Hydroinformatics at VT

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Chapter 1

Introduction

There will be information here about prerequisite resources and suggested readings.

For questions, suggestions, activity answer keys, etc.: jpgannon at vt.edu

1.1 How to use these materials

At the top of each chapter there is a link to a github repository. In each repository is the code that produces each chapter and a version where the code chunks within it are blank. These repositories are all template repositories, so you can easily copy them to your own github space by clicking *Use This Template* on the repo page.

In my class, I work through the each document, live coding with students following along.Typically I ask students to watch as I code and explain the chunk and then replicate it on their computer. Depending on the lesson, I will ask students to try some of the chunks before I show them the code as an in-class activity. Some chunks are explicitly designed for this purpose and are typically labeled a "challenge".

Chapters called ACTIVITY are either homework or class-period-long in-class activities. The code chunks in these are therefore blank. If you would like a key for any of these, please just send me an email.

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Chapter 2

Intro to Plotting

Get this document and a version with empty code chunks at the template repository on github: https://github.com/VT-Hydroinformatics/1-Intro-plotting-R

2.1 Download and install tidyverse library

We will use the tidyverse a lot this semester. It is a suite of packages that handles plotting and data wrangling efficiently.

You only have to install the library once. You have to load it using the library() function each time you start an R session.

```
#install.packages("tidyverse")
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.2     v purrr   0.3.4
## v tibble  3.0.4     v dplyr   1.0.2
## v tidyr   1.1.2     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.0
```

```
## Warning: package 'ggplot2' was built under R version 3.6.2
```

```
## Warning: package 'tibble' was built under R version 3.6.2
```

```
## Warning: package 'tidyr' was built under R version 3.6.2
```

```
## Warning: package 'readr' was built under R version 3.6.2

## Warning: package 'purrr' was built under R version 3.6.2

## Warning: package 'dplyr' was built under R version 3.6.2

## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

2.2 Reading data

The following lines will read in the data we will use for this exercise. Don't worry about this right now beyond running it, we will talk more about it later.

```
Pine <- read_csv("PINE_Jan-Mar_2010.csv")
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   StationID = col_character(),
##   cfs = col_double(),
##   surrogate = col_character(),
##   datetime = col_datetime(format = ""),
##   year = col_double(),
##   quarter = col_double(),
##   month = col_double(),
##   day = col_double()
## )
```

```
SNP <- read_csv("PINE_NFDR_Jan-Mar_2010.csv")
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   StationID = col_character(),
##   cfs = col_double(),
##   surrogate = col_character(),
##   datetime = col_datetime(format = ""),
##   year = col_double(),
##   quarter = col_double(),
##   month = col_double(),
##   day = col_double()
## )
```

```
RBI <- read_csv("Flashy_Dat_Subset.csv")
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   .default = col_double(),
##   STANAME = col_character(),
##   STATE = col_character(),
##   CLASS = col_character(),
##   AGGECOREGION = col_character()
## )
## i Use `spec()` for the full column specifications.
```

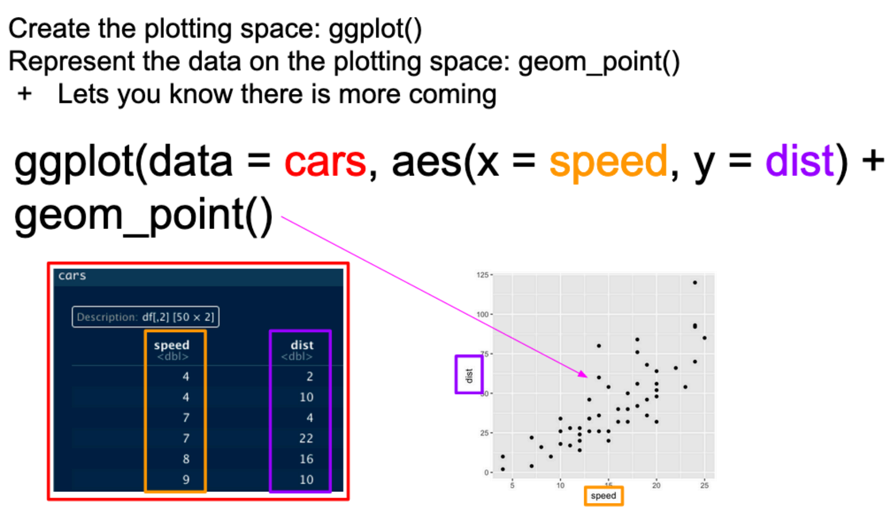
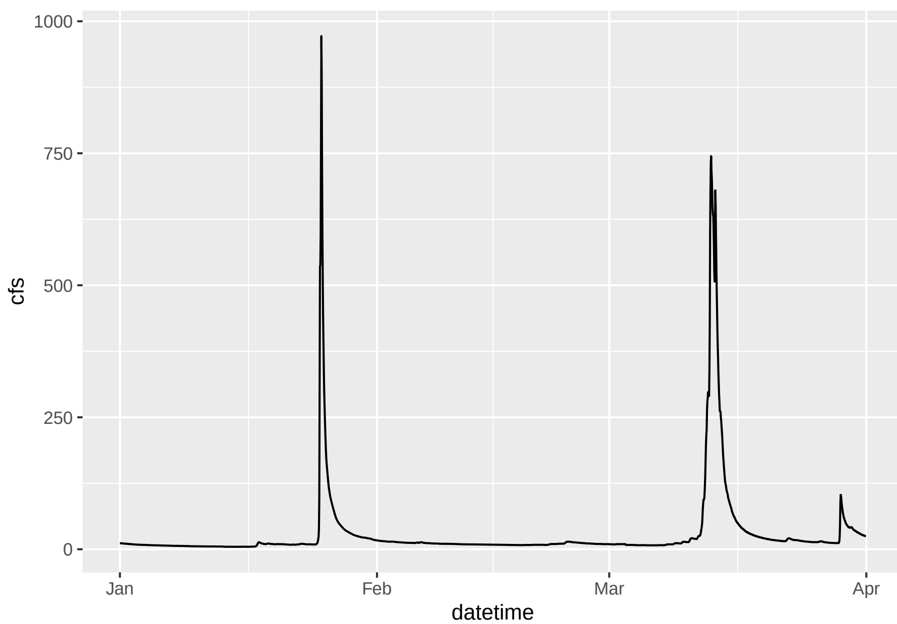


Figure 2.1: Basic ggplot syntax

2.3 Our first ggplot

Let's look at the Pine data, plotting streamflow (the cfs column) by the date (datetime column). We will show the time series as a line.

```
ggplot(data = Pine, aes(x = datetime, y = cfs))+
  geom_line()
```

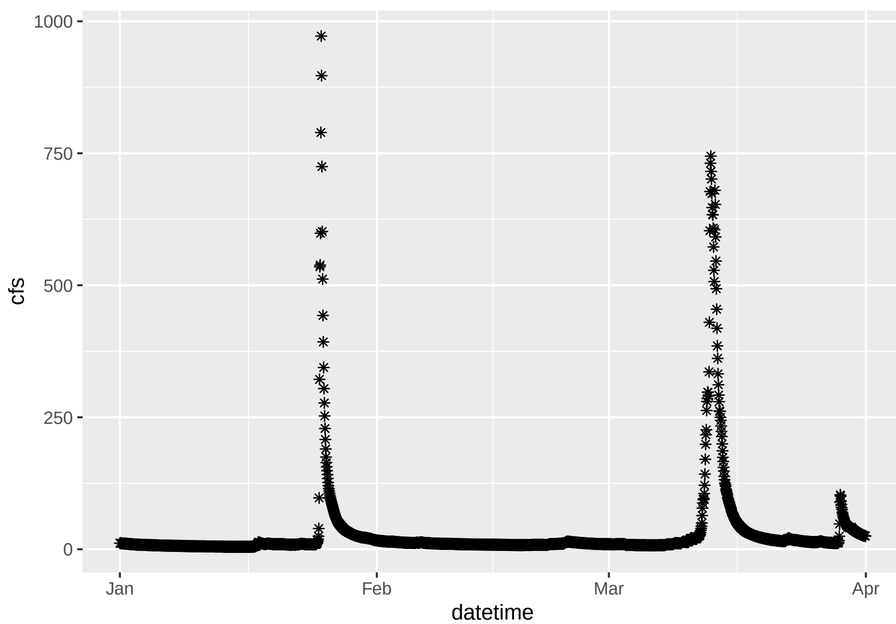


2.4 Change point type

Now let's make the same plot but show the data as points, using the pch parameter in geom_point() we can change the point type to any of the following:

Figure 2.2: pch options from R help file

```
ggplot(data = Pine, aes(x = datetime, y = cfs))+
  geom_point(pch = 8)
```



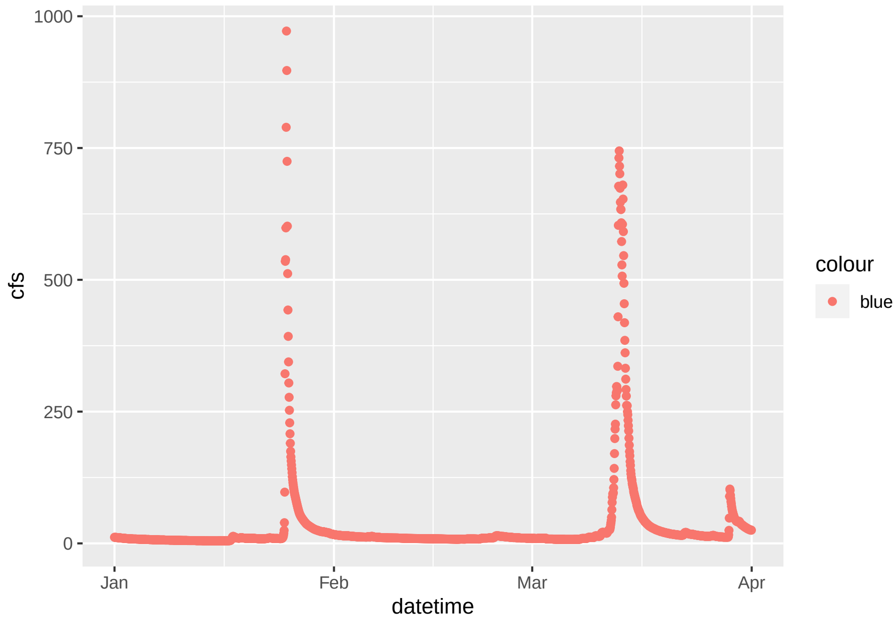
2.5 Set colors

We can also "easily" change the color. Easily is in quotes because this often trips people up. If you put color = "blue" in the aesthetic function, think about what that is telling ggplot. It says "control the color using"blue"". That doesn't make a whole lot of sense, so neither does the output… Try it.

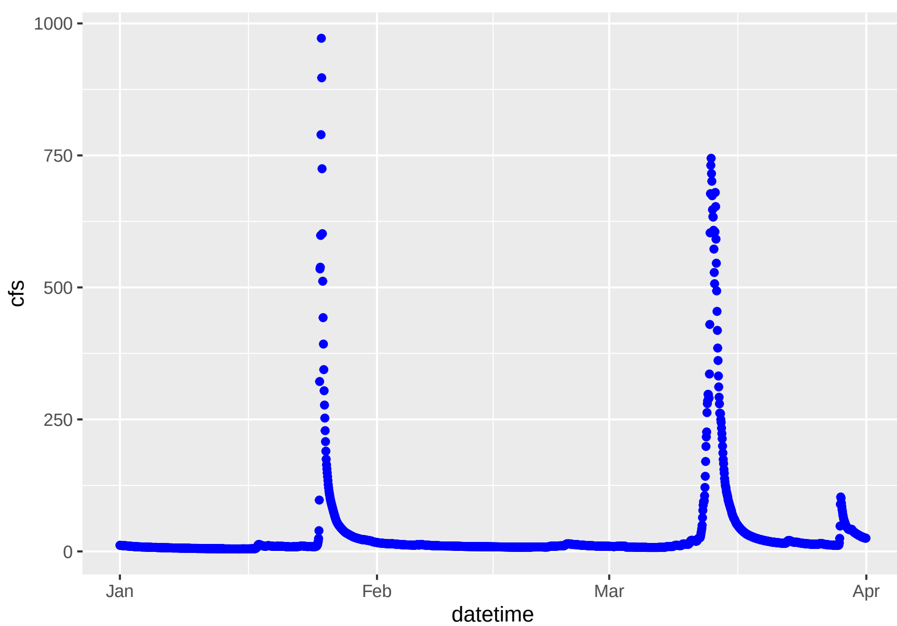
What happens is that if color = "blue" is in the aesthetic, you are telling R that the color used in the geom represents "blue". This is very useful if you have multiple geoms in your plot, are coloring them differently, and are building a legend. But if you are just trying to color the points, it kind of feels like R is trolling you… doesn't it?

Take the color = "blue" out of the aesthetic and you're golden.

```
ggplot(data = Pine, aes(datetime, y = cfs, color = "blue"))+
  geom_point()
```




```
ggplot(data = Pine, aes(x = datetime, y = cfs))+
  geom_point(color = "blue")
```



2.6 Controlling color with a third variable and other functions

Let's plot the data as a line again, but play with it a bit.

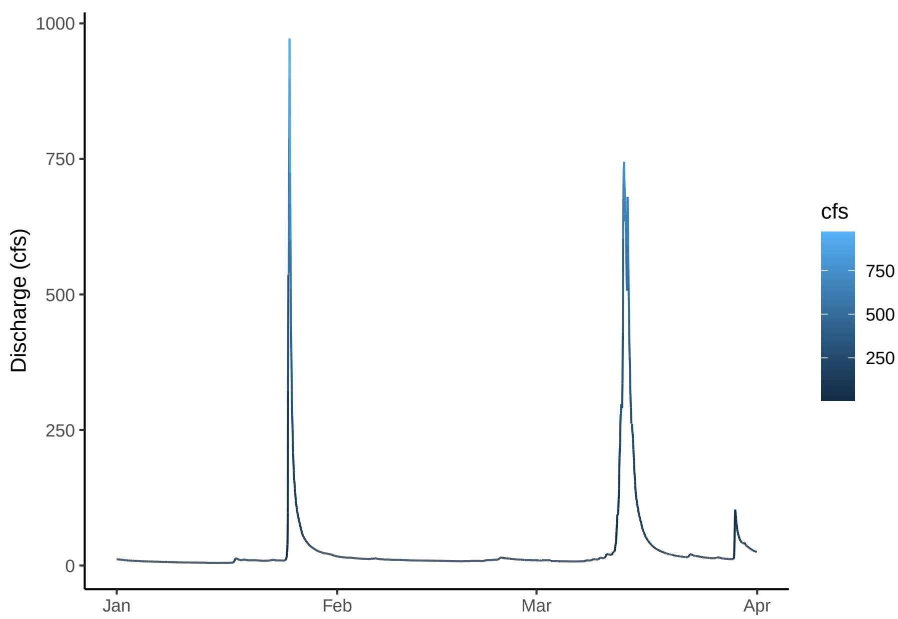
First: make the line blue

Second: change the theme

Third: change the axis labels

Fourth: color by discharge

```
ggplot(data = Pine, aes(x = datetime, y = cfs, color = cfs))+
  geom_line()+
  ylab("Discharge (cfs)")+
  xlab(element_blank())+
  theme_classic()
```



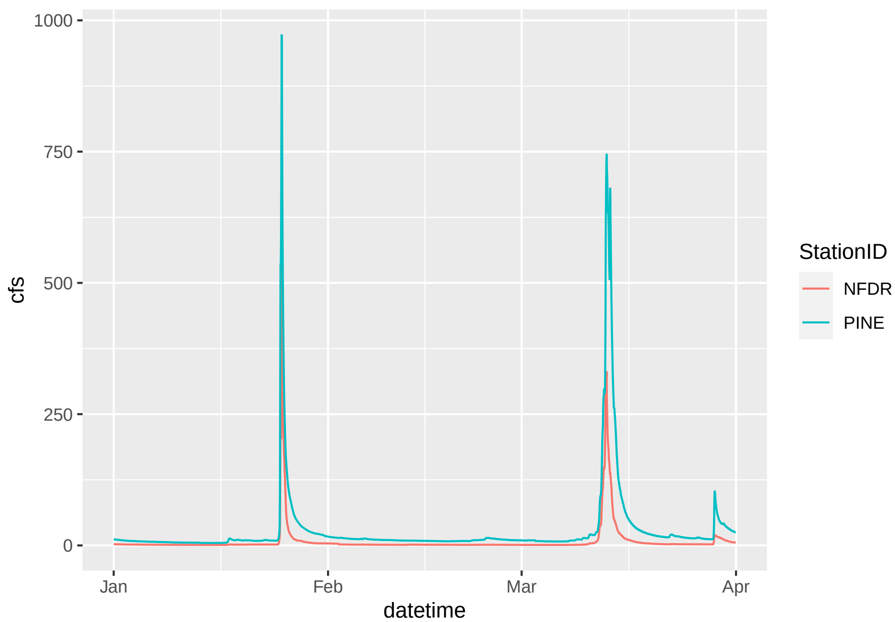
2.7 Plotting multiple groups

The SNP dataset has two different streams: Pine and NFDR

We can look at the two of those a couple of different ways

First, make two lines, colored by the stream by adding color = to your aesthetic.

```
ggplot(data = SNP, aes(x = datetime,y = cfs, color = StationID)) +
  geom_line()
```

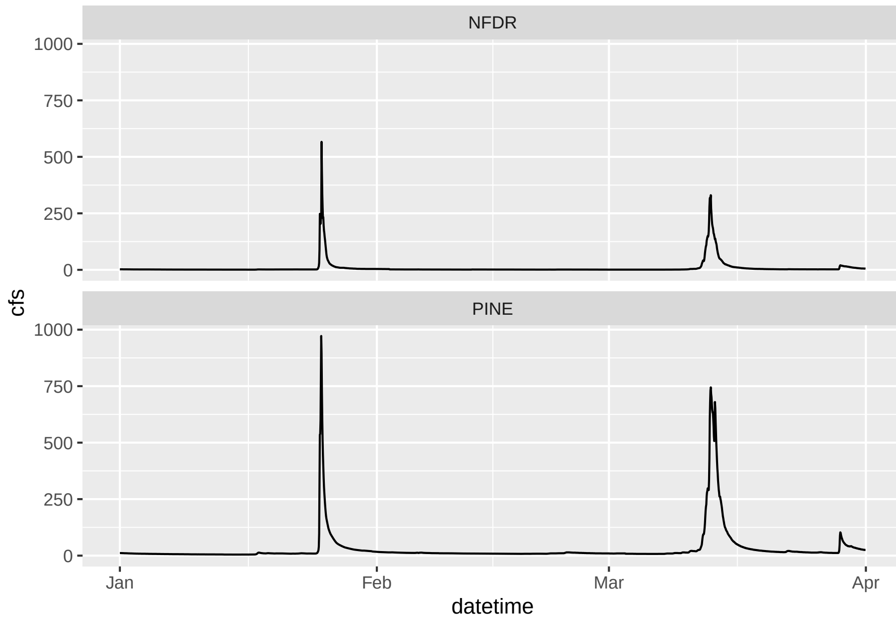


2.8 Facets

We can also use facets.

You must tell the facet_wrap what variable to use to make the separate panels (facet =). It'll decide how to orient them or you can tell it how. We want them to be on top of each other so we are going to tell it we want 2 rows by setting nrow = 2. Note that we have to put the column used to make the facets in quotes after facets =

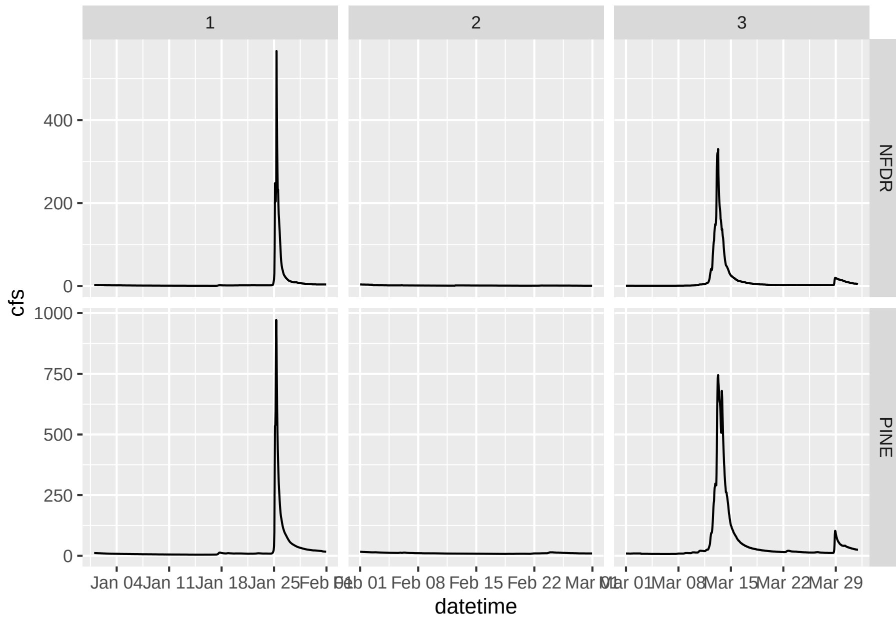
```
ggplot(data = SNP, aes(x = datetime,y = cfs)) +
  geom_line() +
  facet_wrap(facets = "StationID", nrow = 2)
```



2.9 Two variable faceting

You can also use facet_grid() to break your plots up into panels based on two variables. Below we will create a panel for each month in each watershed. Adding scales = "free" allows facet_grid to change the axes. By default, all axes will be the same. This is often what we want, so we can more easily compare magnitudes, but sometimes we are looking for patterns more, so we may want to let the axes have whatever range works for the individual plots.

```
ggplot(data = SNP, aes(x = datetime,y = cfs)) +
  geom_line() +
  facet_grid(StationID ~ month, scales = "free")
```

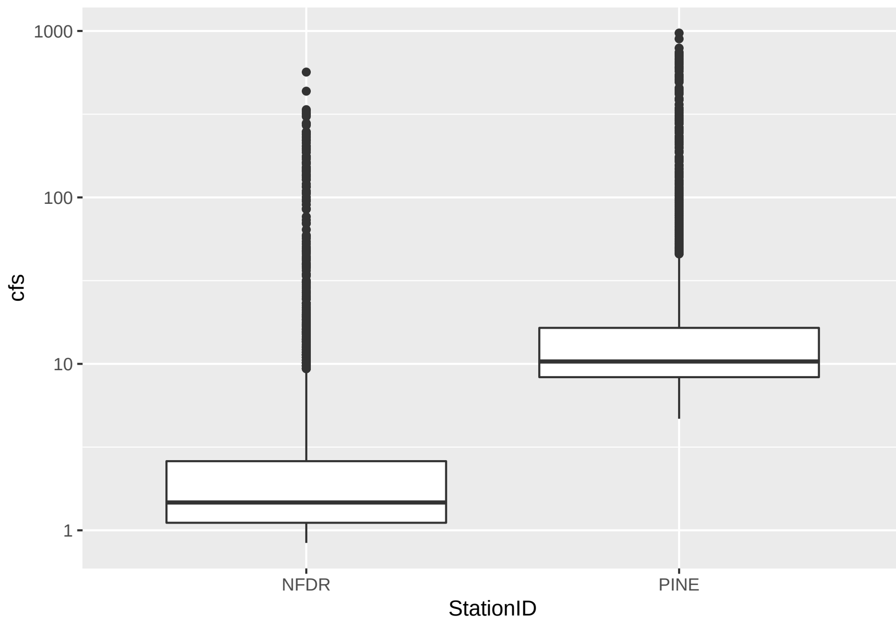


2.10 Boxplots

We can look at these data in other ways as well. A very useful way to look at the variation of two groups is to use a boxplot.

Because the data span several orders of magnitude, we will have to log the y axis to see the differences between the two streams. We do that by adding scale_y_log10()

```
ggplot(data = SNP, aes(x = StationID, y = cfs)) +
  stat_boxplot()+
  scale_y_log10()
```



2.11 More about color, size, etc

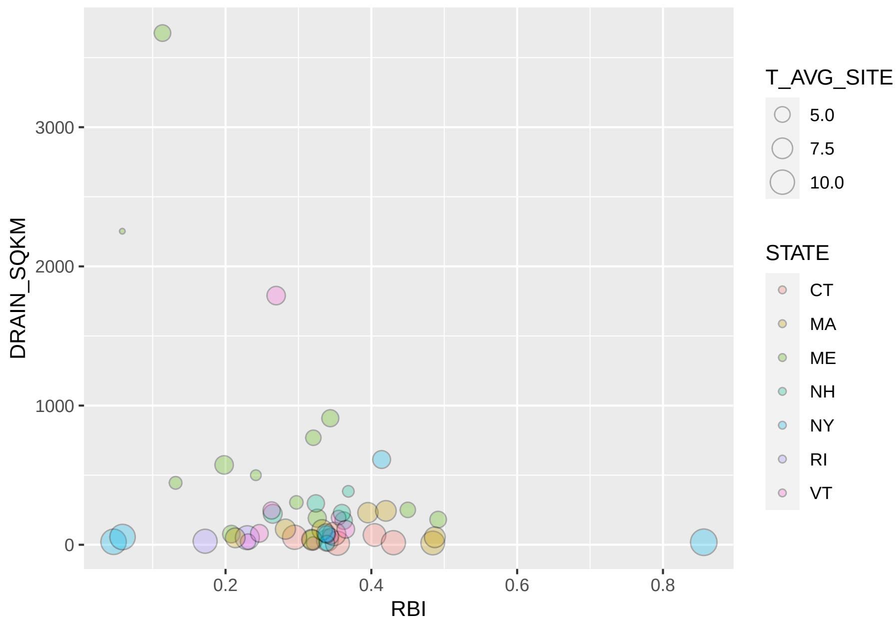
Let's play around a bit with controlling color, point size, etc with other data.

We can control the size of points by putting size = in the aes() and color by putting color =

If you use a point type that has a background, like #21, you can also set the background color using bg =

If points are too close together to see them all you can use a hollow point type or set the alpha lower so the points are transparent (alpha =)

```
ggplot(RBI, aes(RBI, DRAIN_SQKM, size = T_AVG_SITE, bg = STATE))+
  geom_point(pch = 21, alpha = 0.3)
```

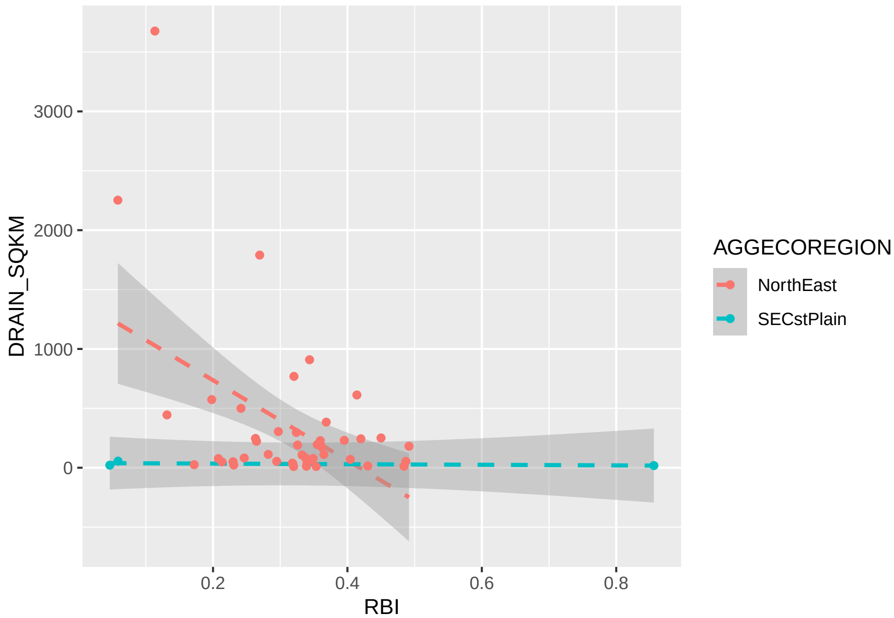


2.12 Multiple geoms

Finally: You can add multiple geoms to the same plot. Examples of when you might want to do this are when you are showing a line fit and want to show the points as well, or maybe showing a boxplot and want to show the data behind it. You simply add additional geom_… lines to add additional geoms.

