R data exploration, wrangling, Github

Dr Simon Dedman

2026-01-28

FIU

University of Southampton

Oceanography with Marine Biology BSc.

2001-2004

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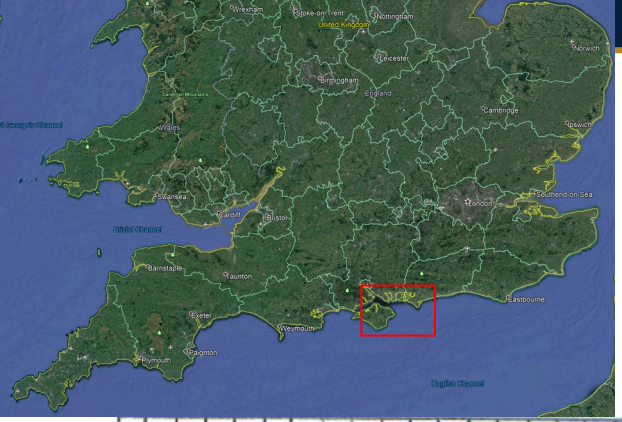
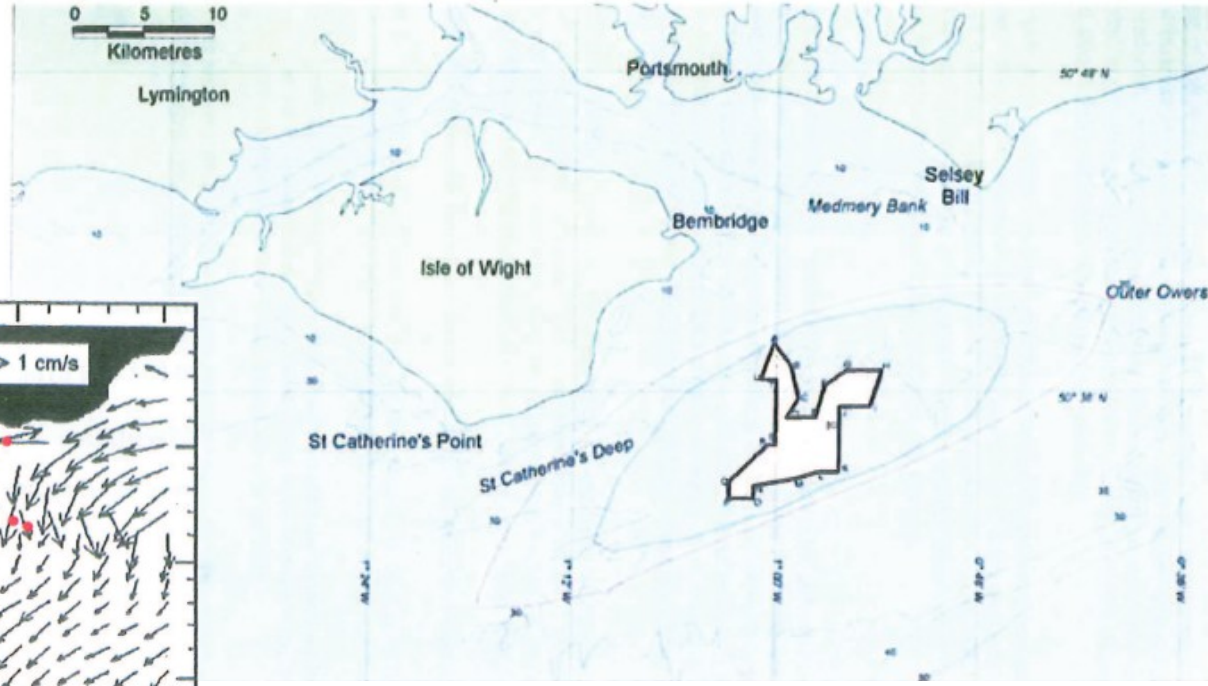
2003 Bachelors thesis

Starry smooth-hound
Mustelus asterias

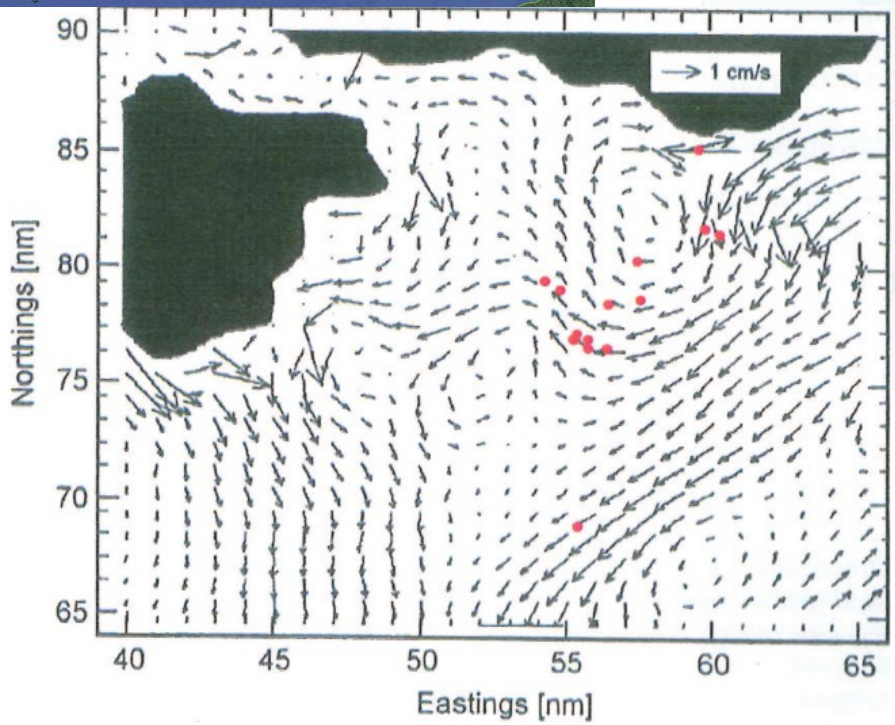
Tope / school shark
Galeorhinus galeus

Elasmobranchs of the East Solent





Gravel extraction area



Currents + study sites

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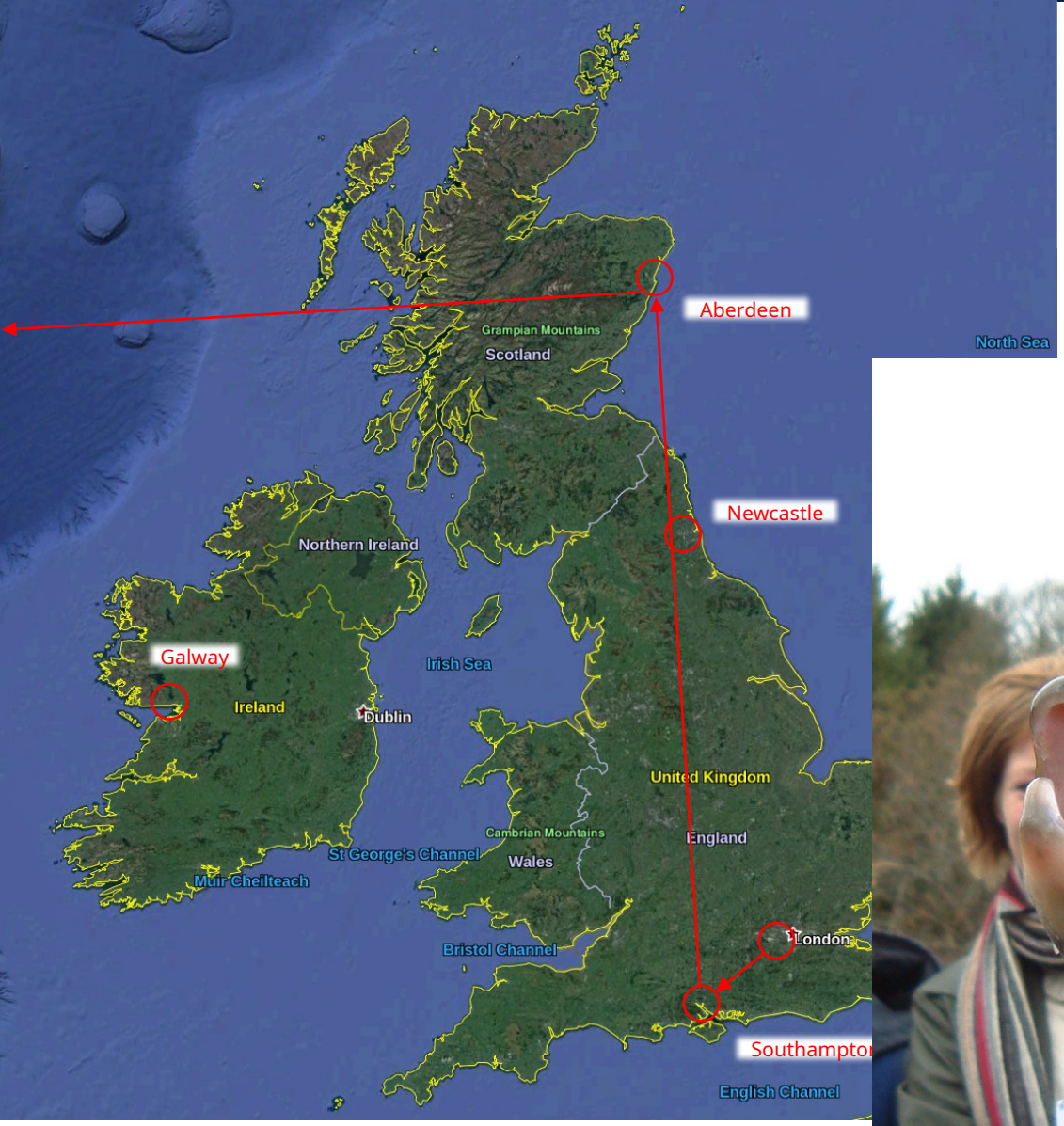
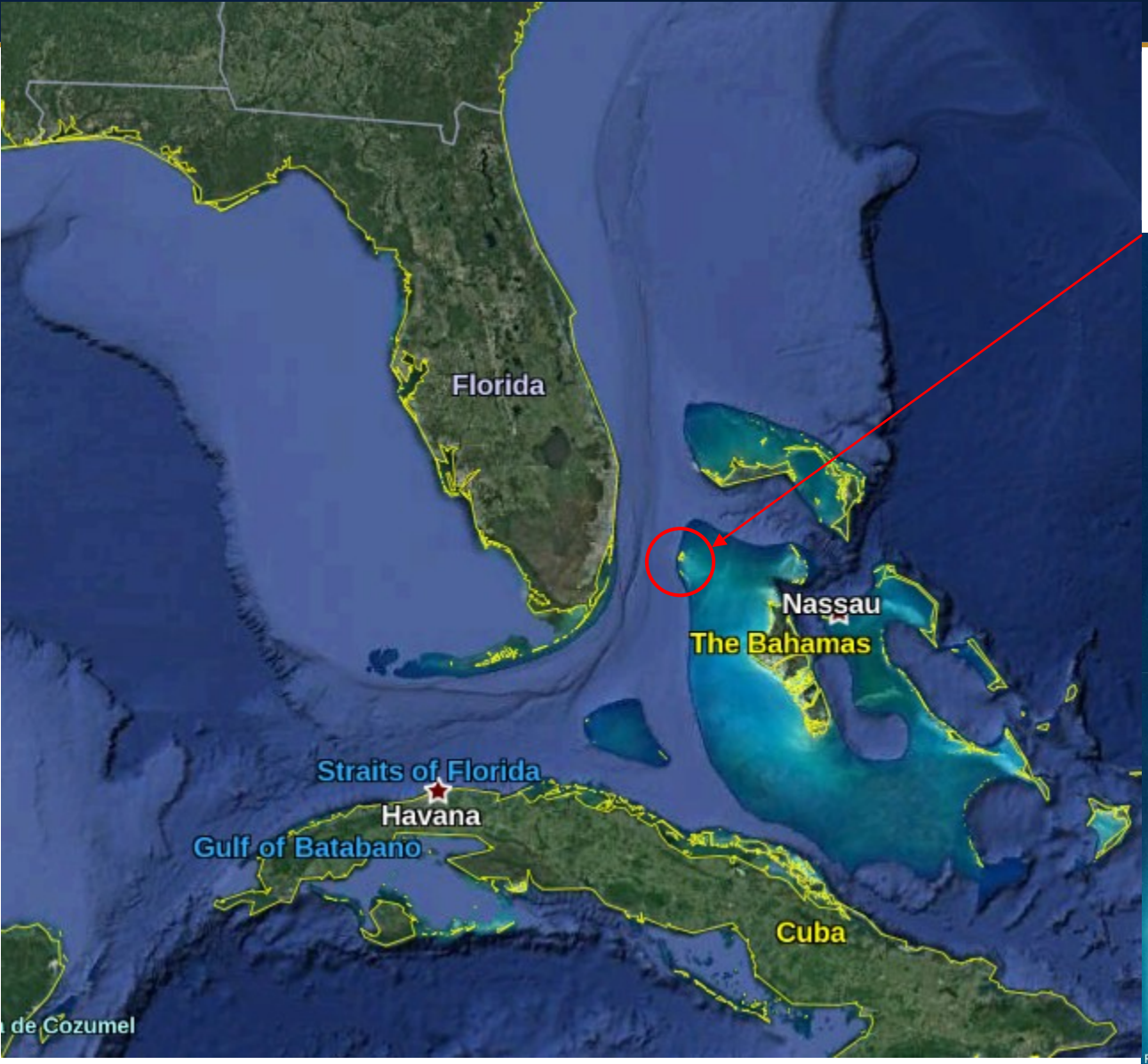
University of Aberdeen

Marine & Fisheries Science MRes.
2005



Bimini, Bahamas, 2006



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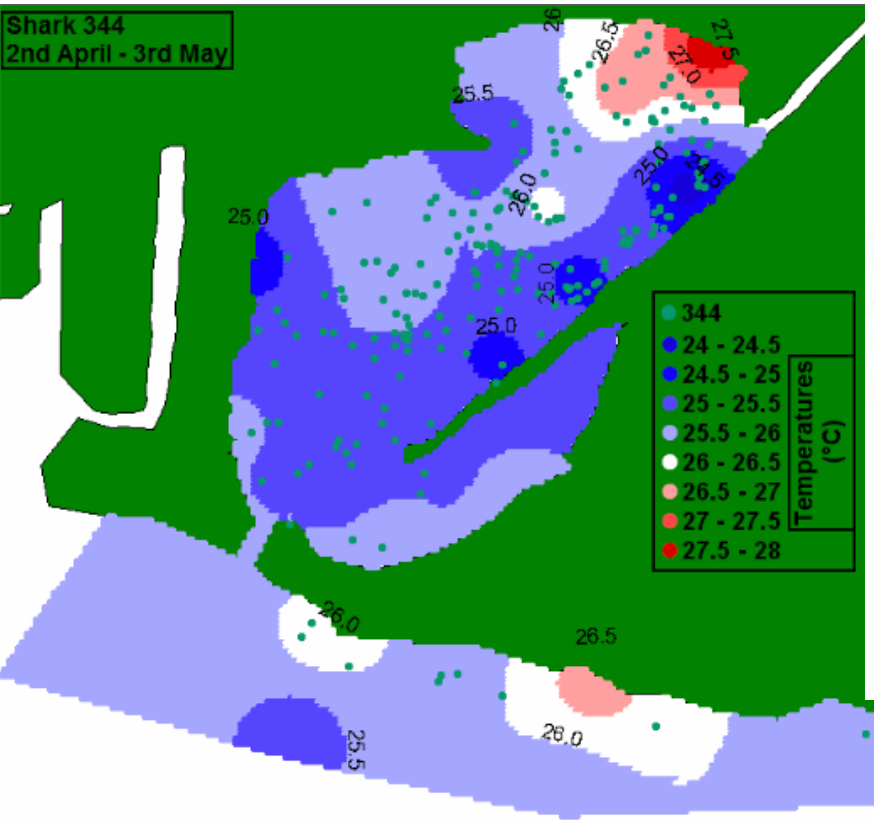
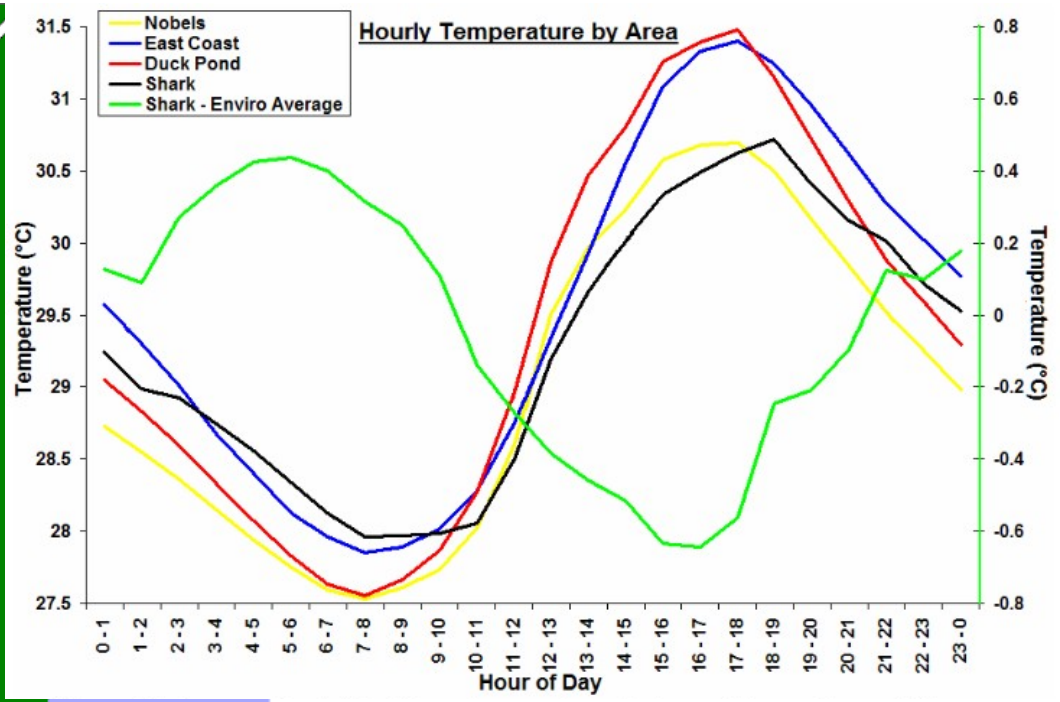
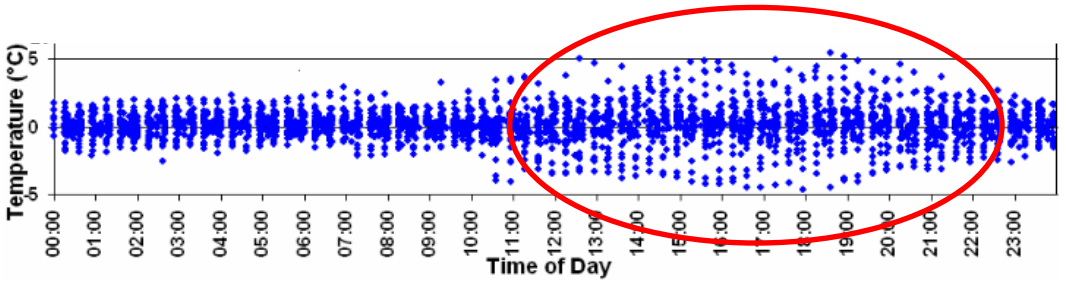


Environmental temperature & shark 344 positions



Temperatures: areas, shark, difference



Shark/environment difference

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- Programme Manager, National Institute for Health Research

Teddington; 2006-2009

- International Quota Manager, Marine Management Organisation

Newcastle/London; 2009-2012

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Galway-Mayo Institute of Technology

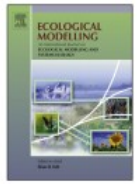
2012-15

Ecological Modelling 312 (2015) 77–90

Contents lists available at ScienceDirect

Ecological Modelling

journal homepage: www.elsevier.com/locate/ecolmodel



Modelling abundance hotspots for data-poor Irish Sea rays

Simon Dedman[a,b,*], Rick Officer[a], Deirdre Brophy[a], Maurice Clarke[b], David G. Reid[b]

[a] Marine and Freshwater Research Centre, Galway-Mayo Institute of Technology, Galway, Ireland
[b] Marine Institute, Rinville, Oranmore, Co., Galway, Ireland

- 4 Irish sea skate/ray species managed as assemblage – not ideal.
- Differentially vulnerable.
- Spatial management recommended but important habitats unknown.
- Boosted Regression Trees had various advantages over Marxan, MaxEnt, GLMs, GAMs – seemed to be the best approach for data-poor species with presence/absence and abundance data.

