std. Error z value Pr(>|z|)
(Intercept)     0.644      1.224   0.527    0.598
lwt            -0.015      0.007  -2.143    0.032
age            -0.040      0.038  -1.032    0.302
ftv             0.051      0.175   0.290    0.772
ht              1.860      0.708   2.627    0.009
race_fblack     1.219      0.533   2.286    0.022
race_fother     0.819      0.450   1.819    0.069
pretermyes      1.219      0.463   2.632    0.008
smoke           0.859      0.410   2.097    0.036
ui              0.719      0.463   1.552    0.121
```

Coefficients output

```
Coefficients:
             Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.99831    0.78529   1.271   0.2036
lwt         -0.01406    0.00617  -2.279   0.0227 *
```

- We have a table of coefficients with standard errors, and hypothesis tests, although these are Wald z-tests, rather than the t tests we saw in linear modeling.
- `lwt` has a Wald Z of -2.279, yielding $p = 0.0227$
  - H_0: `lwt` does not have an effect on the log odds of `low`
  - H_A: `lwt` does have such an effect
- If the coefficient (on the logit scale) for `lwt` was truly 0, this would mean that:
  - the log odds of low birth weight did not change based on `lwt`,
  - the odds of low birth weight were unchanged based on `lwt` (OR = 1), and
  - the probability of low birth weight was unchanged based on the `lwt`.

Confidence Intervals for Coefficients

```
coef(model.1)
```

```
(Intercept)         lwt
 0.99831432 -0.01405826
```

```
confint(model.1, level = 0.95)
```

```
Waiting for profiling to be done...

                   2.5 %       97.5 %
(Intercept) -0.48116701  2.611748138
lwt         -0.02696198 -0.002650036
```

- The coefficient of `lwt` has a point estimate of -0.014 and a 95% confidence interval of (-0.027, -0.003).
- On the logit scale, this isn't that interpretable, but we will often exponentiate to describe odds ratios.

Odds Ratio Interpretation of exp(Coefficient)

```
exp(coef(model.1))
```

```
(Intercept)         lwt
  2.7137035   0.9860401
```

```
exp(confint(model.1, level = 0.95))
```

```
                2.5 %     97.5 %
(Intercept) 0.6180617 13.6228447
lwt         0.9733982  0.9973535
```

- Odds Ratio for `low` based on a one pound increase in `lwt` is 0.986 (95% CI: 0.973, 0,997).
  - Estimated odds of low birth weight will be smaller (odds < 1) for those with larger `lwt` values.
  - Smaller odds(low birth weight) = smaller Prob(low birth weight).

Deviance Residuals

```
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.0951  -0.9022  -0.8018   1.3609   1.9821
```

- The deviance residuals for each individual subject sum up to the deviance statistic for the model, and describe the contribution of each point to the model likelihood function. The formula is in the Course Notes.
- Logistic Regression is a non-linear model, and it doesn't come with either an assumption that the residuals will follow a Normal distribution, or an assumption that the residuals will have constant variance, so when we build diagnostics for the logistic regression model, we'll use different plots and strategies than we used in linear models.

Other New Things

```
(Dispersion parameter for binomial family taken to be 1)

Number of Fisher Scoring iterations: 4
```

- Dispersion parameters matter for some generalized linear models. For binomial family models like the logistic, it's always 1.
- The solution of a logistic regression model involves maximizing a likelihood function. Fisher's scoring algorithm needed just four iterations to perform this fit. The model converged, quickly.

How Well Does Our `model.1` Classify Subjects?

One possible rule: if predicted Pr(low = 1) $\geq$ 0.5, then we predict "low birth weight"

```
mod1.aug$rule.5 <- ifelse(mod1.aug$.fitted >= 0.5,
                          "Predict Low", "Predict Not Low")

table(mod1.aug$rule.5, mod1.aug$low)
```

```
                    0   1
  Predict Not Low 130  59
```

This rule might be a problem for us. What % are correct?

A plot of classifications with the 0.5 rule

How Well Does Our `model.1` Classify Subjects?

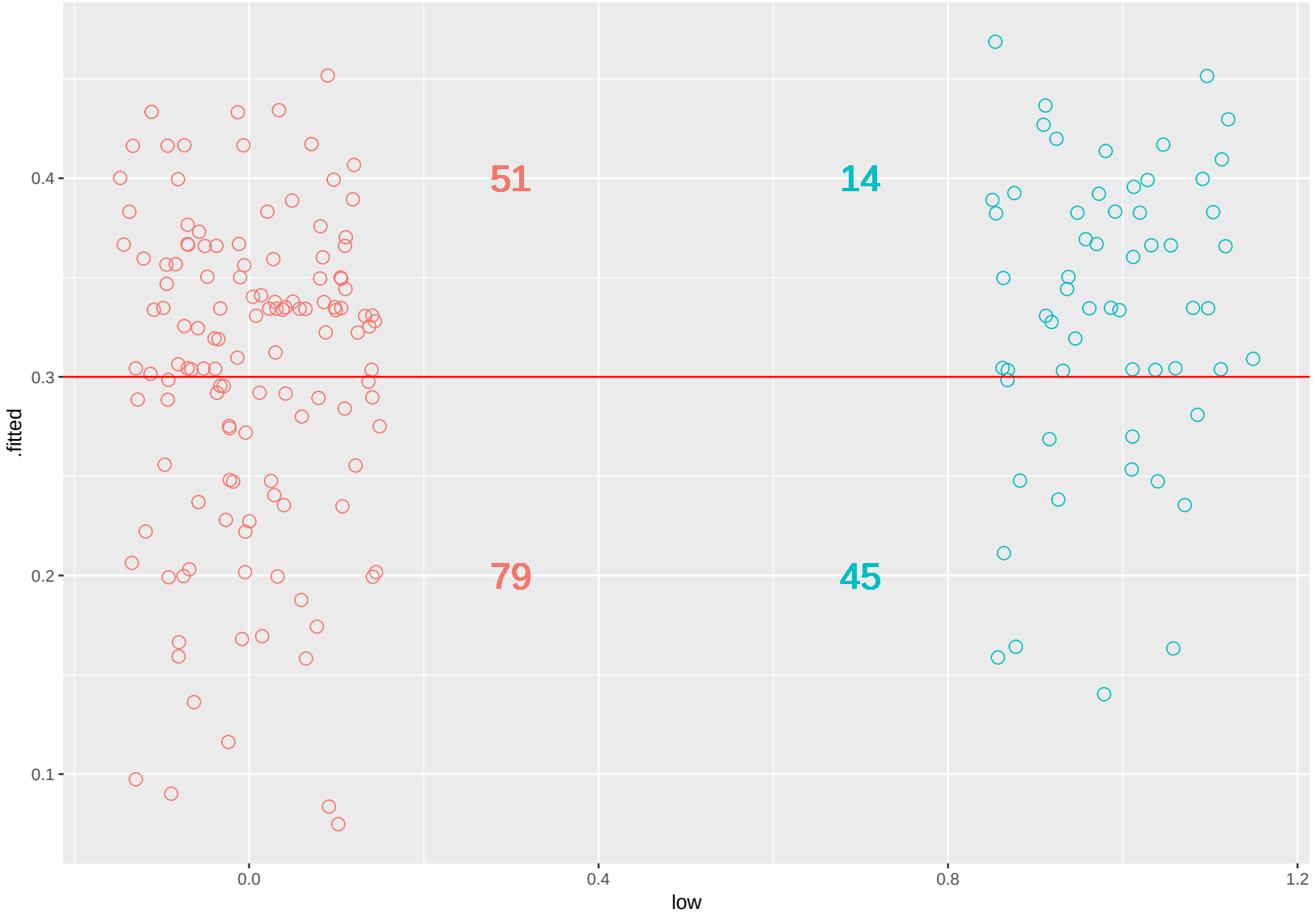
A new rule: if predicted Pr(low = 1) $\geq$ 0.3, then we predict "low birth weight"

```
mod1.aug$rule.3 <- ifelse(mod1.aug$.fitted >= 0.3,
                          "Predict Low", "Predict Not Low")

table(mod1.aug$rule.3, mod1.aug$low)
```

```
                   0  1
  Predict Low     79 45
  Predict Not Low 51 14
```

What percentage of these classifications are correct?

A plot of classifications with the 0.3 rule



The C Statistic (Area under the ROC Curve)

Our Model as Diagnostic Test

We want to assess predictive accuracy of our model.

- One approach: Receiver Operating Characteristic (ROC) curve analysis.
- A common choice for assessing diagnostic tests in medicine.

Consider two types of errors made by our model, in combination with a classification rule.

- Our model uses Mom's weight at last period to predict Pr(low birth weight).
- Lighter moms had higher model probabilities, so our rule would be: Predict low birth weight if Mom's last weight is no more than R pounds.

But the choice of R is available to us. Any value we select can lead to good outcomes (of our prediction) or to errors.

Test Results

- One good outcome of our "model/test" would be if the Mom's weight is less than R and her baby is born at a low birth weight.
- The other good outcome is if Mom's weight is greater than R and her baby is born at a non-low weight.

But we can make errors, too.

- A false positive occurs when we predict Pr(low = 1) to be small, but the baby is born at a low birth weight.
- A false negative occurs when we predict Pr(low = 1) to be large, but the baby is born at a non-low weight.

We identify two key summaries:

- The true positive fraction (TPF) for a specific weight cutoff R is Pr(Mom weight $<$ R | baby actually has low = 1).
- The false positive fraction (FPF) for a specific weight cutoff R is Pr(Mom weight $<$ R | baby has low = 0).

The ROC Curve

Since the cutoff R is not fixed in advanced, we can plot the value of TPF (on the y axis) against FPF (on the x axis) for all possible values of R, and this is what the ROC curve is.

- We calculate AUC = the area under the ROC curve (a value between 0 and 1) and use it to help summarize the effectiveness of the predictions made by the model on the following scale:
  - AUC above 0.9 = excellent discrimination of low = 1 from low = 0
  - AUC between 0.8 and 0.9 = good discrimination
  - AUC between 0.6 and 0.8 = mediocre/fair discrimination
  - AUC of 0.5 = random guessing
  - AUC below 0.5 = worse than guessing

Others refer to the Sensitivity on the Y axis, and 1-Specificity on the X axis, and this is the same idea. The TPF is called the sensitivity. 1 - FPF is the true negative rate, called the specificity.

A Simulation

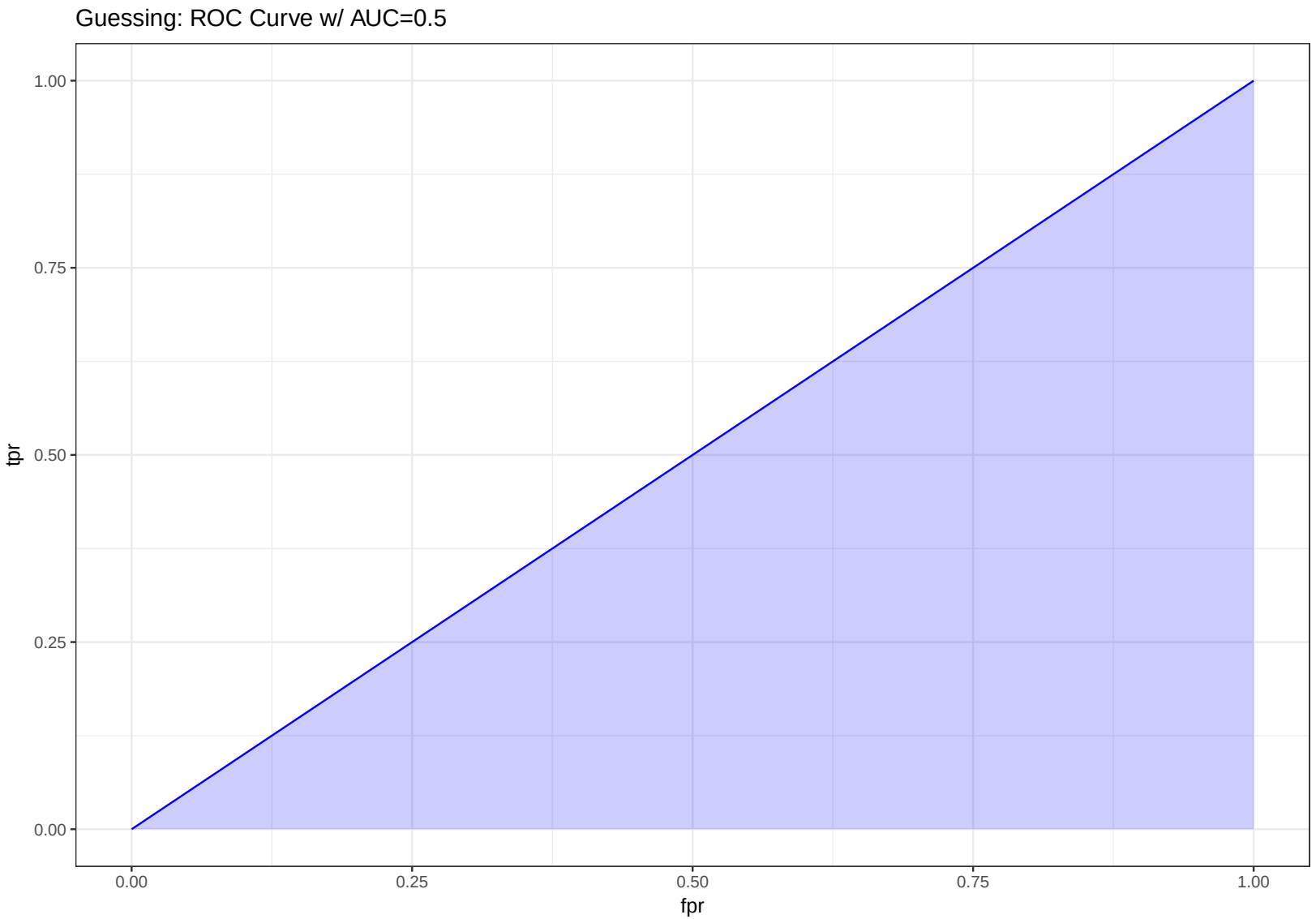
```
set.seed(43223)
sim.temp <- data_frame(x = rnorm(n = 200),
                       prob = exp(x)/(1 + exp(x)),
                       y = as.numeric(1 * runif(200) < prob))