```
ggplot(RBI, aes(RBI, DRAIN_SQKM, color = AGGECOREGION))+
  stat_smooth(method = "lm", linetype = 2)+
  geom_point()
```

```
## `geom_smooth()` using formula 'y ~ x'
```


3000
2000
1000
0
DRAIN_SQKM
0.2
0.4
0.6
0.8
RBI
AGGECOREGION
NorthEast
SECstPlain

Chapter 3

R Tidyverse Programming Basics

Get this document and a version with empty code chunks at the template repository on github: https://github.com/VT-Hydroinformatics/2-Programming-Basics

3.1 Introduction

We have messed around with plotting a bit and you've seen a little of what R can do. So now let's review or introduce you to some basics. Even if you have worked in R before, it is good to be remind of/practice with this stuff, so stay tuned in!

This exercise covers most of the same principles as two chapters in R for Data Science

Workflow: basics (https://r4ds.had.co.nz/workflow-basics.html)

Data transformation (https://r4ds.had.co.nz/transform.html)

3.2 You can use R as a calculator

If you just type numbers and operators in, R will spit out the results

```
1 + 2
```

```
## [1] 3
```

3.3 You can create new objects using <-

Yea yea, = does the same thing. But use <-. We will call <- assignment or assignment operator. When we are coding in R we use <- to assign values to objects and = to set values for parameters in functions. Using <- helps us differentiate between the two. Norms for formatting are important because they help us understand what code is doing, especially when stuff gets complex.

Oh, one more thing: Surround operators with spaces. Don't code like a gorilla.

x <- 1 looks better than x<-1 and if you disagree you are wrong. :)

You can assign single numbers or entire chunks of data using <-

So if you had an object called my_data and wanted to copy it into my_new_data you could do:

my_new_data <- my_data

You can then recall/print the values in an object by just typing the name by itself.

In the code chunk below, assign a 3 to the object "y" and then print it out.

```
y <- 3
y
```

```
## [1] 3
```

If you want to assign multiple values, you have to put them in the function c() c means combine. R doesn't know what to do if you just give it a bunch of values with space or commas, but if you put them as arguments in the combine function, it'll make them into a vector.

Any time you need to use several values, even passing as an argument to a function, you have to put them in c() or it won't work.

```
a <- c(1,2,3,4)
a
```

```
## [1] 1 2 3 4
```

When you are creating objects, try to give them meaningful names so you can remember what they are. You can't have spaces or operators that mean something else as part of a name. And remember, everything is case sensitive.

Assign the value 5.4 to water_pH and then try to recall it by typing "water_ph"

```
water_pH <- 5.4

#water_ph
```

You can also set objects equal to strings, or values that have letters in them. To do this you just have to put the value in quotes, otherwise R will think it is an object name and tell you it doesn't exist.

Try: name <- "JP" and then name <- JP

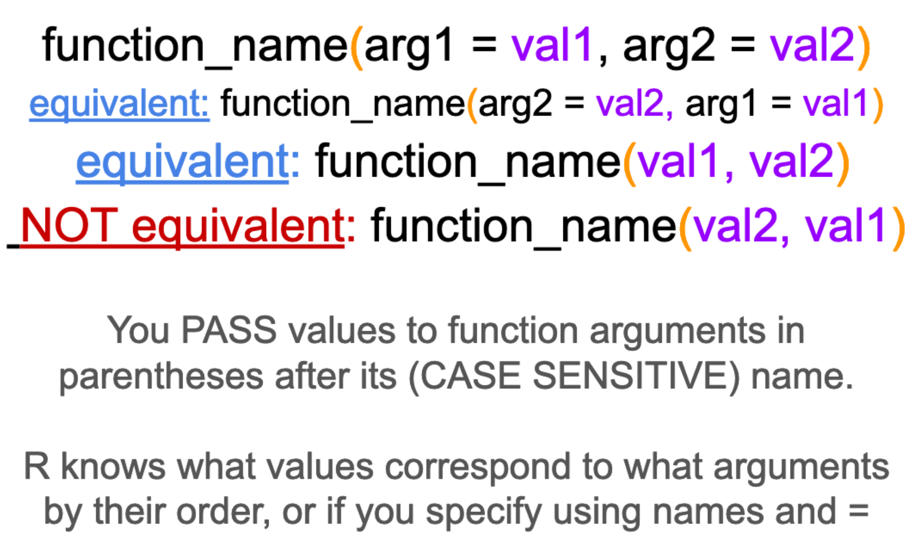
What happens if you forget the ending parenthesis?

Try: name <- "JP

R can be cryptic with it's error messages or other responses, but once you get used to them, you know exactly what is wrong when they pop up.

```
name <- "JP"
#name <- JP
```

3.4 Using functions



As an example, let's try the seq() function, which creates a sequence of numbers.

```
seq(from = 1, to = 10, by = 1)
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10
```

```
#or

seq(1, 10, 1)
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10
```

```
#or

seq(1, 10)
```

```
##  [1]  1  2  3  4  5  6  7  8  9 10
```

```
#what does this do
seq(10,1)
```

```
##  [1] 10  9  8  7  6  5  4  3  2  1
```

3.5 Read in some data.

For the following demonstration we will use the RBI data from a sample of USGS gages we used last class. First we will load the tidyverse library, everything we have done so far is in base R.

Important: read_csv() is the tidyverse csv reading function, the base R function is read.csv(). read.csv() will not read your data in as a tibble, which is the format used by tidyverse functions.

```
library(tidyverse)

rbi <- read_csv("Flashy_Dat_Subset.csv")
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   .default = col_double(),
##   STANAME = col_character(),
##   STATE = col_character(),
##   CLASS = col_character(),
##   AGGECOREGION = col_character()
## )
## i Use `spec()` for the full column specifications.
```

3.6 Wait, hold up. What is a tibble?

Good question. It's a fancy way to store data that works well with tidyverse functions. Let's look at the rbi tibble.

```
head(rbi)
```

```
## # A tibble: 6 x 26
##   site_no    RBI RBIrank STANAME DRAIN_SQKM HUC02 LAT_GAGE LNG_GAGE STATE CLASS
##     <dbl>  <dbl>   <dbl> <chr>        <dbl> <dbl>    <dbl>    <dbl> <chr> <chr>
## 1 1013500 0.0584      35 Fish R~     2253.      1     47.2    -68.6 ME    Ref
## 2 1021480 0.208      300 Old St~       76.7     1     44.9    -67.7 ME    Ref
## 3 1022500 0.198      286 Narrag~      574.      1     44.6    -67.9 ME    Ref
## 4 1029200 0.132      183 Seboei~      445.      1     46.1    -68.6 ME    Ref
## 5 1030500 0.114      147 Mattaw~     3676.      1     45.5    -68.3 ME    Ref
## 6 1031300 0.297      489 Piscat~      304.      1     45.3    -69.6 ME    Ref
## # ... with 16 more variables: AGGECOREGION <chr>, PPTAVG_BASIN <dbl>,
## #   PPTAVG_SITE <dbl>, T_AVG_BASIN <dbl>, T_AVG_SITE <dbl>, T_MAX_BASIN <dbl>,
## #   T_MAXSTD_BASIN <dbl>, T_MAX_SITE <dbl>, T_MIN_BASIN <dbl>,
## #   T_MINSTD_BASIN <dbl>, T_MIN_SITE <dbl>, PET <dbl>, SNOW_PCT_PRECIP <dbl>,
## #   PRECIP_SEAS_IND <dbl>, FLOWYRS_1990_2009 <dbl>, wy00_09 <dbl>
```

Now read in the same data with read.csv() which will NOT read the data as a tibble. How is it different? Output each one in the Console.

Knowing the data type for each column is super helpful for a few reasons.... let's talk about them.

Types: int, dbl, fctr, char, logical

```
rbi_NT <- read.csv("Flashy_Dat_Subset.csv")

head(rbi_NT)
```

```
##   site_no        RBI RBIrank                                    STANAME
## 1 1013500 0.05837454      35            Fish River near Fort Kent, Maine
## 2 1021480 0.20797008     300               Old Stream near Wesley, Maine
## 3 1022500 0.19805382     286     Narraguagus River at Cherryfield, Maine
## 4 1029200 0.13151299     183          Seboeis River near Shin Pond, Maine
## 5 1030500 0.11350485     147 Mattawamkeag River near Mattawamkeag, Maine
## 6 1031300 0.29718786     489        Piscataquis River at Blanchard, Maine
##   DRAIN_SQKM HUC02 LAT_GAGE  LNG_GAGE STATE CLASS AGGECOREGION PPTAVG_BASIN
## 1     2252.7     1 47.23739 -68.58264    ME   Ref    NorthEast        97.42
## 2       76.7     1 44.93694 -67.73611    ME   Ref    NorthEast       115.39
## 3      573.6     1 44.60797 -67.93524    ME   Ref    NorthEast       120.07
```

```
## 4      444.9     1 46.14306 -68.63361    ME   Ref    NorthEast       102.19
## 5     3676.2     1 45.50097 -68.30596    ME   Ref    NorthEast       108.19
## 6      304.4     1 45.26722 -69.58389    ME   Ref    NorthEast       119.83
##   PPTAVG_SITE T_AVG_BASIN T_AVG_SITE T_MAX_BASIN T_MAXSTD_BASIN T_MAX_SITE
## 1       93.53        3.00        3.0        9.67          0.202       10.0
## 2      117.13        5.71        5.8       11.70          0.131       11.9
## 3      129.56        5.95        6.3       11.90          0.344       12.2
## 4      103.24        3.61        4.0        9.88          0.231       10.4
## 5      113.13        4.82        5.4       10.75          0.554       11.7
## 6      120.93        3.60        4.2        9.57          0.431       11.0
##   T_MIN_BASIN T_MINSTD_BASIN T_MIN_SITE   PET SNOW_PCT_PRECIP PRECIP_SEAS_IND
## 1       -2.49          0.269       -2.7 504.7            36.9           0.102
## 2       -0.85          0.123       -0.6 554.2            39.5           0.046
## 3        0.06          0.873        1.4 553.1            38.2           0.047
## 4       -2.13          0.216       -1.5 513.0            36.4           0.070
## 5       -1.49          0.251       -1.2 540.8            37.2           0.033
## 6       -2.46          0.268       -1.7 495.8            40.2           0.030
##   FLOWYRS_1990_2009 wy00_09
## 1                20      10
## 2                11      10
## 3                20      10
## 4                11      10
## 5                20      10
## 6                13      10
```

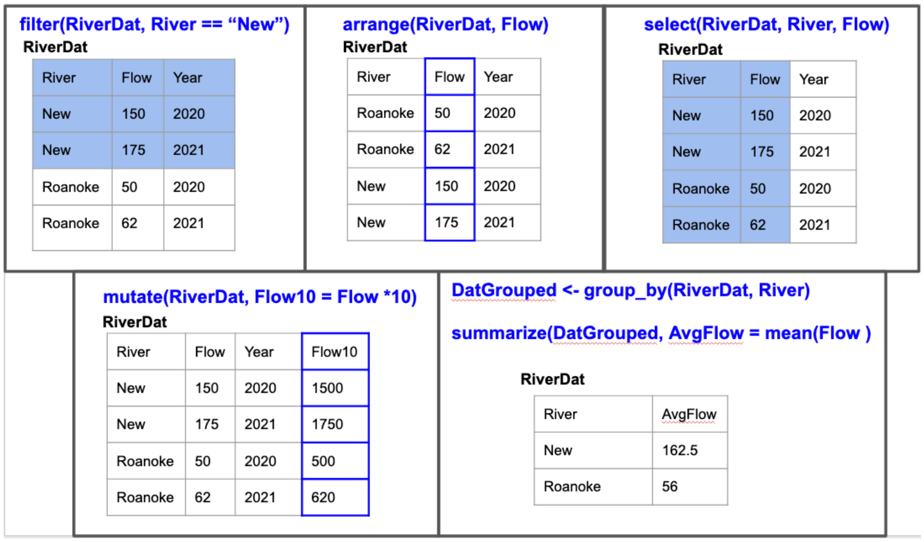
3.7 Data wrangling in dplyr

If you forget syntax or what the following functions do, here is an excellent cheat sheet: https://rstudio.com/wp-content/uploads/2015/02/data-wrangling-cheatsheet.pdf

We will demo five functions below:

- **filter()** - returns rows that meet specified conditions
- **arrange()** - reorders rows
- **select()** - pull out variables (columns)
- **mutate()** - create new variables (columns) or reformat existing ones
- **summarize()** - collapse groups of values into summary stats

With all of these, the first argument is the data and then the arguments after that specify what you want the function to do.



3.8 Filter

Write an expression that returns data in rbi for the state of Maine (ME)

Operators:
== equal
!= not equal
>= , <= greater than or equal to, less than or equal to
>, < greater than or less then
%in% included in a list of values
& and
| or

```
filter(rbi, STATE == "ME")
```

```
## # A tibble: 13 x 26
##    site_no    RBI RBIrank STANAME DRAIN_SQKM HUC02 LAT_GAGE LNG_GAGE STATE CLASS
##      <dbl>  <dbl>   <dbl> <chr>        <dbl> <dbl>    <dbl>    <dbl> <chr> <chr>
##  1 1013500 0.0584      35 Fish R~     2253.      1     47.2    -68.6 ME    Ref
##  2 1021480 0.208      300 Old St~       76.7     1     44.9    -67.7 ME    Ref
##  3 1022500 0.198      286 Narrag~      574.      1     44.6    -67.9 ME    Ref
##  4 1029200 0.132      183 Seboei~      445.      1     46.1    -68.6 ME    Ref
##  5 1030500 0.114      147 Mattaw~     3676.      1     45.5    -68.3 ME    Ref
##  6 1031300 0.297      489 Piscat~      304.      1     45.3    -69.6 ME    Ref
##  7 1031500 0.320      545 Piscat~      769       1     45.2    -69.3 ME    Ref
##  8 1037380 0.318      537 Ducktr~       39       1     44.3    -69.1 ME    Ref
```

```
##  9 1044550 0.242      360 Spence~      500.       1      45.3    -70.2 ME    Ref
## 10 1047000 0.344      608 Carrab~      909.       1      44.9    -70.0 ME    Ref
## 11 1054200 0.492      805 Wild R~      181        1      44.4    -71.0 ME    Ref
## 12 1055000 0.450      762 Swift ~      251.       1      44.6    -70.6 ME    Ref
## 13 1057000 0.326      561 Little~      191.       1      44.3    -70.5 ME    Ref
## # ... with 16 more variables: AGGECOREGION <chr>, PPTAVG_BASIN <dbl>,
## #   PPTAVG_SITE <dbl>, T_AVG_BASIN <dbl>, T_AVG_SITE <dbl>, T_MAX_BASIN <dbl>,
## #   T_MAXSTD_BASIN <dbl>, T_MAX_SITE <dbl>, T_MIN_BASIN <dbl>,
## #   T_MINSTD_BASIN <dbl>, T_MIN_SITE <dbl>, PET <dbl>, SNOW_PCT_PRECIP <dbl>,
## #   PRECIP_SEAS_IND <dbl>, FLOWYRS_1990_2009 <dbl>, wy00_09 <dbl>
```

3.8.1 Multiple conditions

How many gages are there in Maine with an rbi greater than 0.25

```
filter(rbi, STATE == "ME" & RBI > 0.25)
```

```
## # A tibble: 7 x 26
##   site_no   RBI RBIrank STANAME DRAIN_SQKM HUC02 LAT_GAGE LNG_GAGE STATE CLASS
##     <dbl> <dbl>   <dbl> <chr>        <dbl> <dbl>    <dbl>    <dbl> <chr> <chr>
## 1 1031300 0.297     489 Piscat~      304.      1     45.3    -69.6 ME    Ref
## 2 1031500 0.320     545 Piscat~      769       1     45.2    -69.3 ME    Ref
## 3 1037380 0.318     537 Ducktr~       39       1     44.3    -69.1 ME    Ref
## 4 1047000 0.344     608 Carrab~      909.      1     44.9    -70.0 ME    Ref
## 5 1054200 0.492     805 Wild R~      181       1     44.4    -71.0 ME    Ref
## 6 1055000 0.450     762 Swift ~      251.      1     44.6    -70.6 ME    Ref
## 7 1057000 0.326     561 Little~      191.      1     44.3    -70.5 ME    Ref
## # ... with 16 more variables: AGGECOREGION <chr>, PPTAVG_BASIN <dbl>,
## #   PPTAVG_SITE <dbl>, T_AVG_BASIN <dbl>, T_AVG_SITE <dbl>, T_MAX_BASIN <dbl>,
## #   T_MAXSTD_BASIN <dbl>, T_MAX_SITE <dbl>, T_MIN_BASIN <dbl>,
## #   T_MINSTD_BASIN <dbl>, T_MIN_SITE <dbl>, PET <dbl>, SNOW_PCT_PRECIP <dbl>,
## #   PRECIP_SEAS_IND <dbl>, FLOWYRS_1990_2009 <dbl>, wy00_09 <dbl>
```

3.9 Arrange

Arrange sorts by a column in your dataset.

Sort the rbi data by the RBI column in ascending and then descending order

```
arrange(rbi, RBI)
```

```
## # A tibble: 49 x 26
##    site_no    RBI RBIrank STANAME DRAIN_SQKM HUC02 LAT_GAGE LNG_GAGE STATE CLASS
```

```
##      <dbl>  <dbl>   <dbl> <chr>        <dbl> <dbl>    <dbl>    <dbl> <chr> <chr>
##  1 1305500 0.0464      18 SWAN R~       21.3     2     40.8    -73.0 NY    Non-~
##  2 1013500 0.0584      35 Fish R~     2253.      1     47.2    -68.6 ME    Ref
##  3 1306460 0.0587      37 CONNET~       55.7     2     40.8    -73.2 NY    Non-~
##  4 1030500 0.114      147 Mattaw~     3676.      1     45.5    -68.3 ME    Ref
##  5 1029200 0.132      183 Seboei~      445.      1     46.1    -68.6 ME    Ref
##  6 1117468 0.172      244 BEAVER~       25.3     1     41.5    -71.6 RI    Ref
##  7 1022500 0.198      286 Narrag~      574.      1     44.6    -67.9 ME    Ref
##  8 1021480 0.208      300 Old St~       76.7     1     44.9    -67.7 ME    Ref
##  9 1162500 0.213      311 PRIEST~       49.7     1     42.7    -72.1 MA    Ref
## 10 1117370 0.230      338 QUEEN ~       50.5     1     41.5    -71.6 RI    Ref
## # ... with 39 more rows, and 16 more variables: AGGECOREGION <chr>,
## #   PPTAVG_BASIN <dbl>, PPTAVG_SITE <dbl>, T_AVG_BASIN <dbl>, T_AVG_SITE <dbl>,
## #   T_MAX_BASIN <dbl>, T_MAXSTD_BASIN <dbl>, T_MAX_SITE <dbl>,
## #   T_MIN_BASIN <dbl>, T_MINSTD_BASIN <dbl>, T_MIN_SITE <dbl>, PET <dbl>,
## #   SNOW_PCT_PRECIP <dbl>, PRECIP_SEAS_IND <dbl>, FLOWYRS_1990_2009 <dbl>,
## #   wy00_09 <dbl>
```

```
arrange(rbi, desc(RBI))
```

```
## # A tibble: 49 x 26
##    site_no   RBI RBIrank STANAME DRAIN_SQKM HUC02 LAT_GAGE LNG_GAGE STATE CLASS
##      <dbl> <dbl>   <dbl> <chr>        <dbl> <dbl>    <dbl>    <dbl> <chr> <chr>
##  1 1311500 0.856    1017 VALLEY~       18.1     2     40.7    -73.7 NY    Non-~
##  2 1054200 0.492     805 Wild R~      181       1     44.4    -71.0 ME    Ref
##  3 1187300 0.487     800 HUBBAR~       53.9     1     42.0    -72.9 MA    Ref
##  4 1105600 0.484     797 OLD SW~       12.7     1     42.2    -70.9 MA    Non-~
##  5 1055000 0.450     762 Swift ~      251.      1     44.6    -70.6 ME    Ref
##  6 1195100 0.430     744 INDIAN~       14.8     1     41.3    -72.5 CT    Ref
##  7 1181000 0.420     732 WEST B~      244.      1     42.2    -72.9 MA    Ref
##  8 1350000 0.414     721 SCHOHA~      612.      2     42.3    -74.4 NY    Ref
##  9 1121000 0.404     710 MOUNT ~       70.3     1     41.8    -72.2 CT    Ref
## 10 1169000 0.395     688 NORTH ~      231.      1     42.6    -72.7 MA    Ref
## # ... with 39 more rows, and 16 more variables: AGGECOREGION <chr>,
## #   PPTAVG_BASIN <dbl>, PPTAVG_SITE <dbl>, T_AVG_BASIN <dbl>, T_AVG_SITE <dbl>,
## #   T_MAX_BASIN <dbl>, T_MAXSTD_BASIN <dbl>, T_MAX_SITE <dbl>,
## #   T_MIN_BASIN <dbl>, T_MINSTD_BASIN <dbl>, T_MIN_SITE <dbl>, PET <dbl>,
## #   SNOW_PCT_PRECIP <dbl>, PRECIP_SEAS_IND <dbl>, FLOWYRS_1990_2009 <dbl>,
## #   wy00_09 <dbl>
```

3.10 Select

There are too many columns! You will often want to do this when you are manipulating the structure of your data and need to trim it down to only include what you will use.

Select Site name, state, and RBI from the rbi data

Note they come back in the order you put them in in the function, not the order they were in in the original data.

You can do a lot more with select, especially when you need to select a bunch of columns but don't want to type them all out. But we don't need to cover all that today. For a taste though, if you want to select a group of columns you can specify the first and last with a colon in between (first:last) and it'll return all of them. Select the rbi columns from site_no to DRAIN_SQKM.

