



Fostering open science and open data with R

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Made possible by:



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ropensci.github.io/ropensci_intro/

“ Most science is not reproducible or repeatable, even within the same lab group over time.

A reproducibility crisis



The scientific workflow



“ Instructions for preparation of the Biographical Sketch have been revised to rename the Publications section to "Products" and amend terminology and instructions accordingly. This change makes clear that products may include, but are not limited to, publications, data sets, software, patents, and copyrights.

Issuance of a new NSF Proposal & Award Policies and Procedures Guide (October 4th)

PLOS Data Policy

“ the Data Policy states the ‘minimal dataset’ consists “of the dataset used to reach the conclusions drawn in the manuscript with related metadata and methods, and any additional data required to replicate the reported study findings in their entirety. This does not mean that authors must submit all data collected as part of the research, but that they must provide the data that are



“ Enable access to scientific data repositories, full-text of articles, and science metrics and also facilitate a culture shift in the scientific community.



More info @ ropensci.org/packages

Data

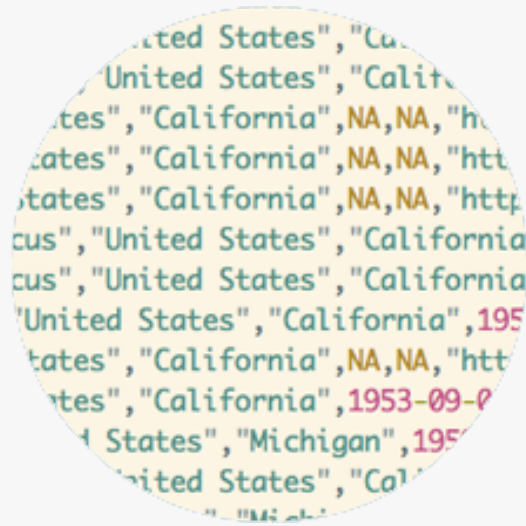
Treebase,
Fishbase,
Flybase,
GBIF, Vertnet
Dryad, ITIS
NPN, Taxize
opensnp

Journals

PLOS
Springer
textmine
pensoft

Data publication

figshare
Mendeley
DataONE,
rAltmetric, EML,
rNEXML



Access all available ecological data

Liberating 400+ million observation records

Full text 100k articles

Data from papers in > 200 journals



Accessing data behind papers – dryad

```
library(rdryad)
dryaddat <- download_url("10.255/dryad.1759")
# Get a file given the URL
file <- dryad_getfile(dryaddat)
dim(file)
```

```
## [1] 131 30
```

Dataset

Biodiversity records from museums

```
library(ecoenigne)
pinus_data <- ee_observations(genus = "Pinus", georeferenced =
TRUE, page = 1:25)
nrow(pinus_data$data)
```

```
## [1] 625
```