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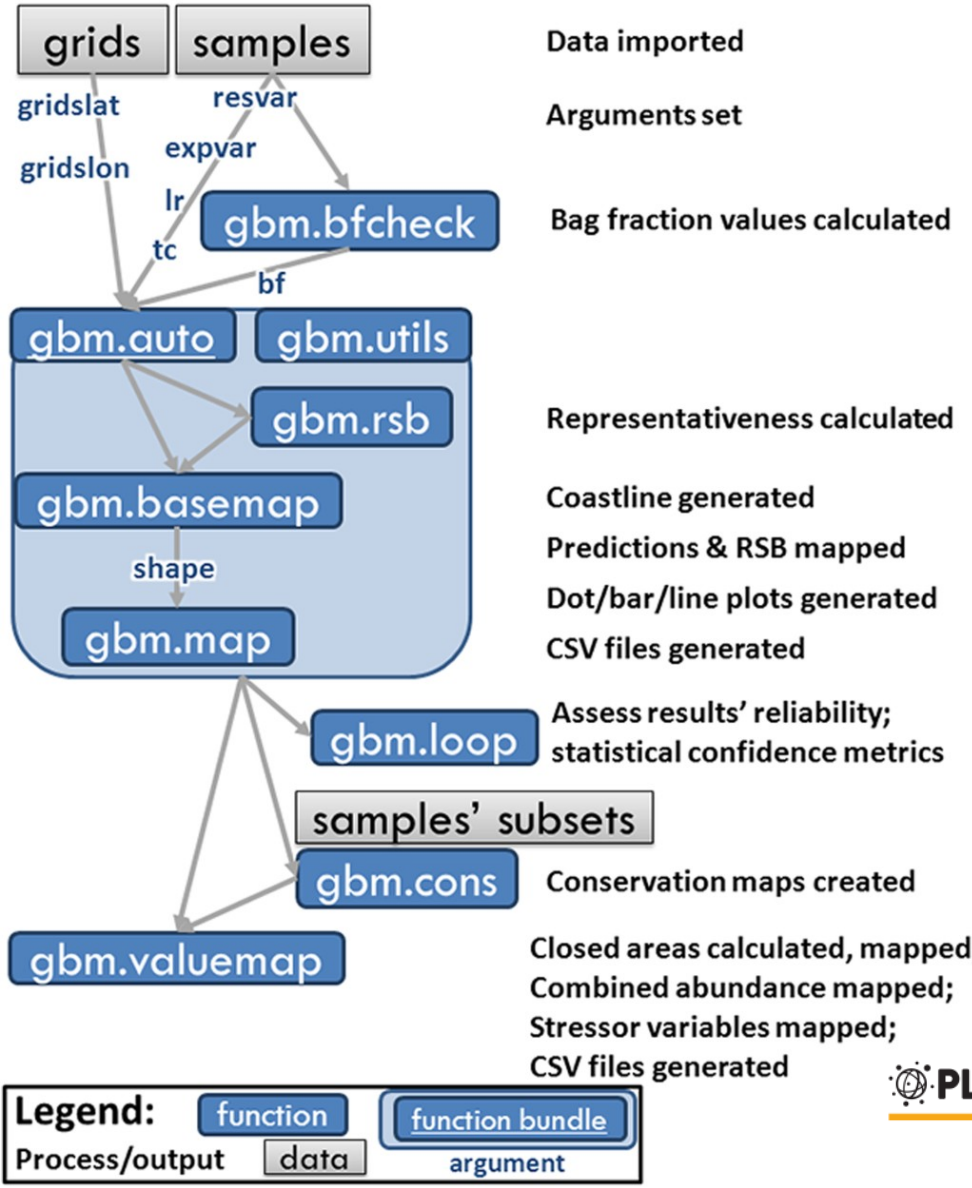


GMIT PhD

2017

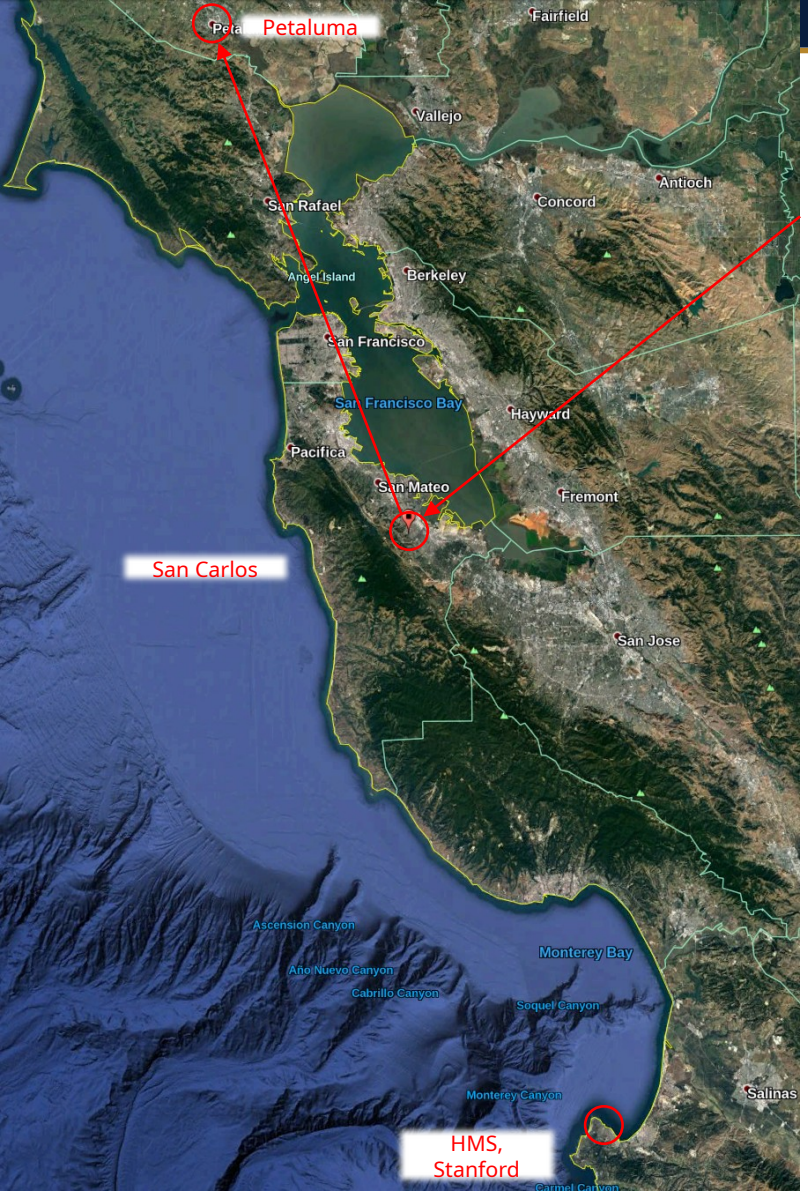
PLOS ONE

RESEARCH ARTICLE

Gbm.auto: A software tool to simplify spatial modelling and Marine Protected Area planning

Simon Dedman[1,2]*, Rick Officer[1], Maurice Clarke[2], David G. Reid[2], Deirdre Brophy[1]

1 Marine and Freshwater Research Centre, Galway-Mayo Institute of Technology, Galway, Ireland, **2** Marine Institute, Rinville, Oranmore, Co. Galway, Ireland



- FishSource (Sustainable Fisheries Partnership, 2017)
- Farallon Institute postdoc (2017-2019)

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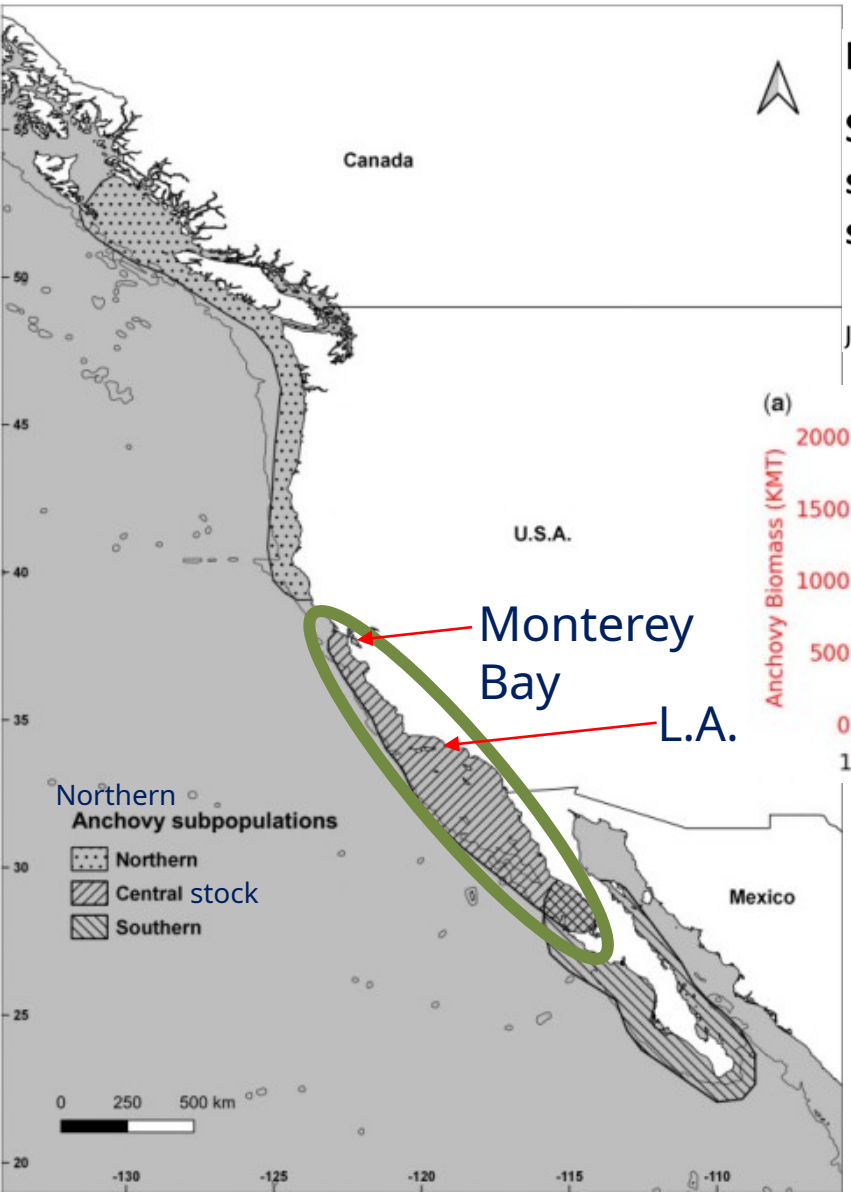
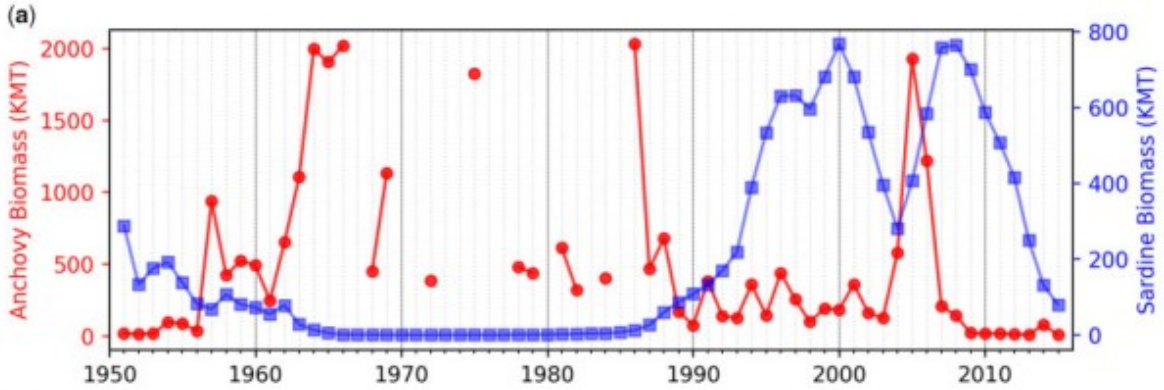


Food for Thought

Sixty-five years of northern anchovy population studies in the southern California Current: a review and suggestion for sensible management

William J. Sydeman *, Simon Dedman, Marisol García-Reyes, Sarah Ann Thompson, Julie A. Thayer, Andrew Bakun, and Alec D. MacCall



CSNA: central stock of northern anchovy

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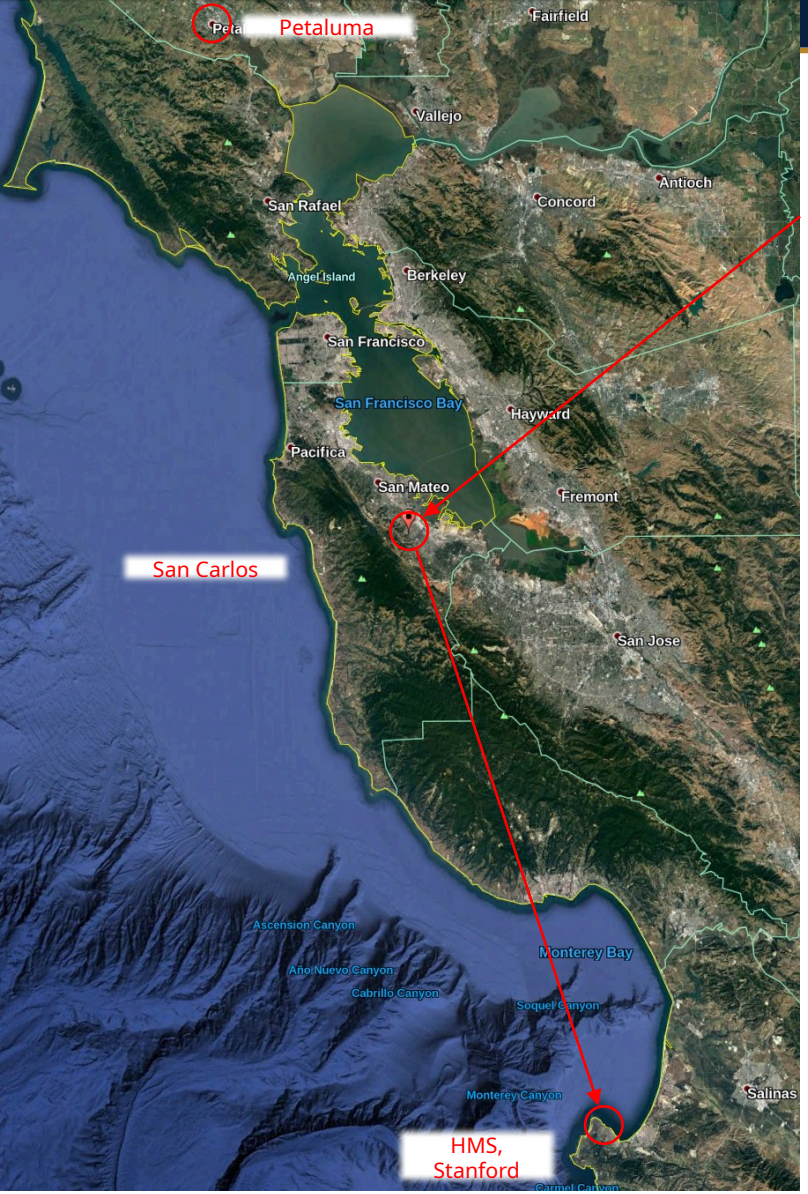

Blocklab, Hopkins Marine Station, Stanford University

Postdoc (2019-2022)

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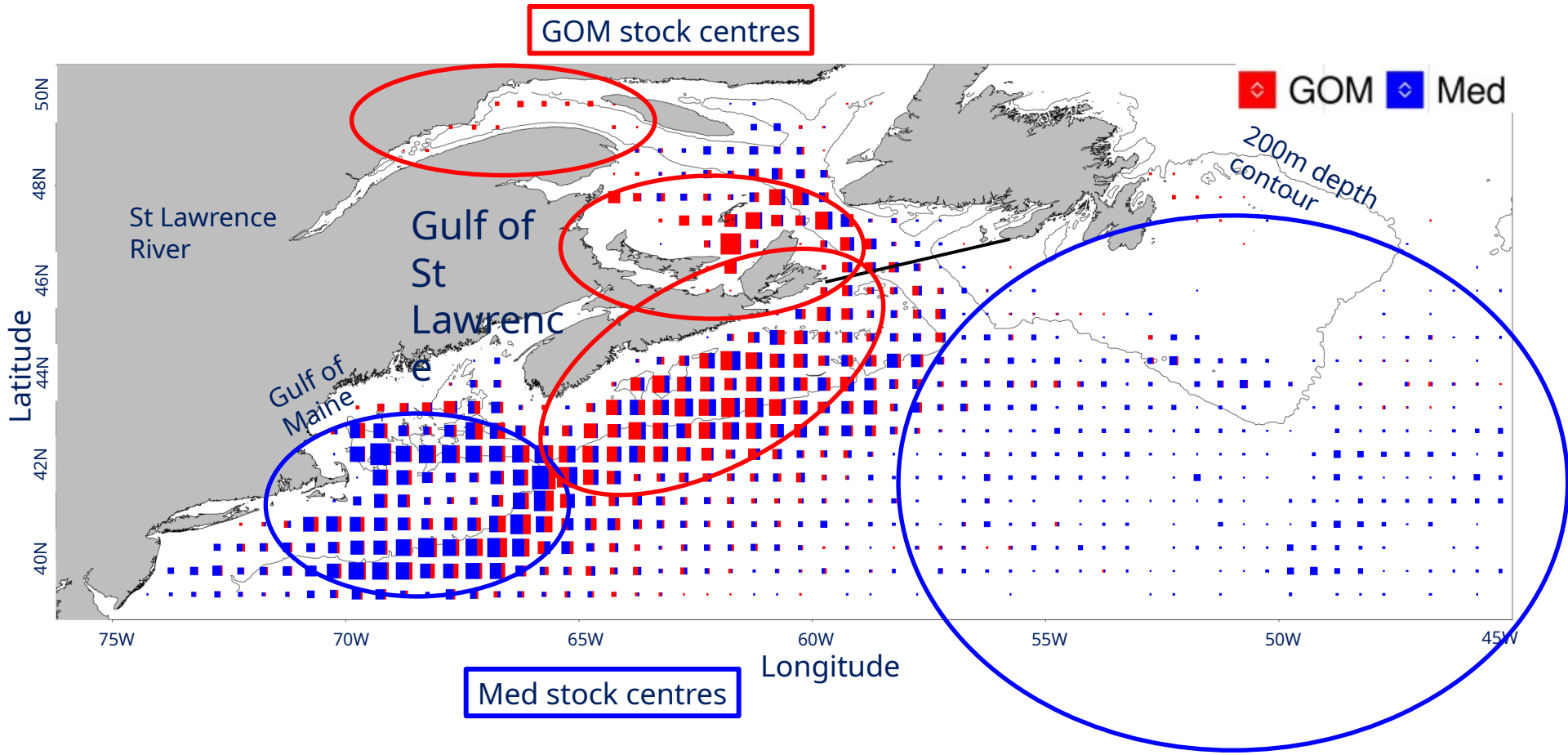

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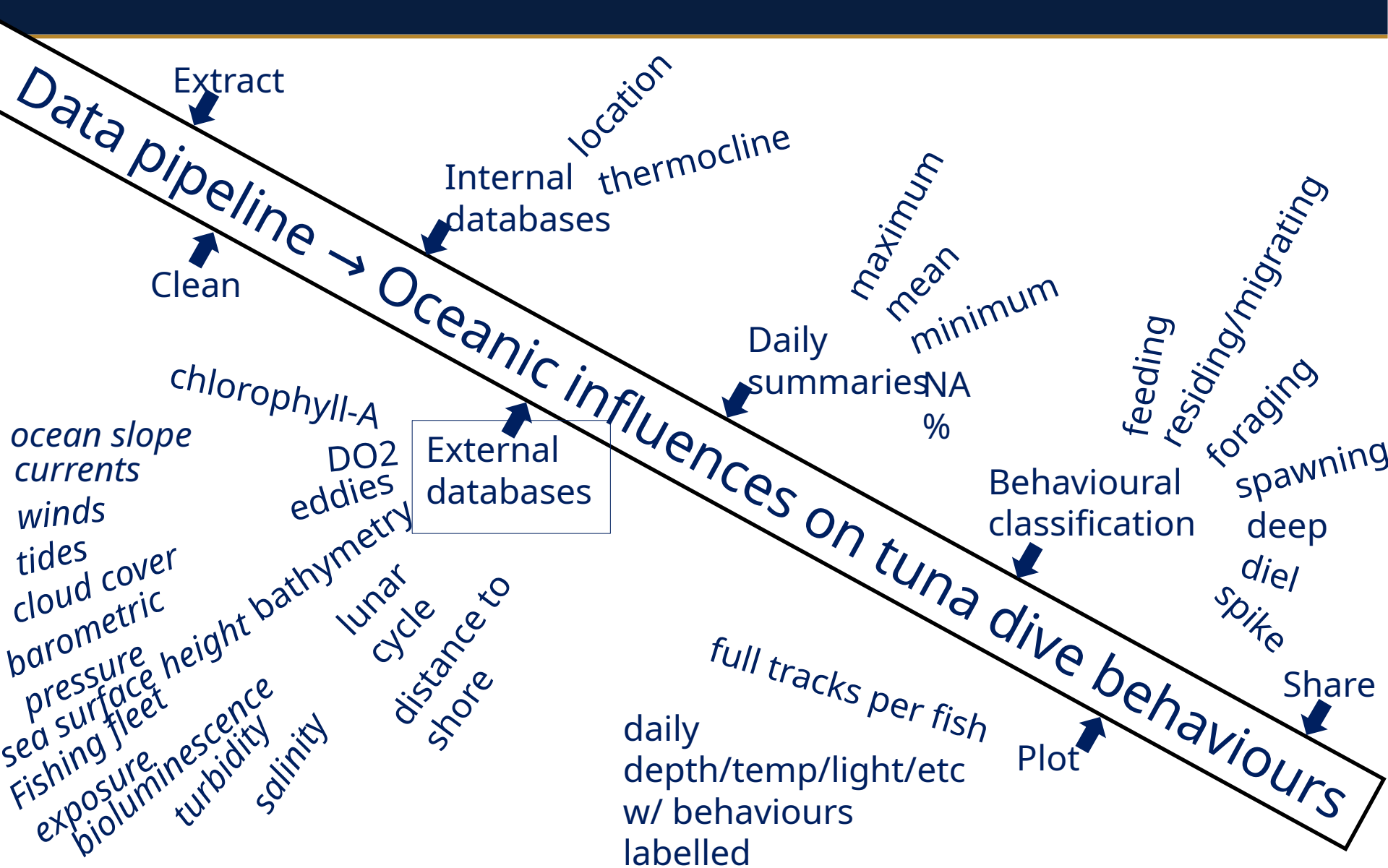

