Basic Tabular Data Manipulation

Alejandro Schuler, adapted from Steve Bagley and based on R for Data Science by Hadley Wickham, updated to include GTEx sample data by Nicole Ferraro
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- filter rows of a dataset based on conditions
- arrange rows of a dataset based on one or more columns
- select columns of a dataset
- mutate existing columns to create new columns
- group and summarize data by one or more columns
- use the pipe to combine multiple operations

dplyr

This section shows the basic data frame functions ("verbs") in the `dplyr` package (part of `tidyverse`).

dplyr verbs

Each operation takes a data frame and produces a new data frame.

- `filter()` picks out rows according to specified conditions
- `select()` picks out columns according to their names
- `arrange()` sorts the row by values in some column(s)
- `mutate()` creates new columns, often based on operations on other columns
- `summarize()` collapses many values in one or more columns down to one value per column

These can all be used in conjunction with `group_by()` which changes the scope of each function from operating on the entire dataset to operating on it group-by-group. These six functions provide the "verbs" for a language of data manipulation.

All work similarly:

1. The first argument is a data frame.
2. The subsequent arguments describe what to do with the data frame, using the variable names (without quotes).
3. The result is a new data frame.

Together these properties make it easy to chain together multiple simple steps to achieve a complex result.

GTEx data

This is a subset of the Genotype Tissue Expression (GTEx) dataset

- **The full dataset.** Includes gene expression data, measured via RNA-sequencing, from 54 post-mortem tissues in ~800 individuals. Whole genome sequencing is also available for these individuals as part of the GTEx v8 release, available through dbGaP.
- **The subsetted dataset.** We are looking at expression data for just 78 individuals here, in four tissues including blood, heart, lung and liver.
- **Data processing** The expression values have been normalized and corrected for technical covariates and are now in the form of Z-scores, which indicate the distance of a given expression value from the mean across all measurements of that gene in that tissue.
- **Goal.** We will use the data here to illustrate different functions for data transformation, often focused on extracting individuals with extremely high or low expression values for a given gene as compared to the distribution across all samples.

NOTE: If copying the code, make sure there are no spaces in the download link (where it wraps to a new line).

```
# Read subsetted data from online file - make sure there are no spaces
gtex_data = read_tsv('https://raw.githubusercontent.com/alejandroschuler/r4ds-
courses/advance-2020/data/gtex.tissue.zscores.advance2020.txt')

# Check number of rows
nrow(gtex_data)
[1] 389922
```

Filter rows with filter()

Filter rows with filter()

- `filter()` lets you filter out rows of a dataset that meet a certain condition
- It takes two arguments: the dataset and the condition

```
filter(gtex_data, Blood >= 12)
# A tibble: 12 x 7
   Gene        Ind         Blood Heart  Lung Liver NTissues
   <chr>       <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 AC012358.7 GTEX-VUSG    13.6 -1.43  1.22 -0.39        4
 2 DCSTAMP    GTEX-12696   13.6 NA    -0.57 -0.91        3
 3 DIAPH2-AS1 GTEX-VUSG    12.2 -0.33  1.18  0.67        4
 4 DNASE2B    GTEX-12696   14.4 -0.82 -0.92  0.35        4
 5 FFAR4      GTEX-12696   12.9 -0.96 -0.67  0.18        4
 6 GAPDHP33   GTEX-UPK5    13.8  1.52 -1.48 -1.84        4
 7 GTF2A1L    GTEX-VUSG    12.2  1.67  0.78  0.09        4
 8 GTF2IP14   GTEX-11NV4   12.2  7.26  5.79  7.06        4
 9 KCNT1      GTEX-1KANB   13.5  3.14  0.62 -0.37        4
10 KLK3       GTEX-147F4   15.7 -0.74 -0.44 -0.02        4
11 NAPSA      GTEX-1CB4J   12.3 -0.29 -0.44 -0.14        4
12 REN        GTEX-U8XE    18.9 -0.57 NA     0.09        3
```

Exercise

- What is the result of running this code?

```
nrow(gtex_data)
[1] 389922
```

```
filter(gtex_data, NTissues <= 2)
filter(gtex_data, Heart <= -5)
nrow(gtex_data)
```

- Remember, functions usually do not change their arguments!

```
low_expression_blood = filter(gtex_data, Blood <= -5)
low_expression_blood_heart = filter(low_expression_blood, Heart <= -5)
nrow(low_expression_blood_heart)
[1] 3
```

Combining constraints in filter

```
filter(gtex_data, Blood <= -5, Heart <= -5)
# A tibble: 3 x 7
  Gene     Ind         Blood  Heart   Lung Liver NTissues
  <chr>    <chr>       <dbl>  <dbl>  <dbl> <dbl>    <dbl>
1 ATP5A1   GTEX-YFC4   -5.35  -6.05  -7.96 -4.4         4
2 GHITM    GTEX-WK11   -5.7   -7.24  -7.37 -4.06        4
3 MTATP6P1 GTEX-1KD5A -9.18 -10.1  -10.3  -9.52        4
```

- This filters by the **conjunction** of the two constraints—both must be satisfied.
- Constraints appear as second (and third…) arguments, separated by commas.

Filtering out all rows

```
filter(gtex_data, NTissues > 5)
# A tibble: 0 x 7
# … with 7 variables: Gene <chr>, Ind <chr>, Blood <dbl>, Heart <dbl>,
#   Lung <dbl>, Liver <dbl>, NTissues <dbl>
```

- If the constraint is too severe, then you will select **no** rows, and produce a zero row sized tibble.

Comparison operators

- == and != test for equality and inequality (do not use = for equality)
- > and < test for greater-than and less-than
- >= and <= are greater-than-or-equal and less-than-or-equal
- these can also be used directly on vectors outside of data frames

```
c(1,5,-22,4) > 0
[1]  TRUE  TRUE FALSE  TRUE
```

Aside: computers are not perfect, so be careful with checking equality

```
sqrt(2) ^ 2 == 2
[1] FALSE
1 / 49 * 49 == 1
[1] FALSE
```

You can use `near()` to check that two numbers are the same (up to "machine precision")

```
near(sqrt(2) ^ 2,  2)
[1] TRUE
near(1 / 49 * 49, 1)
[1] TRUE
```

Comparing to NA

- The other "gotcha" is that == cannot be used to compare to `NA`:

```
x = NA
x == NA
[1] NA
```

- The result actually makes sense though, because I'm asking if "I don't know" is the same as "I don't know". Since either side could be any value, the right answer is "I don't know".
- To check if something is `NA`, use `is.na()`

```
x = NA
is.na(x)
[1] TRUE
```

Logical conjunctions

```
filter(gtex_data, Lung > 6 | Liver < -6)
# A tibble: 73 x 7
   Gene        Ind         Blood Heart  Lung Liver NTissues
   <chr>       <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 ACOT12      GTEX-12WSD  5.43   0.53  8.2   0.71         4
 2 ACSL6       GTEX-X261   2.45   1.04  7.03  2.4          4
 3 ADAL        GTEX-1EWIQ  0.69  -0.15  6.28 -0.52         4
 4 AGAP2       GTEX-1GN73  2.32   1.46  6.1   0.89         4
 5 ALDOB       GTEX-12WSD  0.93  -0.42  6.06 -0.08         4
 6 ALOXE3      GTEX-YFC4  -1.32   0.02  7.5  -1.37         4
 7 AP001610.5  GTEX-X4EP  -1.25   3.12  6.59 -0.48         4
 8 APMAP       GTEX-17HGU -0.13  -1.25  0.87 -6.14         4
 9 APOA1       GTEX-12WSD  5.45  NA     7     0.67         3
10 ATF4P3      GTEX-1GN2E  1.85   0.5   6.95  1.03         4
# … with 63 more rows
```

- The pipe sign `|` stands for "OR"
- The ampersand sign `&` stands for "AND"
- As we have seen, separating conditions by a comma is the same as using `&` inside `filter()`
- Multiple conjunctions can describe complex logical conditions

Logical conjunctions

```
filter(gtex_data, !(Blood < 6 | Lung < 6))
# A tibble: 5 x 7
  Gene            Ind         Blood Heart  Lung Liver NTissues
  <chr>           <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
1 CTAG2           GTEX-17HGU  6.61  0.65  7.4   2.85         4
2 GTF2IP14        GTEX-X3Y1  10.3   7.46  8.12  3.67         4
3 KLK3            GTEX-X261  11.1   0.02  8.39  5.02         4
4 RP11-1228E12.1  GTEX-1KANB  6.18  4.08  9.69  6.63         4
5 TDRD1           GTEX-ZEX8  10.3   3.47  6.19  0.3          4
```

