Lyme stats project code update

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Plan

Here are the variables/parameters we want to have:

$X_{t,s}$: Lyme disease annual case incidence per state

$\Delta X_{t,s} = X_{t,s} - X_{t-1,s}$: delta X or change in incidence per state from year to year

$r_{t,s} = \frac{\Delta X_{t,s}}{X_{t-1,s}}$: rate of change in incidence per state from year to year

$\overline{r}_s = \frac{1}{14}\sum r_{t,s}$: mean rate of incidence change per state (this will be calculated from 2008-2021 data only)

$\tilde{X}_{t,s} = X_{t,s}\overline{r}_s$: predicted annual incidence based on previous step

$k_s = \frac{X_{t,s} - \tilde{X}_{t,s}}{\tilde{X}_{t,s}}$: difference between actual and predicted incidence (discrepancy presumably caused by change in case def.

Goal is to compare the distribution of k_s for high and low incidence areas to then be able to test some simple hypotheses.

Possible hypotheses to test:

1. We expect the mean of the distribution of k_s for low incidence states to be centered on 0.
2. We expect the mean of the distribution of k_s for high incidence states to *not* be centered on 0.
3. We expect the mean of the distribution of k_s for high and low incidence states to be different from each other.

1. Load packages and clean data:

```r
library(tidyverse)
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.1.4     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.1     v tibble    3.2.1
v lubridate 1.9.3     v tidyr     1.3.1
v purrr     1.0.2
-- Conflicts ------------------------------------------ tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()    masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to becor
```

```r
data <- read_csv("data/Lyme_Disease_Incidence_Rates_by_State_or_Locality.csv")
```

```
Rows: 52 Columns: 16
-- Column specification --------------------------------------------------------
Delimiter: ","
chr  (1): State
dbl (15): 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, ...

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.
```

```r
# Remove special characters from "State" column
data$State <- str_remove_all(data$State, "[^[:alnum:] ]")
# Put data in long format
data <- data %>% pivot_longer(!State, names_to = "Year", values_to = "Incidence")

jurisdiction_data <- read_csv("data/Lyme_jurisdiction_data.csv") %>%
  rename("State" = "states")
```

```
Rows: 51 Columns: 8
-- Column specification --------------------------------------------------------
Delimiter: ","
chr (8): states, pre2022_cases, year2022_cases, percent_change, pre2022_inci...

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.
```

```r
data <- data %>%
  left_join(jurisdiction_data, by="State") %>%
  select(State,Year,Incidence,jurisdiction) %>%
  filter(Incidence > 0)
```

2. Calculate variable values

```r
# calculate delta_X
data <- data %>%
  group_by(State) %>%
  mutate(X = Incidence) %>%
  mutate(delta_X = X - lag(X)) %>%
  ungroup()

# calculate r_t
data <- data %>%
  group_by(State) %>%
  mutate(r = delta_X / lag(X)) %>%
  ungroup()

# calculate mean rate of incidence change per state, mean_r
mean_rates <- data %>%
  filter(Year >= 2008, Year <= 2021) %>% # filter years for 2008-2021
  group_by(State) %>%
  summarise(mean_r = mean(r, na.rm = TRUE))

# join mean rates back to main data
data <- data %>%
  left_join(mean_rates, by = "State")
```

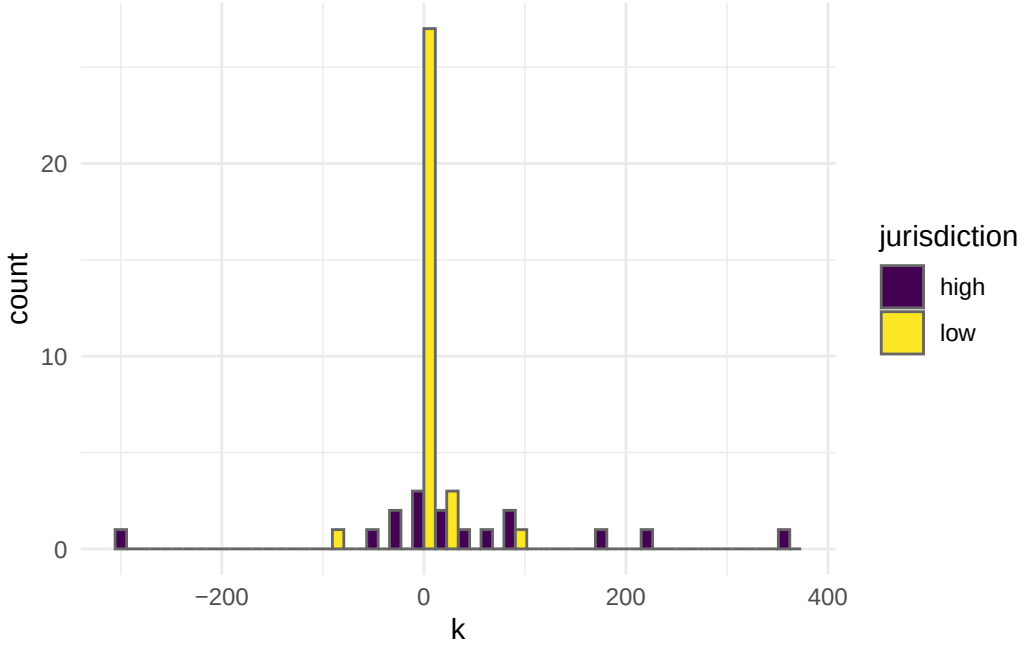
```r
# Calculate X_pred and k
# predicted value for 2022, X_pred
state_data <- data %>%
  group_by(State) %>%
  mutate(X_pred = ifelse(Year == 2022, lag(X) * mean_r, NA)) %>%
  ungroup() %>%
  na.omit()

# difference between predicted value and actual value, k
state_data <- state_data %>%
```

```
  mutate(k = (X - X_pred) / X_pred) %>%
  filter(!is.infinite(k), !is.na(k))
```