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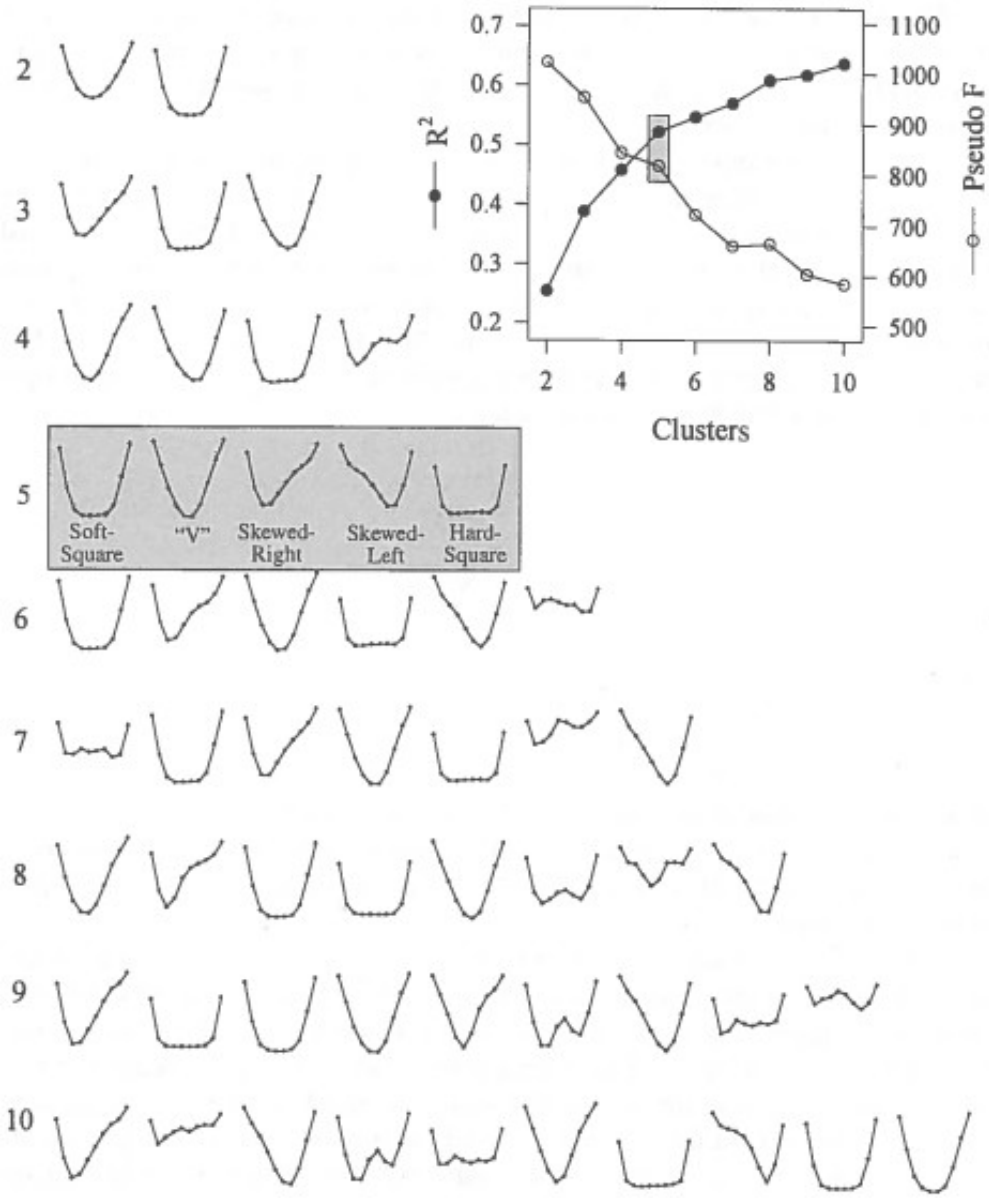
Defining Dive Behaviours

- Manual approach
  - Laborious / slow = small data / ‘proof of concept’
  - Arbitrary / contentious / vague
  - Circular
- Algorithmic approach
  - Very quick = big data
  - Slow/complex to build
  - Universal, citable definitions

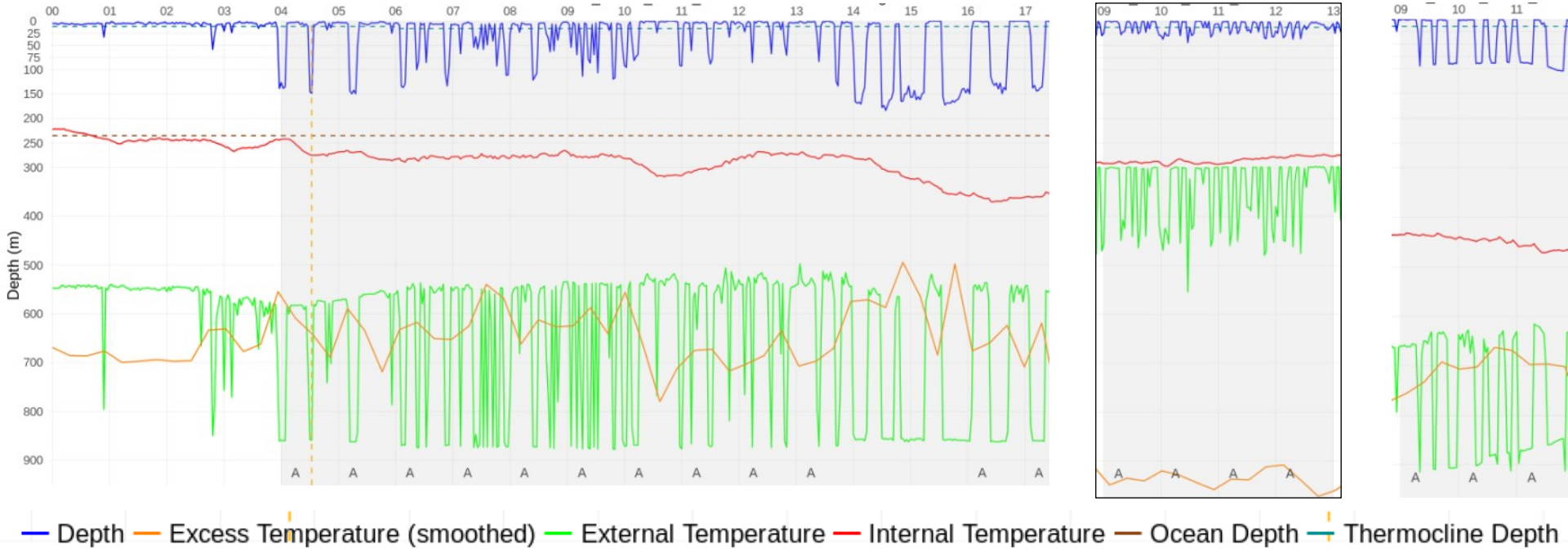


Classification of Dive Profiles: A Comparison of Statistical Clustering Techniques and Unsupervised Artificial Neural Networks

Jason F. Schreer, R. J. O'Hara Hines, and Kit M. Kovacs

Defining Dive Behaviours: Forage A

V aka Bounce A: ~100m depth, steep thermocline



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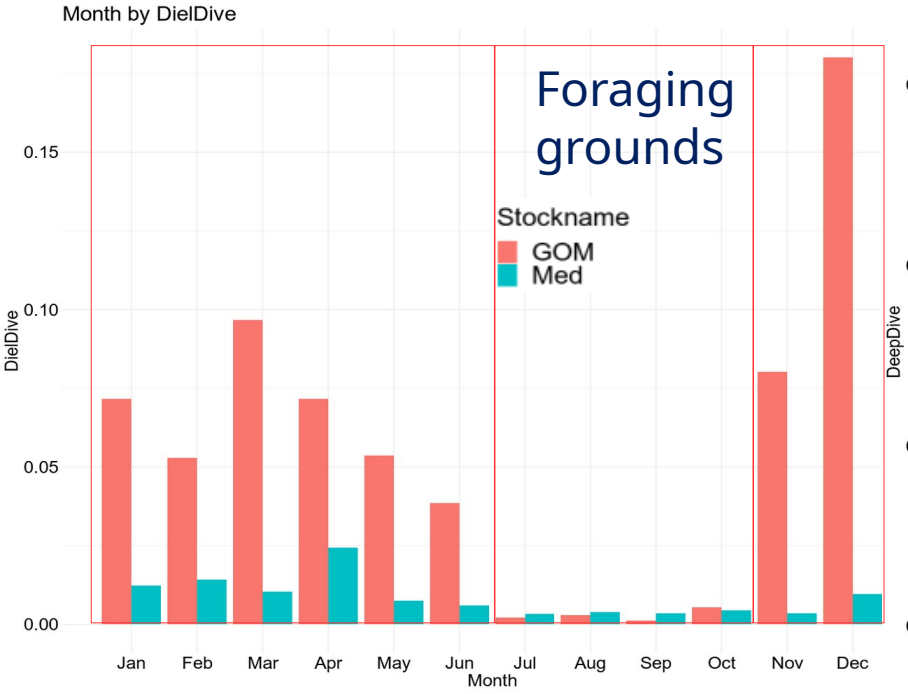

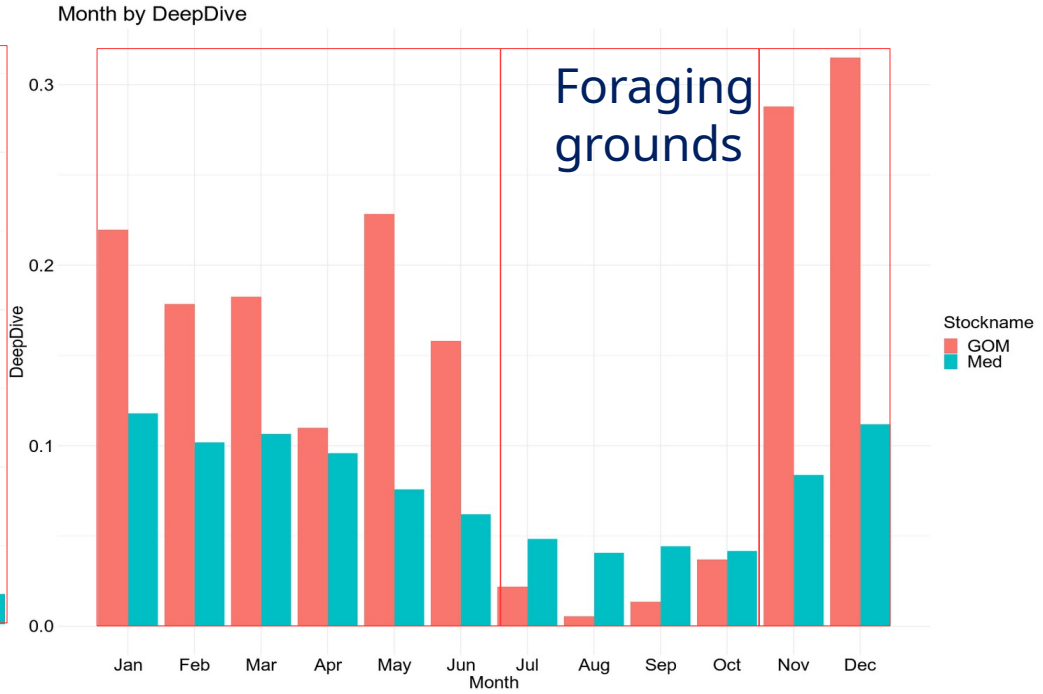

Lots of deep diving.

Hardly any.

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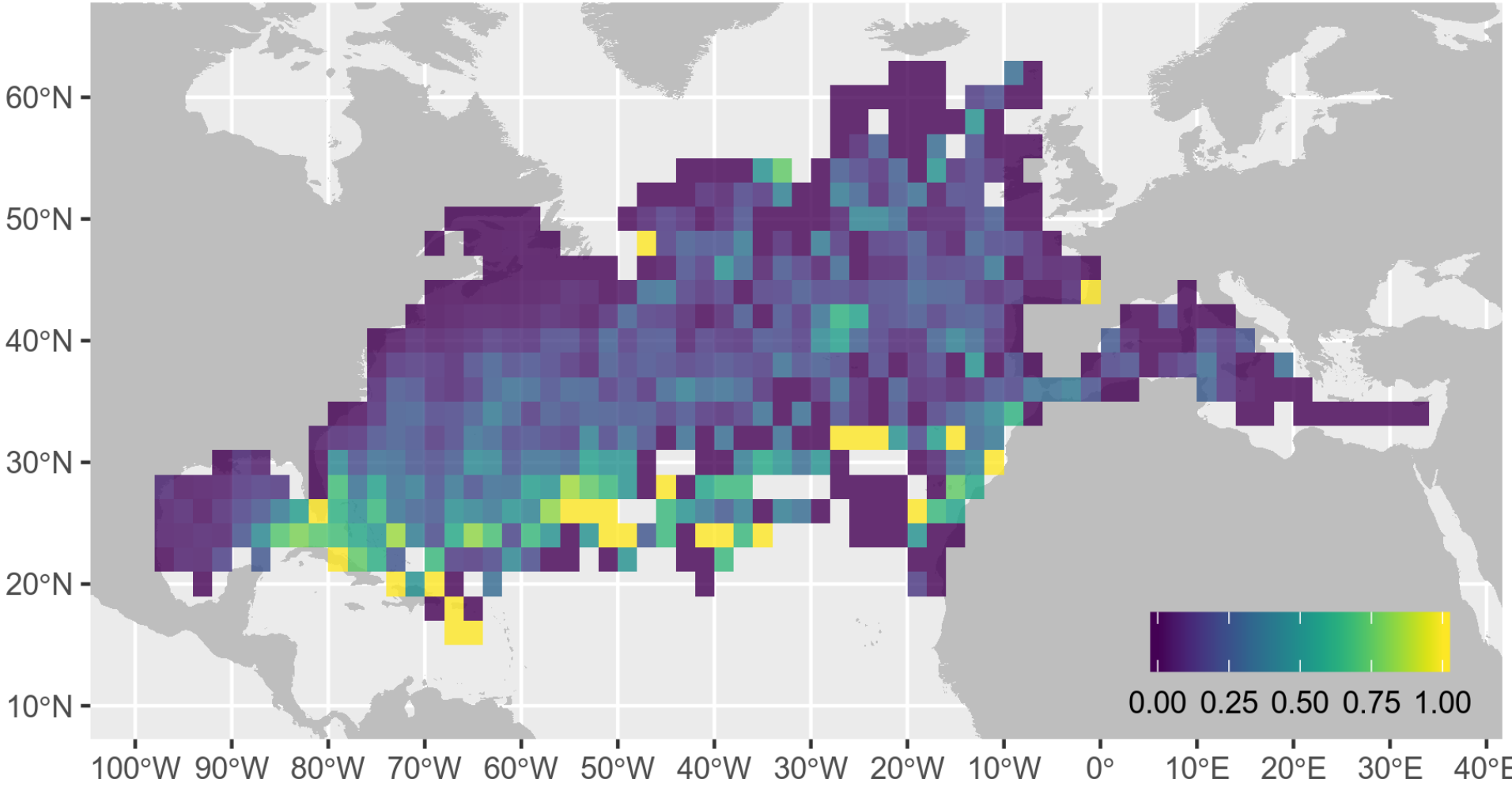
DeepDive

Rasterised into 2° cells, aggregation function: mean



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Florida International University

Mike Heithaus & Yannis Papastamatiou

Postdoc (2022)

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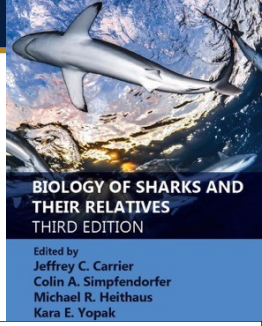
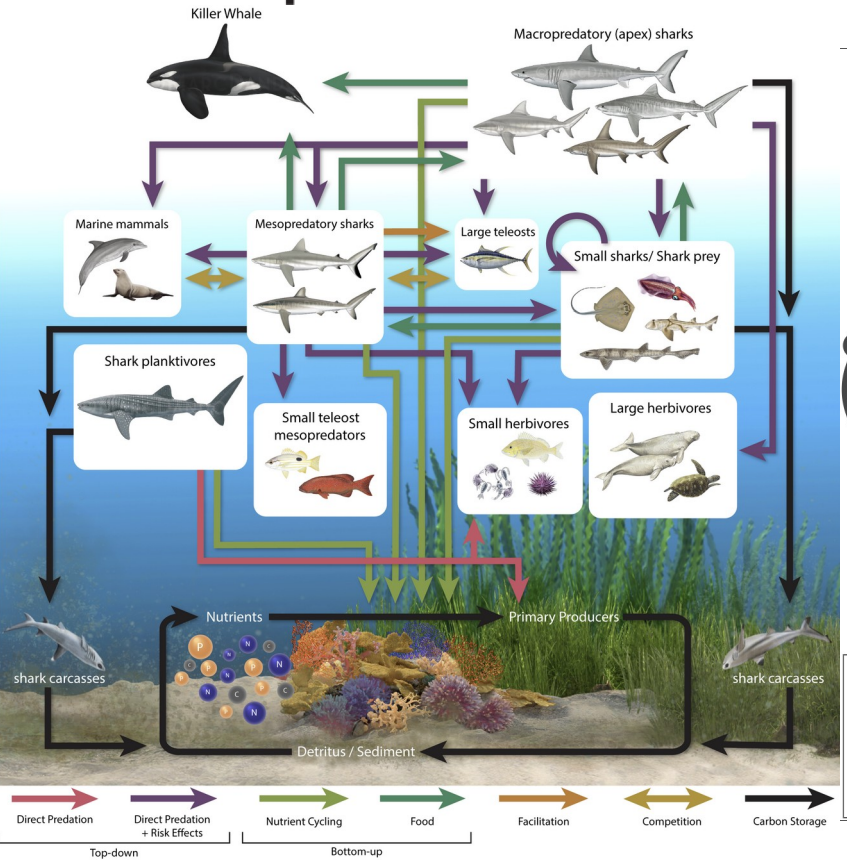
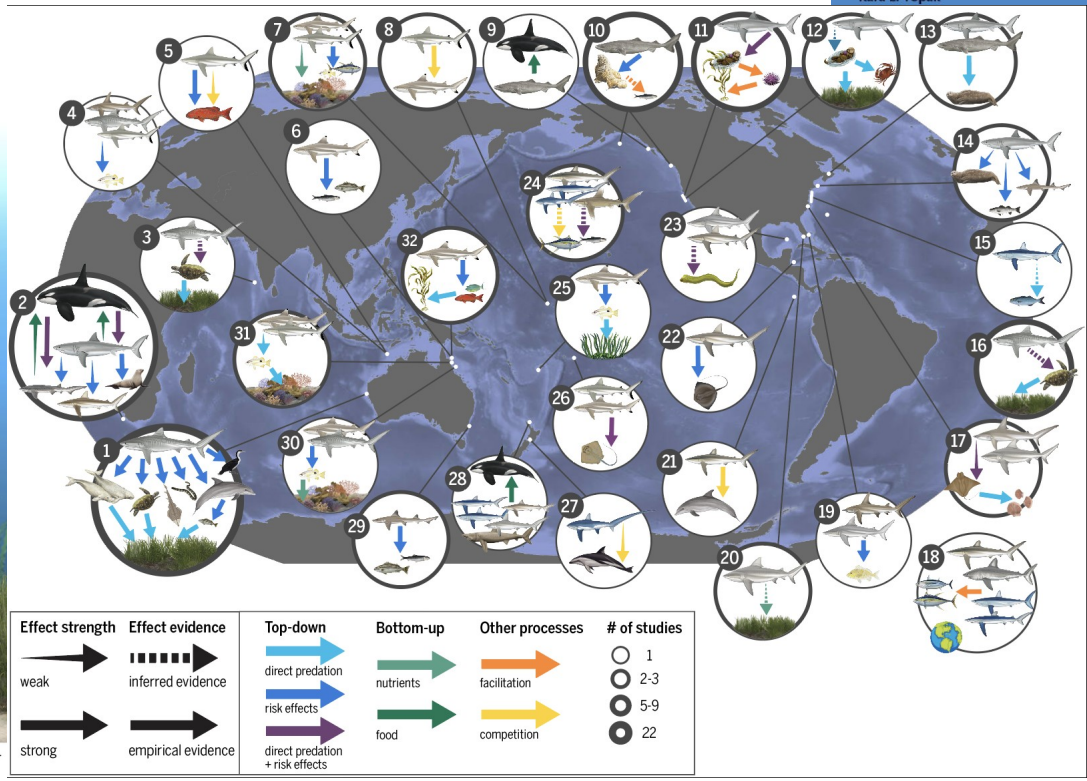
REVIEW

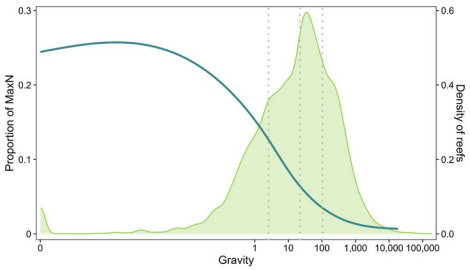
CONSERVATION

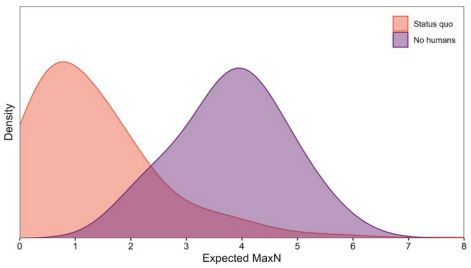
Ecological roles and importance of sharks in the Anthropocene Ocean

