Recoding variables - Interpreting logistic models

Frank Edwards

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Review Homework,

Logistic regression part 2

The logit and logistic functions

$$\text{logit}(p) = \log\left(\frac{p}{1-p}\right) = \alpha$$

$$\text{logit}^{-1}(\alpha) = \text{logistic}(\alpha) = \frac{\exp(\alpha)}{\exp(\alpha)+1}$$

Let's define a function in R for logit

```
logit <- function(p) {
    alpha <- log(p/(1 - p))
    return(alpha)
}
```

- What should we expect to see if we run logit(0.5)

Let's define a function in R for logit

```
logit <- function(p) {
    alpha <- log(p/(1 - p))
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}
```

- What should we expect to see if we run logit(0.5)
- What about logit(0.6)
- logit(0.9)?

What does it do?

```
logit(0.5)
```

```
## [1] 0
```

```
logit(0.6)
```

```
## [1] 0.4054651
```

```
logit(0.9)
```

```
## [1] 2.197225
```

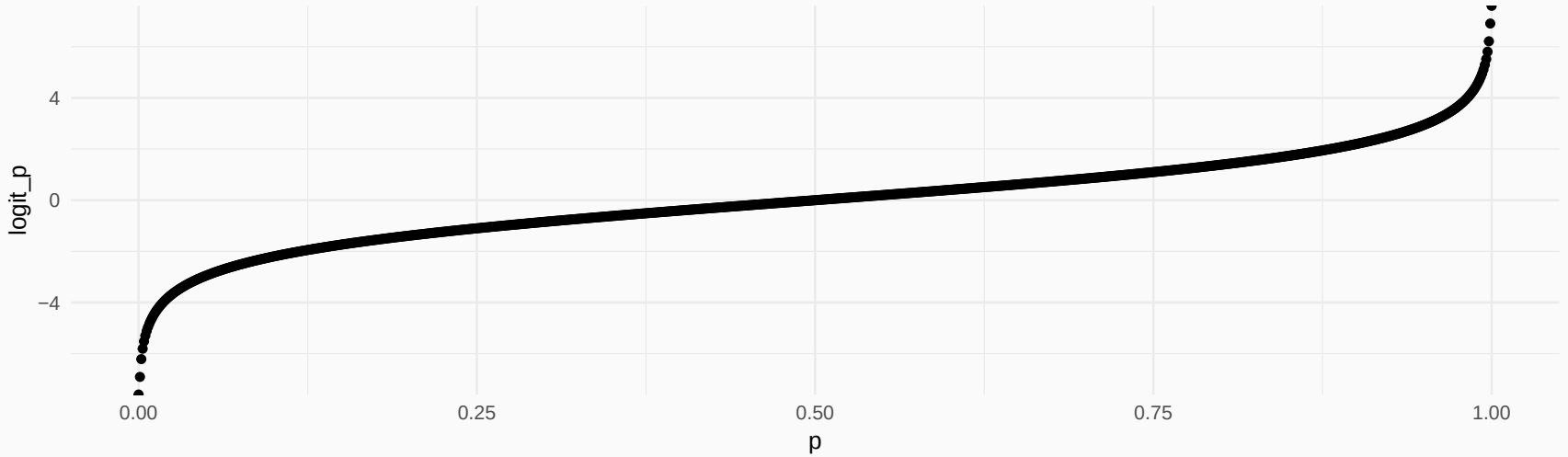
Functions in R can run over vectors!

```
p <- c(0.5, 0.6, 0.9)
logit(p)
```

```
## [1] 0.0000000 0.4054651 2.1972246
```

What does a logit look like with probabilities on [0,1]

```
p <- seq(from = 0, to = 1, by = 0.001)
p_dat <- data.frame(p = p, logit_p = logit(p))
ggplot(p_dat, aes(x = p, y = logit_p)) + geom_point()
```



Defining the inverse logit (logistic) function

Remember:

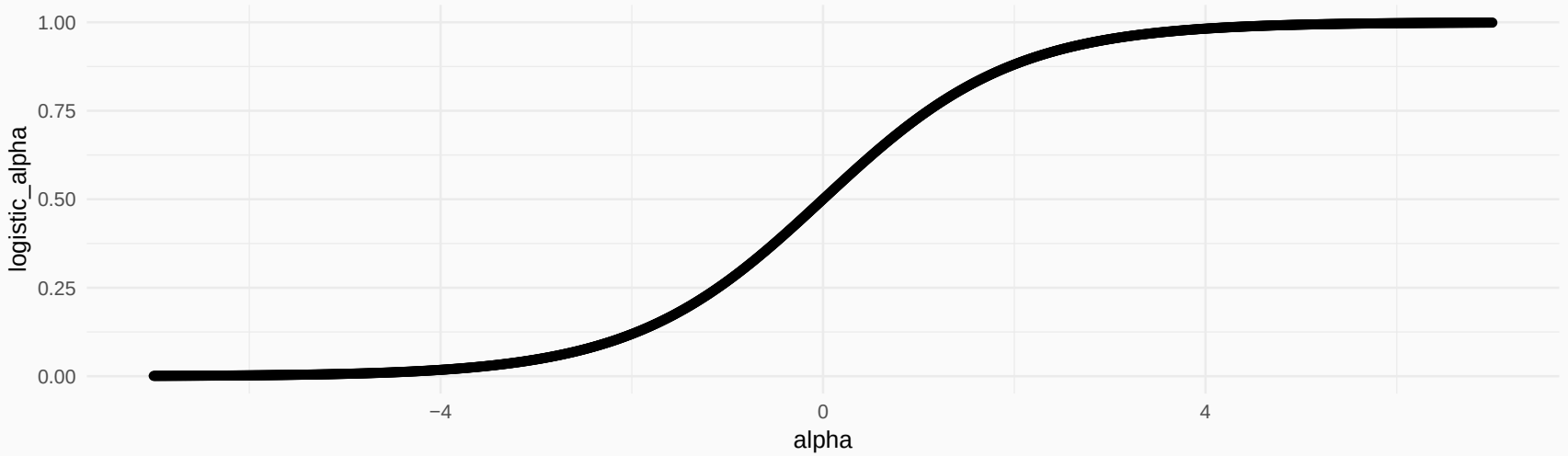
$$\text{logit}^{-1}(\alpha) = \text{logistic}(\alpha) = \frac{\exp(\alpha)}{\exp(\alpha) + 1}$$

```
inv.logit <- function(alpha) {
    p <- exp(alpha)/(exp(alpha) + 1)
    return(p)
}
```

- What does inv.logit(0) return?
- What does inv.logit(10) return?
- What does inv.logit(-10) return?

