HW6: Markdown file

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Problem 1

The Washington Post has gathered data on homicides in 50 large U.S. cities and made the data available through a GitHub repository here. You can read their accompanying article here.

```
raw_homicide_data =
  read_csv("./data/homicide-data.csv") |>
  janitor::clean_names()
```

```
## Rows: 52179 Columns: 12
## ── Column specification ────────────────────────────────────────────────────────
## Delimiter: ","
## chr (9): uid, victim_last, victim_first, victim_race, victim_age, victim_sex...
## dbl (3): reported_date, lat, lon
##
## ℹ Use `spec()` to retrieve the full column specification for this data.
## ℹ Specify the column types or set `show_col_types = FALSE` to quiet this message
```

Data Process

Create a city_state variable (e.g. "Baltimore, MD"), and a binary variable indicating whether the homicide is solved.

Omit cities Dallas, TX; Phoenix, AZ; and Kansas City, MO – these don't report victim race. Also omit Tulsa, AL – this is a data entry mistake. For this problem, limit your analysis those for whom victim_race is white or black. Be sure that victim_age is numeric.

- Omit: Dallas, TX, Phoeniz, AZ, Kansas City, MO, and Tulsa Al
- Include only when victim_race == "white" or "black"
- victim_age has to be numeric

```
processs_homicide_data =
  raw_homicide_data |>

  #Create variable "city_state" which is a concatenation of city + state separated
  mutate(city_state = paste(city, state, sep = ", ")) |>

  #Omit Dallas, Phoenix, Kansas Ciry, and Tulsa
  filter(!grepl("Dallas, TX|Phoenix, AZ|Kansas City, MO|Tulsa, AL", city_state)) |>

  #Include victim_race == "white" or "black"
  filter(grepl("White|Black", victim_race)) |>

  #victim_age is numeric
  mutate(victim_age = as.numeric(victim_age))
```

```
## Warning: There was 1 warning in `mutate()`.
## ℹ In argument: `victim_age = as.numeric(victim_age)`.
## Caused by warning:
## ! NAs introduced by coercion
```

For the city of Baltimore, MD, use the glm function…

to fit a *logistic regression* with resolved vs unresolved as the outcome and victim age, sex and race as predictors.

- Outcome: Resolved vs. Unresolved (1 or 0 Binary)
- PRedictors
  - Age: Continuous
  - Sex: Binary
  - Race: Binary

Resolved vs. Unresolved (Binary Var)

```
#Process Data
resolved_data =
  processs_homicide_data |>

  #create binary variable that is 1 or 0 dpeending on if resolved or not
  mutate(resolve = ifelse(disposition %in% c("Closed without arrest", "Open/No arres

  #NOTE: glm is able to automatically define binary despite the variables being defi
```

Logistic Regression

```
homicide_logistic =
  resolved_data |>
```

Tidy

Save the output of glm as an R object; apply the broom::tidy to this object;

```
#Extract all parameter estimates from logistic regression
homicide_param_est =
  homicide_logistic |>
  broom::tidy() |>
  mutate(OR = exp(estimate), OR_CI = exp(confint(homicide_logistic))) |>
  select(term, log_OR = estimate, OR, OR_CI, p.value)
```

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

OR of Male vs. Female

Obtain the estimate and confidence interval of the adjusted odds ratio for solving homicides comparing male victims to female victims keeping all other variables fixed.

```
homicide_param_est_male_female =
  homicide_param_est |>
  filter(grepl("victim_sexMale", term))
```

- OR Estimate = 0.6028675
  - 95% CI: (0.568848, 0.6388225)

Now run glm for each of the cities in your dataset,

and extract the adjusted odds ratio (and CI) for solving homicides comparing male victims to female victims. Do this within a “tidy” pipeline, making use of purrr::map, list columns, and unnest as necessary to create a dataframe with estimated ORs and CIs for each city.

