# Joining data - Logistic regression

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# Joining data with dplyr

# Kinds of join

- Add new rows to a data frame: rbind()
- Add new columns to a data frame: cbind()
- Join full data frames: left_join()

# When to rbind()

Bind rows to a dataframe when you have new observations to append. The number, type, and names of columns *must* be identical.

I find rbind to be most useful when I need to add a single or small set of observations manually to a data frame.

# How to rbind()

```
tail(gapminder)
```

```
## # A tibble: 6 x 6
##   country  continent  year lifeExp      pop gdpPercap
##   <fct>    <fct>     <int>   <dbl>    <int>     <dbl>
## 1 Zimbabwe Africa     1982    60.4  7636524      789.
## 2 Zimbabwe Africa     1987    62.4  9216418      706.
## 3 Zimbabwe Africa     1992    60.4 10704340      693.
## 4 Zimbabwe Africa     1997    46.8 11404948      792.
## 5 Zimbabwe Africa     2002    40.0 11926563      672.
## 6 Zimbabwe Africa     2007    43.5 12311143      470.
```

```r
new_data <- data.frame(country = "Zimbabwe", continent = "Africa
    lifeExp = 50.2, pop = 12345678, gdpPercap = 500)
new_gap <- rbind(gapminder, new_data)
tail(new_gap)
```

```
## # A tibble: 6 x 6
##   country  continent  year lifeExp      pop gdpPercap
##   <fct>    <fct>     <dbl>   <dbl>    <dbl>     <dbl>
## 1 Zimbabwe Africa     1987    62.4  9216418      706.
## 2 Zimbabwe Africa     1992    60.4 10704340      693.
## 3 Zimbabwe Africa     1997    46.8 11404948      792.
## 4 Zimbabwe Africa     2002    40.0 11926563      672.
## 5 Zimbabwe Africa     2007    43.5 12311143      470.
## 6 Zimbabwe Africa     2012    50.2 12345678      500
```

# When to cbind()

Bind columns to a dataframe when you have a new variable to append. The number of rows *must* be identical in both objects.

I use cbind most often when combining vectors to create data frames.

# How to cbind()

```
captain <- c("Kirk", "Picard", "Janeway", "Sisko")
ship <- c("Enterprise", "Enterprise", "Voyager", "Defiant")
star_trek <- data.frame(cbind(captain, ship))
star_trek
```

```
##   captain       ship
## 1    Kirk Enterprise
## 2  Picard Enterprise
## 3 Janeway    Voyager
## 4   Sisko    Defiant
```

# Joins

Joins are more flexible than cbind() and rbind(). Joins take two data frames and merge them according to your specification.

They are powerful tools for flexibly merging datasets with common identifier variables.

Joins merge data frames based on matching key values.

# Kinds of join: from ?dplyr::join

- inner_join(x,y): Return all rows from x with matching values in y, and all columns from x and y.
- left_join(x,y): My most frequently used join function. Returns all rows from x and all columns from x and y.
- right_join(x,y): Returns all rows from y and all columns from x and y
- full_join(x,y): Return all rows and columns from both x and y
- semi_join(x,y): Return all rows from x with matching values in y, returning only columns in x
- anti_join(x,y): Return all rows from x where there are not matching values in y, keeping only columns from x

# What do joins do?

```
band_members
```

```
## # A tibble: 3 x 2
##   name  band
##   <chr> <chr>
## 1 Mick  Stones
## 2 John  Beatles
## 3 Paul  Beatles
```

```
band_instruments
```

```
## # A tibble: 3 x 2
##   name  plays
##   <chr> <chr>
## 1 John  guitar
## 2 Paul  bass
## 3 Keith guitar
```

```r
band_members %>% inner_join(band_instruments)
```

```
## # A tibble: 2 x 3
##   name  band    plays
##   <chr> <chr>   <chr>
## 1 John  Beatles guitar
## 2 Paul  Beatles bass
```

```r
band_members %>% left_join(band_instruments)
```

```
## # A tibble: 3 x 3
##   name  band    plays
##   <chr> <chr>   <chr>
## 1 Mick  Stones  <NA>
## 2 John  Beatles guitar
## 3 Paul  Beatles bass
```

```
band_members %>% right_join(band_instruments)
```

```
## # A tibble: 3 x 3
##   name  band    plays
##   <chr> <chr>   <chr>
## 1 John  Beatles guitar
## 2 Paul  Beatles bass
## 3 Keith <NA>    guitar
```

```r
band_members %>% full_join(band_instruments)
```

```
## # A tibble: 4 x 3
##   name  band    plays
##   <chr> <chr>   <chr>
## 1 Mick  Stones  <NA>
## 2 John  Beatles guitar
## 3 Paul  Beatles bass
## 4 Keith <NA>    guitar
```

# Filtering joins

```
band_members %>% semi_join(band_instruments)
```

```
## # A tibble: 2 x 2
##   name  band
##   <chr> <chr>
## 1 John  Beatles
## 2 Paul  Beatles
```

# Filtering joins

```
band_members %>% anti_join(band_instruments)
```

```
## # A tibble: 1 x 2
##   name  band
##   <chr> <chr>
## 1 Mick  Stones
```