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?

If we're guessing completely at random, then the model should correctly classify a subject (as died or not died) about 50% of the time, so the TPR and FPR will be equal. This yields a diagonal line in the ROC curve, and an area under the curve (C statistic) of 0.5.

Plot is on the next slide. . .

What if we are guessing?



Building that ROC curve, Code part 1

This approach requires the loading of the ROCR package. . .

```
pred_guess <- prediction(sim.temp$p_guess, sim.temp$y)
perf_guess <- performance(pred_guess, measure = "tpr",
                          x.measure = "fpr")
auc_guess <- performance(pred_guess, measure="auc")

auc_guess <- round(auc_guess@y.values[[1]],3)
roc_guess <- data.frame(fpr=unlist(perf_guess@x.values),
                        tpr=unlist(perf_guess@y.values),
                        model="GLM")
```

Building that ROC curve, Code part 2

```
ggplot(roc_guess, aes(x=fpr, ymin=0, ymax=tpr)) +
    geom_ribbon(alpha=0.2, fill = "blue") +
    geom_line(aes(y=tpr), col = "blue") +
    labs(title = paste0("Guessing: ROC Curve w/ AUC=",
                        auc_guess)) +
    theme_bw()
```

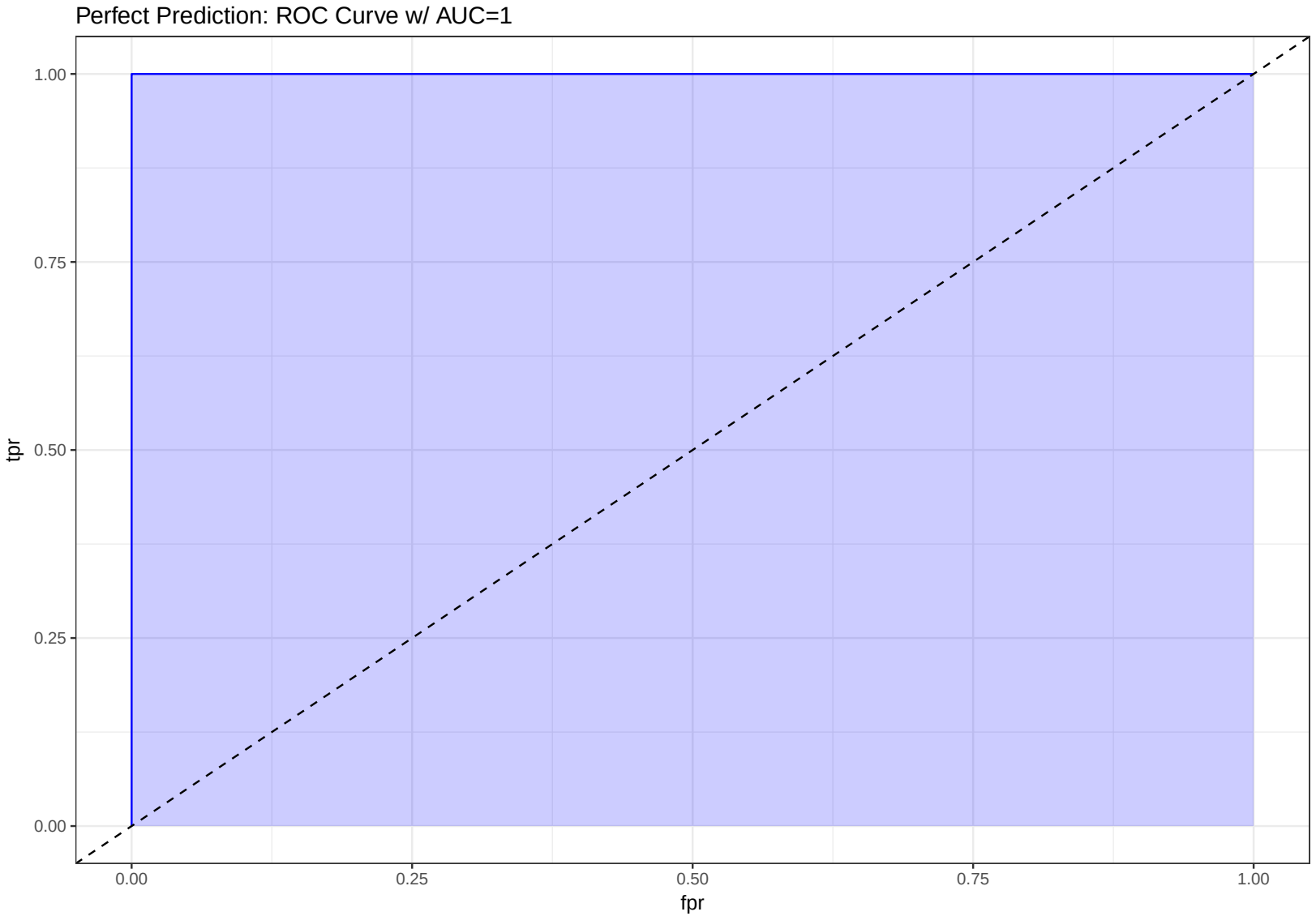
What if our model classifies things perfectly?

If we're classifying subjects perfectly, then we have a TPR of 1 and an FPR of 0.

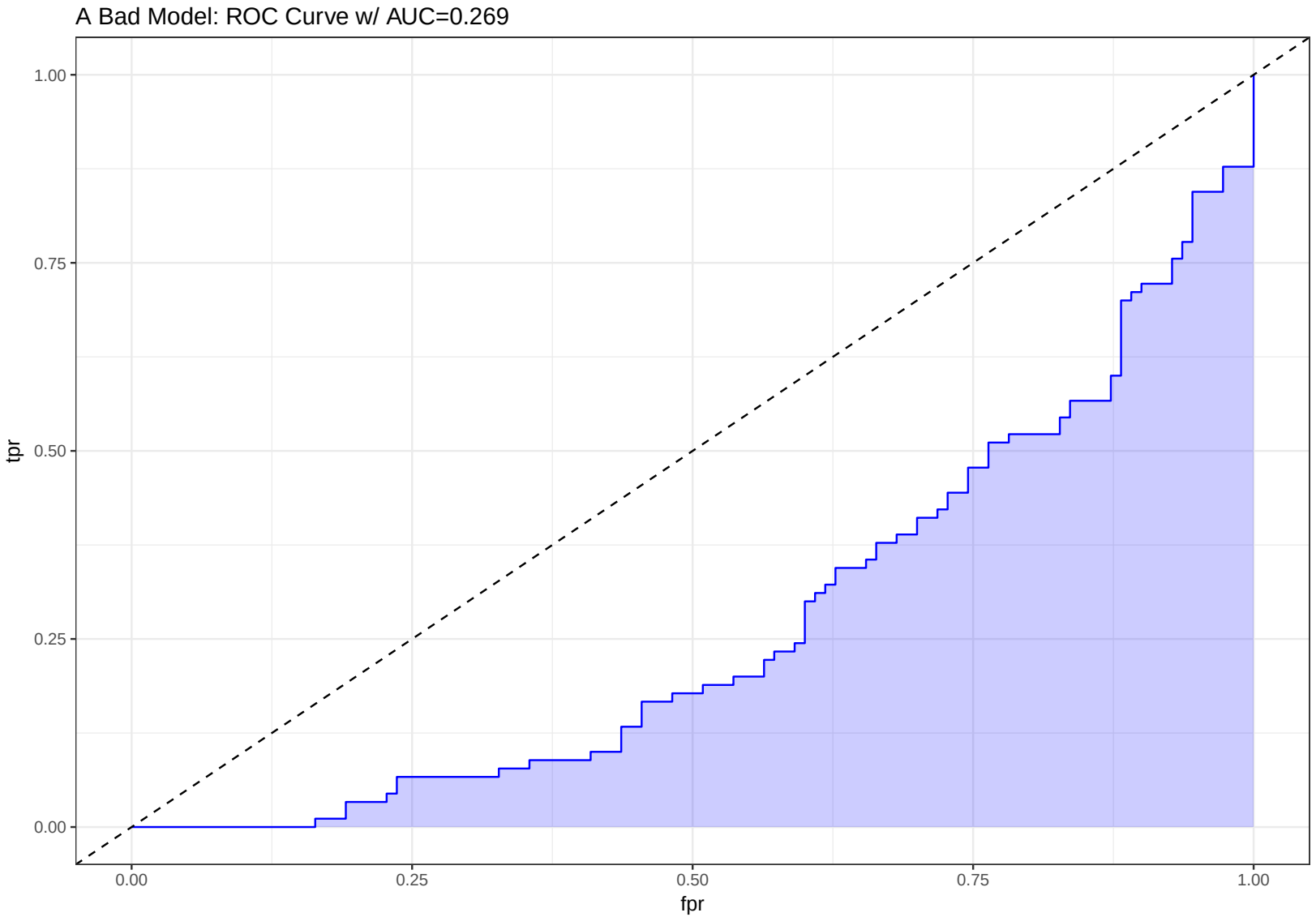
- That yields an ROC curve that looks like the upper and left edges of a box.
- If our model correctly classifies a subject (as died or not died) 100% of the time, the area under the curve (c statistic) will be 1.0.

