

Shinyscholar

A template for creating reproducible Shiny applications in R

Simon Smart and Tim Lucas, School of Medical Sciences, University of Leicester

9th September 2025

Shinyscholar helps create reproducible analytical apps in R

- Creates an empty application with a regular structure
- Analyses can be reproduced outside the app



Shinyscholar helps create reproducible analytical apps in R

- Creates an empty application with a regular structure
- Analyses can be reproduced outside the app
- Make it easier to follow software development best practices
- Developers can concentrate on creating functionality



R has cutting-edge statistical methods but barriers can restrict uptake

- Know how to use R

R has cutting-edge statistical methods but barriers can restrict uptake

- Know how to use R
- Able to comprehend documentation

R has cutting-edge statistical methods but barriers can restrict uptake

- Know how to use R
- Able to comprehend documentation
- Access to specific data

R has cutting-edge statistical methods but barriers can restrict uptake

- Know how to use R
- Able to comprehend documentation
- Access to specific data
- Format data in specific ways

Shiny apps enable anybody to access the power of R

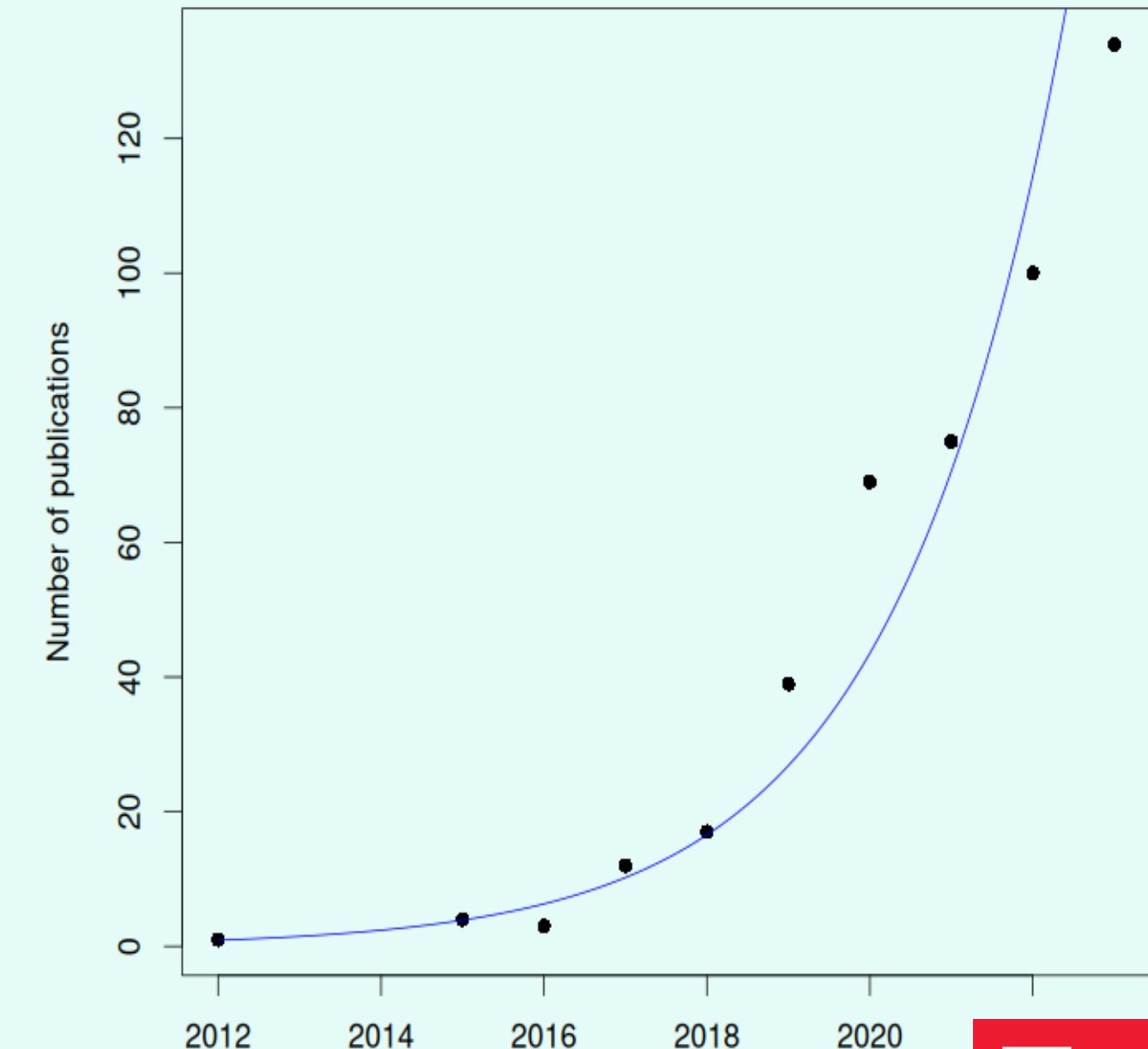
```
ui <- fluidPage(  
  numericInput("number", "Enter a number", value = 5),  
  textOutput("answer"))  
  
server <- function(input, output) {  
  output$answer <- renderText(input$number * 10)  
}  
  
shinyApp(ui, server)
```

