Key tidyverse verbs to accelerate data analysis

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Who am I?

I'm Amy Willis, PhD; I am a tenure-track Assistant Professor in Biostatistics

- Principal Investigator, Statistical Diversity Lab
 - ► Methods for microbiome data analysis
- ▶ PhD in Statistics, Cornell University
- ► I <3 statistics and data analysis; I've worked for Google, Australian Government, macroeconomic forecasting consulting, biotech...
- ▶ 10+ years of R experience
 - ▶ I'm a methods developer; most of my methods are coded in R
 - ▶ packages: breakaway, DivNet, corncob, paramedic...

Please call me Amy; I use she/her pronouns

My favourite toolbox for data analysis

> library(tidyverse)

My favourite tools

tidyverse functions that I use all the time:

- summarize() reduces multiple values to a single summary
- ▶ group_by() groups rows together (useful for summarize)
- ▶ filter() picks rows based on their valuess
- ▶ select() picks columns based on their names
- ► arrange() changes the ordering of the rows

tidyverse functions that I learnt *more recently* and now use **a lot**:

- pivot_longer() and pivot_wider()
- ► across()

Reading in the data

I prefer read_csv because it gives me a tibble - a clever data frame

```
> df <- read csv("TESTIntegratedCaseIn DATA 2021-01-21 for Amy.csv")
-- Column specification
cols(
  .default = col_character(),
  record id = col double(),
  translator_needed = col_double(),
  fever_any = col_double(),
  fever temp taken = col double(),
  fever_temp_measure = col_double(),
  sx headache = col double(),
  sx myalgia = col double(),
  sx_congestion = col_double(),
  sx_pharyngitis = col_double(),
  sx_cough = col_double(),
  sx_dyspnea = col_double(),
  sx pneumonia = col double(),
  sx_nausea = col_double(),
  sx_vomiting = col_double(),
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```

Looking at the data

Using tibbles helps me avoid endless scrolling up

```
> df
# A tibble: 924 x 226
   record_id remote_intervie~
                              specimen_collec~ translator_need~ languag
                                                          <dbl> <chr>
       <dbl> <chr>
                              <chr>>
 1 100924894 5/1/2020 14:11 5/1/2020
                                                               1 ENGLISH
 2 100924893 5/1/2020 14:15 5/1/2020
                                                             NA ENGLISH
 3 100924501 5/1/2020 14:44
                             4/20/2020
                                                               1 ENGLISH
 4 100924671 5/1/2020 14:58
                             4/15/2020
                                                               1 ENGLISH
 5 100924678 5/1/2020 14:58
                             4/23/2020
                                                               1 ENGLISH
 6 100801703 5/1/2020 14:59
                             4/21/2020
                                                               1 ENGLISH
 7 100683673 5/1/2020 14:59
                             4/28/2020
                                                               1 ENGLISH
                                                               1 ENGLISH
 8 100924499 5/1/2020 15:00 4/22/2020
 9 100924576 5/1/2020 15:01 5/24/2020
                                                               1 ENGLISH
10 100924830 5/1/2020 15:04 4/23/2020
                                                             NA ENGLISH
# ... with 914 more rows, and 221 more variables: startexposurenoill <c
    endexposurenoill <chr>, contagiousnoill <chr>, asymptom_cleared <ch
    fever_any <dbl>, fever_temp_taken <dbl>, fever_temp_measure <dbl>,
#
    sx_headache <dbl>, sx_myalgia <dbl>, sx_congestion <dbl>,
    ar phoromoitic (dhl)
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```

Looking at the data: global view

The pipe %>%: the glue that holds tidyverse functions together. Strong recommend for accelerating your data analysis!

```
> # names(df) # alternative
> df %>% names
  [1] "record id"
  [2] "remote_interviewer_timestamp"
  [3] "specimen_collection"
  [4] "translator needed"
  [5] "language"
  [6] "startexposurenoill"
  [7] "endexposurenoill"
  [8] "contagiousnoill"
  [9] "asymptom_cleared"
 [10] "fever_any"
 [11] "fever_temp_taken"
 [12] "fever_temp_measure"
 [13] "sx_headache"
 [14] "sx_myalgia"
 [15] "sx congestion"
```

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Looking at the data: global view

```
> # head(names(df), 15) # alternative
> df %>% names %>% head(15)
 [1] "record_id"
                                     "remote_interviewer_timestamp"
 [3] "specimen_collection"
                                     "translator needed"
 [5] "language"
                                     "startexposurenoill"
                                     "contagiousnoill"
 [7]
    "endexposurenoill"
 [9] "asymptom_cleared"
                                     "fever any"
[11] "fever_temp_taken"
                                     "fever_temp_measure"
[13] "sx headache"
                                     "sx_myalgia"
[15] "sx congestion"
```

Looking at my data: local view

```
> df %>%
    group_by(fever_any) %>%
    summarise(n())
# A tibble: 4 x 2
  fever_any `n()`
      <dbl> <int>
1
               197
              322
3
        100
4
         NA
              403
```

Cleaning my data

Let's not forget this going forward!

