Basic Tabular Data Manipulation

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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.

```
# Read subsetted data from online file
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

Exercise: Low expression

Exercise: High expression in all tissues

Exercise: High and low expression events

Exercise: getting rid of NAs

Filtering by row number

```
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
```

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

Sampling rows

```
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 MELTF       GTEX-14JG1  0.49  0.68  0.27  0.13         4
2 PAPPA       GTEX-18465  0.7   2.44  0.02 -0.16         4
3 AZIN1-AS1   GTEX-X261  -0.7  -2.77  0.35  0.13         4
4 AC002456.2  GTEX-1B932 -2.72  1.55 -1.56  0.47         4
5 CNN3        GTEX-1GN2E  0.26 -0.83  0.3  -0.04         4
```

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

Arrange rows 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 sort 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

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()

- `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
...
```

Exercise: select and filter

Exercise: select text columns

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
 3 A2ML1 GTEX-11NUK -0.08 -0.4  -0.26 -0.13         4      0.08
 4 A2ML1 GTEX-11NV4 -0.37  0.11 -0.42 -0.61         4      0.37
 5 A2ML1 GTEX-11TT1  0.3  -1.11  0.59 -0.12         4      0.3
 6 A2ML1 GTEX-11TUW  0.02 -0.47  0.29 -0.66         4      0.02
 7 A2ML1 GTEX-11ZUS -1.07 -0.41  0.67  0.06         4      1.07
 8 A2ML1 GTEX-11ZVC -0.27 -0.51  0.13 -0.75         4      0.27
 9 A2ML1 GTEX-1212Z -0.3   0.53  0.1  -0.48         4      0.3
10 A2ML1 GTEX-12696 -0.11  0.24  0.96  0.72         4      0.11
# … with 389,912 more rows
```

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

mutate() can create multiple new columns at once

```
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
```

- If you save the result into a column that already exists, it will be overwritten

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).

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: 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.

Piping

Why pipe?

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

```
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

- 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

```
data.frame(name = c("Petunia", "Rose", "Daisy", "Marigold", "Arabidopsis"),
           age = c(10,54,21,99,96)) %>%
    filter(age > 30)
         name age
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

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

Exercise: summarize and plot

Recreate this plot.

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

Data Transformation with dplyr : : CHEAT SHEET

dplyr functions work with pipes and expect **tidy data**. In tidy data:

Each **variable** is in its own **column**

&

Each **observation**, or **case**, is in its own **row**

pipes

x %>% f(y) becomes **f(x, y)**

Summarise Cases

These apply **summary functions** to columns to create a new table of summary statistics. Summary functions take vectors as input and return one value (see back).

summary function

summarise(.data, …)
Compute table of summaries.
summarise(mtcars, avg = mean(mpg))

count(x, ..., wt = NULL, sort = FALSE)
Count number of rows in each group defined by the variables in … Also **tally**().
count(iris, Species)

VARIATIONS

summarise_all() - Apply funs to every column.
summarise_at() - Apply funs to specific columns.
summarise_if() - Apply funs to all cols of one type.

Group Cases

Use **group_by()** to create a "grouped" copy of a table. dplyr functions will manipulate each "group" separately and then combine the results.

mtcars %>%
group_by(cyl) %>%
summarise(avg = mean(mpg))

group_by(.data, ..., add = FALSE)
Returns copy of table grouped by …
g_iris <- group_by(iris, Species)

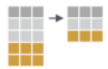
ungroup(x, …)
Returns ungrouped copy of table.
ungroup(g_iris)

Manipulate Cases

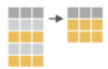
EXTRACT CASES

Row functions return a subset of rows as a new table.

filter(.data, …) Extract rows that meet logical criteria. *filter(iris, Sepal.Length > 7)*



distinct(.data, ..., .keep_all = FALSE) Remove rows with duplicate values.
distinct(iris, Species)



sample_frac(tbl, size = 1, replace = FALSE, weight = NULL, .env = parent.frame()) Randomly select fraction of rows.
sample_frac(iris, 0.5, replace = TRUE)

sample_n(tbl, size, replace = FALSE, weight = NULL, .env = parent.frame()) Randomly select size rows. *sample_n(iris, 10, replace = TRUE)*

slice(.data, …) Select rows by position.
slice(iris, 10:15)

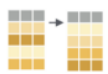
top_n(x, n, wt) Select and order top n entries (by group if grouped data). *top_n(iris, 5, Sepal.Width)*

Logical and boolean operators to use with filter()

<	<=	is.na()	%in%	|	xor()
>	>=	!is.na()	!	&	

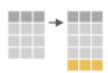
See **?base::logic** and **?Comparison** for help.

ARRANGE CASES



arrange(.data, …) Order rows by values of a column or columns (low to high), use with **desc()** to order from high to low.
arrange(mtcars, mpg)
arrange(mtcars, desc(mpg))

ADD CASES



add_row(.data, ..., .before = NULL, .after = NULL) Add one or more rows to a table.
add_row(faithful, eruptions = 1, waiting = 1)

Manipulate Variables

EXTRACT VARIABLES

Column functions return a set of columns as a new vector or table.

pull(.data, var = -1) Extract column values as a vector. Choose by name or index.
pull(iris, Sepal.Length)

select(.data, …)
Extract columns as a table. Also **select_if()**.
select(iris, Sepal.Length, Species)

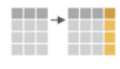
Use these helpers with select (),
e.g. select(iris, starts_with("Sepal"))

contains(match)
ends_with(match)
matches(match)
num_range(prefix, range)
one_of(…)
starts_with(match)
:, e.g. mpg:cyl
-, e.g, -Species

MAKE NEW VARIABLES

These apply **vectorized functions** to columns. Vectorized funs take vectors as input and return vectors of the same length as output (see back).

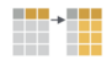
vectorized function



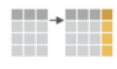
mutate(.data, …)
Compute new column(s).
mutate(mtcars, gpm = 1/mpg)

transmute(.data, …)
Compute new column(s), drop others.
transmute(mtcars, gpm = 1/mpg)

mutate_all(.tbl, .funs, …) Apply funs to every column. Use with **funs()**. Also **mutate_if()**.
mutate_all(faithful, funs(log(.), log2(.)))
mutate_if(iris, is.numeric, funs(log(.)))



mutate_at(.tbl, .cols, .funs, …) Apply funs to specific columns. Use with **funs()**, **vars()** and the helper functions for select().
mutate_at(iris, vars(-Species), funs(log(.)))



add_column(.data, ..., .before = NULL, .after = NULL) Add new column(s). Also **add_count()**, **add_tally()**. *add_column(mtcars, new = 1:32)*

rename(.data, …) Rename columns.
rename(iris, Length = Sepal.Length)