Enter a number

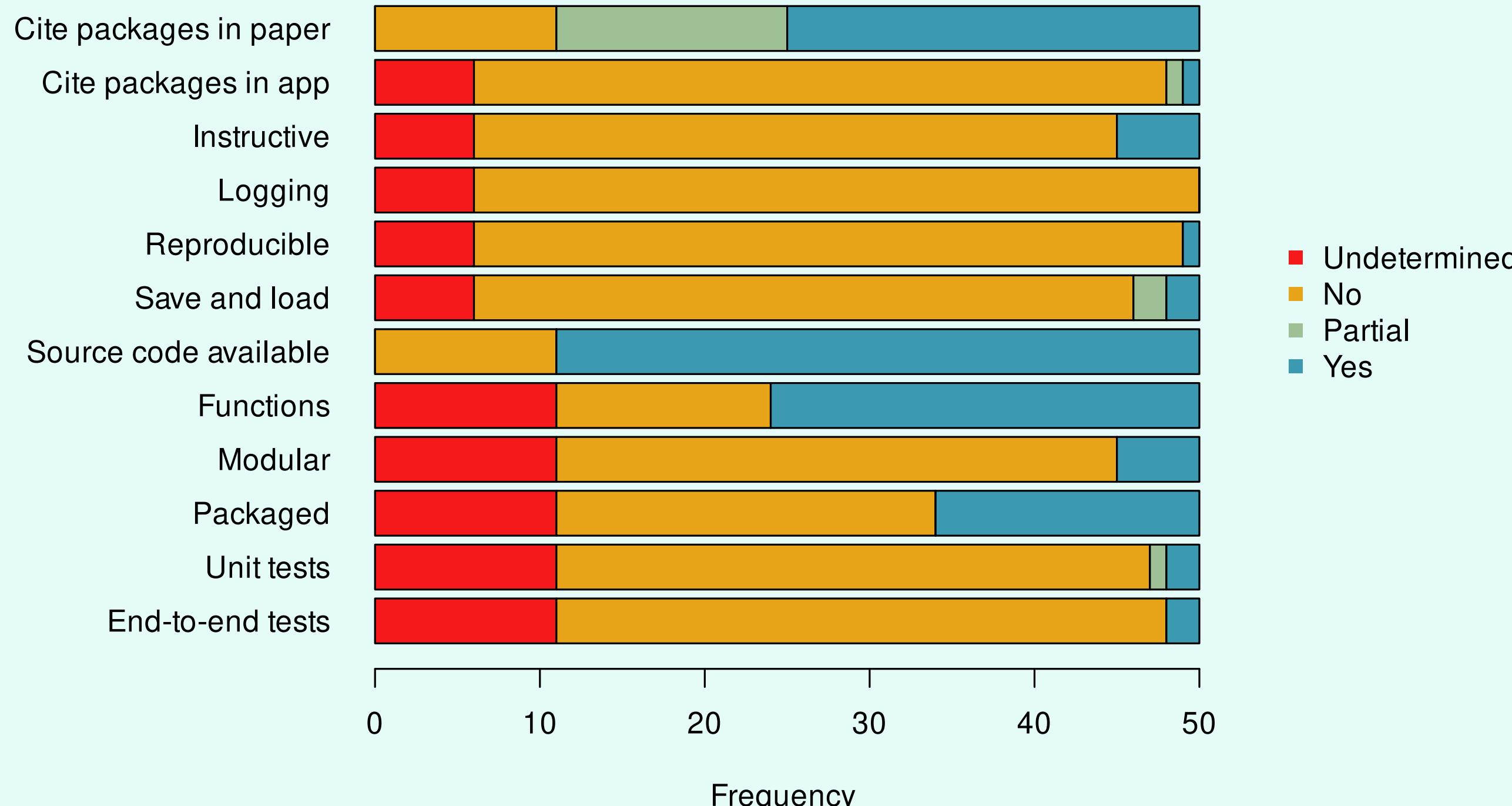
50

Shiny apps are becoming increasingly popular in academia

- The low barrier to entry makes Shiny popular
- Substantially increased apps as a method of dissemination



Current apps do not follow best practices



Wallace bucked the trend

 Intro Occ Data Env Data Process Occs Process Envs Env Space Partition Occs Model Visualize Transfer Reproduce Support 

Species menu

Paraponera_clavata

Component: Obtain Occurrence Data 

Modules Available:

- Query Database (Present)
- User-specified

Module: Query Database (Present) 

R packages: BIEN, spocc

Choose Database

GBIF VertNet BIEN

Keep only occurrences with uncertainty values

Include Data Source Citations

Enter species scientific name

Set maximum number of occurrences

Query Database

Module Developers: Jamie M. Kass, Bruno Vilela, Gonzalo E. Pinilla-Buitrago, Hannah Owens, Cory Merow, Robert P. Anderson

BIEN references
Tools for Accessing the Botanical Information and Ecology Network Database

Package Developers: Brian Maitner

Log window

Please find messages for the user in this log window.

> **Paraponera clavata** | Total gbif records returned [2000] out of [3686] total (limit 2000). Records without coordinates removed [6]. Duplicated records removed [160]. Remaining records [1834].



The map displays a distribution map for the species Paraponera clavata. It shows numerous red circular markers representing occurrence records, primarily concentrated in the Amazon Basin of South America, with smaller clusters in Central America (Panama, Costa Rica, and southern Mexico). The map includes labels for countries like Mexico, Guatemala, Costa Rica, Panama, Colombia, Venezuela, Guyana, Suriname, Ecuador, Peru, Bolivia, Brazil, and Paraguay, along with major cities and river systems.