Get complete and current taxonomic records

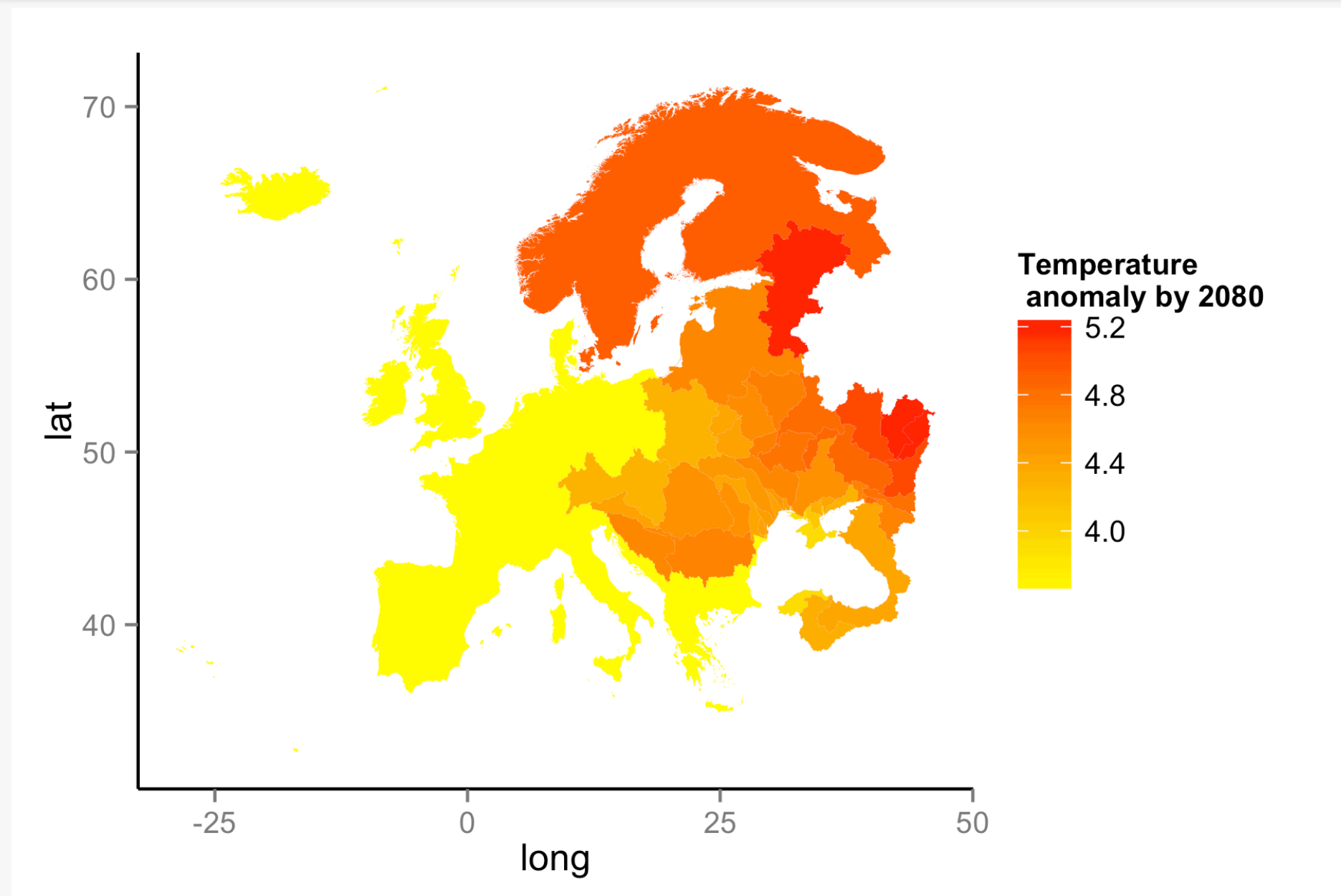
```
classification(c("Helianthus annuus"), db = "ncbi")
```

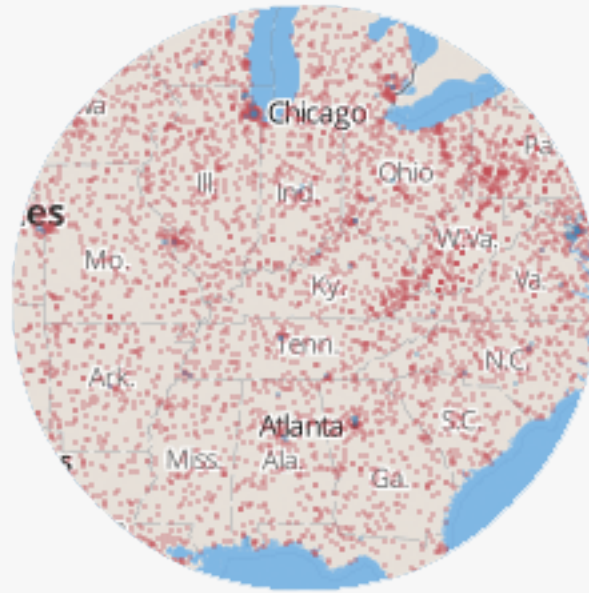
```
## $`Helianthus annuus`  
##           name      rank  
## 1  cellular organisms  no rank  
## 2      Eukaryota superkingdom  
## 3    Viridiplantae  kingdom  
## 4    Streptophyta  phylum  
## 5    Streptophytina  no rank  
... cutoff  
## attr("class")  
## [1] "classification"  
## attr("db")  
## [1] "ncbi"
```

World Bank climate knowledge portal

rWBclimate

```
library(rWBclimate)
eu_basin <- create_map_df(Eur_basin)
eu_basin_dat <- get_ensemble_temp(Eur_basin, "annualanom", 2080, 2100)
```