Broom function

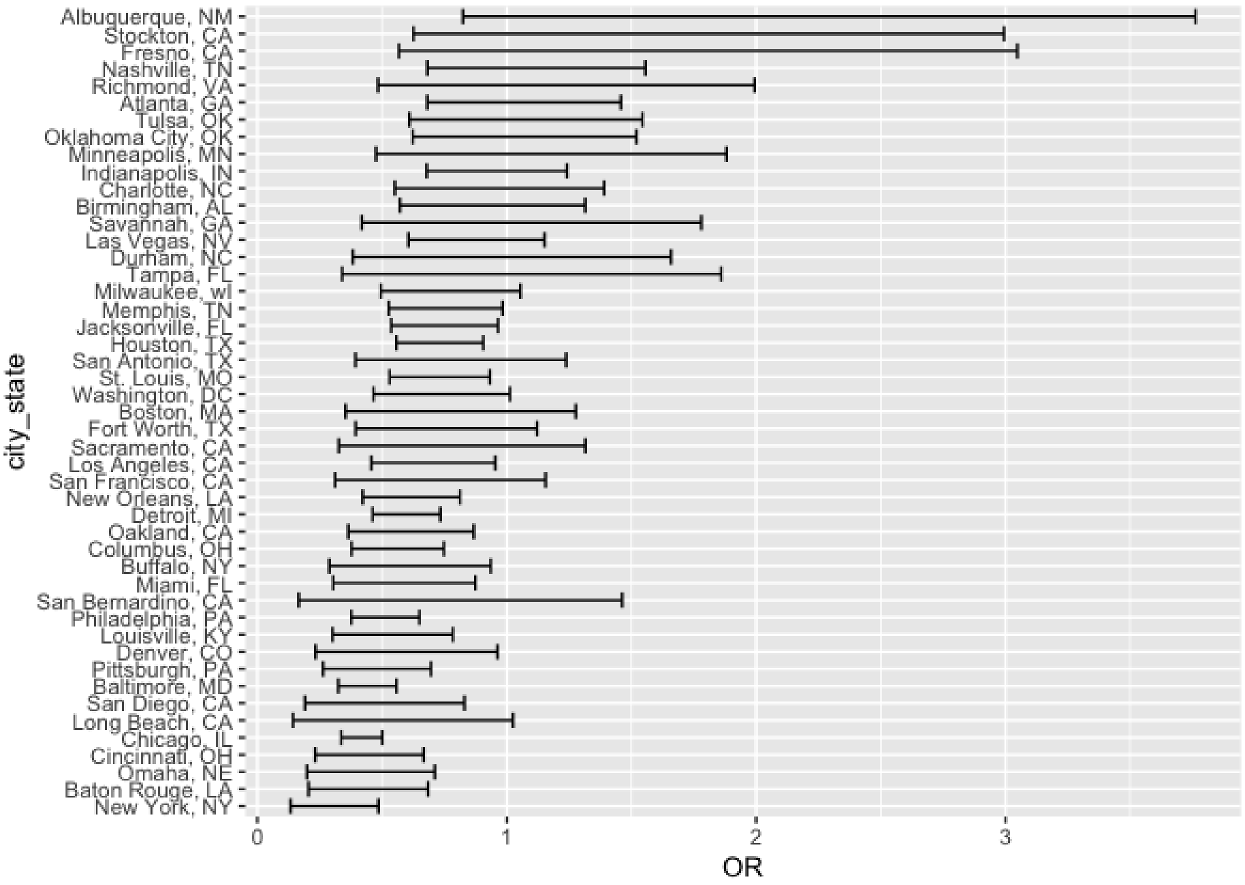
```
broom_conf = function(df) {
  broom::tidy(df, conf.int = TRUE)
}
```

```
citystate_OR_CI_hom =
  resolved_data |>
  nest(data = -city_state) |>
  mutate(
    models = map(data, \(df) glm(resolve ~ victim_age + victim_race + victim_sex, da
    results = map(models, broom_conf)) |>
  select(-data, -models) |>
  unnest(results) |>
  mutate(OR = exp(estimate), lowCI = exp(conf.low), uppCI = exp(conf.high)) |>
  filter(grepl("victim_sexMale", term)) |>
  select(city_state, OR, lowCI, uppCI)
```

```
## Warning: There were 44 warnings in `mutate()`.
## The first warning was:
## ℹ In argument: `results = map(models, broom_conf)`.
## Caused by warning:
## ! glm.fit: fitted probabilities numerically 0 or 1 occurred
## ℹ Run `dplyr::last_dplyr_warnings()` to see the 43 remaining warnings.
```

Create a plot that shows the estimated ORs and CIs for each city. Organize cities according to estimated OR, and comment on the plot.

```
citystate_OR_CI_hom[order(citystate_OR_CI_hom$OR),] |>
  mutate(city_state = factor(city_state, levels = city_state)) |>
  ggplot(aes(x = city_state, y = OR)) +
  geom_errorbar(aes(ymin = lowCI, ymax = uppCI))+
  coord_flip()
```



Problem 2

```
# Central Park Weather Data
weather_df =
  rnoaa::meteo_pull_monitors(
    c("USW00094728"),
    var = c("PRCP", "TMIN", "TMAX"),
    date_min = "2022-01-01",
    date_max = "2022-12-31") |>
  mutate(
    name = recode(id, USW00094728 = "CentralPark_NY"),
    tmin = tmin / 10,
    tmax = tmax / 10) |>
  select(name, id, everything())
```

```
## Registered S3 method overwritten by 'hoardr':
##   method           from
##   print.cache_info httr

## using cached file: /Users/kl/Library/Caches/org.R-project.R/R/rnoaa/noaa_ghcnd/US

## date created (size, mb): 2023-09-28 13:49:36.87383 (8.524)
## file min/max dates: 1869-01-01 / 2022-09-30
```

The boostrap is helpful when you’d like to perform inference for a parameter / value / summary that doesn’t have an easy-to-write-down distribution in the usual repeated sampling framework.

