

CSSS 569 Visualizing Data and Models

Lab 4: Advanced `ggplot2`

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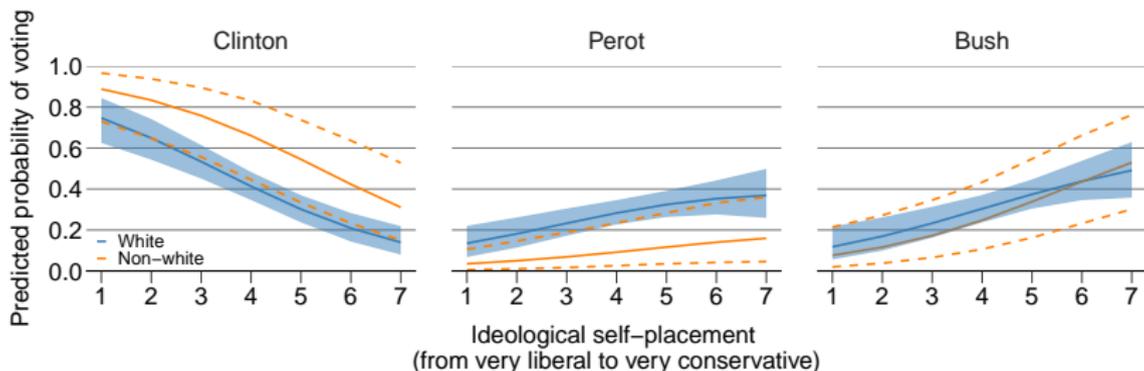
January 28, 2022

Introduction

- ▶ Recap of what we've covered last week
- ▶ Making a scatterplot from scratch in `ggplot2` (from Chris's slides)
 1. Decide on dimensions: aspect ratio, axis limits
 2. Add axis labels, plot titles
 3. Choose data markers: points, symbols, text
 4. Scaling & transformation, add ticks if needed
 5. Choose a color palette
 6. Add annotations: labels, arrows, notes
 7. Add best-fit line(s) & confidence intervals
 8. Add extra plots (e.g., rugs) to make a confection
 9. Repeat as small multiples (`facet_grid` and `facet_wrap`)
 - ▶ Next week we'll implement them using `tile`
- ▶ Unpack the inner working of `ggplot2`
 - ▶ `data`, `aes(...)`, `geom(..., inherit.aes = TRUE)`
- ▶ Customized theme: `theme_caviz.R`
- ▶ Exercise to reproduce a graph

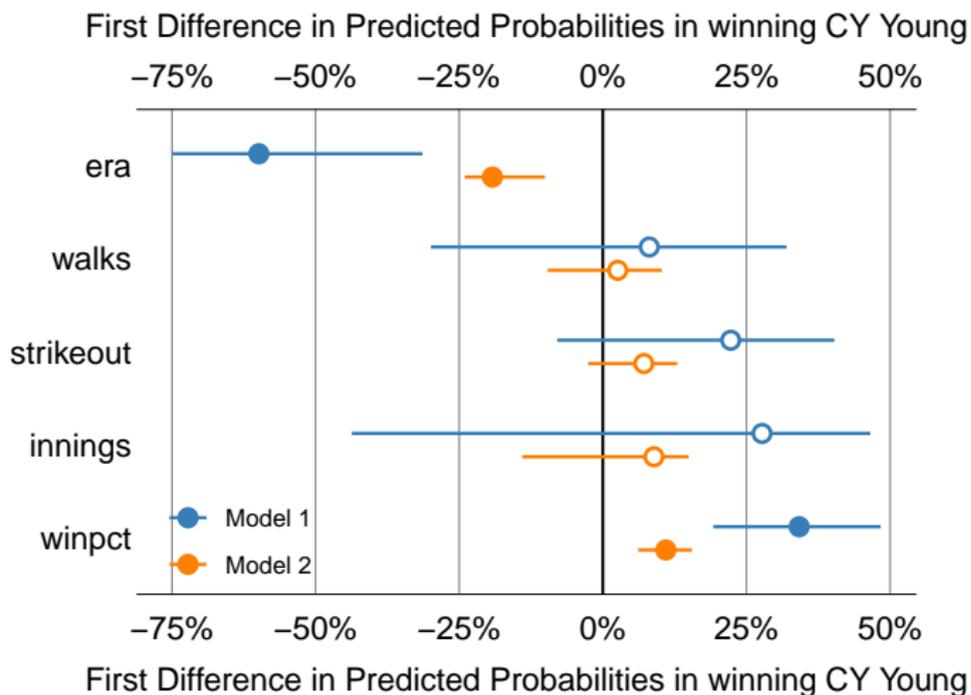
Roadmap for today

Today's lab is structured around three exercises:



Roadmap for today

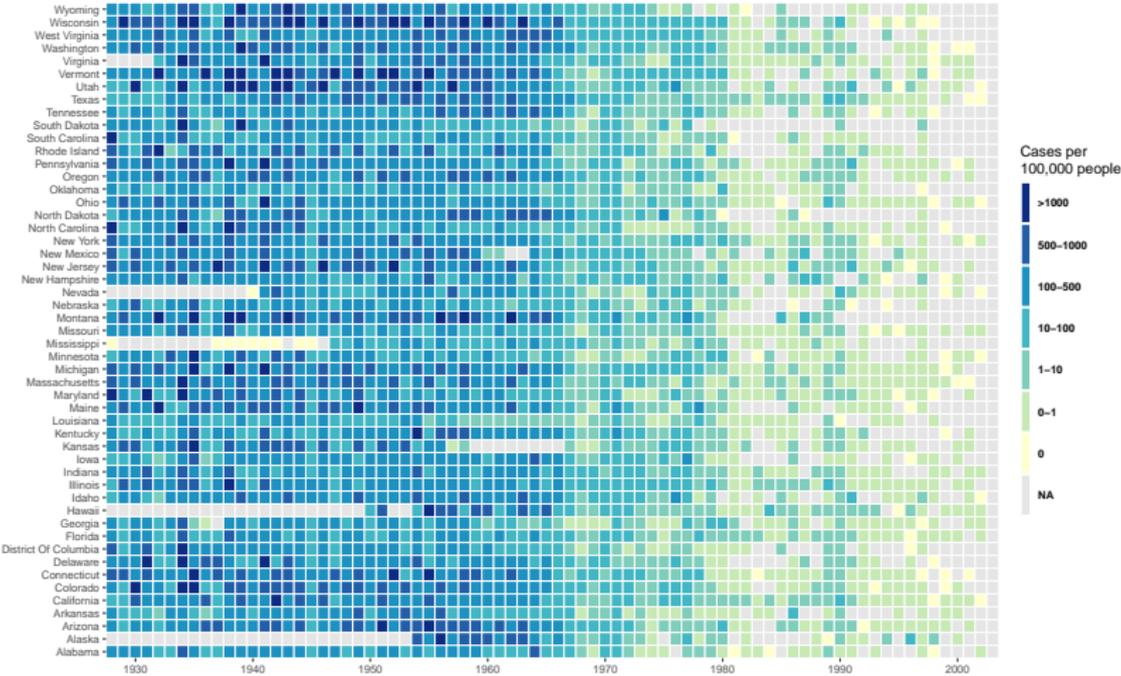
Today's lab is structured around three exercises:



Roadmap for today

Today's lab is structured around three exercises:

Incidence of Measles in the US



Roadmap for today

1. Last exercise: 1992 Presidential Election

Roadmap for today

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 - ▶ Use of `scale_{...}`

Roadmap for today

1. Last exercise: 1992 Presidential Election

- ▶ Use of `scale_{...}`
- ▶ Use of `facet_grid` and facet-specific labels

Roadmap for today

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 - ▶ Use of `scale_{...}`
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2. Ropeladder exercise: Cy Young award

Roadmap for today

1. Last exercise: 1992 Presidential Election
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 - ▶ `pivot_longer` and `pivot_wider`

Roadmap for today

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 - ▶ `pivot_longer` and `pivot_wider`
 - ▶ Sorting using `fct_reorder`

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3. Heatmap exercise: Measles in US

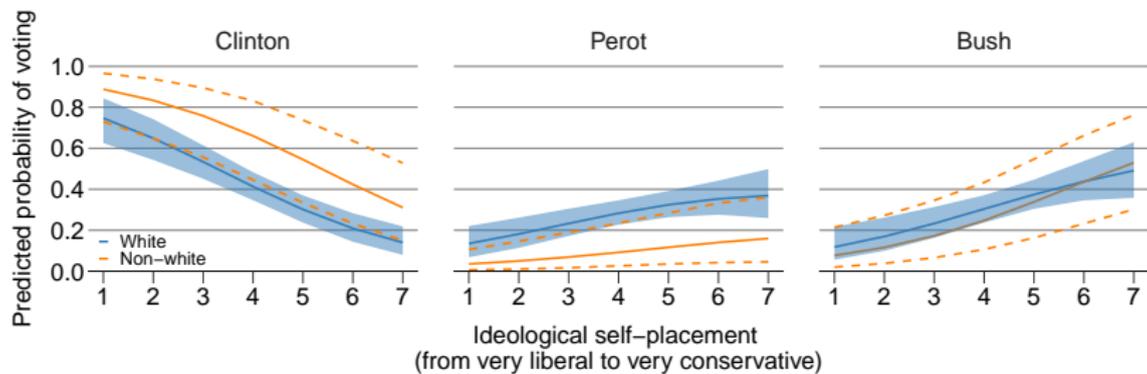
Roadmap for today

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 - ▶ Use of `scale_{...}`
 - ▶ Use of `facet_grid` and facet-specific labels
2. Ropeladder exercise: Cy Young award
 - ▶ `pivot_longer` and `pivot_wider`
 - ▶ Sorting using `fct_reorder`
 - ▶ Use of `scale_{...}`
3. Heatmap exercise: Measles in US
 - ▶ Use of `geom_tile` and various ways to `scale_color/fill_{...}`

Roadmap for today

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2. Ropeladder exercise: Cy Young award
 - ▶ `pivot_longer` and `pivot_wider`
 - ▶ Sorting using `fct_reorder`
 - ▶ Use of `scale_{...}`
3. Heatmap exercise: Measles in US
 - ▶ Use of `geom_tile` and various ways to `scale_color/fill_{...}`
4. Highlight `ggplot2` extension packages ([See more here](#))

Last exercise: 1992 Presidential Election

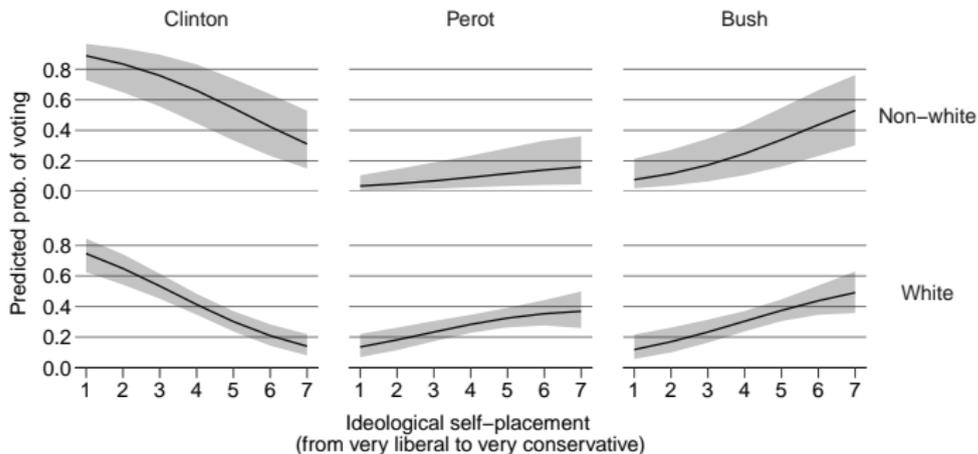


Last exercise: motivation

- ▶ There are many ways to do small multiples:

Last exercise: motivation

- ▶ There are many ways to do small multiples:
 - ▶ `plot + facet_grid(nonwhite ~ vote92)`

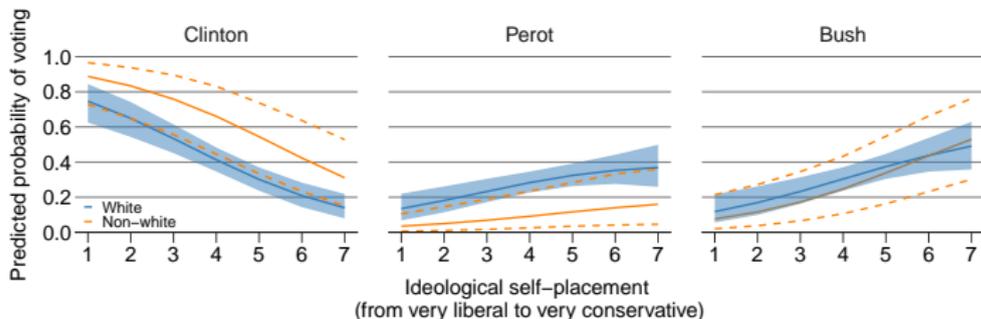


Last exercise: motivation

- ▶ Thoughtful juxtaposition facilitates meaningful comparison and provokes further inquiry