- The exclamation point ! means "NOT", which negates the logical condition

Logical conjunctions

```
filter(gtex_data, NTissues %in% c(1,2)) # equivalent to filter(gtex_data,
NTissues==1 | NTissues==2)
# A tibble: 132 x 7
   Gene        Ind         Blood Heart  Lung Liver NTissues
   <chr>       <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 AC016757.3 GTEX-131YS  1.43  NA    NA    -0.07        2
 2 ACTG1P1    GTEX-15RJE NA     NA    -0.41 -0.1         2
 3 ACVR2B-AS1 GTEX-1GN73 -0.86 NA    NA     0.46        2
 4 ADAMTSL1   GTEX-1LGRB -0.48 NA    NA    -0.76        2
 5 ADGRF5     GTEX-ZPU1  -0.13 NA    NA    -0.68        2
 6 AOAH       GTEX-11GSP -1.27 NA    NA     0.41        2
 7 ARV1       GTEX-12WSD -1.07 NA    NA     1.27        2
 8 BORCS7     GTEX-X261  NA     0.93 NA     0.11        2
 9 C16orf46   GTEX-ZEX8  -0.95 NA    NA     0.21        2
10 C4orf19    GTEX-ZVT3  -0.88 NA    NA     0.82        2
# … with 122 more rows
```

- `%in%` returns true for all elements of the thing on the left that are also elements of the thing on the right. This is actually shorthand for a match function (use `help('%in%')` to learn more)

Caution! `in` (without the flanking percent signs) has a different meaning - it is used to iterate through a sequence rather than as a matching function. For example, to loop through and print all numbers from 1 to 10 we would do the following:

```
for(x in seq(1,10)){ print x }
```

Exercise: High expression

- How many individuals have high expression (Z > 3) for CTAG2 in both blood and lung?

Exercise: High expression

- How many individuals have high expression (Z > 3) for CTAG2 in both blood and lung?

```
nrow(filter(gtex_data, Gene=="CTAG2", Blood > 3, Lung > 3))
[1] 3
```

Exercise: Low expression

- Create a dataset of all individual-gene pairs with low expression (Z < -3) in blood and heart tissues

Exercise: Low expression

- Create a dataset of all individual-gene pairs with low expression (Z < -3) in blood and heart tissues

```
filter(gtex_data, Blood < -3, Heart < -3)
# A tibble: 26 x 7
   Gene                Ind         Blood Heart  Lung Liver NTissues
   <chr>               <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 ABC7-42389800N19.1 GTEX-14E7W -4.24 -3.29 -3.55 -3.2          4
 2 ALDH9A1            GTEX-11NUK -3.45 -4.78 -4.15 -3.8          4
 3 ARPC3              GTEX-1MJIX -4.21 -3.76 -4.56  2.42         4
 4 ATL3               GTEX-ZF29  -5.07 -4.22 -2.77 -2.82         4
 5 ATP5A1             GTEX-YFC4  -5.35 -6.05 -7.96 -4.4          4
 6 CCDC163            GTEX-1KANB -3.06 -3.05 -0.94  0.48         4
 7 COQ6               GTEX-ZEX8  -4.49 -3.11 -0.19 -0.9          4
 8 CRYL1              GTEX-WFON  -3.77 -6.42 -6.14 -4.11         4
 9 CTPS2              GTEX-1E2YA -3.92 -6.71 -4.06 -1.98         4
10 ENGASE             GTEX-147JS -3.96 -3.17 -3.62 -3.22         4
# … with 16 more rows
```

Exercise: High expression in all tissues

- Create a dataset of all individual-gene pairs with high expression (Z > 3) in all four tissues

Exercise: High expression in all tissues

- Create a dataset of all individual-gene pairs with high expression (Z > 3) in all four tissues

```
filter(gtex_data, Blood > 3, Heart > 3, Lung > 3, Liver > 3)
# A tibble: 16 x 7
   Gene            Ind         Blood Heart  Lung Liver NTissues
   <chr>           <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 AC004453.8      GTEX-12WSI   6.2   4.31  4.57  3.77        4
 2 AC004453.8      GTEX-14DAQ   7.76  6.98  5.64  4.81        4
 3 CTAG2           GTEX-YECK    4.73  8.37  6.11  3.11        4
 4 CTD-2525I3.5    GTEX-14E1K   3.27  8.78  5.9   4.76        4
 5 EMC3-AS1        GTEX-1KANB   5.33  4     4.21  4.87        4
 6 GTF2IP14        GTEX-11NV4  12.2   7.26  5.79  7.06        4
 7 GTF2IP14        GTEX-X3Y1   10.3   7.46  8.12  3.67        4
 8 MTATP8P2        GTEX-17EVP   6.35  5.16  5.31  5.44        4
 9 MTATP8P2        GTEX-YECK    4.21  4.04  3.53  4.55        4
10 PSMA6           GTEX-12WSI   4.23  3.92  5.39  3.03        4
11 RP11-1228E12.1  GTEX-1KANB   6.18  4.08  9.69  6.63        4
12 RRP7BP          GTEX-1AX9I   7.49  5.45  5.8   3.94        4
13 TMEM145         GTEX-1JMLX   3.68  7.15  7.98  7.96        4
14 TRBV23-1        GTEX-1A8FM   6.51  8.63  3.15  4.82        4
15 TRBV3-1         GTEX-1E2YA   5.04  3.64  3.34  4.64        4
16 TRMT2B          GTEX-1CB4J   6.56  5.74  5.58  5.29        4
```

Exercise: High and low expression events

- Create a dataset of all high and low expression instances (Z > 3 or < -3) in any tissue (`?abs` may be helpful)

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- Create a dataset of all high and low expression instances (Z > 3 or < -3) in any tissue (`?abs` may be helpful)

```
filter(gtex_data, abs(Blood) > 3 | abs(Heart) > 3 | abs(Lung) > 3 | abs(Liver) >
3)
# A tibble: 10,171 x 7
   Gene    Ind         Blood Heart  Lung Liver NTissues
   <chr>   <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 A2ML1   GTEX-14E7W  0.55 -0.63  3.7   1.6          4
 2 A2ML1   GTEX-1GF9V -0.04  1.44 -0.53  3.65         4
 3 A3GALT2 GTEX-11TUW  0.15 -3.41  0.96 -0.83         4
 4 A3GALT2 GTEX-1BAJH -0.7   0.91  0.16  3.61         4
 5 A3GALT2 GTEX-XBEC   1.03  3.25  0.87  1.51         4
 6 A3GALT2 GTEX-ZF29  -3.61 -2.02 -2.1   0.23         4
 7 A3GALT2 GTEX-ZTPG   0.94  0.5  -1.23  3.22         4
 8 AAMDC   GTEX-12WSG -0.49 -3.38 -2.62 -1.67         4
 9 AAMDC   GTEX-1JMLX  0.65  0.69  0.15  3.43         4
10 AANAT   GTEX-ZTPG   1.02  0.02  0.55  3.78         4
# … with 10,161 more rows
```

Exercise: getting rid of NAs

- Filter out any rows where the value for `Heart` is missing (value is `NA`)

Exercise: getting rid of NAs

- Filter out any rows where the value for `Heart` is missing (value is `NA`)

```
filter(gtex_data, !is.na(Heart))
# A tibble: 383,941 x 7
   Gene  Ind         Blood Heart  Lung Liver NTissues
   <chr> <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 A2ML1 GTEX-11DXZ -0.14 -1.08 NA    -0.66         3
 2 A2ML1 GTEX-11GSP -0.5   0.53  0.76 -0.1          4
 3 A2ML1 GTEX-11NUK -0.08 -0.4  -0.26 -0.13         4
 4 A2ML1 GTEX-11NV4 -0.37  0.11 -0.42 -0.61         4
 5 A2ML1 GTEX-11TT1  0.3  -1.11  0.59 -0.12         4
 6 A2ML1 GTEX-11TUW  0.02 -0.47  0.29 -0.66         4
 7 A2ML1 GTEX-11ZUS -1.07 -0.41  0.67  0.06         4
 8 A2ML1 GTEX-11ZVC -0.27 -0.51  0.13 -0.75         4
 9 A2ML1 GTEX-1212Z -0.3   0.53  0.1  -0.48         4
10 A2ML1 GTEX-12696 -0.11  0.24  0.96  0.72         4
# … with 383,931 more rows
```