# A practical example

```
g_c <- gapminder %>% group_by(continent, year) %>% summarise(gdp_mean_continent = mean(gdpPercap))

gapminder %>% left_join(g_c)
```

```
## # A tibble: 1,704 x 7
##    country     continent  year lifeExp      pop gdpPercap gdp_mean_contine~
##    <fct>       <fct>     <int>   <dbl>    <int>     <dbl>             <dbl>
##  1 Afghanistan Asia       1952    28.8  8425333      779.             5195.
##  2 Afghanistan Asia       1957    30.3  9240934      821.             5788.
##  3 Afghanistan Asia       1962    32.0 10267083      853.             5729.
##  4 Afghanistan Asia       1967    34.0 11537966      836.             5971.
##  5 Afghanistan Asia       1972    36.1 13079460      740.             8187.
##  6 Afghanistan Asia       1977    38.4 14880372      786.             7791.
##  7 Afghanistan Asia       1982    39.9 12881816      978.             7434.
##  8 Afghanistan Asia       1987    40.8 13867957      852.             7608.
##  9 Afghanistan Asia       1992    41.7 16317921      649.             8640.
## 10 Afghanistan Asia       1997    41.8 22227415      635.             9834.
## # ... with 1,694 more rows
```

# Another practical example

```
head(pop)
```

```
## # A tibble: 6 x 5
##    year race  sex    age     pop
##   <dbl> <chr> <chr>  <chr> <dbl>
## 1  1991 amind Female 0     22465
## 2  1991 amind Female 1-4   84894
## 3  1991 amind Female 10-14 97299
## 4  1991 amind Female 15-19 91647
## 5  1991 amind Female 20-24 86044
## 6  1991 amind Female 25-29 92740
```

```
head(mort)
```

```
## # A tibble: 6 x 5
##    year age   race                     sex    deaths
##   <dbl> <chr> <chr>                    <chr>   <dbl>
## 1  2008 0     African American         Female   3807
## 2  2008 0     African American         Male     4761
## 3  2008 0     American Indian/AK Native Female    169
## 4  2008 0     American Indian/AK Native Male      234
## 5  2008 0     Asian/Pacific Islander   Female    448
## 6  2008 0     Asian/Pacific Islander   Male      570
```

# Check values on common variables

```
unique(pop$race)
```

```
## [1] "amind"  "asian"  "black"  "latino" "white"
```

```
unique(mort$race)
```

```
## [1] "African American"          "American Indian/AK Native"
## [3] "Asian/Pacific Islander"    "Latinx"
## [5] "White"
```

# Recode variable for join

```
pop<-pop%>%
  mutate(race = case_when(

    race == "amind" ~ "American Indian/AK Native",

    race == "black" ~ "African American",

    race == "asian" ~ "Asian/Pacific Islander",

    race == "latino" ~ "Latinx",

    race == "white" ~ "White"
  ))
```

# Check values on common variables

```
unique(pop$sex)
```

```
## [1] "Female" "Male"
```

```
unique(mort$sex)
```

```
## [1] "Female" "Male"
```

# Check values on common variables

```
unique(pop$year)
```

```
##  [1] 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2
## [15] 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2
```

```
unique(mort$year)
```

```
##  [1] 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017
```

# Check values on common variables

```
unique(pop$age)
```

```
##  [1] "0"     "1-4"   "10-14" "15-19" "20-24" "25-29" "30-34"
##  [9] "40-44" "45-49" "5-9"   "50-54" "55-59" "60-64" "65-69"
## [17] "75-79" "80-84" "85+"
```

```
unique(mort$age)
```

```
##  [1] "0"       "1-4"     "10-14"   "15-19"   "20-24"   "25-29
##  [8] "35-39"   "40-44"   "45-49"   "5-9"     "50-54"   "55-59
## [15] "65-69"   "70-74"   "75-79"   "80-84"   "85+"     "Missi
```

# Join population onto mortality

```
mort_join <- mort %>% left_join(pop)
```

# Check results

```
head(mort_join)
```

```
## # A tibble: 6 x 6
##    year age   race                     sex    deaths    pop
##   <dbl> <chr> <chr>                    <chr>   <dbl>  <dbl>
## 1  2008 0     African American         Female   3807 341912
## 2  2008 0     African American         Male     4761 353833
## 3  2008 0     American Indian/AK Native Female    169  36155
## 4  2008 0     American Indian/AK Native Male      234  37284
## 5  2008 0     Asian/Pacific Islander   Female    448 111074
## 6  2008 0     Asian/Pacific Islander   Male      570 117174
```

```
nrow(mort)
```

```
## [1] 1996
```

```
nrow(mort_join)
```

```
## [1] 1996
```

```
nrow(pop)
```

```
## [1] 5320
```

# What about a full_join()?

```
mort_join <- mort %>%
full_join(pop) %>%
arrange(year, age, race, sex)
```

# Check results

```
head(mort_join)
```

```
## # A tibble: 6 x 6
##    year age   race                     sex    deaths    pop
##   <dbl> <chr> <chr>                    <chr>   <dbl>  <dbl>
## 1  1991 0     African American         Female     NA 313730
## 2  1991 0     African American         Male       NA 320671
## 3  1991 0     American Indian/AK Native Female     NA  22465
## 4  1991 0     American Indian/AK Native Male       NA  22924
## 5  1991 0     Asian/Pacific Islander   Female     NA  68661
## 6  1991 0     Asian/Pacific Islander   Male       NA  71908
```

```
nrow(mort)
```

```
## [1] 1996
```

```
nrow(mort_join)
```

```
## [1] 5416
```

```
nrow(pop)
```

```
## [1] 5320
```