Last exercise: motivation

- ▶ Thoughtful juxtaposition facilitates meaningful comparison and provokes further inquiry
 - ▶ Sometimes, data overlapping might be an interesting phenomenon



Last exercise: 1992 Presidential Election

```
### Prerequisite
# Load package
library(tidyverse)
library(RColorBrewer)

# Load data
presVoteEV <- read_csv("data/presVoteEV.csv")

# Load theme
source("source/theme_caviz.R")

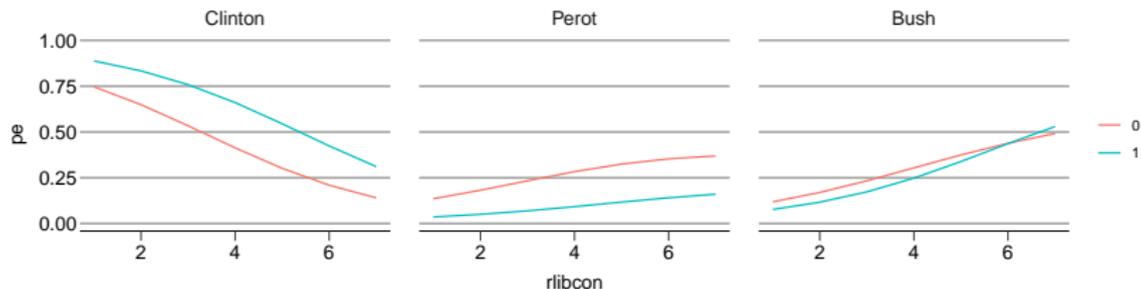
# Get nice color
brewer <- brewer.pal(9, "Set1")
blue <- brewer[2]
orange <- brewer[5]
```

Last exercise: 1992 Presidential Election

```
# Factorize variables
presVoteEV <- presVoteEV %>%
  mutate(
    nonwhite = factor(nonwhite),
    vote92 = factor(vote92, levels = c("Clinton", "Perot", "Bush"))
  )
```

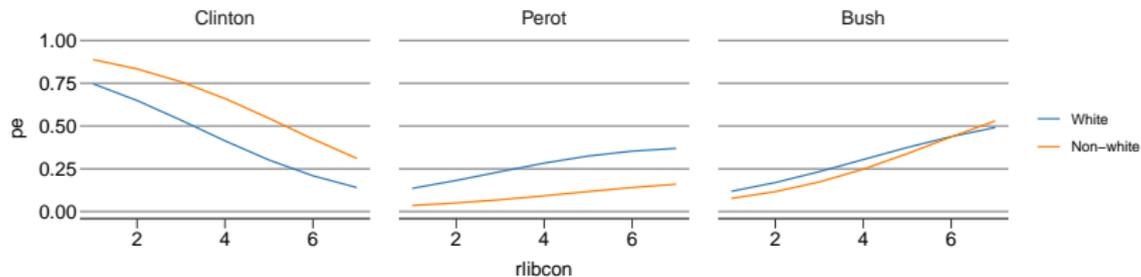
Last exercise: 1992 Presidential Election

```
p <-  
  ggplot(presVoteEV, aes(x = rlibcon,  
                        y = pe, ymin = lower, ymax = upper,  
                        color = nonwhite, fill = nonwhite)) +  
  facet_grid(~ vote92) +  
  geom_line() +  
  theme_caviz_hgrid  
  
print(p)
```



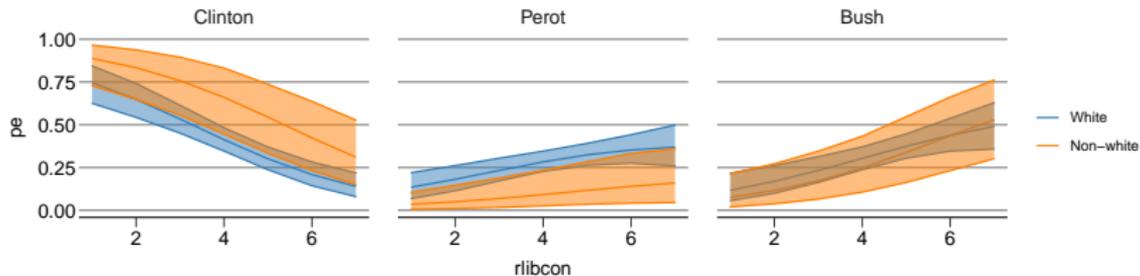
Last exercise: 1992 Presidential Election

```
p <- p +  
  scale_color_manual(values = c(blue, orange),  
                    labels = c("White", "Non-white"))  
  
print(p)
```



Last exercise: 1992 Presidential Election

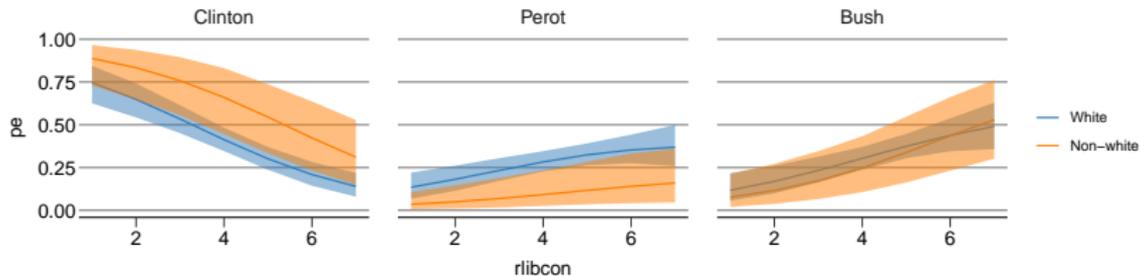
```
p +  
  geom_ribbon(alpha = 0.5, show.legend = FALSE) +  
  scale_fill_manual(values = c(blue, orange))
```



Last exercise: 1992 Presidential Election

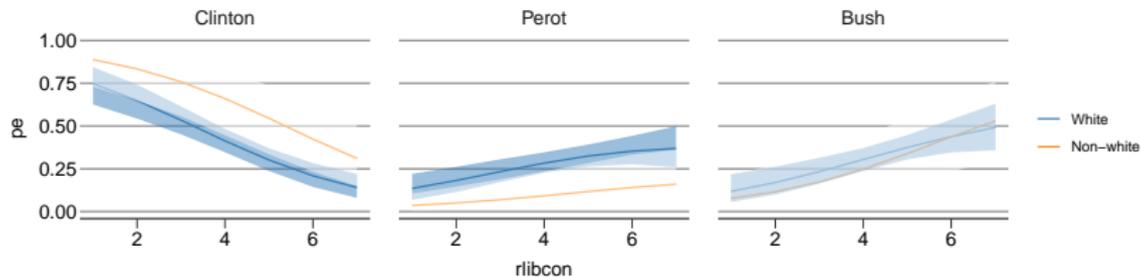
p +

```
geom_ribbon(alpha = 0.5, linetype = 0, show.legend = FALSE) +  
scale_fill_manual(values = c(blue, orange))
```



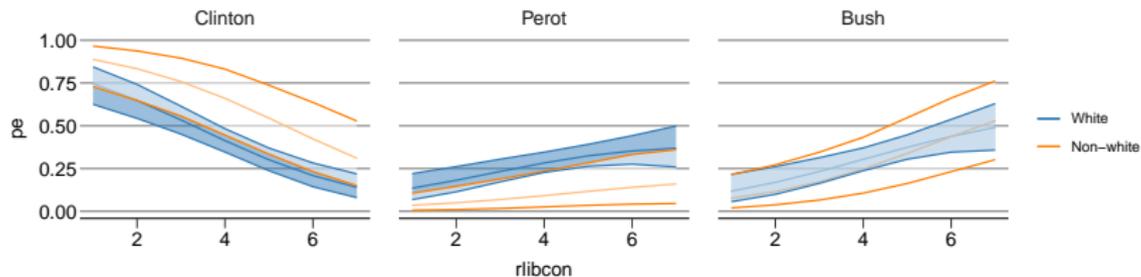
Last exercise: 1992 Presidential Election

```
p <- p +  
  geom_ribbon(alpha = 0.5, linetype = 0, show.legend = FALSE) +  
  scale_fill_manual(values = c(blue, "transparent")) # NA used to work  
  
print(p)
```



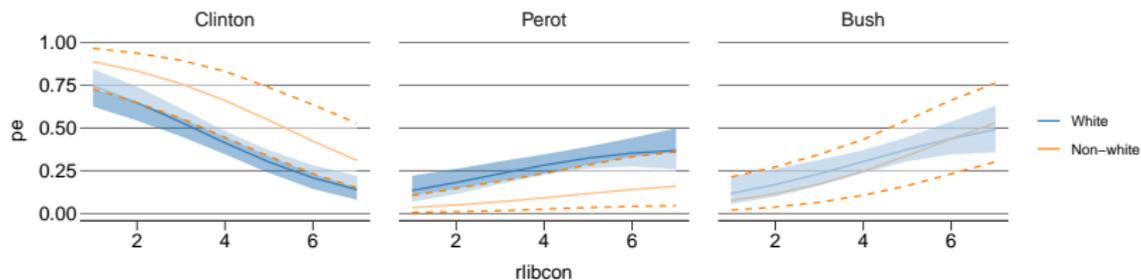
Last exercise: 1992 Presidential Election

```
p +  
  geom_line(aes(y = upper)) +  
  geom_line(aes(y = lower))
```



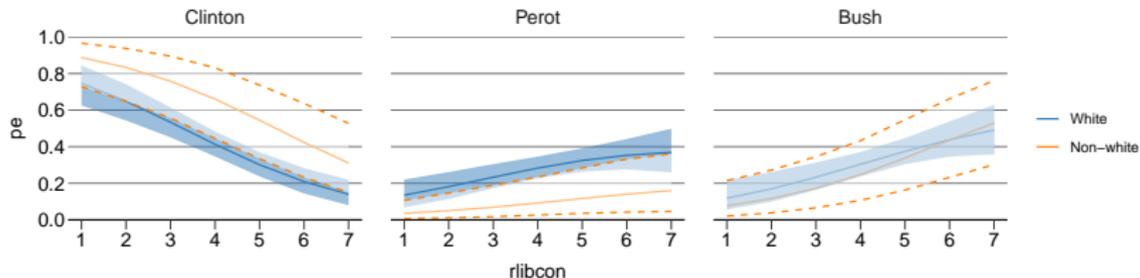
Last exercise: 1992 Presidential Election

```
p <- p +  
  geom_line(aes(y = upper, linetype = nonwhite), show.legend = FALSE) +  
  geom_line(aes(y = lower, linetype = nonwhite), show.legend = FALSE) +  
  scale_linetype_manual(values = c(0, 2)) # 0 = blank; 2 = dashed  
  
print(p)
```



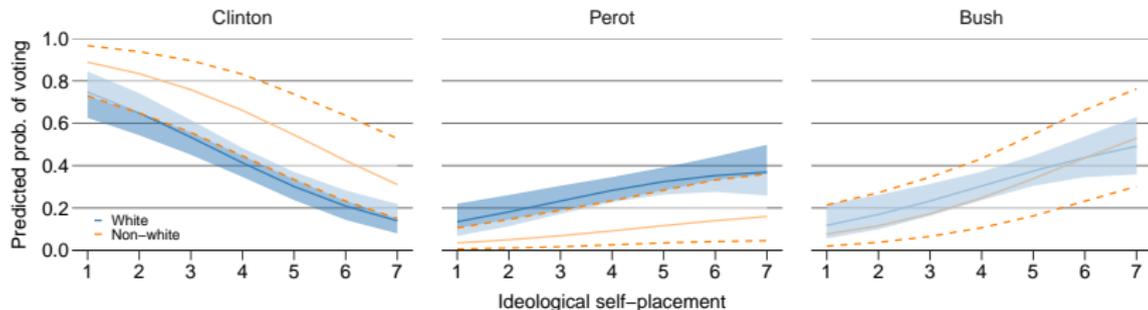
Last exercise: 1992 Presidential Election

```
p <- p +  
  scale_x_continuous(breaks = 1:7) +  
  scale_y_continuous(breaks = seq(0, 1, 0.2),  
                    limits = c(0, 1),  
                    expand = c(0, 0))  
  
print(p)
```



Last exercise: 1992 Presidential Election

```
p <- p +  
  theme(legend.position = c(0.06, 0.13),  
        legend.key.size = unit(0.2, "cm")) +  
  labs(y = "Predicted prob. of voting",  
       x = "Ideological self-placement")  
  
print(p)
```