We’ll focus on a simple linear regression with *tmax* as the response with *tmin* and *prcp* as the predictors, and are interested in the distribution of two quantities estimated from these data: r^2 + log(b1 * b2)

Bootstrap

Use 5000 bootstrap samples and, for each bootstrap sample, produce estimates of these two quantities. Plot the distribution of your estimates, and describe these in words. Using the 5000 bootstrap estimates, identify the 2.5% and 97.5% quantiles to provide a 95% confidence interval for $\hat{r}^2$ and $\log(\hat{\beta}_0 * \hat{\beta}_1)$.

```
weather_boostrap =
  weather_df |>
  select(-name, -id) |>
  modelr::bootstrap(n = 5000) |>
  mutate(
    models = map(strap, \(df) lm(tmax ~ tmin + prcp, data = df) ),
    results_tidy = map(models, broom::tidy),
    results_glance = map(models, broom::glance)) |>
  select(-models) |>
  unnest(results_tidy)
```

r^2 Estimate + Conf. Interval

```
#r^2 estimate plot + CI
r_squared =
  weather_boostrap |>
  select(.id, term, results_glance) |>
  unnest(results_glance) |>
  group_by(.id) |>
  select(r.squared) |>
  distinct()
```

```
## Adding missing grouping variables: `.id`
```

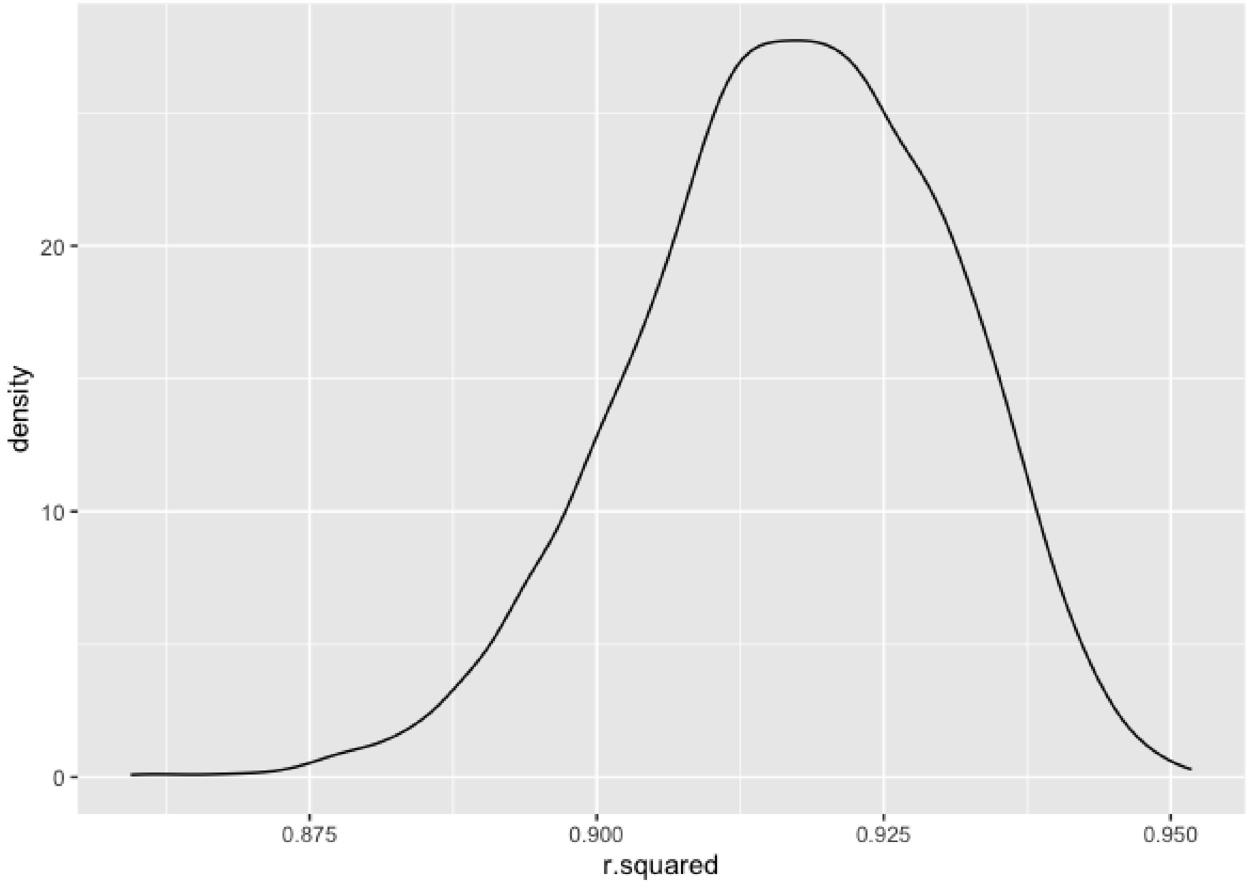
```
zval = qnorm(.975)
r_mean = mean(r_squared$r.squared)
```

```
r_sd = sd(r_squared$r.squared)
count = nrow(r_squared)
me = zval * (r_sd/sqrt(count))
```