The shape of the logistic function

```
alpha <- seq(from = -7, to = 7, by = 0.01)
p_dat <- data.frame(alpha = alpha, logistic_alpha = inv.logit(al
ggplot(p_dat, aes(x = alpha, y = logistic_alpha)) + geom_point()
```



Logit and logistic are inverses

```
p <- c(0.1, 0.3, 0.5, 0.7, 0.9)
alpha <- logit(p)
alpha
```

```
## [1] -2.1972246 -0.8472979  0.0000000  0.8472979  2.1972246
```

```
inv.logit(alpha)
```

```
## [1] 0.1 0.3 0.5 0.7 0.9
```

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- Logistic regression is the special case where g is the logit function: $\mathrm{logit}(y) = \mathrm{X}\beta$
- A logistic regression model returns $\mathrm{X}\beta$ on the logit scale
- How can we convert $\mathrm{x}\beta$ to something useful?

Let's return to the grad school admission example

```
admits <- read_csv("./data/binary.csv")
summary(admits)
```

```
##      admit             gre             gpa             rank
##  Min.   :0.0000   Min.   :220.0   Min.   :2.260   Min.   :1.0
##  1st Qu.:0.0000   1st Qu.:520.0   1st Qu.:3.130   1st Qu.:2.0
##  Median :0.0000   Median :580.0   Median :3.395   Median :2.0
##  Mean   :0.3175   Mean   :587.7   Mean   :3.390   Mean   :2.4
##  3rd Qu.:1.0000   3rd Qu.:660.0   3rd Qu.:3.670   3rd Qu.:3.0
##  Max.   :1.0000   Max.   :800.0   Max.   :4.000   Max.   :4.0
```

Is rank a numeric?

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Not really. Let's make it a factor.

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Is the distance between 1 and 2 symmetric to the distance between 2 and 3?

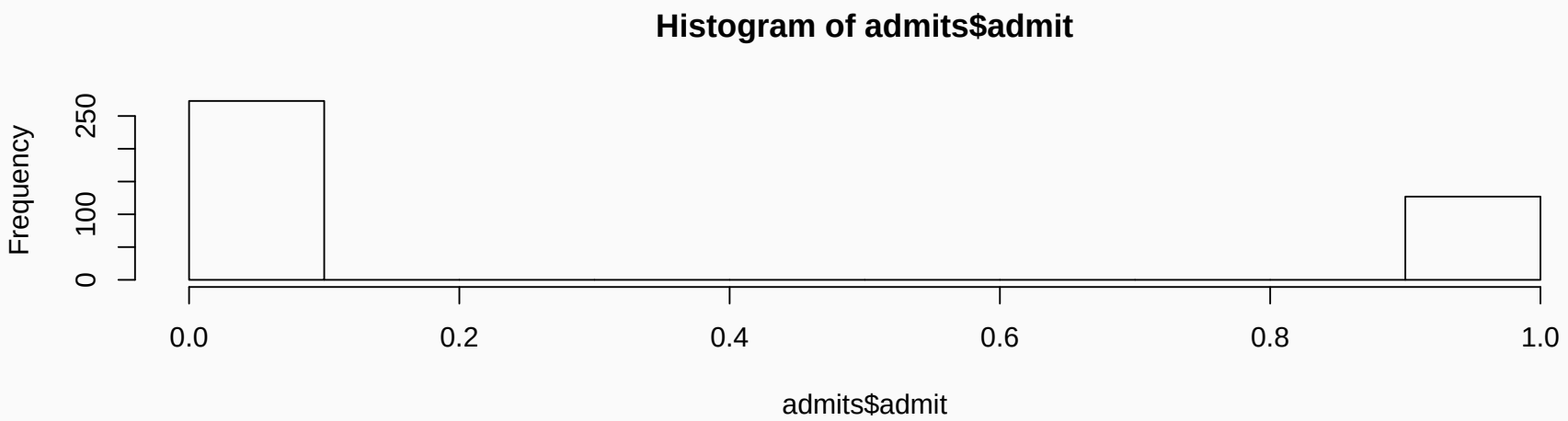
Not really. Let's make it a factor.

```
admits <- admits %>% mutate(rank = factor(rank))
## as.character() would be fine too
```

Let’s explore our outcome

Huh, all this tells us is mean(admits) = 0.3175

```
hist(admits$admit)
```



Let's look at this as the distribution of the probability of admissions across the data

- First, fit an intercept-only logistic regression model

```
m0 <- glm(admit ~ 1, data = admits, family = "binomial")
m0_est <- tidy(m0)
```

- What does this model tell us?

What does this model tell us?

```
m0_est$estimate  ## log odds
```

```
## [1] -0.7652847
```

```
exp(m0_est$estimate)  ## odds
```

```
## [1] 0.4652015
```

```
inv.logit(m0_est$estimate)  ## probability
```

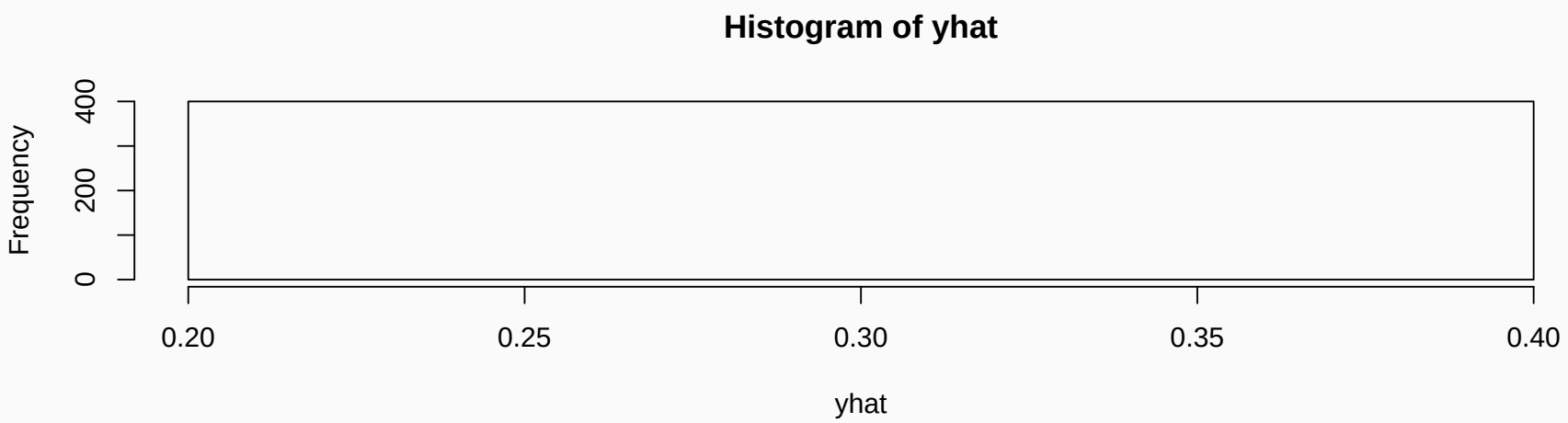
```
## [1] 0.3175
```

```
mean(admits$admit)  ## mean admission probability
```

```
## [1] 0.3175
```