Last exercise: 1992 Presidential Election

Full code to reproduce the graph

```
p <- ggplot(presVoteEV, aes(x = rlibcon, y = pe,
                           color = nonwhite, fill = nonwhite)) +
  # Small multiples by candidates
  facet_grid(~ vote92) +
  # Point estimates lines
  geom_line() +
  scale_color_manual(values = c(blue, orange),
                    labels = c("White", "Non-white")) +
  # CIs for white voters
  geom_ribbon(aes(ymin = lower, ymax = upper),
            alpha = 0.5, linetype = 0, show.legend = FALSE) +
  scale_fill_manual(values = c(blue, "transparent")) +
  # CIs for non-white voters
  geom_line(aes(y = upper, linetype = nonwhite), show.legend = FALSE) +
  geom_line(aes(y = lower, linetype = nonwhite), show.legend = FALSE) +
  scale_linetype_manual(values = c(0, 2)) +
  # Other adjustments
  scale_x_continuous(breaks = 1:7) +
  scale_y_continuous(breaks = seq(0, 1, 0.2), limits = c(0, 1),
                    expand = c(0, 0)) +
  theme_caviz_hgrid +
  theme(legend.position = c(0.06, 0.13), legend.key.size = unit(0.2, "cm")) +
  labs(y = "Predicted prob. of voting", x = "Ideological self-placement")
```

Last exercise: 1992 Presidential Election

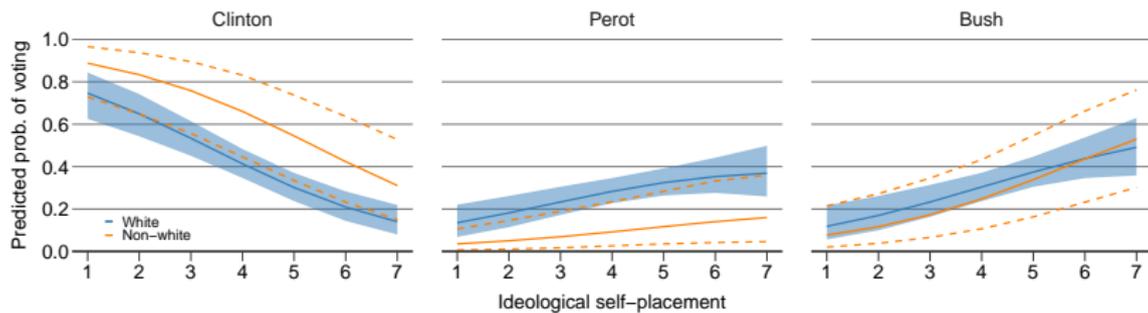
Alternative way: create subsets of data and localize data source for each geom layer

```
whiteData <- filter(presVoteEV, nonwhite == 0)
nonwhiteData <- filter(presVoteEV, nonwhite == 1)

altplot <-
  ggplot(mapping = aes(x = rlibcon, y = pe, ymin = lower, ymax = upper)) +
    # Small multiples by candidates
    facet_grid(~ vote92) +
    # For white voters
    geom_line(data = whiteData, aes(colour = blue)) +
    geom_ribbon(data = whiteData, fill = blue, linetype = 0, alpha = 0.5) +
    # For non-white voters
    geom_line(data = nonwhiteData, aes(colour = orange)) +
    geom_line(data = nonwhiteData, aes(y = lower), colour = orange, linetype = 2)
    geom_line(data = nonwhiteData, aes(y = upper), colour = orange, linetype = 2)
    # To create a legend that recognizes color strings
    scale_color_identity(labels = c("White", "Non-white"), guide = "legend") +
    # Other adjustments
    scale_x_continuous(breaks = 1:7) +
    scale_y_continuous(breaks = seq(0, 1, 0.2), limits = c(0, 1),
                      expand = c(0, 0)) +
    theme_caviz_hgrid +
    theme(legend.position = c(0.07, 0.13), legend.key.size = unit(0.2, "cm")) +
    labs(y = "Predicted prob. of voting", x = "Ideological self-placement")
```

See the result:

```
print(altplot)
```



Last exercise: 1992 Presidential Election

To create facet-specific labels, you need a separate dataframe with the x and y coordinates, labels, and the variable used in `facet_wrap` for identification

```
candidates <- c("Clinton", "Perot", "Bush")

facet_labels <-
  tibble(vote92 = rep(candidates, each = 2),
         nonwhite = rep(c(0, 1), 3),
         label = rep(c("White", "Non-white"), 3),
         x_coord = c(1.5, 6.3, 1.4, 6.6, 1.4, 6.3),
         y_coord = c(0.5, 0.75, 0.32, 0.105, 0.32, 0.13)) %>%
  mutate(vote92 = factor(vote92, levels = candidates),
         nonwhite = factor(nonwhite))

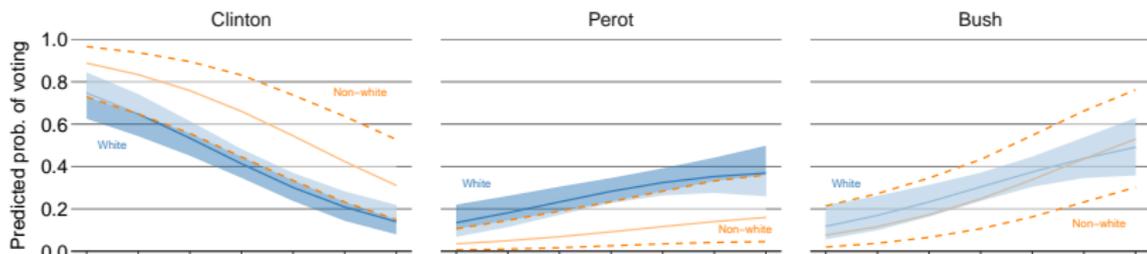
print(facet_labels)
```

```
## # A tibble: 6 x 5
##   vote92 nonwhite label      x_coord y_coord
##   <fct>  <fct>   <chr>    <dbl>  <dbl>
## 1 Clinton 0       White     1.5    0.5
## 2 Clinton 1       Non-white 6.3    0.75
## 3 Perot   0       White     1.4    0.32
## 4 Perot   1       Non-white 6.6    0.105
## 5 Bush    0       White     1.4    0.32
## 6 Bush    1       Non-white 6.3    0.13
```

Last exercise: 1992 Presidential Election

To create facet-specific labels, you need a separate dataframe with the x and y coordinates, labels, and the variable used in `facet_wrap` for identification

```
p +  
  geom_text(data = facet_labels,  
            aes(x = x_coord,  
                y = y_coord,  
                label = label,  
                color = nonwhite),  
            size = 2.5) +  
  theme(legend.position = "none")
```



Ropeladder exercise: Cy Young award

- ▶ Model results `cyyoungFD.csv` can be found on the course website
 - ▶ Background: North American baseball pitchers from 1980 to 2002 competing for the Cy Young Award
 - ▶ Outcome: binary; winning the Cy Young Award or not
 - ▶ Model: logistic regression
 - ▶ Note: estimated quantities of interests (e.g. first differences) are obtained via `simcf`, `Zelig`, or `ggeffects` packages
 - ▶ Variables in the model (not that they are important...):

Rows/Columns	Explanation
<code>winpct</code>	The percentage of games which the pitcher personally won
<code>era</code>	The number of runs the pitcher allows per 9 innings
<code>strikeout</code>	The number of strikeouts the pitcher collected over a season
<code>innings</code>	The number of innings (periods) a pitcher played during the season
<code>walks</code>	The number of walks the pitcher collected over a season
<code>pe</code>	The first difference in expected prob. of winning Cy Young Award
<code>lower</code>	Lower bound of the 95% confidence intervals
<code>upper</code>	Upper bound of the 95% confidence intervals

Ropeladder exercise: Cy Young award

```
cyyoungFD <- read_csv("data/cyyoungFD.csv")  
cyyoungFD
```

```
## # A tibble: 5 x 7  
##   covariate    pe_m1 lower_m1 upper_m1    pe_m2 lower_m2 upper_m2  
##   <chr>      <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>  
## 1 winpct      0.342    0.192    0.484    0.198    0.111    0.280  
## 2 era        -0.599   -0.749   -0.314  -0.347   -0.434   -0.182  
## 3 strikeout  0.223   -0.0793   0.403    0.129   -0.0459   0.233  
## 4 innings    0.277   -0.437    0.465    0.160   -0.253    0.269  
## 5 walks      0.0808  -0.299    0.320    0.0468  -0.173    0.185
```

Ropeladder exercise: Cy Young award

- ▶ Major challenges:

1. How do we reformat the data in a “tidy way”?
2. How do we create a variable that classifies statistically significant covariates from non-significant ones?
 - ▶ How can we indicate statistical non-significance using white-filled circles?
3. How do we plot the model results as a ropeladder?
4. How can we sort the covariates according to their effect sizes?
5. How can we juxtapose two models' results effectively?

Ropeladder exercise: Cy Young award

1. How do we reformat the data in a “tidy way”?
 - ▶ Motivation: create a column model with values {m1, m2} such that we can map model to aesthetics
 - ▶ i.e. `aes(colour = model)`
 - ▶ We need to learn `pivot_longer` and `pivot_wider` (available in the recent tidy versions)
 - ▶ Update by `update.packages("tidyverse")`

```
## # A tibble: 10 x 5
##   covariate model      pe    lower  upper
##   <chr>      <chr> <dbl> <dbl> <dbl>
## 1 winpct    m1     0.342  0.192  0.484
## 2 era      m1    -0.599 -0.749 -0.314
## 3 strikeout m1     0.223 -0.0793 0.403
## 4 innings  m1     0.277 -0.437  0.465
## 5 walks    m1     0.0808 -0.299  0.320
## 6 winpct    m2     0.198  0.111  0.280
## 7 era      m2    -0.347 -0.434 -0.182
## 8 strikeout m2     0.129 -0.0459 0.233
## 9 innings  m2     0.160 -0.253  0.269
## 10 walks   m2     0.0468 -0.173  0.185
```

Ropeladder exercise: Cy Young award

1. How do we reformat the data in a “tidy way”?

```
print(cyyoungFD)
```

```
## # A tibble: 5 x 7
##   covariate    pe_m1 lower_m1 upper_m1    pe_m2 lower_m2 upper_m2
##   <chr>      <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl>
## 1 winpct      0.342    0.192    0.484    0.198    0.111    0.280
## 2 era        -0.599   -0.749   -0.314   -0.347   -0.434   -0.182
## 3 strikeout  0.223   -0.0793    0.403    0.129   -0.0459    0.233
## 4 innings    0.277   -0.437    0.465    0.160   -0.253    0.269
## 5 walks      0.0808  -0.299    0.320    0.0468  -0.173    0.185
```

Ropeladder exercise: Cy Young award

1. How do we reformat the data in a “tidy way”?

```
cyyoungFD %>%  
  pivot_longer(cols = pe_m1:upper_m2,  
               names_to = "col_names",  
               values_to = "value")
```

```
## # A tibble: 30 x 3  
##   covariate col_names  value  
##   <chr>      <chr>    <dbl>  
## 1 winpct    pe_m1      0.342  
## 2 winpct    lower_m1   0.192  
## 3 winpct    upper_m1   0.484  
## 4 winpct    pe_m2      0.198  
## 5 winpct    lower_m2   0.111  
## 6 winpct    upper_m2   0.280  
## 7 era       pe_m1     -0.599  
## 8 era       lower_m1  -0.749  
## 9 era       upper_m1  -0.314  
## 10 era      pe_m2     -0.347  
## # ... with 20 more rows
```

Ropeladder exercise: Cy Young award

1. How do we reformat the data in a “tidy way”?

```
cyyoungFD %>%  
  pivot_longer(cols = pe_m1:upper_m2,  
               names_to = "col_names",  
               values_to = "value") %>%  
  separate(col_names, into = c("stat", "model"), sep = "_")
```

```
## # A tibble: 30 x 4  
##   covariate stat  model  value  
##   <chr>      <chr> <chr> <dbl>  
## 1 winpct    pe     m1     0.342  
## 2 winpct    lower m1     0.192  
## 3 winpct    upper m1     0.484  
## 4 winpct    pe     m2     0.198  
## 5 winpct    lower m2     0.111  
## 6 winpct    upper m2     0.280  
## 7 era      pe     m1    -0.599  
## 8 era      lower m1    -0.749  
## 9 era      upper m1    -0.314  
## 10 era     pe     m2    -0.347  
## # ... with 20 more rows
```

Ropeladder exercise: Cy Young award

1. How do we reformat the data in a “tidy way”?

```
cyyoungFD %>%  
  pivot_longer(cols = pe_m1:upper_m2,  
               names_to = "col_names",  
               values_to = "value") %>%  
  separate(col_names, into = c("stat", "model"), sep = "_") %>%  
  pivot_wider(names_from = stat, values_from = value)
```

```
## # A tibble: 10 x 5  
##   covariate model      pe  lower  upper  
##   <chr>      <chr>  <dbl> <dbl> <dbl>  
## 1 winpct    m1      0.342  0.192  0.484  
## 2 winpct    m2      0.198  0.111  0.280  
## 3 era      m1     -0.599 -0.749 -0.314  
## 4 era      m2     -0.347 -0.434 -0.182  
## 5 strikeout m1      0.223 -0.0793 0.403  
## 6 strikeout m2      0.129 -0.0459 0.233  
## 7 innings  m1      0.277 -0.437  0.465  
## 8 innings  m2      0.160 -0.253  0.269  
## 9 walks    m1      0.0808 -0.299  0.320  
## 10 walks   m2      0.0468 -0.173  0.185
```

