Winter/Summer - stats testing

evidence of meeting PDA outcome 2.6.

Statistical analyses to identify patterns, trends and relationships in the dataset

```
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.2 --
## v ggplot2 3.4.0      v purrr   0.3.5
## v tibble  3.1.8      v dplyr   1.0.10
## v tidyr   1.2.1      v stringr 1.4.1
## v readr   2.1.3      v forcats 0.5.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(infer)
library(lubridate)
```

```
## Loading required package: timechange
##
## Attaching package: 'lubridate'
##
## The following objects are masked from 'package:base':
##
##     date, intersect, setdiff, union
```

define functions

```
source(here::here("r_scripts_and_notebooks/fun_smoother.R"))
source(here::here("r_scripts_and_notebooks/fun_stats_test.R"))
```

some not so successful attempts at setting up code for use in dashboard making it so it will run with any dataset and not just this one note that data must just be one timeries. date must be date format either weekly or monthly.

load data here

```
admissions_spec <- read_csv(here::here("clean_data/weekly_admissions_spec_clean.csv"))
delayed_discharge <- read_csv(here::here("clean_data/delayed_discharge_clean.csv"))
```

```
#define filters
input <- list(dataset = "delayed_discharge", age_group = "All (18plus)", healthboard = "All Scotland")
```

```
#define parametrs to plot
selection <- 1
lookup_dataset <- list("delayed_discharge","admissions_spec")
lookup_param <- list("number_of_delayed_bed_days","number_admissions")
lookup_date <- list("wdate","mdate")
lookup_indicator <- list("weekly","monthly")
```

```
# how to evaluate when passing in variable names?
eval(str2expression(str_c("seldata <- ",input$datase)))
eval(str2expression(str_c("choice1=unique(seldata$",lookup_param[1],")")))
```

start here

this is an example where we need to remove long term trend if we are to reveal any seasonal differences

```
seldata <- delayed_discharge %>%
  filter(hb_name == "All Scotland") %>%
  filter(age_group == "All (18plus)") %>%
  #using this filter - dont expect a significant result
  filter(reason_for_delay == "All Delay Reasons") %>%
  # using this filter expect a significant result
  #filter(reason_for_delay == "Code 9 Non-AWI") %>%
  # here we are selecting just post pandemic data
  filter(mdate > as.Date("2020-04-01")) %>%
  # by just having param it will make app easier
  rename(param = number_of_delayed_bed_days) %>%
  select(mdate, param, iswinter)

data <- seldata[2]
date <- seldata[1]
```

call function to smooth data

this will make it easier to embed in shiny app

```
smoothed_data <- data_smoother(date,seldata)
```

call function to run test and calc p-value

used code from lines below to create this function - we should get similar pvalue. note that because we are using bootstrap pvalues could be slightly different each time we run.

```
p_value2 <- stats_test(smoothed_data)
p_value2
```

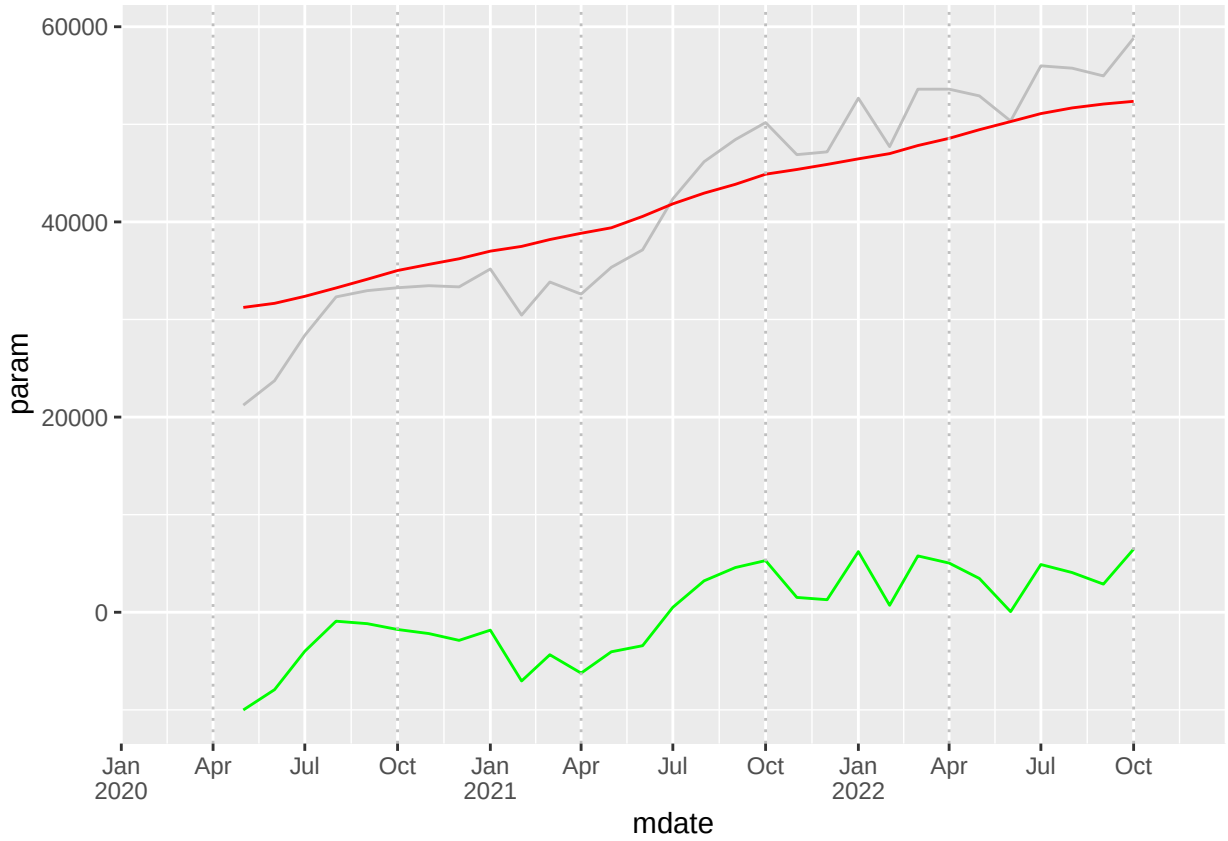
```
## # A tibble: 1 x 1
##   p_value
##     <dbl>
## 1   0.341
```

