Simple process for sharing R code via Docker

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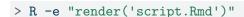
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1 Introduction

Lets assume you have an Rmd file, say script.Rmd, you're written to analyze some data. You now want to share the code with a colleague. How to proceed?

The simplest option is simply to send him/her the "rmd" file containing the code via email/text/slack/discord/USB drive etc.

The next step will be for the code recipient to attempt to load and run the code typically using either of two methods 1) use Rstudio.app to open the file and knit it, or 2) render it from the command line with something like





Sometimes this works. Frequently however the process will fail for any number of reasons. Ideally to facilitate reproducibility the new user will have as similar a computing environment as the original developer. This can be difficult to achieve especially given the dynamic nature of open source software. For example your colleague may have an outdated version of R installed on their workstation, or their R environment may be missing a necessary package, or the package may be present but its the wrong version, or the program may need to source an additional file thats missing, or load some data that it can't find.

All of these problems go away if instead of sending the program as a standalone text file you send it as a docker image. In this post we'll walk through the process of dockerizing the R code.

```
title: "Penguins analysis"
author: "R.G. Thomas"
date: "`r format(Sys.time(), '%B %d, %Y')`"
fontsize: 11pt
geometry: "left=3cm,right=5cm,top=2cm,bottom=2cm"
output:
 pdf_document:
   keep_tex: true
    includes:
      in_header: "~/shr/preamble.tex"
```{r include=F, echo=F}
library(pacman)
p_load(palmerpenguins, tidyverse, knitr)
opts_chunk$set(warning = FALSE, message = FALSE, echo = FALSE, results =
 "asis", dev = "pdf")
Introduction
We can work with the dataset `penguins` included in the package
'palmerpenguins'. One naive approach is to split the dataset and do three
separate analyses:
```

```
```{r}
df1 <- split(penguins, penguins$species)</pre>
foo <- function(df, z) {</pre>
  df |> ggplot(aes(x = bill_length_mm, y = flipper_length_mm)) +
    geom_point(aes(color = island), alpha = .5) +
    geom_smooth() +
    scale_color_manual(values = c("purple", "green", "red")) +
    theme bw() +
    labs(
      title = paste(z, " Penguin Anatomy Comparison"), x = "Flipper length",
      y = "Bill length", color = "Island"
  plotfile_name <- paste0(z, ".pdf")</pre>
  ggsave(plotfile_name)
  cat(paste0("\\includegraphics[height=3cm]{", plotfile_name, "}"), "\n")
  cat("\\vspace{1cm}", "\n")
}
bar <- df1 |> map2(names(df1), foo)
```

The Rmd file runs cleanly and generates the following page. However, we note that the third plot needs additional examination and want to relay the program to our colleague Joe for further analysis.

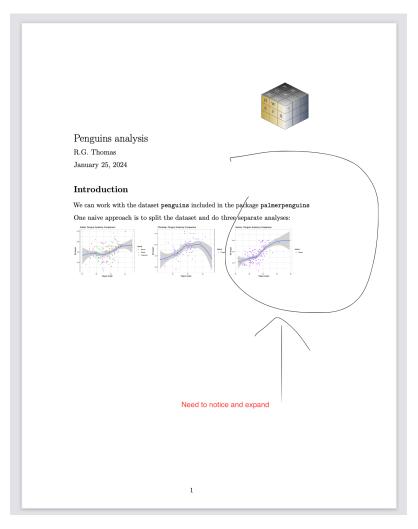


Figure 1: rendered page

Whats the best way to accomplish this?

We start by simply emailing the file to him (rgthomas4747@gmail.com) and asking

him to collaborate.

Joe downloads the attachment. Opens a working directory and attempts to run the Rmd file to see whats what.

Joe has a linux mint desktop

```
> mkdir peng_collaboration
> cd peng_collaboration
> R -e "render('peng.Rmd')"
```

Linux can'f find R

Joe can fix this by installing R > sudo apt install r-base-core

The first problem is that R can not find the function render.

He determines that render is a function in the package rmarkdown

He tries to install rmarkdown with R -e "install.packages('rmarkdown')"

This fails due to inadequate permission on the directory /usr/lib/R/library

After some research he decides to install Rstudio to shortcut some of these problems.

Now try again > R -e "library(rmarkdown); render('peng.Rmd')"

Comes back with an error saying no pacman package.

R -e "install.packages('pacman')"

This is better but something is taking a really long time to install...

Tidyverse is breaking on install. Looks like its missing some libraries. Some research leads to the suggestions:

```
sudo apt install libssl-dev libcurl4-openssl-dev unixodbc-dev libxml2-dev\libmariadb-dev libfontconfig1-dev libharfbuzz-dev libfribidi-dev\libfreetype6-dev libpng-dev libtiff5-dev libjpeg-dev
```

One more try... and the latex engine notes the absence of the file

```
~/shr/preamble.tex
```

So, I need to relay the missing .tex file.

Also the .pdf (sudoku.pdf) logo file.

Finally! success. # Docker approach

Alternatively, consider the "Docker" approach.

Before sending peng.Rmd to Joe we'll dockerize it.

• Prepare a work directory: penguins. We want to send Joe a container that has R and all the preliminaries taken care of so that all he has to do is

run docker > docker run joe_penguin_container

R -e "library(rmarkdown); render('peng.Rmd')"

and if he wants to edit peng.Rmd

vim peng.Rmd

2 REFERENCES

Running your R script in Docker