Filtering by row number

- Use `row_number()` to filter specific rows. This is more useful once you have sorted the data in a particular order, which we will soon see how to do.

```
filter(gtex_data, row_number()<=3)
# A tibble: 3 x 7
  Gene  Ind         Blood Heart  Lung Liver NTissues
  <chr> <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
1 A2ML1 GTEX-11DXZ -0.14 -1.08 NA    -0.66        3
2 A2ML1 GTEX-11GSP -0.5   0.53  0.76 -0.1         4
3 A2ML1 GTEX-11NUK -0.08 -0.4  -0.26 -0.13        4
```

Sampling rows

- You can use `sample_n()` to get `n` randomly selected rows if you don't have a particular condition you would like to filter on.

```
sample_n(gtex_data, 5)
# A tibble: 5 x 7
  Gene         Ind         Blood Heart  Lung Liver NTissues
  <chr>        <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
1 ZNF252P      GTEX-11TT1 -0.5   0.93  2.14 -0.58        4
2 RPP40        GTEX-14E7W -0.48 -0.28  0.17 -0.89        4
3 ZNF292       GTEX-X3Y1  -0.2  NA     0.87  0.63        3
4 RP4-644L1.2  GTEX-X261   0.33  1.94 -0.1  -1.15        4
5 DECR2        GTEX-ZF2S   1.22  0.73  0.99  1.08        4
```

- `sample_frac()` is similar
- Do `?sample_n()` to see how you can sample with replacement or with weights

Sort rows by a column with arrange()

Arrange rows with arrange()

- `arrange()` takes a data frame and a column, and sorts the rows by the values in that column (ascending order).
- Again, the first argument is the data frame and the other arguments tell the function what to do with it

```
arrange(gtex_data, Blood)
# A tibble: 389,922 x 7
   Gene         Ind         Blood  Heart   Lung Liver NTissues
   <chr>        <chr>       <dbl>  <dbl>  <dbl> <dbl>    <dbl>
 1 HBA2         GTEX-11DXZ -9.44  -1.52  -1.44 -2.15        4
 2 MTATP6P1     GTEX-1KD5A -9.18 -10.1  -10.3  -9.52        4
 3 RP11-46D6.1  GTEX-14E1K -7.83  -3.94  -5.22 -4.49        4
 4 CYTH3        GTEX-11NV4 -6.63  -0.6   -0.37 -1.32        4
 5 TRG-AS1      GTEX-11NV4 -6.47   2.39  -0.6  -0.22        4
 6 SMG1P1       GTEX-11ZUS -6.26  -1.68  -1.41 -0.31        4
 7 ZBTB10       GTEX-VUSG  -6.13   0.77   0.51 -0.67        4
 8 RPS29        GTEX-1B8L1 -5.84  -0.8   -0.46 -0.17        4
 9 GHITM        GTEX-WK11  -5.7   -7.24  -7.37 -4.06        4
10 ZNF2         GTEX-VUSG  -5.62   1.52   0.61  0.13        4
# … with 389,912 more rows
```

Arrange can sort by more than one column

- This is useful if there is a tie in sorting by the first column.

```
arrange(gtex_data, NTissues, Blood)
# A tibble: 389,922 x 7
   Gene        Ind         Blood Heart  Lung Liver NTissues
   <chr>       <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 HEATR1      GTEX-1EWIQ -1.63  NA       NA  0.49        2
 2 FOXO1       GTEX-1BAJH -1.58  NA       NA -0.25        2
 3 UCN         GTEX-12WSI -1.57  NA       NA -0.48        2
 4 GPR171      GTEX-132NY -1.53  NA       NA -1.03        2
 5 UCN         GTEX-WFON  -1.46  NA       NA -0.15        2
 6 KIAA1614    GTEX-12WSI -1.35  NA       NA -0.46        2
 7 ENTPD1-AS1  GTEX-11NUK -1.28  NA       NA -0.54        2
 8 TOP3B       GTEX-1A32A -1.28  NA       NA -0.76        2
 9 AOAH        GTEX-11GSP -1.27  NA       NA  0.41        2
10 PRRX2       GTEX-1A8FM -1.13  -1.2     NA NA          2
# … with 389,912 more rows
```

Use the desc function to arrange by descending values

```
arrange(gtex_data, desc(Blood))
# A tibble: 389,922 x 7
   Gene        Ind         Blood Heart  Lung Liver NTissues
   <chr>       <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 REN         GTEX-U8XE    18.9 -0.57 NA     0.09        3
 2 KLK3        GTEX-147F4   15.7 -0.74 -0.44 -0.02        4
 3 DNASE2B     GTEX-12696   14.4 -0.82 -0.92  0.35        4
 4 GAPDHP33    GTEX-UPK5    13.8  1.52 -1.48 -1.84        4
 5 DCSTAMP     GTEX-12696   13.6 NA    -0.57 -0.91        3
 6 AC012358.7 GTEX-VUSG    13.6 -1.43  1.22 -0.39        4
 7 KCNT1       GTEX-1KANB   13.5  3.14  0.62 -0.37        4
 8 FFAR4       GTEX-12696   12.9 -0.96 -0.67  0.18        4
 9 NAPSA       GTEX-1CB4J   12.3 -0.29 -0.44 -0.14        4
10 DIAPH2-AS1 GTEX-VUSG    12.2 -0.33  1.18  0.67        4
# … with 389,912 more rows
```

Exercise: top 5 high expression instances

Use `arrange()` and `filter()` to get the data for the 5 individual-gene pairs with the most extreme expression changes in blood

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Use `arrange()` and `filter()` to get the data for the 5 individual-gene pairs with the most extreme expression changes in blood

```
filter(arrange(gtex_data, desc(Blood)), row_number()<=5) # "nesting" the calls to
filter and arrange
# A tibble: 5 x 7
  Gene     Ind         Blood Heart  Lung Liver NTissues
  <chr>    <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
1 REN      GTEX-U8XE    18.9 -0.57 NA     0.09        3
2 KLK3     GTEX-147F4   15.7 -0.74 -0.44 -0.02        4
3 DNASE2B  GTEX-12696   14.4 -0.82 -0.92  0.35        4
4 GAPDHP33 GTEX-UPK5    13.8  1.52 -1.48 -1.84        4
5 DCSTAMP  GTEX-12696   13.6 NA    -0.57 -0.91        3
```

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Use `arrange()` and `filter()` to get the data for the 5 individual-gene pairs with the most extreme expression changes in blood

```
filter(arrange(gtex_data, desc(Blood)), row_number()<=5) # "nesting" the calls to
filter and arrange
# A tibble: 5 x 7
  Gene     Ind         Blood Heart  Lung Liver NTissues
  <chr>    <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
1 REN      GTEX-U8XE    18.9 -0.57 NA     0.09        3
2 KLK3     GTEX-147F4   15.7 -0.74 -0.44 -0.02        4
3 DNASE2B  GTEX-12696   14.4 -0.82 -0.92  0.35        4
4 GAPDHP33 GTEX-UPK5    13.8  1.52 -1.48 -1.84        4
5 DCSTAMP  GTEX-12696   13.6 NA    -0.57 -0.91        3
```

or

```
gtex_by_blood = arrange(gtex_data, desc(Blood)) # using a temporary variable
filter(gtex_by_blood, row_number()<=5)
# A tibble: 5 x 7
  Gene     Ind         Blood Heart  Lung Liver NTissues
  <chr>    <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
1 REN      GTEX-U8XE    18.9 -0.57 NA     0.09        3
2 KLK3     GTEX-147F4   15.7 -0.74 -0.44 -0.02        4
3 DNASE2B  GTEX-12696   14.4 -0.82 -0.92  0.35        4
4 GAPDHP33 GTEX-UPK5    13.8  1.52 -1.48 -1.84        4
5 DCSTAMP  GTEX-12696   13.6 NA    -0.57 -0.91        3
```

Select columns with select()

Select columns with select()

```
select(gtex_data, Gene, Ind, Blood)
# A tibble: 389,922 x 3
   Gene  Ind         Blood
   <chr> <chr>       <dbl>
 1 A2ML1 GTEX-11DXZ -0.14
 2 A2ML1 GTEX-11GSP -0.5
 3 A2ML1 GTEX-11NUK -0.08
 4 A2ML1 GTEX-11NV4 -0.37
 5 A2ML1 GTEX-11TT1  0.3
 6 A2ML1 GTEX-11TUW  0.02
 7 A2ML1 GTEX-11ZUS -1.07
 8 A2ML1 GTEX-11ZVC -0.27
 9 A2ML1 GTEX-1212Z -0.3
10 A2ML1 GTEX-12696 -0.11
# … with 389,912 more rows
```

- The select function will return a subset of the tibble, using only the requested columns in the order specified.

