Pipelines and workflows

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BIOF 339

BIOF 339: Practical R

Pipes in the tidyverse

Pipes

We've seen two types of pipes in R.

The pipe operator %>% from the **magrittr** package

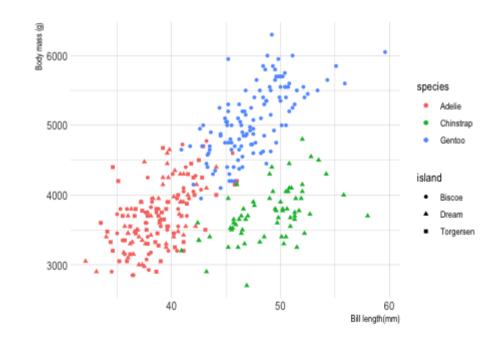
library(tidyverse) # includes magrittr library(palmerpenguins)

The + symbol used as a pipe-like operator in ggplot2

Pipes

You can combine the two pipes into a workflow to create a visualization

The **ggplot** pipe has to be at the end of the workflow. Also note, we're not adding the data argument to **ggplot** since it is tidyverse-compatible and slots the end of the previous pipe into the **data** argument



Rowwise operations

The **dplyr** package allows you to do rowwise operations much more easily than before within a pipe using the **rowwise** function. For example

mpg %>%			
select(manufacturer, year,	cty,	hwy)	%>%
rowwise() %>%			
<pre>mutate(avg_mpg = mean(c(hwy</pre>	/, cty	/)))	

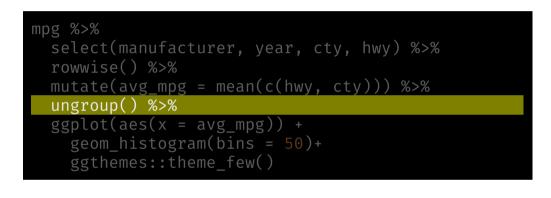
# A tibble: 234	× 5			
<pre># Rowwise:</pre>				
manufacturer	year	cty	hwy	avg_mpg
<chr></chr>	<int></int>	<int></int>	<int></int>	<dbl></dbl>
<mark>1</mark> audi	1999	18	29	23.5
2 audi	1999	21	29	25
3 audi	2008	20	31	25.5
4 audi	2008	21	30	25.5
5 audi	1999	16	26	21
<mark>6</mark> audi	1999	18	26	22
7 audi	2008	18	27	22.5
<mark>8</mark> audi	1999	18	26	22
9 audi	1999	16	25	20.5
10 audi	2008	20	28	24
# with 224 mon	re rows	5		

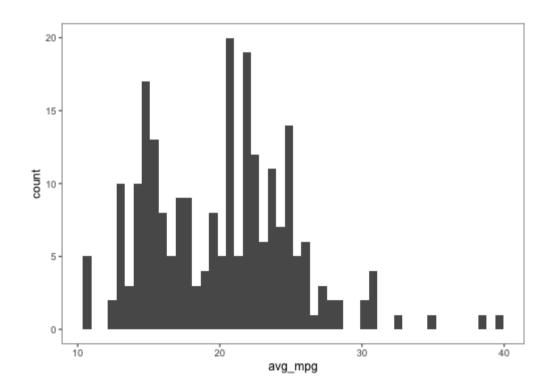
The **rowwise** function creates groups, one per row, and allows operations to occur along rows and across columns.

What would the result be if you omitted the **rowwise** function in the pipe?

Rowwise operations

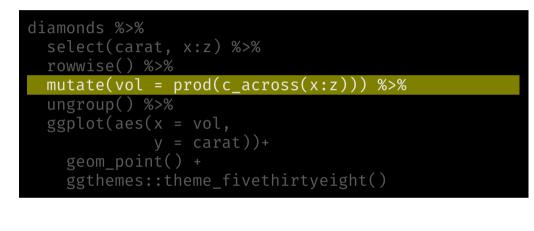
If you want to continue the pipe to incorporate the more traditonal column-wise operations, you need to use **ungroup** before proceeding