# Common join key variables

- Year
- Subject ID
- Geo ID (country, FIPS, state, etc)
- Agency ID
- Anything you want, but probably always a categorical variable

# Break

# Logistic regression

# Read in the data for today

```
admissions <- read.csv("https://stats.idre.ucla.edu/stat/data/binary.csv")
head(admissions)
```

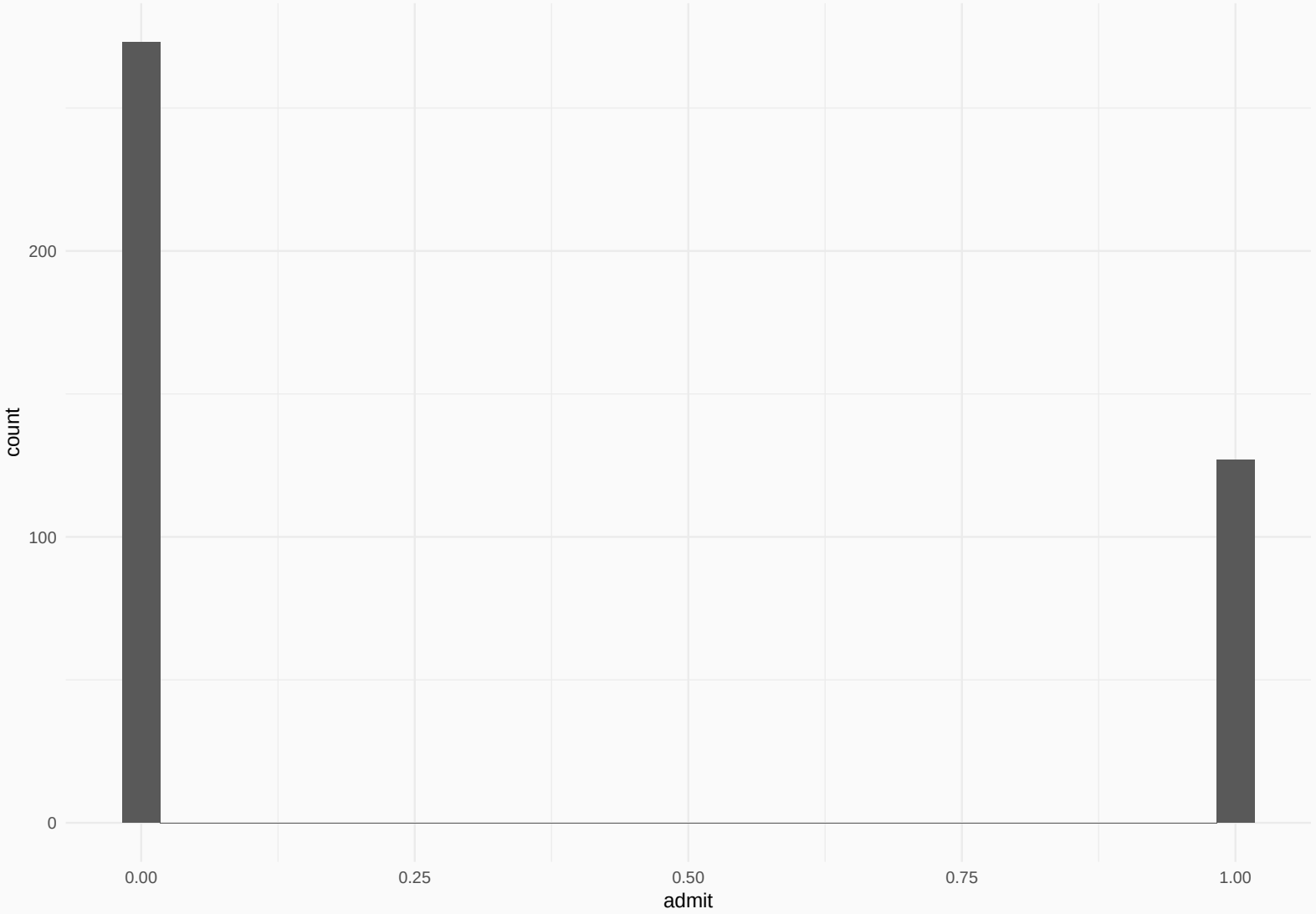
```
##   admit gre  gpa rank
## 1     0 380 3.61    3
## 2     1 660 3.67    3
## 3     1 800 4.00    1
## 4     1 640 3.19    4
## 5     0 520 2.93    4
## 6     1 760 3.00    2
```

```
nrow(admissions)
```

```
## [1] 400
```

# Evaluate distribution of binary admission variable

```
ggplot(admissions, aes(x = admit)) + geom_histogram()
```



# Properties of Bernoulli variables

If $y$ is an i.i.d. Bernoulli variable with probability $p$:

$$y \sim Bernoulli(p)$$

$$\Pr(y = 1) = p = 1 - \Pr(y = 0)$$

$$E(y) = \bar{y} = p$$

$$Var(y) = p(1 - p)$$

# Summary of admit: What can we say about the probability of admission?

```r
mean(admissions$admit)
```

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

```r
sum(admissions$admit == 1)/nrow(admissions)
```

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

```r
var(admissions$admit)
```