I added in a diagonal dashed black line to show how this model compares to random guessing.

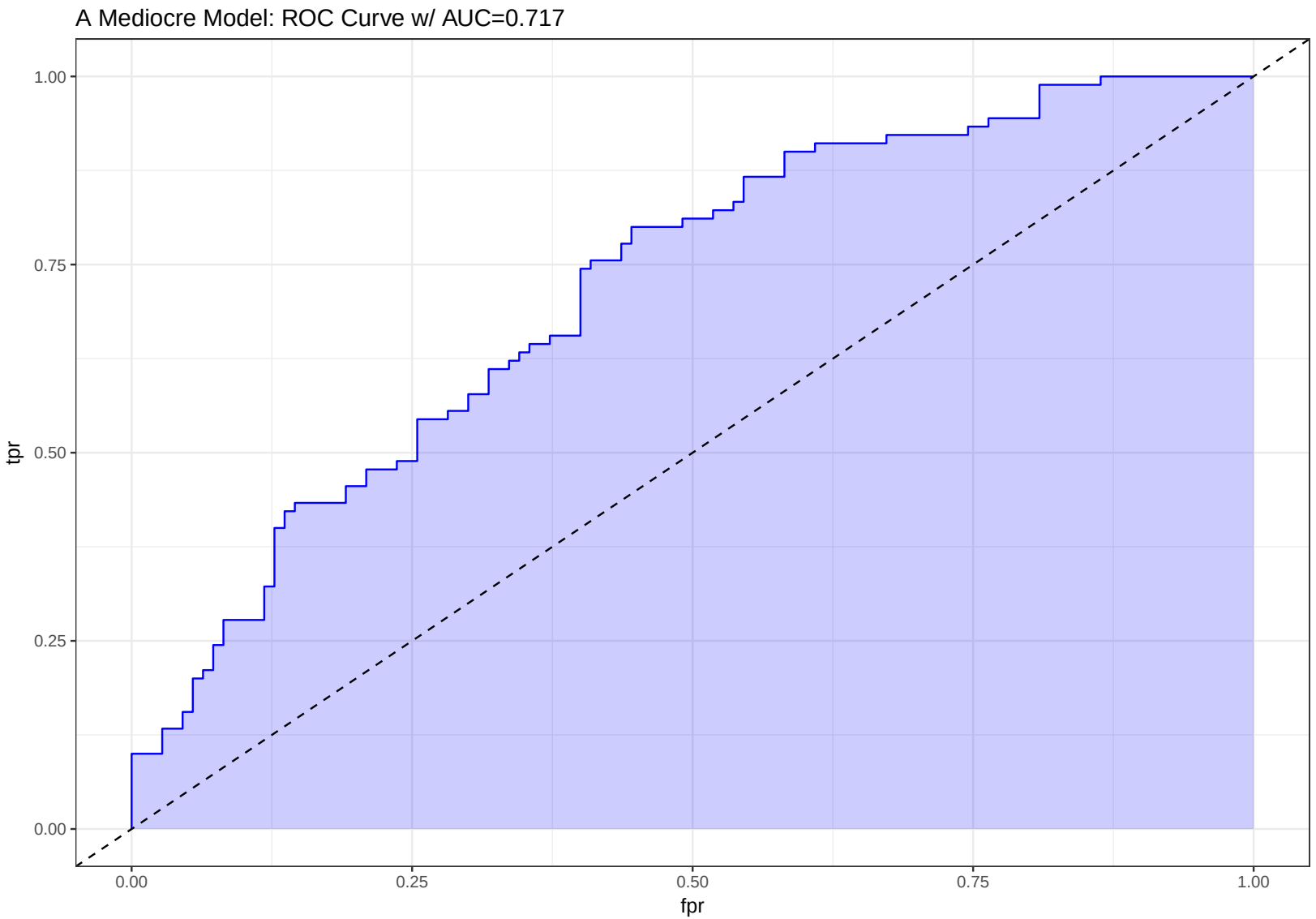
What if our model classifies things perfectly?



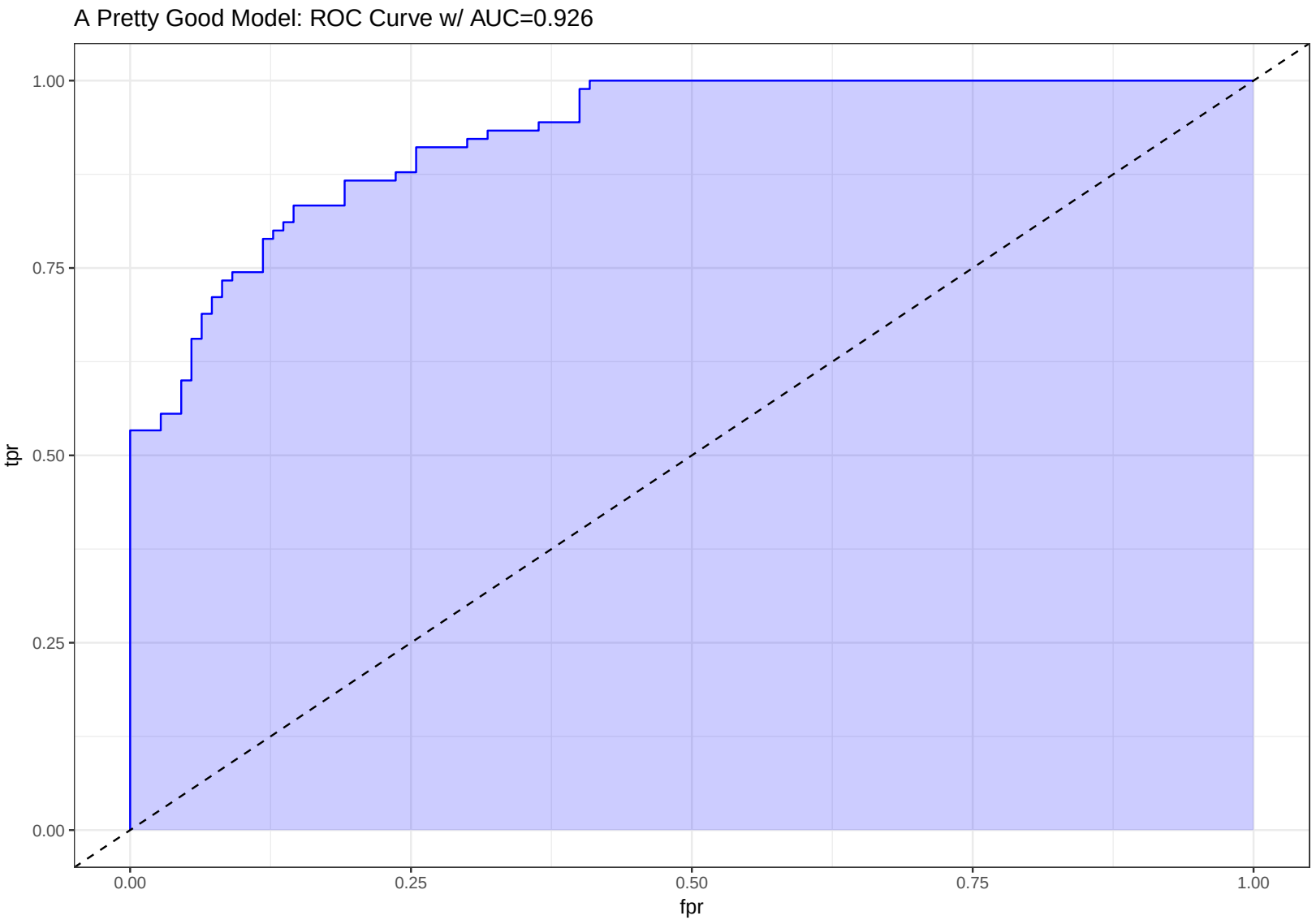
What does "worse than guessing" look like?



What does "better than guessing" look like?



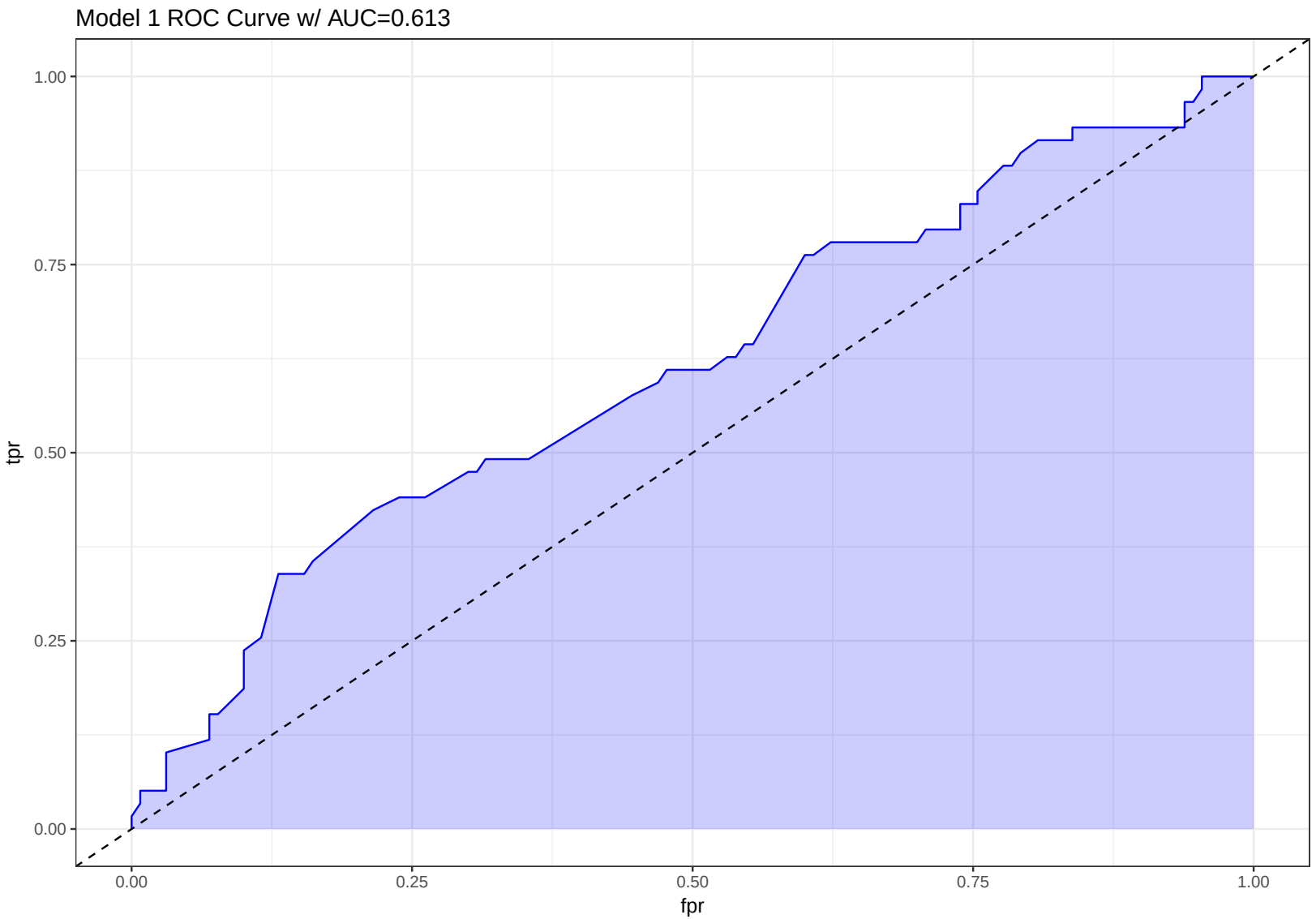
What does “pretty good” look like?