Ropeladder exercise: Cy Young award

1. How do we reformat the data in a “tidy way”?

```
cyyoungFD <- cyyoungFD %>%  
  pivot_longer(cols = pe_m1:upper_m2,  
               names_to = "col_names",  
               values_to = "value") %>%  
  separate(col_names, into = c("stat", "model"), sep = "_") %>%  
  pivot_wider(names_from = stat, values_from = value) %>%  
  arrange(model)  
  
print(cyyoungFD)
```

```
## # A tibble: 10 x 5  
##   covariate model      pe    lower  upper  
##   <chr>      <chr> <dbl> <dbl> <dbl>  
## 1 winpct    m1      0.342  0.192  0.484  
## 2 era      m1     -0.599 -0.749 -0.314  
## 3 strikeout m1      0.223 -0.0793 0.403  
## 4 innings  m1      0.277 -0.437  0.465  
## 5 walks    m1      0.0808 -0.299  0.320  
## 6 winpct    m2      0.198  0.111  0.280  
## 7 era      m2     -0.347 -0.434 -0.182  
## 8 strikeout m2      0.129 -0.0459 0.233  
## 9 innings  m2      0.160 -0.253  0.269  
## 10 walks   m2      0.0468 -0.173  0.185
```

Ropeladder exercise: Cy Young award

2. How do we create a variable that classifies statistically significant covariates from non-significant ones?
 - ▶ How do we know if a covariate's effect is statistically significant or not?

```
print(cyyoungFD)
```

```
## # A tibble: 10 x 5
##   covariate model      pe    lower  upper
##   <chr>      <chr>  <dbl>  <dbl>  <dbl>
## 1 winpct    m1      0.342  0.192  0.484
## 2 era      m1     -0.599 -0.749 -0.314
## 3 strikeout m1      0.223 -0.0793 0.403
## 4 innings  m1      0.277 -0.437  0.465
## 5 walks    m1      0.0808 -0.299  0.320
## 6 winpct    m2      0.198  0.111  0.280
## 7 era      m2     -0.347 -0.434 -0.182
## 8 strikeout m2      0.129 -0.0459 0.233
## 9 innings  m2      0.160 -0.253  0.269
## 10 walks   m2      0.0468 -0.173  0.185
```

Ropeladder exercise: Cy Young award

2. How do we create a variable that classifies statistically significant covariates from non-significant ones?

```
cyyoungFD <- cyyoungFD %>%  
  mutate(  
    signif = case_when(  
      lower > 0 & upper > 0 ~ TRUE, # Both bounds are above zero = signif  
      lower < 0 & upper < 0 ~ TRUE, # Both bounds are below zero = signif  
      TRUE ~ FALSE) # Everything else is not signif  
  )  
print(cyyoungFD)
```

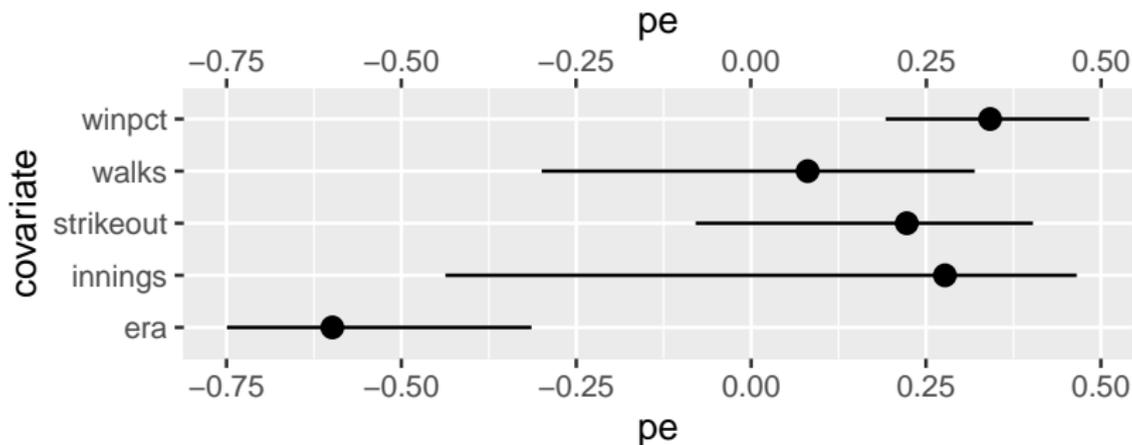
```
## # A tibble: 10 x 6  
##   covariate model      pe  lower  upper signif  
##   <chr>      <chr> <dbl> <dbl> <dbl> <lg1>  
## 1 winpct    m1      0.342  0.192  0.484 TRUE  
## 2 era      m1     -0.599 -0.749 -0.314 TRUE  
## 3 strikeout m1      0.223 -0.0793 0.403 FALSE  
## 4 innings  m1      0.277 -0.437  0.465 FALSE  
## 5 walks    m1      0.0808 -0.299  0.320 FALSE  
## 6 winpct    m2      0.198  0.111  0.280 TRUE  
## 7 era      m2     -0.347 -0.434 -0.182 TRUE  
## 8 strikeout m2      0.129 -0.0459 0.233 FALSE  
## 9 innings  m2      0.160 -0.253  0.269 FALSE  
## 10 walks   m2      0.0468 -0.173  0.185 FALSE
```

Ropeladder exercise: Cy Young award

3. How do we plot the model results as a ropeladder?

- ▶ Practice: focus on model 1 and replicate the graph below
- ▶ Hints: check out `geom_pointrange()`

```
cyyoungFD %>%  
  filter(model == "m1") %>%  
  ggplot(...)
```

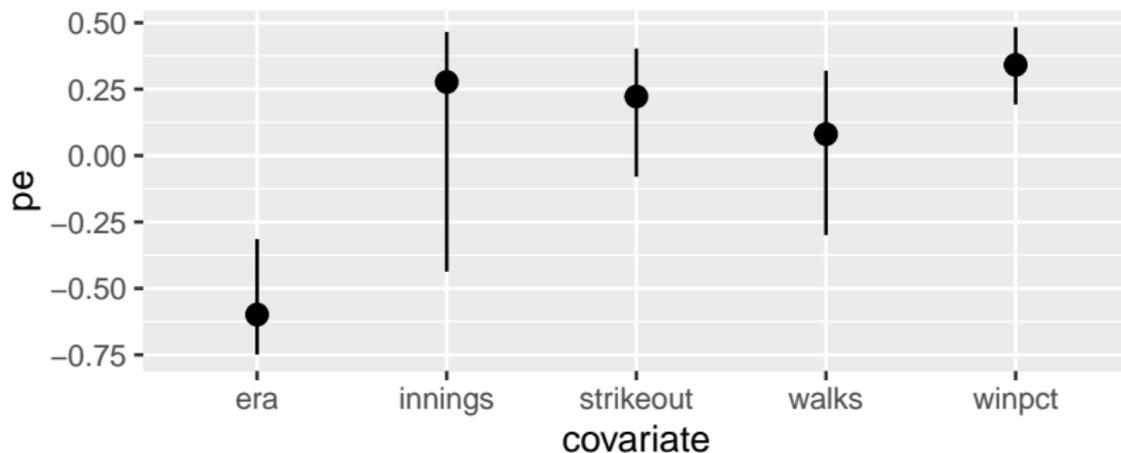


Ropeladder exercise: Cy Young award

3. How do we plot the model results as a ropeladder?

- ▶ Old method: `coord_flip()`

```
cyyoungFD %>%  
  filter(model == "m1") %>%  
  ggplot(aes(x = covariate, y = pe, ymax = upper, ymin = lower)) +  
  geom_pointrange()
```

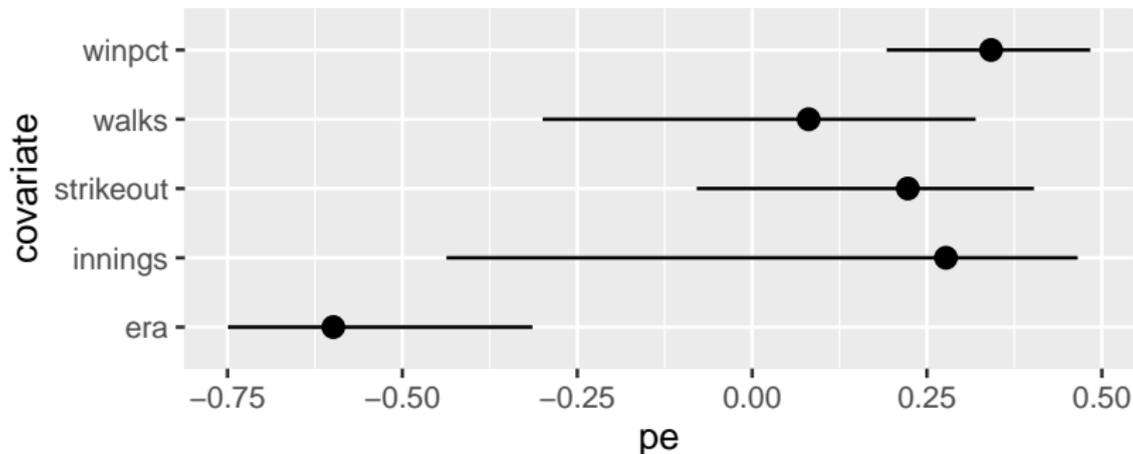


Ropeladder exercise: Cy Young award

3. How do we plot the model results as a ropeladder?

- ▶ Old method: `coord_flip()`

```
cyyoungFD %>%  
  filter(model == "m1") %>%  
  ggplot(aes(x = covariate, y = pe, ymax = upper, ymin = lower)) +  
  geom_pointrange() +  
  coord_flip()
```

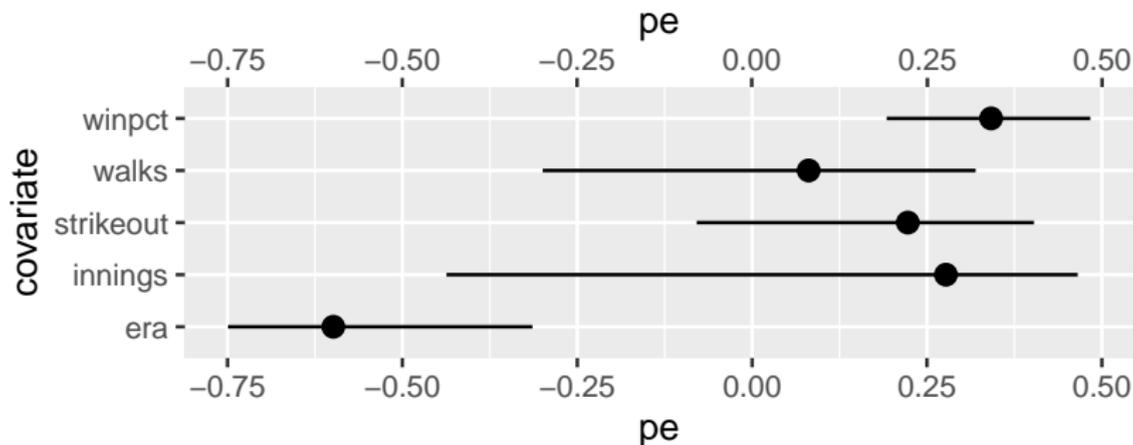


Ropeladder exercise: Cy Young award

3. How do we plot the model results as a ropeladder?

- ▶ Old method: `coord_flip()`

```
cyyoungFD %>%  
  filter(model == "m1") %>%  
  ggplot(aes(x = covariate, y = pe, ymax = upper, ymin = lower)) +  
  geom_pointrange() +  
  coord_flip() +  
  scale_y_continuous(sec.axis = dup_axis(~ .))
```

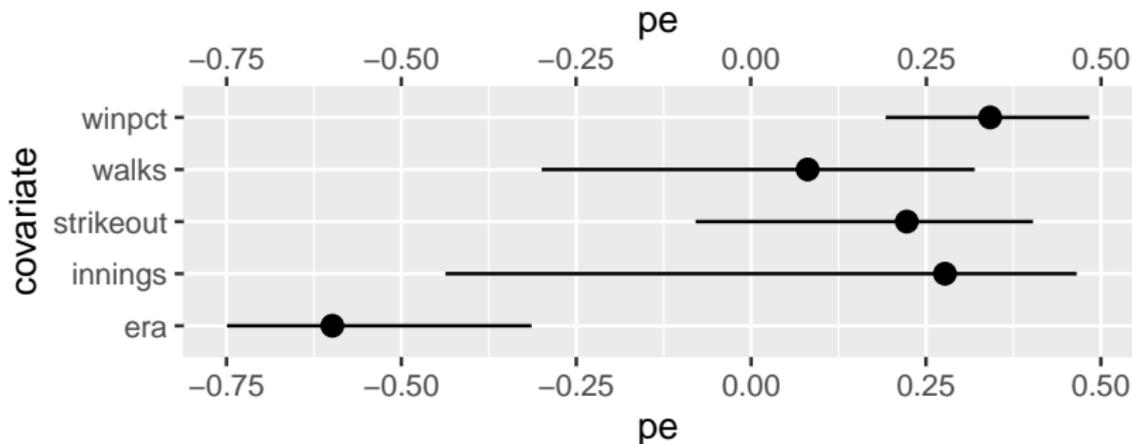


Ropeladder exercise: Cy Young award

3. How do we plot the model results as a ropeladder?

- ▶ New method: native `xmax` and `xmin` inputs in new `ggplot2`
- ▶ But problems with legend keys displayed in wrong orientation

```
cyyoungFD %>%  
  filter(model == "m1") %>%  
  ggplot(aes(y = covariate, x = pe, xmax = upper, xmin = lower)) +  
  geom_pointrange() +  
  scale_x_continuous(sec.axis = dup_axis(~ .))
```