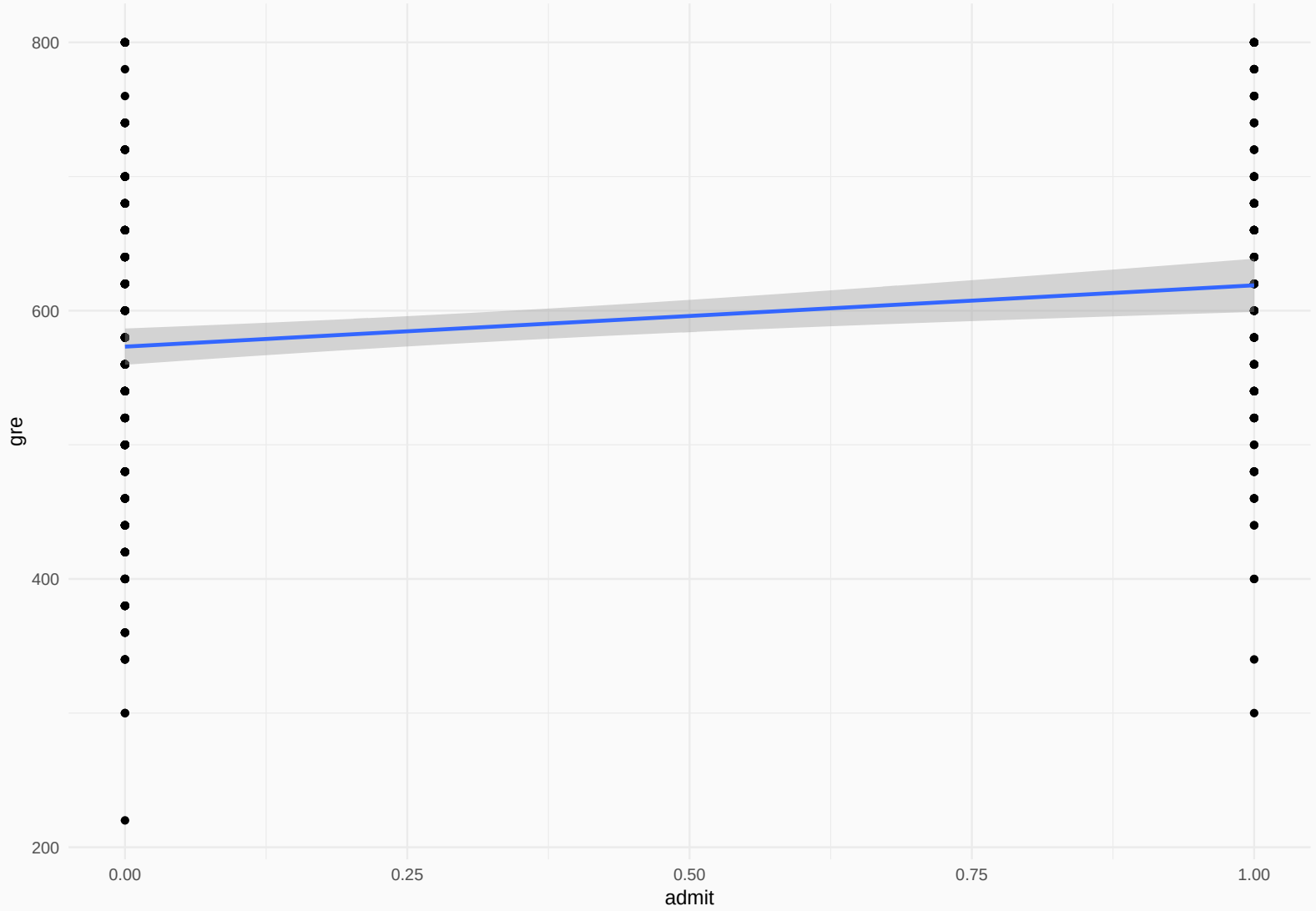
```
## [1] 0.2172368
```

```r
mean(admissions$admit) * (1 - mean(admissions$admit))
```

```
## [1] 0.2166937
```