Compare the distribution of k for low and high incidence states

```
p1 <- ggplot(state_data, aes(x=k, fill = jurisdiction)) +
  geom_histogram(color = "grey40", position="dodge") +
  #facet_wrap(~jurisdiction) +
  theme_minimal() +
  scale_fill_viridis_d()
p1
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



Hypothesis testing

```
low <- state_data %>% filter(jurisdiction == "low")
high <- state_data %>% filter(jurisdiction == "high")
summary(low)
```

```
   State               Year             Incidence     jurisdiction
Length:32          Length:32          Min.   :0.100   Length:32
Class :character   Class :character   1st Qu.:0.275   Class :character
Mode  :character   Mode  :character   Median :0.550   Mode  :character
                                      Mean   :1.241
                                      3rd Qu.:1.450
                                      Max.   :5.500
      X             delta_X              r                 mean_r
Min.   :0.100   Min.   :-6.400   Min.   :-0.75000   Min.   :-0.1250
1st Qu.:0.275   1st Qu.:-0.425   1st Qu.:-0.38125   1st Qu.: 0.1047
Median :0.550   Median :-0.150   Median :-0.11824   Median : 0.1880
Mean   :1.241   Mean   :-0.525   Mean   :-0.06462   Mean   : 0.2261
3rd Qu.:1.450   3rd Qu.: 0.000   3rd Qu.: 0.00000   3rd Qu.: 0.2514
Max.   :5.500   Max.   : 0.700   Max.   : 1.50000   Max.   : 1.0333
    X_pred                k
Min.   :-0.01250   Min.   :-100.000
1st Qu.: 0.04442   1st Qu.:   1.728
Median : 0.12981   Median :   2.760
Mean   : 0.38001   Mean   :   3.361
3rd Qu.: 0.62286   3rd Qu.:   6.183
Max.   : 1.96689   Max.   :  88.105
```

```
summary(high)
```

```
   State               Year             Incidence      jurisdiction
Length:16          Length:16          Min.   : 11.50   Length:16
Class :character   Class :character   1st Qu.: 43.50   Class :character
Mode  :character   Mode  :character   Median : 68.50   Mode  :character
                                      Mean   : 86.93
                                      3rd Qu.:101.03
                                      Max.   :212.00
      X              delta_X              r                  mean_r
Min.   : 11.50   Min.   : -2.10   Min.   : -0.1544   Min.   :-0.1201019
1st Qu.: 43.50   1st Qu.: 17.50   1st Qu.:  0.7316   1st Qu.:-0.0007449
Median : 68.50   Median : 41.55   Median :  1.2931   Median : 0.0454490
Mean   : 86.93   Mean   : 52.02   Mean   : 13.0734   Mean   : 0.1111267
3rd Qu.:101.03   3rd Qu.: 70.03   3rd Qu.:  2.0963   3rd Qu.: 0.1172027
Max.   :212.00   Max.   :185.00   Max.   :179.7500   Max.   : 1.0218642
    X_pred                k
Min.   :-1.80153   Min.   :-291.366
1st Qu.:-0.03965   1st Qu.:  -3.933
Median : 0.82890   Median :  21.446
```

```
 Mean   : 3.95873   Mean   :  44.747
 3rd Qu.: 2.26524   3rd Qu.:  81.703
 Max.   :28.78999   Max.   : 365.113
```

```r
t.test(low$k, mu=0)
```

```
    One Sample t-test

data:  low$k
t = 0.77588, df = 31, p-value = 0.4437
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -5.474598 12.197532
sample estimates:
mean of x
 3.361467
```