The ROC plot for our Model 1 (code)

```
## requires ROCR package
prob <- predict(model.1, lbw1, type="response")
pred <- prediction(prob, lbw1$low)
perf <- performance(pred, measure = "tpr", x.measure = "fpr")
auc <- performance(pred, measure="auc")

auc <- round(auc@y.values[[1]],3)
roc.data <- data.frame(fpr=unlist(perf@x.values),
                       tpr=unlist(perf@y.values),
                       model="GLM")

ggplot(roc.data, 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 ROC plot for our Model 1 (Result)



Interpreting the C statistic (0.613) for Model 1

C statistic	Interpretation
0.90 to 1.00	model does an excellent job at discriminating "yes" 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

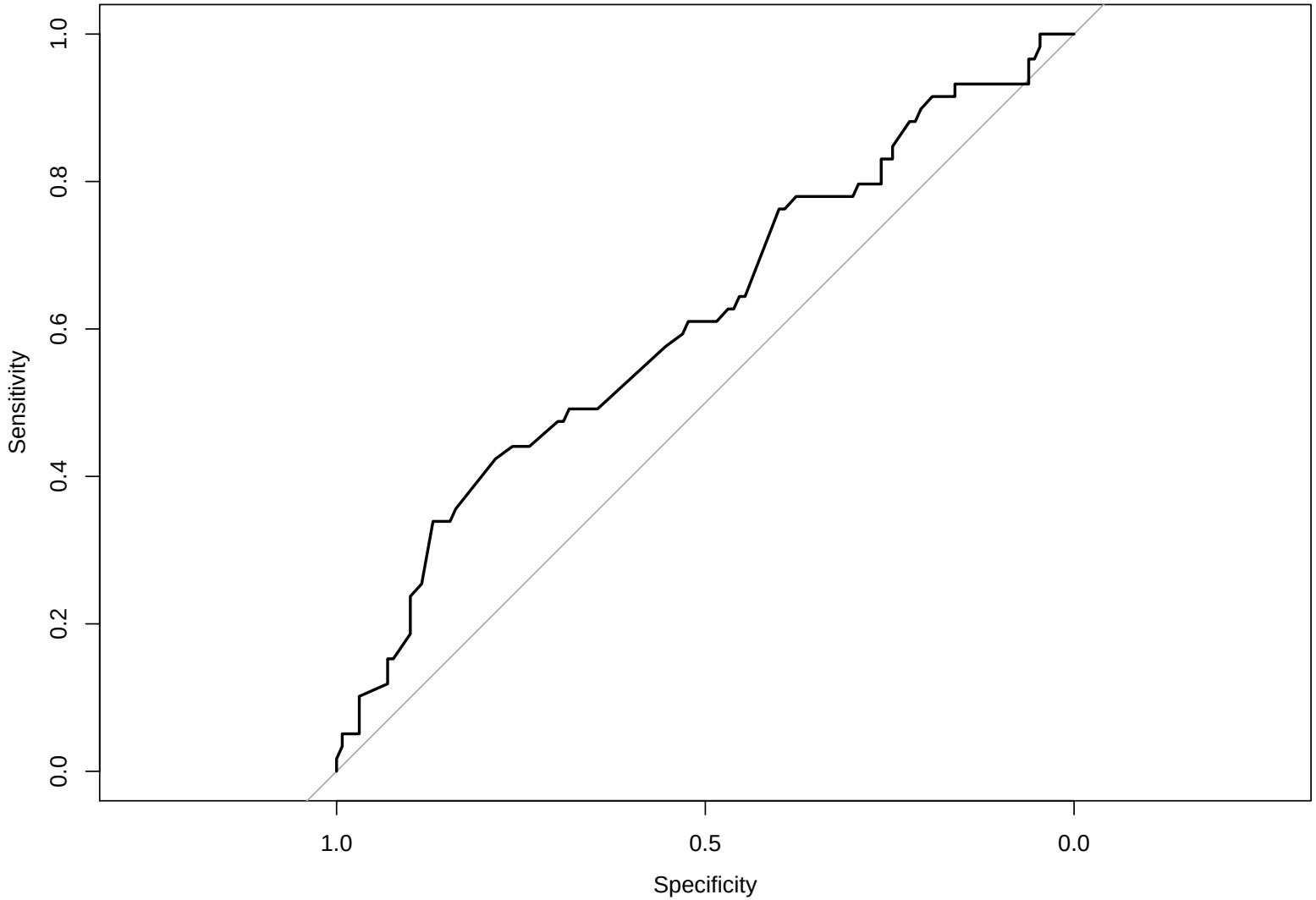
Another way to plot the ROC Curve

If we've loaded the pROC package, we can also use the following (admittedly simpler) approach to plot the ROC curve, without ggplot2, and to obtain the C statistic, and a 95% confidence interval around that C statistic.

```
## requires pROC package
roc.mod1 <-
    roc(lbw1$low ~ predict(model.1, type="response"),
        ci = TRUE)
```

```
> roc.mod1

Call:
roc.formula(formula = lbw1$low ~ predict(model.1, type = "response"),     ci = TRUE)

Data: predict(model.1, type = "response") in 130 controls (lbw1$low 0) < 59 cases (lbw1$low 1).
Area under the curve: 0.6131
95% CI: 0.5245-0.7017 (DeLong)
```

Result of `plot(roc.mod1)`



Plotting Residuals of a Logistic Regression

Residual Plots for `model.1`?

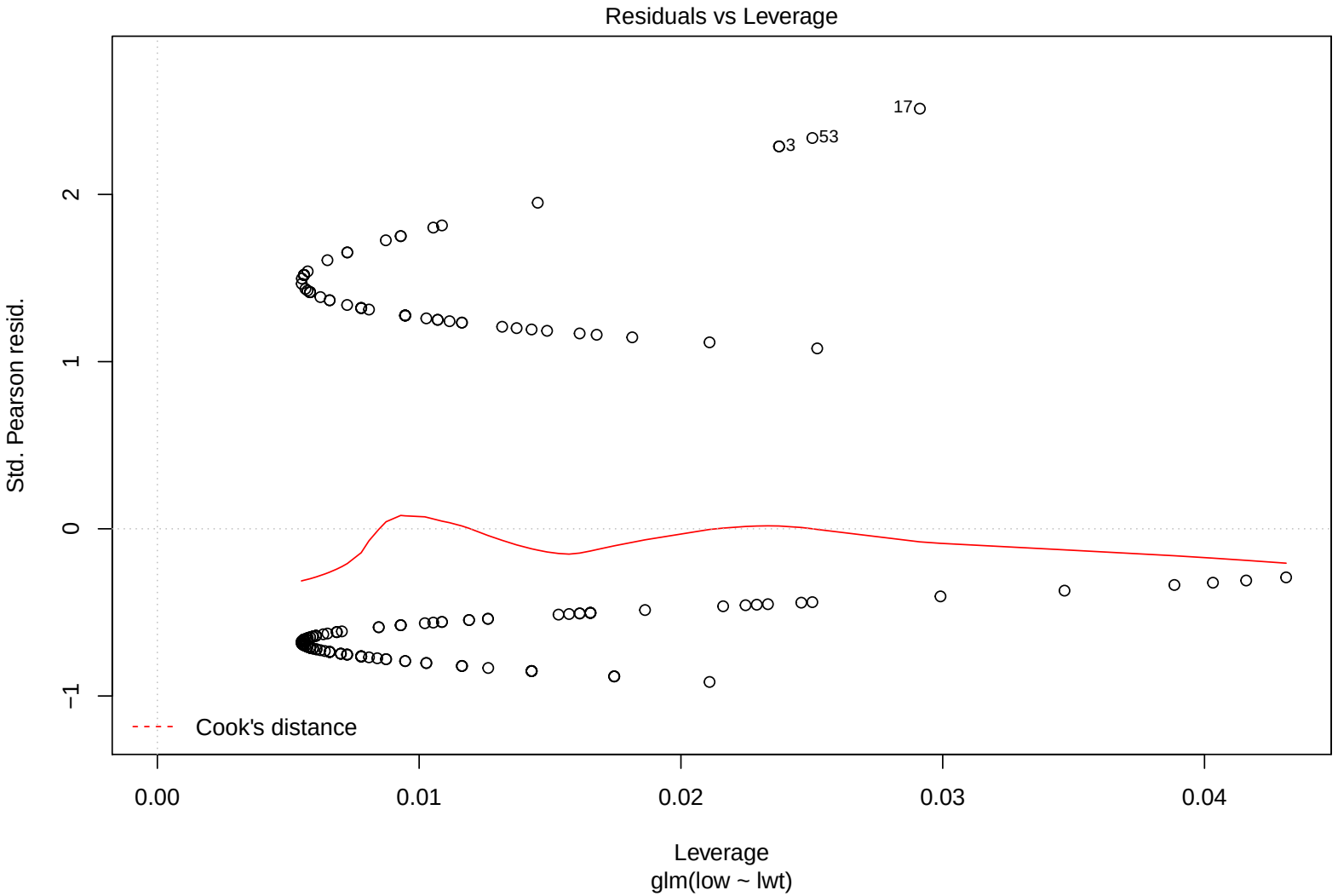
- Yes/No outcomes contain less information than quantitative outcomes
- Residuals cannot be observed - predicted
  - There are several different types of residuals defined
- Assumptions of logistic regression are different
  - Model is deliberately non-linear
  - Error variance is a function of the mean, 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 down the line.

Semi-Useful Residual Plot

```
plot(model.1, which = 5)
```



Building a Bigger Model

Model 2: A "Kitchen Sink" Logistic Regression

```
model.2 <- glm(low ~ lwt + age + ftv + ht + race_f +
                     preterm + smoke + ui,
               data = lbw1, family = binomial)
```

Variable	Description
`low`	indicator of low birth weight ($<$ 2500 g)
`lwt`	mom's weight at last menstrual period (lbs.)
`age`	age of mother in years
`ftv`	physician visits in first trimester (0 to 6)
`ht`	history of hypertension: 1 = yes, 0 = no
`race_f`	race of mom: white, black, other
`preterm`	prior premature labor: 1 = yes, 0 = no
`smoke`	1 = smoked during pregnancy, 0 = did not
`ui`	uterine irritability: 1 = yes, 0 = no

model.2

```
Call:  glm(formula = low ~ lwt + age + ftv + ht + race_f + pre
    smoke + ui, family = binomial, data = lbw1)

Coefficients:
(Intercept)          lwt          age          ftv
    0.64448     -0.01508     -0.03955      0.05090
         ht  race_fblack  race_fother   pretermyes
    1.86043      1.21879      0.81944      1.21851
      smoke           ui
    0.85946      0.71930

Degrees of Freedom: 188 Total (i.e. Null);  179 Residual
Null Deviance:      234.7
Residual Deviance: 196.8    AIC: 216.8
```

Comparing model.2 to model.1

```
anova(model.1, model.2)
```

```
Analysis of Deviance Table

Model 1: low ~ lwt
Model 2: low ~ lwt + age + ftv + ht + race_f + preterm + smoke
  Resid. Df Resid. Dev Df Deviance
1       187     228.69
2       179     196.75  8   31.941
```