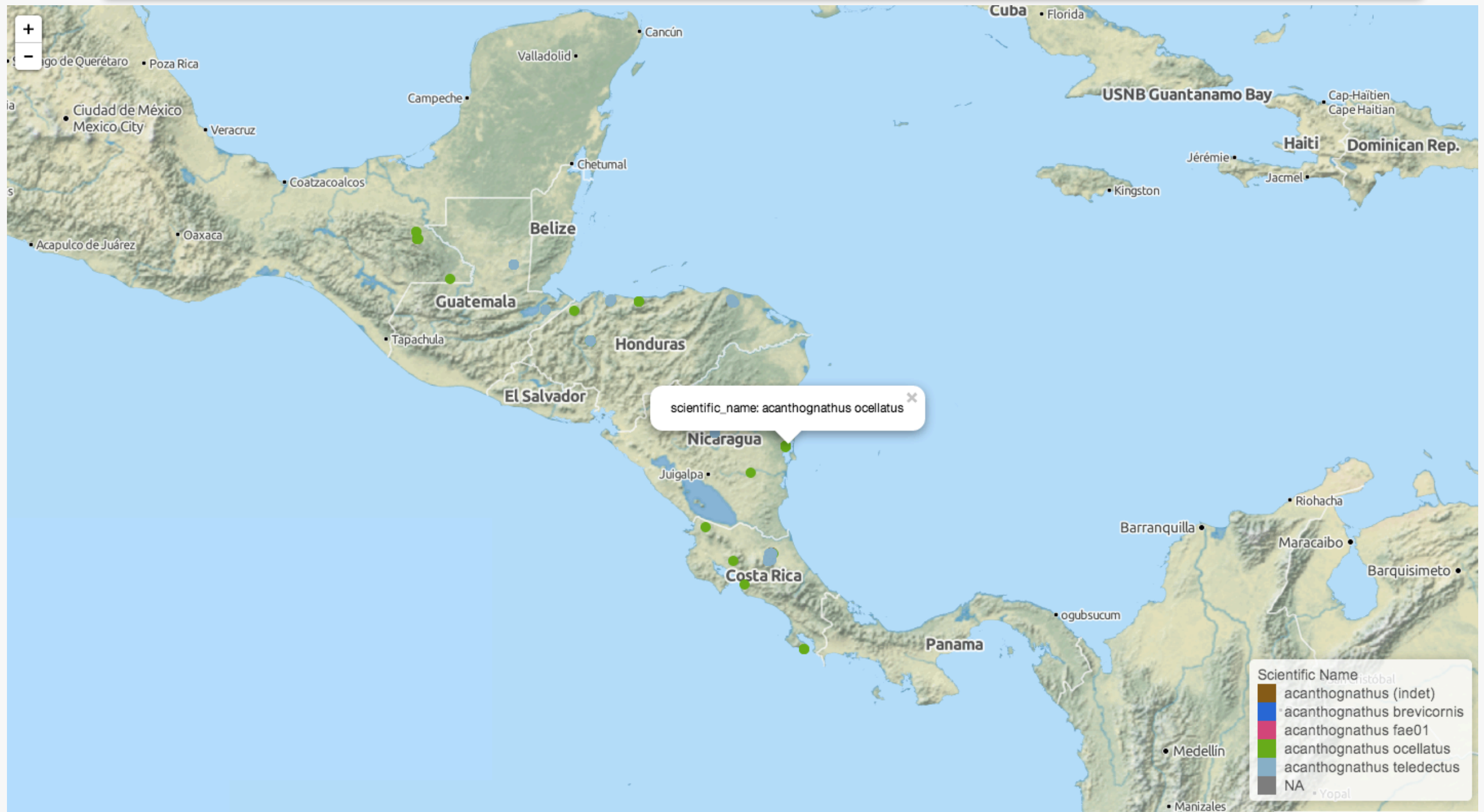


Interactively visualize and analyze data

Explore these data interactively,
including any plots you might make

Taxon specific databases - AntWeb

```
library(AntWeb)
acdd <- aw_data(genus = "acanthognathus")
aw_map(acdd)
```



Sharing data – (figshare)

Using figshare's [API](#) it is possible to share figures, data and any other object generated in **R** and obtain a data citation.

```
library(rfigshare)
id <- fs_create("Fisheries dataset", "A dataset containing
catch for 4 important commercial fish species", "dataset")
fs_upload(id, "dat.csv")
```


A reproducible workflow (in R)

Load your own data

load all raw
untransformed
data.