```r
t.test(high$k, mu = 0)
```

```
    One Sample t-test

data:  high$k
t = 1.2733, df = 15, p-value = 0.2223
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -30.15616 119.64987
sample estimates:
mean of x
 44.74685
```

```r
t.test(k ~ jurisdiction, state_data)
```

```
    Welch Two Sample t-test

data:  k by jurisdiction
t = 1.1688, df = 15.458, p-value = 0.2602
alternative hypothesis: true difference in means between group high and group low is not equa
```

```
95 percent confidence interval:
 -33.89054 116.66131
sample estimates:
mean in group high  mean in group low
         44.746851           3.361467
```

Uncertainty Quantification - Markov Chain Monte Carlo

```r
low_k <- state_data %>% filter(jurisdiction == "low") %>% pull(k)
high_k <- state_data %>% filter(jurisdiction == "high") %>% pull(k)

# Metropolis-Hastings function
mh_sampler <- function(data, n_iter = 10000, proposal_sd = 0.1) {
  # Initialize parameters
  mu_current <- mean(data)  # Start at the sample mean
  samples <- numeric(n_iter)  # Store samples
  sigma <- sd(data)           # Fixed standard deviation (from data)

  # Prior: Normal(0, 10^2)
  prior <- function(mu) {
    dnorm(mu, mean = 0, sd = 10, log = TRUE)
  }

  # Likelihood: Normal(mu, sigma^2)
  likelihood <- function(mu) {
    sum(dnorm(data, mean = mu, sd = sigma, log = TRUE))
  }

  # Posterior: likelihood * prior
  posterior <- function(mu) {
    likelihood(mu) + prior(mu)  # Log-scale
  }

  # MCMC Sampling
  for (i in 1:n_iter) {
    # Propose new mu
    mu_proposed <- rnorm(1, mean = mu_current, sd = proposal_sd)

    # Acceptance ratio
    R <- exp(posterior(mu_proposed) - posterior(mu_current))
```

```
    # Accept or reject
    if (runif(1) < R) {
      mu_current <- mu_proposed
    }

    # Store the current sample
    samples[i] <- mu_current
  }

  return(samples)
}

# Run the sampler for both groups
low_samples <- mh_sampler(low_k, n_iter = 10000)
high_samples <- mh_sampler(high_k, n_iter = 10000)

# Summarize results
summary(low_samples)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
 -0.237   8.094  10.500   9.554  11.934  15.792
```

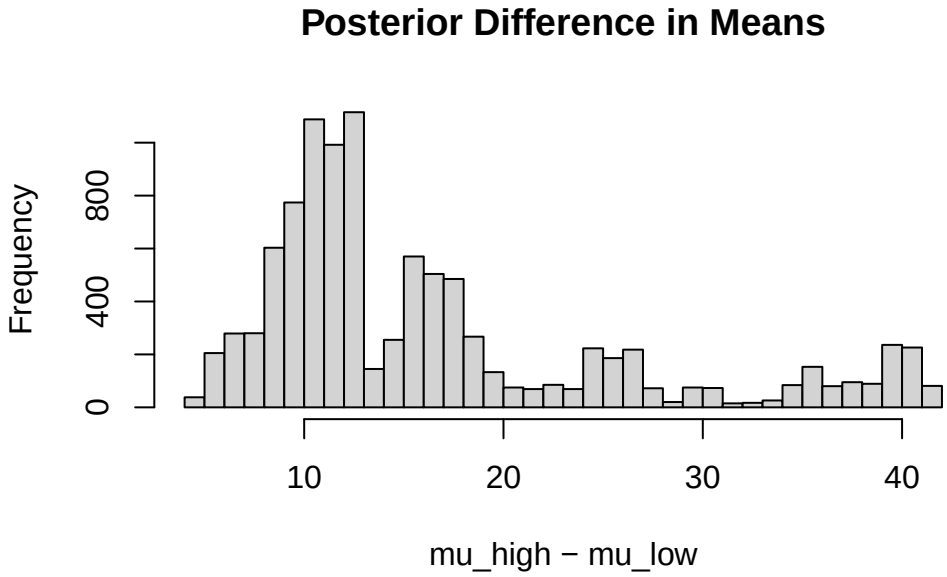
```
summary(high_samples)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  17.11   21.67   23.97   26.04   27.83   45.09
```

```
# Compute posterior difference
diff_samples <- high_samples - low_samples
summary(diff_samples)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
  4.423  10.254  12.520  16.483  18.592  41.890
```

```
# Plot results
hist(diff_samples, breaks = 30, main = "Posterior Difference in Means", xlab = "mu_high - mu
abline(v = 0, col = "red", lwd = 2)
```


Posterior Difference in Means
Frequency
0
400
800
10
20
30
40
mu_high − mu_low