

# Structuring projects

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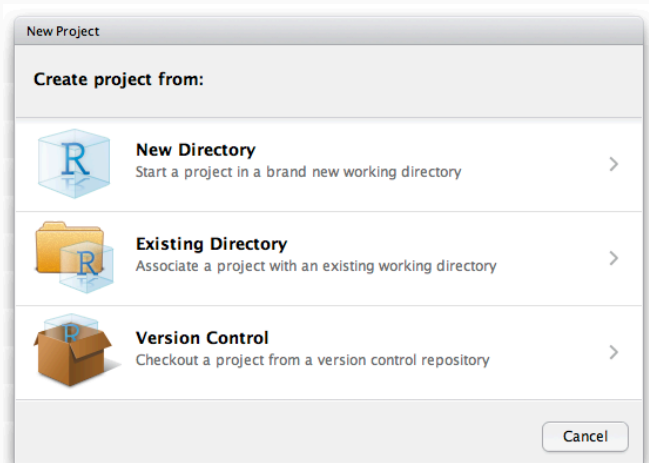
@frod\_san

<https://frodriguezsanchez.net>

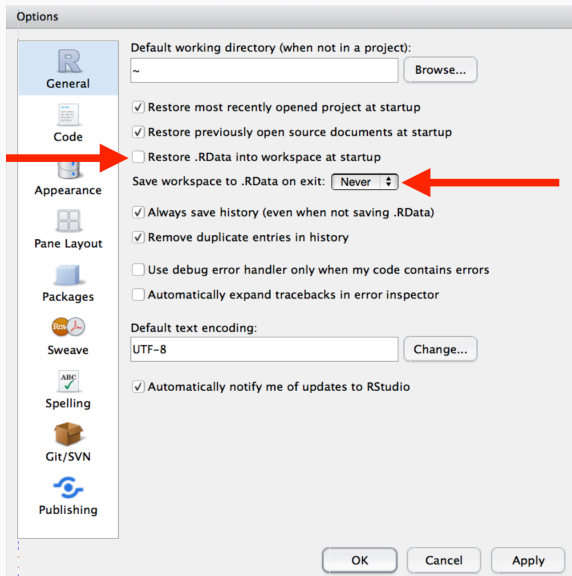
# One Project = One Folder

```
myproject
|
|- data
|
|- code
|
|- output (figures etc)
|
|- manuscript
```

- Self-contained
- Easy to navigate (file paths)
- Easy to share



# Avoid saving workspace



## Use here for file paths



```
setwd('C:/Users/PACO/myproject')
```

```
mydata <- read.csv('data/mydata.csv')
```



```
library('here')
```

```
mydata <- here('data', 'mydata.csv')
```



## fertile package: real-time feedback on reproducibility

```
library('fertile')  
  
setwd("C:/Users/FRS")
```

*Error: setwd() is likely to break reproducibility. Use here::here() instead.*

<https://github.com/baumer-lab/fertile>

## Structuring projects: guidelines

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# Guidelines for structuring projects

- All files in same directory

Noble 2009, Rodriguez-Sanchez et al 2016, Wilson et al 2017

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- **Raw data** separate from **clean data**

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Noble 2009, Rodriguez-Sanchez et al 2016, Wilson et al 2017



# Project organisation example

myproject

- data
  - data-raw
  - data-clean
- code
- output (figures etc)
- manuscript
- README
- License
- Makefile

- What
- Who
- How
- Licence
- Citation
- etc

README.md

## pandanusisotopes



This repository contains the data and code for our paper:

Florin, A. et al. (2020). *Palaeoprecipitation data from Madjedbebe, northern Australia: A novel proxy from ancient pandanus.*

### How to cite

Please cite this compendium as:

Marwick, B., A. Florin et al., (2020). *Compendium of R code and data for Palaeoprecipitation data from Madjedbebe, northern Australia: A novel proxy from ancient pandanus.* Accessed 16 Oct 2020. Online at <https://doi.org/xxx/xxx>

### How to download

You can download the compendium as a zip from from this URL: <https://github.com/benmarwick/pandanusisotopes/archive/master.zip>

### Licenses

**Text and figures** : [CC-BY-4.0](#)

**Code** : See the [DESCRIPTION](#) file

**Data** : [CC-0](#) attribution requested in reuse

## Document your data

<https://docs.ropensci.org/dataspice/>

```
library("dataspice")
create_spice() # create CSV templates for metadata

edit_creators() # open Shiny apps to edit the CSVs
prep_access()
edit_access()
prep_attributes()
edit_attributes()
edit_biblio()

write_spice() # write machine-readable metadata

build_site() # build human-readable metadata report
```

Break up scripts

```
prepare_data.R
```

```
run_analysis.R
```

```
make_figures.R
```

(and `makefile` will run them in the right order)

## makefile runs code in appropriate order

makefile.R

```
source("prepare_data.R")
```

```
source("run_analysis.R")
```

```
source("make_figures.R")
```