```
select(rbi, STANAME, STATE, RBI)
```

```
## # A tibble: 49 x 3
##    STANAME                                      STATE    RBI
##    <chr>                                        <chr>  <dbl>
##  1 Fish River near Fort Kent, Maine             ME    0.0584
##  2 Old Stream near Wesley, Maine                ME    0.208
##  3 Narraguagus River at Cherryfield, Maine      ME    0.198
##  4 Seboeis River near Shin Pond, Maine          ME    0.132
##  5 Mattawamkeag River near Mattawamkeag, Maine  ME    0.114
##  6 Piscataquis River at Blanchard, Maine        ME    0.297
##  7 Piscataquis River near Dover-Foxcroft, Maine ME    0.320
##  8 Ducktrap River near Lincolnville, Maine      ME    0.318
##  9 Spencer Stream near Grand Falls, Maine       ME    0.242
## 10 Carrabassett River near North Anson, Maine   ME    0.344
## # ... with 39 more rows
```

```
select(rbi, site_no:DRAIN_SQKM)
```

```
## # A tibble: 49 x 5
##    site_no    RBI RBIrank STANAME                                      DRAIN_SQKM
##      <dbl>  <dbl>   <dbl> <chr>                                             <dbl>
##  1 1013500 0.0584      35 Fish River near Fort Kent, Maine                2253.
##  2 1021480 0.208      300 Old Stream near Wesley, Maine                     76.7
##  3 1022500 0.198      286 Narraguagus River at Cherryfield, Maine          574.
##  4 1029200 0.132      183 Seboeis River near Shin Pond, Maine              445.
##  5 1030500 0.114      147 Mattawamkeag River near Mattawamkeag, Maine     3676.
##  6 1031300 0.297      489 Piscataquis River at Blanchard, Maine            304.
##  7 1031500 0.320      545 Piscataquis River near Dover-Foxcroft, Mai~      769
##  8 1037380 0.318      537 Ducktrap River near Lincolnville, Maine           39
##  9 1044550 0.242      360 Spencer Stream near Grand Falls, Maine           500.
## 10 1047000 0.344      608 Carrabassett River near North Anson, Maine       909.
## # ... with 39 more rows
```

3.11 Mutate

Use mutate to add new columns based on additional ones. Common uses are to create a column of data in different units, or to calculate something based on two columns. You can also use it to just update a column, by naming the new column the same as the original one (but be careful because you'll lose the original one!). I commonly use this when I am changing the datatype of a column, say from a character to a factor or a string to a date.

Create a new column in rbi called T_RANGE by subtracting T_MIN_SITE from T_MAX_SITE

```
mutate(rbi, T_RANGE = T_MAX_SITE - T_MIN_SITE)
```

```
## # A tibble: 49 x 27
##    site_no    RBI RBIrank STANAME DRAIN_SQKM HUC02 LAT_GAGE LNG_GAGE STATE CLASS
##      <dbl>  <dbl>   <dbl> <chr>        <dbl> <dbl>    <dbl>    <dbl> <chr> <chr>
##  1 1013500 0.0584      35 Fish R~     2253.      1     47.2    -68.6 ME    Ref
##  2 1021480 0.208      300 Old St~       76.7     1     44.9    -67.7 ME    Ref
##  3 1022500 0.198      286 Narrag~      574.      1     44.6    -67.9 ME    Ref
##  4 1029200 0.132      183 Seboei~      445.      1     46.1    -68.6 ME    Ref
##  5 1030500 0.114      147 Mattaw~     3676.      1     45.5    -68.3 ME    Ref
##  6 1031300 0.297      489 Piscat~      304.      1     45.3    -69.6 ME    Ref
##  7 1031500 0.320      545 Piscat~      769       1     45.2    -69.3 ME    Ref
##  8 1037380 0.318      537 Ducktr~       39       1     44.3    -69.1 ME    Ref
##  9 1044550 0.242      360 Spence~      500.      1     45.3    -70.2 ME    Ref
## 10 1047000 0.344      608 Carrab~      909.      1     44.9    -70.0 ME    Ref
## # ... with 39 more rows, and 17 more variables: AGGECOREGION <chr>,
## #   PPTAVG_BASIN <dbl>, PPTAVG_SITE <dbl>, T_AVG_BASIN <dbl>, T_AVG_SITE <dbl>,
## #   T_MAX_BASIN <dbl>, T_MAXSTD_BASIN <dbl>, T_MAX_SITE <dbl>,
## #   T_MIN_BASIN <dbl>, T_MINSTD_BASIN <dbl>, T_MIN_SITE <dbl>, PET <dbl>,
## #   SNOW_PCT_PRECIP <dbl>, PRECIP_SEAS_IND <dbl>, FLOWYRS_1990_2009 <dbl>,
## #   wy00_09 <dbl>, T_RANGE <dbl>
```

When downloading data from the USGS through R, you have to enter the gage ID as a character, even though they are all made up of numbers. So to practice doing this, update the site_no column to be a character datatype

```
mutate(rbi, site_no = as.character(site_no))
```

```
## # A tibble: 49 x 26
##    site_no    RBI RBIrank STANAME DRAIN_SQKM HUC02 LAT_GAGE LNG_GAGE STATE CLASS
##    <chr>    <dbl>   <dbl> <chr>        <dbl> <dbl>    <dbl>    <dbl> <chr> <chr>
##  1 1013500 0.0584      35 Fish R~     2253.      1     47.2    -68.6 ME    Ref
```

```
##  2 1021480 0.208      300 Old St~       76.7      1      44.9    -67.7 ME    Ref
##  3 1022500 0.198      286 Narrag~      574.       1      44.6    -67.9 ME    Ref
##  4 1029200 0.132      183 Seboei~      445.       1      46.1    -68.6 ME    Ref
##  5 1030500 0.114      147 Mattaw~     3676.       1      45.5    -68.3 ME    Ref
##  6 1031300 0.297      489 Piscat~      304.       1      45.3    -69.6 ME    Ref
##  7 1031500 0.320      545 Piscat~      769        1      45.2    -69.3 ME    Ref
##  8 1037380 0.318      537 Ducktr~       39        1      44.3    -69.1 ME    Ref
##  9 1044550 0.242      360 Spence~      500.       1      45.3    -70.2 ME    Ref
## 10 1047000 0.344      608 Carrab~      909.       1      44.9    -70.0 ME    Ref
## # ... with 39 more rows, and 16 more variables: AGGECOREGION <chr>,
## #   PPTAVG_BASIN <dbl>, PPTAVG_SITE <dbl>, T_AVG_BASIN <dbl>, T_AVG_SITE <dbl>,
## #   T_MAX_BASIN <dbl>, T_MAXSTD_BASIN <dbl>, T_MAX_SITE <dbl>,
## #   T_MIN_BASIN <dbl>, T_MINSTD_BASIN <dbl>, T_MIN_SITE <dbl>, PET <dbl>,
## #   SNOW_PCT_PRECIP <dbl>, PRECIP_SEAS_IND <dbl>, FLOWYRS_1990_2009 <dbl>,
## #   wy00_09 <dbl>
```

3.12 Summarize

Summarize will perform an operation on all of your data, or groups if you assign groups.

Use summarize to compute the mean, min, and max rbi

```
summarize(rbi, meanrbi = mean(RBI), maxrbi = max(RBI), minrbi = min(RBI))
```

```
## # A tibble: 1 x 3
##   meanrbi maxrbi minrbi
##     <dbl>  <dbl>  <dbl>
## 1   0.316  0.856 0.0464
```

Now use the group function to group by state and then summarize in the same way as above

```
rbistate <- group_by(rbi, STATE)
summarize(rbistate, meanrbi = mean(RBI), maxrbi = max(RBI), minrbi = min(RBI))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 7 x 4
##   STATE meanrbi maxrbi minrbi
##   <chr>   <dbl>  <dbl>  <dbl>
## 1 CT      0.366  0.430 0.295
## 2 MA      0.367  0.487 0.213
```

```
## 3 ME      0.269  0.492 0.0584
## 4 NH      0.336  0.368 0.265
## 5 NY      0.342  0.856 0.0464
## 6 RI      0.201  0.230 0.172
## 7 VT      0.299  0.365 0.231
```

3.13 Multiple operations with pipes

The pipe operator %>% allows you to perform multiple operations in a sequence without saving intermediate steps. Not only is this more efficient, but structuring operations with pipes is also more intuitive than nesting functions within functions (the other way you can do multiple operations).

3.13.1 Let's say we want to tell R to make a PB&J sandwich by using the pbbread(), jbread(), and joinslices() functions and the data "ingredients". If we do this saving each step if would look like this:

> sando <- pbbread(ingredients)
>
> sando <- jbread(sando)
>
> sando <- joinslices(sando)

3.13.2 If we nest the functions together we get this

> joinslice(jbread(pbbread(ingredients)))

Efficient… but tough to read/interpret

3.13.3 Using the pipe it would look like this

> ingredients %>%
> pbbread() %>%
> jbread() %>%
> joinslices()

Much easier to follow!

3.13.4 When you use the pipe, it basically takes whatever came out of the first function and puts it into the data argument for the next one

so rbi %>% group_by(STATE) is the same as group_by(rbi, STATE)

Take the groupby and summarize code from above and perform the operation using the pipe

```
rbi %>%
  group_by(STATE) %>%
  summarize(meanrbi = mean(RBI), maxrbi = max(RBI), minrbi = min(RBI))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
## # A tibble: 7 x 4
##   STATE meanrbi maxrbi minrbi
##   <chr>   <dbl>  <dbl>  <dbl>
## 1 CT      0.366  0.430 0.295
## 2 MA      0.367  0.487 0.213
## 3 ME      0.269  0.492 0.0584
## 4 NH      0.336  0.368 0.265
## 5 NY      0.342  0.856 0.0464
## 6 RI      0.201  0.230 0.172
## 7 VT      0.299  0.365 0.231
```

3.14 Save your results to a new tibble

We have just been writing everything to the screen so we can see what we are doing… In order to save anything we do with these functions to work with it later, we just have to use the assignment operator (<-) to store the data.

One kind of awesome thing about the assignment operator is that it works both ways…

x <- 3 and 3 -> x do the same thing (WHAT?!)

So you can do the assignment at the beginning of the end of your dplyr workings, whatever you like best.

Use the assignment operator to save the summary table you just made.

```
stateRBIs <- rbi %>%
  group_by(STATE) %>%
  summarize(meanrbi = mean(RBI), maxrbi = max(RBI), minrbi = min(RBI))
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

```
# Notice when you do this it doesn't output the result...
# You can see what you did by clickon in stateRBIs in your environment panel
# or just type stateRBIs

stateRBIs
```

```
## # A tibble: 7 x 4
##   STATE meanrbi maxrbi minrbi
##   <chr>   <dbl>  <dbl>  <dbl>
## 1 CT      0.366  0.430 0.295
## 2 MA      0.367  0.487 0.213
## 3 ME      0.269  0.492 0.0584
## 4 NH      0.336  0.368 0.265
## 5 NY      0.342  0.856 0.0464
## 6 RI      0.201  0.230 0.172
## 7 VT      0.299  0.365 0.231
```

3.15 What about NAs?

We will talk more about this when we discuss stats, but some operations will fail if there are NA's in the data. If appropriate, you can tell functions like mean() to ignore NAs. You can also use drop_na() if you're working with a tibble. But be aware if you use that and save the result, drop_na() gets rid of the whole row, not just the NA. Because what would you replace it with.... an NA?

```
x <- c(1,2,3,4,NA)
mean(x, na.rm = TRUE)
```

```
## [1] 2.5
```

3.16 What are some things you think I'll ask you to do for the activity next class?

Chapter 4

ACTIVITY Intro Skills

Get this document at the template repository on github: https://github.com/VT-Hydroinformatics/3-Activity-Intro-Skills

4.1 Problem 1

Load the tidyverse and lubridate libraries.

Read in the PINE_NFDR_Jan-Mar_2010 csv using read_csv()

Make a plot with the date on the x axis, discharge on the y axis. Show the discharge of the two watersheds as a line, coloring by watershed (StationID)

4.2 Problem 2

Make a boxplot to compare the discharge of Pine to NFDR for February 2010.

Hint: use the pipe operator and the filter() function.

Hint2: when you filter dates, you have to let R know you're giving it a date. You can do this by using the mdy() function from lubridate.

4.3 Problem 3

Read in the Flashy Dat Subset file.

For only sites in ME, NH, and VT: Plot PET (Potential Evapotranspiration) on the X axis and RBI (flashiness index) on the Y axis. Color the points based on what state they are in. Use the classic ggplot theme.

4.4 Problem 4

We want to look at the amount of snow for each site in the flashy dataset. Problem is, we are only given the average amount of total precip (PPTAVG_BASIN) and the percentage of snow (SNOW_PCT_PRECIP).

Create a new column in the dataset called SNOW_AVG_BASIN and make it equal to the average total precip times the percentage of snow (careful with the percentage number).

Make a barplot showing the amount of snow for each site in Maine. Put station name on the x axis and snow amount on the y. You have to add something to geom_bar() to use it for a 2 variable plot… check out the ggplot cheatsheet or do a quick internet search.

The x axis of the resulting plot looks terrible! Can you figure out how to rotate the X axis labels so we can read them?

4.5 Problem 5

Create a new tibble that contains the min, max, and mean PET for each state. Sort the tibble by mean PET from high to low. Give your columns meaningful names within the summarize function or using rename().

Be sure your code outputs the tibble.

4.6 Problem 6

Take the tibble from problem 5. Create a new column that is the Range of the PET (max PET - min PET). Then get rid of the max PET and min PET columns so the tibble just has columns for State, mean PET, and PET range.

Be sure your code outputs the tibble.

Chapter 5

Introduction to Basic Statistics

Get this document and a version with empty code chunks at the template repository on github: https://github.com/VT-Hydroinformatics/4-Intro-Stats

```
library(tidyverse)
library(patchwork)
```

```
## Warning: package 'patchwork' was built under R version 3.6.2
```

```
theme_set(theme_classic())
```

5.1 Reading for this section: Statistical Methods in Water Resources: Chapter 1

https://pubs.usgs.gov/tm/04/a03/tm4a3.pdf

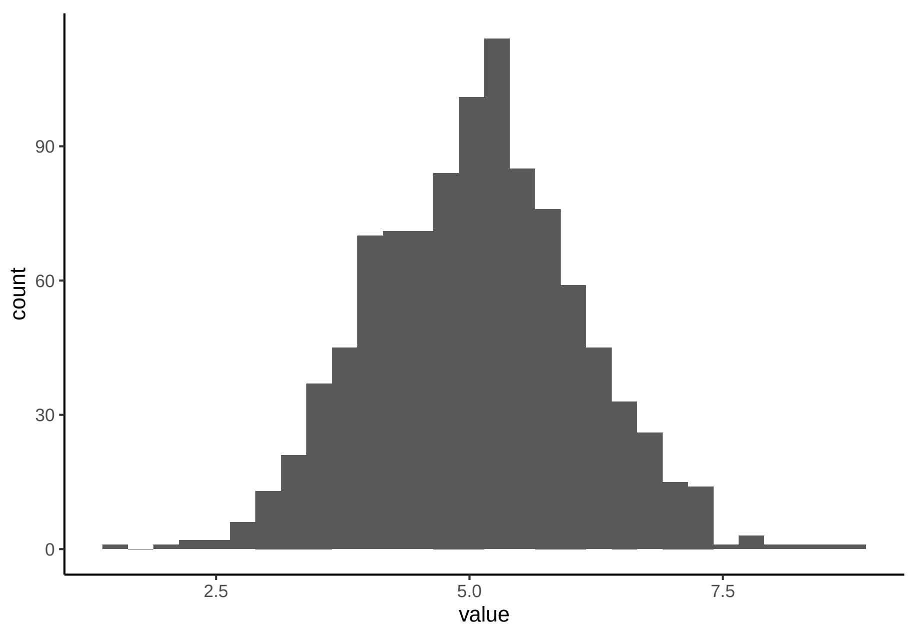
5.2 Questions for today:

- *What is the difference between a sample and a population?*
- *How do we look at the distribution of data in a sample*
- *How do we measure aspects of a distribution*
- *What is a normal distribution?*

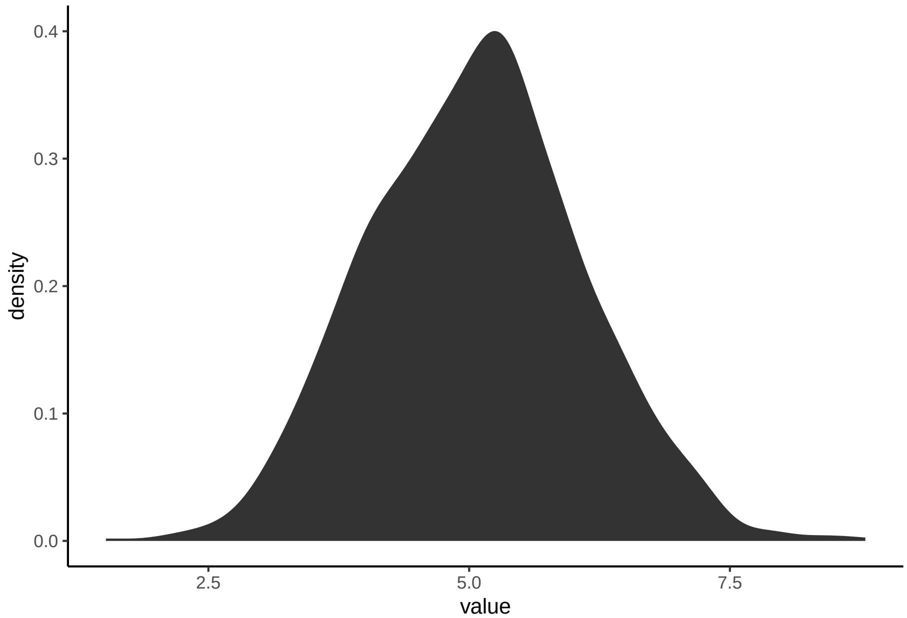
First let's generate some synthetic data and talk about how to visualize it.

```
#generate a normal distribution
ExNorm <- rnorm(1000, mean = 5) %>%
  as_tibble()

#look at distributions
#histogram
ExNorm %>%
  ggplot(aes(value)) +
  geom_histogram()
```

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




```
#pdf
ExNorm %>%
  ggplot(aes(value)) +
  stat_density()
```




```
#Let's generate a plot that makes comparing these two easier
```

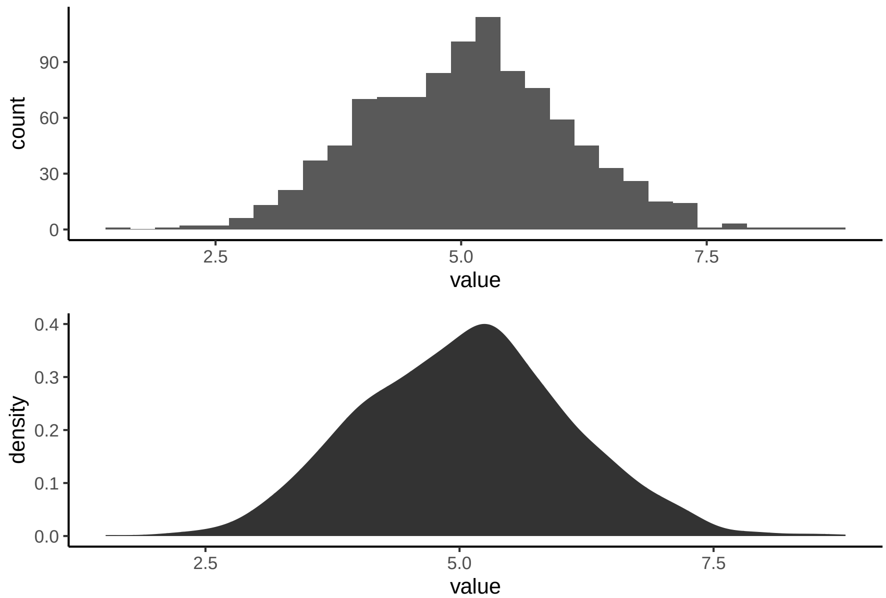
5.2.1 Stack plots to compare histogram and pdf

We will save each plot as ggplot object and then output them using the patchwork package (loaded in the setup chunk).

What is the difference between a histogram and a pdf?
What features of the histogram are preserved? Which are lost?

```
#histogram
exhist <- ExNorm %>%
  ggplot(aes(value)) +
  geom_histogram()

#pdf
expdf <- ExNorm %>%
  ggplot(aes(value)) +
  stat_density()

#put the plots side by side with + or on top of each other with /
exhist/expdf
```

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



5.3 What is the difference between a sample and a population.

Simply put: a population is the thing you are trying to measure. A sample is the data you measure in an effort to measure the population. A sample is a subset of a population.

Let's write some code for an example:

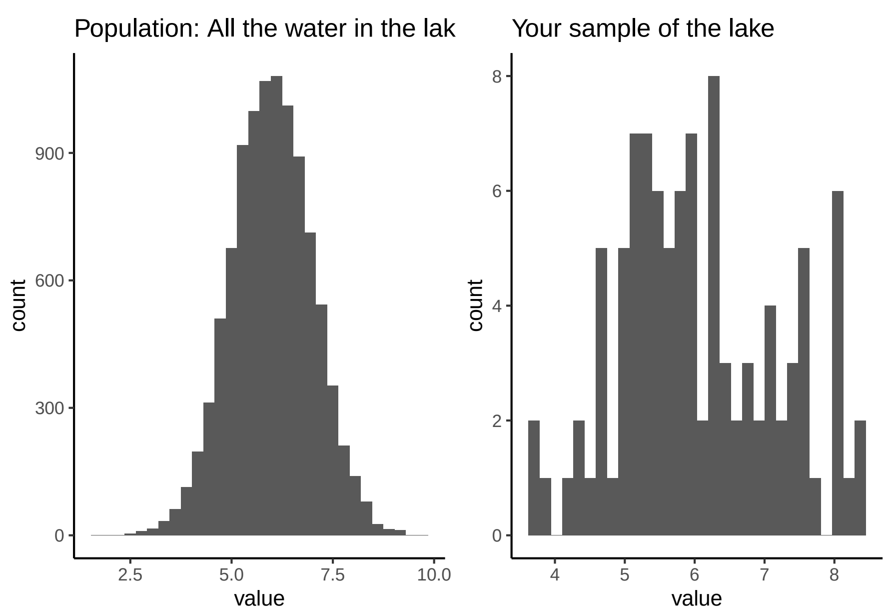
We will create a POPULATION that is a large set of numbers. Think of this is as the concentration of Calcium in every bit of water in a lake. Then we will create a SAMPLE by randomly grabbing values from the POPULATION. This simulates us going around in a boat and taking grab samples in an effort to figure out the concentration of calcium in the lake.

We can then run this code a bunch of times, you'll get a different sample each time. You can also take a smaller or larger number of samples by changing "size" in the sample() function.

How does your sample distribution look similar or different from the population?
Why does the sample change every time you run it?
What happens as you increase or decrease the number of samples?
What happens if you set the number of samples to the size of the population?

```
all_the_water <- rnorm(10000, mean = 6) %>% as_tibble()

sample_of_water <- sample(all_the_water$value, size = 100, replace = FALSE) %>% as_tibble()

population_hist <- all_the_water %>%
  ggplot(aes(value))+
  geom_histogram()+
  ggtitle("Population: All the water in the lake")

sample_hist <- sample_of_water %>%
  ggplot(aes(value))+
  geom_histogram()+
  ggtitle("Your sample of the lake")

population_hist + sample_hist
```

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



5.4 Measuring our sample distribution: central tendency.

When we take a sample of a population, there are a few things we will want to measure about the distribution of values: where is the middle, how variable is it, and is it skewed to one side or another?

The first of these, "where is the middle?" is addressed with measures of central tendency. We will discuss three possible ways to measure this. The mean, median, and weighted mean.

To explain the importance of choosing between the mean and median, we will first import some discharge data. Read in the PINE discharge data.

```
pineQ <- read_csv("PINE_Jan-Mar_2010.csv")
```

```
##
## -- Column specification --------------------------------------------------------
## cols(
##   StationID = col_character(),
##   cfs = col_double(),
##   surrogate = col_character(),
##   datetime = col_datetime(format = ""),
##   year = col_double(),
##   quarter = col_double(),
##   month = col_double(),
##   day = col_double()
## )
```

To find the mean (average), you just sum up all the values in your sample and divide by the number of values.

To find the median, you put the values IN ORDER, and choose the middle value. The middle value is the one where there are the same number of values higher than that value as there are values lower than it.

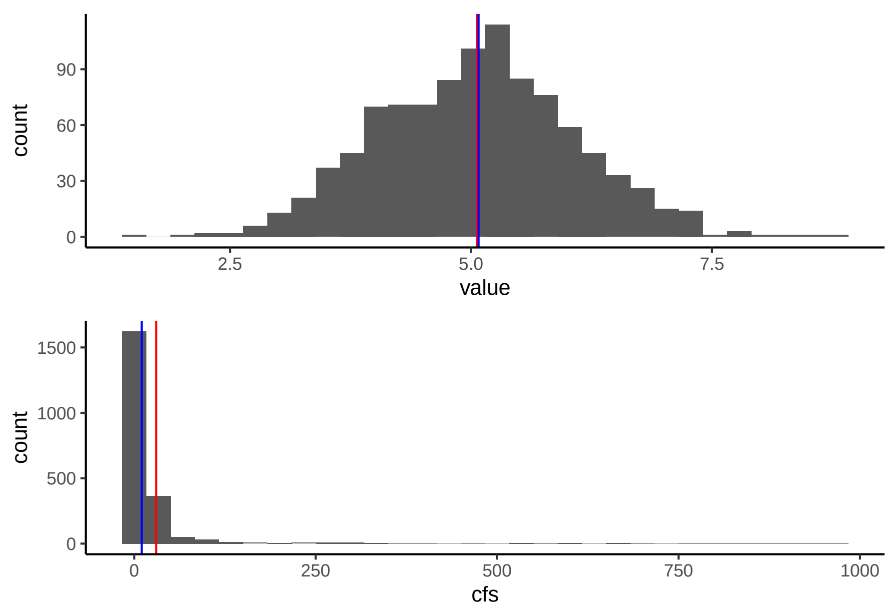
Because it uses the order of the values rather than just the values themselves, the median is resistant to skewed distributions. This means it is less effected by very large or very small values compared to most values in the sample data.

Let's look at our normal distribution from earlier (ExNorm) compared to the Pine watershed discharge (pineQ)

Note that distributions like pineQ, that are positively skewed, are very common in environmental data.

```
#Calculate mean and median for cfs in pineQ and values in ExNorm
pineMean <- mean(pineQ$cfs)
pineMedian <- median(pineQ$cfs)

xmean <- mean(ExNorm$value)
xmedian <- median(ExNorm$value)

#plot mean and median on the ExNorm distribution
Ex <- ExNorm %>% ggplot(aes(value)) +
  geom_histogram()+
  geom_vline(xintercept = xmean, color = "red")+
  geom_vline(xintercept = xmedian, color = "blue")

#plot mean and median on the pineQ discharge histogram
PineP <- pineQ %>% ggplot(aes(cfs)) +
  geom_histogram()+
  geom_vline(xintercept = pineMean, color = "red")+
  geom_vline(xintercept = pineMedian, color = "blue")

Ex / PineP
```

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



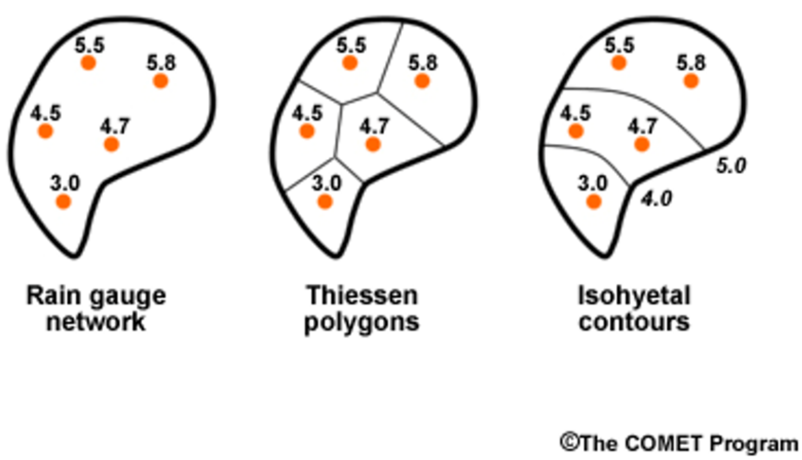
5.4.1 So what's a weighted average?