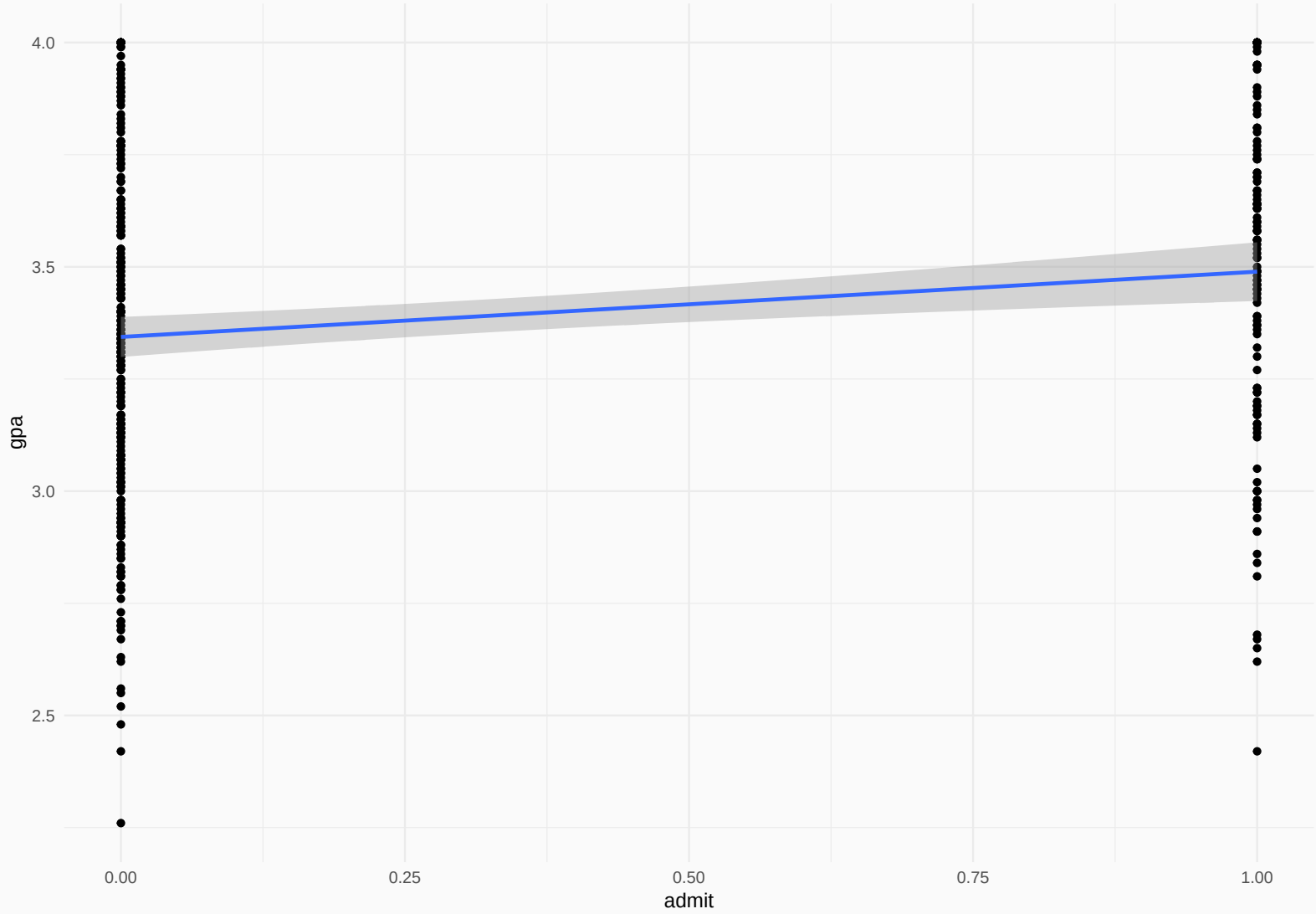
# How does GRE relate to admission?

```
ggplot(admissions, aes(x = admit, y = gre)) + geom_point() + geo
```



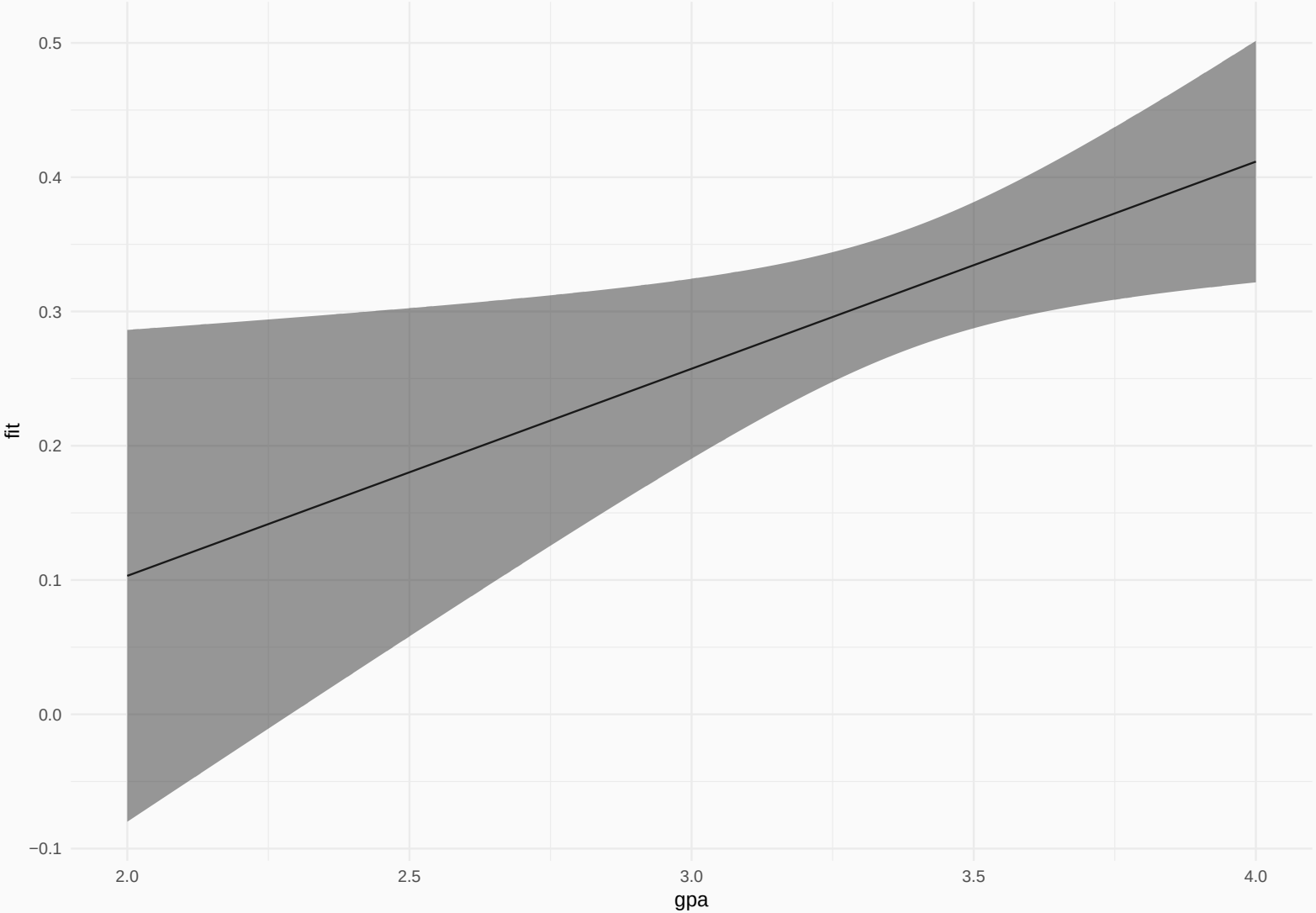
# GPA?

```
ggplot(admissions, aes(x = admit, y = gpa)) + geom_point() + geo
```