Looking at my data: larger view

#

#

Do you have columns of the same type named similarly? Awesome!

```
> df %>%
+ select(starts_with("sx"))
```

```
# A tibble: 924 x 22
   sx_headache sx_myalgia sx_congestion sx_pharyngitis sx_cough sx_dysp
         <dbl>
                                    <dbl>
                                                    <dbl>
                                                              dbl>
                     <dbl>
                                                                          <d
            NA
                                       NA
                                                        NA
                                                                 NA
                        NA
            NΑ
                        NΑ
                                       NΑ
                                                        NΑ
                                                                 NΑ
 3
 5
 6
 8
10
            NΑ
                        NΑ
                                       NΑ
                                                        NA
                                                                 NΑ
  ... with 914 more rows, and 16 more variables: sx_pneumonia <dbl>,
```

sx_nausea <dbl>, sx_vomiting <dbl>, sx_diarrhea <dbl>, sx_abdominal
sx_dysgeusia <dbl>, sx_anosmia <dbl>, sx_other <dbl>, sx_other_det

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Which symptoms were most commonly observed?

How could we answer this?

#

#

```
> df %>%
+ select(starts_with("sx"))
```

```
# A tibble: 924 x 22
   sx_headache sx_myalgia sx_congestion sx_pharyngitis sx_cough sx_dysp
         dbl>
                                    <dbl>
                                                    <dbl>
                                                              dbl>
                     <dbl>
                                                                          <d
            NA
                                       NA
                                                       NA
                                                                 NA
                        NA
             NΑ
                        NΑ
                                       NΑ
                                                       NΑ
                                                                 NΑ
 3
 5
 6
 8
10
            NΑ
                        NΑ
                                       NΑ
                                                       NA
                                                                 NΑ
  ... with 914 more rows, and 16 more variables: sx_pneumonia <dbl>,
```

sx_nausea <dbl>, sx_vomiting <dbl>, sx_diarrhea <dbl>, sx_abdominal
sx_dysgeusia <dbl>, sx_anosmia <dbl>, sx_other <dbl>, sx_other_det

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Which symptoms were most commonly observed?

How could we answer this?

```
> df %>%
+ select(starts_with("sx")) %>%
+ pivot_longer(starts_with("sx"))
```

Error: Can't combine `sx_headache` <double> and `sx_other_det` <charact

Oh no!

What's going on?

> df\$sx_other_det %>% unique

```
[1] NA
 [2] "loose stools"
 [3] "overall weakness and body aches"
 [4] "Sneezing"
 [5] "weakness, low energy"
 [6] "Back ache & feet were tingling"
 [7] "very tired"
 [8] "Lungs felt on fire"
 [9] "Fatigue"
[10] "aching her body/and legs"
[11] "Loss of appetite; fatigue"
[12] "fatigue"
[13] "chills"
[14] "Nose bleed, belly distension, tears"
[15] "Trench Foot"
[16] "Not wanting to eat"
[17] "Seasonal Allergies"
[18] "Soreness in face"
[19] "Farts"
```

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Pivoting: wide to long

```
> df %>%
    select(starts_with("sx")) %>%
    select(where(is.numeric)) %>%
    pivot_longer(starts_with("sx"))
# A tibble: 15,708 x 2
   name
                   value
                   <dbl>
   <chr>>
 1 sx headache
                      NΑ
                      NΑ
 2 sx myalgia
 3 sx_congestion
                      NA
 4 sx_pharyngitis
                     NA
 5 sx_cough
                      NA
 6 sx_dyspnea
                      NA
 7 sx_pneumonia
                      NA
                      NA
 8 sx_nausea
 9 sx_vomiting
                      NA
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```

Which symptoms were most commonly observed?

Now, grab only entries that are neither zero nor NA