Select columns with select()

- `select()` can also be used with handy helpers like `starts_with()` and `contains()`

```
select(gtex_data, starts_with("L"))
# A tibble: 389,922 x 2
    Lung Liver
   <dbl> <dbl>
 1 NA    -0.66
 2  0.76 -0.1
 3 -0.26 -0.13
 4 -0.42 -0.61
 5  0.59 -0.12
 6  0.29 -0.66
 7  0.67  0.06
 8  0.13 -0.75
 9  0.1  -0.48
10  0.96  0.72
# … with 389,912 more rows
```

- Use `?select` to see all the possibilities

Select columns with select()

```
select(gtex_data, contains("N"))
# A tibble: 389,922 x 4
   Gene  Ind          Lung NTissues
   <chr> <chr>       <dbl>    <dbl>
 1 A2ML1 GTEX-11DXZ NA           3
 2 A2ML1 GTEX-11GSP  0.76        4
 3 A2ML1 GTEX-11NUK -0.26        4
 4 A2ML1 GTEX-11NV4 -0.42        4
 5 A2ML1 GTEX-11TT1  0.59        4
 6 A2ML1 GTEX-11TUW  0.29        4
 7 A2ML1 GTEX-11ZUS  0.67        4
 8 A2ML1 GTEX-11ZVC  0.13        4
 9 A2ML1 GTEX-1212Z  0.1         4
10 A2ML1 GTEX-12696  0.96        4
# … with 389,912 more rows
```

- The quotes around the letter `"N"` make it a string. If we did not do this, `R` would think it was looking for a variable called `N` and not just the plain letter.
- We don't have to quote the names of columns (like `Ind`) because the `tidyverse` functions know that we are working within the dataframe and thus treat the column names like they are variables in their own right

select() subsets columns by name

- `select()` can also be used to select everything **except for** certain columns

```
select(gtex_data, -starts_with("L"), -Ind)
# A tibble: 389,922 x 4
   Gene  Blood Heart NTissues
   <chr> <dbl> <dbl>    <dbl>
 1 A2ML1 -0.14 -1.08        3
 2 A2ML1 -0.5   0.53        4
 3 A2ML1 -0.08 -0.4         4
 4 A2ML1 -0.37  0.11        4
 5 A2ML1  0.3  -1.11        4
 6 A2ML1  0.02 -0.47        4
 7 A2ML1 -1.07 -0.41        4
 8 A2ML1 -0.27 -0.51        4
 9 A2ML1 -0.3   0.53        4
10 A2ML1 -0.11  0.24        4
# … with 389,912 more rows
```

select() subsets columns by name

- or even to select only columns that match a certain condition

```
select(gtex_data, where(is.numeric))
# A tibble: 389,922 x 5
   Blood Heart  Lung Liver NTissues
   <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 -0.14 -1.08 NA    -0.66        3
 2 -0.5   0.53  0.76 -0.1         4
 3 -0.08 -0.4  -0.26 -0.13        4
 4 -0.37  0.11 -0.42 -0.61        4
 5  0.3  -1.11  0.59 -0.12        4
 6  0.02 -0.47  0.29 -0.66        4
 7 -1.07 -0.41  0.67  0.06        4
 8 -0.27 -0.51  0.13 -0.75        4
 9 -0.3   0.53  0.1  -0.48        4
10 -0.11  0.24  0.96  0.72        4
# … with 389,912 more rows
```

pull() is a friend of select()

- `select()` has a friend called `pull()` which returns a vector instead of a (one-column) data frame

```
select(gtex_data, Gene)
# A tibble: 389,922 x 1
   Gene
   <chr>
 1 A2ML1
 2 A2ML1
 3 A2ML1
 4 A2ML1
 5 A2ML1
 6 A2ML1
 7 A2ML1
 8 A2ML1
 9 A2ML1
10 A2ML1
# … with 389,912 more rows
```

```
pull(gtex_data, Gene)
    [1] "A2ML1"              "A2ML1"              "A2ML1"
    [4] "A2ML1"              "A2ML1"              "A2ML1"
    [7] "A2ML1"              "A2ML1"              "A2ML1"
   [10] "A2ML1"              "A2ML1"              "A2ML1"
   [13] "A2ML1"              "A2ML1"              "A2ML1"
...
```

Rename column names with rename()

- `select()` can be used to rename variables, but it drops all variables not selected

```
select(gtex_data, number_tissues = NTissues)
# A tibble: 389,922 x 1
   number_tissues
            <dbl>
 1              3
 2              4
 3              4
...
```

- `rename()` is better suited for this because it keeps all the columns

```
rename(gtex_data, number_tissues = NTissues)
# A tibble: 389,922 x 7
   Gene  Ind         Blood Heart  Lung Liver number_tissues
   <chr> <chr>       <dbl> <dbl> <dbl> <dbl>          <dbl>
 1 A2ML1 GTEX-11DXZ -0.14 -1.08 NA    -0.66              3
 2 A2ML1 GTEX-11GSP -0.5   0.53  0.76 -0.1               4
 3 A2ML1 GTEX-11NUK -0.08 -0.4  -0.26 -0.13              4
...
```

Note: `mutate()`, can also change a column name (more on `mutate()` soon)

Exercise: select and filter

- Create a one-column dataframe of the heart expression Z-scores (`Heart`) of all individuals with data present (i.e. not `NA`) for gene WDR34 (`Gene`) in the `gtex_data` dataset.

Exercise: select and filter

- Create a one-column dataframe of the heart expression Z-scores (`Heart`) of all individuals with data present (i.e. not `NA`) for gene WDR34 (`Gene`) in the `gtex_data` dataset.

```
select(filter(gtex_data, Gene == "WDR34", !is.na(Heart)), Heart)
# A tibble: 78 x 1
   Heart
   <dbl>
 1  0.78
 2  0.94
 3  0.29
 4  0.17
 5 -0.6
 6  0.46
 7 -0.97
...
```

Exercise: select and filter

- Create a one-column dataframe of the heart expression Z-scores (`Heart`) of all individuals with data present (i.e. not `NA`) for gene WDR34 (`Gene`) in the `gtex_data` dataset.

```
select(filter(gtex_data, Gene == "WDR34", !is.na(Heart)), Heart)
# A tibble: 78 x 1
   Heart
   <dbl>
 1  0.78
 2  0.94
 3  0.29
 4  0.17
 5 -0.6
 6  0.46
 7 -0.97
...
```

- What is wrong with this?

```
filter(select(gtex_data, Heart), Gene == "WDR34")
```

Exercise: select text columns

- Use select to subset the `gtex_data` dataframe to just those columns that contain text data.
- Can you do this programmatically without specifying the names of each of the desired columns?
- Which base R function will help you determine if a column is textual or not? Use whatever tools you want to find out.