## Don't Repeat Yourself (DRY)

```
dataset %>%  
  filter(species == "Laurus nobilis") %>%  
  ggplot() +  
  geom_point(aes(x, y))
```

```
dataset %>%  
  filter(species == "Laurus azorica") %>%  
  ggplot() +  
  geom_point(aes(x, y))
```

# Don't Repeat Yourself

Write functions (documented + tested)

```
plot_species <- function(sp, data) {  
  data %>%  
    filter(species == sp) %>%  
    ggplot() +  
    geom_point(aes(x, y))  
}
```

# Don't Repeat Yourself

Use functions

```
plot_species(sp = "Laurus nobilis", dataset)
```

```
plot_species(sp = "Laurus azorica", dataset)
```



# Don't Repeat Yourself

Use for loops

```
for (i in species) {  
  plot_species(sp = i, dataset)  
}
```

Good ol' `lapply`

```
lapply(species, plot_species, data = dataset)
```

## Don't Repeat Yourself

```
library("purrr")  
  
map(species, plot_species, data = dataset)
```

Why rather than What

```
## Response is not linear, so fit gam rather than lm  
  
model.height <- gam(height ~ s(diameter), data = trees)
```

## Use meaningful names for objects

```
m1 <- lm(height ~ diameter, data = trees)
m2 <- gam(height ~ s(diameter), data = trees)
```

## Use meaningful names for objects

```
m1 <- lm(height ~ diameter, data = trees)
m2 <- gam(height ~ s(diameter), data = trees)
```

```
model.linear <- lm(height ~ diameter, data = trees)
model.gam <- gam(height ~ s(diameter), data = trees)
```

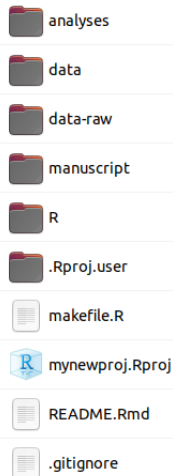
## Project templates

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# Automatic project creation with template

```
library('template')
```

```
new_project("mynewproj",  
            package = FALSE)
```





# template: New projects also on GitHub

```
new_project("mynewproj",  
            package = FALSE,  
            github = TRUE)
```

 Pakillo / mynewproj Private

[Code](#) [Issues](#) [Pull requests](#) [Actions](#) [Projects](#) [Wiki](#) [Security](#) [Insights](#) [Settings](#)

 master  1 branch  0 tags

Go to file

Add file

 Code



**Pakillo** Initial commit

654e46f 2 minutes ago 1 commit



.gitignore

Initial commit

2 minutes ago



README.Rmd

Initial commit

2 minutes ago



makefile.R

Initial commit

2 minutes ago



mynewproj.Rproj

Initial commit

2 minutes ago

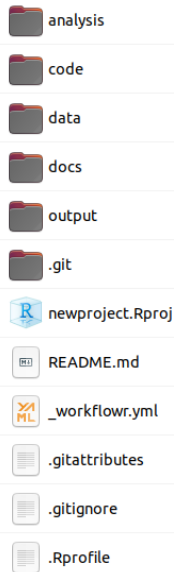


**workflowr:**  
reproducible projects with  
website

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## wflow\_start creates project scaffolding

```
library('workflowr')  
  
wflow_start("newproject")
```



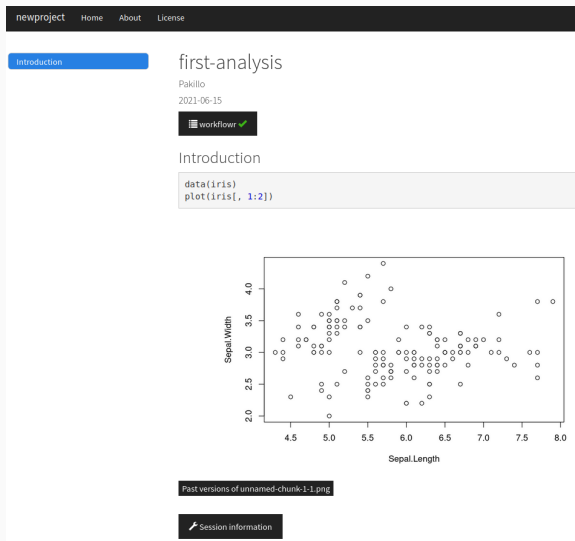
## wflow\_open starts new analysis

```
wflow_open("analysis/first-analysis.Rmd")
```

```
---  
title: "first-analysis"  
author: "Pakillo"  
date: "2021-06-15"  
output: workflowr::wflow_html  
editor_options:  
  chunk_output_type: console  
---  
|  
## Introduction  
  
````{r}  
data(iris)  
plot(iris)  
````
```

# wflow\_build runs analyses and generates website

## wflow\_build()



## wflow\_publish commits changes & updates everything

```
wflow_publish(c("analysis/first-analysis.Rmd",  
               "analysis/index.Rmd",  
               "analysis/about.Rmd",  
               "analysis/license.Rmd"),  
             message = "Publish initial analyses")
```

```
wflow_use_github("Pakillo")
```

```
wflow_git_push()
```