demo that function works

```
## plot data
#calculate difference to create mvar
smoothed_data <- smoothed_data %>%
  mutate(mvar = param - moving_avg)
```

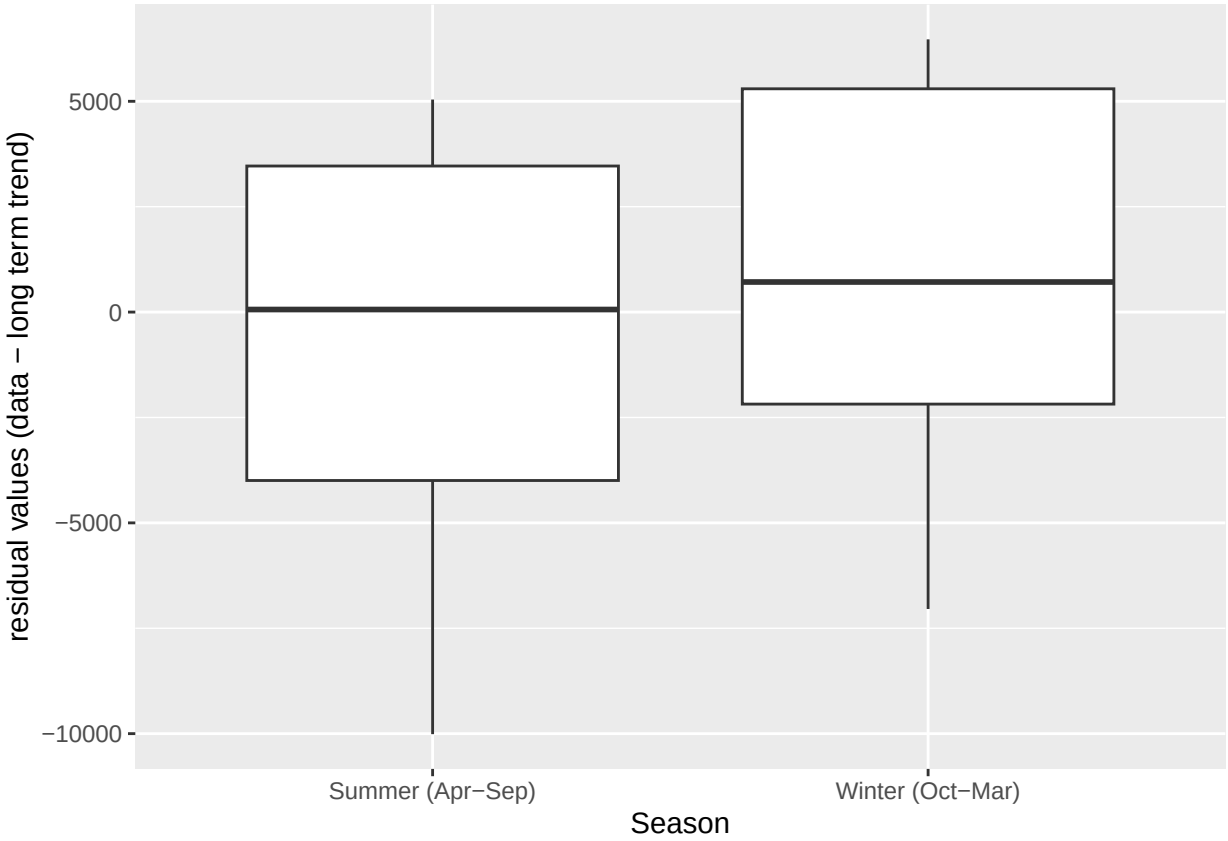
plot - check the smoother makes sense and tweak values if they dont line plot can be added to the app - show pre pandemic and post pandemic in different plots in this plot seasonal var much greater than long term var

```
plotlim <- as.Date(c("2020-01-01","2022-12-31"))
smoothed_data %>%
ggplot() +
  #geom_line(aes(x = mdate, y = c(param, moving_avg, mvar)))
  #above is an attempt to merge them - doesnt work!
  geom_line(aes(x = mdate, y = param), colour = "gray") +
  geom_line(aes(x = mdate, y = moving_avg), colour = "red") +
  geom_line(aes(x = mdate, y = mvar), colour = "green") +
  scale_x_date(limits=plotlim, date_breaks="3 month",
               labels = scales::label_date_short(), expand = c(0,0)) +
    # add dashed lines to show the boundaries
    geom_vline(xintercept=ymd(20201001),color="gray",linetype="dotted", linewidth = 0.5) +
    geom_vline(xintercept=ymd(20211001),color="gray",linetype="dotted", linewidth = 0.5) +
    geom_vline(xintercept=ymd(20221001),color="gray",linetype="dotted", linewidth = 0.5) +
    geom_vline(xintercept=ymd(20200401),color="gray",linetype="dotted", linewidth = 0.5) +
    geom_vline(xintercept=ymd(20210401),color="gray",linetype="dotted", linewidth = 0.5) +
    geom_vline(xintercept=ymd(20220401),color="gray",linetype="dotted", linewidth = 0.5)
```