Kass et al. (2022) DOI: 10.1111/ecog.06547 install.packages("wallace") (not online)

modules contains information about each module

```
modules <- data.frame(  
  "component" = "transform",  
  "long_component" = "Transform numbers",  
  "module" = "multiply",  
  "long_module" = "Multiply a number",  
  "map" = FALSE,  
  "result" = TRUE,  
  "rmd" = TRUE,  
  "save" = TRUE,  
  "download" = FALSE,  
  "async" = FALSE)
```

create_template() creates the skeleton app

```
shinyscholar::create_template(  
  path = file.path("~", "Documents"),  
  name = "demo",  
  author = "Simon Smart",  
  include_map = FALSE,  
  include_table = FALSE,  
  include_code = FALSE,  
  common_objects = "result",  
  modules = modules,  
  install = TRUE)  
  
demo::run_demo()
```

create_template() creates the skeleton app

The screenshot shows the shiny scholar interface with the following components:

- Header:** Intro, Transform numbers (highlighted in blue), Reproduce, Support, and a power icon.
- Left Sidebar (Component View):**
 - Component: Transform numbers** with a help icon.
 - Multiply** button.
 - Module: Multiply a number** with a help icon.
 - R packages:** Run module transform_multiply button.
 - Module developers:** Simon Smart.
- Global settings:** Delete data button.
- Results:** A small number '0'.
- Log window:** Displays the message: ***WELCOME TO DEMO***.