Exercise: select text columns

- Use select to subset the `gtex_data` dataframe to just those columns that contain text data.
- Can you do this programmatically without specifying the names of each of the desired columns?
- Which base R function will help you determine if a column is textual or not? Use whatever tools you want to find out.

```
select(gtex_data, where(is.character))
# A tibble: 389,922 x 2
   Gene  Ind
   <chr> <chr>
 1 A2ML1 GTEX-11DXZ
 2 A2ML1 GTEX-11GSP
 3 A2ML1 GTEX-11NUK
 4 A2ML1 GTEX-11NV4
 5 A2ML1 GTEX-11TT1
 6 A2ML1 GTEX-11TUW
 7 A2ML1 GTEX-11ZUS
 8 A2ML1 GTEX-11ZVC
 9 A2ML1 GTEX-1212Z
10 A2ML1 GTEX-12696
# … with 389,912 more rows
```

Add new variables with mutate()

Add new variables with mutate()

```
mutate(gtex_data, abs_blood = abs(Blood))
# A tibble: 389,922 x 8
   Gene  Ind         Blood Heart  Lung Liver NTissues abs_blood
   <chr> <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>     <dbl>
 1 A2ML1 GTEX-11DXZ -0.14 -1.08 NA    -0.66        3      0.14
 2 A2ML1 GTEX-11GSP -0.5   0.53  0.76 -0.1         4      0.5
...
```

- This uses `mutate()` to add a new column to which is the absolute value of `Blood`.
- The thing on the left of the = is a new name that you make up which you would like the new column to be called
- The expresssion on the right of the = defines what will go into the new column
- **Warning!** If the new variable name already exists, `mutate()` will overwrite the existing one

```
mutate(gtex_data, Blood = Blood *1000)
# A tibble: 389,922 x 7
   Gene  Ind         Blood Heart  Lung Liver NTissues
   <chr> <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 A2ML1 GTEX-11DXZ  -140 -1.08 NA    -0.66        3
 2 A2ML1 GTEX-11GSP  -500  0.53  0.76 -0.1         4
...
```

mutate() can create multiple new columns at once

- `mutate()` can create multiple columns at the same time and use multiple columns to define a single new one

```
mutate(gtex_data, # the newlines make it more readable
       abs_blood = abs(Blood),
       abs_heart = abs(Heart),
       blood_heart_dif = abs_blood - abs_heart
)
# A tibble: 389,922 x 10
   Gene  Ind         Blood Heart  Lung Liver NTissues abs_blood abs_heart
   <chr> <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>     <dbl>     <dbl>
 1 A2ML1 GTEX-11DXZ -0.14 -1.08 NA    -0.66        3      0.14      1.08
 2 A2ML1 GTEX-11GSP -0.5   0.53  0.76 -0.1         4      0.5       0.53
 3 A2ML1 GTEX-11NUK -0.08 -0.4  -0.26 -0.13        4      0.08      0.4
 4 A2ML1 GTEX-11NV4 -0.37  0.11 -0.42 -0.61        4      0.37      0.11
 5 A2ML1 GTEX-11TT1  0.3  -1.11  0.59 -0.12        4      0.3       1.11
 6 A2ML1 GTEX-11TUW  0.02 -0.47  0.29 -0.66        4      0.02      0.47
 7 A2ML1 GTEX-11ZUS -1.07 -0.41  0.67  0.06        4      1.07      0.41
 8 A2ML1 GTEX-11ZVC -0.27 -0.51  0.13 -0.75        4      0.27      0.51
 9 A2ML1 GTEX-1212Z -0.3   0.53  0.1  -0.48        4      0.3       0.53
10 A2ML1 GTEX-12696 -0.11  0.24  0.96  0.72        4      0.11      0.24
# … with 389,912 more rows, and 1 more variable: blood_heart_dif <dbl>
```

- Note that we have also used two columns simultaneously (`Blood` and `Heart`) to create a new column)

mutate() for data type conversion

- Data is sometimes given to you in a form that makes it difficult to do operations on

```
df = tibble(number = c("1", "2", "3"))
df
# A tibble: 3 x 1
  number
  <chr>
1 1
2 2
3 3
mutate(df, number_plus_1 = number + 1)
Error: Problem with `mutate()` column `number_plus_1`.
ℹ `number_plus_1 = number + 1`.
x non-numeric argument to binary operator
```

- `mutate()` is also useful for converting data types, in this case text to numbers

```
mutate(df, number = as.numeric(number))
# A tibble: 3 x 1
  number
   <dbl>
1      1
2      2
3      3
```

Exercise: mutate()

I want to identify genes that have large average expression changes across blood and liver. Can you compute the average of blood and liver expression changes across all gene-individual pairs? Compute the average manually (i.e. don't use the mean function).

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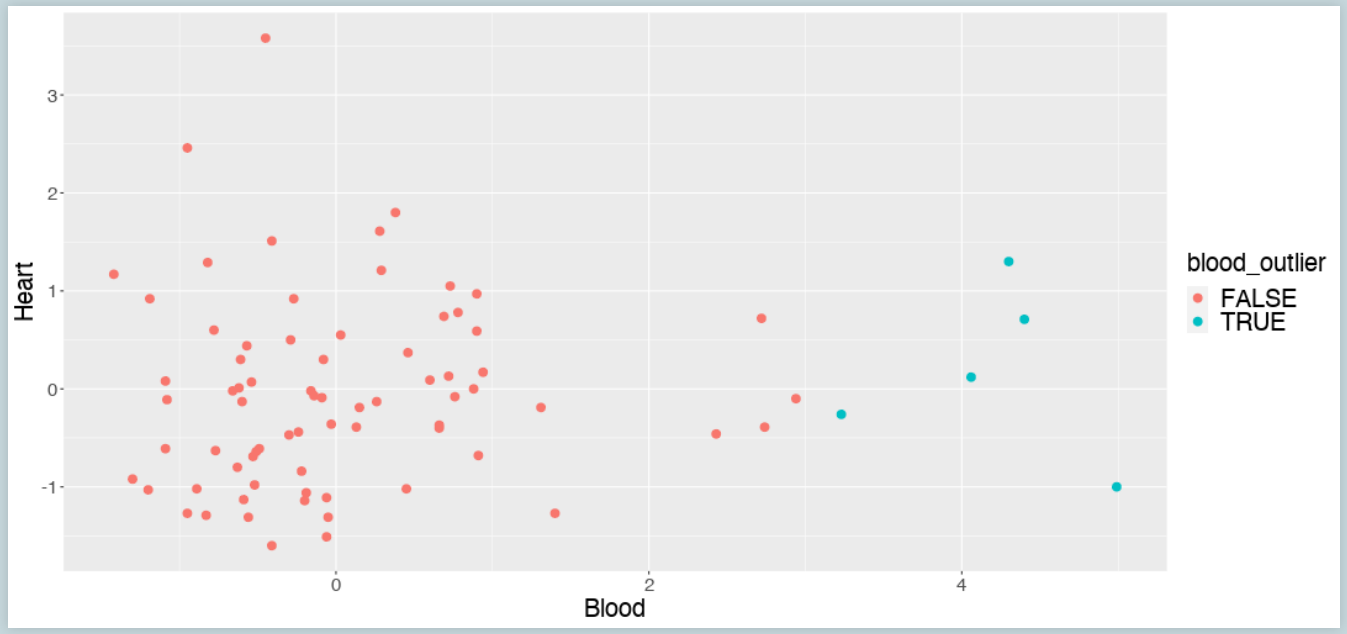
```
mutate(gtex_data, avg_blood_liver = (Blood+Liver)/2)
# A tibble: 389,922 x 8
   Gene  Ind         Blood Heart  Lung Liver NTissues avg_blood_liver
   <chr> <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>           <dbl>
 1 A2ML1 GTEX-11DXZ -0.14 -1.08 NA    -0.66        3          -0.4
 2 A2ML1 GTEX-11GSP -0.5   0.53  0.76 -0.1         4          -0.3
 3 A2ML1 GTEX-11NUK -0.08 -0.4  -0.26 -0.13        4          -0.105
 4 A2ML1 GTEX-11NV4 -0.37  0.11 -0.42 -0.61        4          -0.49
 5 A2ML1 GTEX-11TT1  0.3  -1.11  0.59 -0.12        4           0.09
 6 A2ML1 GTEX-11TUW  0.02 -0.47  0.29 -0.66        4          -0.32
 7 A2ML1 GTEX-11ZUS -1.07 -0.41  0.67  0.06        4          -0.505
 8 A2ML1 GTEX-11ZVC -0.27 -0.51  0.13 -0.75        4          -0.51
 9 A2ML1 GTEX-1212Z -0.3   0.53  0.1  -0.48        4          -0.39
10 A2ML1 GTEX-12696 -0.11  0.24  0.96  0.72        4           0.305
# … with 389,912 more rows
```

Exercise: mutate() and ggplot

Filter `gtex_data` to only include measurements of the MYL1 gene. Then, use mutate to mark which gene-individual pairs have outlier MYL1 expression in blood, defined as Z > 3 or Z < -3. Then, produce a plot showing blood Z-scores vs heart Z-scores and color the blood gene expression outliers in a different color than the other points.

Exercise: mutate() and ggplot

Filter `gtex_data` to only include measurements of the MYL1 gene. Then, use mutate to mark which gene-individual pairs have outlier MYL1 expression in blood, defined as Z > 3 or Z < -3. Then, produce a plot showing blood Z-scores vs heart Z-scores and color the blood gene expression outliers in a different color than the other points.