```
pchisq(31.94, 8, lower.tail = FALSE)
```

```
[1] 9.547465e-05
```

Comparing model.2 to model.1

```
glance(model.2)
```

```
  null.deviance df.null    logLik      AIC      BIC
1       234.672     188 -98.37504 216.7501 249.1676
  deviance df.residual
1 196.7501         179
```

```
glance(model.1)
```

```
  null.deviance df.null    logLik      AIC      BIC
1       234.672     188 -114.3453 232.6907 239.1742
  deviance df.residual
1 228.6907         187
```

Interpreting `model.2`

```
> round(summary(model.2)$coef,3)
             Estimate Std. Error z value Pr(>|z|)
(Intercept)     0.644      1.224   0.527    0.598
lwt            -0.015      0.007  -2.143    0.032
age            -0.040      0.038  -1.032    0.302
ftv             0.051      0.175   0.290    0.772
ht              1.860      0.708   2.627    0.009
race_fblack     1.219      0.533   2.286    0.022
race_fother     0.819      0.450   1.819    0.069
pretermyes      1.219      0.463   2.632    0.008
smoke           0.859      0.410   2.097    0.036
ui              0.719      0.463   1.552    0.121
```

- Larger Mom `lwt` is associated with a smaller log odds of LBW holding all other predictors constant.

Impact of these predictors via odds ratios

```
exp(coef(model.2)); exp(confint(model.2))
```

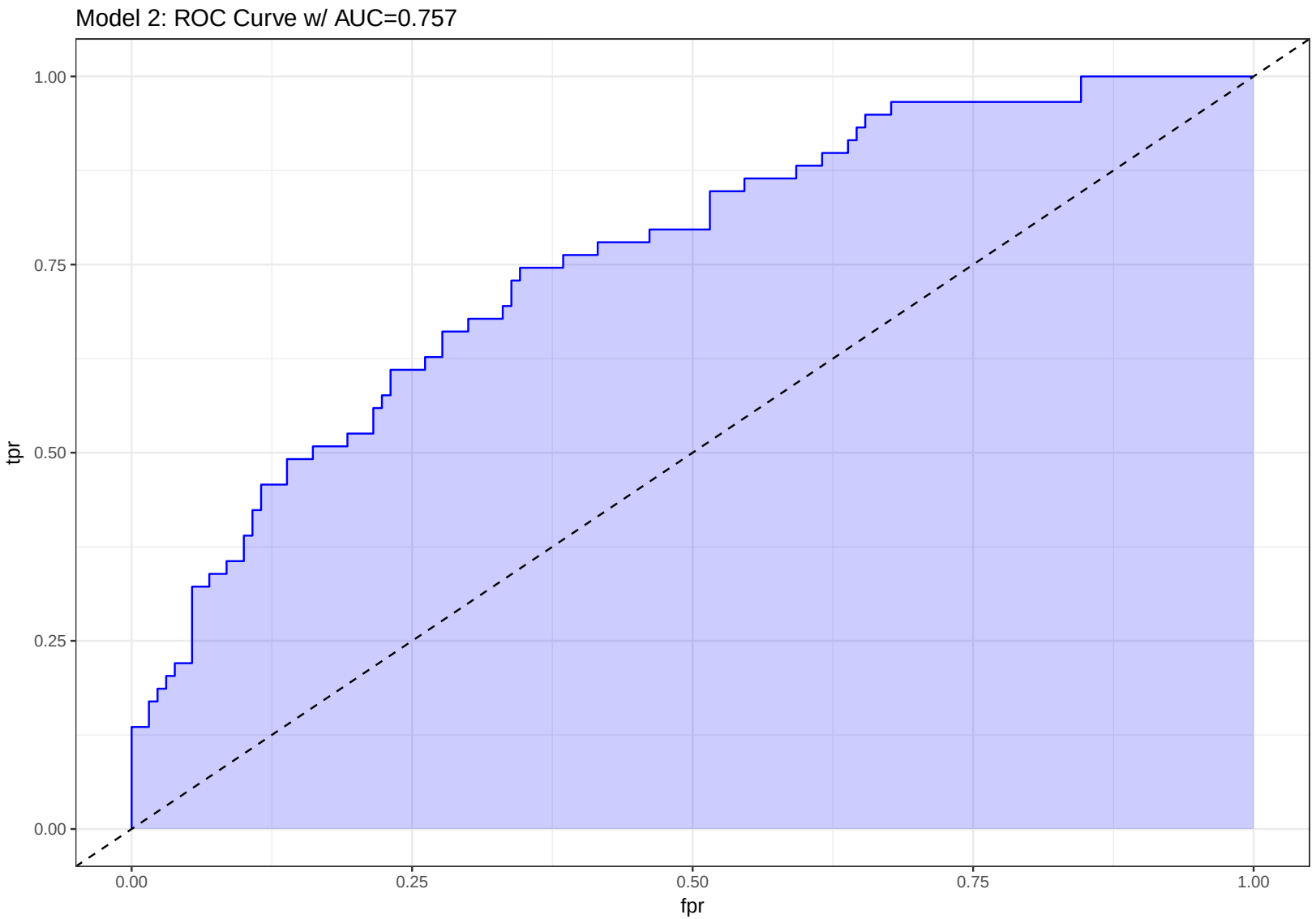
Variable	OR est.	2.5%	97.5%
lwt	0.985	0.971	0.998
age	0.961	0.890	1.035
ftv	1.052	0.739	1.478
ht	6.426	1.662	28.187
race_fblack	3.383	1.192	9.808
race_fother	2.269	0.947	5.597
pretermyes	3.382	1.378	8.575
smoke	2.362	1.067	5.375
ui	2.053	0.818	5.101

- Larger Mom `lwt` is associated with a smaller odds of LBW (est OR 0.985, 95% CI 0.971, 0.998) holding all other predictors constant.
- What appears to be associated with larger odds of LBW?

ROC curve for Model 2 (Code)

```
prob <- predict(model.2, lbw1, type="response")
pred <- prediction(prob, lbw1$low)
perf <- performance(pred, measure = "tpr", x.measure = "fpr")
auc <- performance(pred, measure="auc")

auc <- round(auc@y.values[[1]],3)
roc.data <- data.frame(fpr=unlist(perf@x.values),
                       tpr=unlist(perf@y.values),
                       model="GLM")

ggplot(roc.data, 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 2: ROC Curve w/ AUC=", auc)) +
    theme_bw()
```

ROC curve for Model 2 (Result)

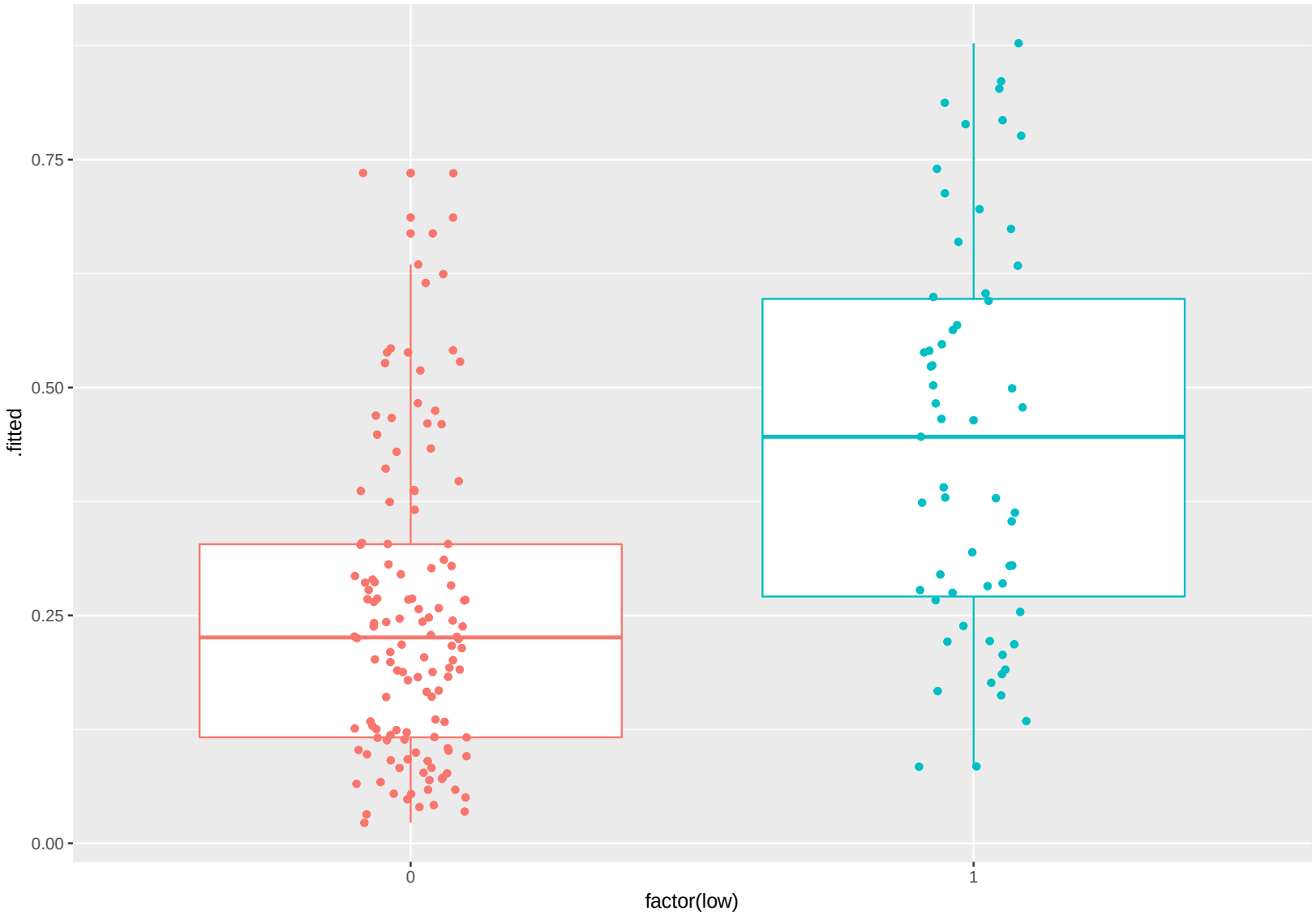


Using augment to capture the fitted probabilities

