Homework 4

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library(here)

here() starts at /Users/kiya/github/ENVS-193DS\_homework-04\_pupa-kiya

library(janitor)

Attaching package: 'janitor'

The following objects are masked from 'package:stats':  
  
 chisq.test, fisher.test

library(tidyverse)

── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──  
✔ dplyr 1.1.1 ✔ readr 2.1.4  
✔ forcats 1.0.0 ✔ stringr 1.5.0  
✔ ggplot2 3.4.2 ✔ tibble 3.2.1  
✔ lubridate 1.9.2 ✔ tidyr 1.3.0  
✔ purrr 1.0.1

── Conflicts ────────────────────────────────────────── tidyverse\_conflicts() ──  
✖ dplyr::filter() masks stats::filter()  
✖ dplyr::lag() masks stats::lag()  
ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors

library(naniar)  
library(visdat)

#reading in files using here function, clean names to make lowercase and more readable, mutate all entries to lowercase  
fish <- read\_csv(here("data", "ntl6\_v12.csv")) %>% clean\_names() %>% mutate\_all(tolower)

Warning: One or more parsing issues, call `problems()` on your data frame for details,  
e.g.:  
 dat <- vroom(...)  
 problems(dat)

Rows: 349229 Columns: 15  
── Column specification ────────────────────────────────────────────────────────  
Delimiter: ","  
chr (8): lakeid, gearid, spname, sampletype, indid, fishpart, spseq, flag  
dbl (5): year4, depth, rep, length, weight  
lgl (1): sex  
date (1): sampledate  
  
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.

#look at data  
str(fish)

tibble [349,229 × 15] (S3: tbl\_df/tbl/data.frame)  
 $ lakeid : chr [1:349229] "al" "al" "al" "al" ...  
 $ year4 : chr [1:349229] "1981" "1981" "1981" "1981" ...  
 $ sampledate: chr [1:349229] "1981-08-04" "1981-08-04" "1981-08-04" "1981-08-04" ...  
 $ gearid : chr [1:349229] "bseine" "bseine" "bseine" "bseine" ...  
 $ spname : chr [1:349229] "blackcrappie" "blackcrappie" "blackcrappie" "blackcrappie" ...  
 $ sampletype: chr [1:349229] NA NA NA NA ...  
 $ depth : chr [1:349229] "-1" "-1" "-1" "-1" ...  
 $ rep : chr [1:349229] "4" "4" "4" "4" ...  
 $ indid : chr [1:349229] "321m1" "321m2" "321m3" "321m4" ...  
 $ length : chr [1:349229] "42" "41" "46" "26" ...  
 $ weight : chr [1:349229] NA NA NA NA ...  
 $ sex : chr [1:349229] NA NA NA NA ...  
 $ fishpart : chr [1:349229] NA NA NA "k" ...  
 $ spseq : chr [1:349229] "3211010-100" "3211010-100" "3211010-100" "3211010-100" ...  
 $ flag : chr [1:349229] NA NA NA NA ...

#Problem 1  
#create new dataframe, filtering by the three years you need and for the mudminnow species  
mudminnow <- fish %>% filter(year4 %in% c("1982", "2002", "2021"), spname %in% c("mudminnow"))  
  
#look at data  
str(mudminnow)

tibble [824 × 15] (S3: tbl\_df/tbl/data.frame)  
 $ lakeid : chr [1:824] "cb" "cb" "cb" "cb" ...  
 $ year4 : chr [1:824] "1982" "1982" "1982" "1982" ...  
 $ sampledate: chr [1:824] "1982-08-09" "1982-08-09" "1982-08-09" "1982-08-09" ...  
 $ gearid : chr [1:824] "fyknet" "fyknet" "fyknet" "fyknet" ...  
 $ spname : chr [1:824] "mudminnow" "mudminnow" "mudminnow" "mudminnow" ...  
 $ sampletype: chr [1:824] NA NA NA NA ...  
 $ depth : chr [1:824] "-1" "-1" "-1" "-1" ...  
 $ rep : chr [1:824] "1" "1" "1" "1" ...  
 $ indid : chr [1:824] "590a1" "590a2" "590a3" "590a4" ...  
 $ length : chr [1:824] "75" "66" "84" "74" ...  
 $ weight : chr [1:824] "3.4" "2.5" "5.8" "4" ...  
 $ sex : chr [1:824] NA NA NA NA ...  
 $ fishpart : chr [1:824] NA NA NA NA ...  
 $ spseq : chr [1:824] "5900220-100" "5900220-100" "5900220-100" "5900220-100" ...  
 $ flag : chr [1:824] NA NA NA NA ...

#view dataframe  
view(mudminnow)

#Problem 2  
trout\_perch <- fish %>% filter(spname == "troutperch")  
str(trout\_perch)

tibble [489 × 15] (S3: tbl\_df/tbl/data.frame)  
 $ lakeid : chr [1:489] "tr" "tr" "tr" "tr" ...  
 $ year4 : chr [1:489] "1981" "1981" "1981" "1981" ...  
 $ sampledate: chr [1:489] "1981-08-10" "1981-08-10" "1981-08-10" "1981-08-10" ...  
 $ gearid : chr [1:489] "bseine" "bseine" "bseine" "bseine" ...  
 $ spname : chr [1:489] "troutperch" "troutperch" "troutperch" "troutperch" ...  
 $ sampletype: chr [1:489] NA NA NA NA ...  
 $ depth : chr [1:489] "-1" "-1" "-1" "-1" ...  
 $ rep : chr [1:489] "1" "1" "1" "1" ...  
 $ indid : chr [1:489] "513h1" "513h2" "513h3" "513h4" ...  
 $ length : chr [1:489] "116" "97" "81" "85" ...  
 $ weight : chr [1:489] "12.5" "7.5" "4.5" "4" ...  
 $ sex : chr [1:489] "false" NA NA "false" ...  
 $ fishpart : chr [1:489] "s" "s" "s" "s" ...  
 $ spseq : chr [1:489] "5130900-100" "5130900-100" "5130900-100" "5130900-100" ...  
 $ flag : chr [1:489] NA NA NA NA ...

view(trout\_perch)