```
> df %>%
+ select(starts_with("sx")) %>%
+ select(where(is.numeric)) %>%
+ pivot_longer(starts_with("sx")) %>%
+ filter(!is.na(value) & value != 0)
```

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```
# A tibble: 3,072 x 2
                 value
   name
   <chr>
                 <dbl>
 1 sx_cough
 2 sx_dysgeusia
 3 sx_anosmia
 4 sx_yesno
 5 sx_ongoing
 6 sx_nausea
   sx abdominal
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```

Which symptoms were most commonly observed?

Then tabulate: group_by, summarise, arrange

> df %>%

```
select(starts_with("sx")) %>%
   select(where(is.numeric)) %>%
   pivot_longer(starts_with("sx")) %>%
   filter(!is.na(value) & value != 0) %>%
  group by(name) %>%
 summarise(n = n()) \%
   arrange(desc(n))
`summarise()` ungrouping output (override with `.groups` argument)
# A tibble: 17 x 2
  name
                     n
  <chr>
                 <int>
                   486
 1 sx_yesno
2 sx_cough
                   347
3 sx headache
               256
4 sx_congestion 195
 5 sx_dysgeusia
                189
6 sx pharvngitis
                   187
```

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Clean up

How can we quickly change all those 100's to 1's?

```
Use mutate + across
```

```
> change_hundreds <- function(x) ifelse(x == 100, 1, x)
> change_hundreds(98:102)
```

```
[1] 98 99 1 101 102
```

- > df %>%
- + select(starts_with("sx")) %>%
 - mutate(across(where(is.numeric), change_hundreds))

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A tibble: 924 x 22

	sx_headache	sx_myalgia	sx_congestion	sx_pharyngitis	sx_cough	sx_dysp
	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<d< td=""></d<>
1	NA	NA	NA	NA	NA	
2	NA	NA	NA	NA	NA	
3	0	0	0	0	1	
4	0	0	0	0	0	
5	0	0	0	0	1	
6	0	0	0	0	1	

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How can we find which investigators set those 100's?

```
> df %>%
    select(investigator,
           starts_with("sx") & where(is.numeric)) %>%
    pivot_longer(!investigator) %>%
    filter(!is.na(value) & value != 0 & value != 1)
# A tibble: 76 \times 3
   investigator name
                                value
          <dbl> <chr>
                                <dbl>
             32 sx_pneumonia
                                  100
             96 sx_dysgeusia
                                  100
 3
             96 sx_anosmia
                                  100
 4
              9 sx_cough
                                  100
 5
             10 sx anosmia
                                  100
 6
             85 sx_congestion
                                  100
             68 sx_congestion
                                  100
             30 sx_pharyngitis
                                  100
 8
 9
           8888 sx_headache
                                  100
10
           8888 sx_myalgia
                                  100
  ... with 66 more rows
```

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How can we find which investigators set those 100's?

```
> df %>%
    select(investigator, starts_with("sx") & where(is.nume)
   pivot_longer(!investigator) %>%
   filter(!is.na(value) & value != 0 & value != 1) %>%
   group_by(investigator) %>%
   summarise(n = n()) \%
+
   arrange(desc(n))
# A tibble: 36 x 2
   investigator
          <dbl> <int>
             22
                    5
           8888
 3
            104
4
            106
 5
            131
                    4
 6
                    3
             12
```

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Scaling up

There is no need to memorise all of this!

Can't remember how to use across? Just type ?across

My cheat list

- ▶ mutate(across(everything(), fun_name))
- ▶ summarise(across(starts_with("sx"), fun_name))
- ▶ mutate(across(contains("Name"), fun_name))
- ► summarise(across(where(is.character), fun_name))
- ▶ mutate(across(FirstCol:LastCol, fun_name))

Recap

tidyverse functions that I use all the time:

- summarize() reduces multiple values to a single summary
- ▶ group_by() groups rows together (useful for summarize)
- ► filter() picks rows based on their valuess
- select() picks columns based on their names
- ► arrange() changes the ordering of the rows

tidyverse functions that I learnt *more recently* and now use **a lot**:

- pivot_longer() and pivot_wider()
- ► across()

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Wrap up

- ► I'm Amy Willis, an Assistant Professor in Biostatistics at the University of Washington in the School of Public Health
- ► I can do many things in R very quickly, and I want you to as well!
- ► This took years of practice... and a few key verbs!
- ▶ I am available for consulting feel free to reach out at adwillis@uw.edu
- ► Slides available at github.com/adw96/presentations
- Keep in touch by e-mail (adwillis@uw.edu) or Twitter (@AmyDWillis)!

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