#### Slides

http://ajstewartlang.github.io/Binder\_slides.pdf

# Binder for fully reproducible research in R (data, code, and computational environment).

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The Turing Way

https://github.com/alan-turing-institute/the-turing-way

# Open and Reproducible Research

- Shared Data we already know this is important for reproducibility.
- Shared Code we already know this is important for reproducibility.
- Shared Computational environment why is this important and how do we do it?

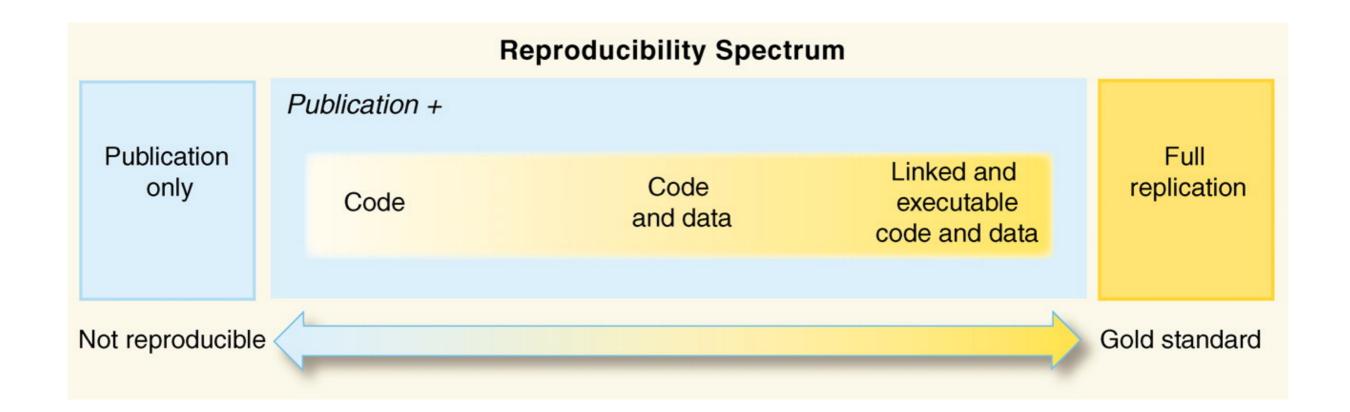
#### PERSPECTIVE

#### Reproducible Research in Computational Science

#### Roger D. Peng

+ See all authors and affiliations

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# Why do we need to reproduce the computational environment?

- Quite often analysis code 'breaks' often in one of two ways:
- Code that worked previously now doesn't maybe a function in an R package was updated (e.g., lsmeans became emmeans so old code using lsmeans wouldn't now run).
- Code that worked previously still works but produces a slightly different result or now throws a warning where it didn't previousy (e.g., convergence/singular fit warnings in lme4 version 1.1-19 vs. version 1.1-20).

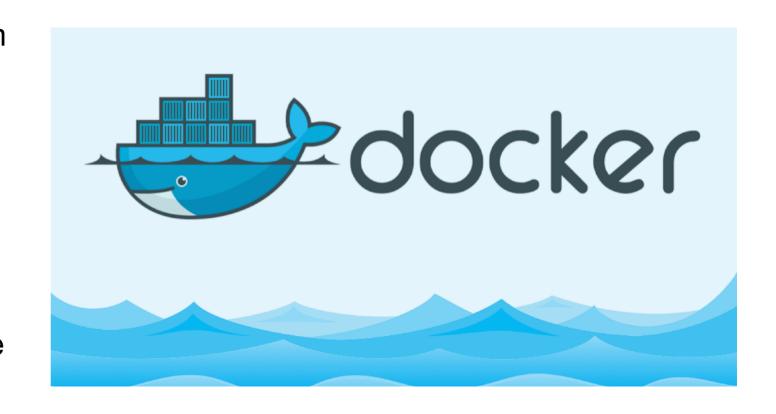
# Capturing your local computational environment

- You need to capture the versions of the different R packages (plus their dependencies).
- May sound trivial but trying running some old R code and be amazed at how many things now don't work as they once did!

### Docker for beginners

Docker packages your data, code and all its dependencies in the form called a docker container to ensure that your application works seamlessly in any environment.

