**Learning Goals**

- Use base R logical indexing to filter rows and select specific columns from a data frame.
- Use the pipe operator (`|>`) to chain multiple steps and interpret a pipeline in plain language.
- Use `filter()`, `arrange()`, and `select()` to subset and order data using readable code.
- Use `rename()`, `mutate()`, and `transmute()` to rename columns and create new variables.

## Key Definitions / Functions

- `|>`:
- `filter()`:
- `arrange()`:
- `select()`:
- `mutate()`:
- `rename()`:

## Practice Problems

For each task below, write the R code you would use *and* briefly describe what you expect the output to look like.

1. Using the built-in `iris` dataset, display only the observations where `Species == "setosa"` and `Sepal.Length > 5`. Then select only the columns `Species`, `Sepal.Length`, and `Sepal.Width`.

2. Using the `iris` dataset, sort the dataset by `Species` first, and within each species sort it by `Petal.Length` from largest to smallest.

3. Using the `iris` dataset, create a new variable called `petal_size` that is `"large"` if `Petal.Length >= 4.5` and `"small"` otherwise. Display the first 6 rows after doing this.

4. Using the `iris` dataset, rename `Sepal.Length` to `SL` and `Petal.Length` to `PL`. Then create a new variable called `length_ratio = SL/PL`. Finally, display only the columns `SL`, `PL`, `length_ratio`, and `Species`.