toolkit for the modern statistician

Solution bit.ly/modern-toolkit

mine çetinkaya-rundel









transformation and tidying with tidyverse



tidyverse

opinionated collection of R packages designed for data science

library(tidyverse)

- ggplot2: data visualization
- **dplyr**: data wrangling
- tidyr: data tidying
- readr: data reading/writing
- forcats: working with factors
- **stringr**: working with strings
- tibble: modern data frames
- **purrr**: functional programming

install.packages(tidyverse) above + a few more



all packages share an underlying design philosophy, grammar, and data structures

• tidy data

data pipelines with %>%

tidy data

each variable must have its own column

tidy data

each variable must have its own column

each observation must have its own row

tidy data

each variable must have its own column

each observation must have its own row
 country
 year
 cases
 population

 Afgarstan
 Image: Stand Stand

Servations

each value must have its own cell

task

I want to find my keys, then start my car, then drive to work, then park my car.

find("keys")

start_car(find("keys"))

drive(start_car(find("keys")), to = "work")

park(drive(start_car(find("keys")), to = "work"))

find("keys")

find("keys") %>% start_car()

find("keys") %>% start_car() %>% drive(to = "work")

find("keys") %>% start_car() %>% park()

drive(to = "work") %>%

ex: ggplot2

library(palmerpenguins) library(tidyverse)

```
ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(aes(color = species, shape = species)) +
  labs(
    title = "Penguin size, Palmer Station LTER",
    subtitle = "Flipper length and body mass
    for Adelie, Chinstrap and Gentoo
    Penguins",
    x = "Flipper length (mm)",
    y = "Body mass (g)",
    color = "Penguin species",
    shape = "Penguin species"
```

visually pleasing defaults!

Penguin species Adelie Chinstrap

Gentoo

```
library(palmerpenguins)
library(tidyverse)
```

```
ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(aes(color = species, shape = species)) +
  labs(
    title = "Penguin size, Palmer Station LTER",
    subtitle = "Flipper length and body mass
    for Adelie, Chinstrap and Gentoo
    Penguins",
    x = "Flipper length (mm)",
    y = "Body mass (g)",
    color = "Penguin species",
    shape = "Penguin species"
```


Chinstrap

Adelie

Penguin species

ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g)) + geom_point(aes(color = species, shape = species), size = 3, alpha = 0.8) + labs(

title = "Penguin size, Palmer Station LTER", subtitle = "Flipper length and body mass for Adelie, Chinstrap and Gentoo Penguins", x = "Flipper length (mm)",

```
y = "Body mass (g)",
```

```
color = "Penguin species",
```

```
shape = "Penguin species"
```

6000 -

Body mass (g)

4000 -

Penguin size, Palmer Station LTER


```
ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(aes(color = species, shape = species), size = 3, alpha = 0.8) +
  labs(
    title = "Penguin size, Palmer Station LTER",
    subtitle = "Flipper length and body mass
    for Adelie, Chinstrap and Gentoo
    Penguins",
    x = "Flipper length (mm)",
    y = "Body mass (g)",
    color = "Penguin species",
    shape = "Penguin species"
    +
                                        6000 -
  scale_color_manual(
    values = c("darkorange",
                "purple",
                                     Body mass (g)
               "cyan4"))
                                        4000 -
```

3000 -

Penguin size, Palmer Station LTER


```
ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(aes(color = species, shape = species), size = 3, alpha = 0.8) +
  labs(
    title = "Penguin size, Palmer Station LTER",
    subtitle = "Flipper length and body mass
    for Adelie, Chinstrap and Gentoo
    Penguins",
    x = "Flipper length (mm)",
    y = "Body mass (g)",
    color = "Penguin species",
    shape = "Penguin species"
  ) +
                                        6000
  scale_color_manual(
    values = c("darkorange",
                "purple",
                                     Body mass (g)
               "cyan4")) +
  theme_minimal()
```

4000

3000

Penguin size, Palmer Station LTER


```
ggplot(data = penguins, aes(x = flipper_length_mm, y = body_mass_g)) +
  geom_point(aes(color = species, shape = species), size = 3, alpha = 0.8) +
  labs(
    title = "Penguin size, Palmer Station LTER",
    subtitle = "Flipper length and body mass
    for Adelie, Chinstrap and Gentoo
    Penguins",
    x = "Flipper length (mm)",
    y = "Body mass (g)",
    color = "Penguin species",
    shape = "Penguin species"
  ) +
                                        6000
  scale_color_manual(
    values = c("darkorange",
                "purple",
                                      (j) 5000
               "cyan4")) +
                                     ) Body mass (
  theme_minimal() +
  theme(
    legend.position = c(0.2, 0.7),
    legend.background =
      element_rect(
        fill = "white",
                                        3000
        color = NA
```

Penguin size, Palmer Station LTER

ex: tidyr

experiment_data

- #>
- #> #> 1 #> 2 #> 3 #> 4
- #> 5 #> б
- # #> #> р #> #> 1 #> 2 #> 3 #> 4
- 5 #> 6
- #>