#now create a boxplot this box plot will be added to the app

```
smoothed_data %>%
  ggplot() +
  aes(x=iswinter, y=mvar) +
  geom_boxplot() +
  ylab("residual values (data - long term trend)") +
  xlab("Season") +
  scale_x_discrete(
    labels=c("FALSE" = "Summer (Apr-Sep)", "TRUE" = "Winter (Oct-Mar)"),
    limits = c("FALSE","TRUE"))
```



Hypothesis Test

Is summer is significantly different to winter?

The null hypothesis is that the average value for summer is the same or lower than the average value for winter.

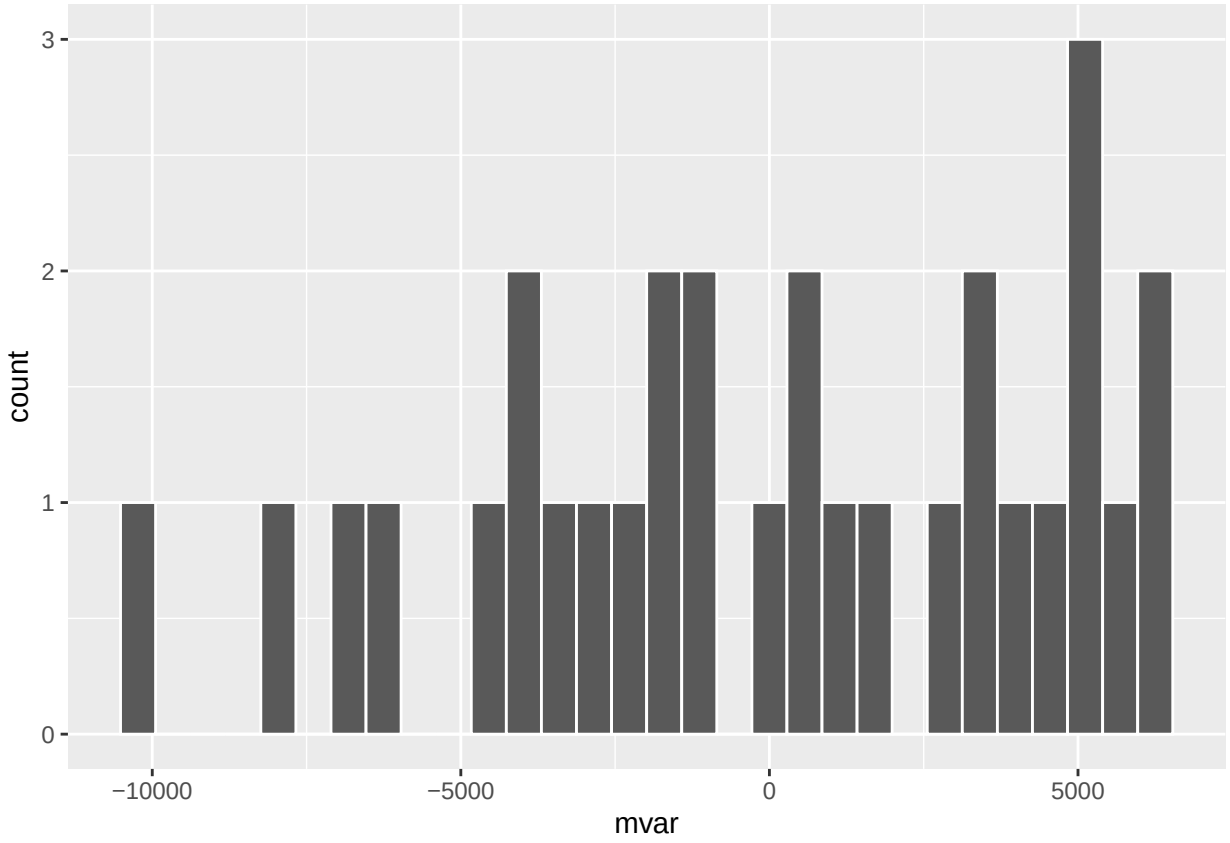
H0 : mean winter - mean summer <= 0 HA : mean winter - mean summer >0

we are setting alpha for this test to be 0.05

```
alpha_test=0.05
```

```
smoothed_data %>%
  ggplot() +
  aes(x = mvar) +
  geom_histogram(col = "white")
```