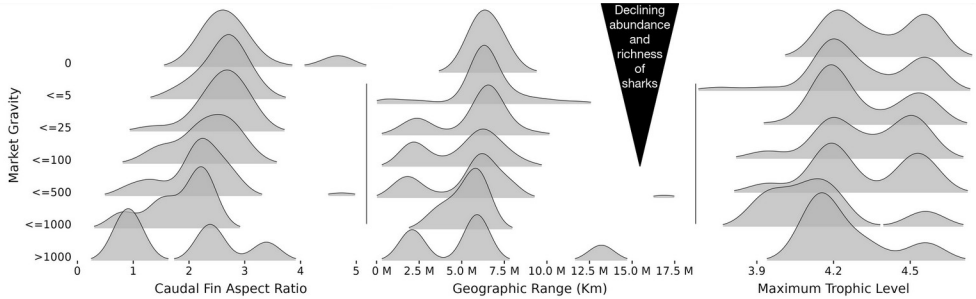




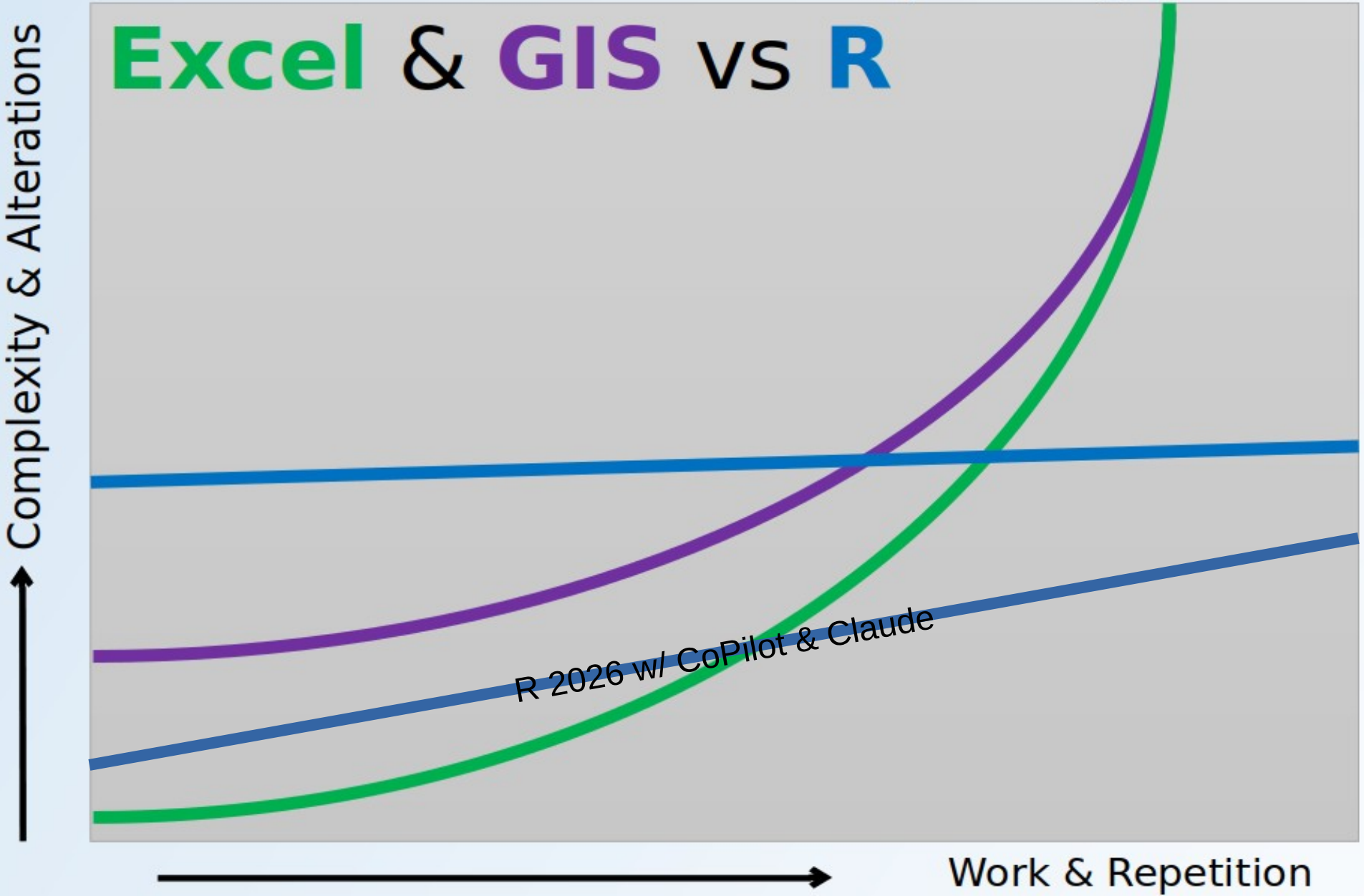




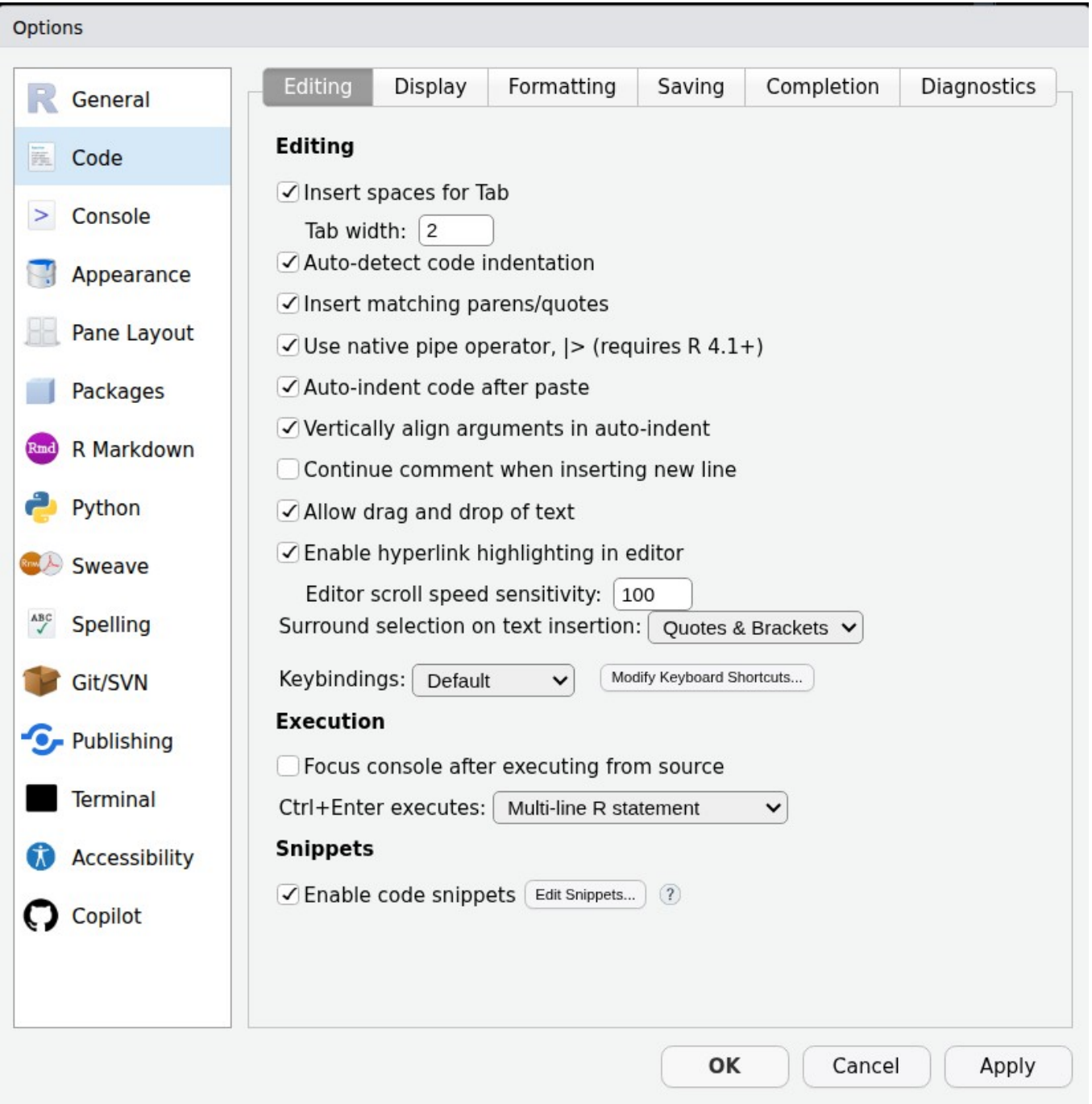




GUI vs Scripting



System setup:
R,
Rstudio



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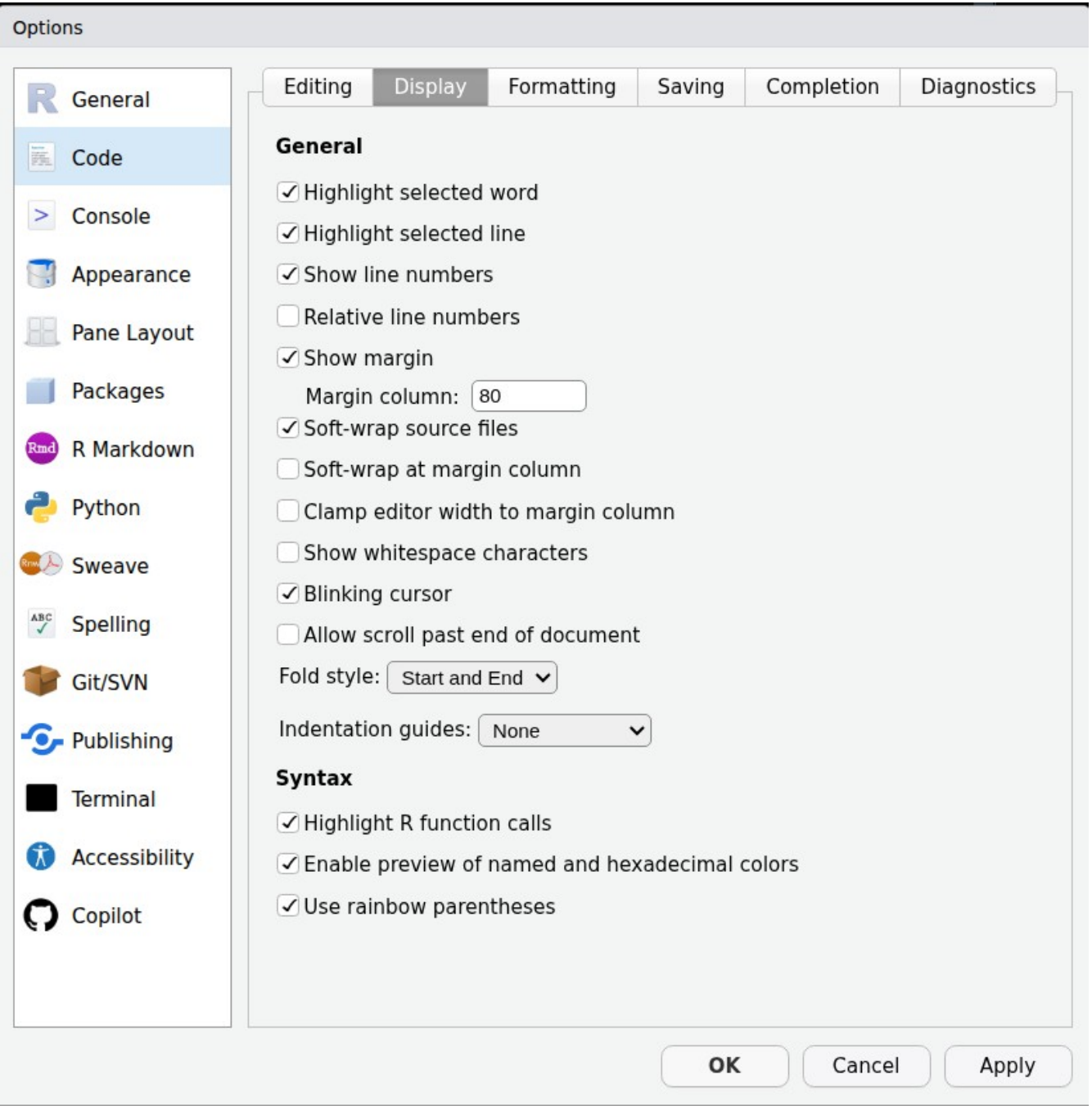

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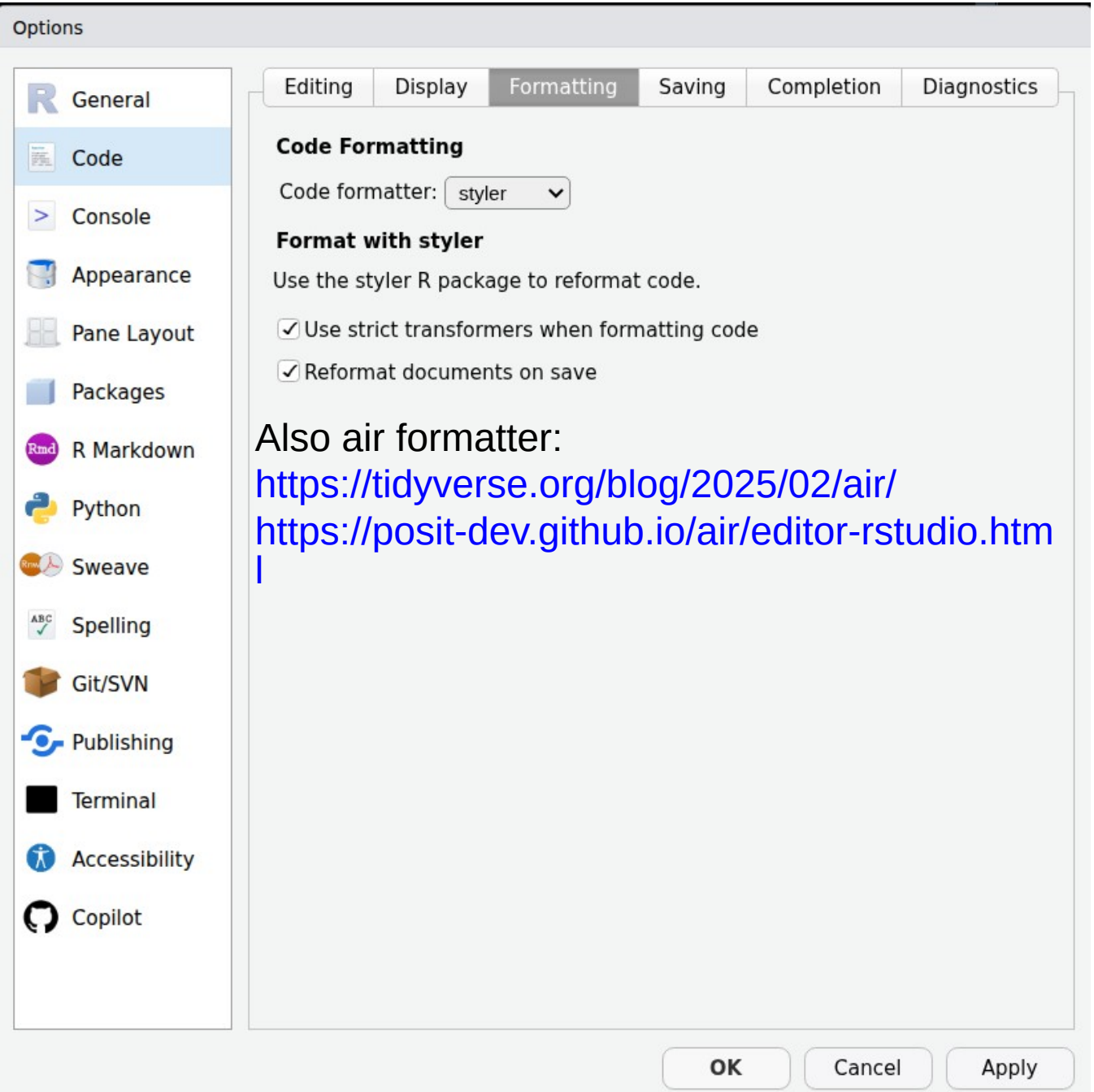
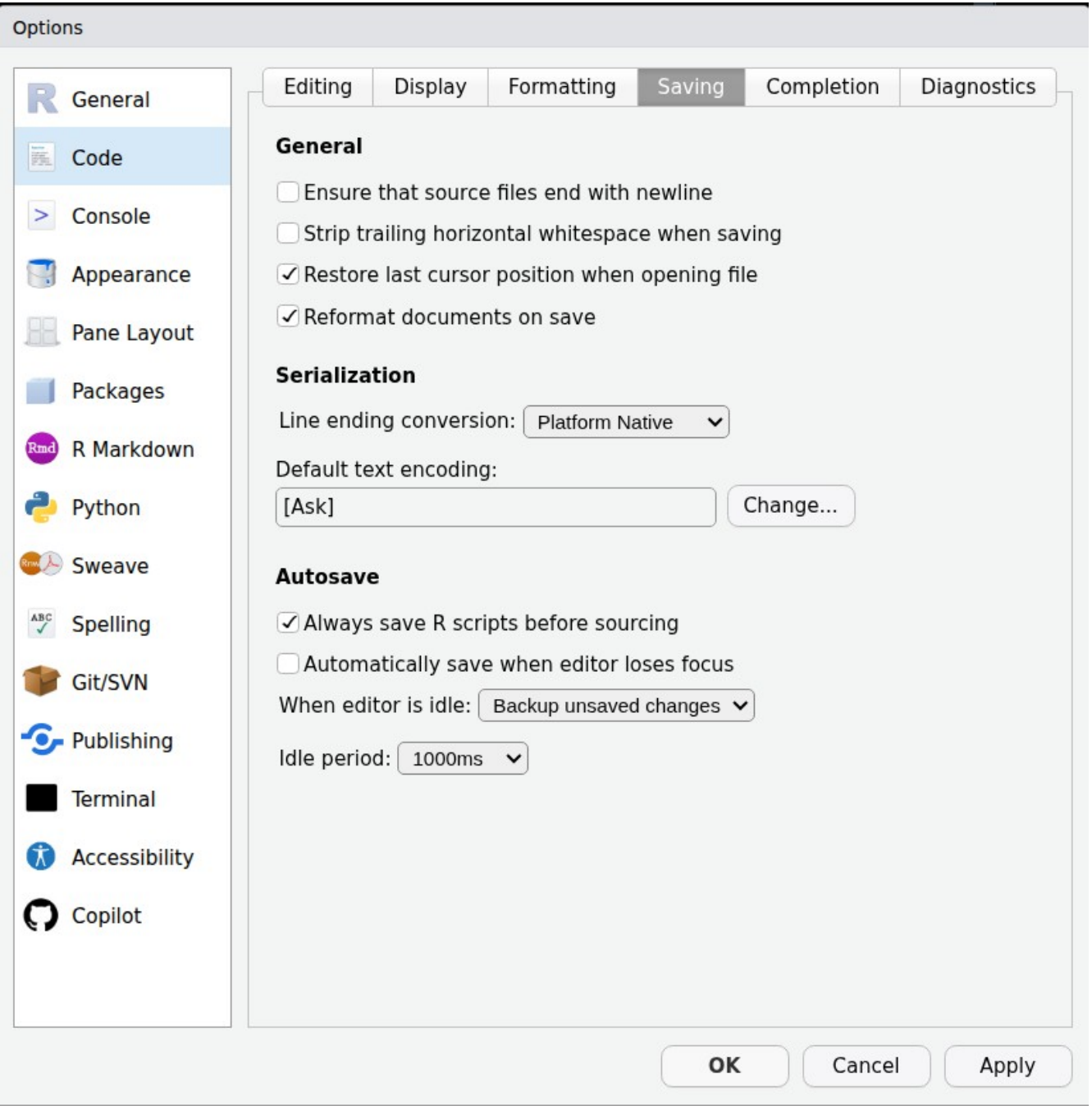


FLORIDA INTERNATIONAL UNIVERSITY



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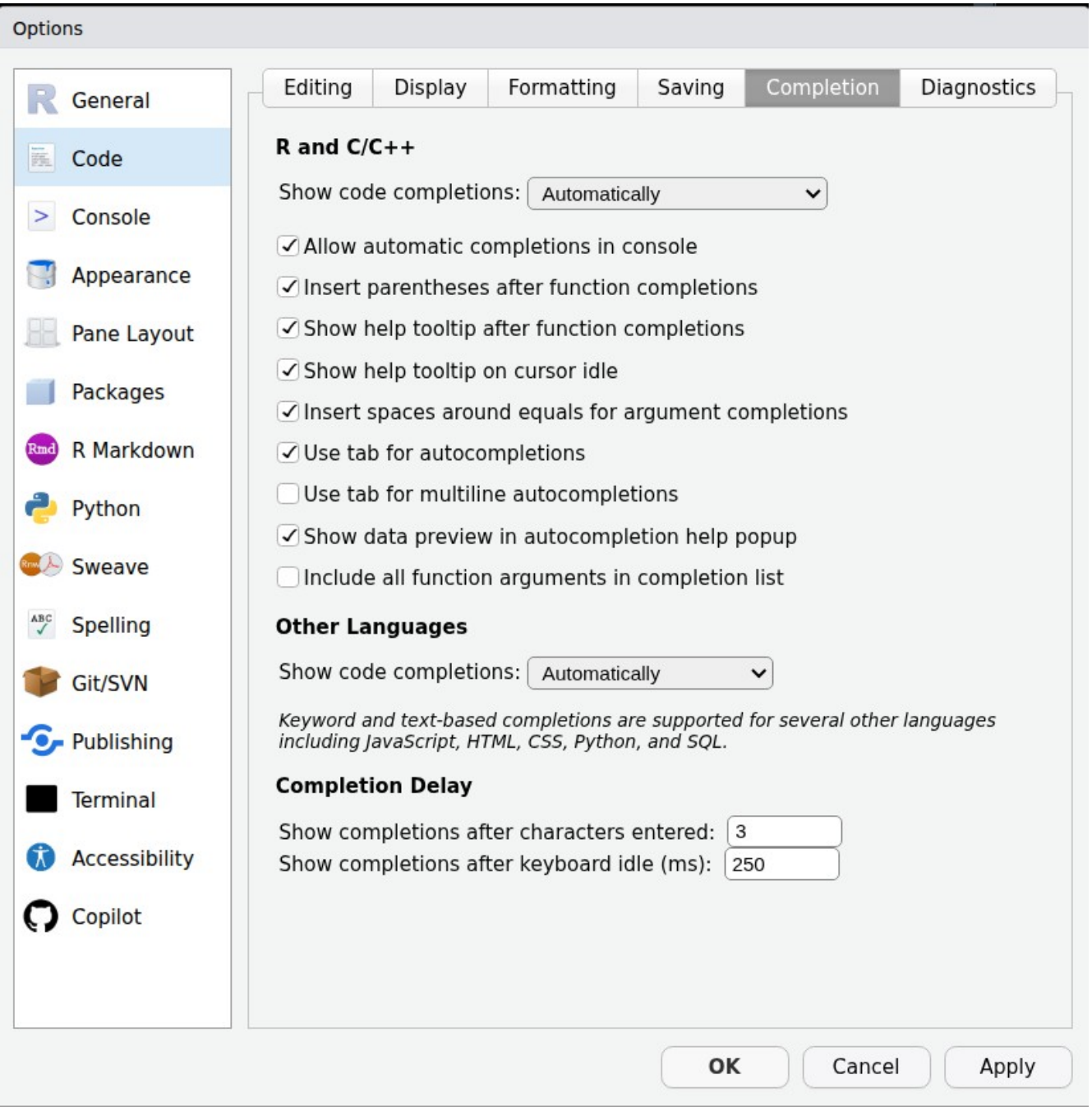