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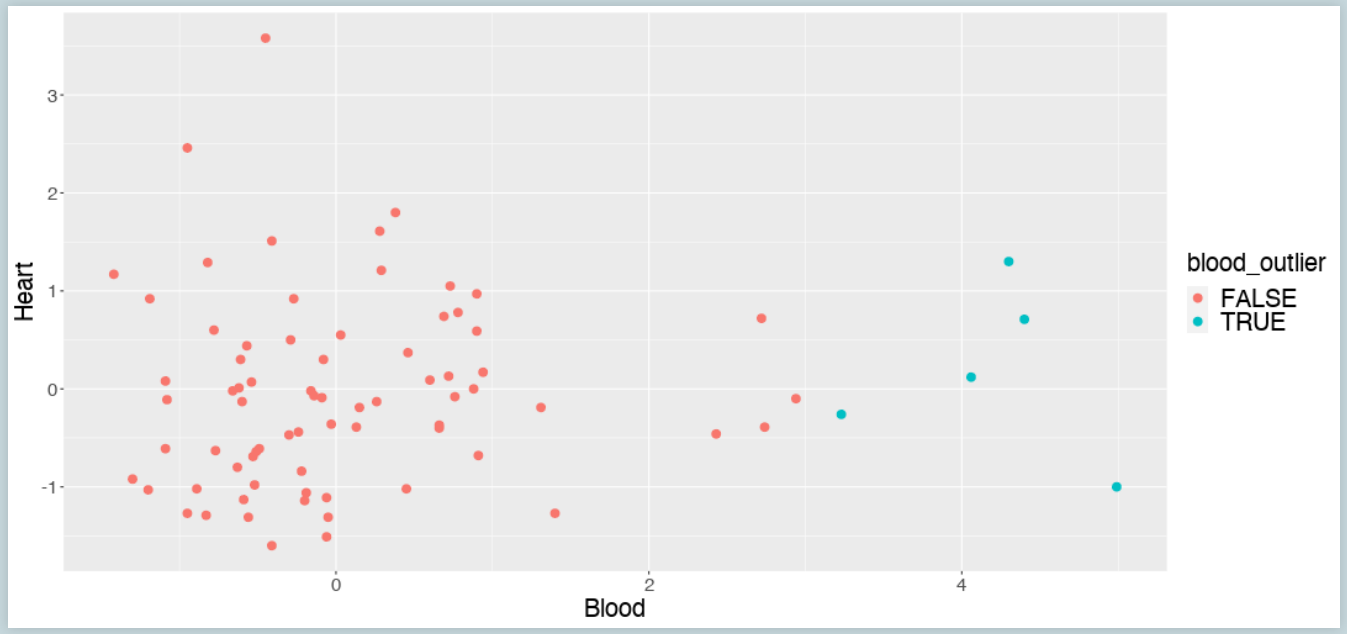
Filter `gtex_data` to only include measurements of the MYL1 gene. Then, use mutate to mark which gene-individual pairs have outlier MYL1 expression in blood, defined as Z > 3 or Z < -3. Then, produce a plot showing blood Z-scores vs heart Z-scores and color the blood gene expression outliers in a different color than the other points.




```
gene_data = filter(gtex_data, Gene == 'MYL1')
blood_outliers = mutate(gene_data, blood_outlier = abs(Blood)>3)
ggplot(blood_outliers) +
  geom_point(aes(x=Blood, y=Heart, color=blood_outlier))
```

Exercise: putting it together

I am interested in identifying individuals that have a large change in gene expression change for any gene between lung tissue and blood tissue, with higher expression in lung.

1. Produce a list of top 10 individual-gene pairs arranged by the expression change for lung compared to blood
2. Only consider individual-gene pairs measured in all four tissues
3. In the output, just show the gene, individual, lung expression, blood expression, and lung-blood differences

Exercise: putting it together

I am interested in identifying individuals that have a large change in gene expression change for any gene between lung tissue and blood tissue, with higher expression in lung.

1. Produce a list of top 10 individual-gene pairs arranged by the expression change for lung compared to blood
2. Only consider individual-gene pairs measured in all four tissues
3. In the output, just show the gene, individual, lung expression, blood expression, and lung-blood differences

```
gtex_data_no_change = filter(gtex_data, NTissues == 4)
gtex_data_ratio = mutate(gtex_data_no_change, lung_blood_dif = Lung - Blood)
sorted = arrange(gtex_data_ratio, desc(lung_blood_dif))
top_10 = filter(sorted, row_number()<=10)
select(top_10, Gene, Ind, Lung, Blood, lung_blood_dif)
# A tibble: 10 x 5
   Gene            Ind         Lung Blood lung_blood_dif
   <chr>           <chr>      <dbl> <dbl>          <dbl>
 1 TMEM151A        GTEX-ZEX8  12.0  -0.77          12.8
 2 DSG3            GTEX-14PJO 10.3  -0.04          10.4
 3 KNG1            GTEX-12WSD 11.6   1.74           9.82
 4 NPIPA8          GTEX-XXEK   9.23  0.03           9.2
 5 ALOXE3          GTEX-YFC4   7.5  -1.32           8.82
 6 ETNPPL          GTEX-1CB4J  8.47 -0.31           8.78
 7 EGR4            GTEX-13FTZ  7.79 -0.75           8.54
 8 IGHV2-26        GTEX-YECK   7.82 -0.63           8.45
 9 LINC00342       GTEX-1A32A  6.01 -2.16           8.17
10 RP11-1260E13.4  GTEX-11ZVC  6.96 -1.17           8.13
```

Piping

Why pipe?

- In our last exercise, we used a number of different function applications to arrive at our answer. Shown below, we used temporary variables to keep our code clean.

```
gtex_data_no_change = filter(gtex_data, NTissues == 4)
gtex_data_ratio = mutate(gtex_data_no_change, lung_blood_dif = Lung - Blood)
sorted = arrange(gtex_data_ratio, desc(lung_blood_dif))
top_10 = filter(sorted, row_number()<=10)
select(top_10, Gene, Ind, Lung, Blood, lung_blood_dif)
```

Why pipe?

- In our last exercise, we used a number of different function applications to arrive at our answer. Shown below, we used temporary variables to keep our code clean.

```
gtex_data_no_change = filter(gtex_data, NTissues == 4)
gtex_data_ratio = mutate(gtex_data_no_change, lung_blood_dif = Lung - Blood)
sorted = arrange(gtex_data_ratio, desc(lung_blood_dif))
top_10 = filter(sorted, row_number()<=10)
select(top_10, Gene, Ind, Lung, Blood, lung_blood_dif)
```

- Compare that to the same code using nested calls (instead of storing in temporary variables):

```
select(
  filter(
    arrange(
      mutate(
        filter(
          gtex_data, NTissues == 4),
        lung_blood_dif = Lung - Blood),
      desc(lung_blood_dif)),
    row_number()<=10),
  Gene, Ind, Lung, Blood, lung_blood_dif
)
```

- What makes either of these hard to read or understand?

The pipe operator

- Tidyverse solves these problems with the pipe operator %>%

```
gtex_data %>%
  filter(NTissues == 4) %>%
  mutate(lung_blood_dif = Lung - Blood) %>%
  arrange(desc(lung_blood_dif)) %>%
  filter(row_number()<=10) %>%
  select(Gene, Ind, Lung, Blood, lung_blood_dif)
```

The pipe operator

- Tidyverse solves these problems with the pipe operator %>%

```
gtex_data %>%
  filter(NTissues == 4) %>%
  mutate(lung_blood_dif = Lung - Blood) %>%
  arrange(desc(lung_blood_dif)) %>%
  filter(row_number()<=10) %>%
  select(Gene, Ind, Lung, Blood, lung_blood_dif)
```

- How does this compare with our code before? What do you notice?

```
gtex_data_no_change = filter(gtex_data, NTissues == 4)
gtex_data_ratio = mutate(gtex_data_no_change, lung_blood_dif = Lung - Blood)
sorted = arrange(gtex_data_ratio, desc(lung_blood_dif))
top_10 = filter(sorted, row_number()<=10)
select(top_10, Gene, Ind, Lung, Blood, lung_blood_dif)
```

Pipe details: What happens to an object when it gets ”piped in”?

When `df1` is piped into `fun(x)` (`fun` is just some fake function)

```
df1 %>% fun(x)
```

is converted into:

```
fun(df1, x)
```

- That is: the thing being piped in is used as the *first* argument of `fun`.
- The tidyverse functions are consistently designed so that the first argument is a data frame, and the result is a data frame, so you can push a dataframe all the way through a series of functions

Pipe details: What objects can be piped?