- r^2 Mean: 0.9169099
- r^2 95% CI: (0.9165334, 0.9172864)

r^2 plot

```
r_squared |>
  ggplot(aes(x = r.squared)) +
  geom_density()
```

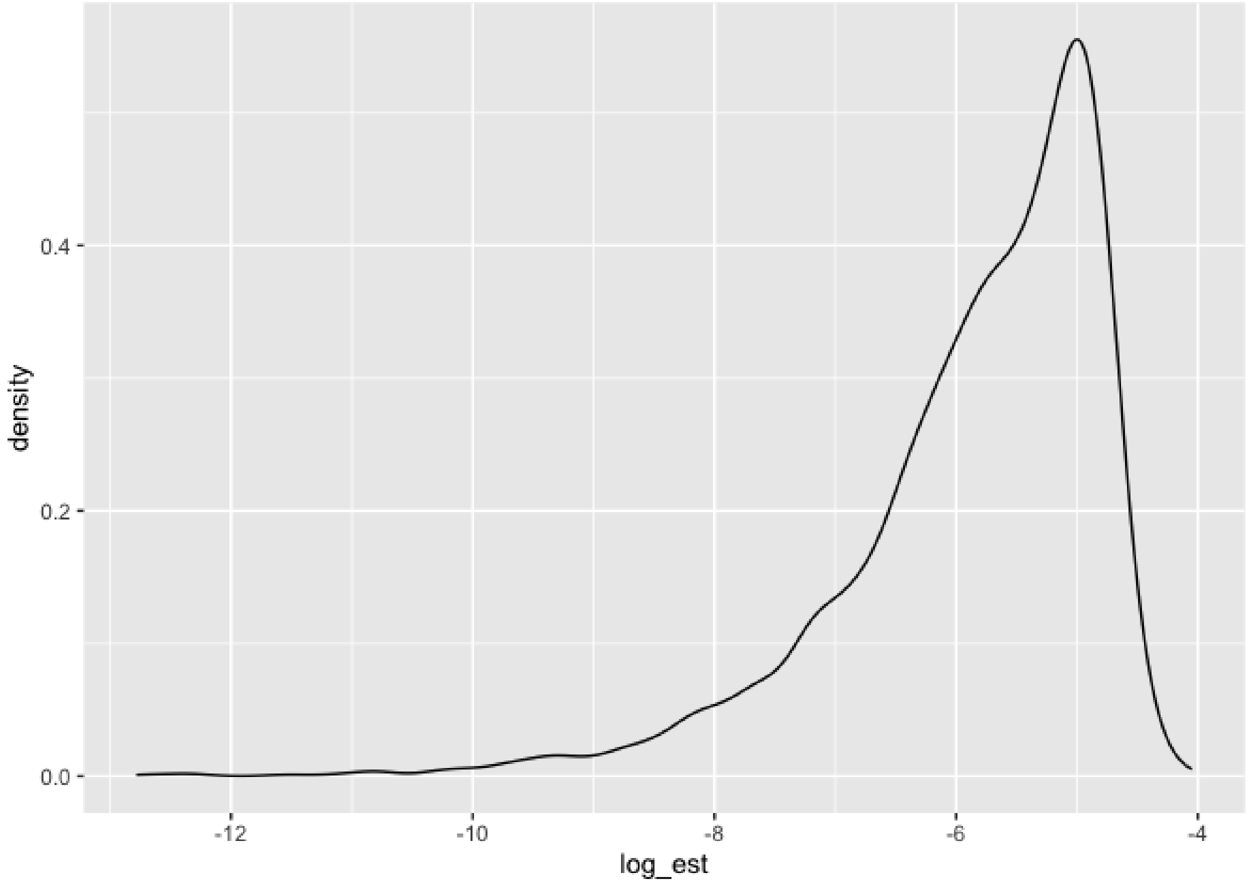


log(beta1 * beta2)

```
log_b1_b2_df =
  weather_boostrap |>
  select(.id, term, estimate) |>
  pivot_wider(
    names_from = term,
    values_from = estimate
  ) |>
  mutate(log_est = log(abs(tmin * prcp)))
```

Plot log(b1 * b2)

```
log_b1_b2_df |>
  ggplot(aes(x = log_est)) +
  geom_density()
```



Problem 3

In this problem, you will analyze data gathered to understand the effects of several variables on a child's birthweight. This dataset, available here, consists of roughly 4000 children and includes the following variables:

Load and clean the data for regression analysis (i.e. convert numeric to factor where appropriate, check for missing data, etc.).