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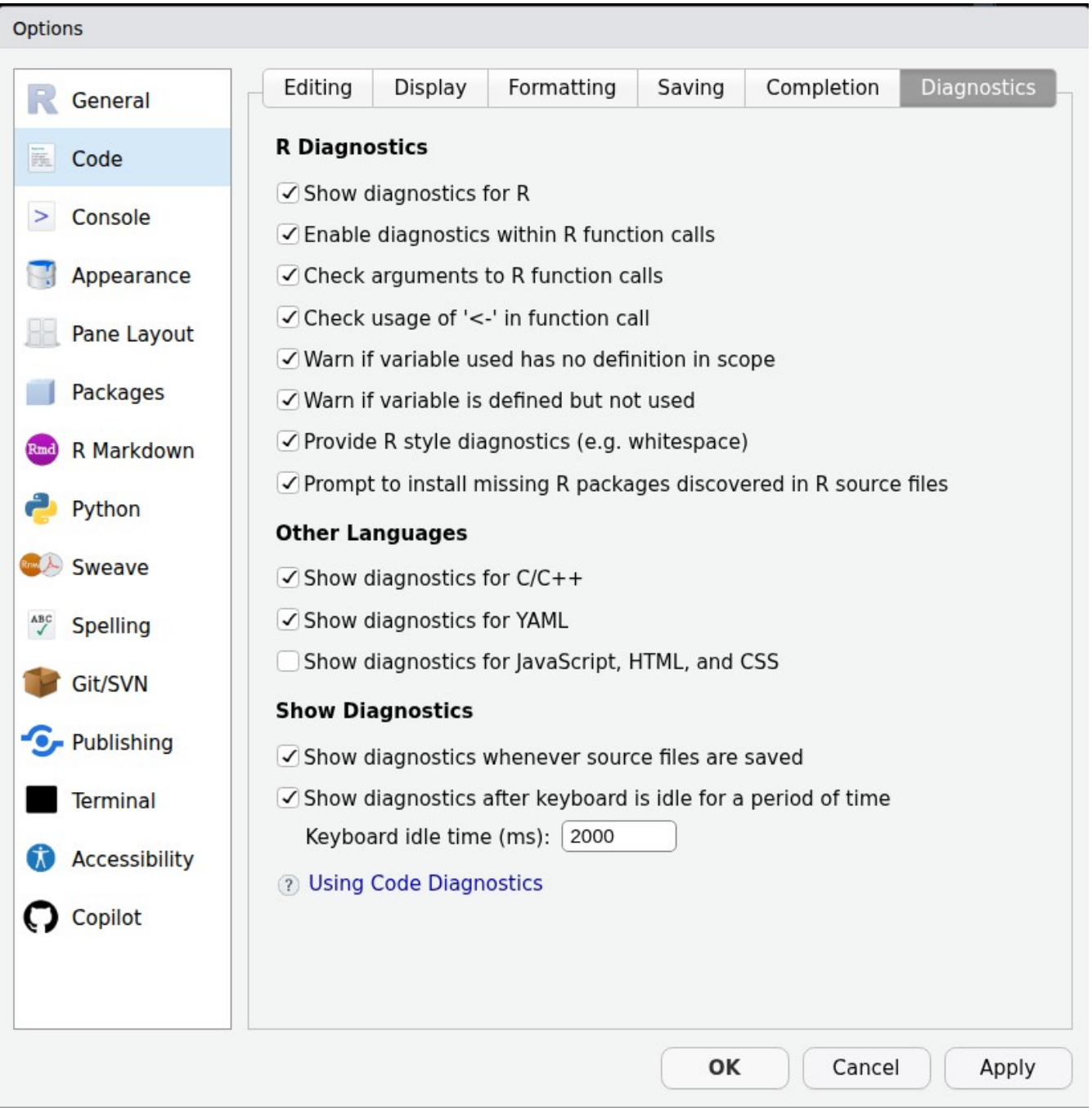

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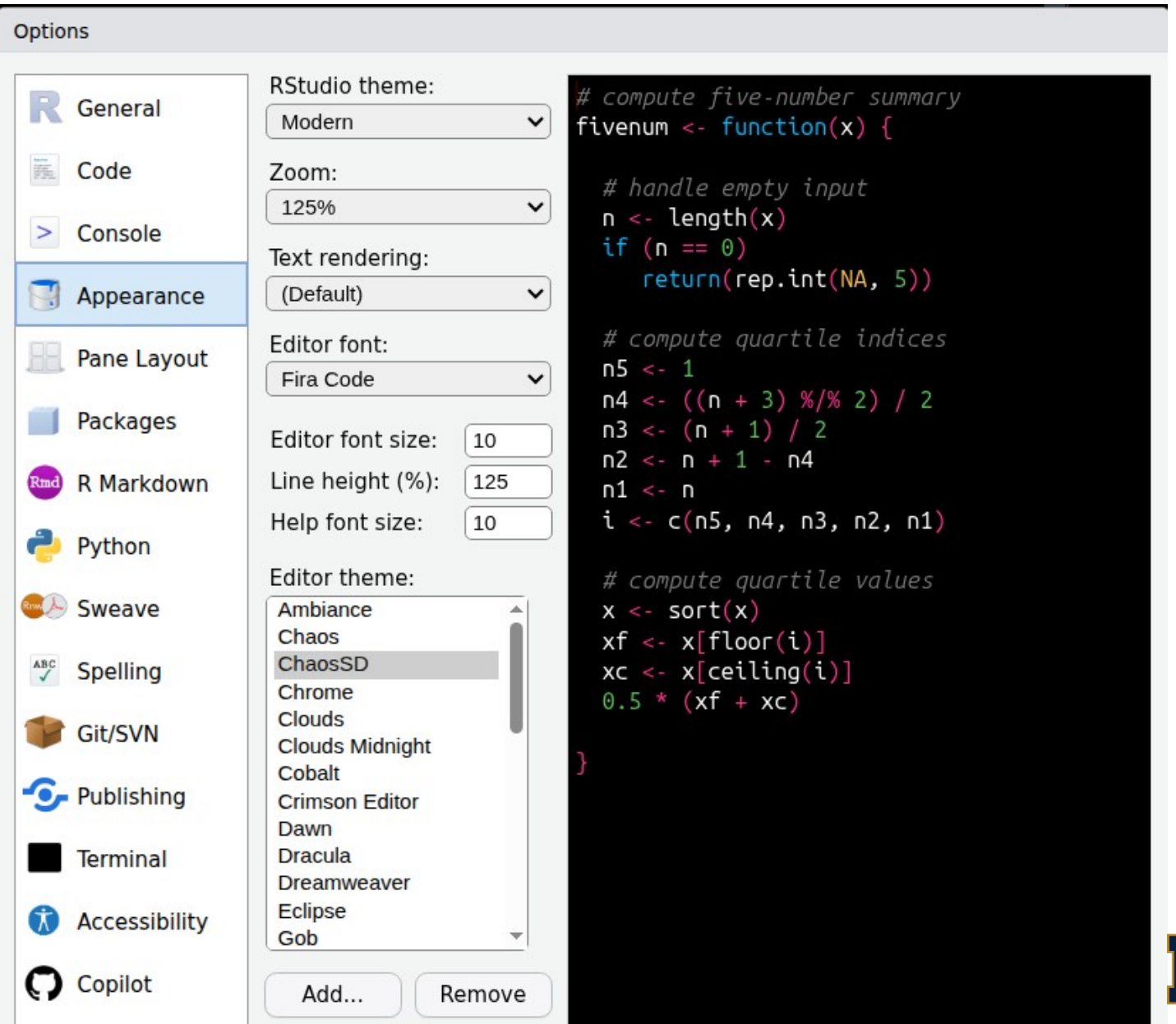

https://github.com/tonsky/FiraCode

chaosSD in Canvas

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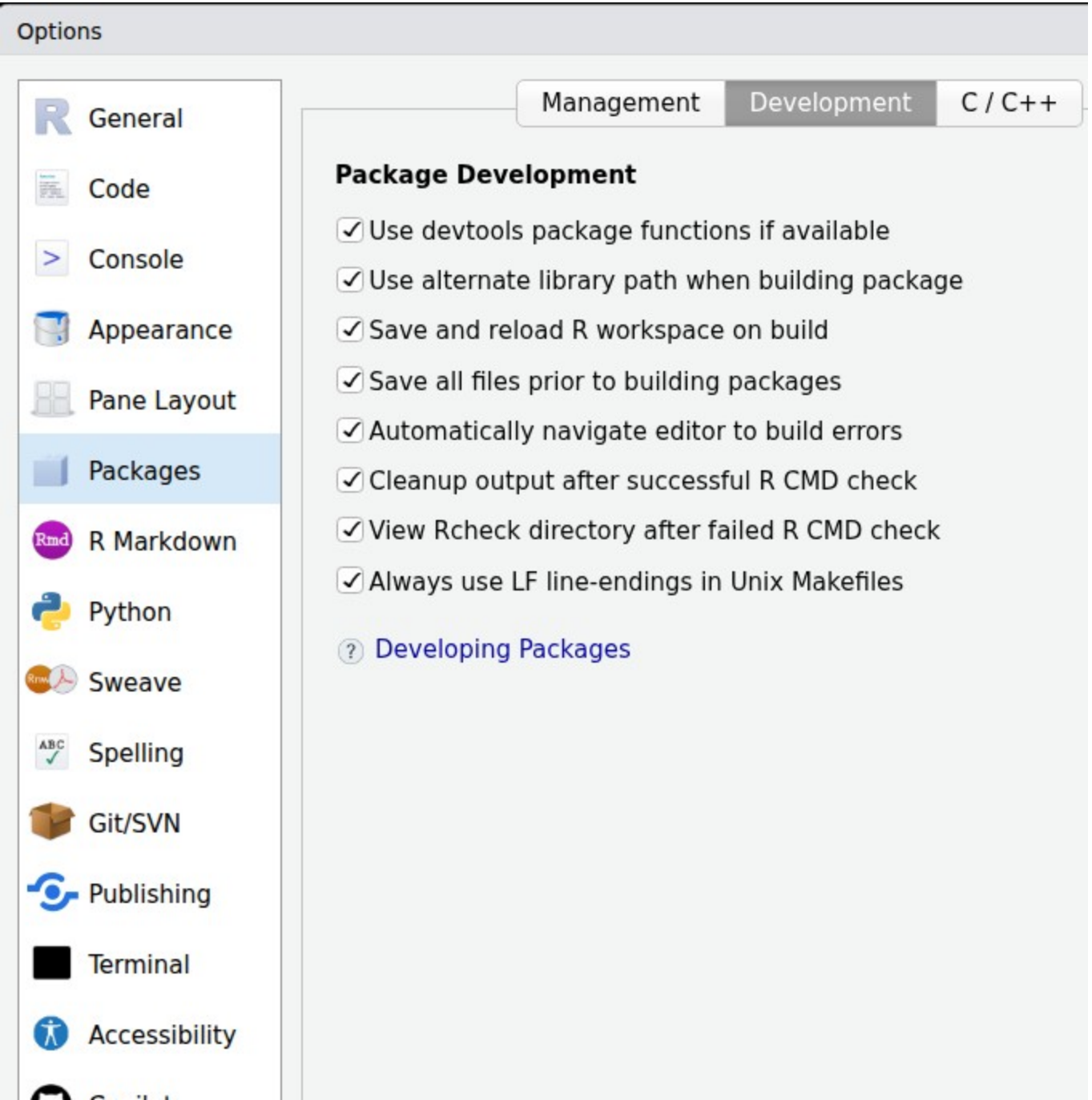

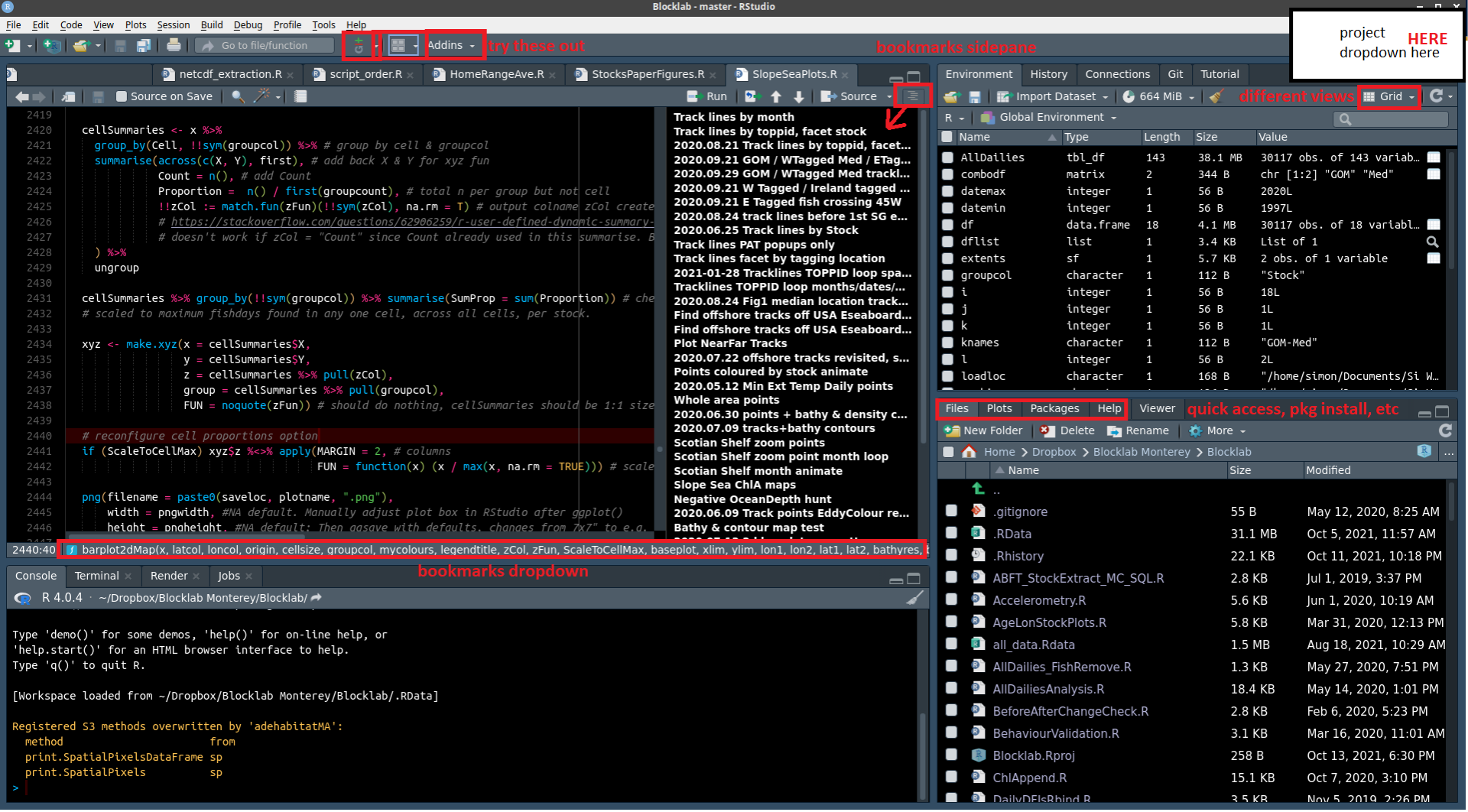

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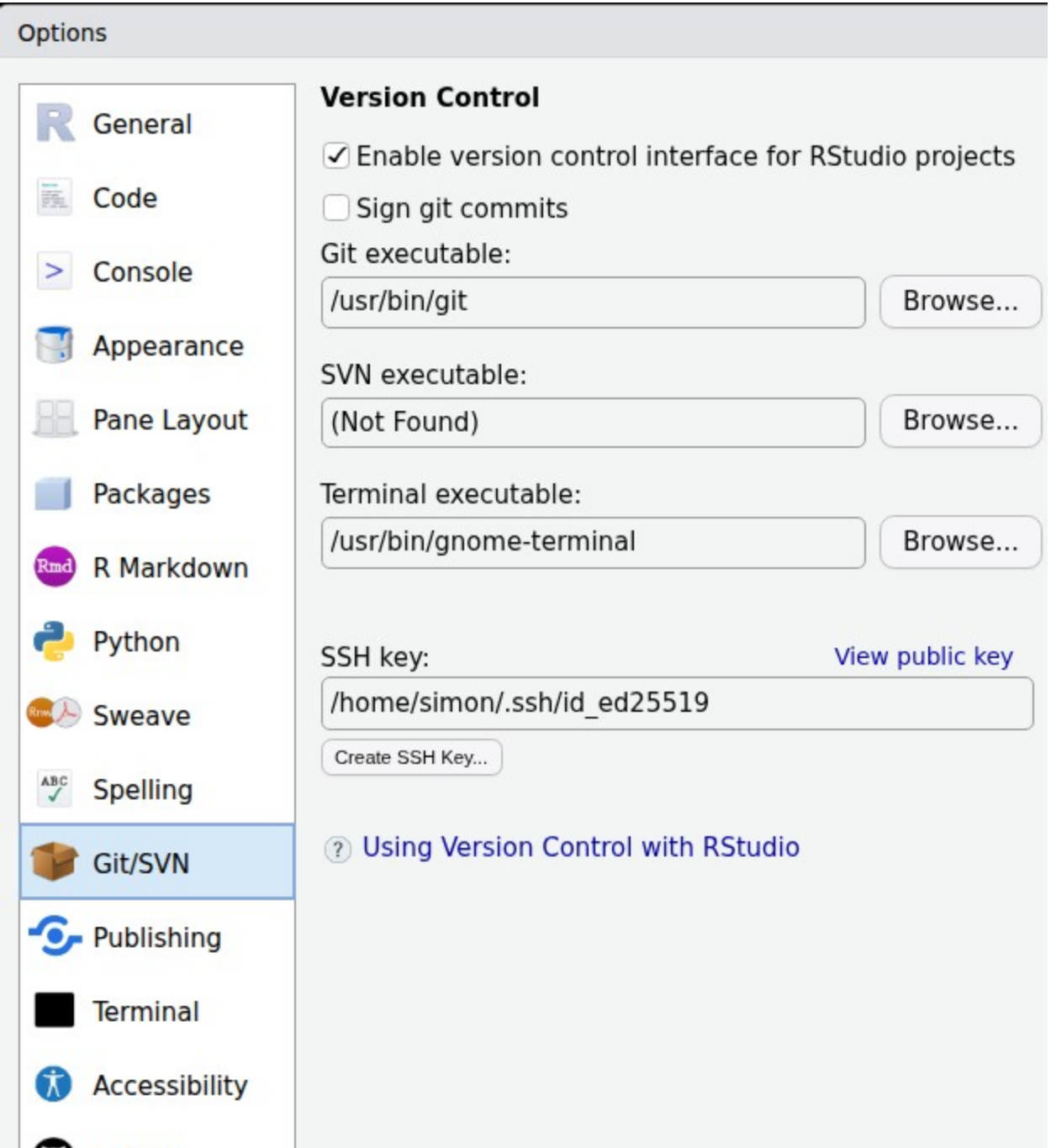

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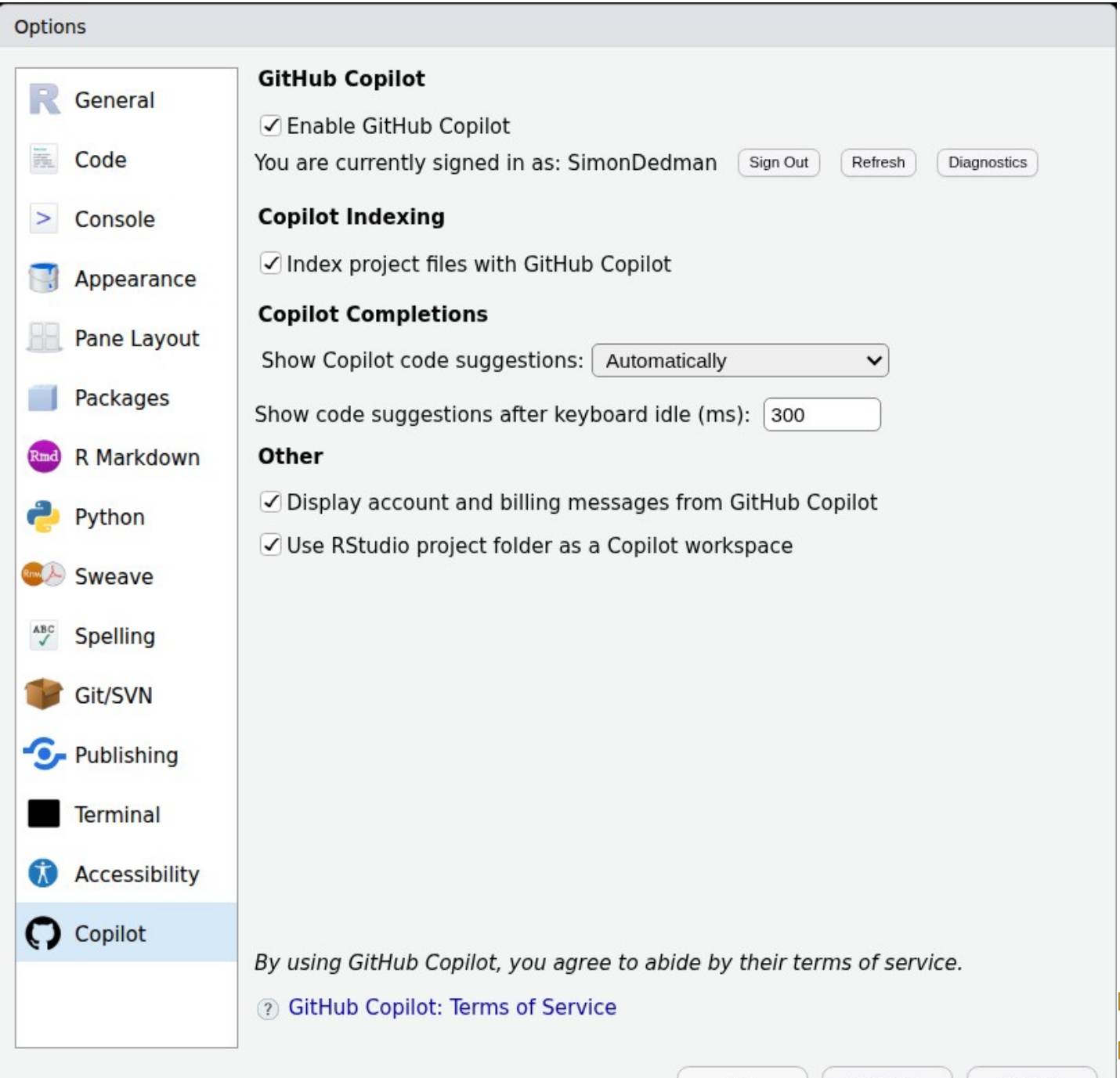

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What IS GitHub?

1. Dropbox/Google Docs but with precise version control
2. Each projects is called a Repository
3. README.md (markdown document) becomes the front page of the repo.
4. 1 person can use it as cloud storage others can see, download, install.
5. 2+ people can collab work on code.
6. Others can fork your repo and work on it themselves.
7. They can propose Pull Requests to fix issues, or go in new directions.
8. Projects gain traction informally here before becoming CRAN packages.
9. You can host HTML on the github.io branch of your repo e.g. https://github.com/SimonDedman/CarsOrSharks
10. Your GitHub homepage hosts all your repos and some personal info.