```
mod2_aug <- augment(model.2, lbw1,
                    type.predict = "response")
head(mod2_aug, 3)
```

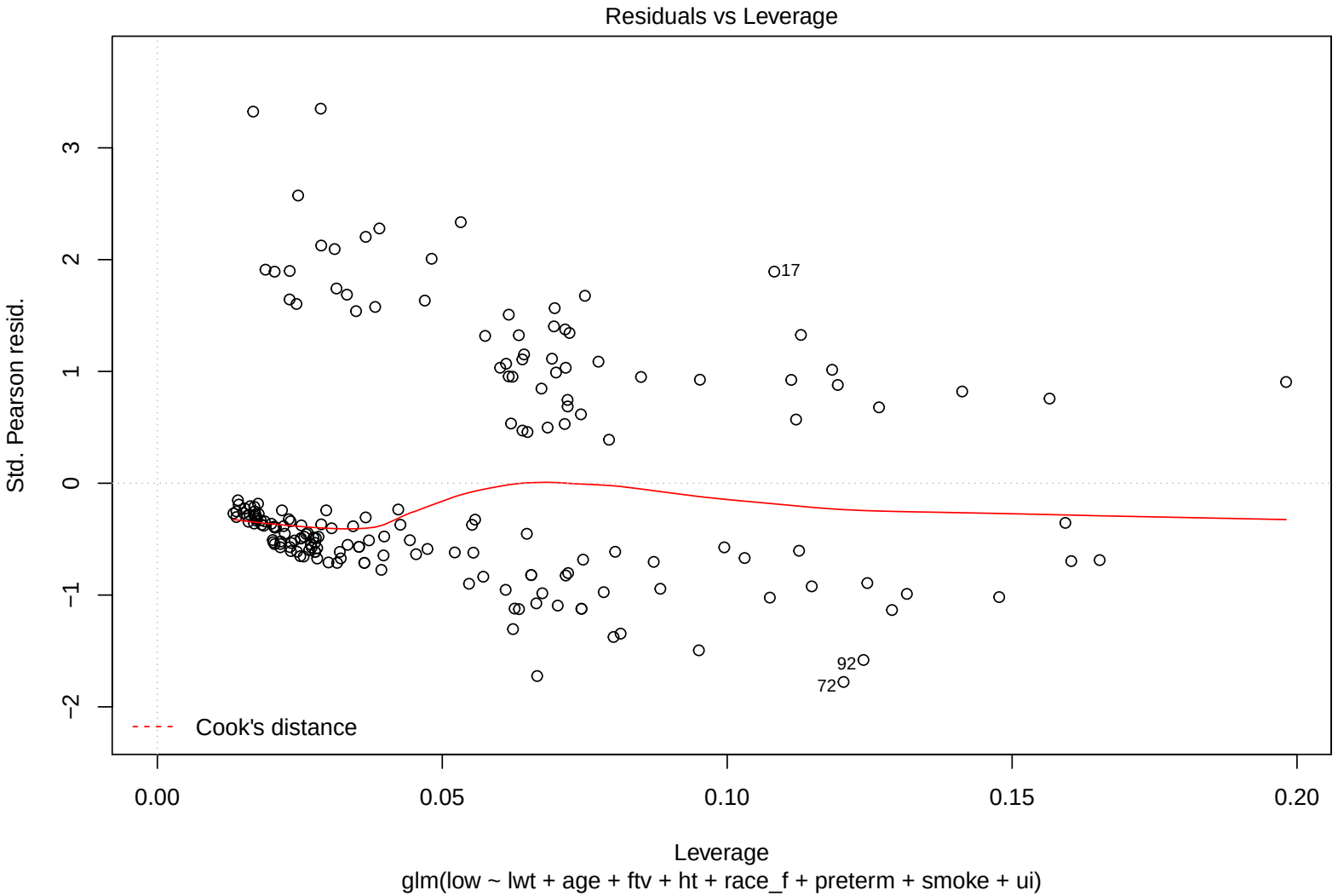
```
  subject low lwt age ftv ht race_f preterm smoke ui
1       4   1 120  28   0  0  other     yes     1  1
2      10   1 130  29   2  0  white      no     0  1
3      11   1 187  34   0  1  black      no     1  0
    .fitted    .se.fit    .resid       .hat   .sigma
1 0.7932350 0.10827348 0.6806406 0.07148005 1.050016
2 0.1622751 0.08507415 1.9070723 0.05324823 1.041036
3 0.6032496 0.21773929 1.0054096 0.19808668 1.047977
      .cooksd .std.resid
1 0.002161114  0.7063537
2 0.030667798  1.9599685
3 0.020259128  1.1227403
```

Plotting Model 2 Fits by Observed LBW status



Residuals, Leverage and Influence

```
plot(model.2, which = 5)
```



Logistic Regression using the `lrm` function

Fitting Model 2 again (as Model 3)

```
dd <- datadist(lbw1)
options(datadist = "dd")

model.3 <- lrm(low ~ lwt + age + ftv + ht + race_f +
                     preterm + smoke + ui,
               data = lbw1, x = TRUE, y = TRUE)
```

model.3 output

```
> model.3
Logistic Regression Model

 lrm(formula = low ~ lwt + age + ftv + ht + race_f + preterm +
     smoke + ui, data = lbw1, x = TRUE, y = TRUE)

                      Model Likelihood     Discrimination    Rank Discrim.
                         Ratio Test           Indexes           Indexes
 Obs             189    LR chi2      37.92    R2       0.256    C       0.757
  0              130    d.f.             9    g        1.263    Dxy     0.514
  1               59    Pr(> chi2) <0.0001    gr       3.538    gamma   0.515
 max |deriv| 0.0003                          gp       0.228    tau-a   0.222
                                             Brier    0.174

              Coef    S.E.   Wald Z Pr(>|Z|)
 Intercept     0.6445 1.2239  0.53  0.5985
 lwt          -0.0151 0.0070 -2.14  0.0321
 age          -0.0395 0.0383 -1.03  0.3019
 ftv           0.0509 0.1755  0.29  0.7717
 ht            1.8604 0.7082  2.63  0.0086
 race_f=black  1.2188 0.5332  2.29  0.0223
 race_f=other  0.8194 0.4505  1.82  0.0689
 preterm=yes   1.2185 0.4630  2.63  0.0085
 smoke         0.8595 0.4098  2.10  0.0360
 ui            0.7193 0.4634  1.55  0.1206
```

The Top Section

```
> model.3
Logistic Regression Model

 lrm(formula = low ~ lwt + age + ftv + ht + race_f + preterm +
     smoke + ui, data = lbw1, x = TRUE, y = TRUE)

                       Model Likelihood     Discrimination    Rank Discrim.
                          Ratio Test           Indexes           Indexes
 Obs              189    LR chi2      37.92   R2        0.256   C         0.757
  0               130    d.f.             9   g         1.263   Dxy       0.514
  1                59    Pr(> chi2) <0.0001   gr        3.538   gamma     0.515
 max |deriv| 0.0003                          gp        0.228   tau-a     0.222
                                             Brier     0.174
```

- Likelihood ratio test = drop in deviance test
- R2 = Nagelkerke R^2 = not a percentage of anything
- C = Area under the ROC curve
- Dxy = Somers' d, and note C = 0.5 + Dxy/2

The Coefficients Summary

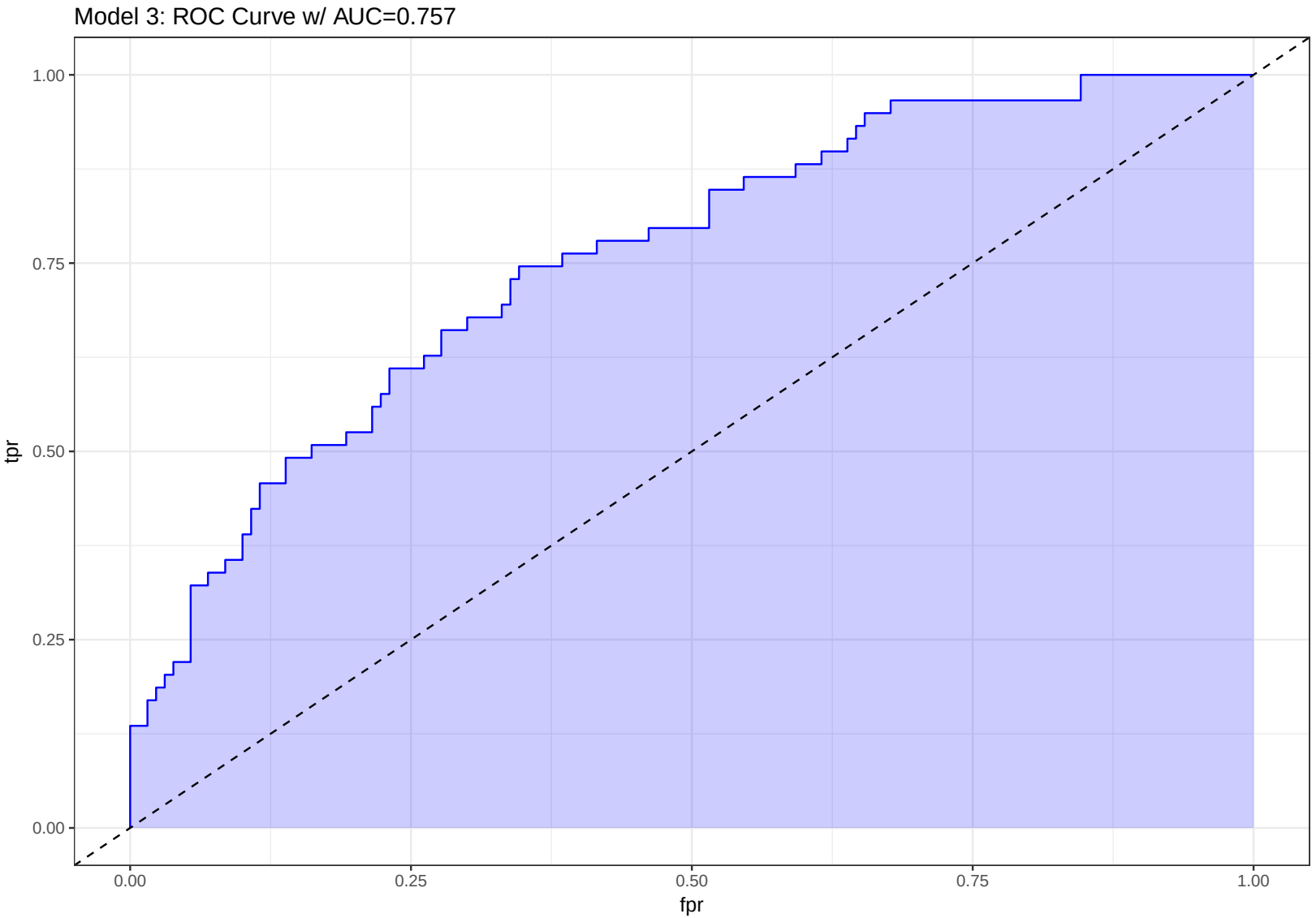
	Coef	S.E.	Wald Z	Pr(>|Z|)
Intercept	0.6445	1.2239	0.53	0.5985
lwt	-0.0151	0.0070	-2.14	0.0321
age	-0.0395	0.0383	-1.03	0.3019
ftv	0.0509	0.1755	0.29	0.7717
ht	1.8604	0.7082	2.63	0.0086
race_f=black	1.2188	0.5332	2.29	0.0223
race_f=other	0.8194	0.4505	1.82	0.0689
preterm=yes	1.2185	0.4630	2.63	0.0085
smoke	0.8595	0.4098	2.10	0.0360
ui	0.7193	0.4634	1.55	0.1206

ROC Curve Analysis (code)

- Note: change `prob` to describe `type = "fitted"`
- Note: make sure `lbw1` in `prob` is a data frame