#> # A tibble: 6 x 5 patient group bp_1 bp_3 bp_2 <dbl> <chr> <chr> <chr> <chr> 120/80 135/93 125/90 1 treatment 2 control 172/105 171/82 161/117 3 treatment 140/89 133/92 121/86 4 control 151/92 112/109 150/83 5 treatment 175/93 173/90 120/118 180/85 6 control 173/94 174/106

A tibble: 18×5

#>		patient	group	measurement	systolic	diast
#>		<dbl></dbl>	<chr></chr>	<chr></chr>	<int></int>	<
#>	1	1	treatment	1	120	
#>	2	1	treatment	2	135	
#>	3	1	treatment	3	125	
#>	4	2	control	1	172	
#>	5	2	control	2	171	
#>	б	2	control	3	161	
#>	#	with 1	12 more rov	NS		

experiment_d	ata %>%		
pivot_long	er(
cols = c	ontains(<mark>"bp</mark> "	·) ,	
names_to	= "measurem	nent",	
names_pr	efix = "bp_"	· /	
values_t	o = "value"		
)			
#> # A tibbl	e: 18 x 4		
<pre>#> patien</pre>	t group	measurement	value
#> <dbl< td=""><td>> <chr></chr></td><td><chr></chr></td><td><chr></chr></td></dbl<>	> <chr></chr>	<chr></chr>	<chr></chr>
#> 1	1 treatment	1	120/80
#> 2	1 treatment	2	135/93
#> 3	1 treatment	3	125/90
#> 4	2 control	1	172/10
#> 5	2 control	2	171/82
#> 6	2 control	3	161/11
#> # with	12 more rows	ő	

exp	bei	riment_da	ata			
#>	#	A tibble	e: 6 x 5			
#>		patient	group	<i>bp_1</i>	bp_2	bp_3
#>		<dbl></dbl>	<chr></chr>	<chr></chr>	<chr></chr>	<chr></chr>
#>	1	1	treatment	120/80	135/93	125/90
#>	2	2	control	172/105	171/82	161/117
#>	3	3	treatment	140/89	133/92	121/86
#>	4	4	control	151/92	112/109	150/83
#>	5	5	treatment	175/93	173/90	120/118
#>	6	6	control	180/85	173/94	174/106

experiment_data %>% pivot_longer(cols = contains("bp"), names_to = "measurement", names_prefix = "bp_", values_to = "value") %>% separate(value, into = c("systolic", "diastolic"), convert = TRUE) #> # A tibble: 18 x 5 patient group measurement systol #> <dbl> <chr> <dbl> <chr> #> <int #> 1 1 treatment 1 1 1 treatment 2 #> 2 #> 3 1 treatment 3 #> 4 2 control #> 5 2 control 2 #> 6 2 control 3 #> # ... with 12 more rows

#>	# A	tibble	2:	18 x 4		
#>	Z	patient		group	measurement	valu
#>		<dbl></dbl>	>	<chr></chr>	<chr></chr>	<chr< td=""></chr<>
#>	1	- -	1	treatment	1	120/
#>	2	- -	1	treatment	2	135/
#>	3	- -	1	treatment	3	125/
#>	4		2	control	1	172/
#>	5		2	control	2	171/
#>	6		2	control	3	161/
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ic	diastolic
t>	<int></int>
20	80
35	93
25	90
72	105
71	82
61	117

modeling and machine learning with tidymodels

tidymodels

WW

w.rstudio.com

tidymodels

- collection of packages for modeling and machine learning using tidyverse principles
- parsnip: unified interface to models that can be used to try a range of models without getting bogged down in the syntactical minutiae of the underlying packages
- recipes: tidy interface to data preprocessing tools for feature engineering
- rsample: efficient resampling for estimation and model evaluation
- "many models" in a single data frame to avoid environment clutter and easy access with helper functions

a vast tidy ecosystem

work with data pipelines

data cleaning

pretty (complex) tables for PDF output

kableExtra

work with ggplot2 layers

share and communicate with rmarkdown

rmarkdown

- Create computational documents that knit together text, code, results, and figures into polished outputs that are easy to read and share
- reproducible by default
- **bookdown**: and make them into books...
- **xaringan**: and make them into slides...
- **blogdown / distill**: and make them into websites...
- rticles: and make them into manuscripts...

interact with shiny

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per of second any infected persons resulting from a infected person. If R>L, the number of in constant.	l'ected persons will increase. If R<1, the number of in/ected persons will
	rt.live
	covid19-projections.com
	UCLA

version control and collaborate with git and github

xkcd.com/1597

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GitHub

- web hosting for projects version controlled with Git
- Collaboration and project management
- discoverability and publishing (with ghpages)
- where the technical side of the R community lives:
 - Iook for code samples
 - make feature requests
 - contribute to packages