GitHub Setup

1. Install R - https://www.r-project.org/
2. Install RStudio - https://posit.co/download/rstudio-desktop/
3. Install Git - https://happygitwithr.com/install-git
4. Register a GitHub account - https://github.com & https://happygitwithr.com/github-acct
5. Setup Personal Access Token for HTTPS (done next) https://happygitwithr.com/https-pat
6. Or for SSH - https://happygitwithr.com/ssh-keys
7. DON'T Open a new repository on GitHub yet

Bookmark & follow https://happygitwithr.com

Initialise Project & Connect to GitHub

1. Follow Sarah Popov's presentation: https://popovs.github.io/r-pkg-slides
2. install.packages("devtools", "usethis") library(devtools) library(usethis)
3. usethis::create_package("~/Documents/R/fjoRds")
   (replace 'fjoRds' with the name of the project/folder/package you want to create, which doesn't exist)
4. usethis::use_r("myfunction")
   (give it a real name & add content)
5. Code > Insert Roxygen skeleton
6. Edit DESCRIPTION file, usethis::use_package_doc(), usethis::use_readme_md(), usethis::use_vignette("function_explain"), usethis::use_data_raw(), usethis::use_data(), usethis::use_test(), use_gpl_license(version = 3, include_future = TRUE), usethis::use_code_of_conduct("your@email"), devtools::document(),
7. usethis::use_git(), usethis::use_github(), usethis::create_github_token(), gitcreds::gitcreds_set(), replace credentials.
8. Tools > terminal: git push -u origin master *(may be needed)*
9. Edit, save

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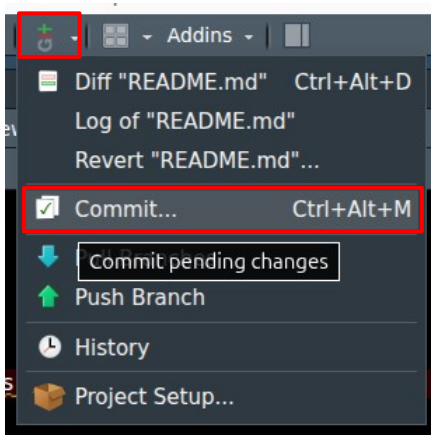
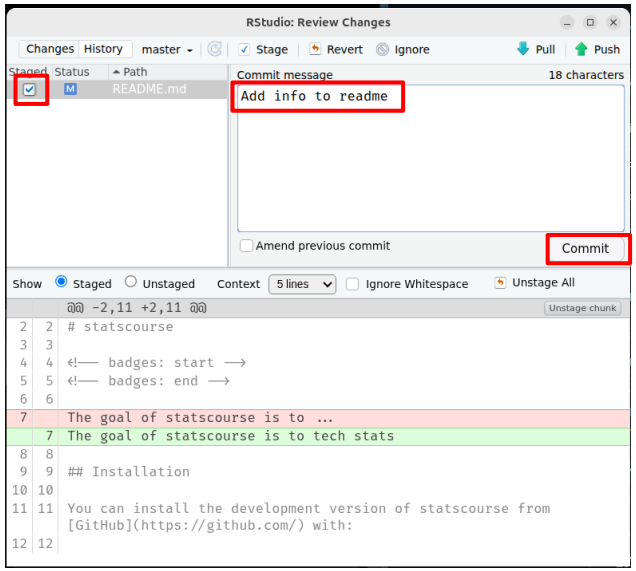
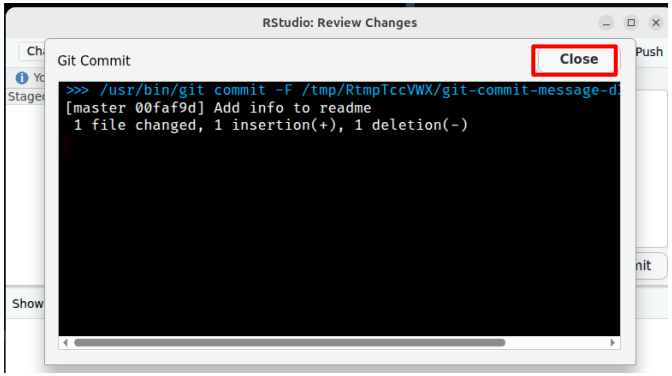
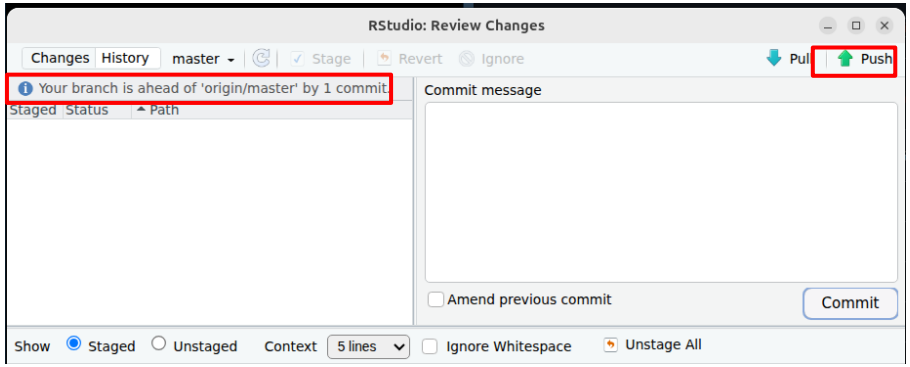
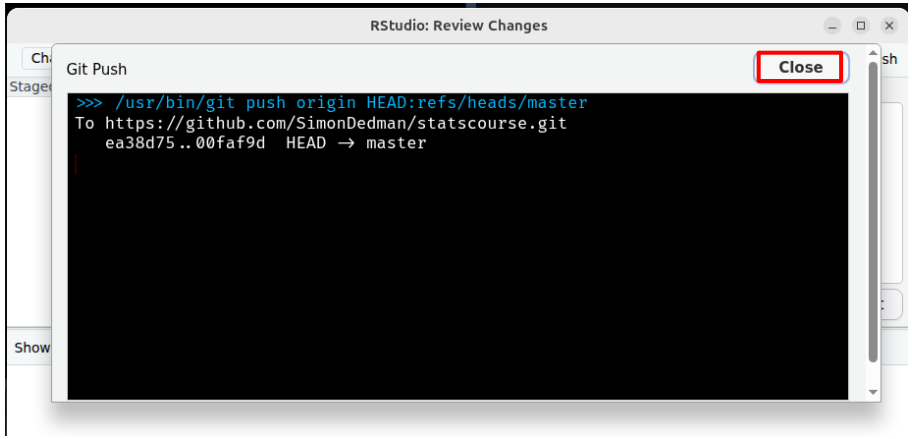
Edit, Save, Stage, Comment, Commit, Push, to Github











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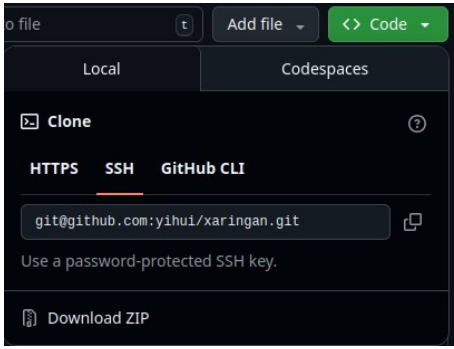
Github Pull Requests: contribute to other packages

1. Fork a project on github (top right).

2. In your GitHub forked project, click green "code" button, copy git address.



3. In a folder on your filesystem: "git clone [gitaddress]".
4. Go to new subfolder, open Rproj in RStudio.
5. Make changes in your local files in RStudio, test, devtools::document(), 'git commit push' to your own Github fork.

6. Go to original (other person's) package, pull requests, create, "compare across forks", select your fork as the right hand side. "Create pull request" button.

7. If it's not automatically named correctly, name it well. See https://docs.github.com/en/issues/tracking-your-work-with-issues/linking-a-pull-request-to-an-issue
8. Example: https://github.com/r-lib/usethis/pull/1898
9. https://docs.github.com/en/pull-requests/collaborating-with-pull-requests/proposing-changes-to-your-work-with-pull-requests/creating-a-pull-request?tool=desktop

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System setup:
Theme, Font

Resources:
Guides, Concepts, Code

Name	Created	Last Modified	Modified By	Size
Others Code Dumps	7:35pm	7:35pm		--
R Cheat Sheets	6:45pm	6:45pm		--
2019.06.25_Stanford_Universit...	4:26pm	5:30pm	Simon Dedman	7.1 MB
2021-10-13_Emil_Aalto_Coding...	4:26pm	8:17pm	Simon Dedman	370 KB
2021-10-13_Emil_Lab_Meeting...	4:26pm	8:17pm	Simon Dedman	885 KB
2023-11-16_MyLabMeeting.pptx	8:27pm	8:27pm	Simon Dedman	12.4 MB
chaosSD.rstheme	4:27pm	4:27pm	Simon Dedman	29 KB
Data_Organization_SOP.docx	8:27pm	8:27pm	Simon Dedman	203 KB
Excel-vs-GIS-vs-R.png	4:32pm	4:32pm	Simon Dedman	68 KB
Filazzola_Lortie.2022.Call_clean...	4:32pm	5:51pm	Simon Dedman	2.1 MB
JennyBryan.NamingPubsCarpet...	4:32pm	5:51pm	Simon Dedman	5.9 MB
JennyBryan.NamingThings.pdf	4:32pm	5:51pm	Simon Dedman	2.3 MB
Project_Organisation_Metadata...	8:27pm	8:27pm	Simon Dedman	89 KB
template_organised.R	8:04pm	8:04pm	Simon Dedman	50 KB

- Various presentations on coding tips
- Especially my bits in Emil Lab Meeting
- chaosSD.rstheme RStudio custom theme has colours for all elements (some otherwise unhelpfully missing colours)
- template_organised: freshly organised code repository from my years of learning R.

Others code dumps. See also: https://github.com/SimonDedman/MiscScripts

- Spatial autocorrelation tests
- Accelerometer, stocks, age/length, dive behaviour, variables acquire, sensor fixing, depth bins, day/night stats, distance to shore, home range, maps, KS tests, linearity index, plots, scales, etc
- Graphics & utility functions
- Lags, logs, pairplots, population modelling
- Animated SST fish tracks
- Pairplots, KS test, XY plots, basic plots
- Raincloud plots – sideways violins
- Data cleaning, munging, mapping, analyses, reports, track filtering ARGOS & foieGras
- Maps, bins, utility functions.

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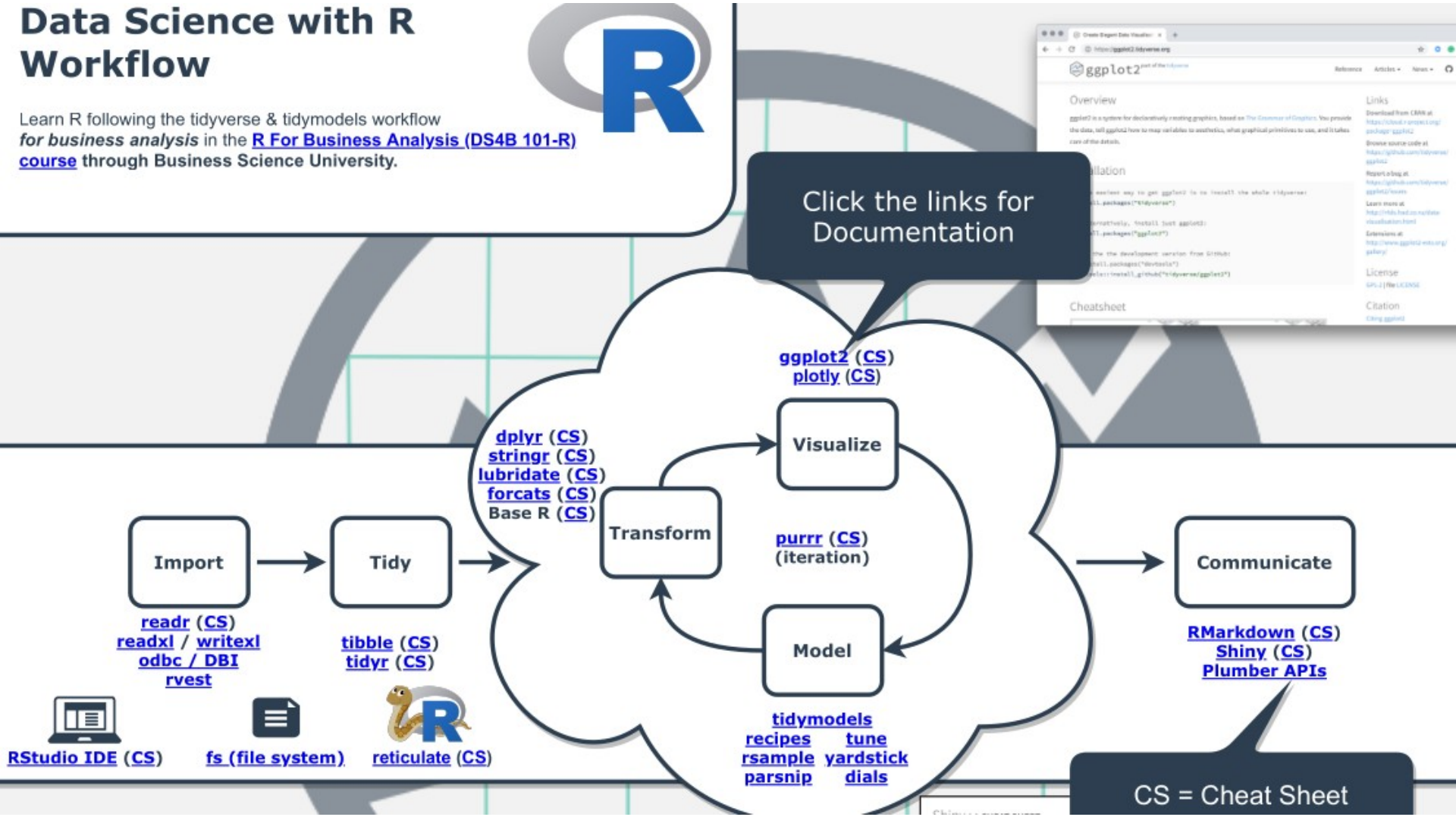
R cheat sheets



42 files: R misc, wrangling, import, data table, factors, ggplot, cloud compute, ML, dates, leaflet/Shiny online plots & maps, colours, markdown, spatial, text strings, survival models

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Base R vs TidyVerse (Dplyr/Pipes)

```r
# Base R
df ← data.frame(
  Lat = c(25.1, 25.2, 25.3),
  Lon = c(121.5, 121.6, 121.7),
  Depth = c(10, 20, 30)
)
df[1,3] # 10. [rows,columns] [radio,control]
df[3,1] # 25.3
df$Lon[3] # 121.7
df$Depth[c(1,3)] # 10 30
df[1,3] ← 20
df[1,3] # 20
dfdepth ← df$Depth
str(dfdepth) # num [1:3] 10 20 30
is.vector(dfdepth) # TRUE
dfdepth ← df ▷ select(Depth) # becomes tibble

# Tidyverse
library(tidyverse)
df ← tibble(
  Lat = c(25.1, 25.2, 25.3),
  Lon = c(121.5, 121.6, 121.7),
  Depth = c(10, 20, 30)
)
df ▷ slice(1) ▷ pull(Depth) # 10
df ▷ slice(3) ▷ pull(Lat) # 25.3
df ▷ pull(Lon) ▷ .[3] # 121.7
df ▷ select(Depth) ▷ slice(c(1,3)) ▷ pull() # 10 30
length(df$Depth) # 3
tbldepth ← df ▷ select(Depth) # tibble
```

tidyverse.org/blog/

Tidyverse Packages

Posts

ragnar 0.3.0 package

Tomasz Kalinowski

The new release of ragnar adds faster ingestion, new embedding providers, improved retrieval, and new integrations for using ragnar stores from tools.

2026/01/27

plumber2 0.2.0 package

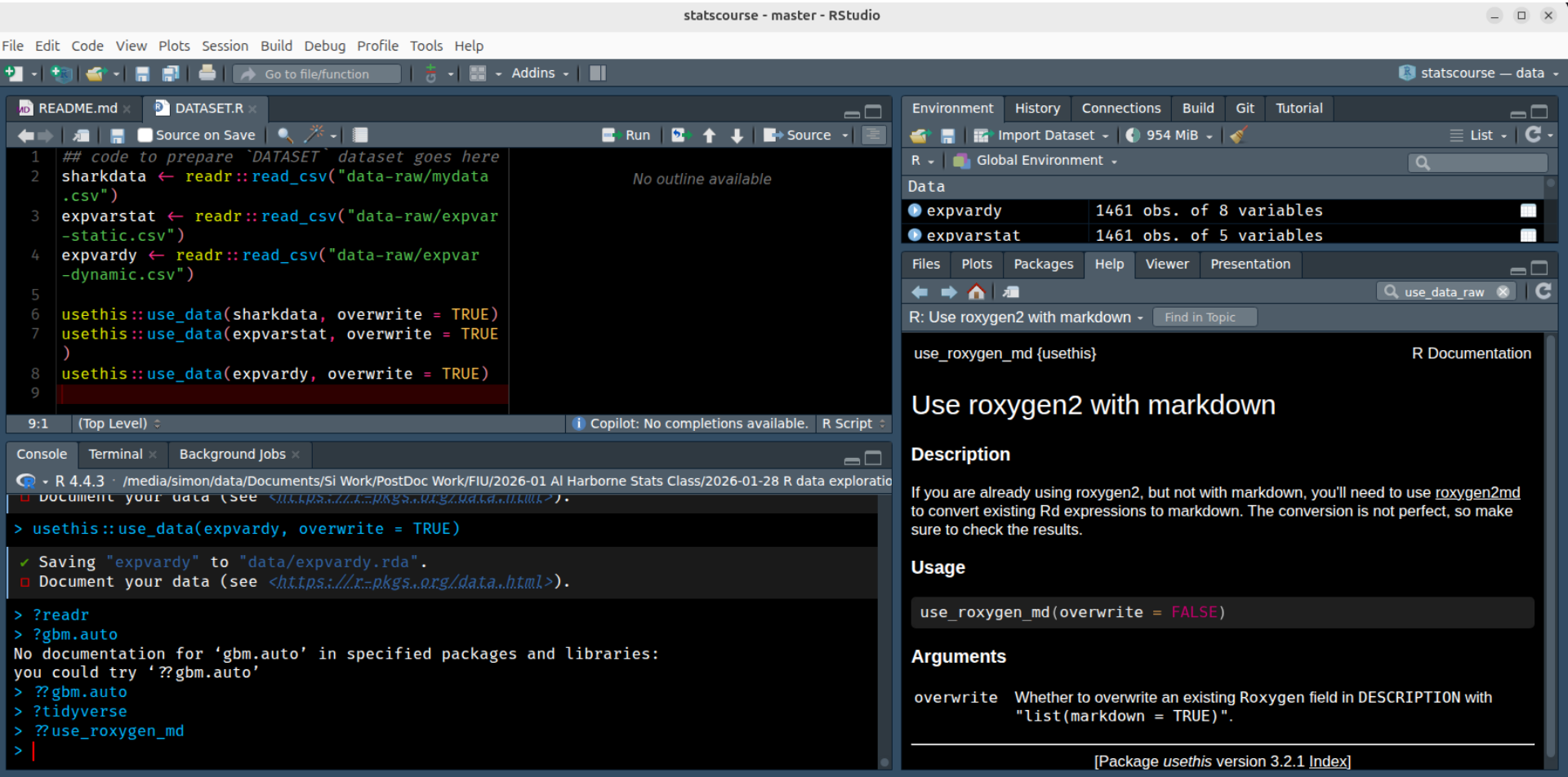
Thomas Lin Pedersen

The next version of plumber2 has hit CRAN. Read all about the new features such as OpenTelemetry (OTEL) support, authentication, new tags, and performance improvements here.

2026/01/20

Coding, Errors, & Help

- Commenting concepts: help your future self. Script organisation, layout, headings, markdown formatting.
- Errors: AI is nice but the first pass is to actually READ the error messages, run traceback, bring up the ?help file, READ the help file. Loads of people ask me how to fix errors/warnings which are well documented (see gbm.auto help file).