```
prob <- predict(model.3, data.frame(lbw1), type="fitted")
pred <- prediction(prob, lbw1$low)
perf <- performance(pred, measure = "tpr", x.measure = "fpr")
auc <- performance(pred, measure="auc")
auc <- round(auc@y.values[[1]],3)
roc.data <- data.frame(fpr=unlist(perf@x.values),
                       tpr=unlist(perf@y.values),
                       model="GLM")

ggplot(roc.data, 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 3: ROC Curve w/ AUC=", auc)) +
    theme_bw()
```

ROC Curve Analysis (resulting plot)



Validating Logistic Model Summary Statistics

`lrm` has a `validate` tool to help perform resampling validation of a model, with or without backwards step-wise variable selection. Here, we'll validate our model's summary statistics using 100 bootstrap replications.

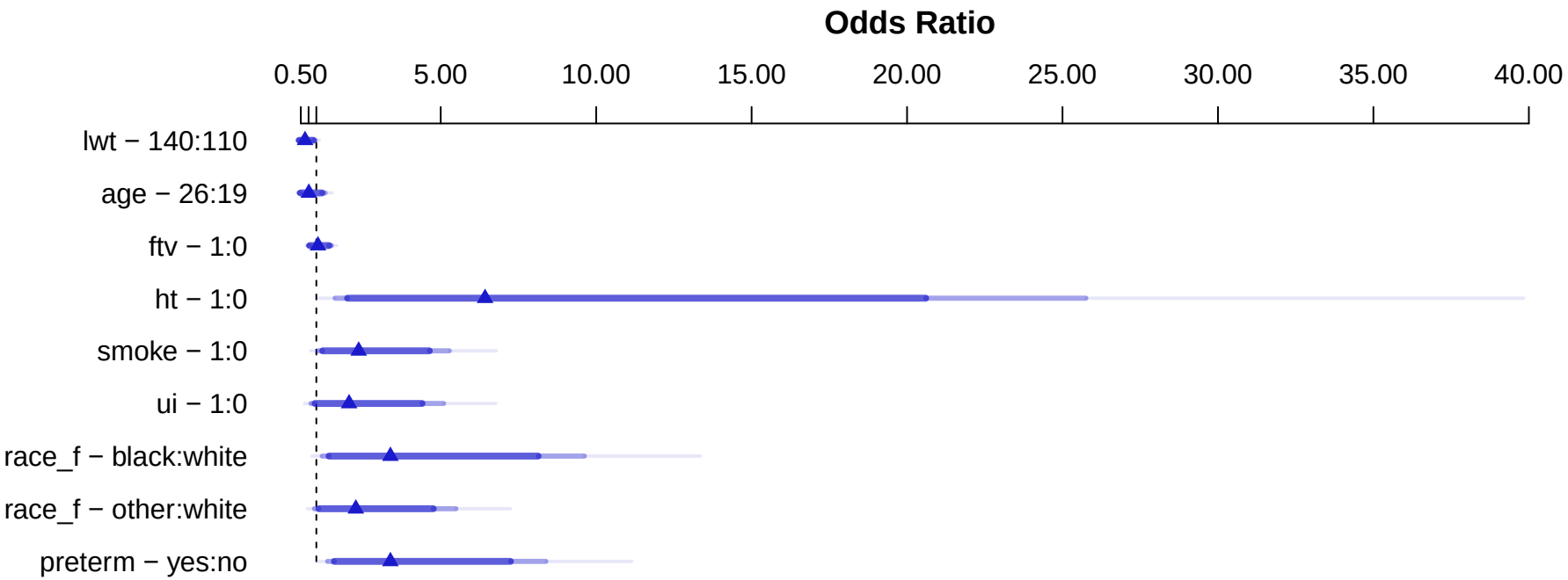
```
set.seed(432001)
validate(model.3, B = 100)
```

```
> set.seed(432001)
> validate(model.3, B = 100)
          index.orig training    test optimism index.corrected   n
Dxy           0.5142   0.5620  0.4640   0.0980          0.4162 100
R2            0.2557   0.3031  0.2041   0.0991          0.1566 100
Intercept     0.0000   0.0000 -0.1649   0.1649         -0.1649 100
Slope         1.0000   1.0000  0.7502   0.2498          0.7502 100
```

Plotting the Summary of the `lrm` approach

The `summary` function applied to an `lrm` fit shows the effect size comparing the 25th to the 75th percentile of each predictor.

```
plot(summary(model.3))
```



summary(model.3)

```
> summary(model.3)
            Effects                  Response : low

 Factor                Low High Diff. Effect   S.E.     Lower 0.95 Upper 0.95
 lwt                   110 140   30    -0.45233 0.21103 -0.865940  -0.038713
  Odds Ratio           110 140   30     0.63615       NA  0.420660   0.962030
 age                    19  26    7    -0.27684 0.26814 -0.802390   0.248710
  Odds Ratio            19  26    7     0.75818       NA  0.448260   1.282400
 ftv                     0   1    1     0.05090 0.17546 -0.292990   0.394790
  Odds Ratio             0   1    1     1.05220       NA  0.746030   1.484100
 ht                      0   1    1     1.86040 0.70817  0.472430   3.248400
  Odds Ratio             0   1    1     6.42650       NA  1.603900  25.750000
 smoke                   0   1    1     0.85946 0.40985  0.056170   1.662700
  Odds Ratio             0   1    1     2.36190       NA  1.057800   5.273800
 ui                      0   1    1     0.71930 0.46343 -0.189000   1.627600
  Odds Ratio             0   1    1     2.05300       NA  0.827790   5.091600
 race_f - black:white    1   2   NA     1.21880 0.53318  0.173780   2.263800
  Odds Ratio             1   2   NA     3.38310       NA  1.189800   9.619600
 race_f - other:white    1   3   NA     0.81944 0.45048 -0.063487   1.702400
  Odds Ratio             1   3   NA     2.26920       NA  0.938490   5.486900
 preterm - yes:no        1   2   NA     1.21850 0.46302  0.311010   2.126000
  Odds Ratio             1   2   NA     3.38220       NA  1.364800   8.381400
```

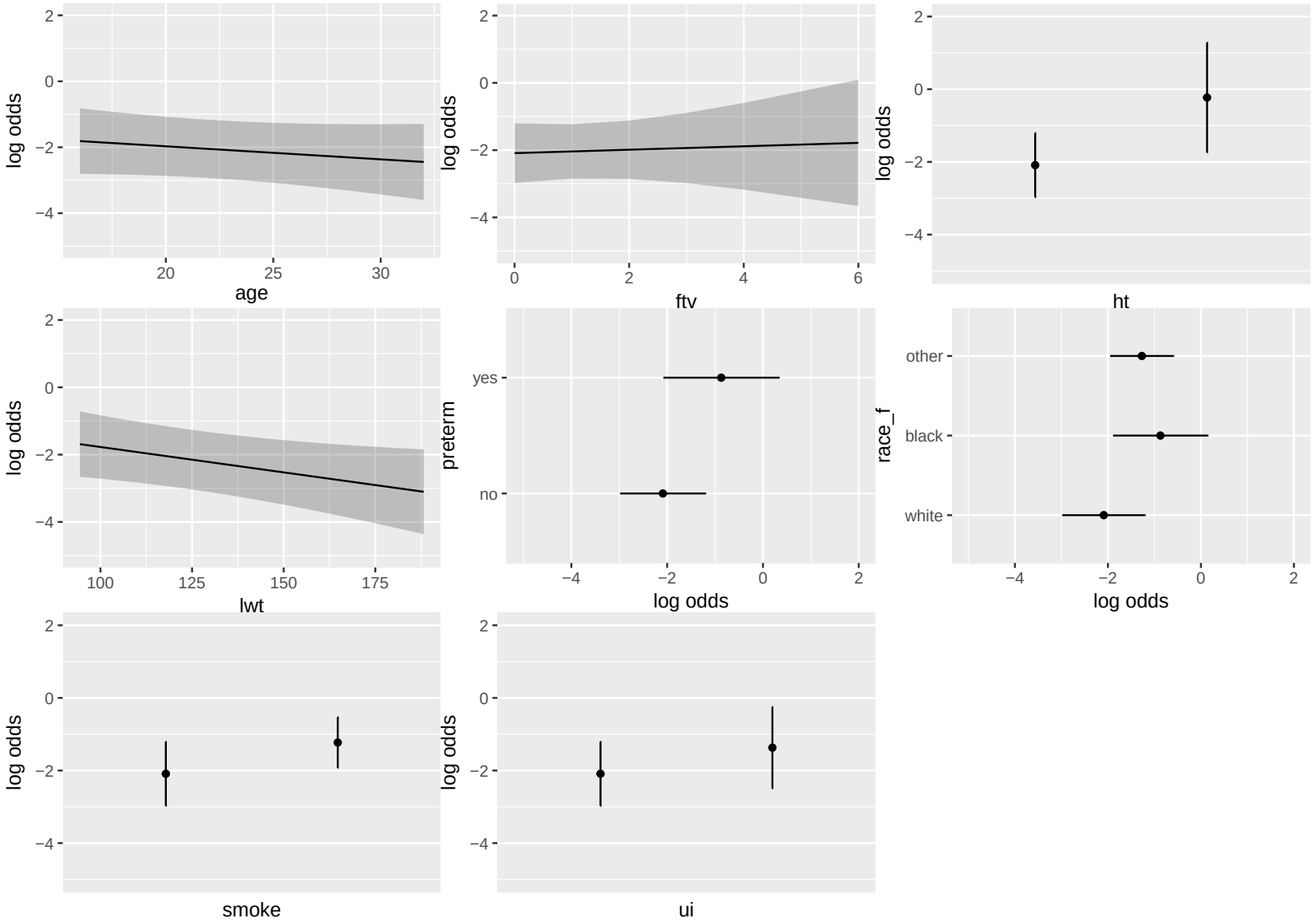
Plot In-Sample Predictions from Model 3

```
ggplot(Predict(model.3))
```

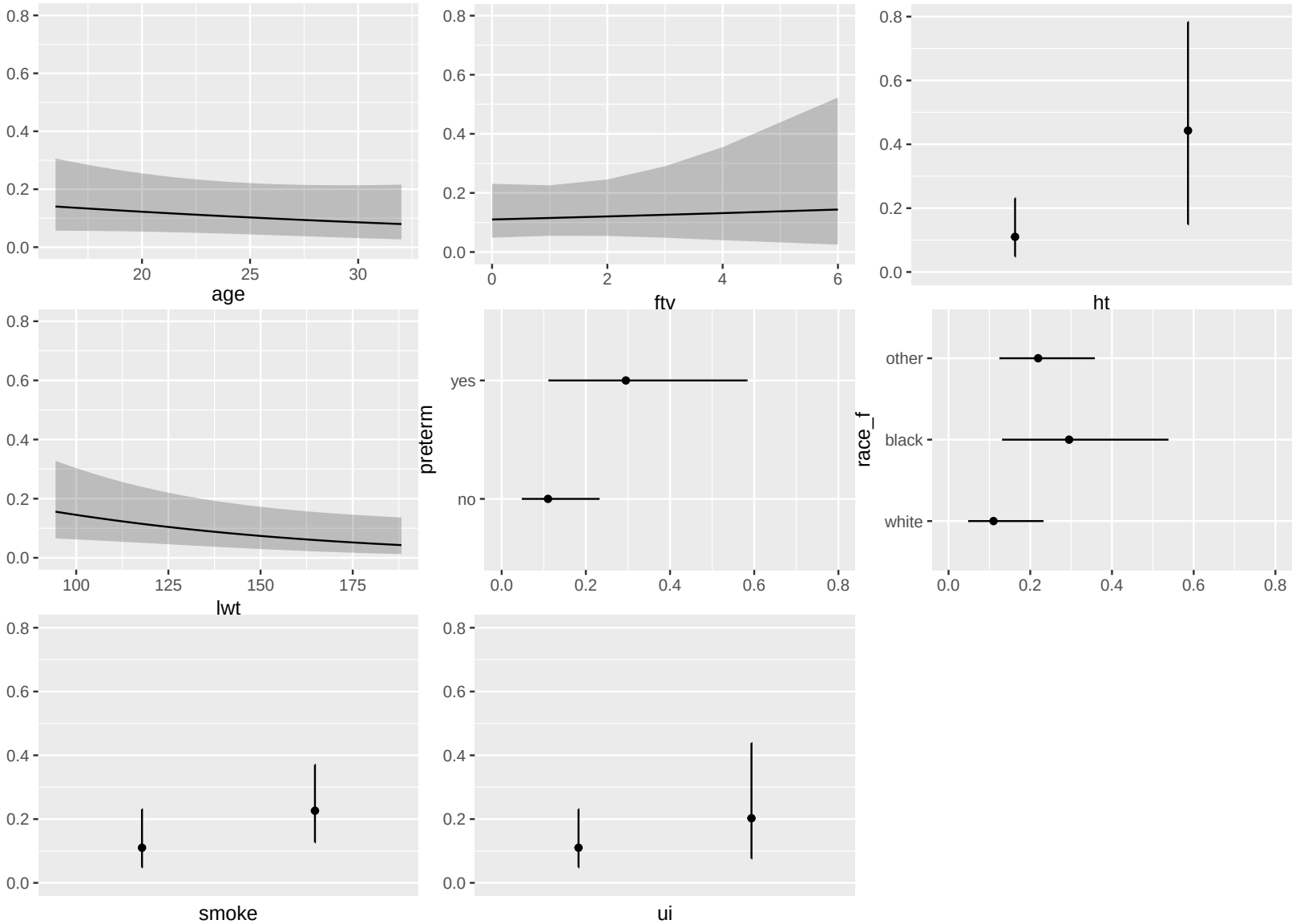
This will plot the effect of each predictor variable (and 95% CI for that effect) across the range of observed values for that predictor, on the log odds of low birth weight. (see next slide)

- To get these plots on the **probability** scale, we add `fun = plogis` (see two slides from now)

ggplot(Predict(model.3))



ggplot(Predict(model.3, fun = plogis))



ANOVA from the `lrm` approach