When you compute a standard mean or median, you are giving equal weight to each measurement. Adding up all the values in a sample and dividing by the number of samples is the same as multiplying each value by 1/# of samples. For instance if you had ten samples, to calculate the mean you would add them up and divide by 10. This is the same as multiplying each value by 1/10 and then adding them up. Each value is equally weighted at 1/10.

There are certain situations in which this is not the ideal way to calculate an average. A common one in hydrology is that you have samples that are supposed to represent different portions of an area. One sample may be taken to measure a forest type that takes up 100 ha of a watershed while another sample represents a forest type that only takes up 4 ha. You may not want to simply average those values!

Another example is precipitation gages. In the image below, you see there are 5 rain gages. To get a precipitation number for the watershed, we could just average them, or we could assume they represent an area of the watershed and then weight their values by the area they represent. One method of designating the areas is by using Theissen polygons (the middle watershed). Another method of weighting is isohyetal contours, but we won't worry about that for now!

In the weighted situation, we find the average by multiplying each precipitation values by the proportion of the watershed it represents, shown by the Thiessen polygons, and then add them all together. Let's do an example.



source: https://edx.hydrolearn.org/assets/courseware/v1/e5dc65098f1e8c5faacae0e171e28ccf/asset-v1:HydroLearn+HydroLearn401+2019_S2+type@asset+block/l2_image004.png

The precip values for the watershed above are 4.5, 5.5, 5.8, 4.7, and 3.0

We will assume the proportions of the watershed that each gauge represents are 0.20, 0.15, 0.40, 0.15, 0.10, respectively (or 20%, 15%, 40%, 15%, 10%)

Write some code to compute the regular mean precip from the values, and then the weighted mean.

```
precip <- c(4.5, 5.5, 5.8, 4.7, 3.0)
weights <- c(0.2, 0.15, 0.4, 0.15, 0.1)

mean(precip)
```

```
## [1] 4.7
```

```
sum(precip * weights)
```

```
## [1] 5.05
```

5.5 Measures of variability

Measures of variability allow us to measure the width of our sample data histogram or pdf. If all the values in our sample are close together, we would have small measures of variability, and a pointy pdf/histogram. If they vary more, we would have larger measures of variability and a broad pdf/histogram.

We will explore four measures of variability:

5.5.0.1 Variance:

Sum of the squared difference of each value from the mean divided by the number of samples minus 1. var()

$$s^2 = \sum_{i=1}^{n} \frac{\left(X_i - \bar{X}\right)^2}{(n-1)}$$

(https://pubs.usgs.gov/tm/04/a03/tm4a3.pdf) source: https://pubs.usgs.gov/tm/04/a03/tm4a3.pdf

5.5.0.2 Standard deviation:

The square root of the variance sd()

**Both variance and standard deviation are sensitive to outliers.

5.5.0.3 CV: Coefficient of Variation

CV is simply the standard deviation divided by the mean of the data. Because you divide by the mean, CV is dimensionless. This allows you to use it to compare the variation in samples with very different magnitudes.

5.5.0.4 IQR: Interquartile Range

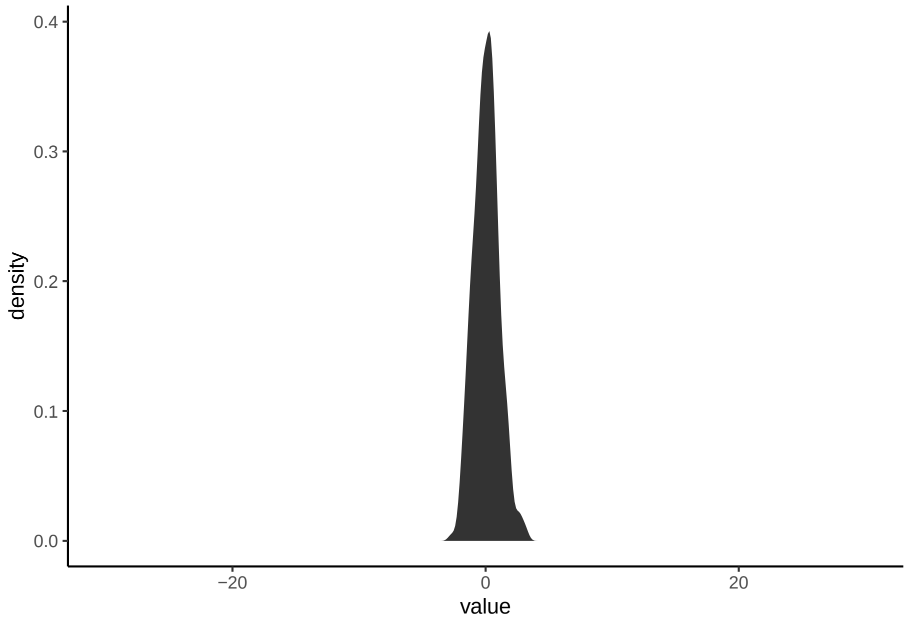
IQR is resistant to outliers because it works like a median. It measures the range of the middle 50% of the data in your distribution. So the IQR is the difference between the value between the 75th and 25th percentiles of your data, where the 75th percentile means 75% of the data is BELOW that value and the 25th percentile means 25% is below that value. Using the same vocabulary, the median is the same as the 50th percentile of the data.

If you ask R for the QUANTILES of your sample data, it will give you the values at which 0%, 25%, 50%, 75%, and 100% of the data are below. These are the 1,2,3,4, and 5th quantiles. Therefore, the IQR is the difference between the 4th and 2nd quantile.

Okay, code time.

First, let's explore how changing the variability of a distribution changes the shape of it's distribution. Create a plot a random normal distribution using rnorm() and set sd to different numbers. Make the mean of the distribution 0, the sample size 300, and the standard deviation 1 to start. Then increase the standard deviation incrementally to 10 and see what happens. Make the limits of the x axis on the plot -30 to 30.

```
rnorm(300, mean = 0, sd = 1) %>% as_tibble %>%
  ggplot(aes(value))+
  stat_density()+
  xlim(c(-30,30))
```



Now let's calculate the standard deviation, variance, coefficient of variation, and IQR of the Pine discharge data.

```
#standard deviation
sd(pineQ$cfs)
```

```
## [1] 84.47625
```

```
#variance
var(pineQ$cfs)
```

```
## [1] 7136.237
```

```
#coefficient of variation
sd(pineQ$cfs)/mean(pineQ$cfs)
```

```
## [1] 2.800221
```

```
#IQR using the IQR funciton
IQR(pineQ$cfs)
```

```
## [1] 8.1325
```

```
#IQR using the quantile function
quants <- quantile(pineQ$cfs)
quants[4] - quants[2]
```

```
##    75%
## 8.1325
```

5.5.0.5 What about how lopsided the distribution is?

There are several ways to measure this as well, but we are just going to look at one: The Quartile skew. The quartile skew is the difference between the upper quartiles (50th-75th) and the lower quartiles (25th-50th) divided by the IQR (75th-25th).

$$qs = \frac{\left(P_{0.75} - P_{0.50}\right) - \left(P_{0.50} - P_{0.25}\right)}{P_{0.75} - P_{0.25}}$$

source: https://pubs.usgs.gov/tm/04/a03/tm4a3.pdf

Let's look at the quartile skew of the two distributions we've been measuring. Calculate it for the pineQ discharge data and the random normal distribution we generated.

Which one is more skewed?

```
quantsP <- quantile(pineQ$cfs)

((quantsP[3]-quantsP[2]) - (quantsP[2] - quantsP[1])) / quantsP[3] - quantsP[1]
```

```
##       50%
## -4.837233
```

```
quantsX <- quantile(ExNorm$value)

((quantsX[3]-quantsX[2]) - (quantsX[2] - quantsX[1])) / quantsX[3] - quantsX[1]
```

```
##       50%
## -1.928711
```

5.6 What is a normal distribution and how can we determine if we have one?

The distribution we generated with rnorm() is a normal distribution. The distribution of pineQ discharge is not normal. Now that we've looked at different ways to characterize distributions, we have the vocabulary to describe why.

Normal distributions:

- mean = median, half values to the right, half to the left
- symmetric (not skewed)
- single peak

Many statistical tests require that the distribution of the data you put into them is normally distributed. BE CAREFUL! There are also tests that use ranked data. Similar to how the median is resistant to outliers, these rank-based tests are resistant to non-normal data. Two popular ones are Kruskal-Wallis and Wilcoxon rank-sum.

But how far off can you be before you don't consider a distribution normal? Seems like a judgement call!

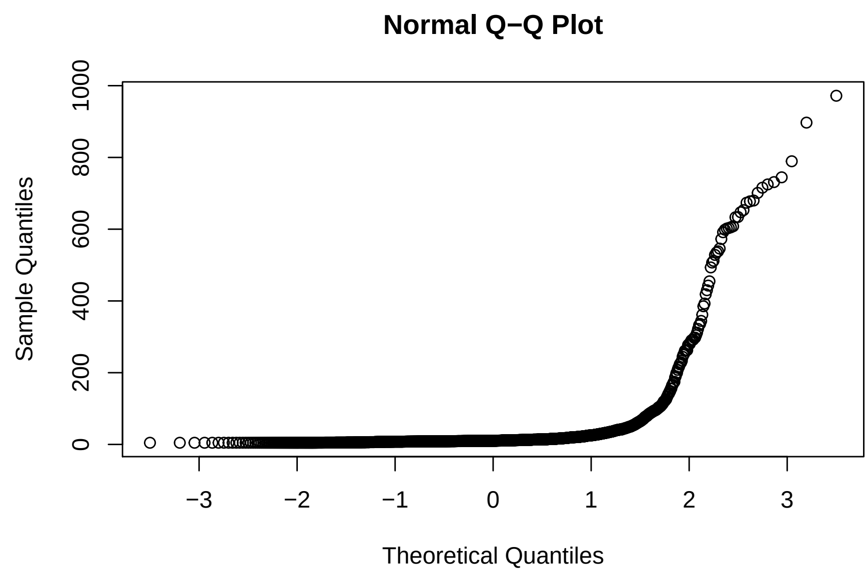
R to the rescue! There is a built in test for normality called shapiro.test(), which performs the Shapiro-Wilk test of normality. The hypothesis this test tests is "The distribution is normal." So if this function returns a p-value less than 0.05, you reject that hypothesis and your function is NOT normal.

You can also make a quantile-quantile plot. A straight line on this plot indicates a normal distribution, a non-straight line indicates it is not normal.

```
shapiro.test(pineQ$cfs)
```

```
##
##  Shapiro-Wilk normality test
##
## data:  pineQ$cfs
## W = 0.27155, p-value < 2.2e-16
```

```
qqnorm(pineQ$cfs)
```


Normal Q−Q Plot
Sample Quantiles
Theoretical Quantiles
0
200
400
600
800
1000
−3
−2
−1
0
1
2
3

Chapter 6

ACTIVITY Intro Stats

Get this document at the template repository on github: https://github.com/VT-Hydroinformatics/5-Intro-Stats-Activity

Address each of the questions in the code chunk below and/or by typing outside the chunk (for written answers).

6.1 Problem 1

Load the tidyverse and patchwork libraries and read in the Flashy and Pine datasets.

6.2 Problem 2

Using the flashy dataset, make a pdf of the average basin rainfall (PPTAVG_BASIN) for the NorthEast AGGECOREGION. On that pdf, add vertical lines showing the mean, median, standard deviation, and IQR. Make each a different color and note which is which in a typed answer below this question. (or if you want an extra challenged, make a custom legend that shows this)

6.3 Problem 3

Perform a Shapiro-Wilk test for normality on the data from question 2. Using the results from that test and the plot and stats from question 2, discuss whether or not the distribution is normal.

6.4 Problem 4

Make a plot that shows the distribution of the data from the PINE watershed and the NFDR watershed (two pdfs on the same plot). Log the x axis.

6.5 Problem 5

You want to compare how variable the discharge is in each of the watersheds in question 4. Which measure of spread would you use and why? If you wanted to measure the central tendency which measure would you use and why?

6.6 Problem 6

Compute 3 measures of spread and 2 measures of central tendency for the PINE and NFDR watershed. (hint: use group_by() and summarize()) Be sure your code outputs the result. Which watershed has higher flow? Which one has more variable flow? How do you know?

Chapter 7

Joins, Pivots, and USGS dataRetrieval

Get this document and a version with empty code chunks at the template repository on github: https://github.com/VT-Hydroinformatics/6-Get-Format-Plot-HydroData

Readings: Introduction to the dataRetrieval package https://cran.r-project.org/web/packages/dataRetrieval/vignettes/dataRetrieval.html

Chapter 12 & 13 of R for Data Science https://r4ds.had.co.nz/tidy-data.html

7.1 Goals for today

- Get familiar with the dataRetrieval package
- Intro to joins
- Learn about long vs. wide data and how to change between them

Prep question: How would you get data from the USGS (non-R)?

Install the dataRetrieval package. Load it and the tidyverse.

```
#install.packages("dataRetrieval")
library(dataRetrieval)
library(tidyverse)
library(lubridate)
```

```
## Warning: package 'lubridate' was built under R version 3.6.2
```

7.2 Exploring what dataRetrieval can do.

Think about the dataRetrieval as a way to interact with same public data you can access through waterdata.usgs.gov but without having to click on buttons and search around. It makes getting data or doing analyses with USGS data much more reproducible and fast!

To explore a few of the capabilities (NOT ALL!!) we will start with the USGS gage on the New River at Radford. The gage number is 03171000.

The documentation for the package is extremely helpful: https://cran.r-project.org/web/packages/dataRetrieval/vignettes/dataRetrieval.html

I always have to look up how to do things because the package is very specialized! This is the case with most website APIs, in my experience. It's a good argument for getting good at navigating package documentation! Basically you just look through and try to piece together the recipe for what you want to do using the examples they give in the document.

First, let's get information about the site using the readNWISsite() and whatNWISdata() functions. Try each out and see what they tell you.

Remember, all the parameter codes and site names get passed to dataRetrieval functions as characters, ao they must be in quotes.

```
#important: note the site number gets input as a character
site <- "03171000"

#Information about the site
siteinfo <- readNWISsite(site)

#What data is available for the site?
#Daily values, mean values
dataAvailable <- whatNWISdata(siteNumber = site, service = "dv", statCd = "00003")

dataAvailable
```

```
##   agency_cd  site_no               station_nm site_tp_cd dec_lat_va dec_long_va
## 2      USGS 03171000 NEW RIVER AT RADFORD, VA         ST   37.14179   -80.56922
## 3      USGS 03171000 NEW RIVER AT RADFORD, VA         ST   37.14179   -80.56922
## 4      USGS 03171000 NEW RIVER AT RADFORD, VA         ST   37.14179   -80.56922
##   coord_acy_cd dec_coord_datum_cd  alt_va alt_acy_va alt_datum_cd   huc_cd
## 2            U              NAD83  1711.99       0.13       NAVD88 05050001
## 3            U              NAD83  1711.99       0.13       NAVD88 05050001
## 4            U              NAD83  1711.99       0.13       NAVD88 05050001
##   data_type_cd parm_cd stat_cd  ts_id loc_web_ds medium_grp_cd parm_grp_cd
## 2           dv   00010   00003 241564         NA           wat        <NA>
## 3           dv   00060   00003 145684         NA           wat        <NA>
```

```
## 4          dv   00095   00003 145685         NA            wat         <NA>
##    srs_id access_cd begin_date   end_date count_nu
## 2 1645597         0 2006-12-20 2009-03-18      704
## 3 1645423         0 1907-10-01 2021-02-24    32654
## 4 1646694         0 2006-12-20 2008-09-29      534
```

7.3 Joins

When we look at what whatNWISdata returns, we see it gives us parameter codes, but doesn't tell us what they mean. This is a common attribute of databases: you use a common identifier but then have the full information in a lookup file. In this case, the look-up information telling us what the parameter codes mean is in "parameterCdFile" which loads with the dataRetrieval package.

So, you could look at that and see what the parameters mean.

OR We could have R do it and add a column that tells us what the parameters mean. Enter JOINS!

Joins allow us to combine the data from two different data sets that have a column in common. At its most basic, a join looks for a matching row with the same key in both datasets (for example, a USGS gage number) and then combines the rows. So now you have all the data from both sets, matched on the key.

But you have to make some decisions: what if a key value exists in one set but not the other? Do you just drop that observation? Do you add an NA? Let's look at the different options.

Take for example the two data sets, FlowTable and SizeTable. The SiteName values are the key values and the MeanFlow and WSsize values are the data.

FlowTable

SiteName	MeanFlow
River1	100
River2	125
River3	80

SizeTable

SiteName	WSsize
River1	800
River2	950
River5	700

Figure 7.1: Join Setup

Note River1 and River2 match up, but River3 and River5 only exist in one data set or the other.

The first way to deal with this is an **INNER JOIN: inner_join()** In an inner join, you only keep records that match. So the rows for River3 and River5 will be dropped because there is no corresponding data in the other set. See below:

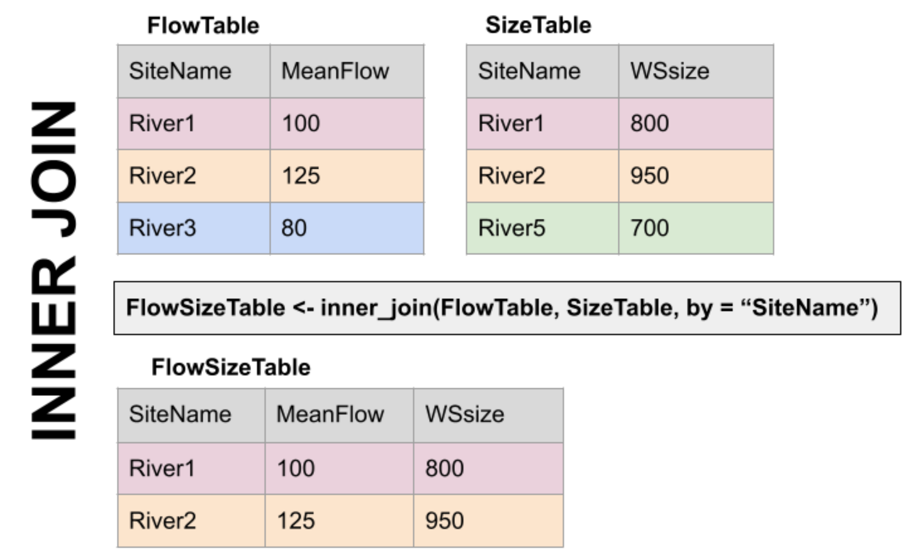


Figure 7.2: Inner Join

But what if you don't want to lose the values in one or the other or both?!

For instance, let's say you have a bunch of discharge data for a stream, and then chemistry grab samples. You want to join the chemistry to the discharge based on the dates and times they were taken. But when you do this, you don't want to delete all the discharge data where there is no chemistry! We need another option. Enter OUTER JOINS

LEFT JOIN, left_join(): Preserves all values from the LEFT data set, and pastes on the matching ones from the right. This creates NAs where there is a value on the left but not the right. (this is what you'd want to do in the discharge - chemistry example above)

RIGHT JOIN, right_join(): Preserves all values from the RIGHT data set, and pastes on the matching ones from the left. This creates NAs where there is a value on the right but not the left.

FULL JOIN, full_join(): KEEP EVERYTHING! The hoarder of the joins. No matching record on the left? create an NA on the right! No matching value on the right? Create an NA on the left! NAs for everyone!

When you do this in R, you use the functions identified in the descriptions with the following syntax (see example below):

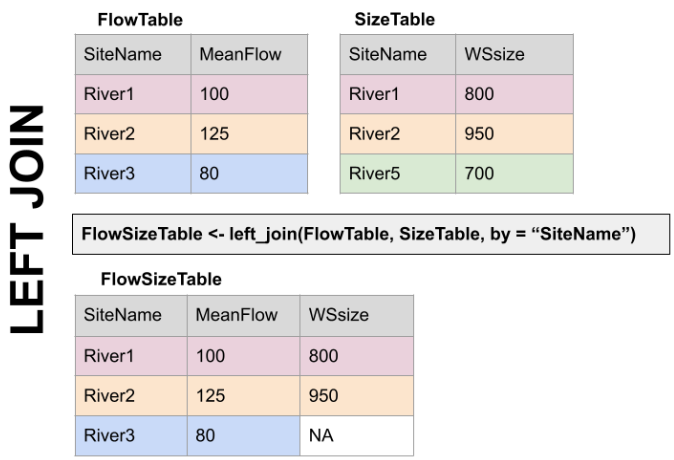


Figure 7.3: Left Join

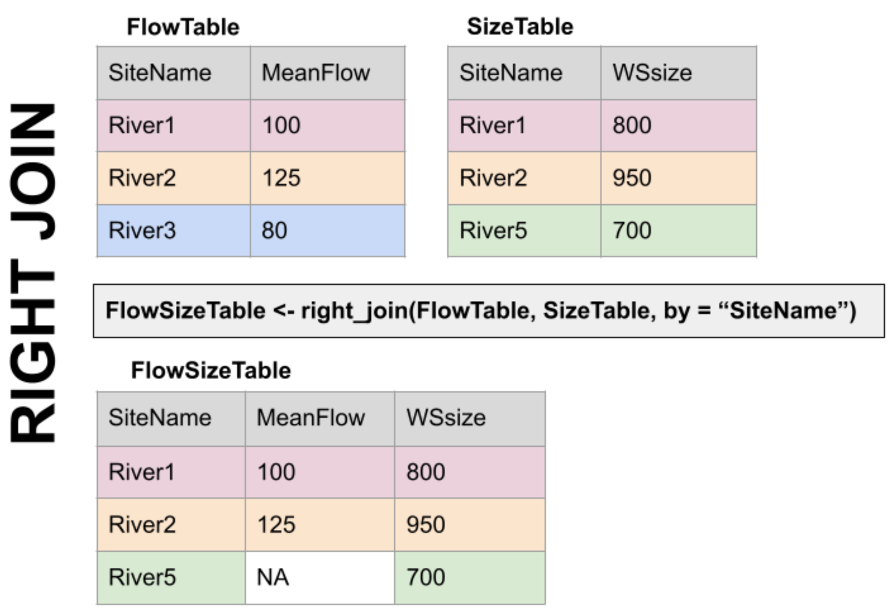


Figure 7.4: Right Join

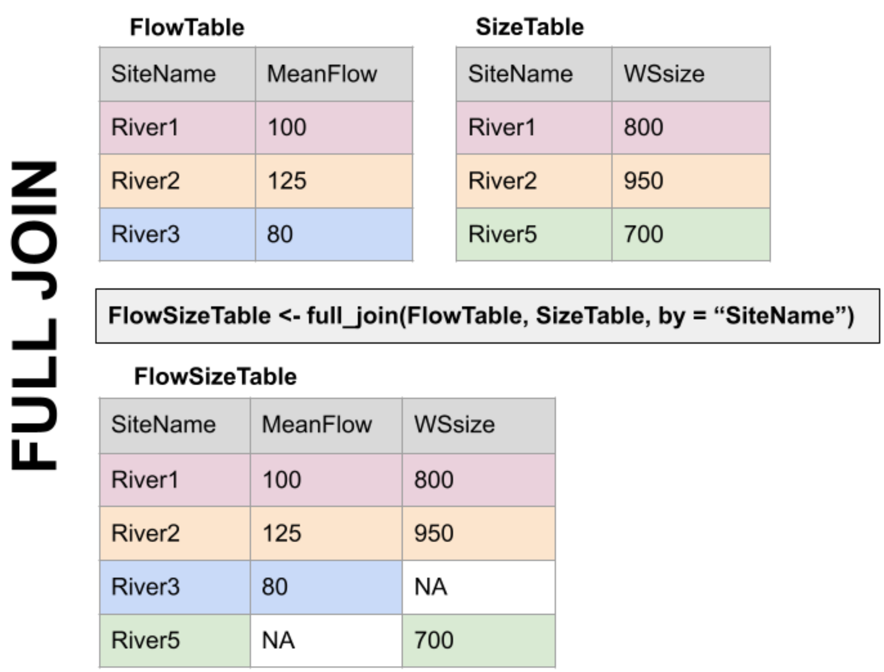


Figure 7.5: Full Join

if the column is named the same in both data sets > xxx_join(left_tibble, right_tibble, by = “key_column”)**

if the column is named differently in both data sets > xxx_join(left_tibble, right_tibble, by = c(“left_key” = “right_key”)

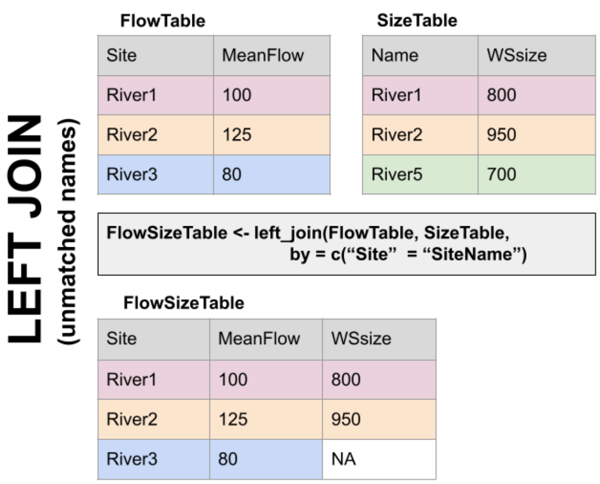


Figure 7.6: Left Join Differing Col Names

Note in both of the above, when you specify which column to use as “by” you have to put it in quotes.