- The pipe works for all variables and functions (not just tidyverse functions)

Piping with an array

```
c(1,44,21,0,-4) %>%
    sum() # instead of sum(c(1,44,21,0,-4))
[1] 62
```

Piping with a scalar

```
1 %>% `+`(1) # `+` is just a function that takes two arguments!
[1] 2
```

Piping with a data frame

```
tibble(name = c("Petunia", "Rose", "Daisy", "Marigold", "Arabidopsis"),
           age = c(10,54,21,99,96)) %>%
    filter(age > 30)
# A tibble: 3 x 2
  name          age
  <chr>       <dbl>
1 Rose           54
2 Marigold       99
3 Arabidopsis    96
```

Piping to another position

- The pipe typically pipes into the first argument of a function, but you can use `.` to represent the object you're piping into the function

```
# install.packages("slider")
library(slider)
mean %>%
  slide_vec(1:10, ., .before=2)
 [1] 1.0 1.5 2.0 3.0 4.0 5.0 6.0 7.0 8.0 9.0
```

- Also notice how I've piped in a *function* to a function! (yes, functions are just objects like anything else in R)
- More about this in the functional programming section

Exercise: Pipe to ggplot

- Run this code to see what it does. Then rewrite it using the pipe operator and get it to produce the same output.

```
gene_data = filter(gtex_data, Gene == 'MYBL2')
outliers = mutate(gene_data, blood_outlier = abs(Blood) > 2)
ggplot(outliers) +
  geom_bar(aes(x=blood_outlier)) +
  scale_x_discrete("Class", labels=c("Other", "Outlier")) +
  ggtitle("How many individuals have outlier MYBL2 expression in blood?")
```

Exercise: Pipe to ggplot

- Run this code to see what it does. Then rewrite it using the pipe operator and get it to produce the same output.

```
gene_data = filter(gtex_data, Gene == 'MYBL2')
outliers = mutate(gene_data, blood_outlier = abs(Blood) > 2)
ggplot(outliers) +
  geom_bar(aes(x=blood_outlier)) +
  scale_x_discrete("Class", labels=c("Other", "Outlier")) +
  ggtitle("How many individuals have outlier MYBL2 expression in blood?")
```

```
gtex_data %>%
  filter(Gene == 'MYBL2') %>%
  mutate(blood_outlier = abs(Blood) > 2) %>%
ggplot() +
  geom_bar(aes(x=blood_outlier)) +
  scale_x_discrete("Class", labels=c("Other", "Outlier")) +
  ggtitle("How many individuals have outlier MYBL2 expression in blood?")
```

Grouped summaries with summarise()

Grouped summaries with summarise()

```
summarize(gtex_data, tissue_avg=mean(NTissues))
# A tibble: 1 x 1
  tissue_avg
       <dbl>
1       3.97
```

- `summarize()` boils down the data frame according to the conditions it gets. In this case, it creates a data frame with a single column called `tissue_avg` that contains the mean of the `NTissues` column
- As with `mutate()`, the name on the left of the = is something you make up that you would like the new column to be named.
- `mutate()` transforms columns into new columns of the same length, but `summarize()` collapses down the data frame into a single row
- Summaries are more useful when you apply them to subgoups of the data, which we will soon see how to do.

Grouped summaries with summarise()

- note that you can also pass in multiple conditions that operate on multiple columns at the same time

```
gtex_data %>%
summarize( # newlines not necessary, again just increase clarity
  tissue_avg = mean(NTissues),
  blood_max = max(Blood, na.rm=T),
  blood_lung_dif_min = min(Blood - Lung, na.rm=T)
)
# A tibble: 1 x 3
  tissue_avg blood_max blood_lung_dif_min
       <dbl>     <dbl>              <dbl>
1       3.97      18.9              -12.8
```

Grouped summaries with summarise()

- Summaries are more useful when you apply them to subgoups of the data

```
gtex_data %>%
  group_by(Gene) %>%
  summarize(max_blood = max(Blood))
# A tibble: 4,999 x 2
   Gene                max_blood
   <chr>                   <dbl>
 1 A2ML1                    2.08
 2 A3GALT2                  2.77
 3 A4GALT                   2.78
 4 AAMDC                   NA
 5 AANAT                    1.71
 6 AAR2                     2.52
 7 AARSD1                   1.89
 8 AB019441.29              2.31
 9 ABC7-42389800N19.1       1.98
10 ABCA5                    2.3
# … with 4,989 more rows
```

Multiple columns can be used to group the data simultaneously

```
gtex_data %>%
  group_by(Gene,Ind) %>%
  summarize(max_blood = max(Blood))
# A tibble: 389,922 x 3
# Groups:   Gene [4,999]
   Gene  Ind         max_blood
   <chr> <chr>           <dbl>
 1 A2ML1 GTEX-11DXZ      -0.14
 2 A2ML1 GTEX-11GSP      -0.5
 3 A2ML1 GTEX-11NUK      -0.08
 4 A2ML1 GTEX-11NV4      -0.37
 5 A2ML1 GTEX-11TT1       0.3
 6 A2ML1 GTEX-11TUW       0.02
 7 A2ML1 GTEX-11ZUS      -1.07
 8 A2ML1 GTEX-11ZVC      -0.27
 9 A2ML1 GTEX-1212Z      -0.3
10 A2ML1 GTEX-12696      -0.11
# … with 389,912 more rows
```

- The result has the summary value for each unique combination of the grouping variables

Computing the number of rows in each group

- The `n()` function counts the number of rows in each group:

```
gtex_data %>%
  filter(!is.na(Blood)) %>%
  group_by(Gene) %>%
  summarize(how_many = n())
# A tibble: 4,999 x 2
   Gene                how_many
   <chr>                  <int>
 1 A2ML1                     78
 2 A3GALT2                   78
 3 A4GALT                    78
 4 AAMDC                     77
 5 AANAT                     78
 6 AAR2                      78
 7 AARSD1                    78
 8 AB019441.29               78
 9 ABC7-42389800N19.1        78
10 ABCA5                     78
# … with 4,989 more rows
```

- You can also use `count()`, which is just a shorthand for the same thing

```
gtex_data %>%
  filter(!is.na(Blood)) %>%
  group_by(Gene) %>%
  count()
```

Computing the number of distinct elements in a column, per group

- `n_distinct()` counts the number of unique elements in a column

```
gtex_data %>%
  group_by(Ind) %>%
  summarize(n_genes = n_distinct(Gene))
# A tibble: 78 x 2
   Ind         n_genes
   <chr>         <int>
 1 GTEX-11DXZ     4999
 2 GTEX-11GSP     4999
 3 GTEX-11NUK     4999
 4 GTEX-11NV4     4999
 5 GTEX-11TT1     4999
 6 GTEX-11TUW     4999
 7 GTEX-11ZUS     4999
 8 GTEX-11ZVC     4999
 9 GTEX-1212Z     4999
10 GTEX-12696     4999
# … with 68 more rows
```

Exercise: top expression per tissue

- Ignoring NAs, what is the highest liver expression value seen for each gene in the `gtex_data` dataset?
- What about the lowest?

Exercise: top expression per tissue

- Ignoring NAs, what is the highest liver expression value seen for each gene in the `gtex_data` dataset?
- What about the lowest?

```
gtex_data %>%
  group_by(Gene) %>%
  summarize(
    max_liver = max(Liver, na.rm=T),
    min_liver = min(Liver, na.rm=T)
  )
# A tibble: 4,999 x 3
   Gene                max_liver min_liver
   <chr>                   <dbl>     <dbl>
 1 A2ML1                    3.65     -1.94
 2 A3GALT2                  3.61     -1.3
 3 A4GALT                   2.22     -1.76
 4 AAMDC                    3.43     -2.62
 5 AANAT                    3.78     -2.22
 6 AAR2                     2.32     -3.23
 7 AARSD1                   2.77     -2.75
 8 AB019441.29              3.36     -1.53
 9 ABC7-42389800N19.1       2.51     -3.2
10 ABCA5                    3.27     -3.27
# … with 4,989 more rows
```

Exercise: summarize and plot

Recreate this plot.