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




```
seasonal_avg <- smoothed_data  %>%
  group_by(iswinter) %>%
  summarise(mean= mean(mvar, na.rm=TRUE))

seasonal_avg
```

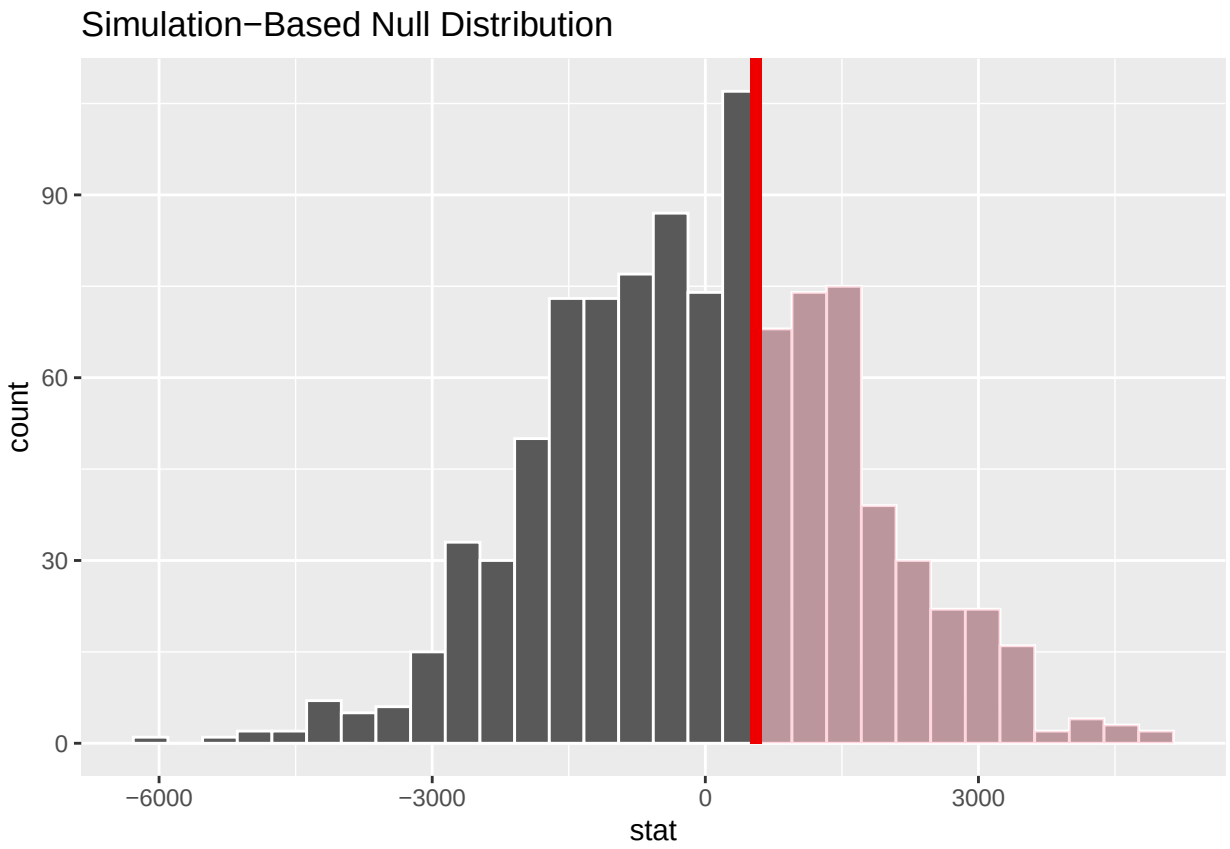
```
## # A tibble: 2 x 2
##   iswinter  mean
##   <lgl>    <dbl>
## 1 FALSE    -530.
## 2 TRUE      555.
```

```
observed_stat = seasonal_avg$mean[seasonal_avg$iswinter ==TRUE]
            -seasonal_avg$mean[seasonal_avg$iswinter ==FALSE]
```

```
## [1] 529.8216
```

```
null_distribution <- smoothed_data  %>%
  specify(response = mvar, explanatory = iswinter) %>%
  hypothesize(null = "independence") %>%
  generate(reps = 1000, type = "permute") %>%
  calculate(stat = "diff in means", order = c(TRUE,FALSE)) #winter - summer
```

```
null_distribution %>%
  visualise(bins = 30) +
shade_p_value(obs_stat = observed_stat
              , direction = "greater")
```




```
p_value <- null_distribution %>%
get_p_value(obs_stat = observed_stat
              , direction = "greater") %>%
pull()
```

```
p_value
```

```
## [1] 0.36
```