7.4 Join example

So in the chunk below let’s get add information about the parameters in dataAvailable by joining it with the key file: parameterCdFile. The column with the parameter codes is called parm_cd in dataAvailable and parameter_cd in parameterCdFile

```
dataAvailable <- left_join(dataAvailable, parameterCdFile, by = c("parm_cd" = "parameter_cd"))

dataAvailable
```

```
##   agency_cd  site_no               station_nm site_tp_cd dec_lat_va dec_long_va
## 1      USGS 03171000 NEW RIVER AT RADFORD, VA         ST   37.14179   -80.56922
## 2      USGS 03171000 NEW RIVER AT RADFORD, VA         ST   37.14179   -80.56922
## 3      USGS 03171000 NEW RIVER AT RADFORD, VA         ST   37.14179   -80.56922
##   coord_acy_cd dec_coord_datum_cd   alt_va alt_acy_va alt_datum_cd   huc_cd
```

```
## 1           U              NAD83  1711.99       0.13       NAVD88 05050001
## 2           U              NAD83  1711.99       0.13       NAVD88 05050001
## 3           U              NAD83  1711.99       0.13       NAVD88 05050001
##   data_type_cd parm_cd stat_cd  ts_id loc_web_ds medium_grp_cd parm_grp_cd
## 1           dv   00010   00003 241564         NA           wat        <NA>
## 2           dv   00060   00003 145684         NA           wat        <NA>
## 3           dv   00095   00003 145685         NA           wat        <NA>
##    srs_id access_cd begin_date   end_date count_nu parameter_group_nm
## 1 1645597         0 2006-12-20 2009-03-18      704           Physical
## 2 1645423         0 1907-10-01 2021-02-24    32654           Physical
## 3 1646694         0 2006-12-20 2008-09-29      534           Physical
##                                                                         para
## 1                                                          Temperature, water, degrees
## 2                                                             Discharge, cubic feet pe
## 3 Specific conductance, water, unfiltered, microsiemens per centimeter at 25 degrees
##   casrn                  srsname parameter_units
## 1  <NA>       Temperature, water           deg C
## 2  <NA> Stream flow, mean. daily          ft3/s
## 3  <NA>     Specific conductance      uS/cm @25C
```

```
#that made a lot of columns, let's clean it up
dataAvailClean <- dataAvailable %>% select(site_no,
                                           station_nm,
                                           parm_cd,
                                           srsname,
                                           parameter_units,
                                           begin_date,
                                           end_date)

dataAvailClean
```

```
##    site_no              station_nm parm_cd                  srsname
## 1 03171000 NEW RIVER AT RADFORD, VA   00010       Temperature, water
## 2 03171000 NEW RIVER AT RADFORD, VA   00060 Stream flow, mean. daily
## 3 03171000 NEW RIVER AT RADFORD, VA   00095     Specific conductance
##   parameter_units begin_date   end_date
## 1           deg C 2006-12-20 2009-03-18
## 2           ft3/s 1907-10-01 2021-02-24
## 3      uS/cm @25C 2006-12-20 2008-09-29
```

7.5 Finding IDs to download USGS data

You can find sites via map and just enter the id like we did in the chunks above:
https://maps.waterdata.usgs.gov/mapper/index.html

Below we will look at two other ways to get sites: using a bounding box of a geographic region, or search terms like State and drainage area

```
#find sites in a bounding box
#coords of bottom left, top right
swva <- c(-81.36, 36.72, -80.27, 37.32)

#get sites in this bounding box that have daily water temperature and discharge
swva_sites <- whatNWISsites(bBox = swva,
                            parameterCd = c("00060", "00010"),
                            hasDataTypeCd = "dv")

swva_sites
```

```
##    agency_cd  site_no                                 station_nm
## 1       USGS 03473500           M F HOLSTON RIVER AT GROSECLOSE, VA
## 2       USGS 03175140         WEST FORK COVE CREEK NEAR BLUEFIELD, VA
## 3       USGS 03177710              BLUESTONE RIVER AT FALLS MILLS, VA
## 4       USGS 03177700                BLUESTONE RIVER AT BLUEFIELD, VA
## 5       USGS 03166000                  CRIPPLE CREEK NEAR IVANHOE, VA
## 6       USGS 03164500                      NEW RIVER NEAR GRAYSON, VA
## 7       USGS 03165500                        NEW RIVER AT IVANHOE, VA
## 8       USGS 03166880  WEST SP AT NAT FISH HAT NEAR GRAHAMS FORGE, VA
## 9       USGS 03166800                GLADE CREEK AT GRAHAMS FORGE, VA
## 10      USGS 03166900 BOILING SP AT NAT FISH HAT NR GRAHAMS FORGE, VA
## 11      USGS 03167000                 REED CREEK AT GRAHAMS FORGE, VA
## 12      USGS 03175500                     WOLF CREEK NEAR NARROWS, VA
## 13      USGS 03168500                       PEAK CREEK AT PULASKI, VA
## 14      USGS 03168000                      NEW RIVER AT ALLISONIA, VA
## 15      USGS 03167500          BIG REED ISLAND CREEK NEAR ALLISONIA, VA
## 16      USGS 03172500              WALKER CREEK AT STAFFORDSVILLE, VA
## 17      USGS 03173000                        WALKER CREEK AT BANE, VA
## 18      USGS 03171500                      NEW RIVER AT EGGLESTON, VA
## 19      USGS 03171000                        NEW RIVER AT RADFORD, VA
## 20      USGS 03170000                 LITTLE RIVER AT GRAYSONTOWN, VA
## 21      USGS 03169500             LITTLE RIVER NEAR COPPER VALLEY, VA
##    site_tp_cd dec_lat_va dec_long_va colocated           queryTime
## 1          ST   36.88873   -81.34733     FALSE 2021-02-25 15:01:41
## 2          ST   37.18428   -81.32982     FALSE 2021-02-25 15:01:41
## 3          ST   37.27151   -81.30482     FALSE 2021-02-25 15:01:41
## 4          ST   37.25595   -81.28177     FALSE 2021-02-25 15:01:41
## 5          ST   36.85984   -80.98036     FALSE 2021-02-25 15:01:41
## 6          ST   36.75985   -80.95619     FALSE 2021-02-25 15:01:41
## 7          ST   36.83485   -80.95258     FALSE 2021-02-25 15:01:41
## 8          SP   36.93429   -80.90313     FALSE 2021-02-25 15:01:41
```

```
## 9          ST   36.93095   -80.90036     FALSE 2021-02-25 15:01:41
## 10         SP   36.93068   -80.89619     FALSE 2021-02-25 15:01:41
## 11         ST   36.93901   -80.88730     FALSE 2021-02-25 15:01:41
## 12         ST   37.30568   -80.84980     FALSE 2021-02-25 15:01:41
## 13         ST   37.04734   -80.77618     FALSE 2021-02-25 15:01:41
## 14         ST   36.93762   -80.74563     FALSE 2021-02-25 15:01:41
## 15         ST   36.88901   -80.72757     FALSE 2021-02-25 15:01:41
## 16         ST   37.24179   -80.71090     FALSE 2021-02-25 15:01:41
## 17         ST   37.26818   -80.70951     FALSE 2021-02-25 15:01:41
## 18         ST   37.28957   -80.61673     FALSE 2021-02-25 15:01:41
## 19         ST   37.14179   -80.56922     FALSE 2021-02-25 15:01:41
## 20         ST   37.03763   -80.55672     FALSE 2021-02-25 15:01:41
## 21         ST   36.99652   -80.52144     FALSE 2021-02-25 15:01:41
```

```
#find sites with other criteria, VA, less than 20 sqmi, other criteria can be used..
#check out the CRAN documentation
smallVA <- readNWISdata(service = "dv",
                           stateCd = "VA",
                           parameterCd = "00060",
                           drainAreaMax = "20",
                           statCd = "00003")
```

7.6 OK let's download some data!

We are going to use readNWISdv(), which downloads daily values.

We will tell it which sites to download, which parameters to download, and then what time period to download.

siteNumber gets the sites we want to download, USGS site numbers, as a character. We will use the swva_sites data we generated (yep, you can download multiple sites at once!)

startDate and endDate get the…. start and end dates. IMPORTANT: These must be in YYY-MM-DD format, but you don't have to tell R they are dates before you give them to the function, it'll do that for you.

parameterCd get the parameters you want to download. We want water temperature and discharge, which are "00060" and "00010", respectively.

Once we have the data, the column names correspond to the keys that identify them, for example, discharge will be 00060 something something. Fortunately the dataRetrieval package also provides "renameNWISColumns()" which translates these into words, making them more easily understood by humans. We can pipe the results of our download to that function after we get the data to make the column names easier to understand.

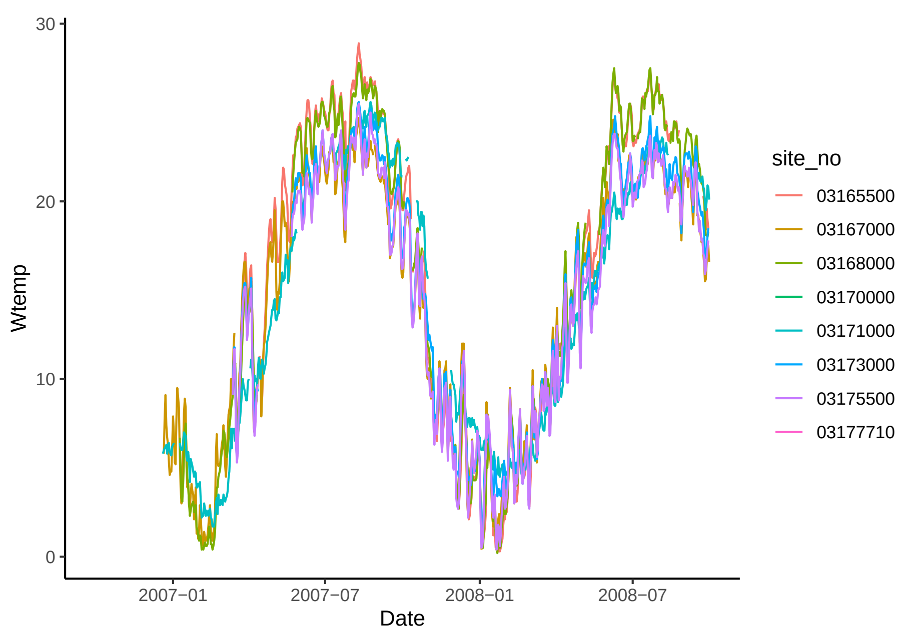
```
start <- "2006-10-01"
end <- "2008-09-30"
params <- c("00010", "00060")

swva_dat <- readNWISdv(siteNumber = swva_sites$site_no,
                       parameterCd = params,
                       startDate = start,
                       endDate = end) %>%
            renameNWISColumns()
```

Let's plot the water temperature data as a line and control the color of the lines with the different sites.

What could be better about this plot?

```
swva_dat %>% ggplot(aes(x = Date, y = Wtemp, color = site_no)) +
  geom_line()
```

```
## Warning: Removed 2218 row(s) containing missing values (geom_path).
```



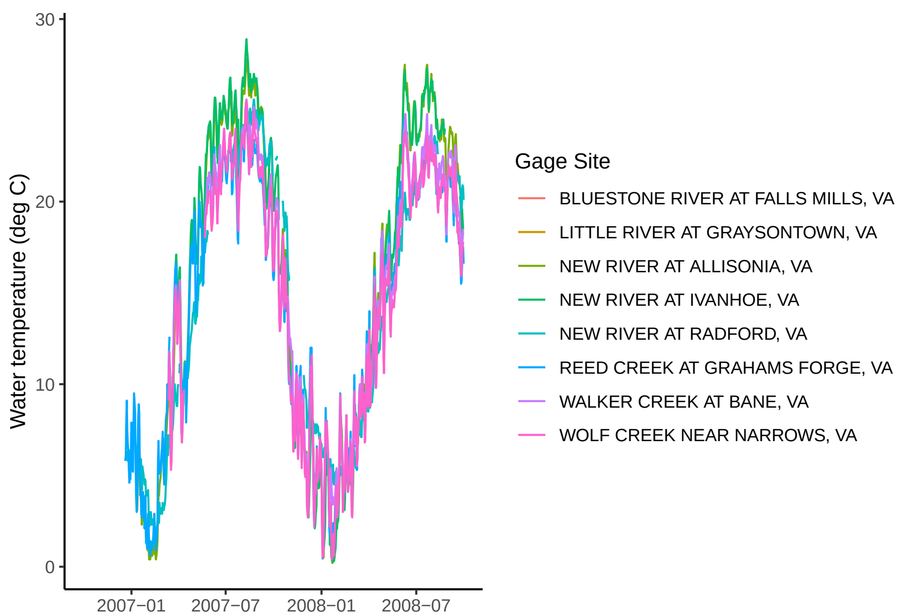
We can add site names with….More joins! Our swva_sites data has the names of the sites in human-friendly language. The column in the downloaded data and in the swva_sites data is called "site_no" so we just give that to the "by" argument. Perform a left join to add the names of the sites to the data.

Then use select to remove some of the unnecessary columns.

Then make the plot and then snazz it up with labels and a non-junky theme.

```
swva_dat_clean <- left_join(swva_dat, swva_sites, by = "site_no") %>%
  select(station_nm, site_no, Date, Flow, Wtemp, dec_lat_va, dec_long_va)

swva_dat_clean %>% ggplot(aes(x = Date, y = Wtemp, color = station_nm)) +
  geom_line()+
  ylab("Water temperature (deg C)")+
  xlab(element_blank())+
  labs(color = "Gage Site")+
  theme_classic()
```

```
## Warning: Removed 2218 row(s) containing missing values (geom_path).
```



7.7 Pivoting: wide and long data

Okay, so with the data above: what would you do if you wanted to subtract the discharge or temperature of one gage from another on the same river: to compute rate of change between the two sites, for instance.

You could split them into two objects, then join based on date?

Or…now hear me out… you could PIVOT them.

A two-dimensional object can be either long or wide. Each has it's advantages.

LONG

Each observation has it's own row. In the first image below, the table on the left is long because each measure of "cases" has it's own row. It's year and country are identified by a second column, and the values in that column repeat a lot. (Look at country and year in the table on the left)

WIDE

Observations of different things have their own columns. In the second image below, notice in the right hand table there is a "cases" and "population" column rather than an identifier in a separate column like in the table on the left.

Why?

Long and wide data are more efficient for different things. Think about plotting a data set with 10 stream gages. If they are in a long format, you can just add color = Gage to your ggplot aes(). If they are in a wide format, meaning each gage has it's own column, you'd have to write a new geom for EACH gage, because they're all in separate columns.

Now imagine you want to do some math to create new data: let's say cases divided by population in the second image below…. How would you even do that using the data on the left? With the wide data on the right it is simply mutate(casesPERpop = cases / population).

Finally, which table is easier to read in TABLE format (not a plot) in each of the two images below? Wide data is much more fitting for tables.

dplyr, part of the tidyverse, has functions to convert data between wide and long data. I have to look up the syntax every single time I use them. But they are VERY useful.

7.8 Pivot Examples

Back to our original question: I want to subtract the flow at Ivanhoe from the flow at Radford on the new river to see how much flow increases between the two sites through time.

To do this I am going to use pivot_wider() to give Ivanhoe and Radford discharges their own column.

First, we will use select to trim the data to just what we need, then call pivot_wider telling it which data to use for the new column names (names_from = station_nm) and what values we want to pivot into the data under those columns (values_from = Flow).

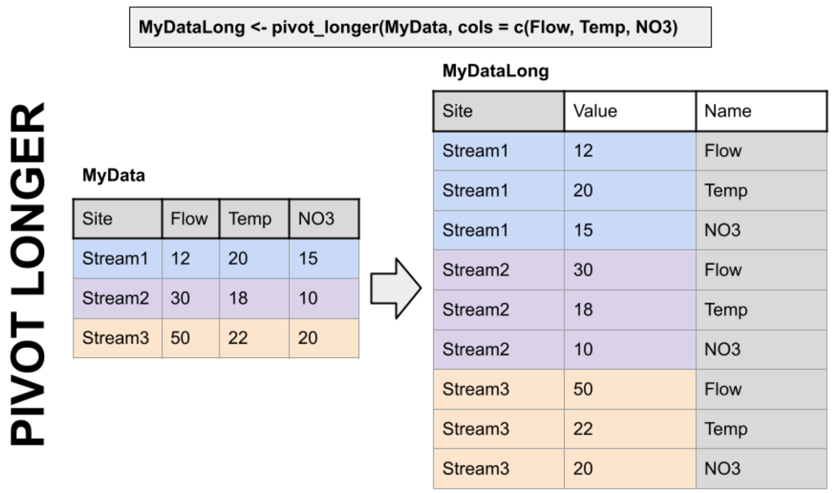


Figure 7.7: Pivoting to a longer format

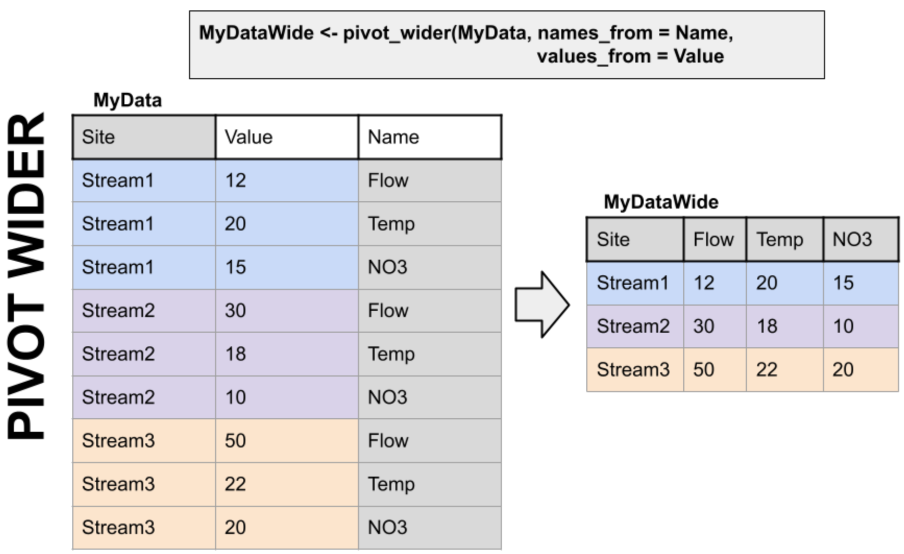
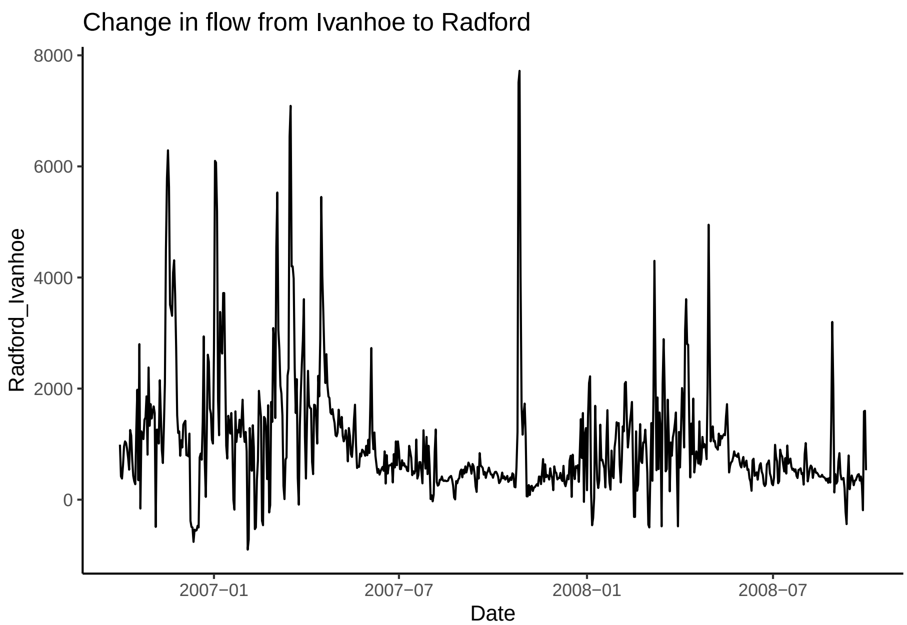


Figure 7.8: Pivoting to a wider format

Then, subtract the two and make a plot!

```
#Pivot so we can compute diffs between one river and others

swva_wide <- swva_dat_clean %>% select(station_nm, Flow, Date) %>%
  pivot_wider(names_from = station_nm, values_from = Flow)

swva_wide <- swva_wide %>% mutate(Radford_Ivanhoe = `NEW RIVER AT RADFORD, VA` - `NEW RIVER AT IV

ggplot(swva_wide, aes(x = Date, y = Radford_Ivanhoe))+
  geom_line()+
  ggtitle("Change in flow from Ivanhoe to Radford")+
  theme_classic()
```



To further illustrate how to move between long and wide data and when to use them, let's grab some water quality data. This process will also review some of the other concepts from this topic.

In the chunk below we will look to see what sites have data for nitrate and chloride in our swva bounding box from above. We will them filter them to just stream sites (leave out groundwater and springs). And finally we will download the nitrate and chloride data for those sites.

```
#Nitrate as nitrate and chloride
params <- c("00940", "71851")
```

```
#what sites in our bounding box have cloride and nitrate
swva_chem_sites <- whatNWISsites(bBox = swva,
                                 parameterCd = params)

#filte to just stream water
swva_chem_sites <- filter(swva_chem_sites, site_tp_cd == "ST")

wqdat <- readNWISqw(siteNumber = swva_chem_sites$site_no,
                    parameterCd = params)

comment(wqdat)
```

```
##   [1] "#"
##   [2] "# File created on 2021-02-25 15:01:48 EST"
##   [3] "#"
##   [4] "# U.S. Geological Survey"
##   [5] "# "
##   [6] "# This file contains selected water-quality data for stations in the National
##   [7] "# Information System water-quality database.  Explanation of codes found in t
##   [8] "# followed by the retrieved data. "
##   [9] "#"
##  [10] "# The data you have secured from the USGS NWISWeb database may include data t
##  [11] "# not received Director's approval and as such are provisional and subject to
##  [12] "# The data are released on the condition that neither the USGS nor the United
##  [13] "# Government may be held liable for any damages resulting from its authorized
##  [14] "# unauthorized use."
##  [15] "#"
##  [16] "# To view additional data-quality attributes, output the results using these
##  [17] "# one result per row, expanded attributes.  Additional precautions are at:"
##  [18] "# https://help.waterdata.usgs.gov/tutorials/water-quality-data/help-using-the
##  [19] "#"
##  [20] "#  agency_cd                     - Agency Code"
##  [21] "#  site_no                       - USGS site number"
##  [22] "#  sample_dt                     - Begin date"
##  [23] "#  sample_tm                     - Begin time"
##  [24] "#  sample_end_dt                 - End date"
##  [25] "#  sample_end_tm                 - End time"
##  [26] "#  sample_start_time_datum_cd - Time datum"
##  [27] "#  tm_datum_rlbty_cd             - Time datum reliability code"
##  [28] "#  coll_ent_cd                   - Agency Collecting Sample Code"
##  [29] "#  medium_cd                     - Sample Medium Code"
##  [30] "#  project_cd                    - Project code"
##  [31] "#  aqfr_cd                       - Geologic unit code"
##  [32] "#  tu_id                         - Taxonomic unit code"
```

```
## [33] "#  body_part_id              - Body part code"
## [34] "#  hyd_cond_cd               - Hydrologic Cond Code"
## [35] "#  samp_type_cd              - Sample Type Code"
## [36] "#  hyd_event_cd              - Hydrologic Event Code"
## [37] "#  sample_lab_cm_tx          - Message from lab"
## [38] "#  parm_cd                   - Parameter code"
## [39] "#  remark_cd                 - Remark code"
## [40] "#  result_va                 - Parameter value"
## [41] "#  val_qual_tx               - Result value qualifier code"
## [42] "#  meth_cd                   - Method code"
## [43] "#  dqi_cd                    - Data-quality indicator code"
## [44] "#  rpt_lev_va                - Reporting level"
## [45] "#  rpt_lev_cd                - Reporting level type"
## [46] "#  lab_std_va                - Lab standard deviation"
## [47] "#  prep_set_no               - Prep set number"
## [48] "#  prep_dt                   - Result prep date"
## [49] "#  anl_set_no                - Analysis set number"
## [50] "#  anl_dt                    - Result analysis date"
## [51] "#  result_lab_cm_tx          - Lab result comment"
## [52] "#  anl_ent_cd                - Analyzing entity code"
## [53] "#"
## [54] "# The following parameters are included:"
## [55] "#  00940  - Chloride, water, filtered, milligrams per liter"
## [56] "#  71851  - Nitrate, water, filtered, milligrams per liter as nitrate"
## [57] "#"
## [58] "# Description of sample_start_time_datum_cd:"
## [59] "# EST  - Eastern Standard Time"
## [60] "# EDT  - Eastern Daylight Time"
## [61] "#"
## [62] "# Description of tm_datum_rlbty_cd:"
## [63] "# K  - Known"
## [64] "# T  - Transferred"
## [65] "#"
## [66] "# Description of coll_ent_cd and anl_ent_cd:"
## [67] "# USGS-WRD  - U.S. Geological Survey-Water Resources Discipline"
## [68] "# USGS-NYL  - USGS-NY WSC Low Ionic Strength Lab,Troy(formerly Albany)"
## [69] "#"
## [70] "# Description of medium_cd:"
## [71] "# WS  - Surface water"
## [72] "#"
## [73] "# Description of aqfr_cd:"
## [74] "#"
## [75] "# Description of tu_id:"
## [76] "# https://www.itis.gov/"
## [77] "#"
## [78] "# Description of body_part_id:"
```

```
##  [79] "#"
##  [80] "# Description of hyd_cond_cd:"
##  [81] "# 4  - Stable, low stage"
##  [82] "# 5  - Falling stage"
##  [83] "# 6  - Stable, high stage"
##  [84] "# 8  - Rising stage"
##  [85] "# 9  - Stable, normal stage"
##  [86] "# A  - Not determined"
##  [87] "#"
##  [88] "# Description of samp_type_cd:"
##  [89] "# 7  - Replicate"
##  [90] "# 9  - Regular"
##  [91] "#"
##  [92] "# Description of hyd_event_cd:"
##  [93] "# 9  - Routine sample"
##  [94] "#"
##  [95] "# Description of remark_cd:"
##  [96] "#"
##  [97] "# Description of val_qual_tx:"
##  [98] "#"
##  [99] "# Description of meth_cd:"
## [100] "# ALGOR  - Computation by NWIS algorithm"
## [101] "# CL031  - Chloride, wf, ASF thiocyanate"
## [102] "# IC022  - Anions, wf, IC"
## [103] "# IC034  - Anions, wf, IC (USGS-NYL)"
## [104] "#"
## [105] "# Description of dqi_cd:"
## [106] "# A  - Historical data"
## [107] "# R  - Reviewed and approved"
## [108] "#"
## [109] "# Description of rpt_lev_cd:"
## [110] "# MRL  - Minimum reporting level"
## [111] "#"
## [112] "# Data for the following sites are included:"
## [113] "#  USGS 03165500 NEW RIVER AT IVANHOE, VA"
## [114] "#  USGS 03167000 REED CREEK AT GRAHAMS FORGE, VA"
## [115] "#  USGS 03167500 BIG REED ISLAND CREEK NEAR ALLISONIA, VA"
## [116] "#  USGS 03168000 NEW RIVER AT ALLISONIA, VA"
## [117] "#  USGS 03168500 PEAK CREEK AT PULASKI, VA"
## [118] "#  USGS 03170000 LITTLE RIVER AT GRAYSONTOWN, VA"
## [119] "#  USGS 03171000 NEW RIVER AT RADFORD, VA"
## [120] "#  USGS 03171500 NEW RIVER AT EGGLESTON, VA"
## [121] "#  USGS 03172500 WALKER CREEK AT STAFFORDSVILLE, VA"
## [122] "#  USGS 03173000 WALKER CREEK AT BANE, VA"
## [123] "#  USGS 03175500 WOLF CREEK NEAR NARROWS, VA"
## [124] "#  USGS 03473500 M F HOLSTON RIVER AT GROSECLOSE, VA"
```