Or visually - fascinating!

```
yhat <- predict(m0, type = "response")
hist(yhat)
```



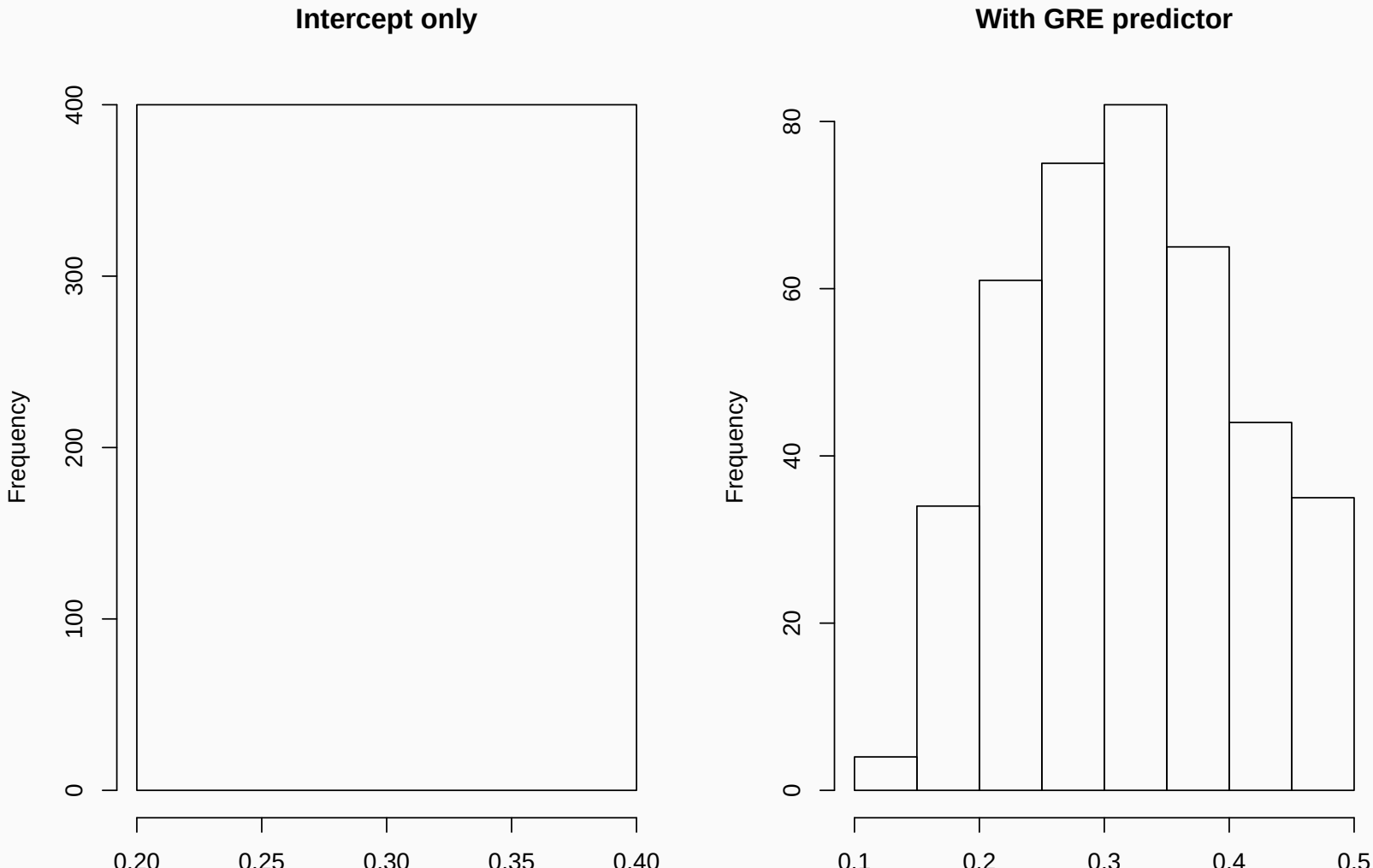
Let's add a predictor

```
m1 <- glm(admit ~ 1 + gre, data = admits, family = "binomial")
m1_est <- tidy(m1)
m1_est
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic    p.value
##   <chr>          <dbl>     <dbl>     <dbl>      <dbl>
## 1 (Intercept) -2.90     0.606        -4.79 0.00000169
## 2 gre          0.00358  0.000986      3.63 0.000280
```

Before and after - what's going on?

```
par(mfrow = c(1, 2))
hist(predict(m0, type = "response"), main = "Intercept only")
hist(predict(m1, type = "response"), main = "With GRE predictor")
```



To ease interpretation, let's scale gre

Scale mean-centers and SD scales variables: $\mathrm{scale}(x_i) = \frac{x_i - \bar{x}}{sd(x)}$

Re-estimate the model: much nicer to look at

```
admits <- admits %>% mutate(gre = as.numeric(scale(gre)))
m1 <- glm(admit ~ 1 + gre, data = admits, family = "binomial")
m1_est <- tidy(m1)
m1_est
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic  p.value
##   <chr>          <dbl>     <dbl>     <dbl>    <dbl>
## 1 (Intercept)   -0.796     0.111     -7.20 6.01e-13
## 2 gre            0.414     0.114      3.63 2.80e- 4
```

Interpret the model

```
m1_est
```

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Remember: $\text{logit}(y) = \text{X}\beta = \log\left(\frac{y}{1-y}\right)$

So: $y = \text{logit}^{-1}(\text{X}\beta) = \frac{\exp(\text{X}\beta)}{\exp(\text{X}\beta)+1}$

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- What is β_0?

Interpret the model

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- What is β_0?
- What is β_1?

Refresher on exponentials

$$e^{y_1+y_2} = e^{y_1}e^{y_2}$$

Refresher on exponentials

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and

$$e^{y_1-y_2} = \frac{e^{y_1}}{e_2^y}$$

Refresher on exponentials

$$e^{y_1+y_2} = e^{y_1}e^{y_2}$$

and

$$e^{y_1-y_2} = \frac{e^{y_1}}{e_2^y}$$

so how can we rewrite:

$$\exp(\text{logit}(y)) = \frac{y}{1-y} = e^{\beta_0+\beta_1 x_1}$$

Non-linear relationships

On the log scale, β_0 and β_1 are related to y multiplicatively because

$$e^{\beta_0+\beta_1 x_1} = e^{\beta_0} e^{\beta_1 x_1}$$

Odds

Odds are defined as the probability of the event occurring divided by the probability of probability of the event not occurring. To obtain odds in a logistic regression, we exponentiate both sides:

$$\frac{y}{1-y} = e^{\beta_0 + \beta_1 x_1}$$

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$$\frac{y}{1-y} = e^{\beta_0 + \beta_1 x_1}$$

The odds of $y == 1$ are simply $e^{X\beta}$

Odds ratios

The odds ratio is the ratio of two odds - or the proportional change in odds. We can obtain an isolated estimate for the relationship between $\beta_1 x_{1i}$ and y this way:

$$\frac{Odds(y|x_1 = 1)}{Odds(y|x_1 = 0)} = \frac{e^{X\beta+\beta_1}}{e^{X\beta}} = \frac{e^{X\beta} \times e^{\beta_1}}{e^{X\beta}} = e^{\beta_1}$$

The odds ratio can be interpreted as the change in odds of $y == 1$ for a one-unit change in x_1.