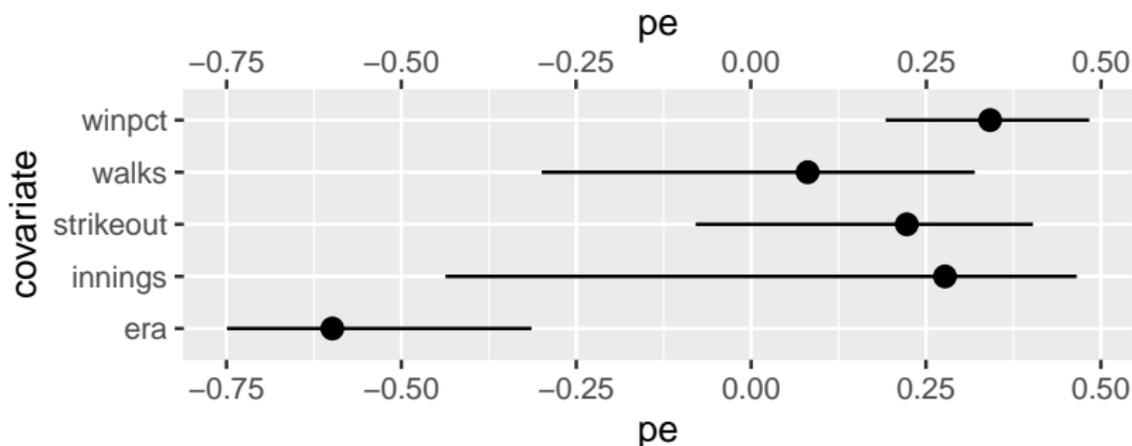
Ropeladder exercise: Cy Young award

3. How do we plot the model results as a ropeladder?

- ▶ Preferred method: ggstance package implements horizontal versions of different geoms with correctly oriented legend keys

```
library(ggstance)

cyyoungFD %>%
  filter(model == "m1") %>%
  ggplot(aes(y = covariate, x = pe, xmax = upper, xmin = lower)) +
  geom_pointrangeh() + # note the "h" at the end
  scale_x_continuous(sec.axis = dup_axis(~ .))
```

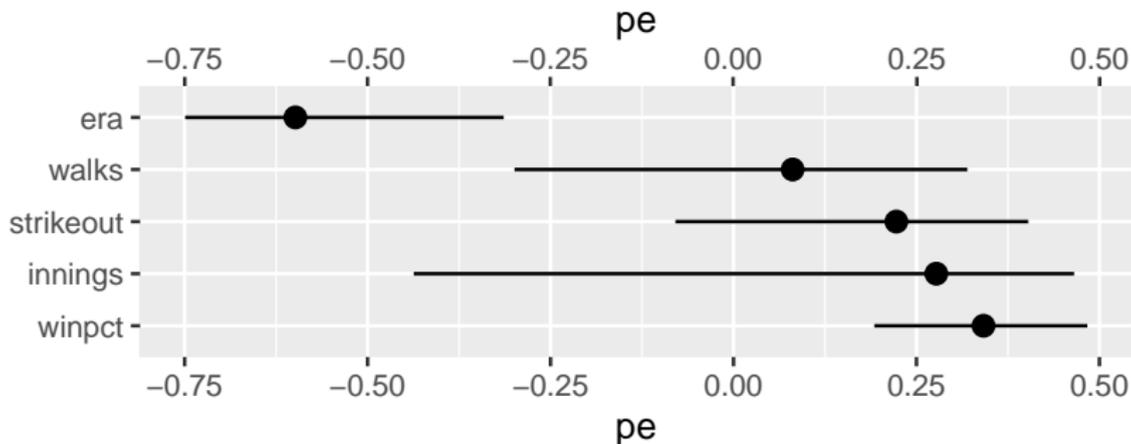


Ropeladder exercise: Cy Young award

4. How can we sort the covariates according to their effect sizes?

▶ `fct_reorder()` from `forcats` package (in `tidyverse`)

```
cyyoungFD %>%  
  filter(model == "m1") %>%  
  mutate(covariate = fct_reorder(covariate, pe, .desc = TRUE)) %>%  
  ggplot(aes(y = covariate, x = pe, xmax = upper, xmin = lower)) +  
  geom_pointrange() +  
  scale_x_continuous(sec.axis = dup_axis(~ .)) +  
  labs(y = NULL)
```

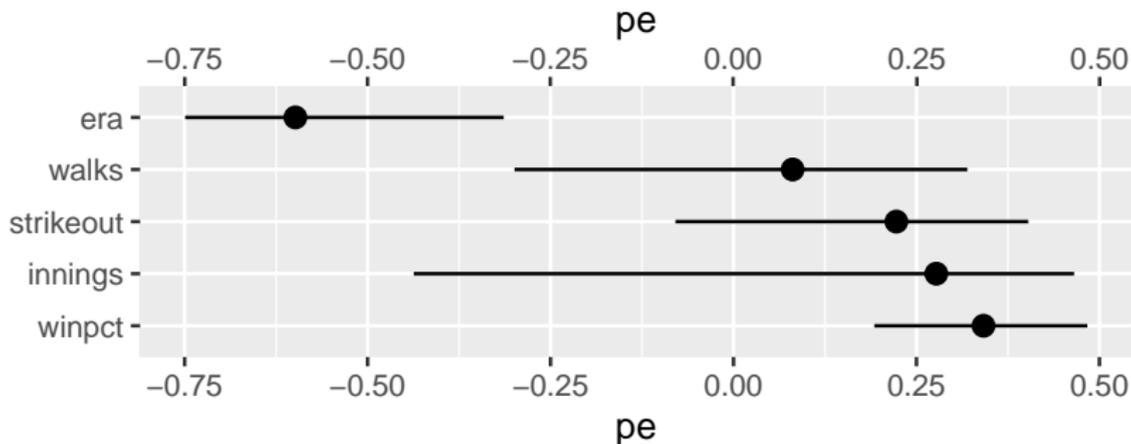


Ropeladder exercise: Cy Young award

4. How can we sort the covariates according to their effect sizes?

▶ `fct_reorder()` from `forcats` package (in `tidyverse`)

```
cyyoungFD %>%  
  filter(model == "m1") %>%  
  ggplot(aes(y = fct_reorder(covariate, pe, .desc = TRUE),  
            x = pe, xmax = upper, xmin = lower)) +  
  geom_pointrangeh() +  
  scale_x_continuous(sec.axis = dup_axis(~ .)) +  
  labs(y = NULL)
```

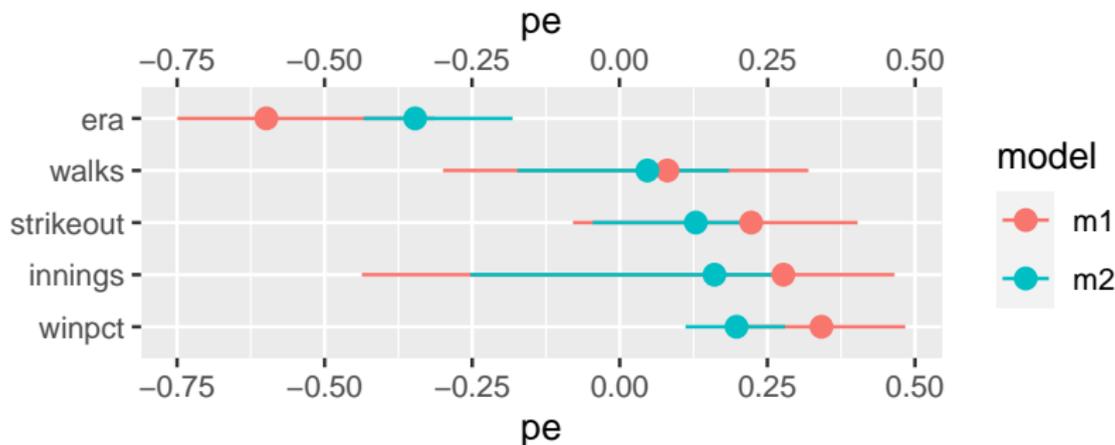


Ropeladder exercise: Cy Young award

5. How can we juxtapose two models' results effectively?

- ▶ If you simply map model to colour...

```
ggplot(cyyoungFD, aes(y = fct_reorder(covariate, pe, .desc = TRUE),  
  x = pe, xmax = upper, xmin = lower,  
  colour = model)) +  
  geom_pointrangeh() +  
  scale_x_continuous(sec.axis = dup_axis(~ .)) +  
  labs(y = NULL)
```

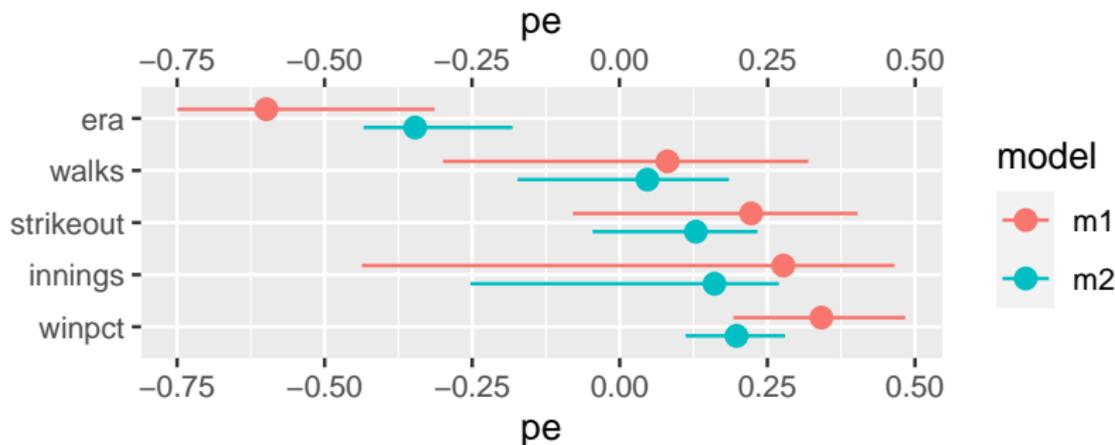


Ropeladder exercise: Cy Young award

5. How can we juxtapose two models' results effectively?

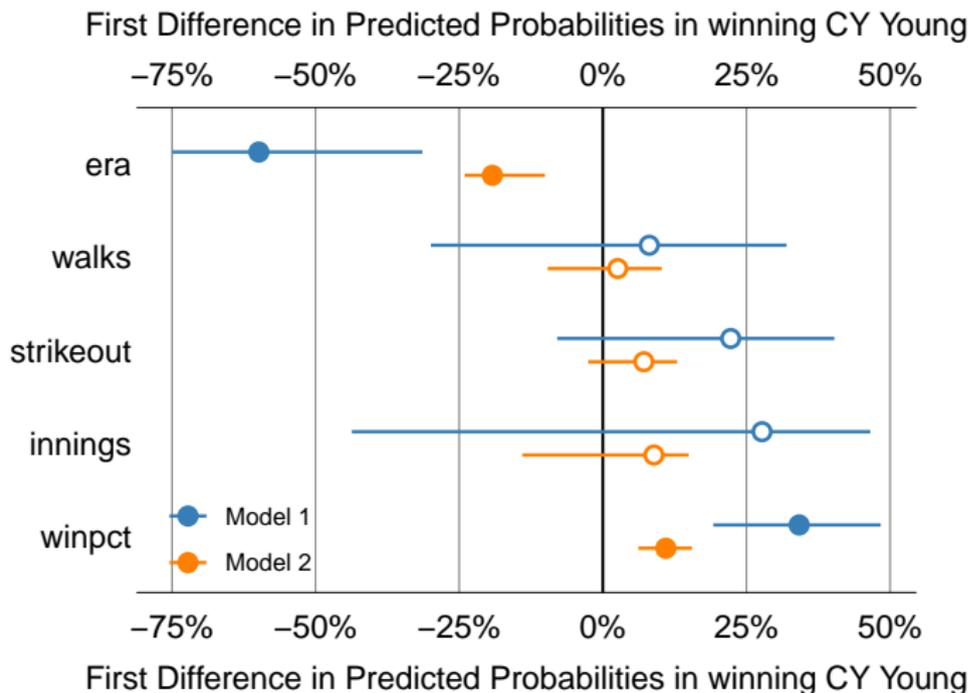
- ▶ Use `position_dodge2v` inside `geom_pointrange()`

```
ggplot(cyyoungFD, aes(y = fct_reorder(covariate, pe, .desc = TRUE),  
                      x = pe, xmax = upper, xmin = lower,  
                      colour = model)) +  
  geom_pointrangeh(position = position_dodge2v(height = 0.7)) +  
  scale_x_continuous(sec.axis = dup_axis(~.)) +  
  labs(y = NULL)
```



Ropeladder exercise: Cy Young award

- ▶ Remaining challenge: How can we indicate statistical non-significance using white-filled circles?