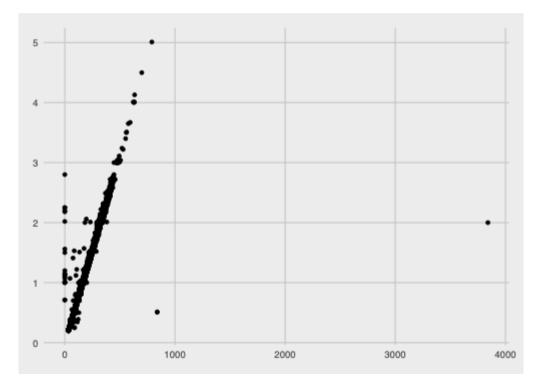




Rowwise operations

There are some nice shortcuts, in line with the **select** function, even with rowwise operations





Much more details about the possibilities of the **rowwise** function are available here

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Prepping data for modeling

The idea of the recipes package is to define a recipe or blueprint that can be used to sequentially define the encodings and preprocessing of the data (i.e. "feature engineering")

This is done in the context of supervised modeling, e.g. regression, decision trees

The idea is to define the dependent and independent variables, and then creating a pipeline to modify the independent variables through various statistical procedures.

We'll start with the credit data in the modeldata package

library(recipes)
library(modeldata)
data("credit_data")

glimpse(credit_data)

Rows: 4,454

Columns: 14

<fct> good, good, bad, good, good, good, good, good, bad, go... \$ Status \$ Seniority <int> 9, 17, 10, 0, 0, 1, 29, 9, 0, 0, 6, 7, 8, 19, 0, 0, 15, 33, ... \$ Home <fct> rent, rent, owner, rent, rent, owner, owner, parents, owner,... \$ Time <int> 60, 60, 36, 60, 36, 60, 60, 12, 60, 48, 48, 36, 60, 36, 18, ... \$ Age <int> 30, 58, 46, 24, 26, 36, 44, 27, 32, 41, 34, 29, 30, 37, 21, ... \$ Marital <fct> married, widow, married, single, single, married, married, s... \$ Records \$ Job <fct> freelance, fixed, freelance, fixed, fixed, fixed, fix... \$ Expenses <int> 73, 48, 90, 63, 46, 75, 75, 35, 90, 90, 60, 60, 75, 75, 35, ... \$ Income <int> 129, 131, 200, 182, 107, 214, 125, 80, 107, 80, 125, 121, 19... \$ Assets <int> 0, 0, 3000, 2500, 0, 3500, 10000, 0, 15000, 0, 4000, 3000, 5... \$ Debt <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 2500, 260, 0, 0, 0, 2000... \$ Amount <int> 800, 1000, 2000, 900, 310, 650, 1600, 200, 1200, 1200, 1150,... \$ Price <int> 846, 1658, 2985, 1325, 910, 1645, 1800, 1093, 1957, 1468, 15...

Create an initial recipe based on the model that will be fit

rec <- recipe(Status ~ Seniority + Time + Age + Records, data = credit_data)</pre>

rec

Data Recipe	9		
Inputs:			
role	#variables		
outcome	1		
predictor	4		
predictor	4		

summary(rec, original=TRUE)

# A tibble:	5 × 4			
variable	type	role	source	
<chr></chr>	<chr></chr>	<chr></chr>	<chr></chr>	
1 Seniority	numeric	predictor	original	
2 Time				
3 Age		predictor		
4 Records		predictor		
5 Status	nominal	outcome	original	

Add a step to convert nominal variables into dummies

(dummied <- rec %>% step_dummy(Records))
Data Recipe
Inputs:
role #variables
outcome 1
predictor 4
Operations:
Dummy variables from Records

Then apply it to your data

<pre>dummied <- prep(dummied, training = credit_data) with_dummy <- bake(dummied, new_data = credit_data) head(with_dummy)</pre>					
#	A tibble:	6 × 5			
			Age	Status	Records_yes
	<int></int>	<int></int>	<int></int>	<fct></fct>	<dbl></dbl>
1	9	60	30	good	Θ
2	17	60	58	good	Θ
3	10		46	bad	1
4	Θ	60	24	good	Θ
5	Θ	36	26	good	Θ
6	1	60	36	good	Θ

The **recipes** package provides a rich variety of data steps that can be used to prepare a data set.

```
iris_recipe <- iris %>%
  recipe(Species ~ .) %>%
  step_corr(all_predictors()) %>%
  step_center(all_predictors(), -all_outcomes()) %>%
  step_scale(all_predictors(), -all_outcomes()) %>%
  prep()
iris_recipe
```

Data Recipe

Inputs:

```
role #variables
outcome 1
predictor 4
```

Training data contained 150 data points and no missing data.