If pvalue is less than alpha we can reject null hypothesis If pvalue is greater than alpha we cannot reject null hypothesis

```
if(p_value > alpha_test){
 print("We cannot reject the null hypothesis. The average winter values in
       this data are the same as the average summer values")
}else{
    print("We can reject the null hypothesis in favour of the alternative
          hypothesis. The average winter values in this data are
          significantly different to the average winter values")}
```

```
## [1] "We cannot reject the null hypothesis. The average winter values in \n       this data are the s
```

#Notes smoother not perfect, hard to remove long term trend in a short dataset maybe need to smooth less? this will do for now though ...

repeat of code with diff filter

this is an example where we definitely expect winter summer to be different

```
seldata <- delayed_discharge %>%
  filter(hb_name == "All Scotland") %>%
  filter(age_group == "All (18plus)") %>%
  #using this filter - dont expect a significant result
  #filter(reason_for_delay == "All Delay Reasons") %>%
  # using this filter expect a significant result
  filter(reason_for_delay == "Code 9 Non-AWI") %>%
  # here we are selecting just post pandemic data
  filter(mdate > as.Date("2020-04-01")) %>%
  # by just having param it will make app easier
  rename(param = number_of_delayed_bed_days) %>%
  select(mdate, param, iswinter)

data <- seldata[2]
date <- seldata[1]
```

call function to smooth data

this will make it easier to embed in shiny app

```
smoothed_data <- data_smoother(date,seldata)
```

call function to run test and calc p-value

used code from lines below to create this function - we should get similar pvalue. note that because we are using bootstrap pvalues could be slightly different each time we run.

```
p_value2 <- stats_test(smoothed_data)
p_value2
```

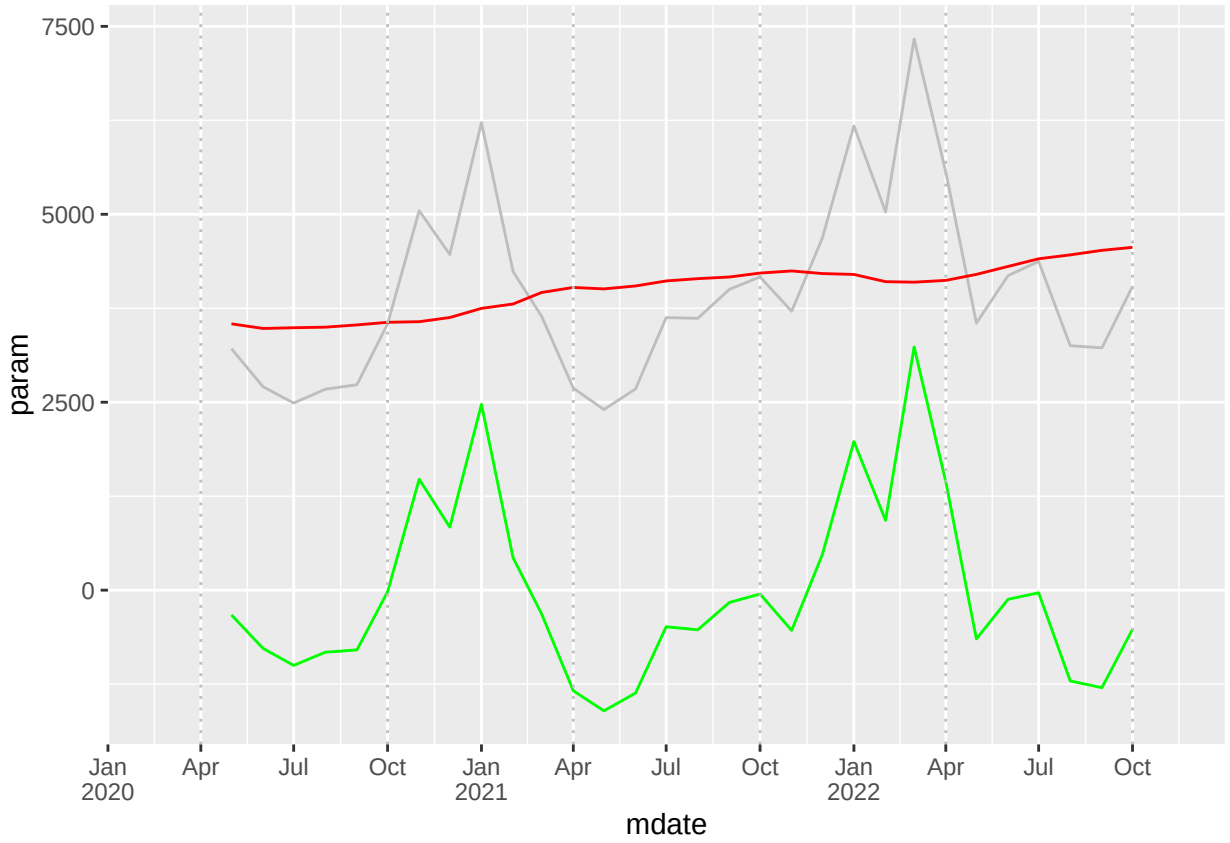
```
## # A tibble: 1 x 1
##   p_value
##     <dbl>
## 1   0.028
```