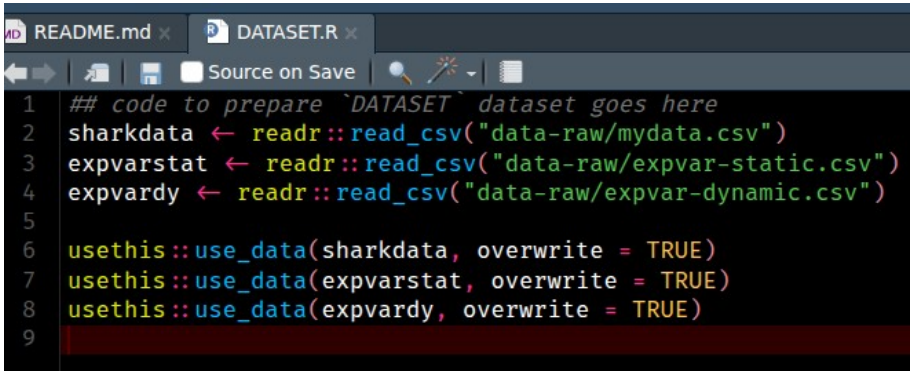


Typical workflow

- Folder setup, Github & R package, here::here https://github.com/jennybc/here_here
- Import: core & additional data
- Tidy: explore, find errors & outliers, conditional format colour scale, clean
- Transform: join, next slides, plus more, see docx
- Visualise: check autocorrelation, plots
- Model [BRT & hopefully tidymodels 4th March]
- Communicate

Import

- Fork/clone my repo https://github.com/SimonDedman/statscourse
- or start your own with the CSV & R files
- usethis::use_data_raw() then edit it (DATASET.R)



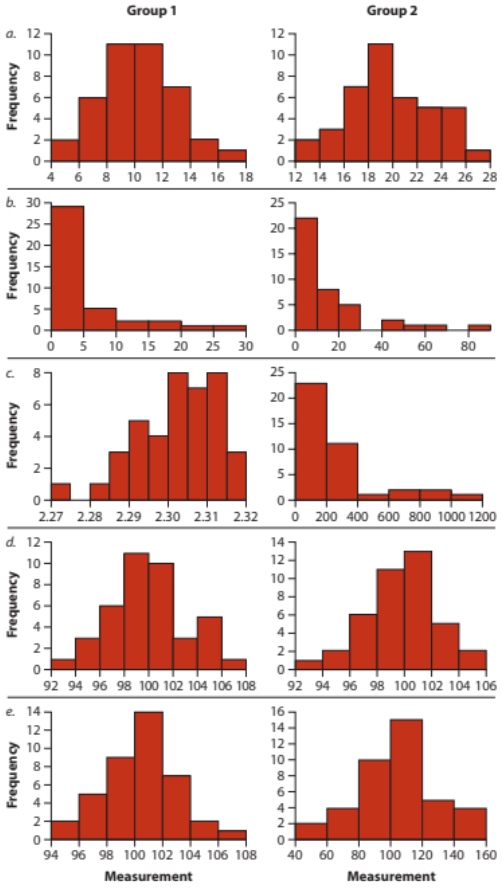
Tidy inc. Plot

- 01_tidy-data.R example
- mydata-bad.csv colour condition example (drumline, no Gibson)

Transform

- Join, assess outliers again
- template_organised.R L1-858 SKIM
- Summarise, pivot, mutate, group, etc

Evaluating Parametric Assumptions & Data Transformations



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Common Parametric Test Assumptions

(1) Errors independent & identically distributed

a. Treatments are applied independently to replicates
b. A given replicate does not affect other replicates
c. No autocorrelation among replicates

(2) Homogeneity of variances among treatment groups (homoscedasticity)

(3) Data are normally distributed

Overview: Assumption Checking

- Use tests & graphical examination of residuals to evaluate assumptions
- Minor to moderate violations of assumptions usually not a problem; tests are still reliable
- If assumptions are severely violated, then:

  1) try transforming data & retest assumptions
  2) rank transform data before analysis
     (equivalent to a nonparametric test)
  3) redo experiment with appropriate changes in design

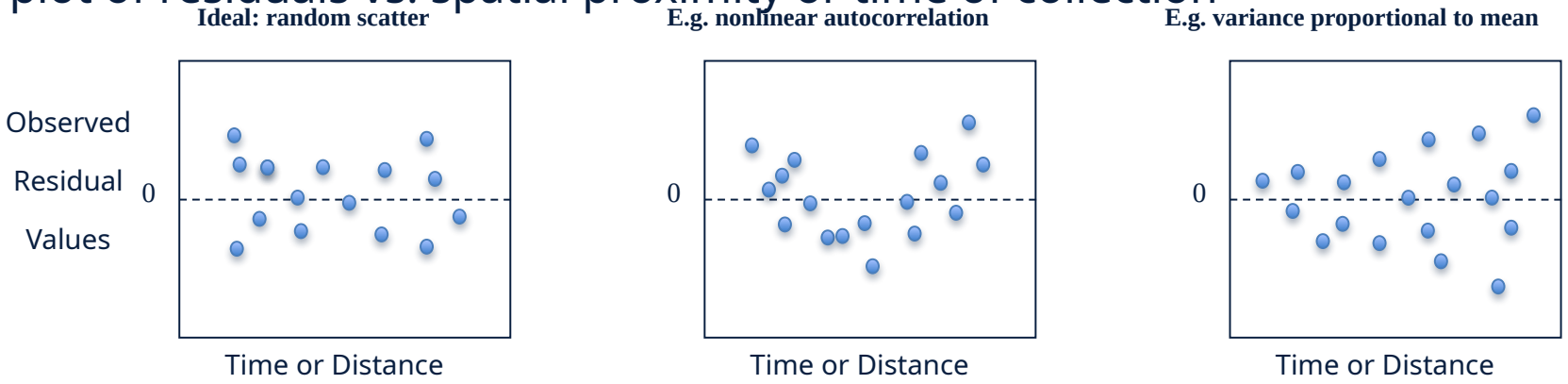
Note: Best to test assumptions using residuals for each datum (i.e., group mean – datum value), not the raw data

Independence of Error

Effect: ruins the analysis; inflates type I error; lowers precision of variance estimate.

Test: difficult to test, often requires detailed info on experimental protocol (e.g., physical proximity replicates, time order of sampling, etc.) and knowledge of system (e.g., likely sources of non-independence)

<u>If you suspect a problem:</u>
- try plot of residuals vs. spatial proximity or time of collection



<u>Solution:</u> None. If violated, can only redesign and repeat experiment correctly

Homogeneity of Variance

Effect: a problem when you have unequal n and a small # of treatment groups

- often disappears if normality problem corrected first
- general rule: ratio of largest variance to smallest should be <3

a) Bartlett's test – Poor test if data are also non-normal

b) Levene's test – better; doesn't depend on normality of data

```
bartlett.test(response ~ group, data = df)
car::leveneTest(response ~ group, data = df)
```

Test of Homogeneity of Variance

		Levene Statistic	df1	df2	Sig.
RI	Based on Mean	.291	1	18	.596
	Based on Median	.444	1	18	.514
	Based on Median and with adjusted df	.444	1	16.024	.515
	Based on trimmed mean	.291	1	18	.596

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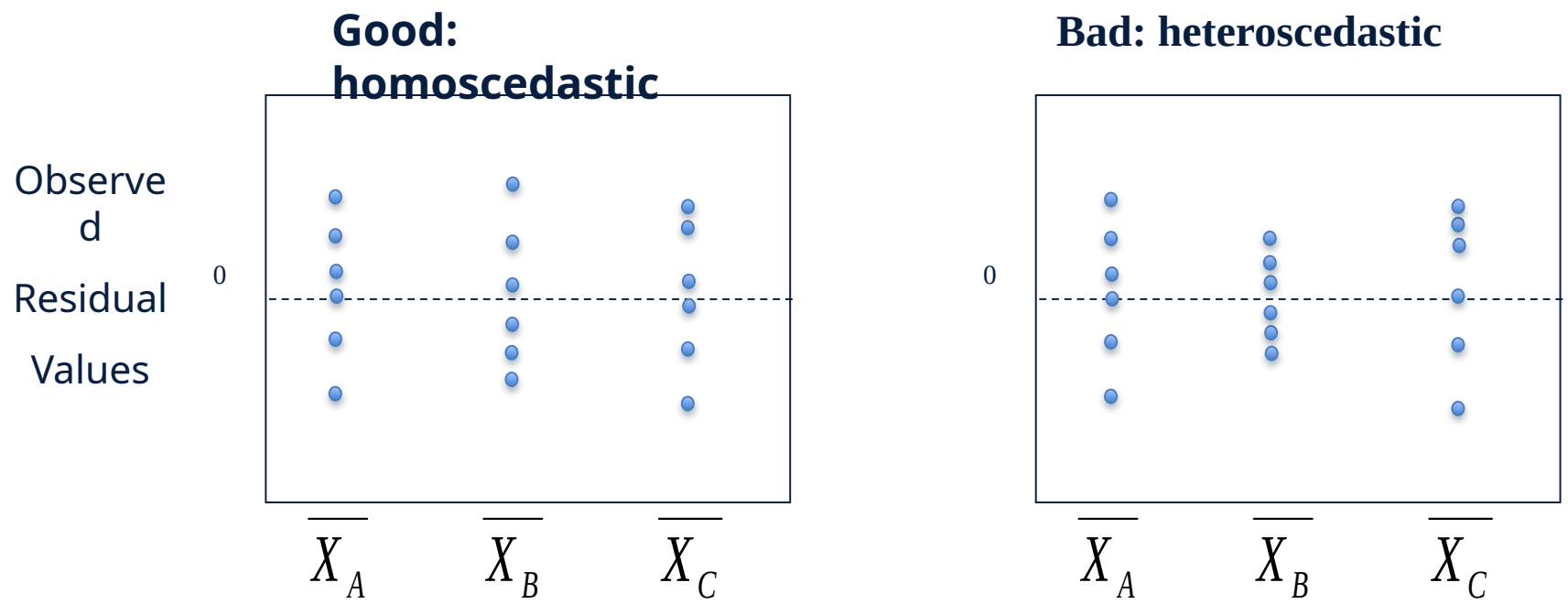
Homogeneity of Variance

Plot Inspection:

Plot of Residuals ($\overline{x_{ij}} - X_j$) vs. Treatment Means




```
ggplot(df, aes(x = fitted, y = residuals)) +
  geom_point() + geom_hline(yintercept = 0)
```

Normality

Effect:

- not usually a problem, if n > 10
- may be problem if n < 10 and unequal sample sizes among treatments
- minor to moderate violations of this assumption usually not a problem; hypothesis tests are still reliable

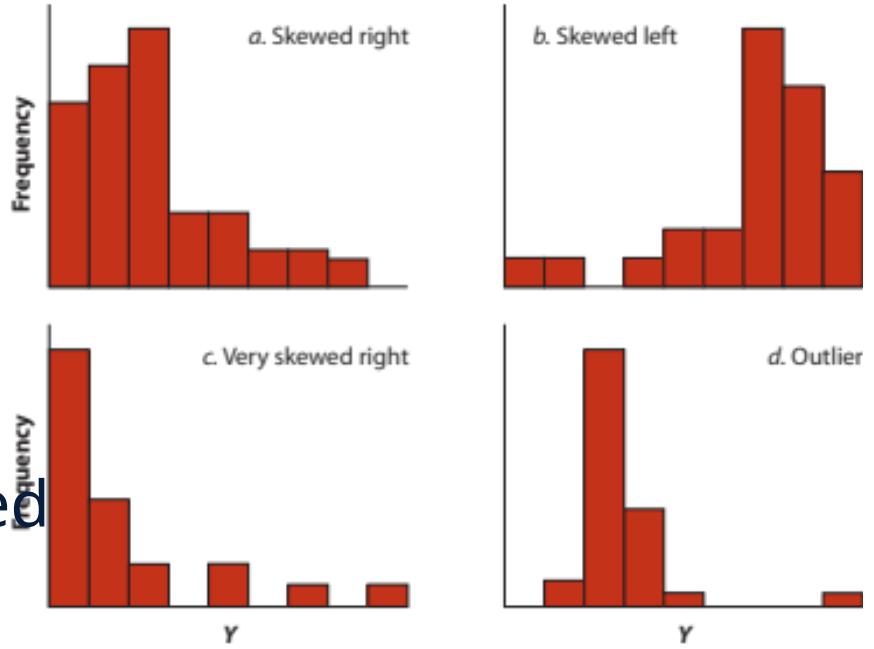
Evaluate: Graphically or with statistical tests:

Graphical Approaches:

a) plot histogram of residuals

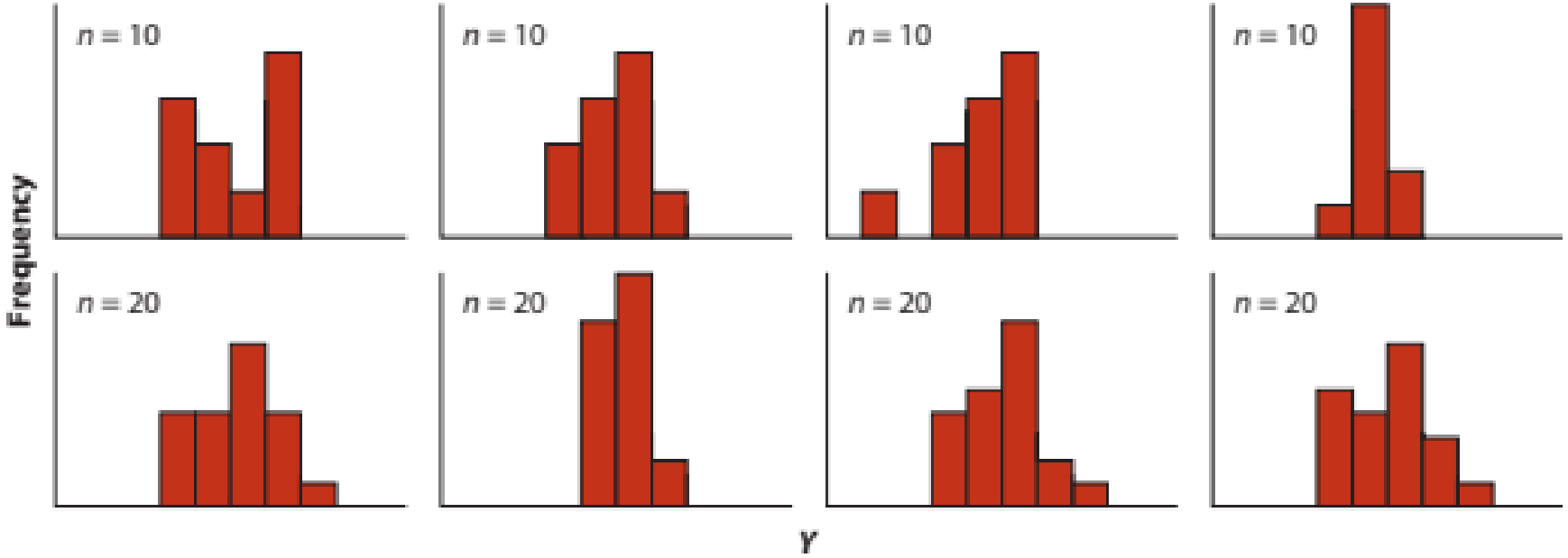
b) normal probability plot (quantile plot)

Inspection of Normality using frequency histograms of data



Problem:

- sample size dependency
- Subjective; not recommended



Inspection of Normality

Top:

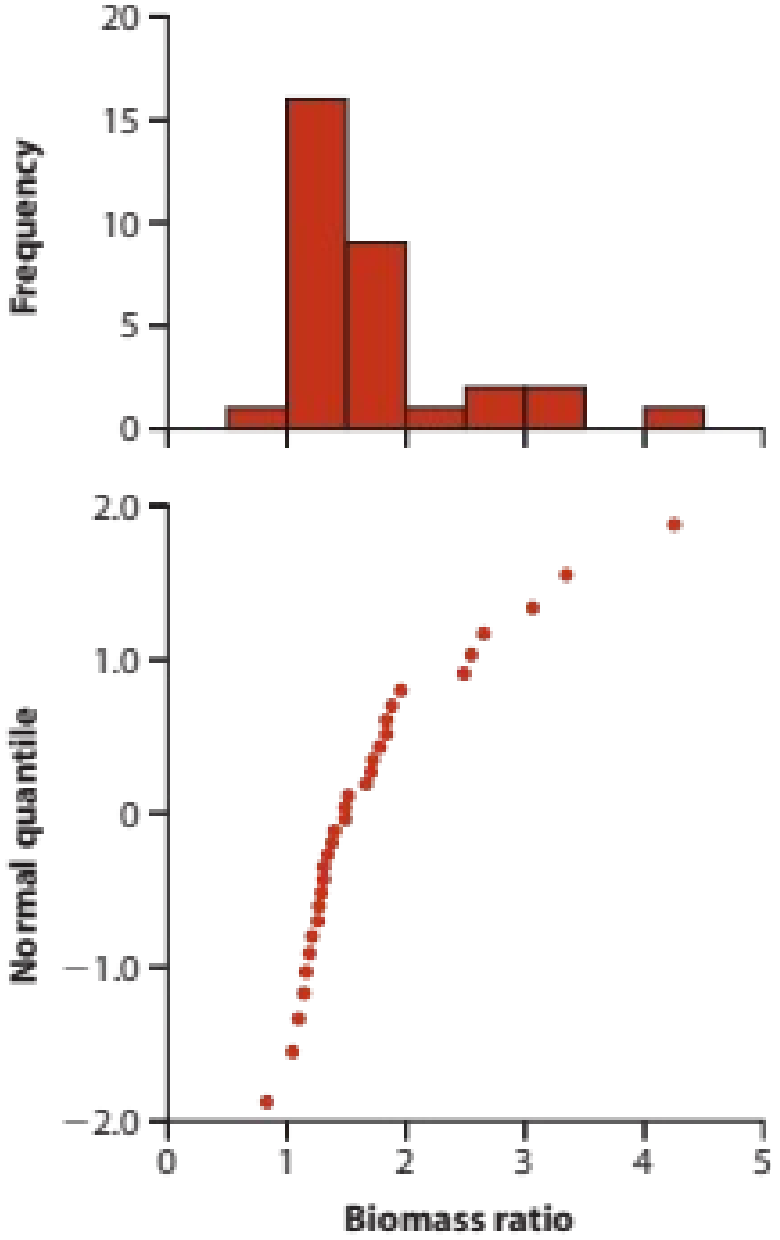
- frequency histogram

```
ggplot(df, aes(x = residuals)) +
  geom_histogram(bins = 20)
```

Bottom:

- quantile plot (normal probability plot)

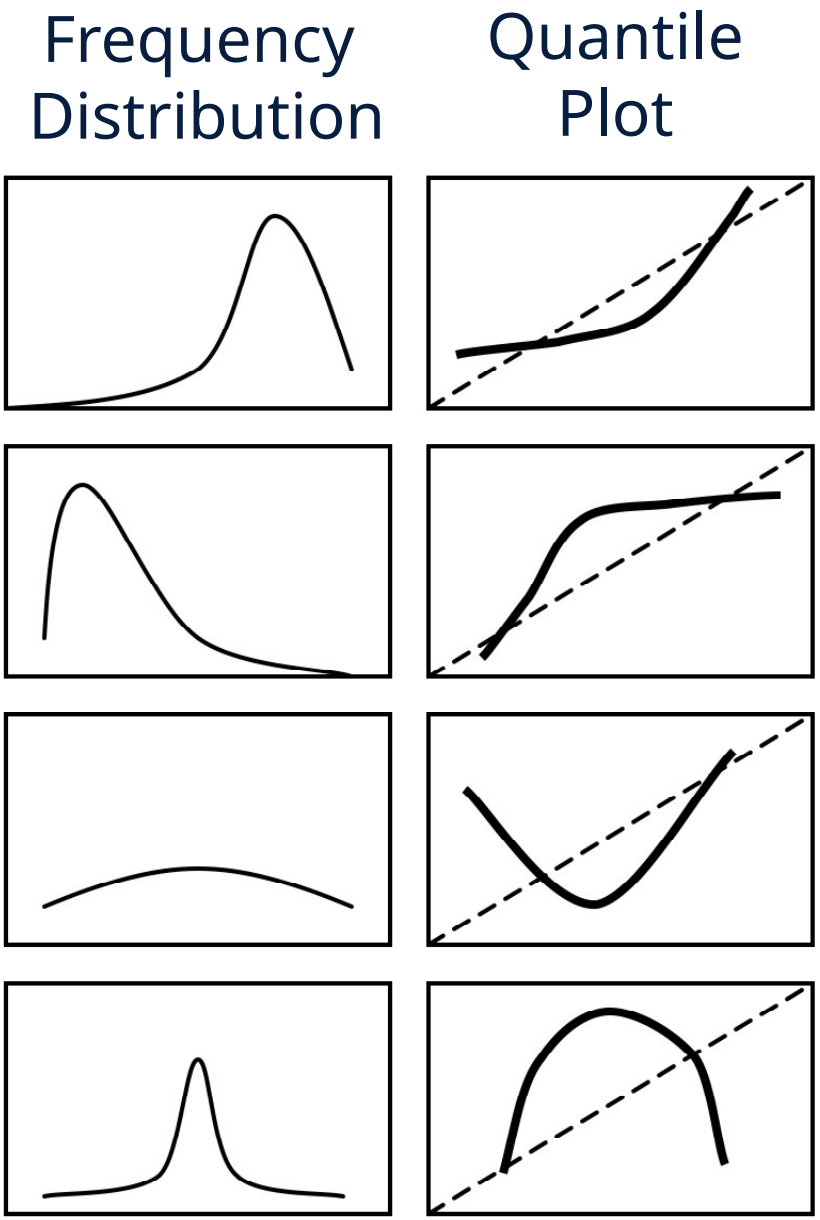
```
ggplot(df, aes(sample = residuals)) +
  stat_qq() + stat_qq_line()
```