Exercise: summarize and plot

Recreate this plot.


```
gtex_data %>%
  filter(Gene %in% c('FFAR4', 'KLK3', 'PLOD2', 'MLPH')) %>%
  group_by(Gene, NTissues) %>%
  summarize(max_heart = max(Heart ,na.rm=T)) %>%

ggplot() +
  geom_point(aes(y=Gene, x=max_heart)) +
  facet_grid(. ~ NTissues , labeller = label_both)
```

Grouped mutates and filters

Filtering grouped data

- `filter()` is aware of grouping. When used on a grouped dataset, it applies the filtering condition separately in each group

```
gtex_data %>%
  group_by(Gene) %>%
  filter(NTissues == max(NTissues))
# A tibble: 376,883 x 7
# Groups:   Gene [4,999]
   Gene  Ind         Blood Heart  Lung Liver NTissues
   <chr> <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 A2ML1 GTEX-11GSP -0.5   0.53  0.76 -0.1          4
 2 A2ML1 GTEX-11NUK -0.08 -0.4  -0.26 -0.13         4
 3 A2ML1 GTEX-11NV4 -0.37  0.11 -0.42 -0.61         4
 4 A2ML1 GTEX-11TT1  0.3  -1.11  0.59 -0.12         4
 5 A2ML1 GTEX-11TUW  0.02 -0.47  0.29 -0.66         4
 6 A2ML1 GTEX-11ZUS -1.07 -0.41  0.67  0.06         4
 7 A2ML1 GTEX-11ZVC -0.27 -0.51  0.13 -0.75         4
 8 A2ML1 GTEX-1212Z -0.3   0.53  0.1  -0.48         4
 9 A2ML1 GTEX-12696 -0.11  0.24  0.96  0.72         4
10 A2ML1 GTEX-12WSD  0.53  0.36  0.2   0.51         4
# … with 376,873 more rows
```

- Why do we get back multiple rows per `class`?
- This is an extremely convenient idiom for finding the rows that minimize or maximize a condition

Exercise: Max expression change in blood and lung

Which are the individual pairs that have both the max blood expression change *and* max lung expression change among all individuals with measurements for the same gene?

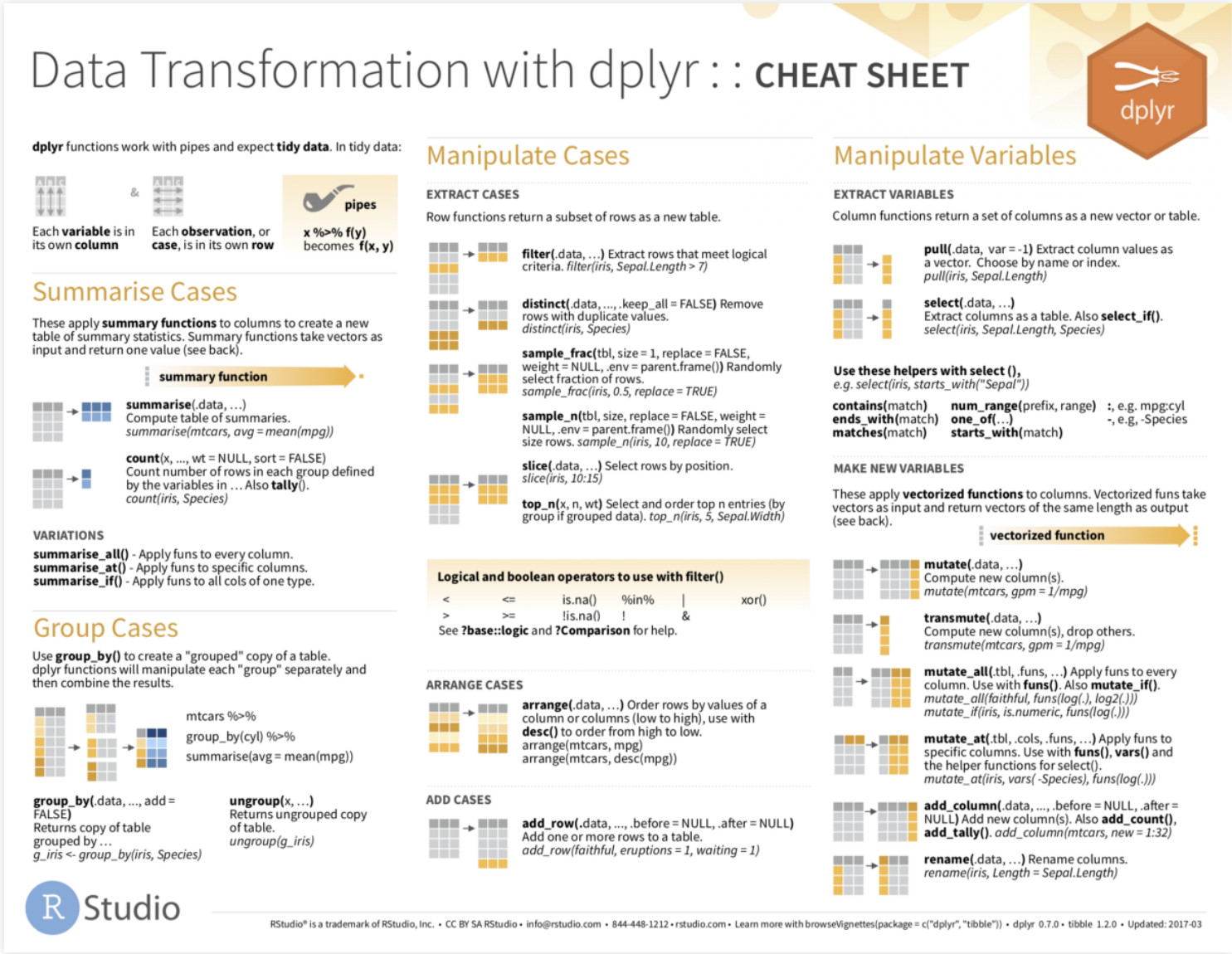
```
gtex_data %>%
  group_by(Gene) %>%
  filter(Blood == max(Blood), Lung==max(Lung))
# A tibble: 64 x 7
# Groups:   Gene [64]
   Gene         Ind         Blood Heart  Lung Liver NTissues
   <chr>        <chr>       <dbl> <dbl> <dbl> <dbl>    <dbl>
 1 A4GALT       GTEX-12696  2.78 -1.02  2.31 -0.23         4
 2 ABHD1        GTEX-VUSG   6.33  0.41  2.04 -0.04         4
 3 AL162151.3   GTEX-WZTO   2.37 -0.19  4.23 -1.22         4
 4 ANKRD36B     GTEX-12WSD  2.72  0.74  2.66  1.22         4
 5 APOA1        GTEX-12WSD  5.45 NA     7     0.67         3
 6 C14orf119    GTEX-11ZUS  2.51  0.76  1.85 -0.99         4
 7 CD1D         GTEX-1B996  3.05  2.85  2.78  2.1          4
 8 CTB-131B5.2  GTEX-1GN73  6.29 -1.17  5.51 -0.96         4
 9 CTC-448F2.6  GTEX-131YS  4.1   0.75  2.67 -0.24         4
10 EVC          GTEX-UPK5   4.31  0.21  2.6  -0.61         4
# … with 54 more rows
```

Mutating grouped data

- `mutate()` is aware of grouping. When used on a grouped dataset, it applies the mutation separately in each group

```
gtex_data %>%
  group_by(Gene) %>%
  mutate(blood_diff_from_min = Blood - min(Blood)) %>%
  select(Gene, Ind, Blood, blood_diff_from_min)
# A tibble: 389,922 x 4
# Groups:   Gene [4,999]
   Gene  Ind         Blood blood_diff_from_min
   <chr> <chr>       <dbl>               <dbl>
 1 A2ML1 GTEX-11DXZ -0.14                1.26
 2 A2ML1 GTEX-11GSP -0.5                 0.9
 3 A2ML1 GTEX-11NUK -0.08                1.32
 4 A2ML1 GTEX-11NV4 -0.37                1.03
 5 A2ML1 GTEX-11TT1  0.3                 1.7
 6 A2ML1 GTEX-11TUW  0.02                1.42
 7 A2ML1 GTEX-11ZUS -1.07                0.33
 8 A2ML1 GTEX-11ZVC -0.27                1.13
 9 A2ML1 GTEX-1212Z -0.3                 1.1
10 A2ML1 GTEX-12696 -0.11                1.29
# … with 389,912 more rows
```

- As always, mutate does not change the number of rows in the dataset



Source: Rstudio Cheat Sheets. Download the full dplyr cheat sheet here.