demo that function works

```
## plot data
#calculate difference to create mvar
smoothed_data <- smoothed_data %>%
  mutate(mvar = param - moving_avg)
```

plot - check the smoother makes sense and tweak values if they dont line plot can be added to the app - show pre pandemic and post pandemic in different plots in this plot seasonal var much greater than long term var

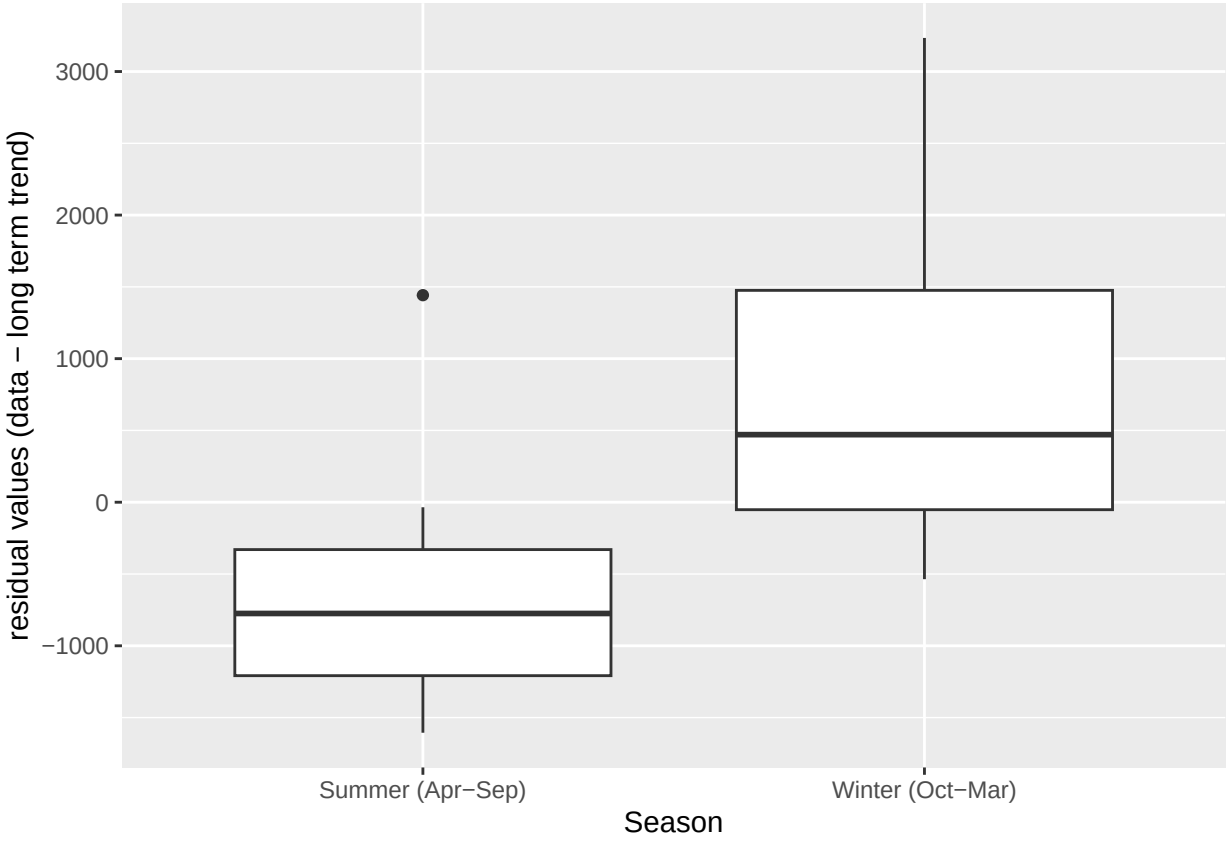
```
plotlim <- as.Date(c("2020-01-01","2022-12-31"))
smoothed_data %>%
ggplot() +
  #geom_line(aes(x = mdate, y = c(param, moving_avg, mvar)))
  #above is an attempt to merge them - doesnt work!
  geom_line(aes(x = mdate, y = param), colour = "gray") +
  geom_line(aes(x = mdate, y = moving_avg), colour = "red") +
  geom_line(aes(x = mdate, y = mvar), colour = "green") +
  scale_x_date(limits=plotlim, date_breaks="3 month",
               labels = scales::label_date_short(), expand = c(0,0)) +
    # add dashed lines to show the boundaries
    geom_vline(xintercept=ymd(20201001),color="gray",linetype="dotted", linewidth = 0.5) +
    geom_vline(xintercept=ymd(20211001),color="gray",linetype="dotted", linewidth = 0.5) +
    geom_vline(xintercept=ymd(20221001),color="gray",linetype="dotted", linewidth = 0.5) +
    geom_vline(xintercept=ymd(20200401),color="gray",linetype="dotted", linewidth = 0.5) +
    geom_vline(xintercept=ymd(20210401),color="gray",linetype="dotted", linewidth = 0.5) +
    geom_vline(xintercept=ymd(20220401),color="gray",linetype="dotted", linewidth = 0.5)
```