```
anova(model.3)
```

```
                Wald Statistics          Response: low

 Factor     Chi-Square d.f. P
 lwt         4.59      1    0.0321
 age         1.07      1    0.3019
 ftv         0.08      1    0.7717
 ht          6.90      1    0.0086
 race_f      6.23      2    0.0444
 preterm     6.93      1    0.0085
 smoke       4.40      1    0.0360
 ui          2.41      1    0.1206
 TOTAL      28.62      9    0.0008
```

Wald test for the model as a whole shows p = 0.0008

Any influential points?

```
inf.3 <- which.influence(model.3, cutoff=0.3)
inf.3
```

```
$Intercept
[1] "40" "53"

$lwt
[1] "17" "53" "72"

$age
[1] "11" "92"

$ftv
[1] "48" "52"

$ht
[1] "72"  "110"
```

Influence within the Data Frame

```
show.influence(object = inf.3, dframe = data.frame(lbw1))
```

```
    Count  lwt age ftv ht race_f ui
2       1  130  29   2  0  white *1
11      1  105 *32   0  0  white  0
17      2 *200  21   2  0  black *1
40      2  110  15   0  0 *white  0
48      1  120  17  *3  0  white  0
52      1  105  20  *3  0  other  0
53      2 *190  26   0  0  white  0
72      2 * 95  22   0 *1  other  0
92      2  121 *35   1  0 *black  0
110     1  120  22   1 *1  white  0
```

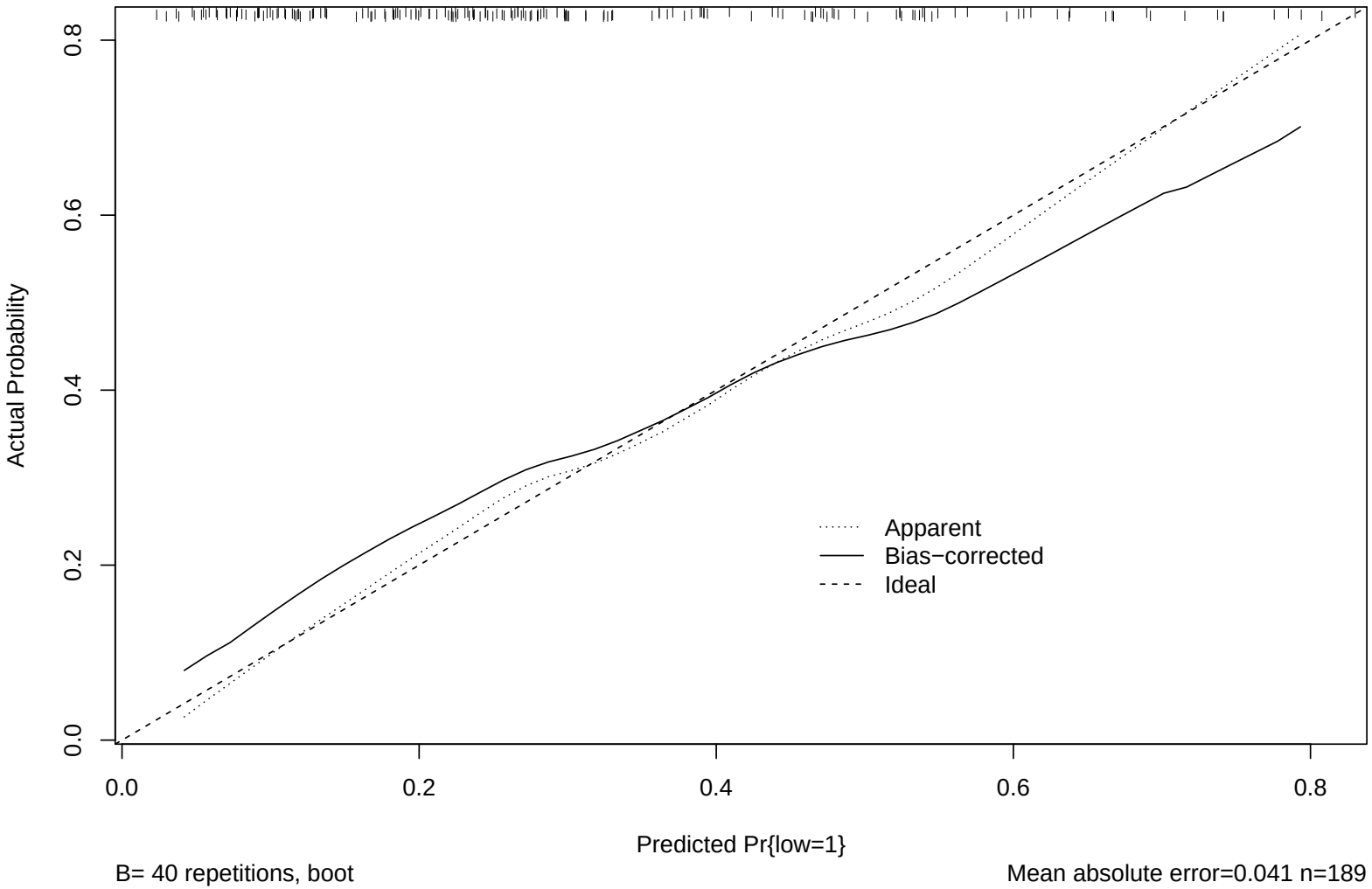
A plot of the model's calibration curve

The `calibrate` function applied to a `lrm` fit provides an assessment of the impact of overfitting on our model.

- The function uses bootstrapping (or cross-validation) to get bias-corrected estimates of predicted vs. observed values based on nonparametric smoothers for logistic regressions.
- In order to obtain this curve, you need to set both `x = TRUE` and `y = TRUE` when fitting the model.
- The errors here refer to the difference between the model predicted values and the corresponding bias-corrected calibrated values.

```
plot(calibrate(model.3))
```

Calibration Curve Plot



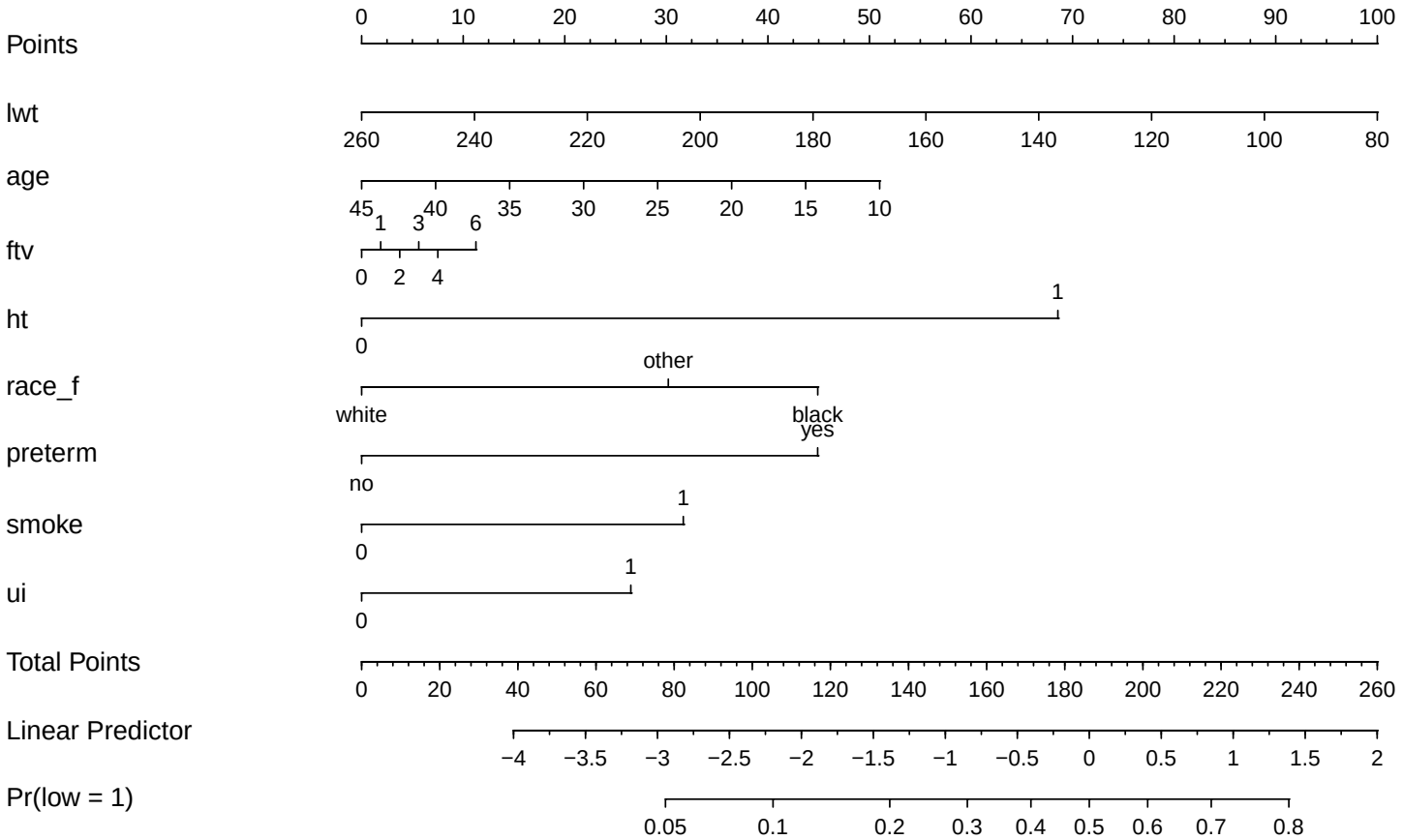
A Nomogram for Model 3

With `lrm`, we can fit a nomogram.

- We use the `plogis` function within a nomogram call to get R to produce fitted probabilities (of our outcome, `low`) in this case.

```
plot(nomogram(model.3, fun=plogis,
              fun.at=c(0.05, seq(0.1, 0.9, by = 0.1), 0.95),
              funlabel="Pr(low = 1)"))
```

Model 3 Nomogram



Next Up...

Linear Regression using the `ols` function