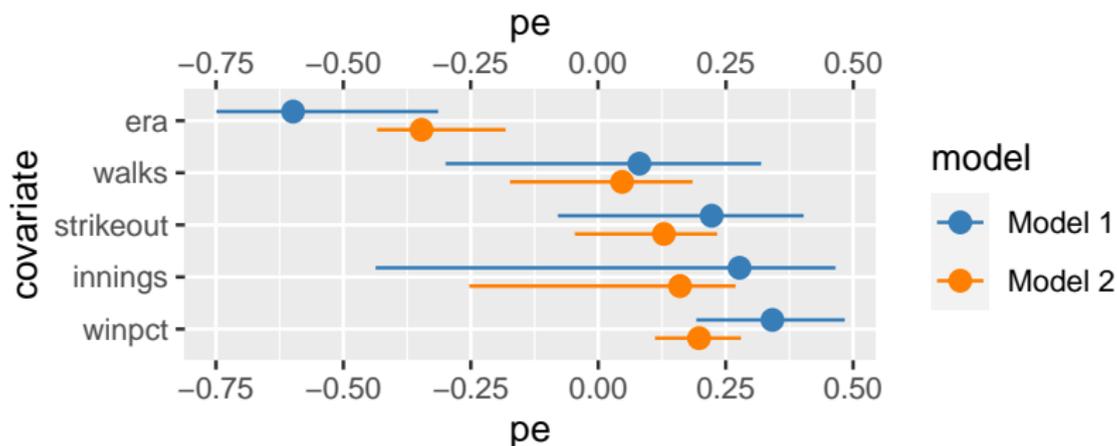
Ropeladder exercise: Cy Young award

```
# Wrangle data before visualization
cyyoungFD <- cyyoungFD %>%
  mutate(covariate = fct_reorder(covariate, pe, .desc = TRUE),
         model = case_when(model == "m1" ~ "Model 1",
                          model == "m2" ~ "Model 2"))

# Get nice colors
brewer <- brewer.pal(9, "Set1")
blue <- brewer[2]
orange <- brewer[5]
```

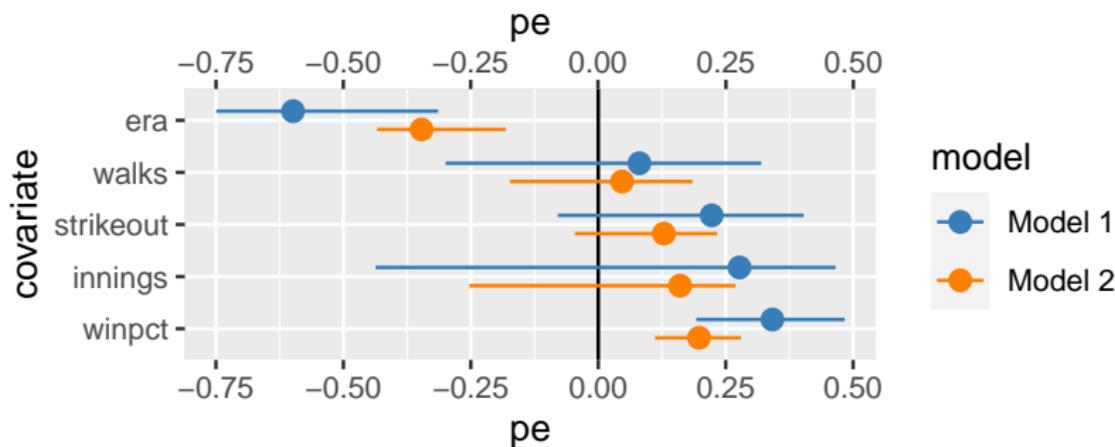
Ropeladder exercise: Cy Young award

```
ggplot(cyyoungFD, aes(y = covariate, x = pe, xmax = upper, xmin = lower,
                      colour = model)) +
  geom_pointrangeh(position = position_dodge2v(height = 0.7)) +
  scale_colour_manual(values = c(blue, orange)) +
  scale_x_continuous(sec.axis = dup_axis(~ .))
```



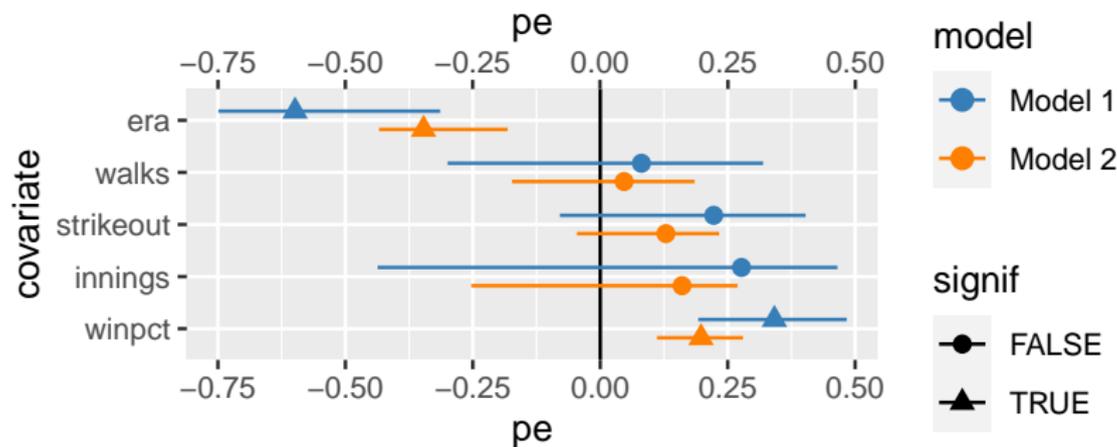
Ropeladder exercise: Cy Young award

```
ggplot(cyyoungFD, aes(y = covariate, x = pe, xmax = upper, xmin = lower,
                      colour = model)) +
  geom_vline(xintercept = 0) +
  geom_pointrangeh(position = position_dodge2v(height = 0.7)) +
  scale_colour_manual(values = c(blue, orange)) +
  scale_x_continuous(sec.axis = dup_axis(~.))
```



Ropeladder exercise: Cy Young award

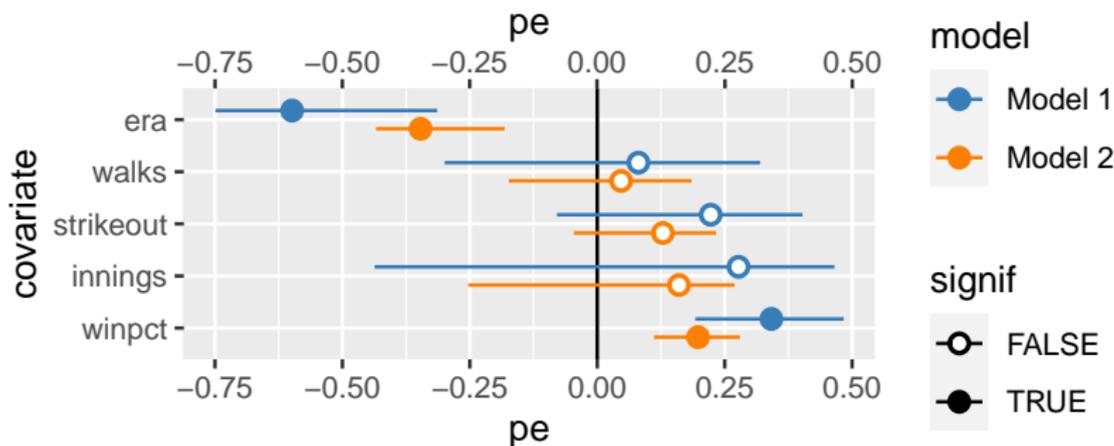
```
ggplot(cyyoungFD, aes(y = covariate, x = pe, xmax = upper, xmin = lower,
                      colour = model, shape = signif, fill = signif)) +
  geom_vline(xintercept = 0) +
  geom_pointrangeh(position = position_dodge2v(height = 0.7)) +
  scale_colour_manual(values = c(blue, orange)) +
  scale_x_continuous(sec.axis = dup_axis(~.))
```



Ropeladder exercise: Cy Young award

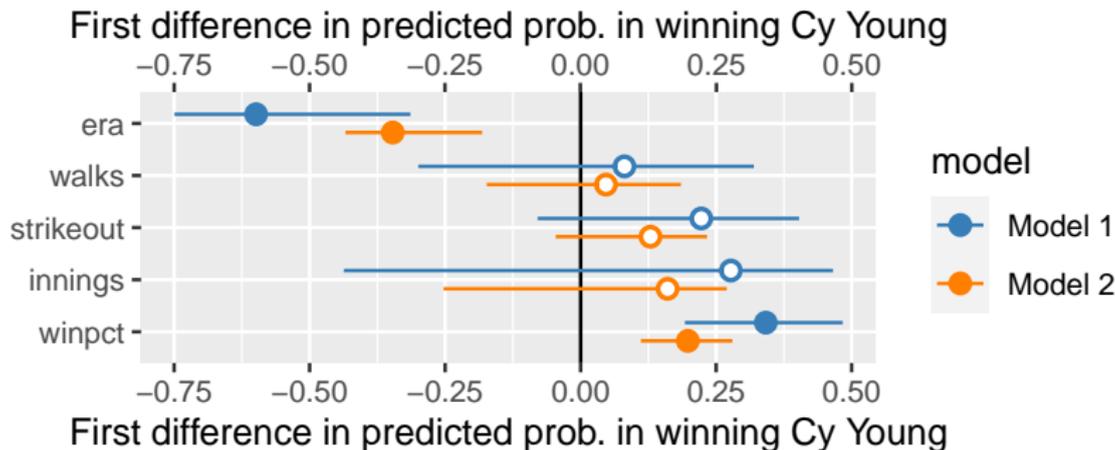
- ▶ See all possible shapes [here](#)
- ▶ 21 = fillable circle; 19 = solid (non-fillable) circle

```
ggplot(cyyoungFD, aes(y = covariate, x = pe, xmax = upper, xmin = lower,
                      colour = model, shape = signif, fill = signif)) +
  geom_vline(xintercept = 0) +
  geom_pointrangeh(position = position_dodge2v(height = 0.7)) +
  scale_colour_manual(values = c(blue, orange)) +
  scale_shape_manual(values = c(21, 19)) + #Non-signif-> fillable circle(21)
  scale_fill_manual(values = c("white", NA)) + #Non-signif-> fill it w. white
  scale_x_continuous(sec.axis = dup_axis(~.))
```



Ropeladder exercise: Cy Young award

```
ggplot(cyyoungFD, aes(y = covariate, x = pe, xmax = upper, xmin = lower,
                      colour = model, shape = signif, fill = signif)) +
  geom_vline(xintercept = 0) +
  geom_pointrangeh(position = position_dodge2v(height = 0.7)) +
  scale_colour_manual(values = c(blue, orange)) +
  scale_shape_manual(values = c(21, 19)) +
  scale_fill_manual(values = c("white", NA)) +
  scale_x_continuous(sec.axis = dup_axis(~ .)) +
  guides(shape = "none", fill = "none") +
  labs(y = NULL, x = "First difference in predicted prob. in winning Cy Young")
```

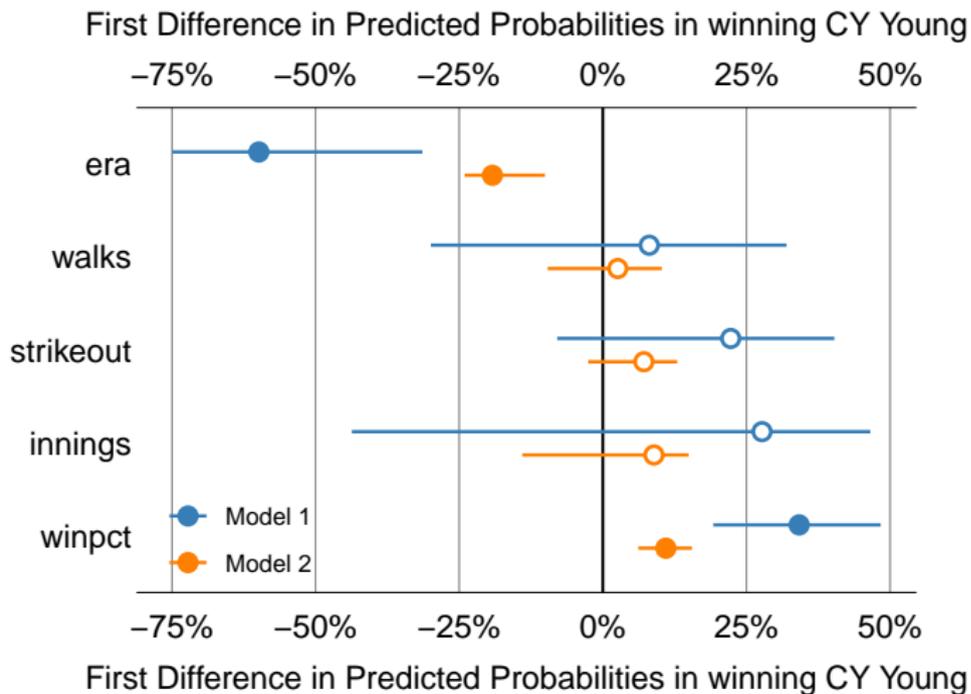


Ropeladder exercise: Cy Young award

Full code:

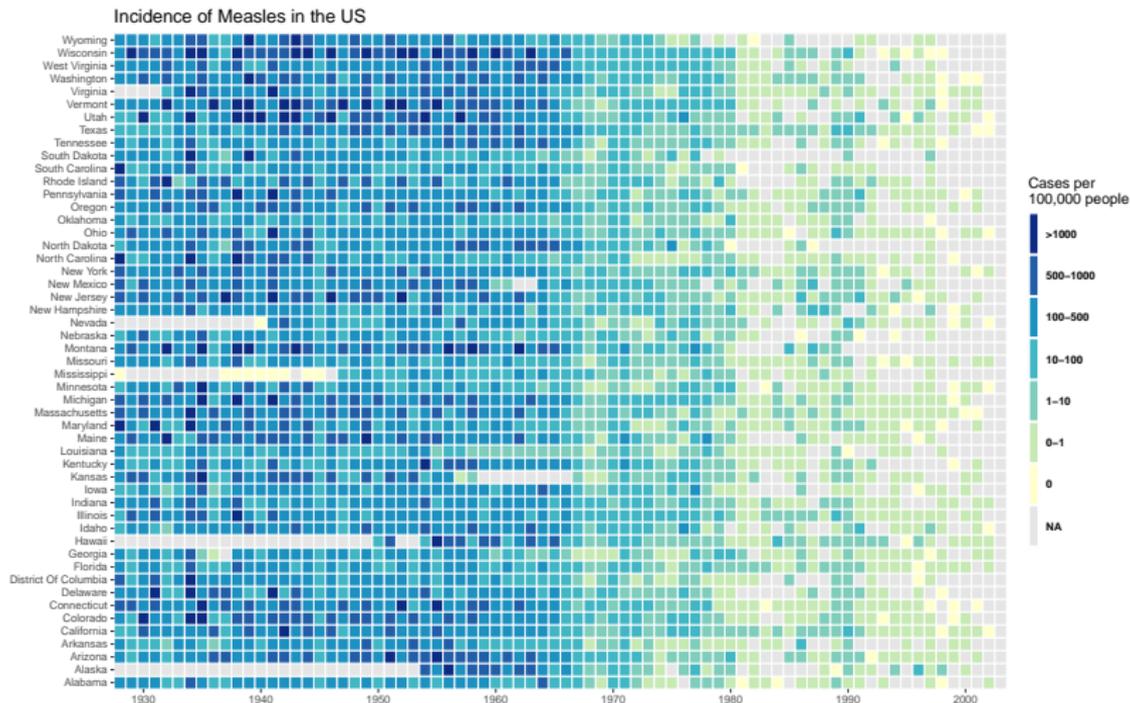
```
ggplot(cyyoungFD, aes(y = covariate, x = pe, xmax = upper, xmin = lower,
                      colour = model, shape = signif, fill = signif)) +
  geom_vline(xintercept = 0) +
  geom_pointrangeh(position = position_dodge2v(height = 0.7)) +
  scale_colour_manual(values = c(blue, orange)) +
  scale_shape_manual(values = c(21, 19)) +
  scale_fill_manual(values = c("white", NA)) +
  scale_x_continuous(sec.axis = dup_axis(~ .), labels = scales::percent) +
  guides(shape = "none", fill = "none") +
  labs(y = NULL, x = "First difference in predicted prob. in winning Cy Young")
theme_caviz_vgrid +
theme(legend.position = c(0.13, 0.125), axis.ticks.x = element_blank())
```

Ropeladder exercise: Cy Young award



Heatmap exercise: scaling colour and fill

- ▶ This example is taken from Francis (2019)
 - ▶ Data: Measles level 1 incidence (cases per 100,000 people)
 - ▶ Coverage: 51 US states; 76 years (3,876 observations)



Heatmap exercise: scaling colour and fill

```
# Load data
```

```
measles <- read_csv("data/measles.csv")
```

```
## Rows: 3876 Columns: 4
```

```
## -- Column specification -----
```

```
## Delimiter: ","
```

```
## chr (2): state, countCat
```

```
## dbl (2): year, count
```

```
##
```

```
## i Use 'spec()' to retrieve the full column specification
```

```
## i Specify the column types or set 'show_col_types = FALSE'
```

```
head(measles)
```

```
## # A tibble: 6 x 4
```

```
##   year state      count countCat
```

```
##   <dbl> <chr>      <dbl> <chr>
```

Heatmap exercise: scaling colour and fill

```
# Factorize variables
levels <- rev(c("0", "0-1", "1-10", "10-100", "100-500", "500-1000", ">1000"))

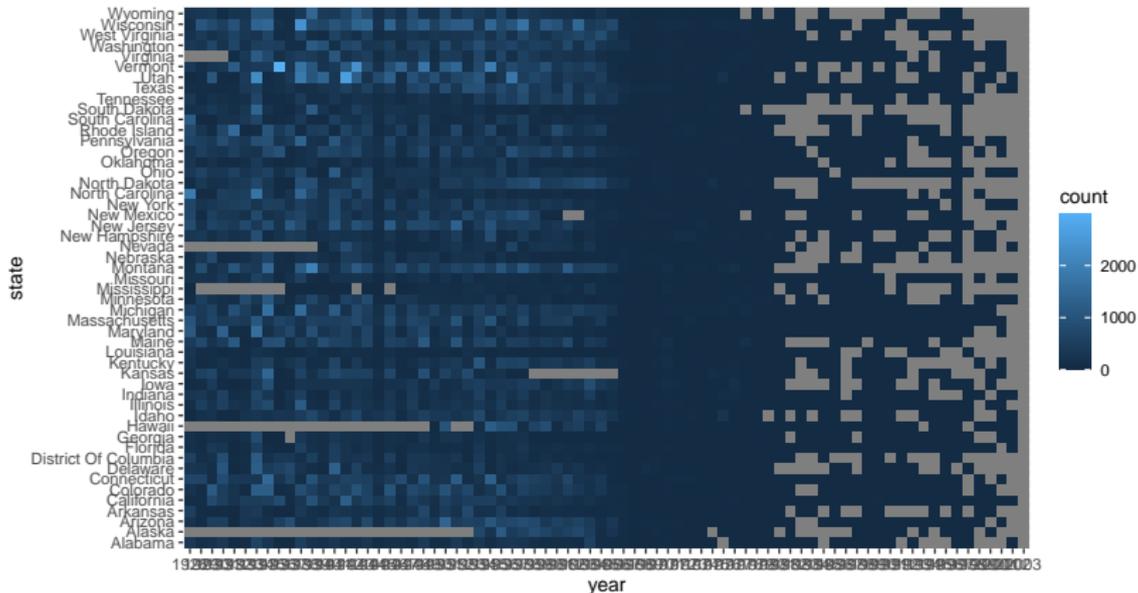
measles <- measles %>%
  mutate(
    year = factor(year),
    state = factor(state),
    countCat = factor(countCat, levels = levels)
  )

head(measles)
```

```
## # A tibble: 6 x 4
##   year  state    count countCat
##   <dbl> <fct>    <dbl> <fct>
## 1 1928  Alabama  335.  100-500
## 2 1928  Alaska    NA    <NA>
## 3 1928  Arizona   201.  100-500
## 4 1928  Arkansas  482.  100-500
## 5 1928  California 69.2  10-100
## 6 1928  Colorado  207.  100-500
```

Heatmap exercise: scaling colour and fill

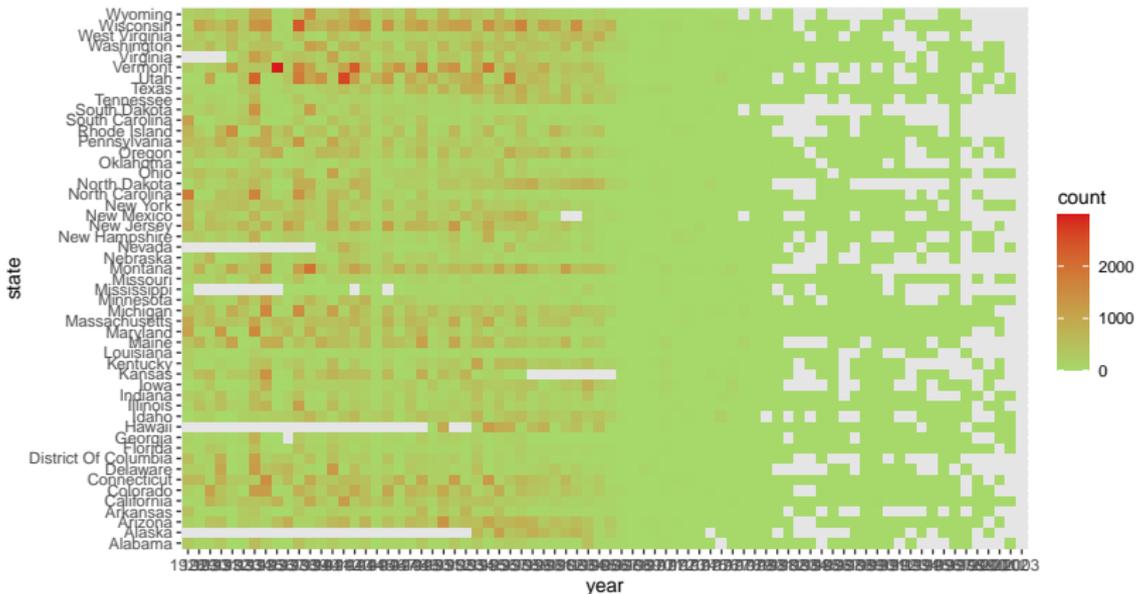
```
ggplot(measles, aes(x = year, y = state, fill = count))+  
  geom_tile()
```



Heatmap exercise: scaling colour and fill

- ▶ For continuous color values, use `scale_fill_gradient`
- ▶ To pick colors, reference [here](#)

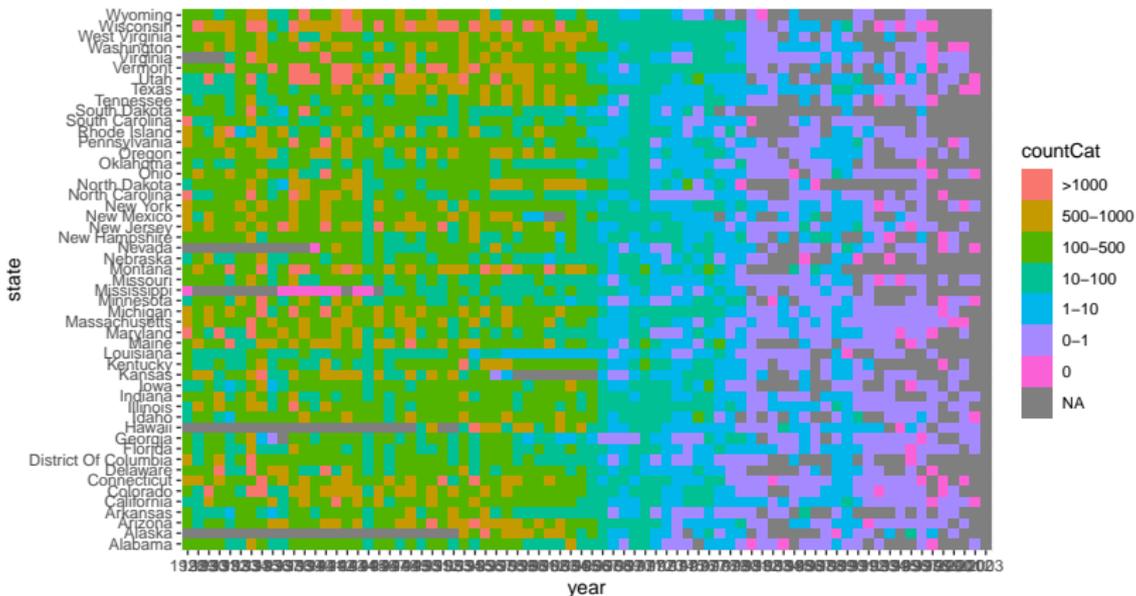
```
ggplot(measles, aes(x = year, y = state, fill = count)) +  
  geom_tile() +  
  scale_fill_gradient(high = "#d7191c", low = "#a6d96a", na.value = "grey90")
```