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covid19-	٠r		Packages	
This repo links to	a collection of analyses on and representations o	f COVID19 data in R. Inclusion on the list does	No packages published Publish your first package	
not mean the ana analysis / data m	lysis was verified by me or that I endorse the find ght be out of date, so these should not be viewed	ings. It should also be noted that some of the I, by default, as current findings.		
I'm collecting the	m as they get posted online so that I can come ba	ack to them later to develop educational	Contributors 10	
thoroughly the personally affect	ed by the pandemic.	greatly and it's possible some students are		
Subheadings are	in flux as of now, as more analyses get added I m	ight recategorize them.		
If you have exam	ples to add, please open an issue or make a pull r	equest.	Environments 1	
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	Source Your GitHub Pages site is currently being built from the master branch. Learn more.
	Pranch: master - Image: / (root) - Save
	Select a theme to publish your site with a Jekyll theme. Learn more. Your site is currently using the Minimal theme. Change theme
	Custom domain Custom domains allow you to serve your site from a domain other than mine-cetinkaya-rundel.github.io. Learn more.
	Enforce HTTPS — Required for your site because you are using the default domain (mine-cetinkaya-rundel.github.io) HTTPS provides a layer of encryption that prevents others from sncoping on or tampering with traffic to your site. When HTTPS is enforced, your site will only be served over HTTPS. Learn more.
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0

Contributor Covenant v2.0 adopted

covid19-r

This repo links to a collection of analyses on and representations of COVID19 data in R. Inclusion on the list does not mean the analysis was rerified by me or that I endorse the findings. It should also be noted that ome of the analysis / data might be out of date, so these should not be iewed, by default, as current findings.

'm collecting them as they get posted online so that I can come back to hem later to develop educational examples based on theses data. I should ilso note that one should think about using these as class examples horoughly – the situation is affecting all of us (and our students) greatly and it's possible some students are personally affected by the pandemic.

ubheadings are in flux as of now, as more analyses get added I might ecategorize them.

f you have examples to add, please open an issue or make a pull request.

Blog posts

- Simulating COVID-19 interventions with R
- Analysing COVID-19 (2019-nCoV) outbreak data with R part 1
- Analysing COVID-19 (2019-nCoV) outbreak data with R part 2
- Modelling the effects of public health interventions on COVID-19 transmission using R - part 1
- Modelling the effects of public health interventions on COVID-19 transmission using R - part 2
- COVID-19: The Case of Germany
- Map Visualization of COVID-19 Across the World with R
- COVID-19 cumulative observed case fatality rate over time
- Impact of a country's age breakdown on COVID-19 case fatality rate
- COVID-19 Tracker: Days since N
- COVID-19 Has Become a Partisan Issue (How to Make Dumbbell Plots in R.
- Get Your Epidemiology from Epidemiologists
- Flatten the COVID-19 curve
- A Beginner's Guide to Creating a Corona "Dashboard"
- Infectious diseases and nonlinear differential equations
- COVID-19: The Case of Spain
- Epidemic modelling of COVID-19 in the UK using an SIR model

stay current and connected with #rstats community

rst

ask (good) questions

- make reproducible examples
- make them as minimal as you can
- available in a package
- Interpret take care of checking for reproducibility and formatting for you!

If asking publicly (RStudio Community, Stack Overflow, etc.) try to use data

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-	📰 🔚 🖸 Source on Save 🔍 🥕 🚽 📃	-+ Run
1	library(tidyverse)	
2	library(palmerpenguins)	
3		
4	penguins <- penguins %>%	
5	<pre>mutate(body_mass_kg = body_mass_g / 1000)</pre>	
6		
7	penguins %>%	
8	group_by(species) %>%	
9	<pre>summarise(mean = mean(body_mass_kg)) </pre>	
10		
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RStudio

🔋 Project: (None) 👻

R Studio Community				
NAs when calculating means				
Incategorized	 tags key packages, functions, & topics 			
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2	library(palmerpe	nguins)	
3			
4	penguins <- peng	uins %>%	
5	mutate(body_ma	ss_kg = body_mass_g / 1000)	
6			
7	penguins %>%		
8	group_by(speci	es) %>%	
9	summarise(mean	= mean(body_mass_kg))	
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RStudio

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community

- #rstats on Twitter
- R Weekly newsletter: <u>rweekly.org</u>
- TidyTuesday: <u>github.com/rfordatascience/tidytuesday</u>
- RLadies: <u>rladies.org</u> + community Slack
- groups
- talk to each other (including your students!) about computing

useR groups: <u>r-consortium.org/blog/2019/09/09/r-community-explorer-r-user-</u>

resources

learn

- tidyverse: tidyverse.org/learn
- tidymodels: <u>tidymodels.org/start</u>
- rmarkdown: rmarkdown.rstudio.com/lesson-1.html
- RStudio visual editor: <u>rstudio.github.io/visual-markdown-editing/#</u>
- shiny: <u>shiny.rstudio.com/tutorial</u>
- Git and GitHub: <u>happygitwithr.com</u>
- teach: datasciencebox.org

toolkit for the modern statistician

bit.ly/modern-toolkit

@minebocek mine-cetinkaya-rundel cetinkaya.mine@gmail.com