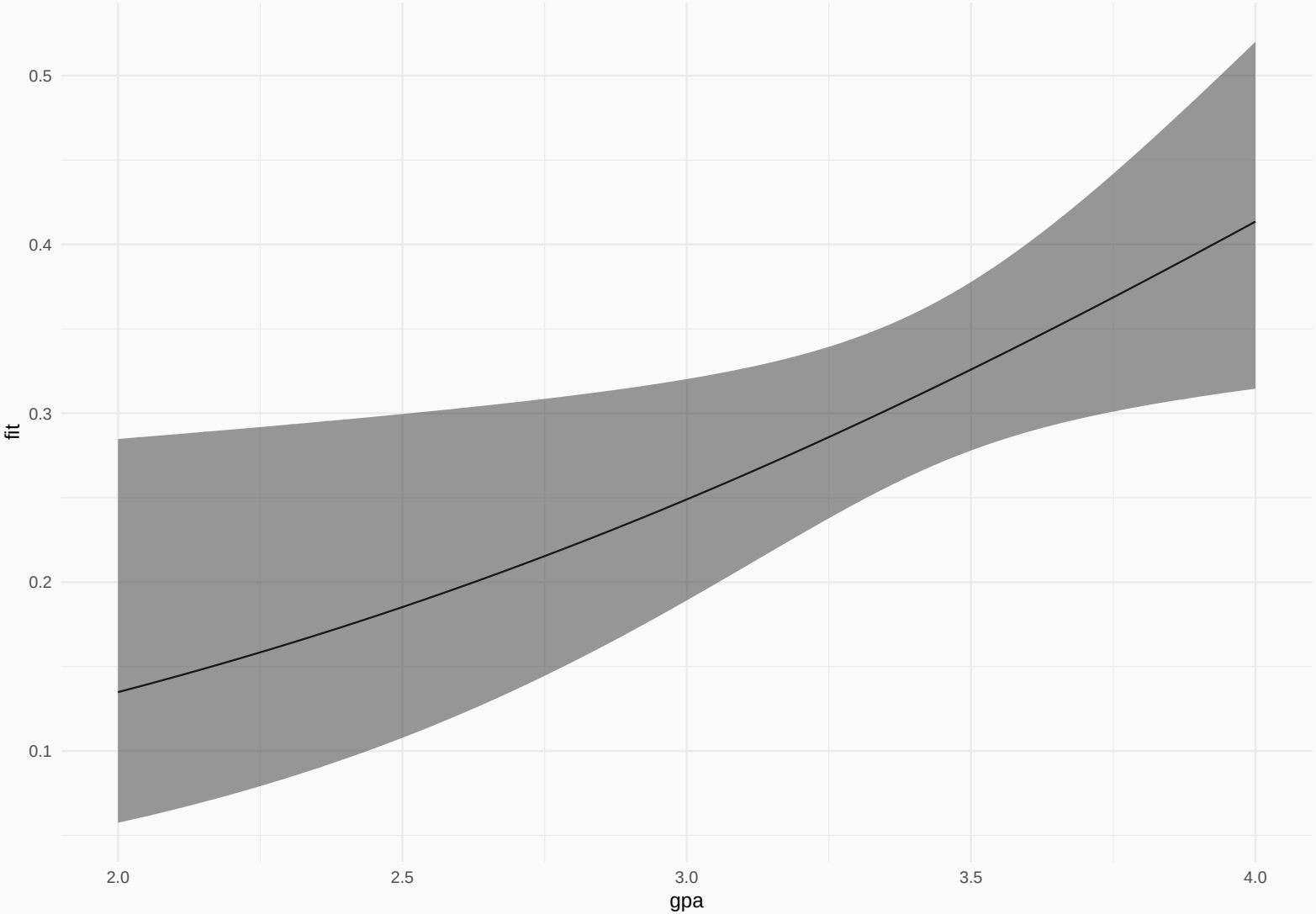
# Can we fit a model to predict admission?

```
m1 <- lm(admit ~ gre + gpa, data = admissions)
```



# Let's try a different approach

```
m2 <- glm(admit ~ gre + gpa, data = admissions, family = "binomial")
```



# A generalized linear model

Our linear probability model was:

$$Pr(admit = 1) = \beta_0 + \beta_1 GRE + \beta_2 GPA + \beta_3 Rank + \varepsilon$$

Our logistic regression model takes the form:

$$logit(Pr(admit = 1)) = \beta_0 + \beta_1 GRE + \beta_2 GPA + \beta_3 Rank$$

The logit function is our link between the linear predictor term $X\beta$ and the outcome *admit*.