Interpreting odds ratios

- Odds ratios appear convenient - e^{β_1} is a percent change in y for a one-unit change in x_1

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How do they work?

In our example: what do these figures mean?

```
new_dat <- c(1, 0)  # for scale(gre) == 0, mean score
odds_0 <- exp(new_dat %*% m1_est$estimate)
odds_0
```

```
##           [,1]
## [1,] 0.4510945
```

```
new_dat1 <- c(1, 1)
odds_1 <- exp(new_dat1 %*% m1_est$estimate)
odds_1
```

```
##           [,1]
## [1,] 0.6823082
```

```
odds_1/odds_0  # odds ratio
```

```
##          [,1]
## [1,] 1.512562
```

```
exp(m1_est$estimate[2])  # exp(beta_1)
```

```
## [1] 1.512562
```

Interpreting the odds ratio

The odds of admission are `exp(m1_est$estimate[2])` times higher for a student with a GRE score one standard deviation above the mean than they are for a student with a mean GRE score.

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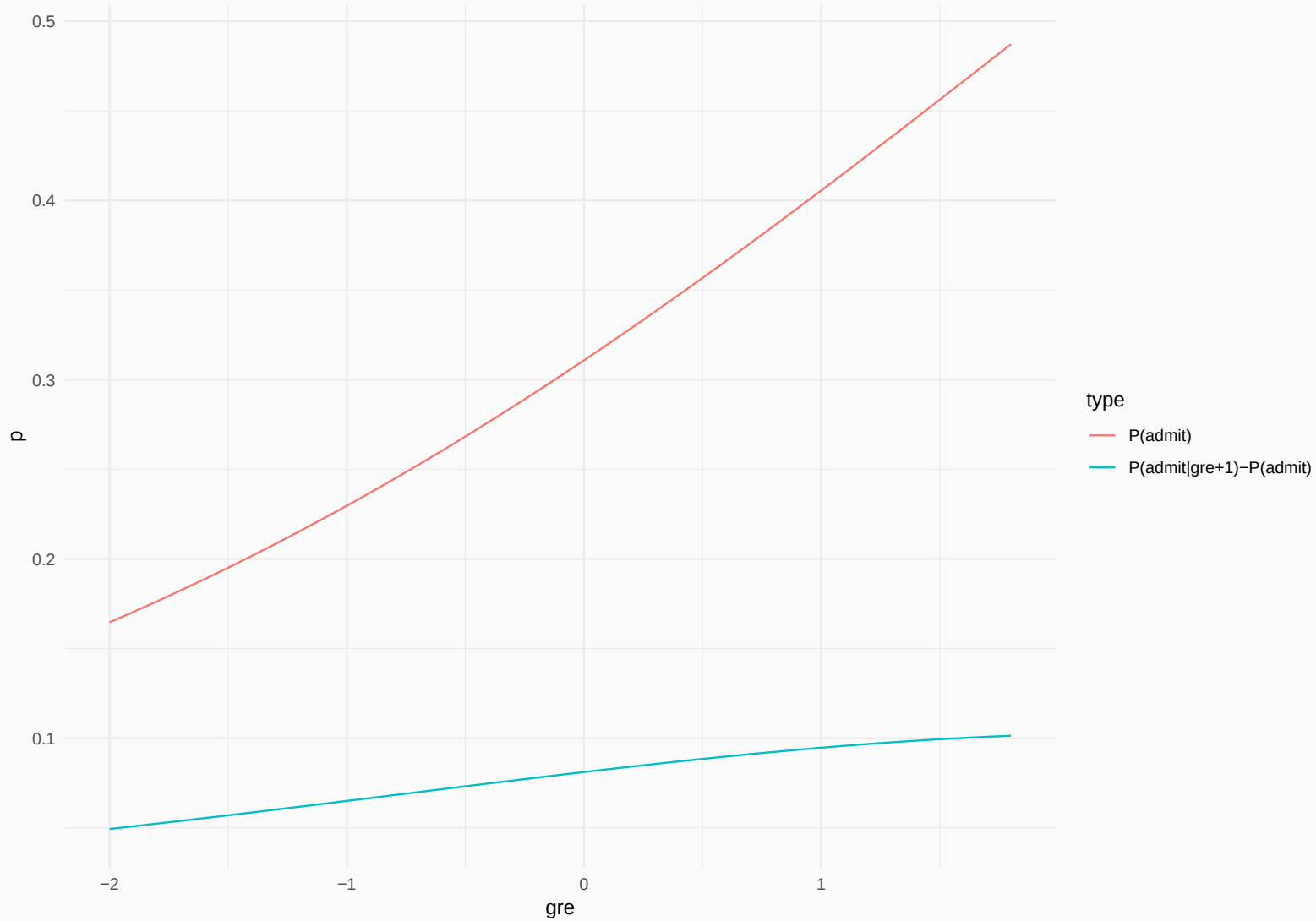
Problems with the odds ratio

```
p <- c(0.1, 0.2, 0.5, 0.8, 0.9)
odds <- function(p) {
    p/(1 - p)
}
inv_odds <- function(o) {
    o/(1 + o)
}
odds_p <- odds(p)
OR <- exp(m1_est$estimate[2])
inv_odds(OR + (OR * odds_p)) - p
```

```
## [1] 0.52695254 0.45406328 0.25156041 0.08321588 0.03798687
```

A visual example: the “effect” of 1 SD increase in GRE scores on Pr(admit==1)