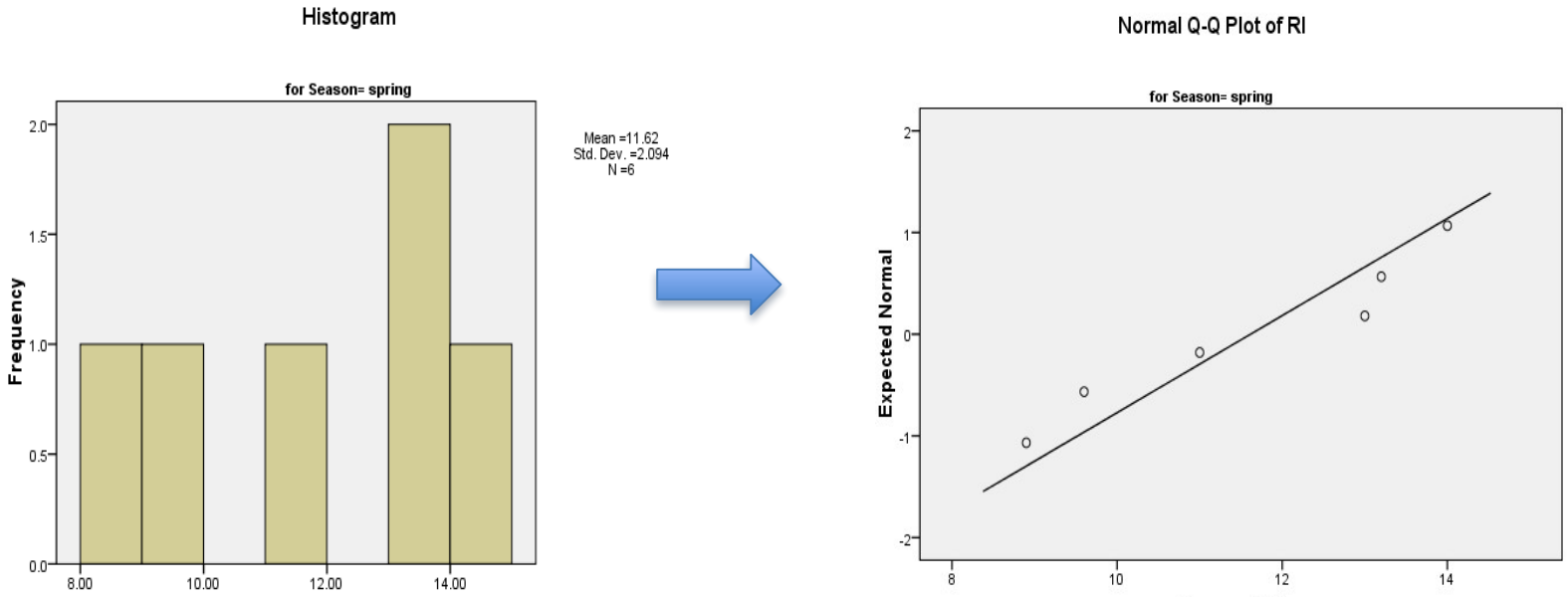


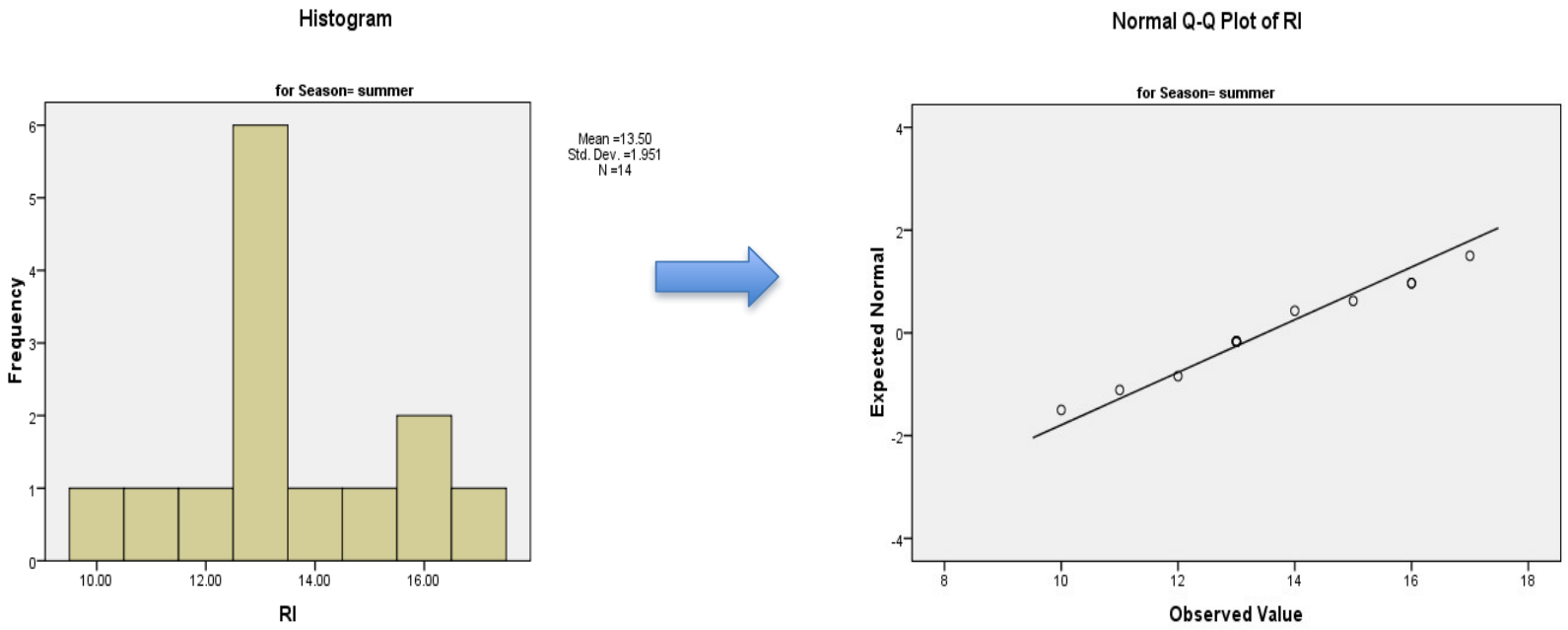
Comparing Normality

Frequency histograms vs. Quantile Plots

Note: The expected distribution of a normally distributed data set in a quantile plot is a straight line




Histogram
for Season= spring
Mean =11.62
Std. Dev. =2.094
N =6
Frequency
2.0
1.5
1.0
0.5
0.0
8.00
10.00
12.00
14.00
Normal Q-Q Plot of RI
for Season= spring
Expected Normal
2
1
0
-1
-2
8
10
12
14


Histogram
for Season= summer
Mean =13.50
Std. Dev. =1.951
N =14
Frequency
6
5
4
3
2
1
0
10.00
12.00
14.00
16.00
RI
Normal Q-Q Plot of RI
for Season= summer
Expected Normal
4
2
0
-2
-4
8
10
12
14
16
18
Observed Value

Statistical Tests for Normality

a) test if skewness & kurtosis are each different from 0

- can do this with a 1-sample t-test

b) Shapiro-Wilk test (n < 50); or Kolmogorov-Smirnov test (n > 50)

If Normality is violated:

- transform data or perform a nonparametric test (e.g., on ranks)

Tests of Normality

		Kolmogorov-Smirnov[a]			Shapiro-Wilk		
	Season	Statistic	df	Sig.	Statistic	df	Sig.
RI	spring	.246	6	.200*	.910	6	.434
	summer	.244	14	.023	.935	14	.355

a. Lilliefors Significance Correction

*. This is a lower bound of the true significance.

```
t.test(skewness, mu = 0)  # 1-sample t-test
shapiro.test(residuals)   # n < 50
ks.test(residuals, "pnorm", mean(residuals), sd(residuals))
```

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Outliers

Effect: strong effect (bias) on tests that compare means

How to investigate:

A) plot residuals vs. treatment means

B) Histogram

Solution:

If value is impossible or can attribute it to known cause (error):

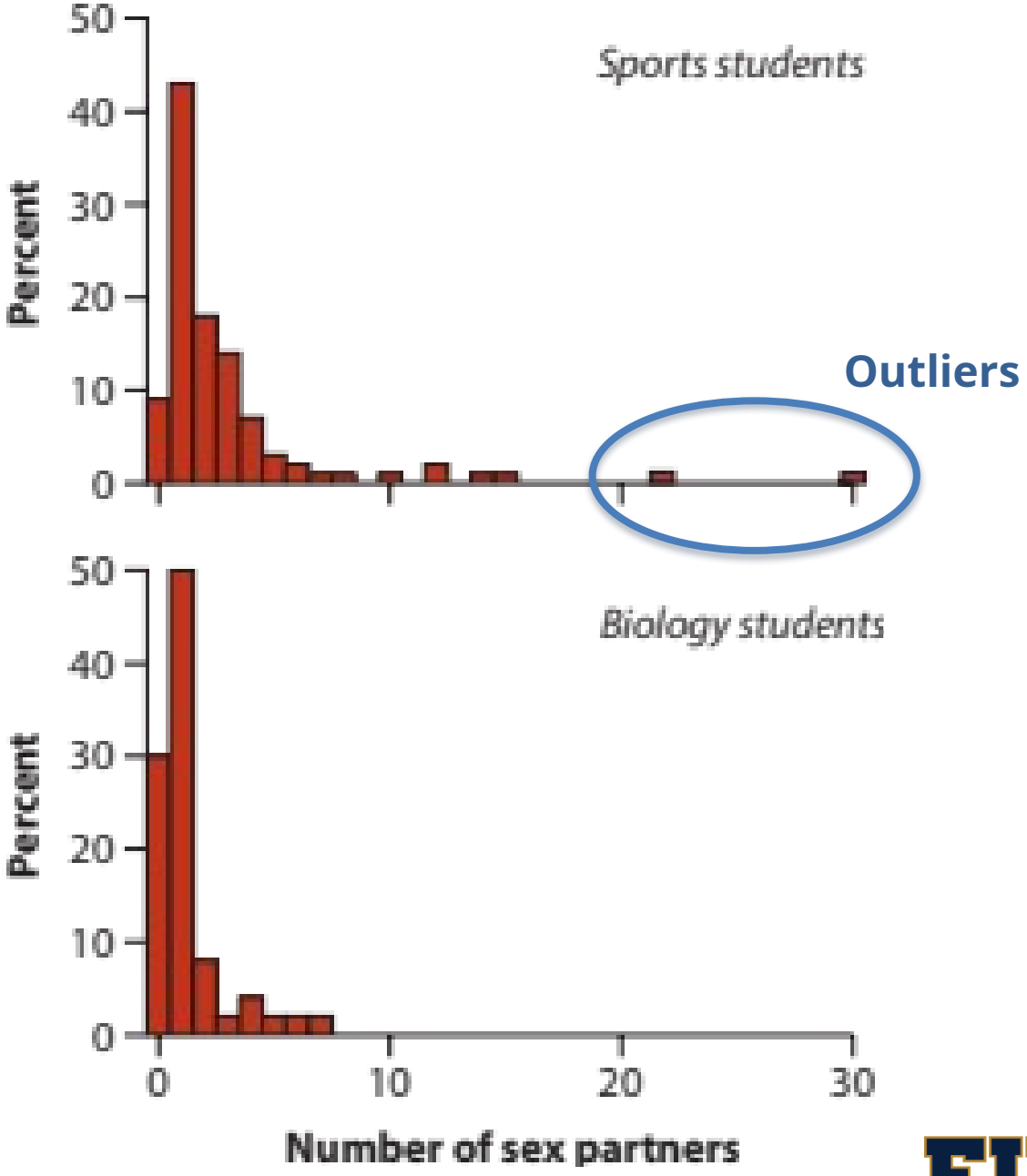
a) omit it

b) Winsorize: replace with mean value and subtract 1 df from error term in analysis

```
DescTools::Winsorize(x, probs = c(0.05, 0.95))
```

BUT ALWAYS report how you handled outliers in your document

If value is possible or you can not attribute to cause – leave it in!



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What to do when the assumptions are not met?

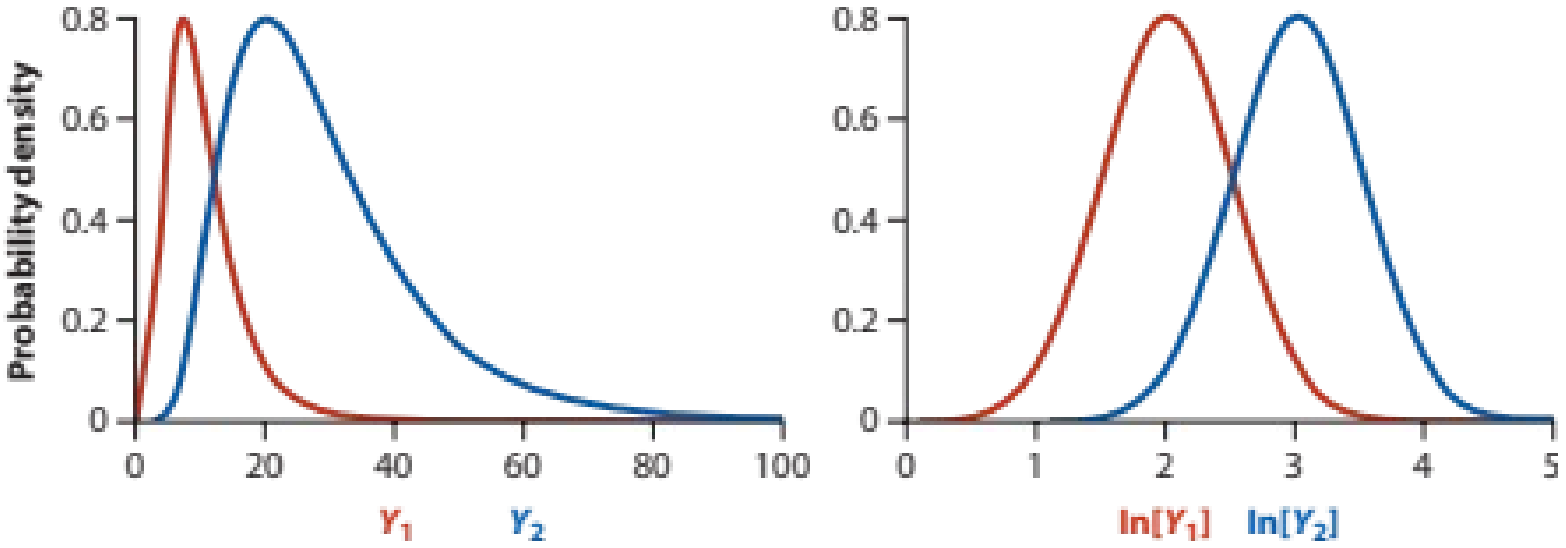
1. Obtain more data

2. Try to improve the fit of the data by employing a data transformation

3. Use a procedure that does not depend on parametric assumptions:
   - Rank the data & perform a non-parametric test
   - Resampling methods
   - Generalized Linear Models
   - Etc…

Data Transformations

- A data transformation changes each data point by some simple mathematical formula
- It is not “magic”, nor is it unethical




```
log(x)      # natural log (ln)
log10(x)    # log base 10
log1p(x)    # log(x + 1), safe for zeros
```

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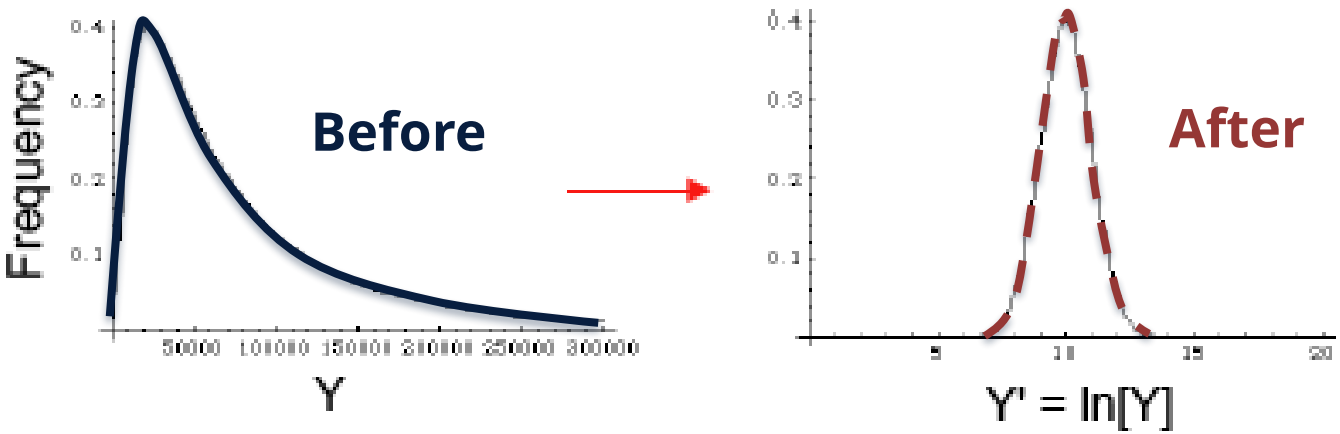
Valid Transformations

- Require the same transformation be applied to each data point (except for a few types of transformations where “0” and “1” are undefined)
- Must be backwards convertible to the original value without ambiguity
- Must have one-to-one correspondence to original value
- Should not be overly complex
- Theoretically there are infinite number of possible transformations, but a few are common:

Log Transformation

$$Y' = \ln[Y]$$



Various Options:

- log10 or ln (X)
- log10 or ln (X + 1) - if zeros in data
- log10 or ln (X x 10 or 100 or 1000, etc.) - if values between 0 and 1

```
log(x); log10(x); log1p(x)
```

Square Root Transformation

$$\sqrt{x_i}$$

$\sqrt{x_i}$ + 0.001 - if zeros in data

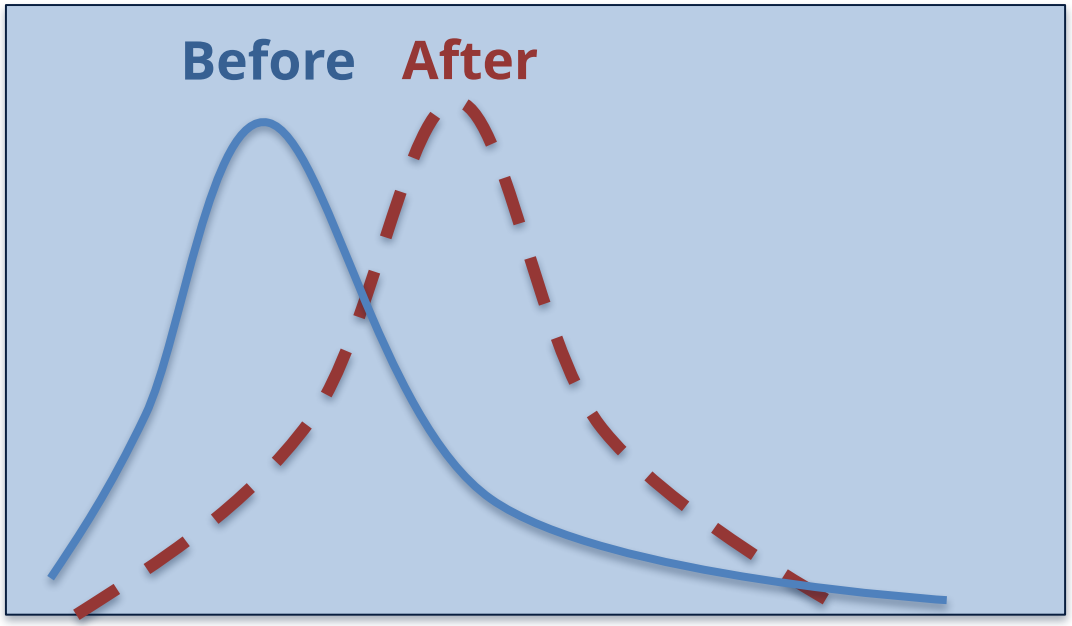
- data are positively skewed ($g_1 > 0$)
- not as “strong” effect on data as log transformation

Reciprocal Transformation

1/X

1/ (x + 1) - use if data contain zeros

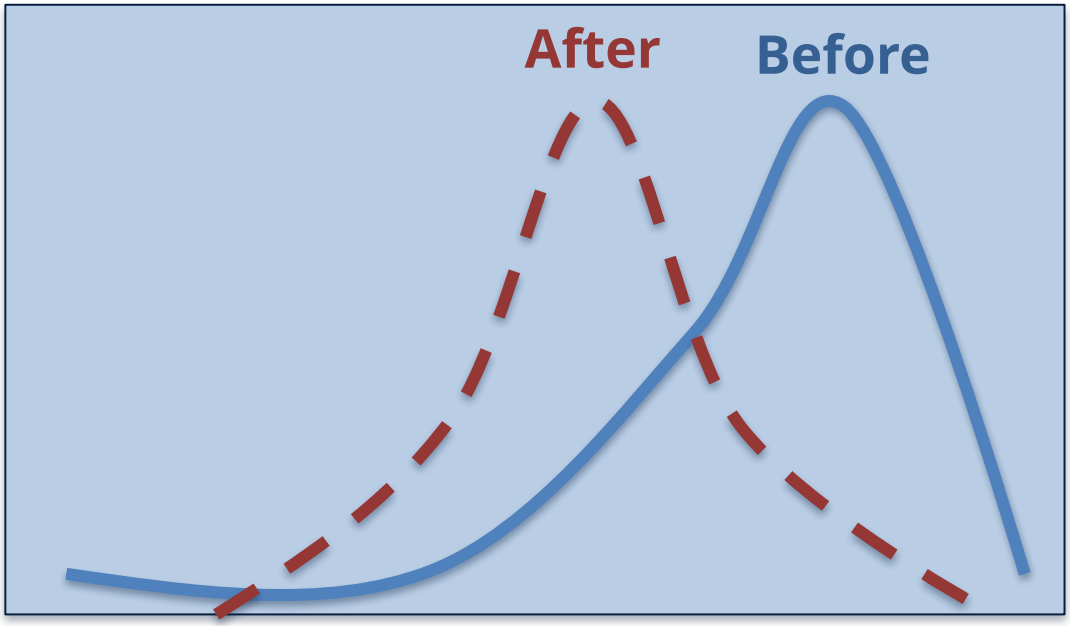
- errors are nonlinear & data positively skewed



Power Transformation

X^y (where y = 2, 3, etc.)

- data distributions are negatively skewed ($g_1 < 0$)



Angular Transformation

inverse or arcsin $\left(\sqrt{x_i}\right)$

arcsin $\left(\sqrt{\frac{1}{4N}}\right)$ (for 0 values)

arcsin $\left(\sqrt{\frac{1}{1-4N}}\right)$ (for 1.00 values); N = sample #

- data are proportions or percentages or binomial data
- often not needed if values between 0.3 and 0.7
- data distribution often diamond shaped pattern in residual vs. mean plot
- Controversial: new stats papers don't recommend using this

Standardization

- *stdize*
- centre
- scale to SD
- rescale 0-1

```
df$var_std <- stdize(df$var)
```

```
df$var_original <- unstdize(df$var_std)
```

Range Standardization

- Linear rescale to 0-1, doesn't centre on mean nor scale by SD. Preserves original distribution shape.
- Steinley, D. 2006a. K-means clustering: a half-century synthesis. British Journal of Mathematical and Statistical Psychology 59:1–34.
- Steinley, D. 2006b. Profiling local optima in K-means clustering: developing a diagnostic technique. Psychological Methods 11:178–192.

```
df$var_range <- range_stdize(df$var)
df$var_original <- unrange_stdize(df$var_range)
```

One Hot Encoding

- Aka ‘binarize wide’
- Convert a single categorical variable to multiple columns of binary variables
- Used by ML models & ML dorksters

```
df |> one_hot_encode(category_column)
```

Rank Transformation
(non-parametric transformation)

Method:

- Rank each data point from lowest to highest regardless of treatment group
- DO NOT retest data to see if parametric assumptions are met. It is unnecessary because the resulting test is now considered a non-parametric test in which the assumptions of homogeneity of variances and normality no longer apply.

Thanks. Any questions?

- Projects coded in R & (aim to) require minimal R knowledge
- Code / figures / contact / links to all papers & thesis: simondedman.com
- github.com/SimonDedman/gbm.auto & /MarSpatAuto & /movegroup
- simondedman@gmail.com

Thanks to Dr Chuck Bangley, beta tester

- AI and the Future of Marine Science (medium.com/@SimonDedman)
- Delta sensitivity, or why your results may not reflect true biological preferences (medium.com/@SimonDedman)
- Please let me know criticisms/praise/suggestions by email or in person

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M. Castleton, B. Whitlock, A. Carlisle, J. Ganong, A. Boustany, S. Teo, S. Wilson, MJW. Stokesbury.
TAG: Robbie Schallert. TAG/TOPP Data Management. NOAA BTRP. Tag a Giant Fund of The Ocean Foundation, Wildlife Computers & Lotek, Inc.