→ **Acquire additional data from the web**

e.g., resolve
taxonomic names,
acquire additional
datasets.

→ **Document everything with metadata**

The EML package
makes it really easy
to add valid EML to
your data

→ **Submit to a persistent repository**

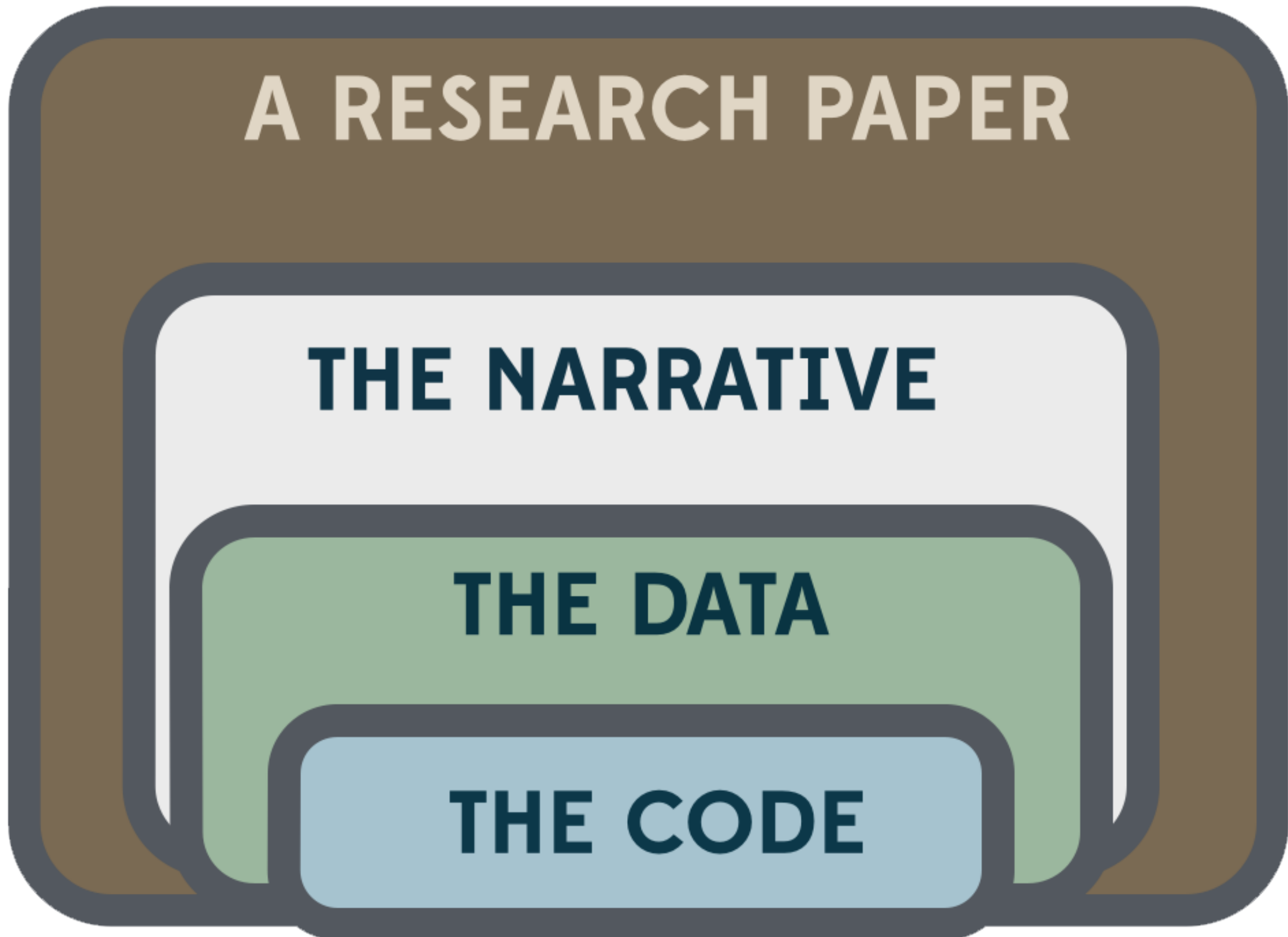
Share your data by
submitting to figshare
or one at your
institution

Generate interactive
maps, viewers

The scientific workflow



The open scientific workflow



ropensci.org

ropensci on GitHub

@ropensci on Twitter

Questions or comments to: info@ropensci.org