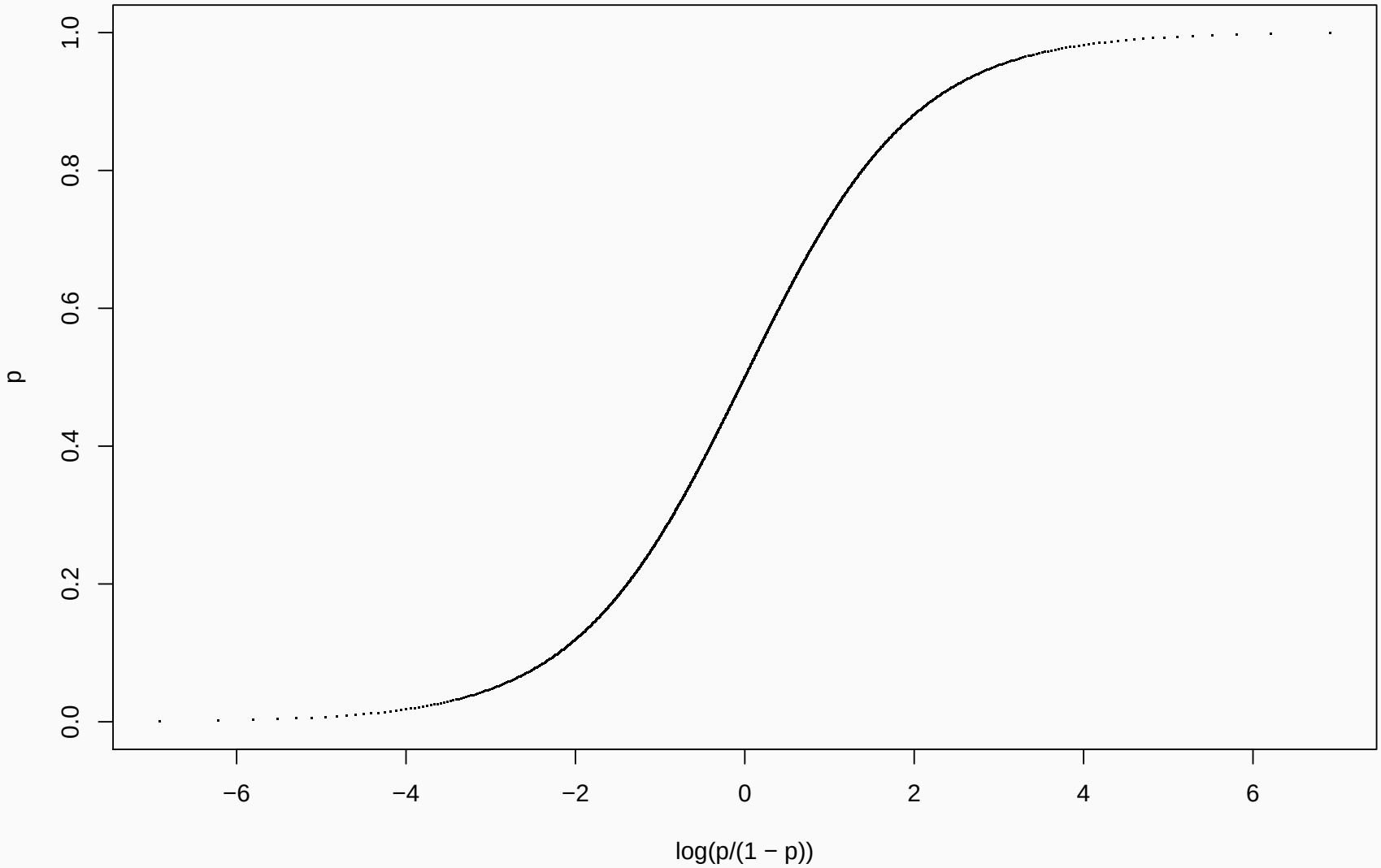
# The logit function

The logit function transforms a probability value on $[0, 1]$ to a continuous distribution

$$logit(p) = log \frac{p}{1 - p}$$

# The logit function

```
p <- seq(0, 1, 0.001)
plot(log(p/(1 - p)), pch = ".", p)
```



# Logistic regression is a GLM with a logit link

A generalized linear model with link function $g$ takes the form:

$$g(y) = X\beta$$

For OLS, the link function is the identity function $g(y) = y$

For logistic regression, the link function is the logit function

$$logit(y) = X\beta$$

$$y = logit^{-1}(X\beta)$$

# Defining logit and its inverse

$$logit(p) = log\frac{p}{1-p}$$

$$logit^{-1}(x) = \frac{exp(x)}{exp(x)+1}$$

We can use these functions to transform values back and forth from our logit-linear scale and the probability scale.

# Logistic regression

Uses the logit function to model the probability of a binary outcome being equal to 1. The logit function transforms the bounded interval $[0, 1]$ to a continuous distribution, allowing us to proceed with building a regression model as we ordinarily would.

Logistic regression may have more accurate uncertainty estimates than a linear probability model for binary outcomes. Logistic regression also constrains model predictions to $[0, 1]$.

# Running logistic models in R: the glm() function

```
m1 <- glm(admit ~ gpa, data = admissions, family = "binomial")
tidy(m1)
```

```
## # A tibble: 2 x 5
##   term        estimate std.error statistic   p.value
##   <chr>          <dbl>     <dbl>     <dbl>     <dbl>
## 1 (Intercept)    -4.36     1.04      -4.21 0.0000257
## 2 gpa             1.05     0.299      3.52 0.000437
```

How do we interpret the coefficients?