Load

```
raw_birthweight_data =
  read_csv("./data/birthweight.csv") |>
  janitor::clean_names()
```

```
## Rows: 4342 Columns: 20
## ── Column specification ────────────────────────────────────────────────────────
## Delimiter: ","
## dbl (20): babysex, bhead, blength, bwt, delwt, fincome, frace, gaweeks, malf...
##
## ℹ Use `spec()` to retrieve the full column specification for this data.
## ℹ Specify the column types or set `show_col_types = FALSE` to quiet this message
```

Clean

```
birthweight_df =
  raw_birthweight_data |>

  #convert frace to categorical var, convert to factor
  mutate(frace = factor(frace)) |>

  #convert mrace to categorical var, convert to factor
  mutate(mrace = factor(mrace))
```

Propose + Compare your Models

Proposed Model

The proposed model will be a linear regression as the outcome is a continuous variable. - BirthWeight = length, gestational age, sex, mrace, frace - Hypothesis: race of mother/father may act as social factors that may significantly affect birthweight.

```
proposed_model = lm(bwt ~ blength + gaweeks + babysex + mrace + frace, data = birthw
```

Main Effect Model

- BirthWeight = Length at Birth + Gestational Age

```
main_model = lm(bwt ~ blength + gaweeks, data = birthweight_df)
```

Three Way Model

- BirthWeight = Head Circumference, Length, Baby Sex, and All Interactions

```
interaction_model = lm(bwt ~ blength + bhead + babysex + blength:bhead + blength:bab
```

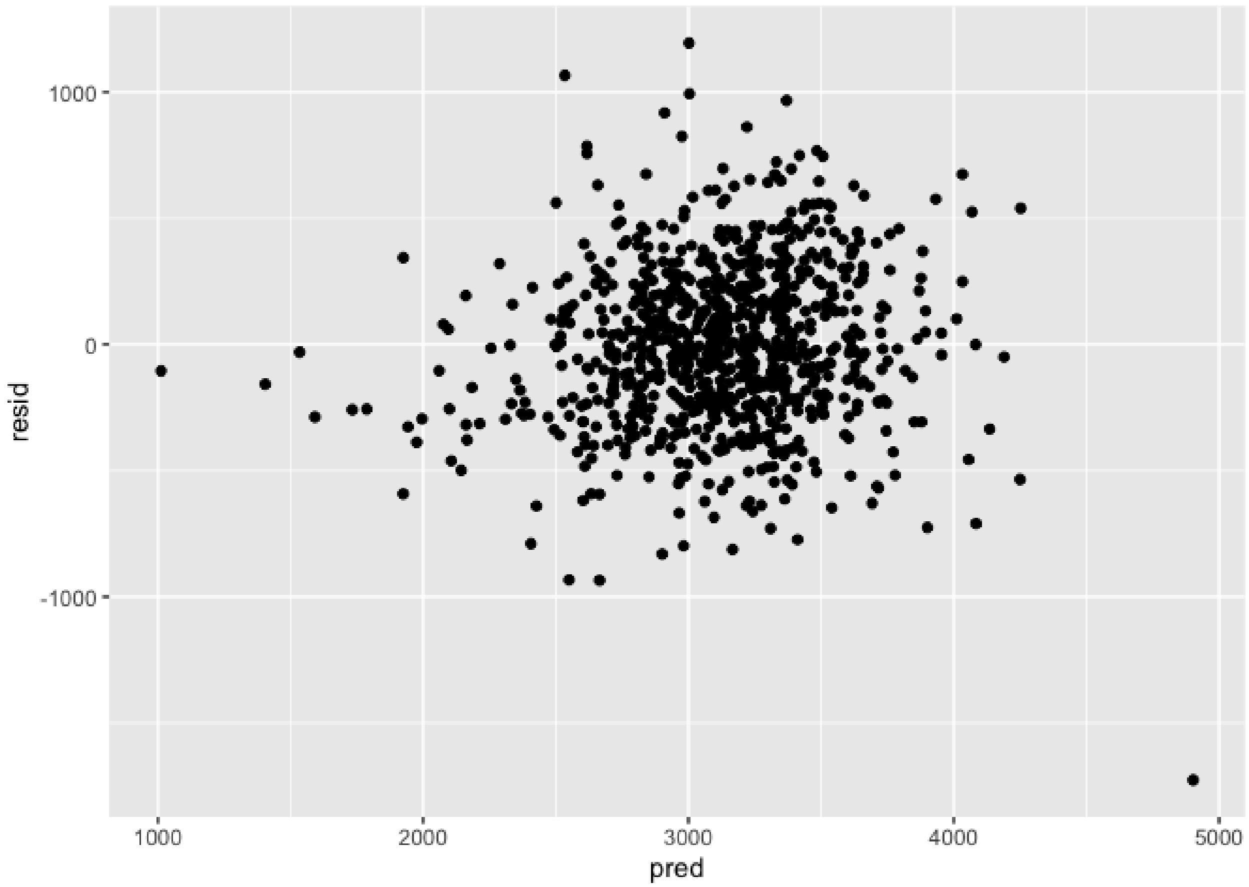
Comparing Models: Residuals vs. Predicted