#now create a boxplot this box plot will be added to the app

```
smoothed_data %>%
  ggplot() +
  aes(x=iswinter, y=mvar) +
```

```
  geom_boxplot() +
  ylab("residual values (data - long term trend)") +
  xlab("Season") +
  scale_x_discrete(
    labels=c("FALSE" = "Summer (Apr-Sep)", "TRUE" = "Winter (Oct-Mar)"),
    limits = c("FALSE","TRUE"))
```



Hypothesis Test

Is summer is significantly different to winter?

The null hypothesis is that the average value for summer is the same or lower than the average value for winter.

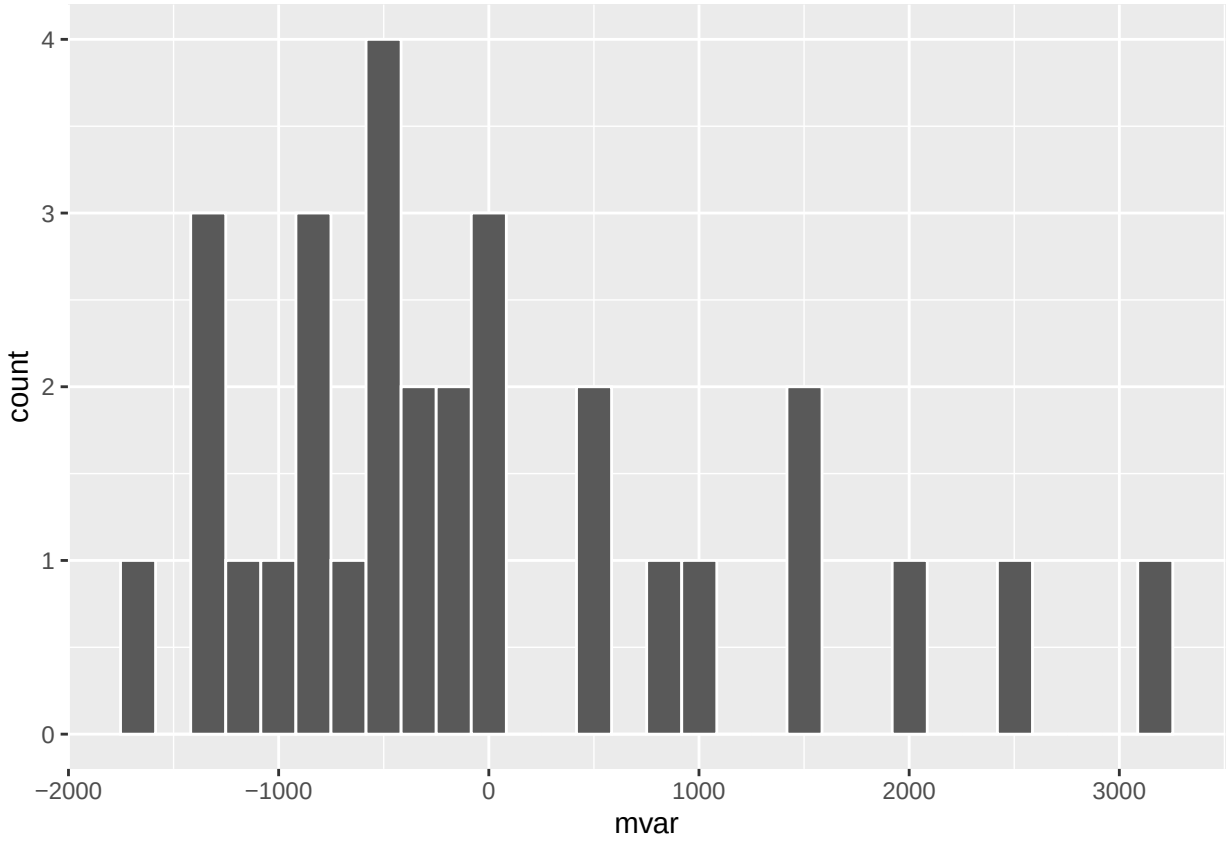
H0 : mean winter - mean summer <= 0 HA : mean winter - mean summer >0

we are setting alpha for this test to be 0.05

```
alpha_test=0.05
```

```
smoothed_data %>%
  ggplot() +
  aes(x = mvar) +
  geom_histogram(col = "white")
```

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




```
seasonal_avg <- smoothed_data  %>%
  group_by(iswinter) %>%
  summarise(mean= mean(mvar, na.rm=TRUE))

seasonal_avg
```