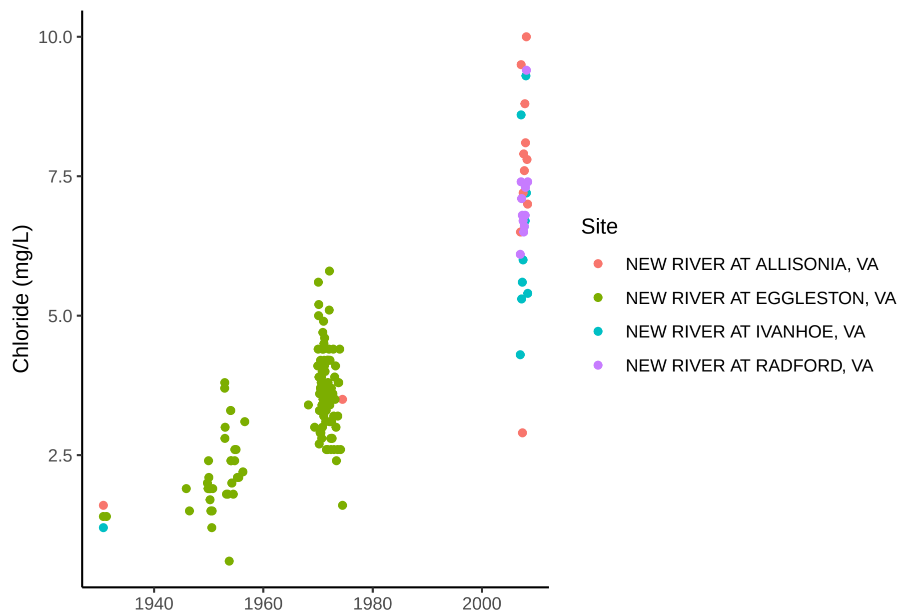
```
## [125] "#  USGS 371852081031201 006.0 EAST RIVER NEAR ENGLESIDE, W. VA."
## [126] "#  USGS 370853081003801 AT 23045 UNNAMED EPHEMERAL TRIB TO WALKER CREEK VA"
## [127] "#  USGS 370941081005201 AT 23045.5 UNNAMED INTERMIT TRIB TO KIMBERLING CR"
## [128] "#  USGS 370847081055101 AT 23046 KIMBERLING CREEK VA"
## [129] "#  USGS 371250080511401 AT 22014 DISMAL CREEK VA"
## [130] "#  USGS 370534081144701 AT 22013 HUNTING CAMP CREEK VA"
## [131] "#  USGS 370603081120801 AT 22013.5 LAUREL CR AT MOUTH OF LITTLE WOLF CR VA"
## [132] "#"
```

Now, let's clean things up a bit.

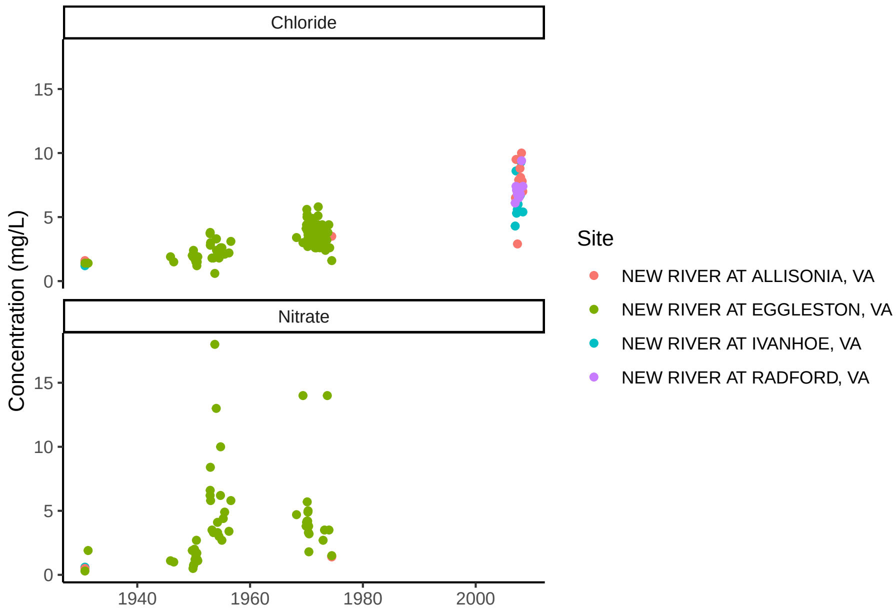
Join the parameter names from parameterCdFile and then join the site names from swva_chem_site. Then select just the columns we want, and finally filter the remaining data to just look at sites from the New River.

To illustrate the functionality of the data in this format, plot Chloride for each site, and then plot Chloride AND Nitrate, using the parameter name in facet_wrap.

```
wqdat_clean <- wqdat %>%
  left_join(parameterCdFile, by = c("parm_cd" = "parameter_cd")) %>%
  left_join(swva_chem_sites, by = "site_no") %>%
  select(station_nm, sample_dt, sample_tm, result_va, srsname, parameter_units) %>%
  filter(str_detect(station_nm, "NEW RIVER"))

wqdat_clean %>% filter(srsname == "Chloride") %>%
  ggplot(aes(x = sample_dt, y = result_va, color = station_nm)) +
  geom_point()+
  ylab("Chloride (mg/L)")+
  xlab(element_blank())+
  labs(color = "Site")+
  theme_classic()
```




```
wqdat_clean %>%
  ggplot(aes(x = sample_dt, y = result_va, color = station_nm)) +
  geom_point()+
  facet_wrap(facets = "srsname", nrow = 2)+
  ylab("Concentration (mg/L)")+
  xlab(element_blank())+
  labs(color = "Site")+
  theme_classic()
```



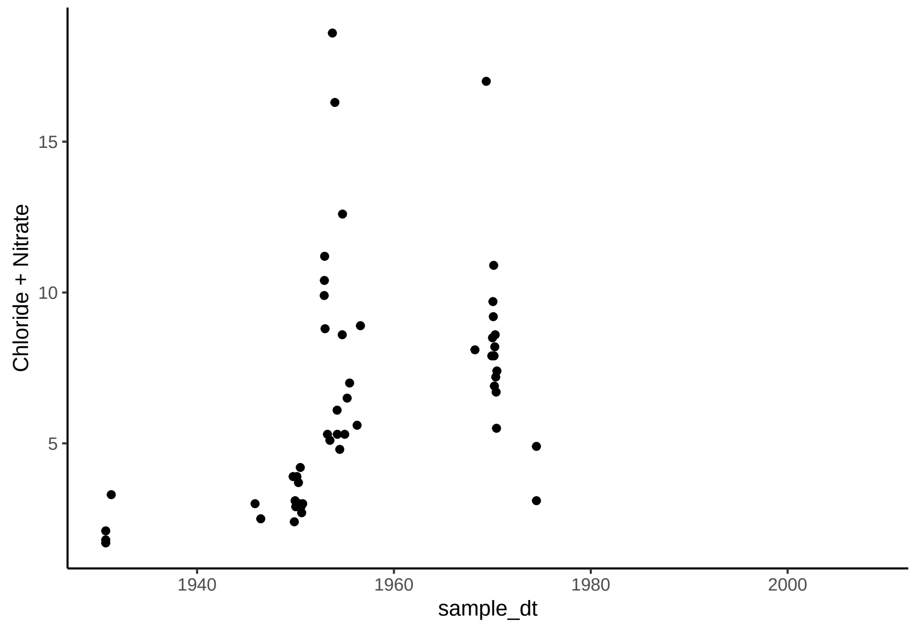
Now let's say we want to calculate something with chloride and nitrate. We need to make the data wide so we have a nitrate column and a chloride column. Do that below. What goes into values_from? what goes into names_from?

Next, plot Chloride + Nitrate. Could you do this with the data in the previous format?

Finally, use pivot_longer to transform the data back into a long format. Often you'll get data in a wide format and need to convert it to long, and we haven't tried that yet. The only argument you'll need to pass to pivot_longer() in this case is to tell it what columns to turn into the new DATA column (using the cols =) parameter.

```
#make wqdat_clean wide

wqdat_wide <- wqdat_clean %>% select(-parameter_units) %>%
  pivot_wider(values_from = result_va, names_from = srsname)

ggplot(wqdat_wide, aes(x = sample_dt, y = Chloride + Nitrate)) +
  geom_point()
```

```
## Warning: Removed 106 rows containing missing values (geom_point).
```




```
wqlonger <- wqdat_wide %>%
  pivot_longer(cols = c("Chloride", "Nitrate"))
```

Chapter 8

ACTIVITY Joins Pivots dataRetrieval

Get this document at the template repository on github: https://github.com/VT-Hydroinformatics/7-Activity-Joins-Pivots_dataRetrieval

8.1 Load the tidyverse, dataRetrieval, and patchwork packages.

```
library(tidyverse)
library(dataRetrieval)
library(patchwork)
```

8.2 Problem 1

Using readNWISqw(), read all the chloride (00940) data for the New River at Radford (03171000). Use the head() function to print the beginning of the output from readNWISqw.

8.3 Problem 2

Using the readNWISdv (daily values) function, download discharge (00060), temperature (00003), and specific conductivity (00095) for the New River at

Radford from 2007 to 2009 (regular year). Use renameNWIScolumns() to rename the output of the download. Use head() to show the beginning of the results of your download.

8.4 Problem 3

Do a left join on newphys and newriver to add the chloride data to the daily discharge, temp, and conductivity data. hint: you will join on the date. Preview your data below the chunk using head().

8.5 Problem 4

Create a line plot of Date (x) and Flow (y). Create a scatter plot of Date (x) and chloride concentration (y). Put the graphs on top of each other using the patchwork library.

8.6 Problem 5

Create a scatter plot of Specific Conductivity (y) and Chloride (x). Challenge: what could you do to get rid of the warning this plot generates about NAs.

8.7 Problem 6

Read in the GG chem subset data and plot Mg_E1 (x) vs Ca_E1 (y) as points.

8.8 Problem 7

We want to look at concentrations of each element in the #6 dataset along the stream (Distance), which is difficult in the current format. Pivot the data into a long format, the data from Ca, Mg, and Na _E1 columns should be pivoted. Make line plots of each element where y is the concentration and x is distance. Use facet_wrap() to create a separate plot for each element and use the "scales" argument of facet_wrap to allow each plot to have different y limits.

Chapter 9

ACTIVITY Summative 1

Get this document at the template repository on github: https://github.com/VT-Hydroinformatics/8-Test_1

9.0.1 Instructions

Please read carefully!

Write your code in the provided code chunks and answer any questions by typing outside the chunk.

Comment your code to let me know what you are trying to do, in case something doesn't work.

Turn in a knitted rmd (html or pdf). If you can't get your document to knit when you go to turn it in, just comment out the lines of code that are causing the knit to fail, knit the document, and submit.

9.1 Problem 1

Load the tidyverse, lubridate, and dataRetrieval packages.

9.2 Problem 2

Read in the McDonald Hollow dataset in the project folder.

What are the data types of the first three columns?

How long is the data (number of rows)?

What is the name of the last column?

9.3 Problem 3

Plot the stage of the stream (Stage_m_pt) on the y axis as a line and the date on the x. These stage data are in meters, convert them to centimeters for the plot.

For all plots in this test, label axes properly and use a theme other than the default.

9.4 Problem 4

We want to look at the big event that happens from November 11, 2020 to November 27, 2020. Filter the dataset down to this time frame and save it separately. Make a plot with the same setup as in #3 with these newly saved data.

9.5 Problem 5

For this storm, we are curious about how conductivity changes with the stream level. To do this, make a scatter plot that shows Stage on the x axis and specific conductivity (SpC_mScm) on the y. (units: mScm) Color the points on the plot using the datetime column. Use the plot to describe how specific conductivity changes with stream stage throughout the storm. (not functionally, just how the values change)

9.6 Problem 6

Continuing to look at the storm, as an exploratory data analysis, we want to create a plot that shows all the parameters measured. To do this, pivot the STORM EVENT data so there is a column that has the values for all the parameters measured as individual rows, along with another column that identifies the type of measurement. Then use facet_wrap with the "name" column (or whatever you call it) as the facet. Be sure to set the parameters of facet_wrap such that the y axes are all allowed to be different ranges.

EX:
Date Value Name

10/1/20 12 Stage
10/1/20 6 Temp
….

9.7 Problem 7

We want to create a table that clearly shows the differences in water temperature for the three months at the two locations (flow and pool) in the FULL data set (not the storm subset). To do this: Create a new column in the full dataset called "month" and set it equal to the month of the datetime column using the month() function. Then group your dataset by month and summarize temperature at each location by mean. Save these results to a new object and output it so it appears below your chunk when you knit. Be sure the object has descriptive column names.

You can do this all in one statement using pipes.

9.8 Problem 8

Plot the distribution of the flow temperature and show as vertical lines on the plot the mean, median, and IQR. Be careful about how you show IQR. Look at the definition and then think about how you would put it on the plot. Describe in the text above the chunk what color is what statistic in the plot. Using the shape of the distribution and the measures you plotted, explain why you think the distribution is normal or not. What statistical test could you perform to see if it is normal?

9.9 Problem 9

In this question we will get and format data for three USGS gages.

Gages: 03177710, 03173000, 03177480
Discharge in cubic feet per second (cfs) code: 00060

a. Read and save the gage information for the three gages using readNWISsite().
b. Use the readNWISdv() function to read and save the daily discharge values for the following three gages for the 2020 water year (10-01-2019 to 9-30-2020). And then use the renameNWIScolumns() function to make the names human-friendly.
c. Join the gage site information from (a) to the data from (b) so you can reference the gages by their names.

9.10 Problem 10

Using the data from #9, Plot flow on the y axis and date on the x axis, showing the data as a line, and coloring by gage name.

Chapter 10

Flow Duration Curves

Get this document and a version with empty code chunks at the template repository on github: https://github.com/VT-Hydroinformatics/9-Flow-Duration-Curves

Alright team. So far we have learned to wrangle data, make plots, and look at data distributions. Now it is time to put all that knowledge to use.

We are on our way to doing analyses of extreme discharge events: low flow statistics and floods. But in order to do that, we need to understand a common way to look at data distributions in hydrology: the flow duration curve. As you'll see below, this is basically just a different way of looking at a pdf, and it can take some getting used to. But it is also a very useful tool!

As always let's load the packages we will use: tidyverse, dataRetrieval, lubridate, and patchwork. Patchwork will help us make a multi-panel graph in the last part of the exercise.

We will also use theme_set() in this chunk so we don't have to change the ggplot theme every time we make a plot.

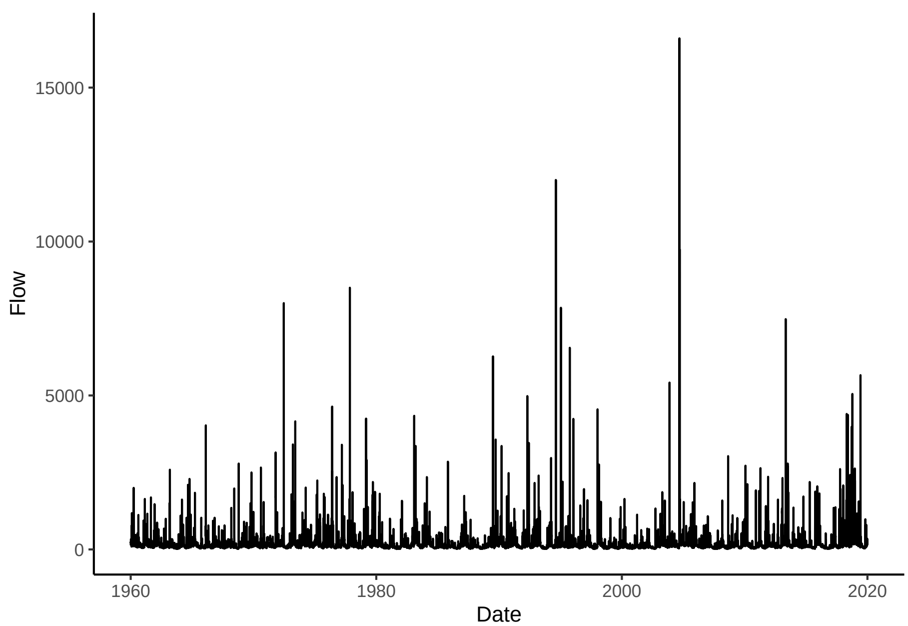
```
library(tidyverse)
library(dataRetrieval)
library(lubridate)
library(patchwork)

#set plot theme for the document so we
#don't have to do it in every plot
theme_set(theme_classic())
```

10.1 Get data

To start, let's grab the USGS discharge data for the gage in Linville NC from 1960 to 2020.

We will download the data using USGS dataRetrieval and look at a line plot.

```
siteno <- "02138500" #Linville NC
startDate <- "1960-01-01"
endDate <- "2020-01-01"
parameter <- "00060"

Qdat <- readNWISdv(siteno, parameter, startDate, endDate) %>%
  renameNWISColumns()

#Look at the data
Qdat %>% ggplot(aes(x = Date, y = Flow))+
  geom_line()
```

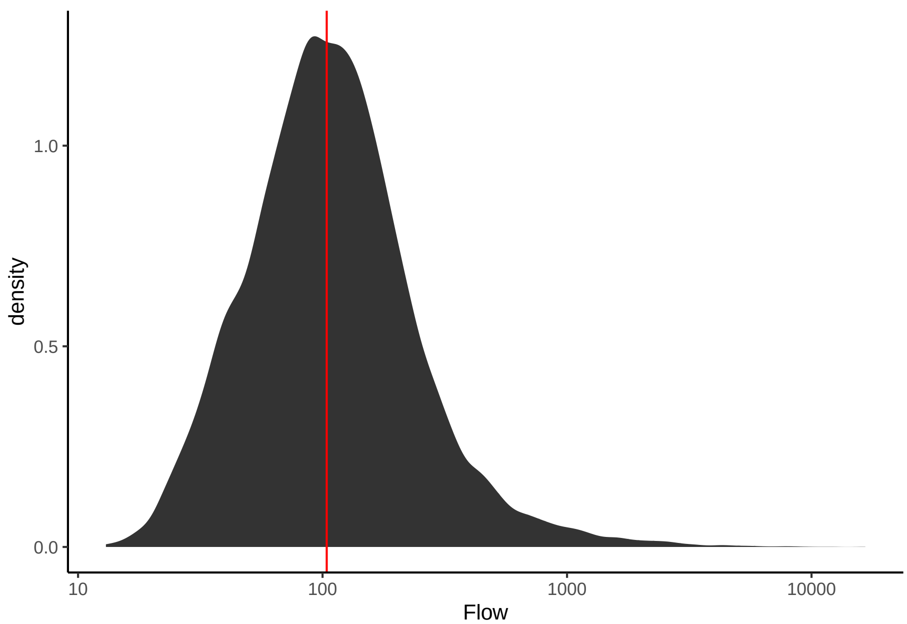


10.2 Review: describe the distribution

Make a plot to view the distribution of the discharge data.

- What is the median flow value?
- What does this tell us about flow at that river?
- How often is the river at or below that value?
- Could you pick that number off the plot?
- What about the flow the river is at or above only 5% of the time?

```
Qdat %>% ggplot(aes(Flow))+
  stat_density()+
  scale_x_log10()+
  geom_vline(xintercept = median(Qdat$Flow), color = "red")
```



10.3 ECDFs

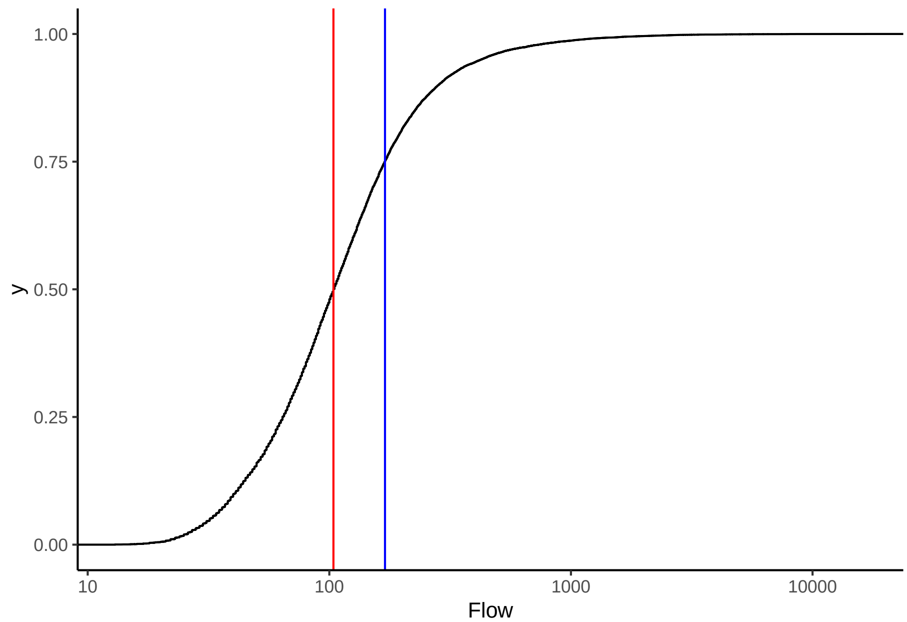
Let's look at an Empirical Cumulative Density Function (ECDF) of the data.

Look at this carefully, what does it show? How is it different from the pdf of the data?

Plot the median again. Without the line on the plot, how would you tell where the median is?

Given your answer to the question above, can you determine the flow the river is at or above only 25% of the time? Think carefully about what the y axis of the ECDF means.

```
Qdat %>% ggplot(aes(Flow))+
  stat_ecdf()+
  scale_x_log10()+
  geom_vline(xintercept = median(Qdat$Flow), color = "red")+
  geom_vline(xintercept = quantile(Qdat$Flow)[4], color = "blue")
```



10.4 Calculate flow exceedence probabilities

In hydrology, it is common to look at a similar representation of flow distributions, but with flow on the Y axis and "% time flow is equaled or exceeded" on the X axis. There are a number of ways we could make this plot: for example we could transform the axes of the plot above or we could use the function that results from the ECDF function in R to calculate exceedence probabilities at flow throughout our range of flows. But for our purposes, we are just going to calculate it manually.

We are going to calculate our own exceedence probabilities because knowing how to do this will hopefully help us understand what a flow duration curve is AND we will need to do similar things in our high and low flow analyses.

The formula for exceedence probability (P) is below. What do we need to calculate this?

Exceedence probability (P), Probability a flow is equaled or exceeded

$P = 100 * [M/(n + 1)]$

M = Ranked position of the flow n = total number of observations in data record

Here's a description of what we will do: > Pass our Qdat data to mutate and create a new column that is equal to the ranks of the discharge column. > Then pass that result to mutate again and create another column equal exceedence probability (P) * 100, which will give us %.

```
#Flow is negative in rank() to make
#high flows ranked low (#1)
Qdat <- Qdat %>%
  mutate(rank = rank(-Flow)) %>%
  mutate(P = 100 * (rank / (length(Flow) + 1)))
```

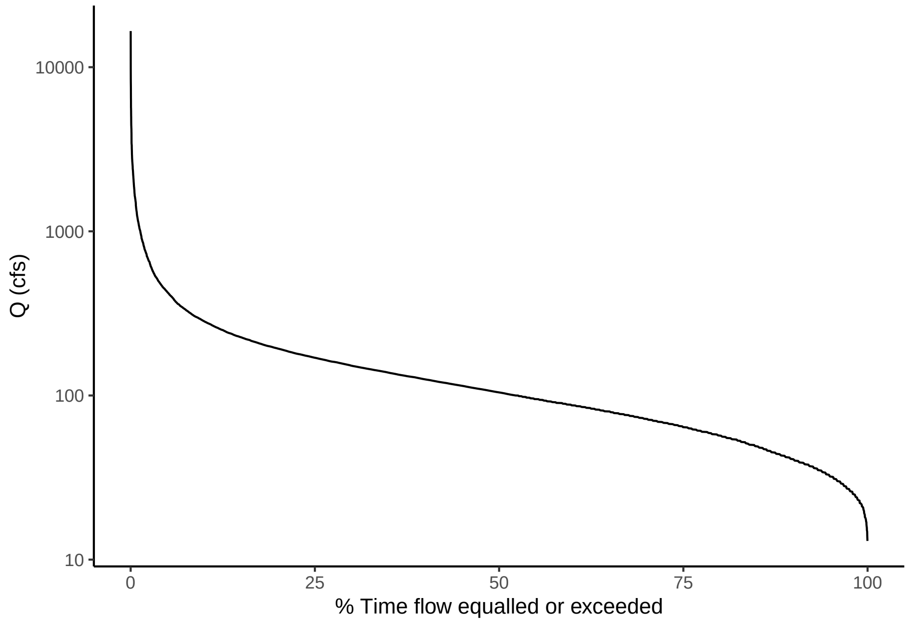
10.5 Plot a Flow Duration Curve using the probabilities

Now construct the following plot: A line with P on the x axis and flow on the y axis. Name the x axis "% Time flow equaled or exceeded" and log the y axis.