It is easy enough to work on the probability scale

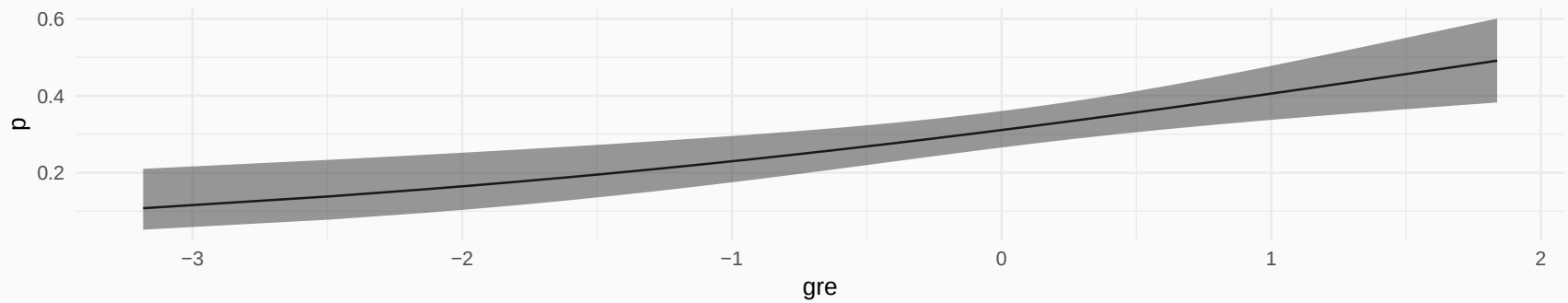
To obtain predicted probabilities of the observed:

- p_hat<-inv.logit(predict(m1))
- p_hat<-predict(m1, type = “response”)

To obtain intervals

```
preds <- predict(m1, se.fit = TRUE)
p_hat <- data.frame(gre = admits$gre, p = inv.logit(preds$fit), upper = inv.logi
    2 * preds$se.fit), lower = inv.logit(preds$fit - 2 * preds$se.fit))

ggplot(p_hat, aes(x = gre, y = p, ymin = lower, ymax = upper)) + geom_line() +
    geom_ribbon(alpha = 0.5)
```



Logistic regression as a classifier

We can use logistic regression to predict values of a binary variable. We can then assess how well our model performs relative to classifying cases relative to the observations.

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What is the meaning of a:

- a true positive rate (sensitivity)?

Logistic regression as a classifier

We can use logistic regression to predict values of a binary variable. We can then assess how well our model performs relative to classifying cases relative to the observations.

What is the meaning of a:

- a true positive rate (sensitivity)?
- a true negative rate (specificity)?

Returning to our model

$$Pr(admit = 1) = logit^{-1}(\beta_0 + \beta_1 GRE)$$

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What does our model predict for each applicant?

```
phat <- predict(m1, type = "response")
head(cbind(phat, admits))
```

```
##        phat admit        gre  gpa rank
## 1 0.1765202     0 -1.7980110 3.61    3
## 2 0.3688660     1  0.6258844 3.67    3
## 3 0.4911072     1  1.8378321 4.00    1
## 4 0.3523492     1  0.4527490 3.19    4
## 5 0.2614213     0 -0.5860633 2.93    4
## 6 0.4554030     1  1.4915613 3.00    2
```

Evaluating our predictions and its performace

```
phat <- predict(m1, type = "response")
summary(phat)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.1078  0.2614  0.3050  0.3175  0.3689  0.4911
```

```
threshold <- quantile(phat, 0.75)
preds <- data.frame(obs = admits$admit == 1, pred = phat > threshold)
table(preds$obs, preds$pred)
```

```
##
##          FALSE TRUE
##   FALSE    214   59
##   TRUE      87   40
```

```
sum((preds$obs == 1) & (preds$pred == 1))/sum(preds$obs == 1)  # True positive r
```

```
## [1] 0.3149606
```

```
sum((preds$obs == 0) & (preds$pred == 0))/sum(preds$obs == 0)  # True negative r
```



```
## [1] 0.7838828
```

What happens to predictive performance when we add a predictor to the model?

```
m2 <- glm(admit ~ gre + gpa, data = admits, family = "binomial")
phat <- predict(m2, type = "response")
threshold <- quantile(phat, 0.75)
preds <- data.frame(obs = admits$admit == 1, pred = phat > threshold)
sum((preds$obs == 1) & (preds$pred == 1))/sum(preds$obs == 1)  # True positive
```

```
## [1] 0.3307087
```

```
sum((preds$obs == 0) & (preds$pred == 0))/sum(preds$obs == 0)  # True negative
```

```
## [1] 0.7875458
```

What happens to predictive performance when we add a predictor to the model?

```
m3 <- glm(admit ~ gre + gpa + rank, data = admits, family = "binomial")
phat <- predict(m3, type = "response")
threshold <- quantile(phat, 0.75)
preds <- data.frame(obs = admits$admit == 1, pred = phat > threshold)
sum((preds$obs == 1) & (preds$pred == 1))/sum(preds$obs == 1)  # True positive
```

```
## [1] 0.4173228
```

```
sum((preds$obs == 0) & (preds$pred == 0))/sum(preds$obs == 0)  # True negative
```

```
## [1] 0.8278388
```

How can we use this to make decisions? ROC Curves

```
roc_dat <- data.frame(obs = admits$admit, phat = phat)

simple_roc <- function(labels, scores) {
    labels <- labels[order(scores, decreasing = TRUE)]
    data.frame(TPR = cumsum(labels)/sum(labels), FPR = cumsum(!labels)/sum(!labels),
        labels, probs = scores[order(scores, decreasing = TRUE)])
}

roc_out <- simple_roc(roc_dat$obs, roc_dat$phat)
1/sum(roc_dat$obs)
```

```
## [1] 0.007874016
```