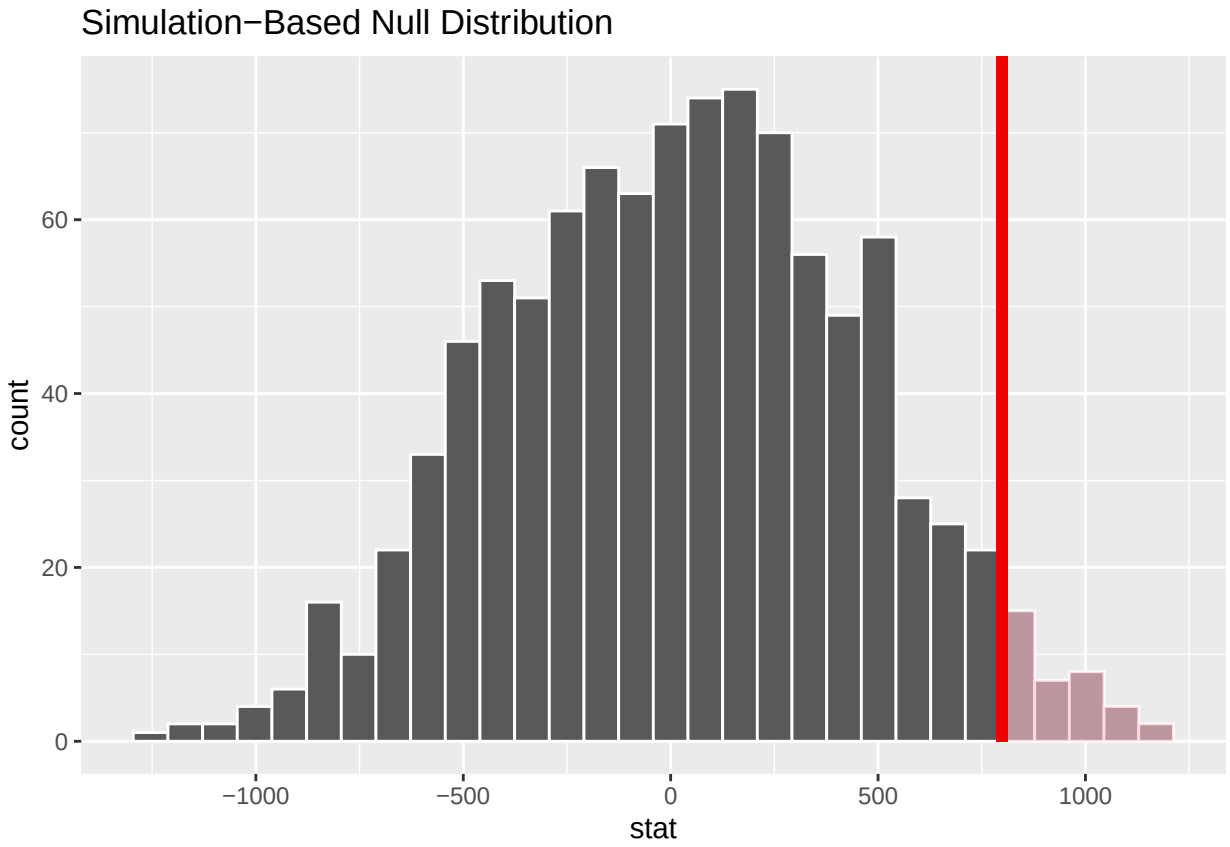
```
## # A tibble: 2 x 2
##   iswinter  mean
##   <lgl>    <dbl>
## 1 FALSE    -652.
## 2 TRUE      798.
```

```
observed_stat = seasonal_avg$mean[seasonal_avg$iswinter ==TRUE]
            -seasonal_avg$mean[seasonal_avg$iswinter ==FALSE]
```

```
## [1] 652.2753
```

```
null_distribution <- smoothed_data  %>%
  specify(response = mvar, explanatory = iswinter) %>%
  hypothesize(null = "independence") %>%
  generate(reps = 1000, type = "permute") %>%
  calculate(stat = "diff in means", order = c(TRUE,FALSE)) #winter - summer
```

```
null_distribution %>%
  visualise(bins = 30) +
shade_p_value(obs_stat = observed_stat
              , direction = "greater")
```




```
p_value <- null_distribution %>%
get_p_value(obs_stat = observed_stat
              , direction = "greater") %>%
pull()
```

```
p_value
```

```
## [1] 0.035
```

If pvalue is less than alpha we can reject null hypothesis If pvalue is greater than alpha we cannot reject null hypothesis

```
if(p_value > alpha_test){
 print("We cannot reject the null hypothesis. The average winter values in
       this data are the same as the average summer values")
}else{
    print("We can reject the null hypothesis in favour of the alternative
          hypothesis. The average winter values in this data are
          significantly different to the average winter values")}
```

```
## [1] "We can reject the null hypothesis in favour of the alternative \n          hypothesis. The avera
```