Operations:

Correlation filter removed Petal.Length [trained] Centering for Sepal.Length, Sepal.Width, Petal.Width [trained] Scaling for Sepal.Length, Sepal.Width, Petal.Width [trained]

This recipe can then be applied to the same or a different dataset

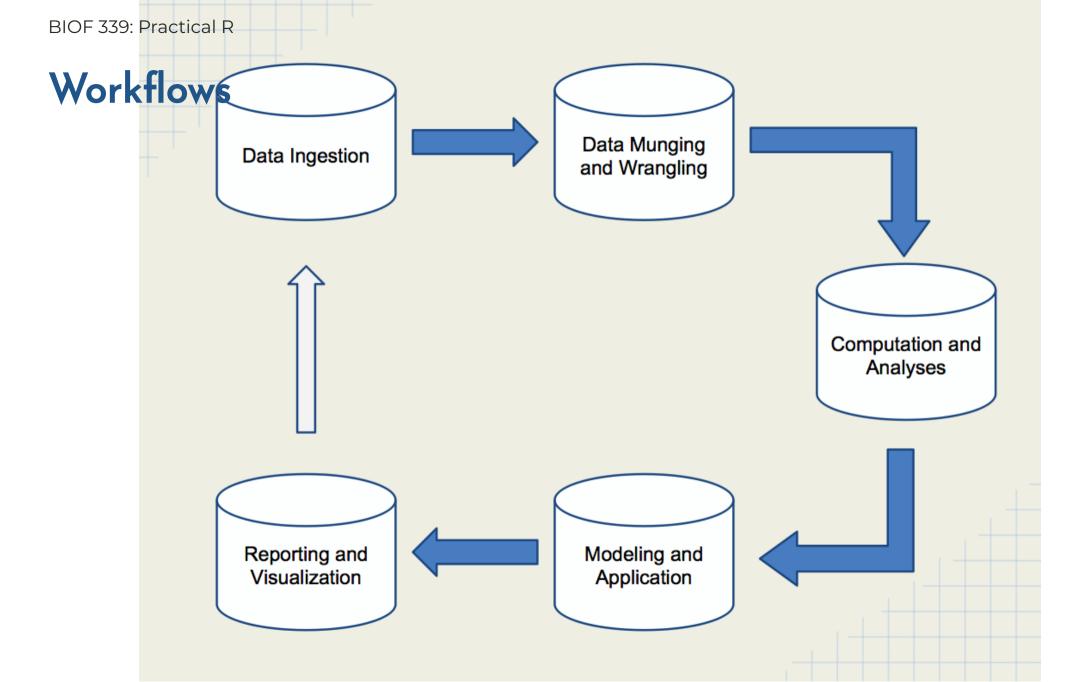
iris1 <- bake(iris_recipe, iris)
glimpse(iris1)</pre>

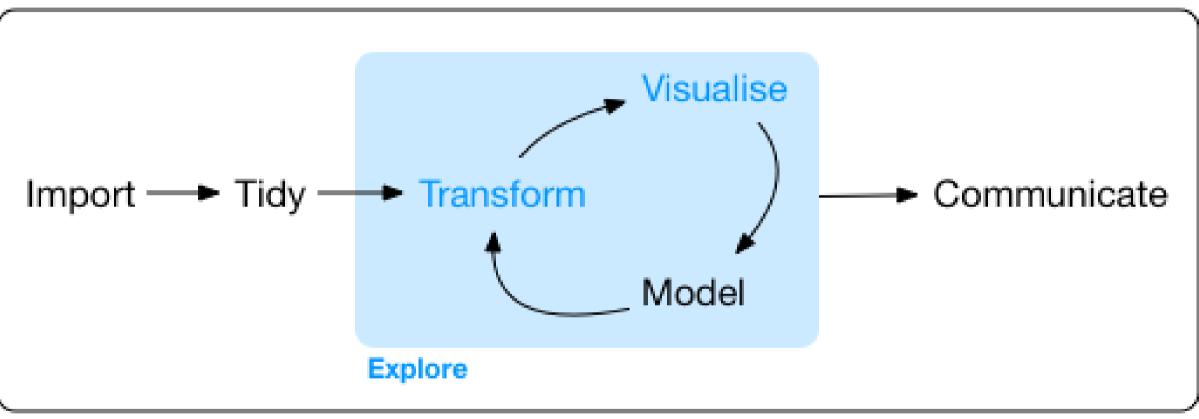
Rows: 150 Columns: 4 \$ Sepal.Length <dbl> -0.89767388, -1.13920048, -1.38072709, -1.50149039, -1.01... \$ Sepal.Width <dbl> 1.01560199, -0.13153881, 0.32731751, 0.09788935, 1.245030... \$ Petal.Width <dbl> -1.3110521, -1.3110521, -1.3110521, -1.311052... \$ Species <fct> setosa, setosa, setosa, setosa, setosa, setosa, setosa, setosa, s...