Reproducibility relies on each module calling one function

Create the function:

```
transform_multiply <- function(number) number * 10
```

Reproducibility relies on each module calling one function

Create the function:

```
transform_multiply <- function(number) number * 10
```

Use it in the module and store the input:

```
common$result <- transform_multiply(input$number)  
common$meta$transform_multiply$number <- input$number
```

Reproducibility relies on each module calling one function

Create the function:

```
transform_multiply <- function(number) number * 10
```

Use it in the module and store the input:

```
common$result <- transform_multiply(input$number)  
common$meta$transform_multiply$number <- input$number
```

In the Rmarkdown:

```
result <- transform_multiply('{{transform_multiply_number}}')
```

Reproducibility relies on each module calling one function

Create the function:

```
transform_multiply <- function(number) number * 10
```

Use it in the module and store the input:

```
common$result <- transform_multiply(input$number)  
common$meta$transform_multiply$number <- input$number
```

In the Rmarkdown:

```
result <- transform_multiply('{{transform_multiply_number}}')
```

metadata() takes care of a lot of the boring code

Disagapp for disaggregation regression

 Intro **Response** Covariates Aggregation Prepare Fit Predict Reproduce ☰ Support ▾

Component: Response Data [?](#)

- [Upload shapefile](#)
- [Upload spreadsheet](#)
- [Combine spreadsheet and shapefile](#)
- Example datasets**
- [Edit data](#)
- [Simplify polygons](#)

Module: Load example datasets [?](#)

R packages: *sf, SpatialEpi*

Dataset

Malaria in Madagascar [▼](#)

Delete existing data?

[Load data](#)

Module developers: Simon E H Smart

sf: Simple Features for R

Package Developers: Edzer Pebesma, Roger Bivand, Etienne Racine, Michael Sumner, Ian Cook, Tim Keitt, Robin Lovelace, Hadley Wickham, Jeroen Ooms, Kirill Müller, Thomas Lin Pedersen, Dan Baston, Dewey Dunnington

[CRAN | documentation](#)

SpatialEpi: Methods and Data for Spatial Epidemiology

Package Developers: Cici Chen, Albert Y. Kim, Michelle Ross, Jon Wakefield, Mikael Moise

[CRAN | documentation](#)

Log window

- ✓ Response data has been loaded and is summarised in the results tab
- ✓ Covariate data has been uploaded
- ✓ Aggregation data has been uploaded

There are currently no tasks running

Map Results [Component guidance](#) [Module guidance](#) [Save](#)

Background map: ESRI Topographic

Leaflet | Tiles © Esri — Esri, DeLorme, NAVTEQ, TomTom, Intermap, iPC, USGS, FAO, NPS, NRCAN, GeoBase, Kadaster NL, Ordnance Survey, Esri Japan, METI, Esri China (Hong Kong), and the GIS User Community



MetalInsight for network metaanalysis

Component: Frequentist NMA

- Forest plot**
- Comparisons
- Inconsistency
- Summary forest plot

Module: Forest plot

R packages: *netmeta, meta*

Generate plots

All studies **Selected studies excluded**

Limits of the x-axis for all studies:

Minimum	Maximum
-0.7	0.5

Limits of the x-axis without excluded studies:

Minimum	Maximum
-0.7	0.5

▶ Module attribution

Model: Random effect (RE) Fixed effect (FE)

Plot download format: PDF PNG SVG

Studies to exclude: Nothing selected

Log window

- ✓ Default continuous data has been loaded
- ✓ The analysis has been configured
- ⌚ Running initial frequentist analysis
- ✓ Initial frequentist analysis is complete

Data table (Click to open / hide this panel)

Results **Guidance**

Results for all studies
Between-study standard deviation: 0.28
Number of studies: 45, Number of treatments: 4

Treatment	Comparison: other vs 'Placebo' (Random Effects Model)	MD	95%-CI
Gabapentinoids		-0.24	[-0.41; -0.08]
Glucocorticoids		-0.12	[-0.62; 0.38]
Ketamine		-0.08	[-0.29; 0.13]

Results with selected studies excluded
Between-study standard deviation: 0.28
Number of studies: 45, Number of treatments: 4

Treatment	Comparison: other vs 'Placebo' (Random Effects Model)	MD	95%-CI
Gabapentinoids		-0.24	[-0.41; -0.08]
Glucocorticoids		-0.12	[-0.62; 0.38]
Ketamine		-0.08	[-0.29; 0.13]



Learn more

- `install.packages("shinyscholar")`
- Example app at <https://simonsmart.shinyapps.io/shinyscholar/>
`install.packages("shinyscholar",
dependencies = TRUE)`
- README guide to development at <https://simon-smart88.github.io/shinyscholar/>
- Workshop for Ukraine

Acknowledgments

- Wellcome for funding
- Wallace developers especially Rob Anderson
- Tim Lucas