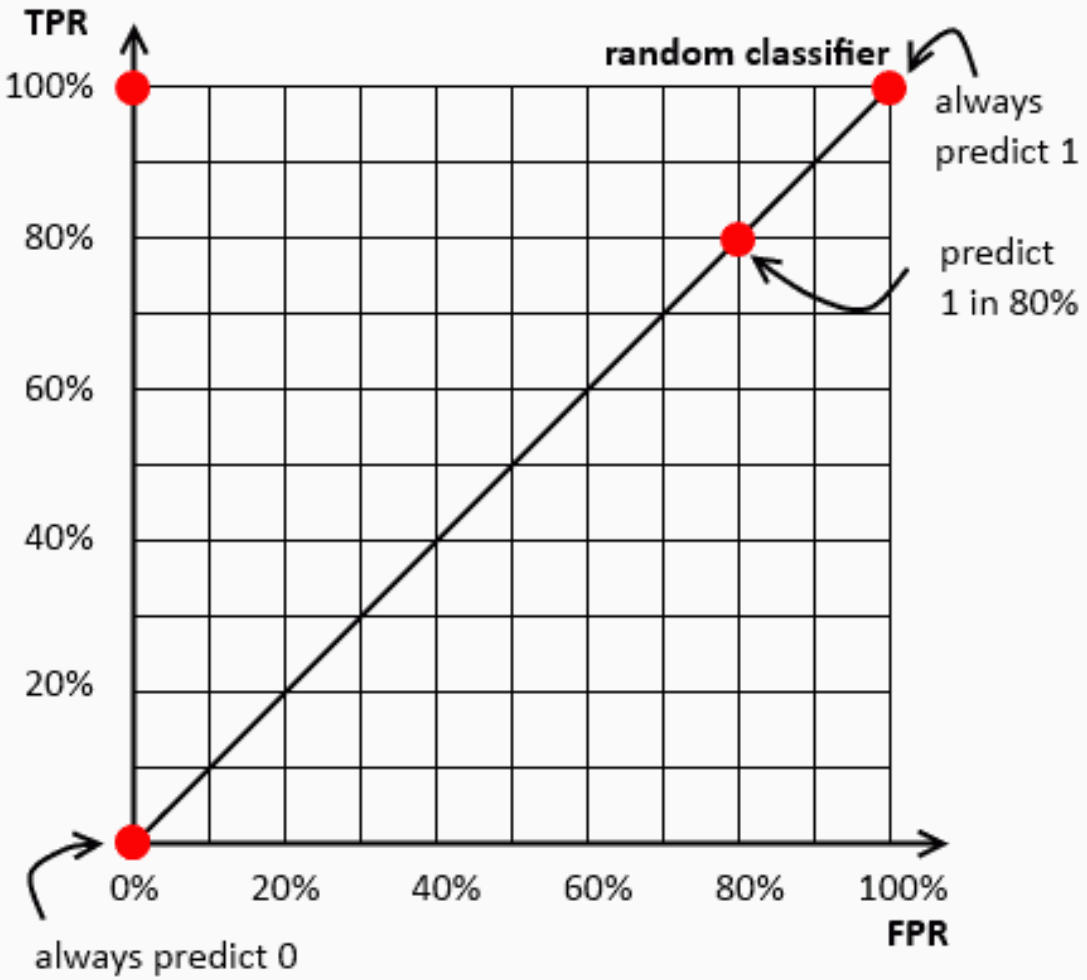
```
1/sum(!(roc_dat$obs))
```

```
## [1] 0.003663004
```

```
slope <- sum(!(admits$admit))/sum(admits$admit)
head(roc_out)
```

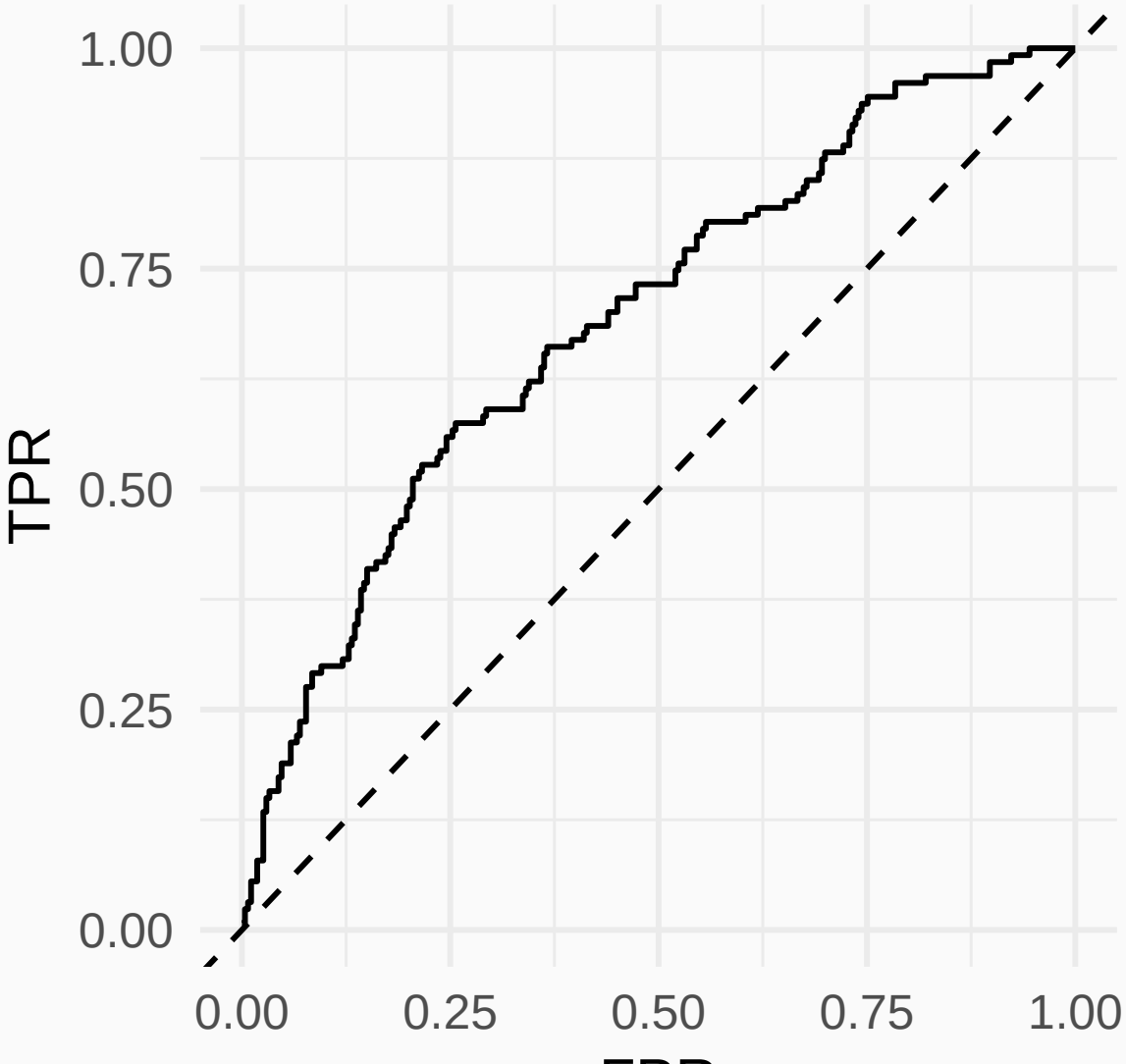
```
##           TPR         FPR labels     probs
## 1 0.007874016 0.000000000      1 0.7384082
## 2 0.007874016 0.003663004      0 0.7337223
## 3 0.015748031 0.003663004      1 0.7205386
## 4 0.023622047 0.003663004      1 0.6960719
## 5 0.023622047 0.007326007      0 0.6943683
## 6 0.031496063 0.007326007      1 0.6923799
```

Plotting in ROC space



Plotting the ROC curve

```
ggplot(roc_out, aes(x = FPR, y = TPR)) + geom_line() + geom_abli
    lty = 2)
```