Create Test/Training Data

```
cv_bwt_df =
  crossv_mc(birthweight_df, 100) |>
  mutate(
    train = map(train, as_tibble),
    test = map(test, as_tibble)) |>
  mutate(
      prop_mod = map(train, \(df) lm(bwt ~ blength + gaweeks + babysex + mrace + fra
      main_mod = map(train, \(df) lm(bwt ~ blength + gaweeks, data = df)),
      inter_mod = map(train, \(df) lm(bwt ~ blength + bhead + babysex + blength:bhea
      ) |>
  mutate(
    rmse_prop = map2_dbl(prop_mod, test, \(mod, df) rmse(model = mod, data = df)),
    rmse_main    = map2_dbl(main_mod, test, \(mod, df) rmse(model = mod, data = df)
    rmse_inter = map2_dbl(inter_mod, test, \(mod, df) rmse(model = mod, data = df))
```

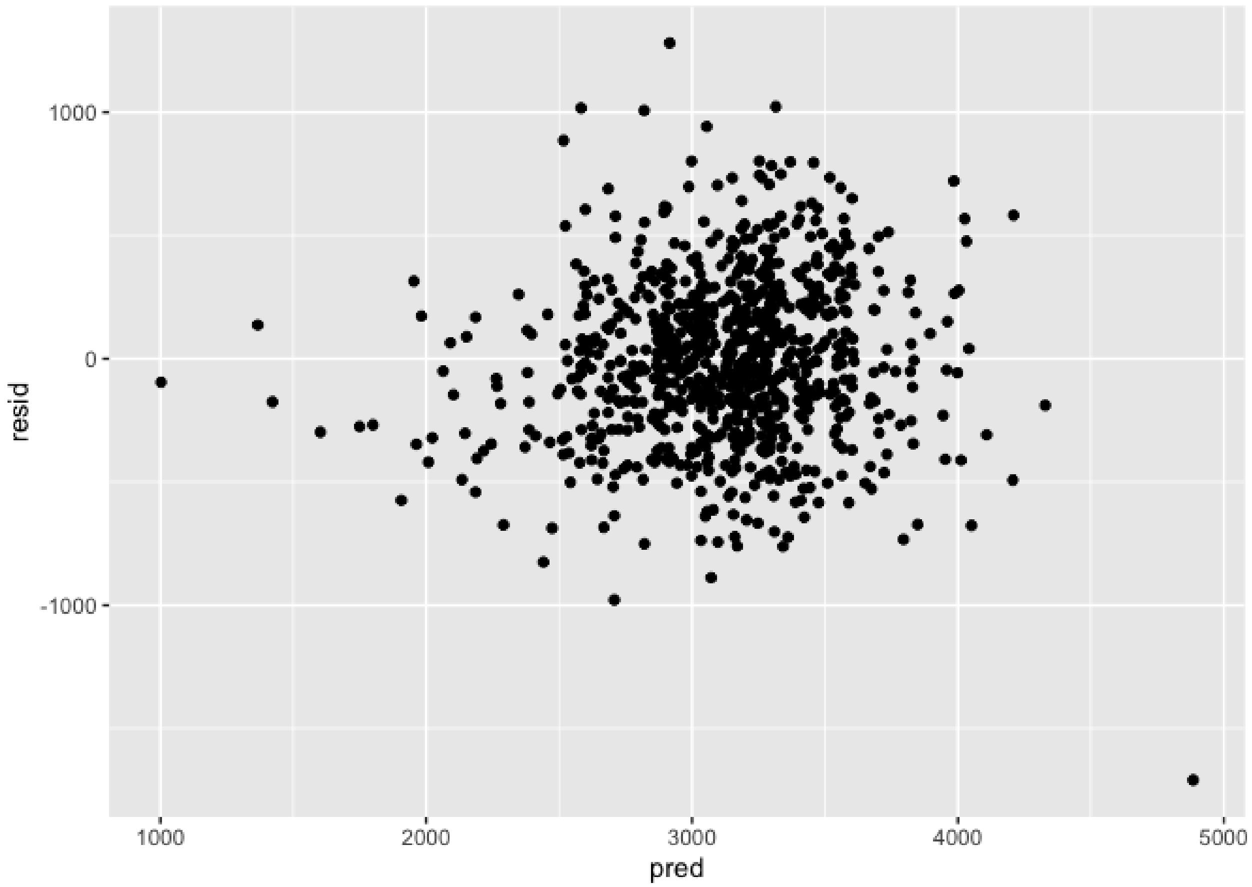
Proposed Model: Residuals vs. Predictors

```
#Take one test sample + plot the predictoed vs. residuals for each sample.
cv_bwt_df |>
  pull(test) |>
  nth(1) |>
  as_tibble() |>
  add_predictions(proposed_model) |>
  add_residuals(proposed_model) |>
  ggplot(aes(x = pred, y = resid)) +
  geom_point()
```