# Common interpretations

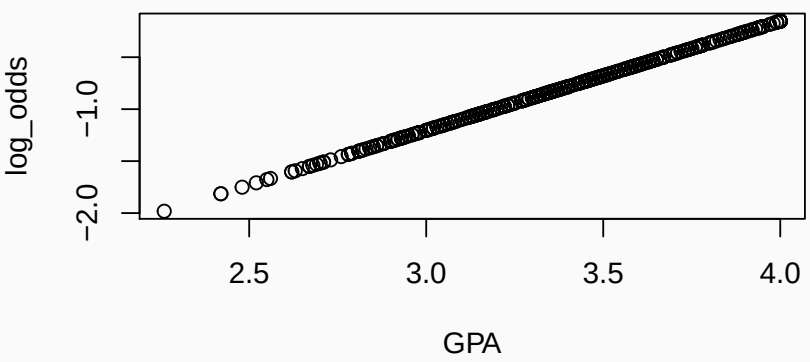
- Log odds: $\beta_1$
- Odds ratio: $e^{\beta_1}$
- Probability: $logit^{-1}(x) = \frac{exp(X\beta)}{exp(X\beta)+1}$

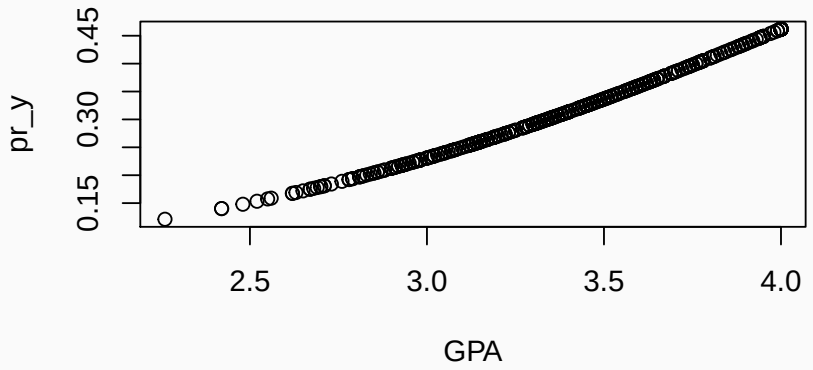
I tend to prefer transforming to a probability scale, as log odds and odds ratios are a bit confusing to define and are not especially intuitive.

# To get predicted probabilities from m1

We need $X\beta$, then apply the logit inverse function

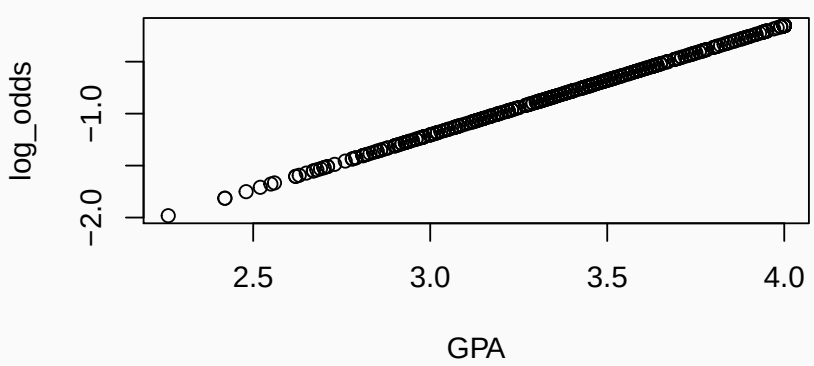
```
x <- cbind(rep(1, nrow(admissions)), admissions$gpa)
log_odds <- coef(m1) %*% t(x)
pr_y <- exp(log_odds)/(exp(log_odds) + 1)
par(mfrow = c(1, 2))
plot(x[, 2], log_odds, xlab = "GPA")
plot(x[, 2], pr_y, xlab = "GPA")
```

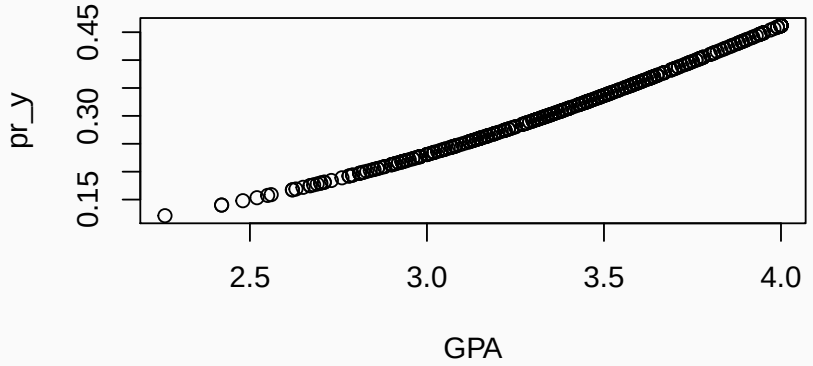


# Alternatively

```
log_odds <- predict(m1)
pr_y <- predict(m1, type = "response")
```



# Reminder

- Complete paper proposal due next week: Provide me with a 200 - 500 word abstract that describes your proposed research. This proposal should be accompanied by a description or visualization of key variables if available. If not available, explain your plans for obtaining and working with the data in a timely fashion.
- Hw 4 is also due next week. Sorry to double up!