Heatmap exercise: scaling colour and fill

- ▶ Plot the categorical variable, countCat, instead

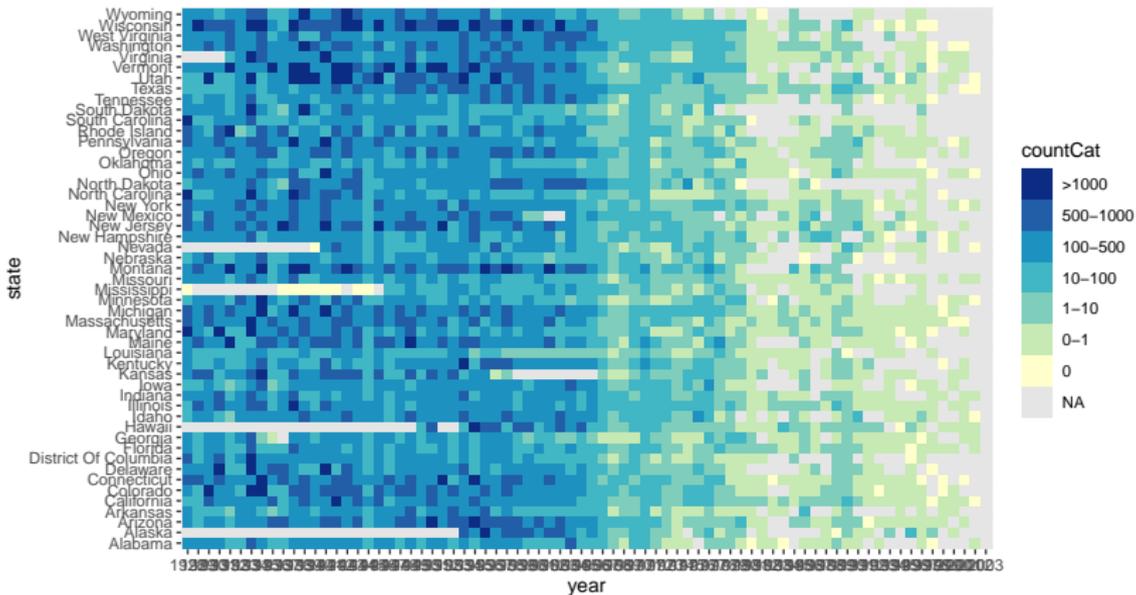
```
ggplot(measles, aes(x = year, y = state, fill = countCat)) +  
  geom_tile()
```



Heatmap exercise: scaling colour and fill

- ▶ For categorical color values, use `scale_fill_brewer`
- ▶ Run `RColorBrewer::display.brewer.all()` for all palettes

```
ggplot(measles, aes(x = year, y = state, fill = countCat)) +  
  geom_tile() +  
  scale_fill_brewer(palette = "YlGnBu", direction = -1, na.value = "grey90")
```

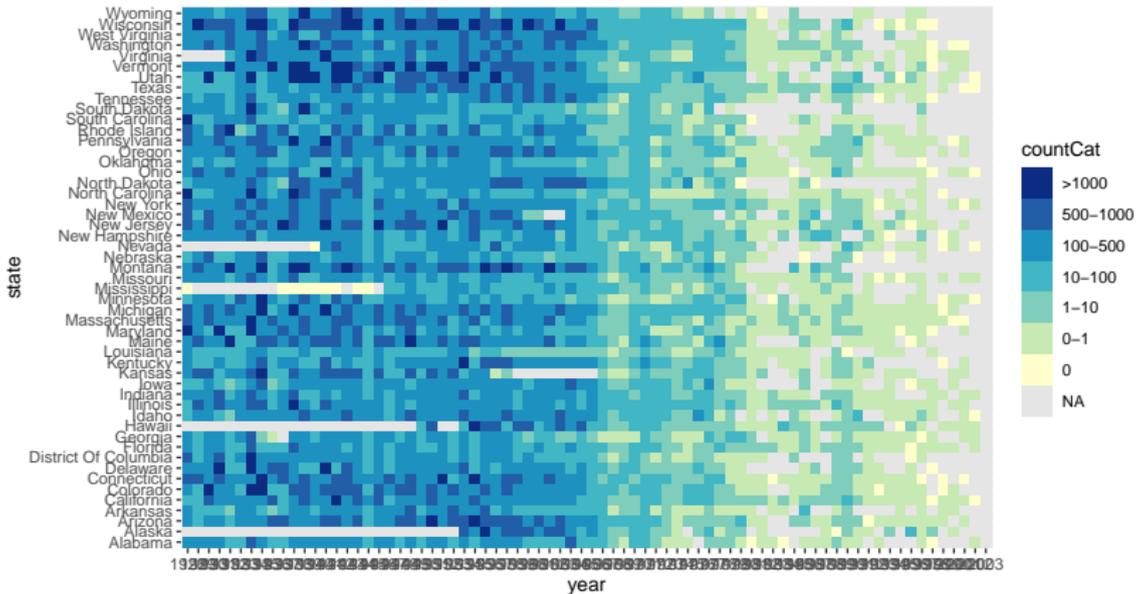


Heatmap exercise: scaling colour and fill

- ▶ Alternatively, use `RColorBrewer` and `scale_fill_manual`

```
blues <- rev(brewer.pal(7, "YlGnBu"))
```

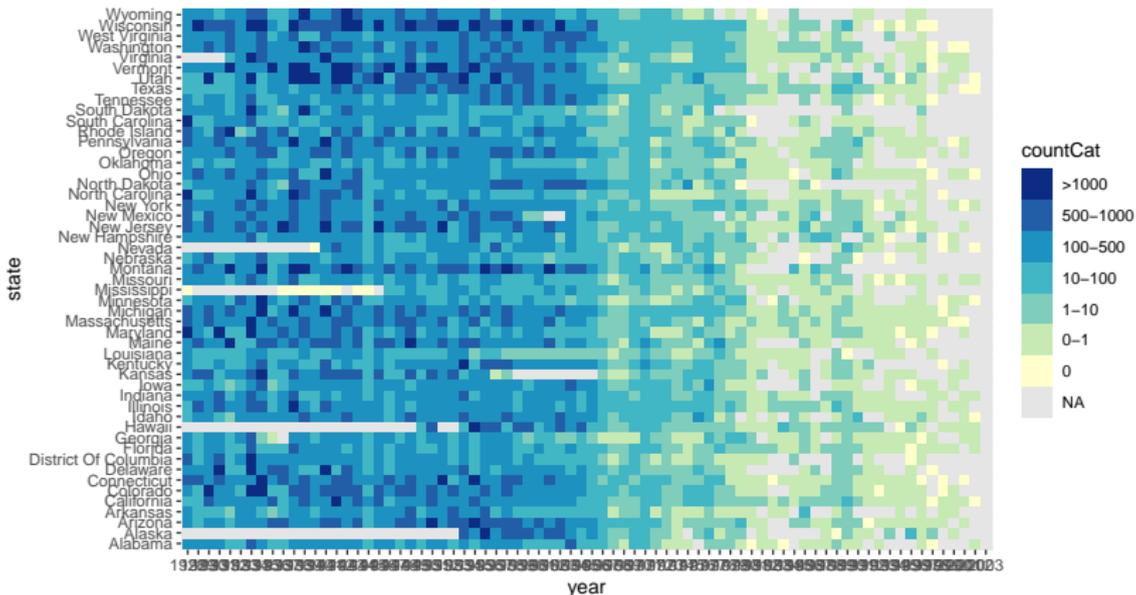
```
ggplot(measles, aes(x = year, y = state, fill = countCat)) +  
  geom_tile() +  
  scale_fill_manual(values = blues, na.value = "grey90")
```



Heatmap exercise: scaling colour and fill

- Use cluster analysis to sort the states

```
ggplot(measles, aes(x = year, y = state, fill = countCat)) +  
  geom_tile() +  
  scale_fill_manual(values = blues, na.value = "grey90")
```

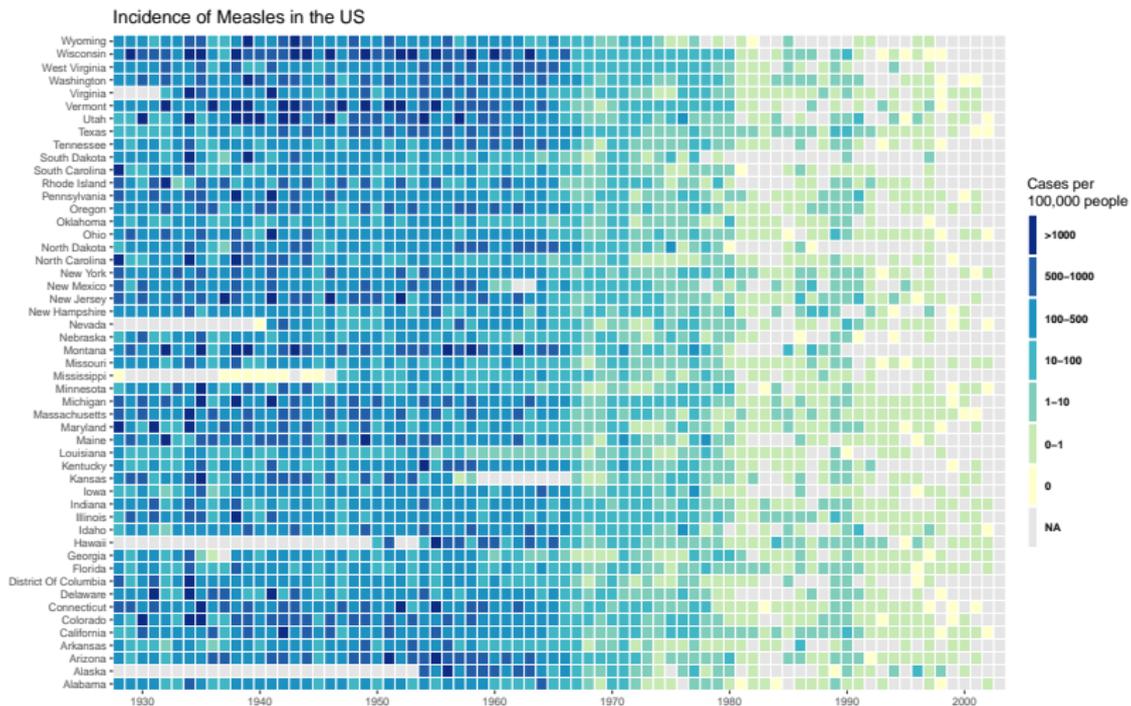


Heatmap exercise: scaling colour and fill

- ▶ Final product; see more details [here](#):

```
hm <-  
ggplot(measles, aes(x = year, y = state, fill = countCat)) +  
  # add border white colour of line thickness 0.25  
  geom_tile(colour = "white", size = 0.25) +  
  # scale fill with "YlGnBu" palette  
  scale_fill_brewer(palette = "YlGnBu", direction = -1, na.value = "grey90") +  
  # define new breaks on x-axis  
  scale_x_discrete(expand = c(0, 0), breaks = seq(1930, 2000, 10)) +  
  # remove extra space  
  scale_y_discrete(expand = c(0, 0)) +  
  # set a base size for all fonts  
  theme_grey(base_size = 8) +  
  # theme options  
  theme(  
    # bold font for legend text  
    legend.text = element_text(face = "bold"),  
    # set thickness of axis ticks  
    axis.ticks = element_line(size = 0.4),  
    # remove plot background  
    plot.background = element_blank(),  
    # remove plot border  
    panel.border = element_blank(),  
    # reshape the legend keys  
    legend.key.height = grid::unit(0.8, "cm"),  
    legend.key.width = grid::unit(0.2, "cm")  
  ) +  
  # legend title  
  guides(fill = guide_legend(title = "Cases per\n100,000 people")) +  
  # remove x and y axis labels; define title  
  labs(x = NULL, y = NULL, title = "Incidence of Measles in the US")
```

Heatmap exercise: scaling colour and fill



ggplot2 extension packages

- ▶ With ggplot2 as the core package, an ecosystem of supporting packages have been developed

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 - ▶ See the gallery [here](#)

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- ▶ I highlight several packages

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 - ▶ We've used: `ggrepel`, `ggstance`

ggplot2 extension packages

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- ▶ I highlight several packages
 - ▶ We've used: `ggrepel`, `ggstance`
 - ▶ `gghighlight`

ggplot2 extension packages

- ▶ With ggplot2 as the core package, an ecosystem of supporting packages have been developed
 - ▶ See the gallery [here](#)
- ▶ I highlight several packages
 - ▶ We've used: `ggrepel`, `ggstance`
 - ▶ `gghighlight`
 - ▶ `ggridges`

ggplot2 extension packages

- ▶ With ggplot2 as the core package, an ecosystem of supporting packages have been developed
 - ▶ See the gallery [here](#)
- ▶ I highlight several packages
 - ▶ We've used: `ggrepel`, `ggstance`
 - ▶ `gghighlight`
 - ▶ `ggribes`
 - ▶ `cowplot`