You can go into more details at tidymodels.org, with a nice introduction here

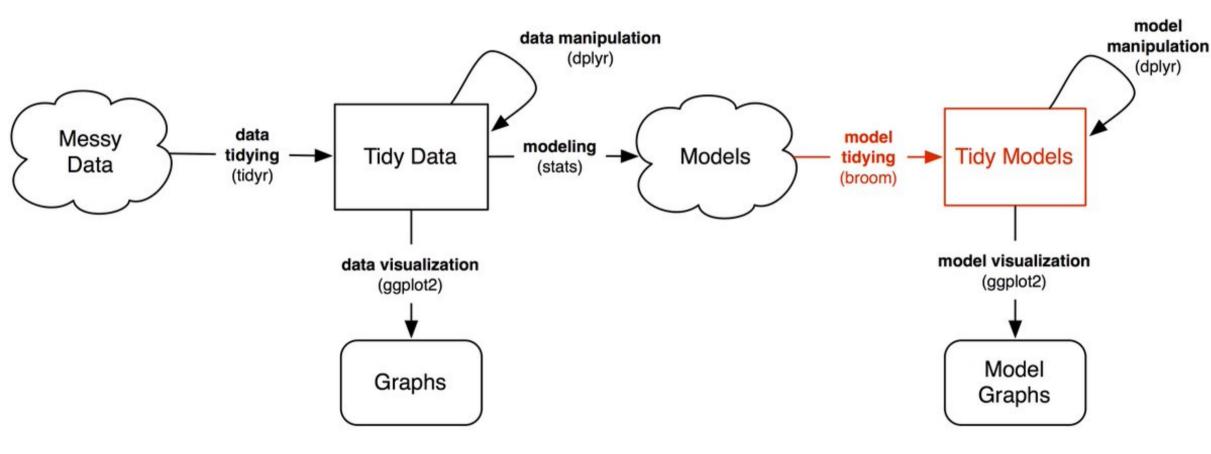
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Workflows





Program



- Create one script file for each node in your workflow
- Save intermediate data or objects using saveRDS so that
 - they can be imported quickly by the next step
 - Each link in the chain can be checked and verified
- You can summarize your entire workflow within one script:

source('01-ingest.R')
source('02-munge.R')
source('03-exploreviz.R')
source('04-eda.R')
source('05-models.R')
source('06-results.R')

A personal story

I wrote a paper using R Markdown with a reasonable pipeline for data analyses, modeling and visualization

Output to Word for submission to a journal

Three months later, reviews came in asking for using updated data

Changed the data at the beginning of my workflow, ran the workflow, and had revised manuscript in 10 minutes.

Quickest turnaround ever!!

Some ideas (*Efficient Programming* by Gillespie and Lovelace)

- 1. Start without writing code but with a clear mind and perhaps a pen and paper. This will ensure you keep your objectives at the forefront of your mind, without getting lost in the technology.
- 2. Make a plan. The size and nature will depend on the project but timelines, resources and 'chunking' the work will make you more effective when you start.
- 3. Select the packages you will use for implementing the plan early. Minutes spent researching and selecting from the available options could save hours in the future.
- 4. Document your work at every stage; work can only be effective if it's communicated clearly and code can only be efficiently understood if it's commented.
- 5. Make your entire workflow as reproducible as possible. knitr can help with this in the phase of documentation.