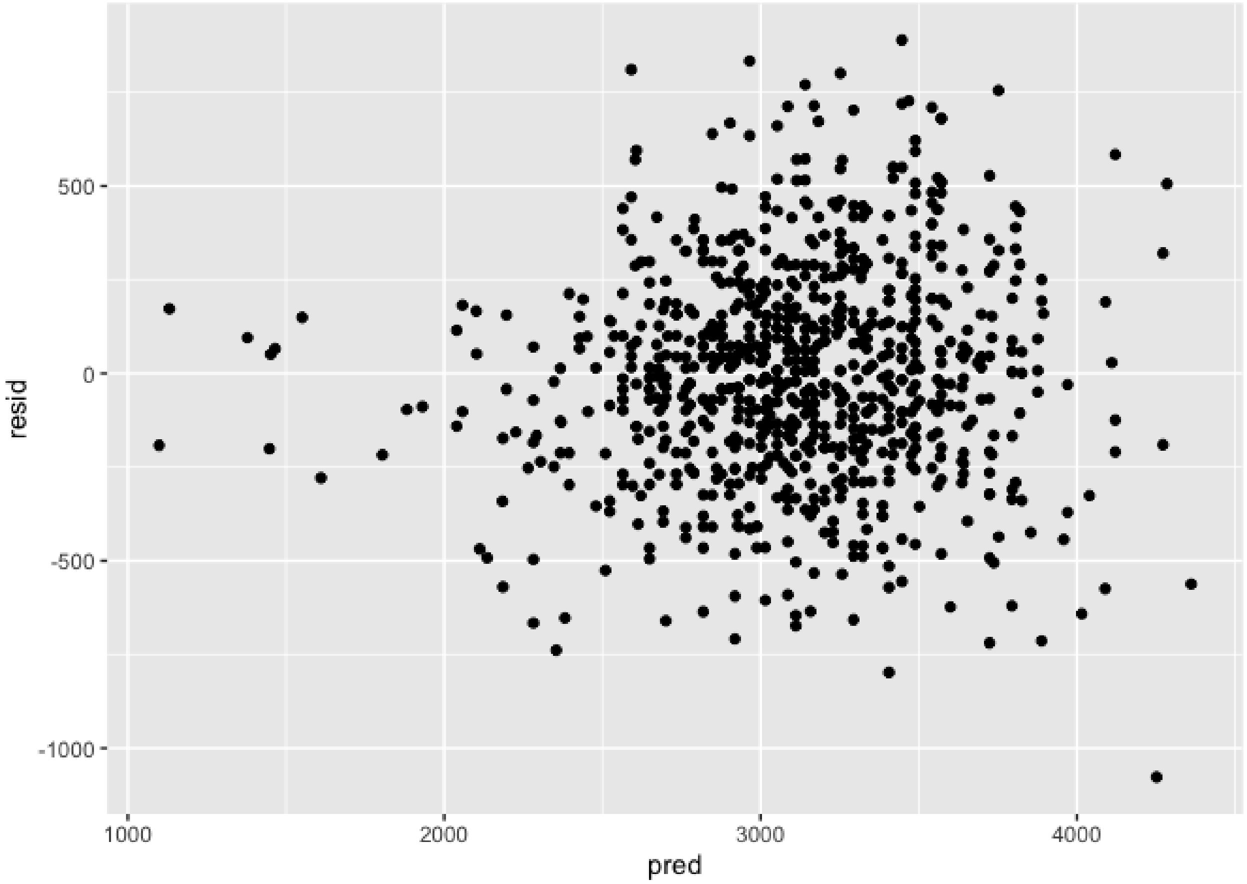
Main Model: Residuals vs. Predictors

```
cv_bwt_df |>
  pull(test) |>
  nth(1) |>
  as_tibble() |>
  add_predictions(main_model) |>
  add_residuals(main_model) |>
  ggplot(aes(x = pred, y = resid)) +
  geom_point()
```