Comparing models

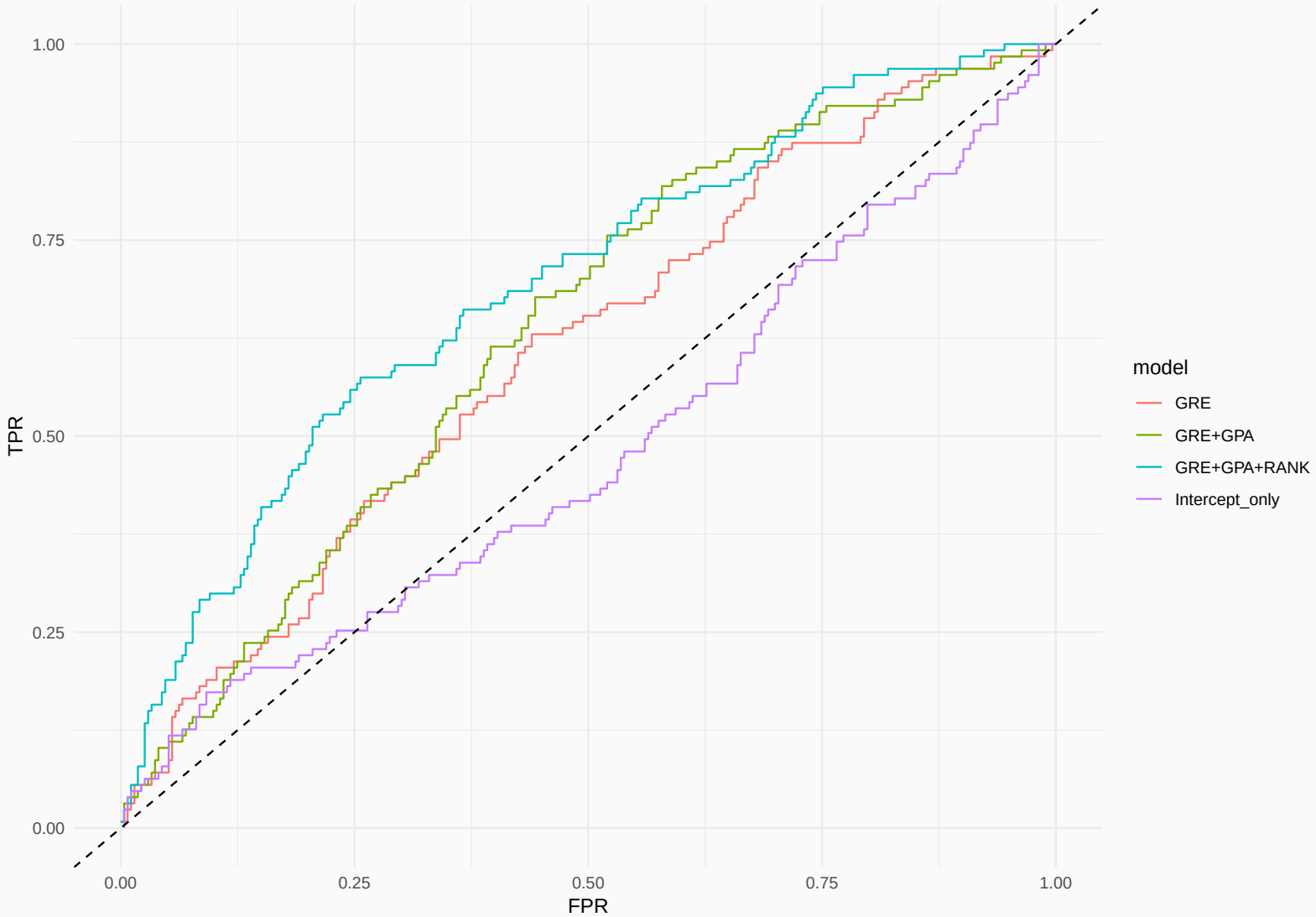
```r
models <- list(m0, m1, m2, m3)
preds <- lapply(models, function(x) {
    predict(x, type = "response")
})
str(preds)
```

```
## List of 4
##  $ : Named num [1:400] 0.318 0.318 0.318 0.318 0.318 ...
##   ..- attr(*, "names")= chr [1:400] "1" "2" "3" "4" ...
##  $ : Named num [1:400] 0.177 0.369 0.491 0.352 0.261 ...
##   ..- attr(*, "names")= chr [1:400] "1" "2" "3" "4" ...
##  $ : Named num [1:400] 0.231 0.4 0.555 0.306 0.208 ...
##   ..- attr(*, "names")= chr [1:400] "1" "2" "3" "4" ...
##  $ : Named num [1:400] 0.173 0.292 0.738 0.178 0.118 ...
##   ..- attr(*, "names")= chr [1:400] "1" "2" "3" "4" ...
```

Comparing models (cont.)

```
roc_temp <- list()
for (i in 1:length(preds)) {
    roc_temp[[i]] <- simple_roc(labels = admits$admit, scores =
}
roc_dat <- bind_rows(roc_temp)
roc_dat <- roc_dat %>% mutate(model = rep(c("Intercept_only", "G
    "GRE+GPA+RANK"), each = nrow(admits)))
```