That's a flow duration curve!

Questions about the flow duration curve: * How often is a flow of 100 cfs exceeded at this gage? * Is flow more variable for flows exceeded 0-25% or of the time or 75-100% * of the time? * How can you tell? * These data are daily observations. Given that, what is a more accurate name for the x axis? * What would the X axis be called if we were using maximum yearly data?

```
Qdat %>% ggplot(aes(x = P, y = Flow))+
  geom_line()+
  scale_y_log10()+
  xlab("% Time flow equalled or exceeded")+
  ylab("Q (cfs)")
```

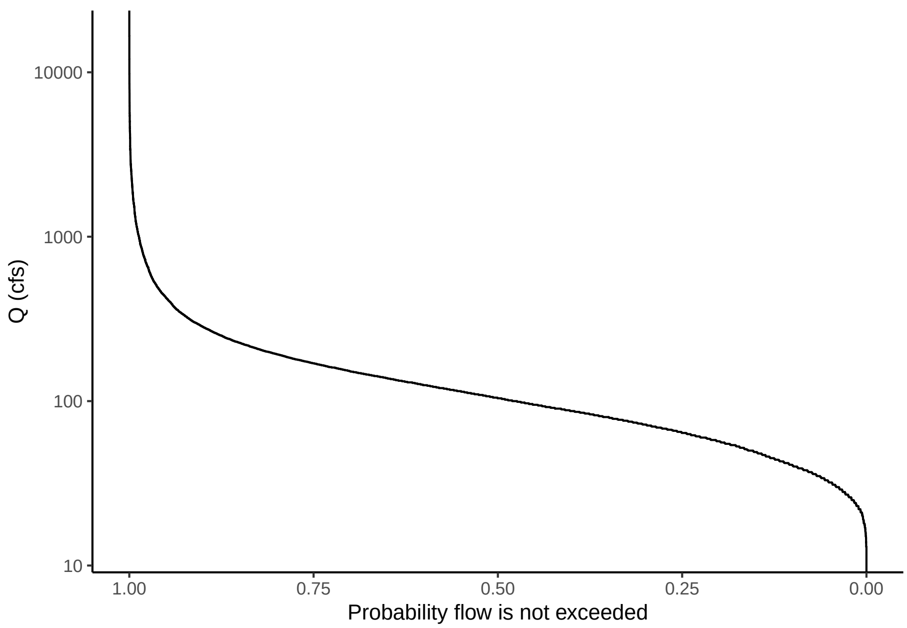


10.6 Make an almost FDC with stat_ecdf

Below is an example of making a very similar plot with the stat_ecdf() geometry in ggplot. Notice how similar the result is to the one we calculated manually.

To make the plot similar, we will reverse the y axis of the ecdf plot with scale_y_reverse and flip the axes (change the x to y and the y to x) with coord_flip()

```
Qdat %>% ggplot(aes(Flow))+
  stat_ecdf()+
  scale_x_log10()+
  scale_y_reverse()+
  coord_flip()+
  xlab("Q (cfs)")+
  ylab("Probability flow is not exceeded")
```



10.7 Example use of an FDC

Let's explore one potential use of flow duration curves: examining the differences between two sets of flow data.

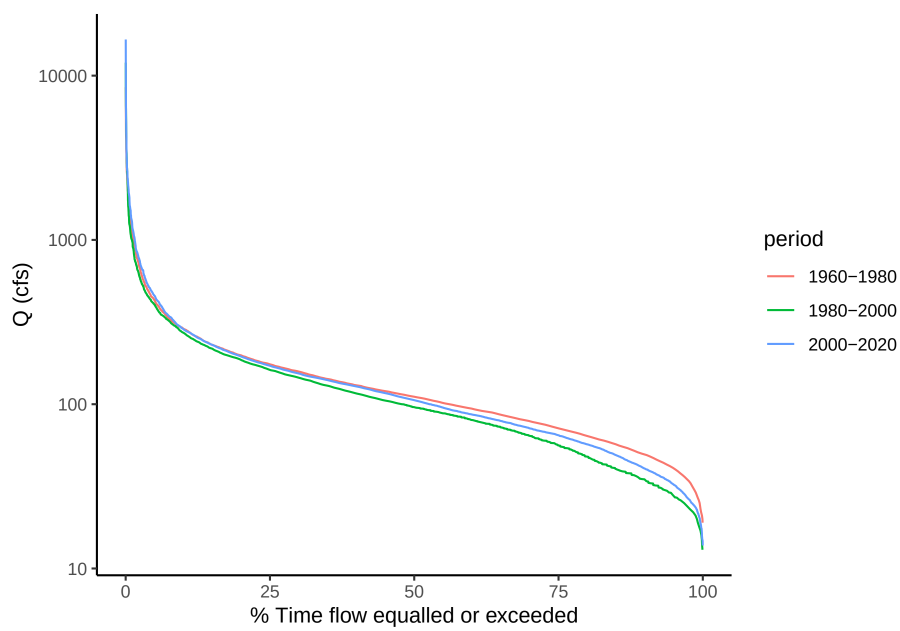
From the line plot of the discharge, it looked like the flow regime may have shifted a bit in the data between the early years and newer data. Let's use flow duration curves to examine potential differences. We can come up with groups and then use group_by to run the analysis by groups instead of the whole dataset.

We are introducing a new function here called case_when(). This allows you to assign values to a new column based on values in another column. In our case, we are going to name different time periods in our data.

We will then group the data by these periods and calculate exceedence probabilities for each. The procedure works the same, except we add a group_by statement to group by our time period column before we create the rank and P columns. Then, when we plot, we can just tell ggplot to create different colored lines based on the time period names and it will plot a separate flow duration curve for each. Tidyverse FOR THE WIN!

Describe the differences in flow regime you see between the three periods of 1960-1980, 1980-2000, and 2000-2020.

```
Qdat <- Qdat %>%
  mutate(year = year(Date)) %>%
  mutate(period = case_when( year <= 1980 ~ "1960-1980",
                             year > 1980 & year <= 2000 ~ "1980-2000",
                             year > 2000 ~ "2000-2020"))

Qdat <- Qdat %>%
  group_by(period) %>%
  mutate(rank = rank(-Flow)) %>%
  mutate(P = 100 * (rank / (length(Flow) + 1)))

Qdat %>% ggplot(aes(x = P, y = Flow, color = period))+
  geom_line()+
  scale_y_log10()+
  xlab("% Time flow equalled or exceeded")+
  ylab("Q (cfs)")
```

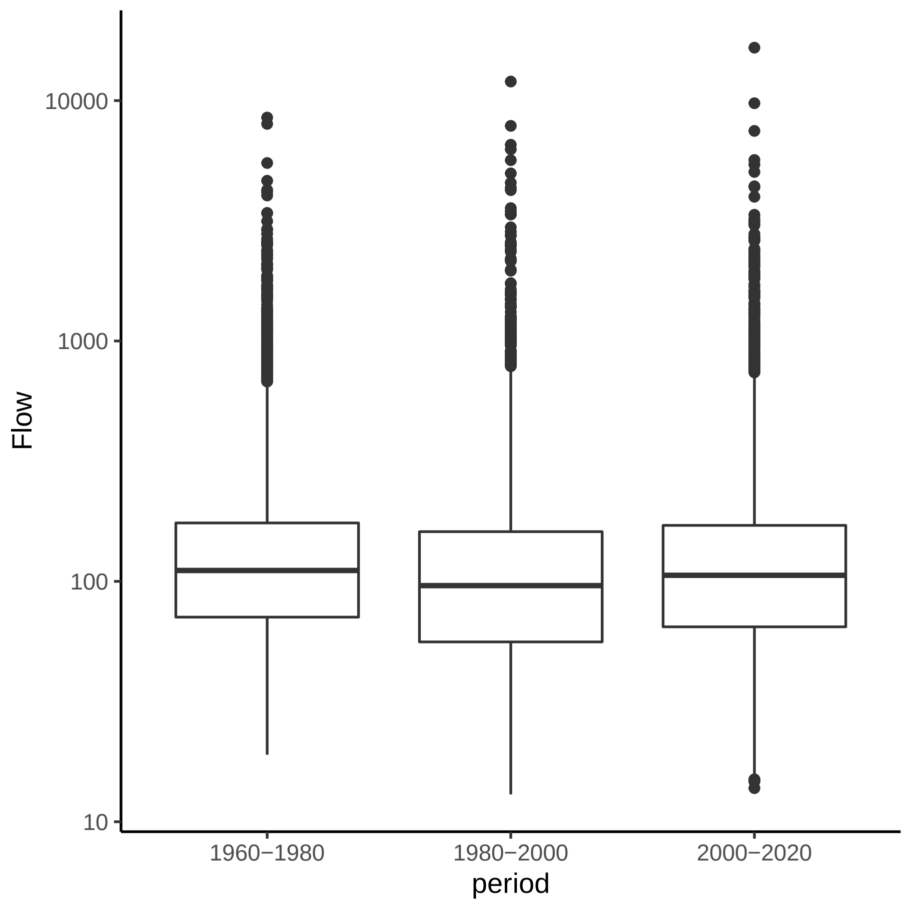


10.8 Compare to a boxplot of the same data

We are really just looking at the data distribution here. Remember another good way to compare distributions is a boxplot. Let's create a boxplot showing flows from these time periods. (we will also mess with the dimensions of the plot so the boxes aren't so wide using fig.width and fig.height in the "' header above the code chunk)

What are the advantages/disadvantages of the flow duration curves vs. boxplots?

```
Qdat %>% ggplot(aes(x = period, y = Flow)) +
  geom_boxplot()+
  scale_y_log10()
```

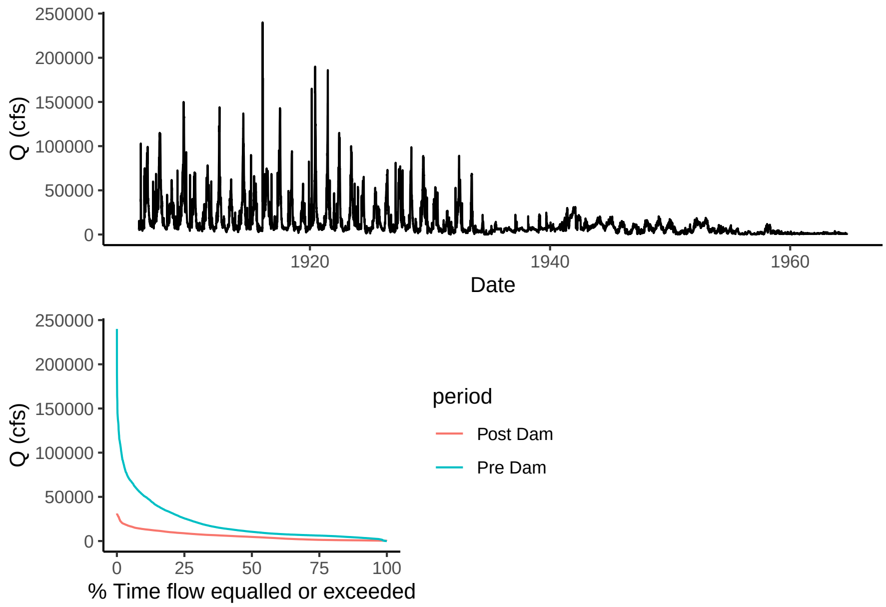


10.9 Challenge: Examining flow regime change at the Grand Canyon

The USGS Gage "Colorado River at Yuma, AZ" is below the Hoover dam. The Hoover Dam closed in 1936, changing the flow of the Colorado River below. Load average daily discharge data from 10-01-1905 to 10-01-1965 from the Yuma gage. Use a line plot of discharge and flow duration curves to examine the differences in discharge for the periods: 1905 - 1936, 1937 - 1965.

How does the FDC show the differences you observed in the line plot?

```
siteid <- "09521000"
startDate <- "1905-10-01"
endDate <- "1965-10-01"
parameter <- "00060"

WS <- readNWISdv(siteid, parameter, startDate, endDate) %>%
  renameNWISColumns() %>%
  mutate(year = year(Date)) %>%
  mutate(period = case_when( year <= 1936 ~ "Pre Dam",
                             year > 1936  ~ "Post Dam")) %>%
  group_by(period) %>%
  mutate(rank = rank(-Flow)) %>%
  mutate(P = 100 * (rank / (length(Flow) + 1)))

flow <- ggplot(WS, aes(Date, Flow))+#, color = period))+
  geom_line()+
  ylab("Q (cfs)")

fdc <- WS %>% ggplot(aes(x = P, y = Flow, color = period))+
  geom_line()+
  #scale_y_log10()+
  xlab("% Time flow equalled or exceeded")+
  ylab("Q (cfs)")

flow / (fdc + plot_spacer())
```



That's it! Next we will apply some of these principles to look at low-flow statistics.

Chapter 11

Low Flow Analysis

Get this document and a version with empty code chunks at the template repository on github: https://github.com/VT-Hydroinformatics/10-Low-Flow-Analysis

Pre-activity reading:

https://www.epa.gov/ceam/definition-and-characteristics-low-flows#1Q10

Analysis based on:

https://github.com/DEQdsobota/Oregon7Q10/blob/master/R/Oregon7Q10.R

https://nepis.epa.gov/Exe/ZyPDF.cgi?Dockey=P100BK6P.txt

Load packages for analysis. zoo will allow us to easily perform rolling means, and moments will allow easy calculation of skewness.

```
library(zoo)
library(tidyverse)
library(dataRetrieval)
library(lubridate)
library(moments)

theme_set(theme_classic())
```

11.1 What are low flow statistics?

Low flow design flows can be specified based on hydrological or biological data. Biological methods look more at water quality standards relevant to biota. The hydrologic method just looks at the statistical distribution of low flows over a period of time.

- Just from this simple definition, can you think of a management situation where it would make sense to use the biological method? the hydrologic method? What are the advantages to each?

We will focus on hydrologic methods. What a surprise! You will most frequently see low flow stats in the format of xQy. So for example 7Q10 or 1Q10 are common design flows. Let's look at the EPA definition of these and then break them down.

"The 1Q10 and 7Q10 are both hydrologically based design flows. The 1Q10 is the lowest 1-day average flow that occurs (on average) once every 10 years. The 7Q10 is the lowest 7-day average flow that occurs (on average) once every 10 years." -EPA https://www.epa.gov/ceam/definition-and-characteristics-low-flows#1Q10

So the first number, **the 7 in 7Q10** is how many days we will average flow over to calculate the statistic. Why does does this matte? Why not always use a 1 day flow record?

Then the second number is the return-interval of the flow, or the probability that a flow of that magnitude or lower will occur any given year. **The 10 in 7Q10** means there is a 10 percent chance that the associated 7-day average flow or below will occur in any given year. Another way of saying this is that a flow of that magnitude or below occurs on average once every 10 years. **However** expressing it this way can be dangerous, especially with the opposite type of extreme flows: Floods. Why do you think it could be dangerous to say a flow of this magnitude or below will happen on average once every 10 years?

So, to calculate a 7Q10 we need: * 7-day mean-daily flows * The minumum value per year of those 7-day mean-daily flows * The return intervals of those flows minimum yearly flows

Because a 7Q10 flow means * There is a 10% chance (return interval = 10) that a river will have a average weekly flow of that level or below in a given year.

11.2 Get data

Let's get started on an example. We will calculate the 7Q10 low flow statistic for the Linville NC usgs gage (02138500) using daily discharge data from 1922-1984. (parameter = 00060)

```
siteno <- "02138500"
startDate <- "1922-01-01"
endDate <- "1984-01-01"
parameter <- "00060"

Qdat <- readNWISdv(siteno, parameter, startDate, endDate) %>%
  renameNWISColumns()
```

11.3 Create the X days average flow record

Remember the 7 in 7Q10 means we are looking at the 7-day average flow. We just have daily values from the USGS gage, so we need to create this data record.

To do this we will calculate a rolling average, also called a moving-window average. This just means you grab the first 7 days, average them, then move the window of the days you are averaging forward a day, and average again… all the way through the record.

For your rolling mean you can have the window look forward, backward, or forward and backward. For example, a forward window takes the average of X number of records and places the value at the beginning. Backward places that value at the end, and both would put it in the middle. In the function we will use to do this, forward is a left align, backward is right align, and both is centered.

For example

> data window = 1, 2, 3, 4, 5 (lots of values before and after this)
>
> mean = 3
>
> forward window/left align: 3, NA, NA, NA, NA
>
> backward window/right align: NA, NA, NA, NA, 3
>
> both/center align: NA, NA, 3, NA, NA

We could certainly set up some code to calculate this, but there is a nice and fast function in the zoo package for calculating rolling means.

As we write the code to do this analysis, we are going to keep in mind that we may want to calculate a different type of low flow, like a 1Q10, so we are going to store the x and y of the xQy low flow statistic as objects rather than including them several places in the code. That way we can just change them in one place and run the analysis to compute a different statistic.

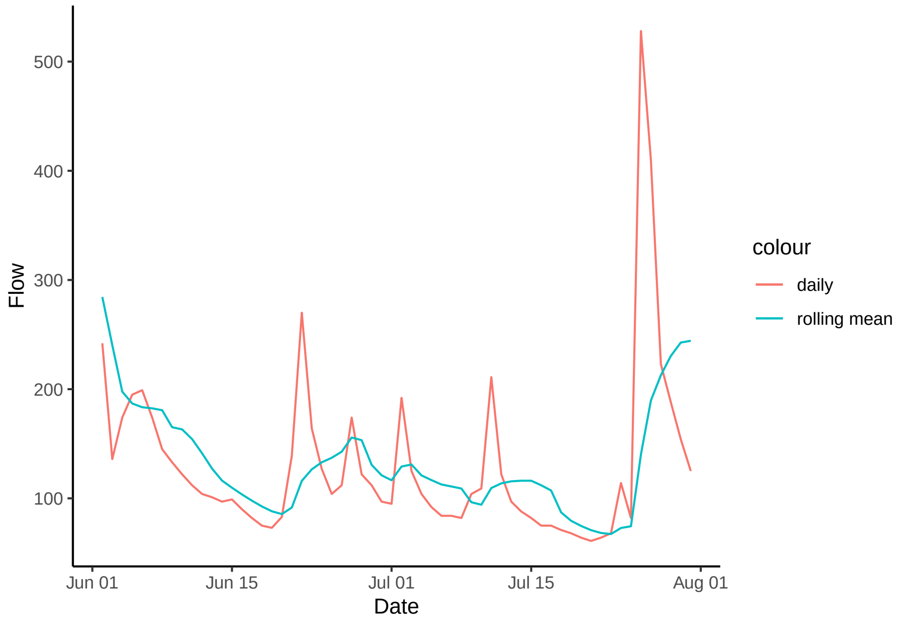
```
#set x and y for xQy design flow
Xday <- 7
YrecInt <- 10

#X day rolling mean, don't fill the ends of the timeseries,
#don't ignore NAs, use a backward-looking window (right align)
Qdat <- Qdat %>% mutate(xdaymean = rollmean(Flow,
                                            Xday,
                                            fill = NA,
                                            na.rm = F,
                                            align = "right"))
```

11.4 Look at what a rolling mean does.

We just added a new column with the rolling mean, so let's plot it and see what it did to the discharge record.

Let's look at June-August 1960. You can't see too well what is going on in the full record.

```
Qdat %>%
  filter(Date > mdy("06-01-1960") & Date < mdy("08-01-1960")) %>%
  ggplot(aes(Date, Flow, color = "daily"))+
    geom_line()+
    geom_line(aes(x = Date, y = xdaymean, color = "rolling mean"))
```



11.5 Calculate yearly minimums

Okay, we have our X-day rolling mean. Now we need to calculate the probability that a given magnitude flow or below will happen in a given year. Because we are concerned with *a given year* we need the lowest flow per year.

We will calculate minimum flow per year by creating a *Year* column, grouping by that column, and using the summarize function to calculate the minimum flow per year. The code we are going to write will also drop any years that are missing too much data by dropping years missing 10% or more days.

```
#missing less than 10% of each year and 10% or fewer NAs
QyearlyMins <- Qdat %>% mutate(year = year(Date)) %>%
                        group_by(year) %>%
                        summarize(minQ = min(xdaymean, na.rm = T),
                                  lenDat = length(Flow),
                                  lenNAs = sum(is.na(xdaymean))) %>%
                        filter(lenDat > 328 & lenNAs / lenDat < 0.1)
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
```

11.6 Calculate return interval

Now that we have an object that contains our yearly minimum flows, we can calculate the return interval as

$$ReturnInterval = (n + 1)/rank$$

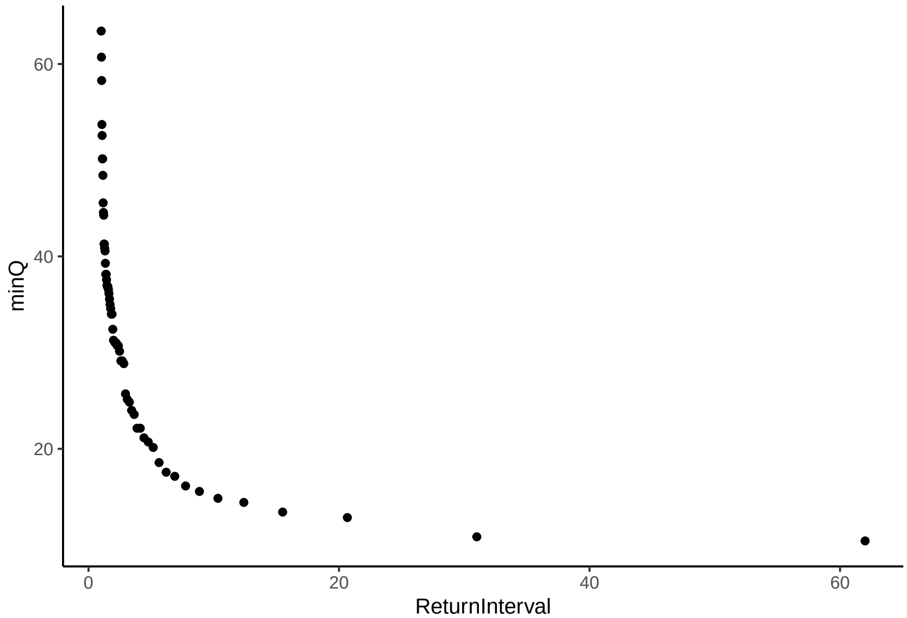
Where n is the number of records in the data (number of years) and rank is the rank of each year's low flow (lowest flow = rank 1 and so on). We can calculate the rank with the rank() function in base R. In the rank function we will specify that in the case of a tie, the first value gets the lower rank using ties.method = "first".

We can then transform that to an exceedence probability as

$$ExceedenceProbability = 1/ReturnInterval$$

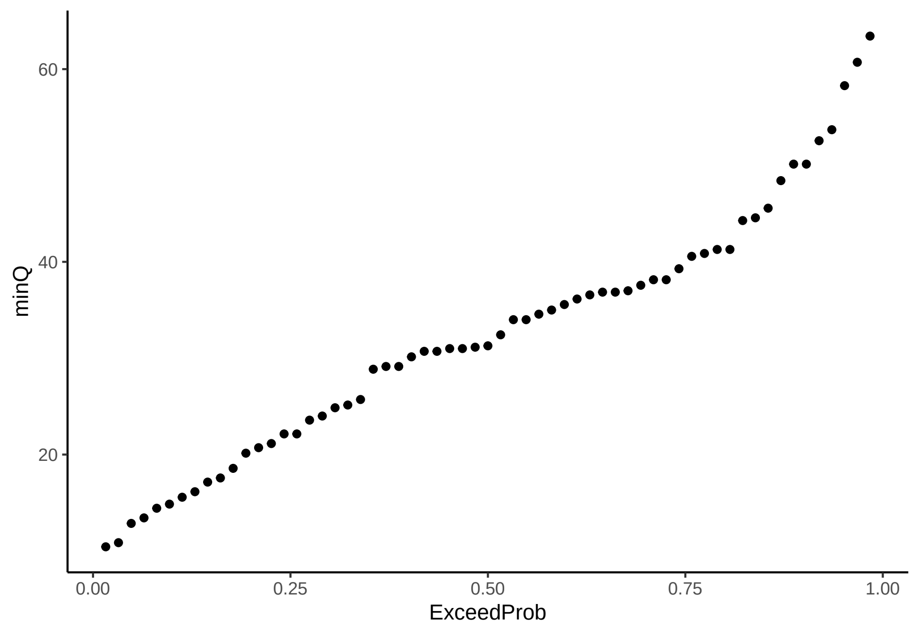
Once we calculate the return interval and exceedence probability we will plot the return interval against the minimum discharge.

```
# add rank column and return interval column
QyearlyMins <- QyearlyMins %>%
               mutate(rank = rank(minQ, ties.method = "first")) %>%
               mutate(ReturnInterval = (length(rank) + 1)/rank) %>%
               mutate(ExceedProb = 1 / ReturnInterval)

ggplot(QyearlyMins, aes(x = ReturnInterval, y = minQ))+
  geom_point()
```



Challenge question How is this similar to a flow duration curve? Could you make a "flow duration curve" from these data? What would it tell you?

```
ggplot(QyearlyMins, aes(x = ExceedProb, y = minQ))+
  geom_point()
```



11.7 Fit to Pearson Type II distribution

Source for these calculations: https://water.usgs.gov/osw/bulletin17b/dl_flow.pdf

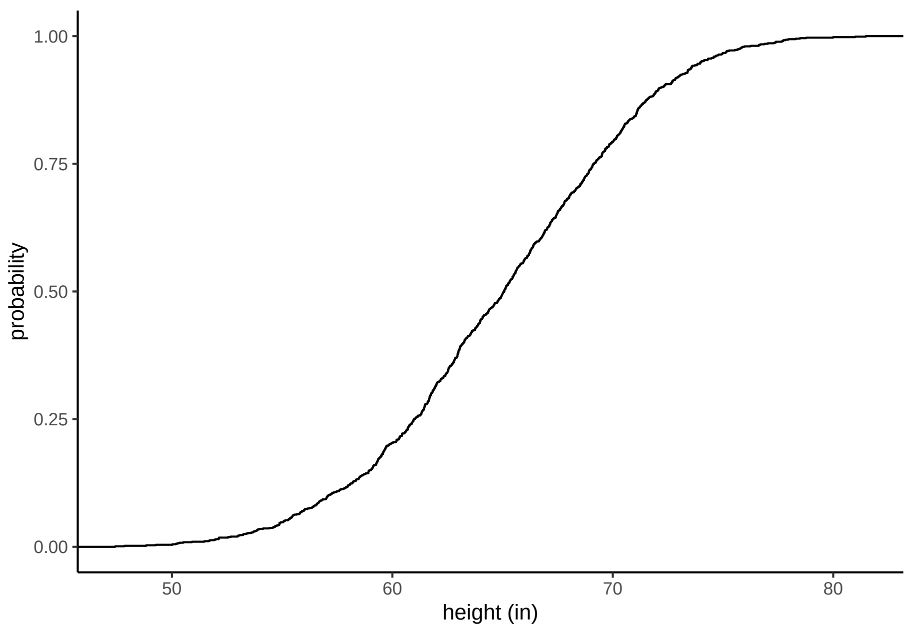
We now have everything we need to calculate what the 10-year return interval flow is (the 0.1 probability flow). To do this, we have to fit a distribution to our data and then use that fitted distribution to predict the value of the 10-year return interval flow.