3 Way Model: Residuals vs. Predictors

```
cv_bwt_df |>
  pull(test) |>
  nth(1) |>
  as_tibble() |>
  add_predictions(interaction_model) |>
  add_residuals(interaction_model) |>
  ggplot(aes(x = pred, y = resid)) +
  geom_point()
```

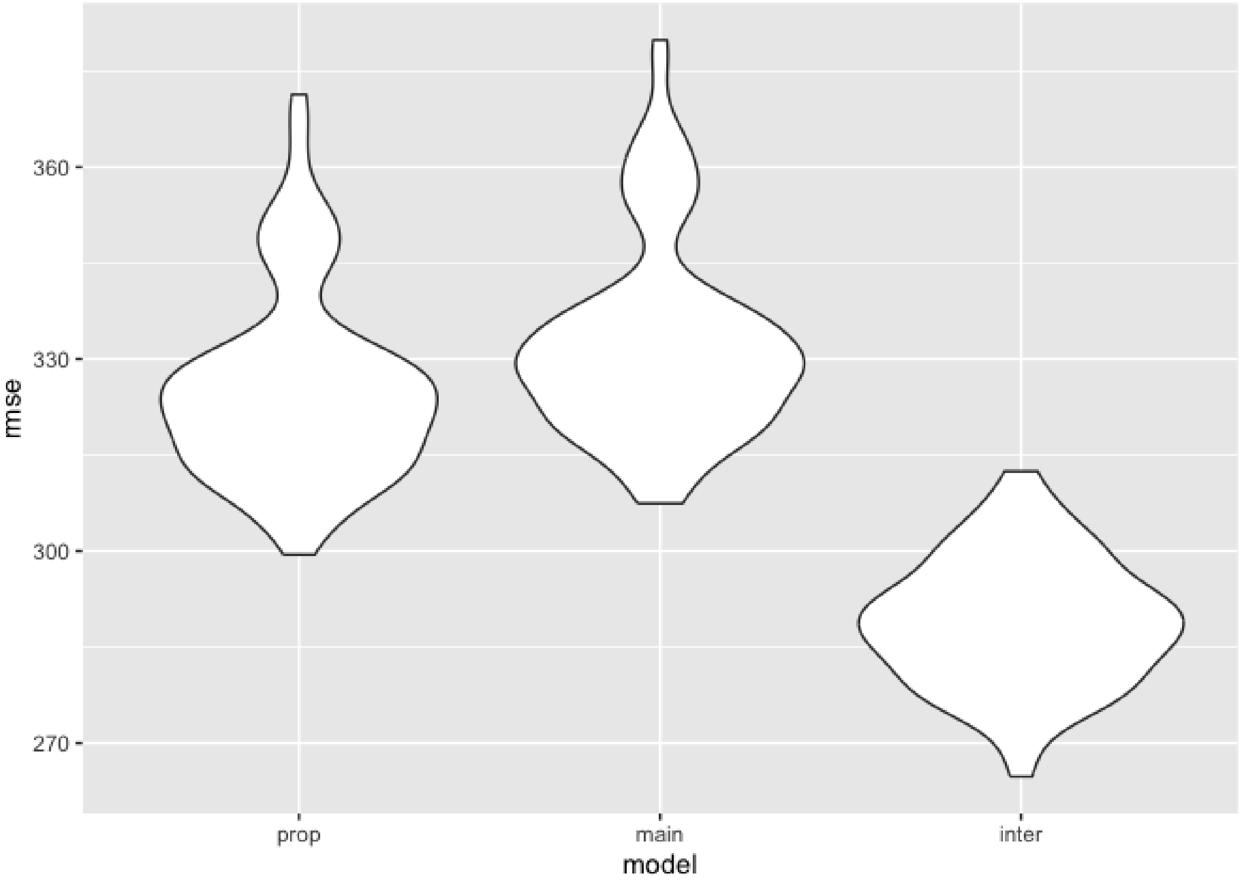


By comparing the models based on residuals and predictors, it seems they all fit quite similarly.

- In more detail, it seems that the 3 way model fits this particular test sample a bit better as the scatterplot is more tightly comppacted around the resid = 0 line.

Comparing Models: MSE

```
cv_bwt_df |>
  select(starts_with("rmse")) |>
  pivot_longer(
    everything(),
    names_to = "model",
    values_to = "rmse",
    names_prefix = "rmse_") |>
  mutate(model = fct_inorder(model)) |>
  ggplot(aes(x = model, y = rmse)) + geom_violin()
```


360
330
300
270
rmse
prop
main
inter
model