Plotting this monstrosity

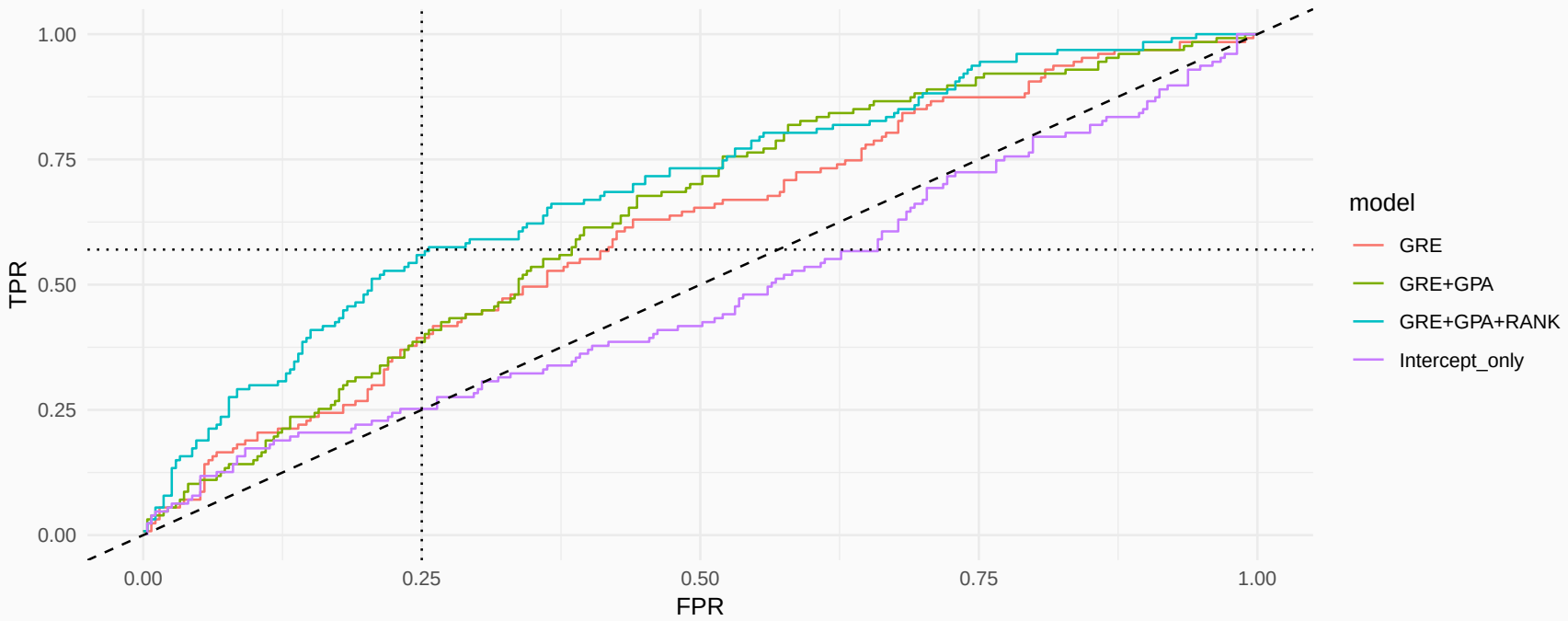


Selecting a threshold

We can use many thresholds:

- We can optimize overall accuracy - this will be the inflection point in the curve

Selecting a threshold




```
##   threshold       FPR       TPR
## 1 0.3589025 0.2490842 0.5590551
```

Selecting a threshold

We can use many thresholds:

- We can optimize overall accuracy - this will be the inflection point in the curve
- We can set arbitrary thresholds (i.e. 10 percent false positive)

```
roc_dat %>% filter(model == "GRE+GPA+RANK") %>% filter(FPR < 0.1
    FPR = max(FPR), TPR = max(TPR))
```

```
##   threshold       FPR       TPR
## 1 0.4675591 0.0989011 0.2992126
```

Bonus points

- This model was fit to our observed data

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- Then predicted itself...

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- This model was fit to our observed data
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- Can it predict new cases?

Out of sample validation

- We could use this model to predict next year's admits to target high and low likelihood cases

Out of sample validation

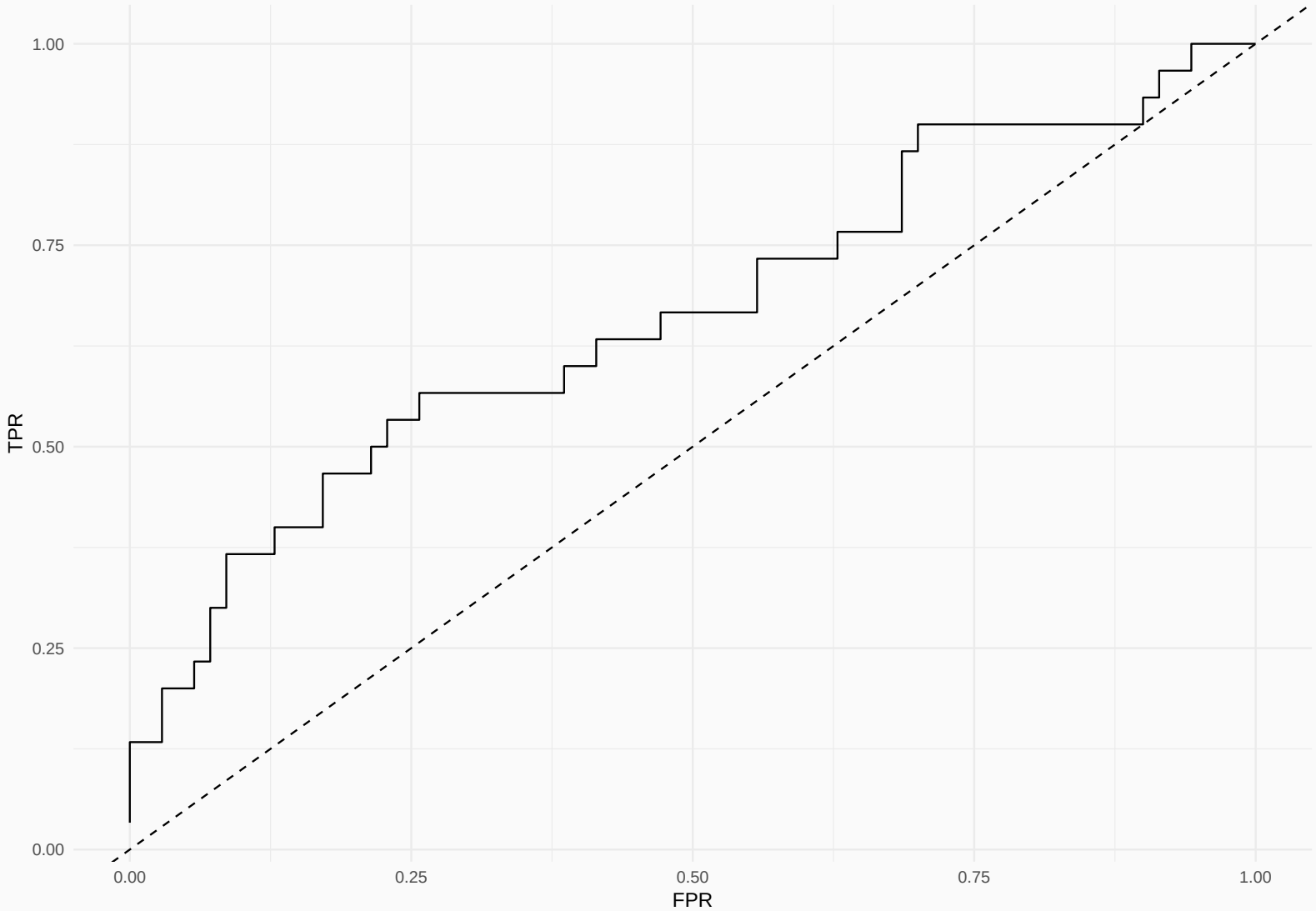
- We could use this model to predict next year's admits to target high and low likelihood cases
- But we only have one year of data. We can split our data into two sets: one for fitting the model (training) and one for evaluating the model fit (test data)

Example with the admissions data

Let's fit the data to a 75 percent subset, then test it against the remaining 25 percent

```
sample_size <- trunc(nrow(admits) * 0.25)
test_rows <- sample(1:nrow(admits), sample_size, replace = FALSE)
training_dat <- admits[-test_rows, ]
test_dat <- admits[test_rows, ]
model_validation <- glm(admit ~ gre + gpa + rank, data = admits, family = "binomial")
yhat <- predict(model_validation, newdata = test_dat, type = "response")
```

Now check out the ROC curve



Out of sample validation is crucial for prediction

- Using the same data to train and test a model leads to overfitting
- New data is necessary to effectively check the performance of your model
- Especially in real world settings where mistakes can be dangerous/costly