This may sound a little complex, but let's think about it this way:

- You have some data, let's say: heights of students at Virginia Tech
- You did some tests on it and know it is a normal distribution
- If you measure the mean and standard deviation of that distribution, you could create a "fitted" representation of your distrubtion by generating a normal distribution with the same mean and standard deviation with the rnorm() function.
- Now you could plot that fitted, synthetic distribution as an ECDF and read the plot to determine, say, 10% of students (0.1 probability) are at or above what height?

Assume the average height from your data was 65 inches and the standard deviation was 6 inches (this is 100% made up), let's look at it.

```
fitteddistribution <- rnorm(1000, mean = 65, sd = 6) %>%
  as_tibble()

ggplot(fitteddistribution, aes(x = value))+
  stat_ecdf()+
  xlab("height (in)")+
  ylab("probability")
```



To get our 10 year return period (0.1 exceedence probability) we are going to do the same thing, except we know the distribution of the data isn't normal, so we have to use a different distribution.

There are a bunch of "extreme value" distributions used in these type of analyses. When we talk about floods we will use the Gumbel distribution, for example. For this type of analysis, it is common to use the Pearson Type III distribution.

When we used the normal distribution example, we let R produce the distribution that fit our data. In this case we will use the equation that describes the Person Type III distribution. To predict flow at a given recurrence interval we will need the mean of the logged discharges (Xbar), the frequency factor (K), the standard deviation of the log discharges (S), skewness (g), and the standard normal variate (z). We will first compute this for all of the values in our dataset to see how the fitted values fit our calculated values.

Pearson Type III

$Flow = exp(Xbar + KS)$

where:

Xbar = mean of the log discharge you are investigating

K = frequency factor

S = standard deviation of log discharges

Frequency Factor

$K = (2/g) * ((1 + (g * z))/6 - ((g^2)/36))^3 - 1)$

Skewness

g = skewness() from moments package

Standard normal variate

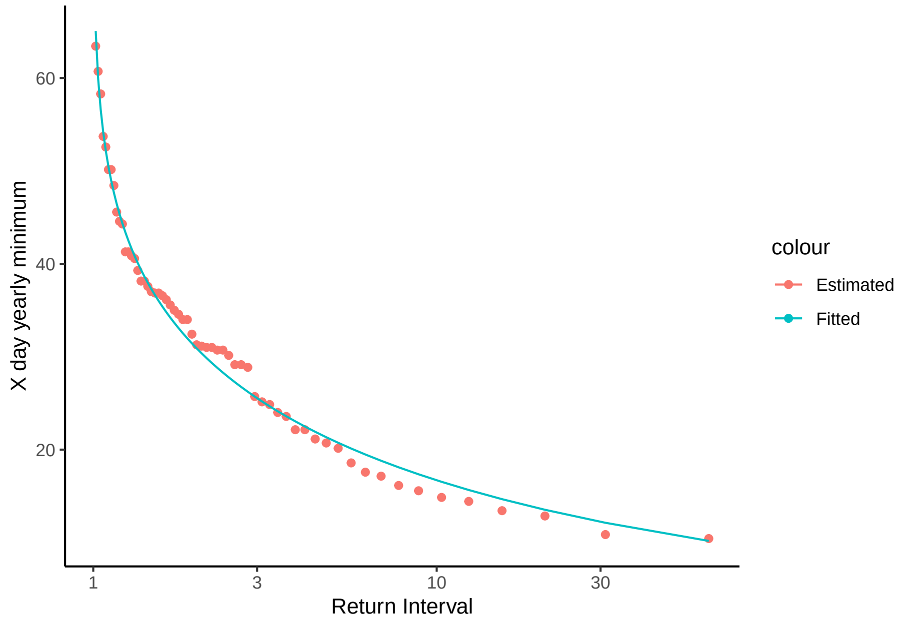
$z = 4.91 * ((1/y)^{0.14} - (1 - (1/y))^{0.14})$

y = recurrence interval

```
#Measures of the distribution
Xbar <- mean(log(QyearlyMins$minQ))
S    <- sd(log(QyearlyMins$minQ))
g    <- skewness(log(QyearlyMins$minQ))

#calculate z, K, to plot the fitted Pearson Type III
QyearlyMins <- QyearlyMins %>%
  mutate(z = 4.91 * ((1 / ReturnInterval) ^ 0.14 - (1 - 1 / ReturnInterval) ^ 0.14)) %>
  mutate(K = (2 / g) * (((1 + (g * z) / 6 - (g ^ 2) / 36) ^ 3) - 1) ) %>%
  mutate(Qfit = exp(Xbar + K * S))
```

Let's look our results and see how they fit. Plot the return interval on the x axis and flow on the y. Plot minQ, the minimum Q data, and Qfit, the data from the the model fit.

```
QyearlyMins %>%
  ggplot(aes(x = ReturnInterval, y = minQ, color = "Estimated"))+
  geom_point()+
  geom_line(aes(x = ReturnInterval, y = Qfit, color = "Fitted"))+
  theme_classic()+
  scale_x_log10()+
  ylab("X day yearly minimum")+
  xlab("Return Interval")
```



Above we calculated z, K and the flow for each return interval in our data record to see how the distribution fit our data. We can see it fits quite well.

We can use the same calculations as we used on the entire record to calculate a specific return period of interest. In our case, the 10 year return period for the 7Q10.

We will set y equal to YrecInt, which we set above. This way we can just change it at the top of the code to run whatever xQy metric we want.

```
#xQy ei: 7Q10
y = YrecInt

#Find these values based on established relationships
z    <- 4.91 * ((1 / y) ^ 0.14 - (1 - 1 / y) ^ 0.14)
K    <- (2 / g) * (((1 + (g * z) / 6 - (g ^ 2) / 36) ^ 3) - 1)

PearsonxQy <- exp(Xbar + K * S)
```

So, our 7Q10 flow in cfs for this gage is....

```
#Low flow stat (7Q10 in exercise)
PearsonxQy
```

```
## [1] 16.70488
```

11.8 Distribution-free method

We won't go over this in the same detail, but the xQy flow can also be calculated using a formula that does not assume a specific distribution. The expression, and code to perform it, is below.

The expression for xQy is:

$xQy = (1 - e)X(m1) + eX(m2)$

where: [ ] indicates the value is truncated

$X(m)$ = the m-th lowest annual low flow of record

$m1 = [(n + 1)/y]$

$m2 = [(n + l)/y] + 1$

$[z]$ = the largest integer less than or equal to z

$e = (n + l)/y - [(n + l)/y]$

This method is only appropriate when the desired return period is less than n/5 years

```
x <- Xday
y <- YrecInt
n <- length(QyearlyMins$minQ)

m1 <- trunc((n + 1)/y)
m2 <- trunc(((n + 1)/y) + 1)

e <- ((n + 1)/y) - m1

Xm1 <- QyearlyMins$minQ[QyearlyMins$rank == m1]
Xm2 <- QyearlyMins$minQ[QyearlyMins$rank == m2]

DFxQy <- (1-e) * Xm1 + e * Xm2

DFxQy
```

```
## [1] 15
```

Chapter 12

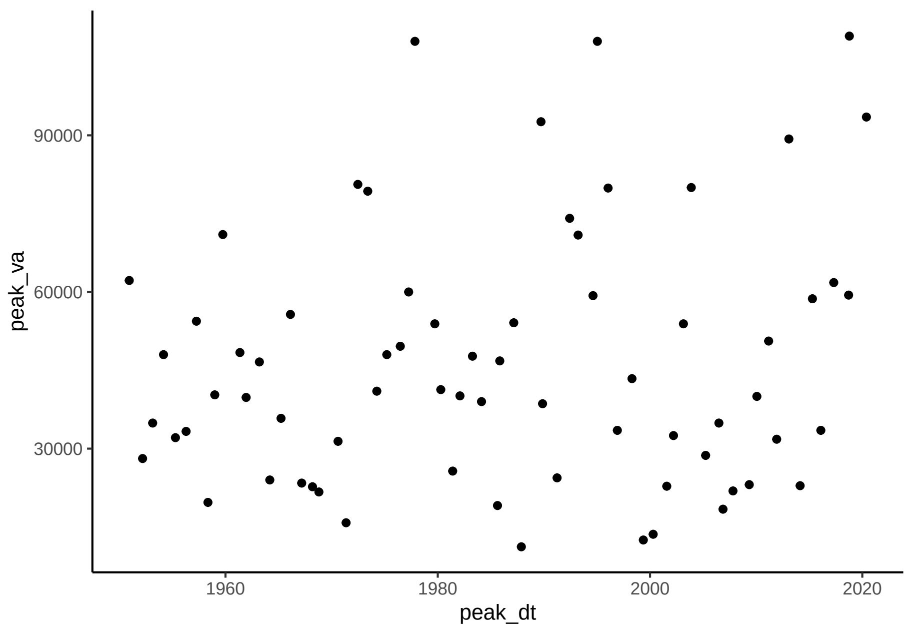
DRAFT Flood Frequency Analysis

Load packages

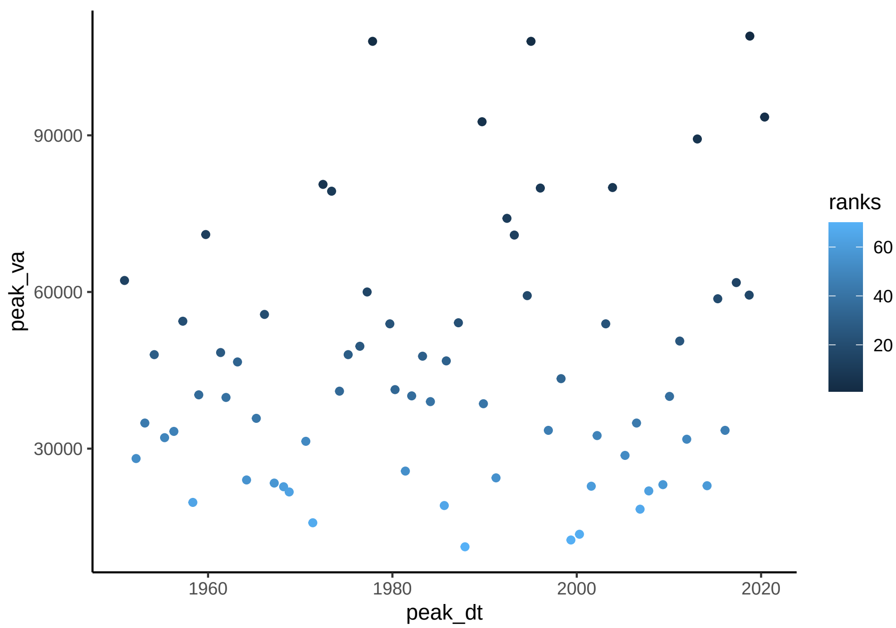
```
library(tidyverse)
library(dataRetrieval)
```

Get peak flow data and plot it

```
radford <- "03171000"

peakflows <- readNWISpeak(radford, startDate = "1950-01-01")

ggplot(peakflows, aes(peak_dt, peak_va))+
  geom_point()
```




```
#create rank column (minus flips the ranking)
#then clean it up, pull out only peak value, date, rank
peakflows <- peakflows %>% mutate(ranks = rank(-peak_va)) %>%
              select(peak_dt, peak_va, ranks)

#look at it
ggplot(peakflows, aes(peak_dt, peak_va, color = ranks))+
  geom_point()
```




```
head(peakflows)
```

```
##      peak_dt peak_va ranks
## 1 1950-12-08   62200  14.0
## 2 1952-03-11   28100  53.0
## 3 1953-02-21   34900  43.5
## 4 1954-03-01   48000  28.5
## 5 1955-04-15   32100  49.0
## 6 1956-04-16   33300  47.0
```

$$q_i = \frac{i - a}{N + 1 - 2a}$$

Figure 12.1: Plotting Position Formula

qi = Exceedance probability

N = Number of observations in your record

i = Rank of specific observation, i = 1 is the largest, i = N is the smallest.

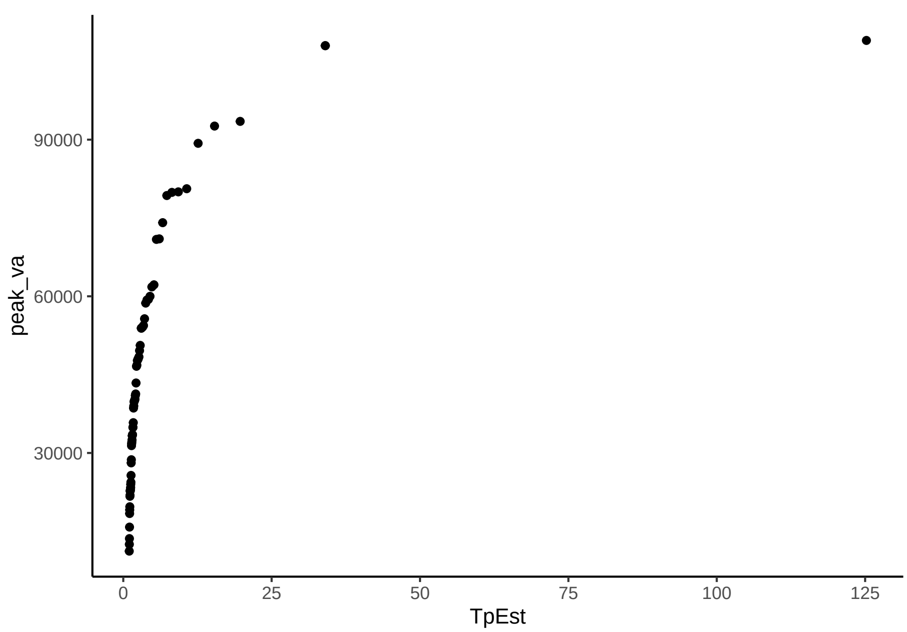
a = constant for estimation = 0.44

Non-exceedence probability = pi = 1 - qi

Return period

Tp = 1/(1-p)

```
N <- length(peakflows$peak_dt)
a <- 0.44

#calculate exceedence/non-exceedence with gringorten and return period
peakflows <- peakflows %>% mutate(qi = (ranks - a) / (N + 1 - (2*a))) %>%
                           mutate(pi = 1 - qi) %>%
                           mutate(TpEst = 1 / (1-pi))

#Plot peak flows on y and est return period on the x
peakflows %>% ggplot(aes(x = TpEst, y = peak_va)) +
  geom_point()
```



Need to fit these data to a distribution in order to make a continuous relationship we can use to predict the discharge of specific return intervals.

There are many distributions but a common one used is the Gumbel extreme value distribution.

$$F_x(x) = \exp\left[-\exp\left(-\frac{x-u}{\alpha}\right)\right] = p$$

x is observed discharge data, u and x are parameters that shape the distribution.

We can calculate u and x in order to create a distribution that best fits our data with the following equations. Notice x bar is mean and sx2 is variance. We will need to find sx, which is the square root of the variance, also known as the standard deviation.

$$\bar{x} = \sum_{i=1}^{n} \frac{x_i}{n}$$

$$s_x{}^2 = \frac{1}{(n-1)} \sum_{i=1}^{n} (x_i - \bar{x})^2$$

$$u = \bar{x} - 0.5772\alpha$$

$$\alpha = \frac{\sqrt{6}s_x}{\pi}$$

Figure 12.2: Gumbel parameters

```
xbar <- mean(peakflows$peak_va)

sx <- sd(peakflows$peak_va)

alpha <- (sqrt(6)*sx) / pi

u <- xbar - (0.5772 * alpha)
```

Now that we have the parameters that best represent our data as a Gumbel Distribution, we can use the formula to create the theoretical values for the return interval according to that distribution.

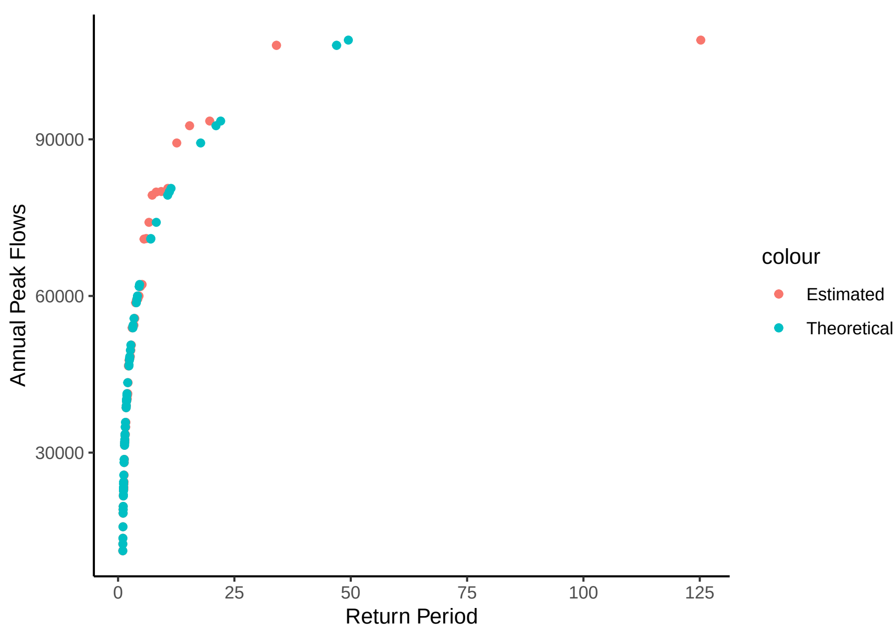
$$F_x(x) = \exp\left[-\exp\left(-\frac{x-u}{\alpha}\right)\right] = p$$

First calculate p theoretical with the

equation above.

Then calculate Tp theoretical (the return period) as T was calculated above Tp = 1 / (1-p)

```
peakflows <- peakflows %>% mutate(pTheoretical =
                                    exp(-exp(-((peak_va - u) / alpha)))) %>%
                           mutate(TpTheoretical = (1 / (1-pTheoretical)))


peakflows %>% ggplot(aes(x = TpEst, y = peak_va, color = "Estimated")) +
  geom_point()+
  geom_point(aes(x = TpTheoretical, y = peak_va, color = "Theoretical"))+
  ylab("Annual Peak Flows")+
  xlab("Return Period")+
  theme_classic()
```



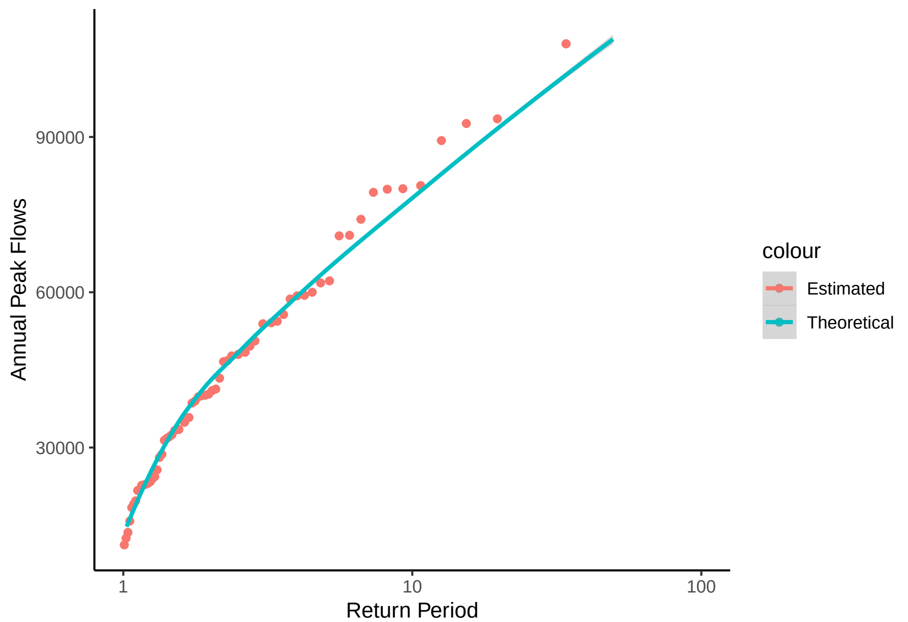
Make the same plot but show the theoretical values as a line and log the x axis with limits set to 1 - 100.

With this plot you could look up the return period for any flood or the discharge level for any return period.

```
peakflows %>% ggplot(aes(x = TpEst, y = peak_va, color = "Estimated")) +
  geom_point()+
  geom_smooth(aes(x = TpTheoretical, y = peak_va, color = "Theoretical"))+
```

```
  ylab("Annual Peak Flows")+
  xlab("Return Period")+
  scale_x_log10(limits = c(1,100))+
  theme_classic()
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'

## Warning: Removed 1 rows containing missing values (geom_point).
```



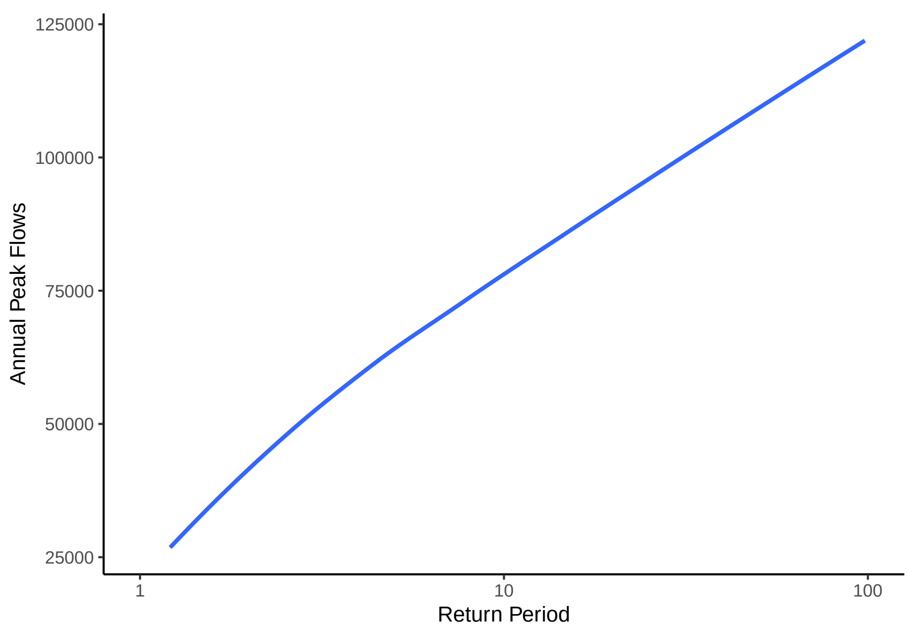
We can create a function that returns the return period for a flood of any magnitude for the gage we are investigating. Creating functions is a great way to streamline your workflow. You can write a function that performs an operation you need to perform a bunch of times, then just use the function rather than re-writing the code.

```
ReturnPeriod <- function(flow, u, alpha){

  pTheoretical = exp(-exp(-((flow - u) / alpha)))
  TpTheoretical = (1 / (1-pTheoretical))

  TpTheoretical
}

ReturnPeriod(120000, u, alpha)
```

```
## [1] 88.25008
```

```
Flows <- seq(25000, 150000, by = 1000)

RPFlows <- ReturnPeriod(Flows, u, alpha)

newline <- tibble(Flows, RPFlows)

ggplot(newline, aes(x = RPFlows, y = Flows))+
        geom_smooth()+
        ylab("Annual Peak Flows")+
        xlab("Return Period")+
        scale_x_log10(limits = c(1,100))+
        theme_classic()
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'

## Warning: Removed 28 rows containing non-finite values (stat_smooth).
```



12.1 Challenge: Create a function

Create a function that returns the theoretical return period for a given flood magnitude when given the the flood magnitude you want to investigate, the gage id, startdate, and enddate for the records you want.

```
RPusgs <- function(magnitude, gageid, startDate, endDate){

  #Read data from USGS
  peakflows <- readNWISpeak(gageid, startDate = startDate, endDate = endDate)

  #Create rank column and clean up
  peakflows <- peakflows %>% mutate(ranks = rank(-peak_va)) %>%
              select(peak_dt, peak_va, ranks)

  #Set N and a constants
  N <- length(peakflows$peak_dt)
  a <- 0.44

  #calculate exceedence/non-exceedence with gringorten and return period estimates
  peakflows <- peakflows %>% mutate(qi = (ranks - a) / (N + 1 - (2*a))) %>%
                         mutate(pi = 1 - qi) %>%
                         mutate(TpEst = 1 / (1-pi))

  #calculate parameters for Gumbel distribution
  xbar <- mean(peakflows$peak_va)

  sx <- sd(peakflows$peak_va)

  alpha <- (sqrt(6)*sx) / pi

  u <- xbar - (0.5772 * alpha)

  #Calculate p and Tp (return interval) with Gumbel distribution
  pTheoretical = exp(-exp(-((magnitude - u) / alpha)))
  TpTheoretical = (1 / (1-pTheoretical))

  TpTheoretical
}

RPusgs(120000, radford, "1950-01-01", "2021-01-01")
```

```
## [1] 88.25008
```