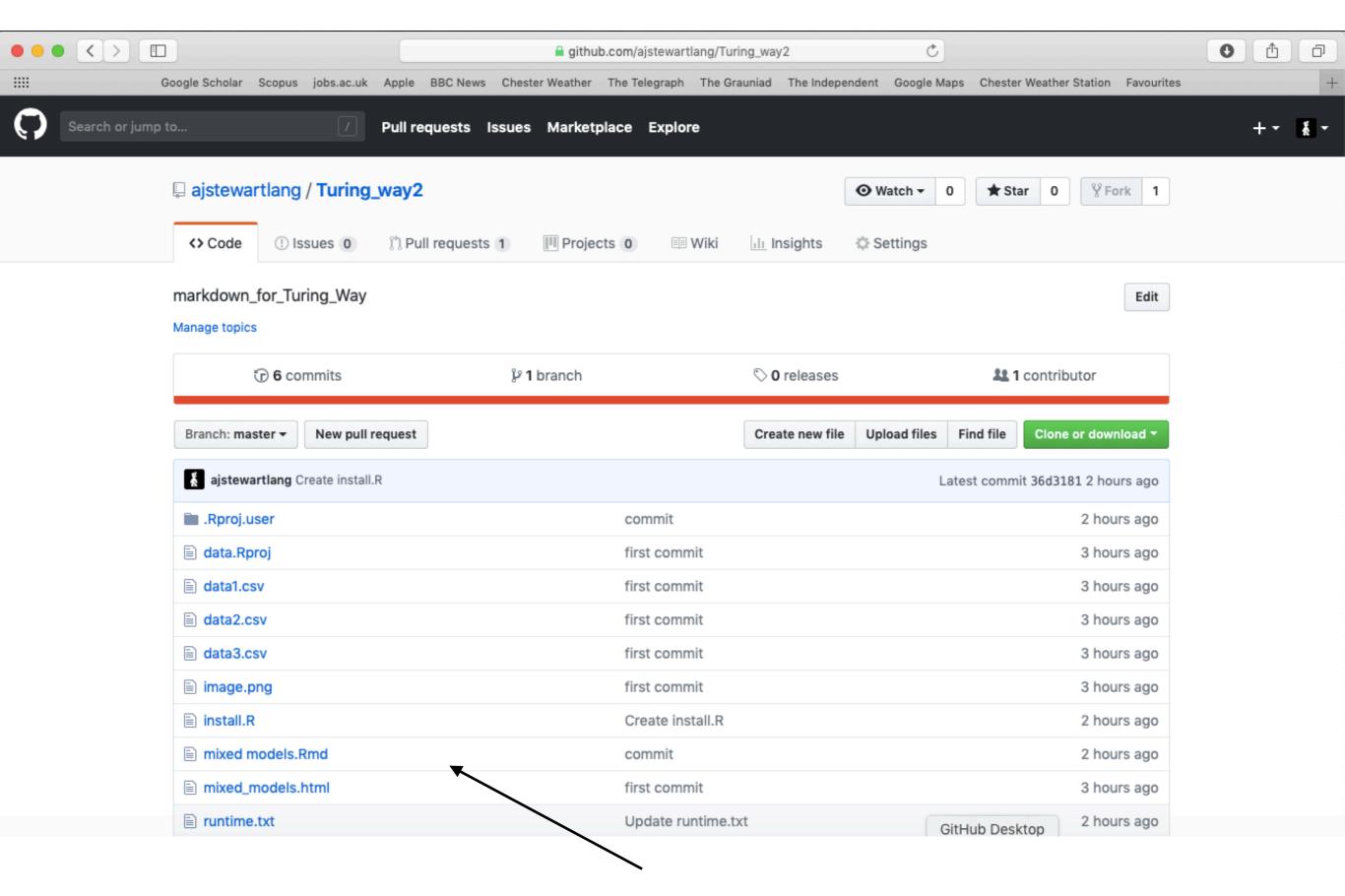
When you run a docker container it's like running your analysis on a virtual computer that has the same configuration as our own one at the point in time when you ran the analysis.



https://medium.com/the-andela-way/docker-for-beginners-61e8e0ce6a19

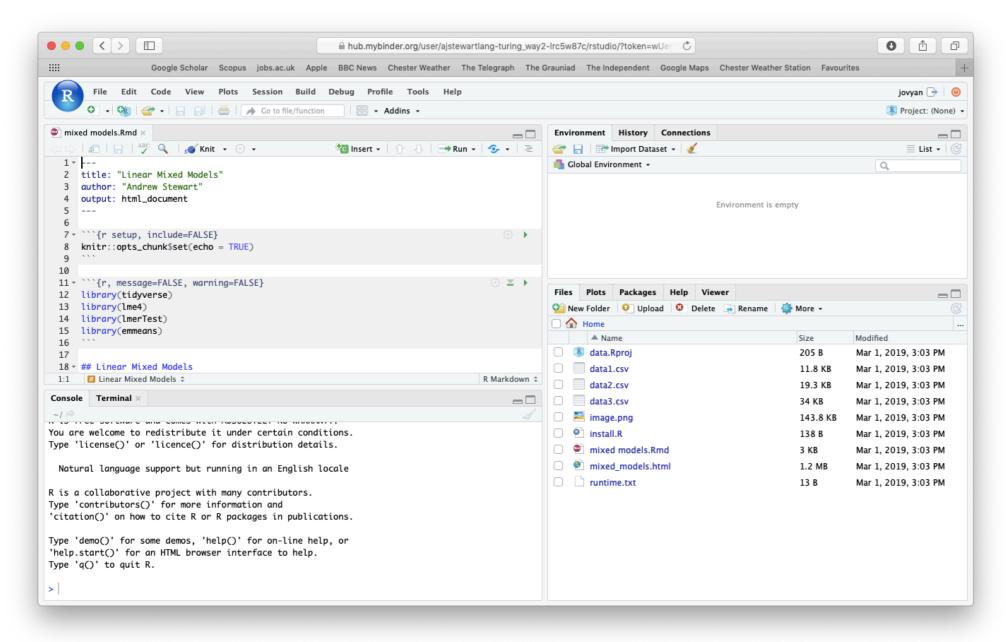
### So what's Binder?

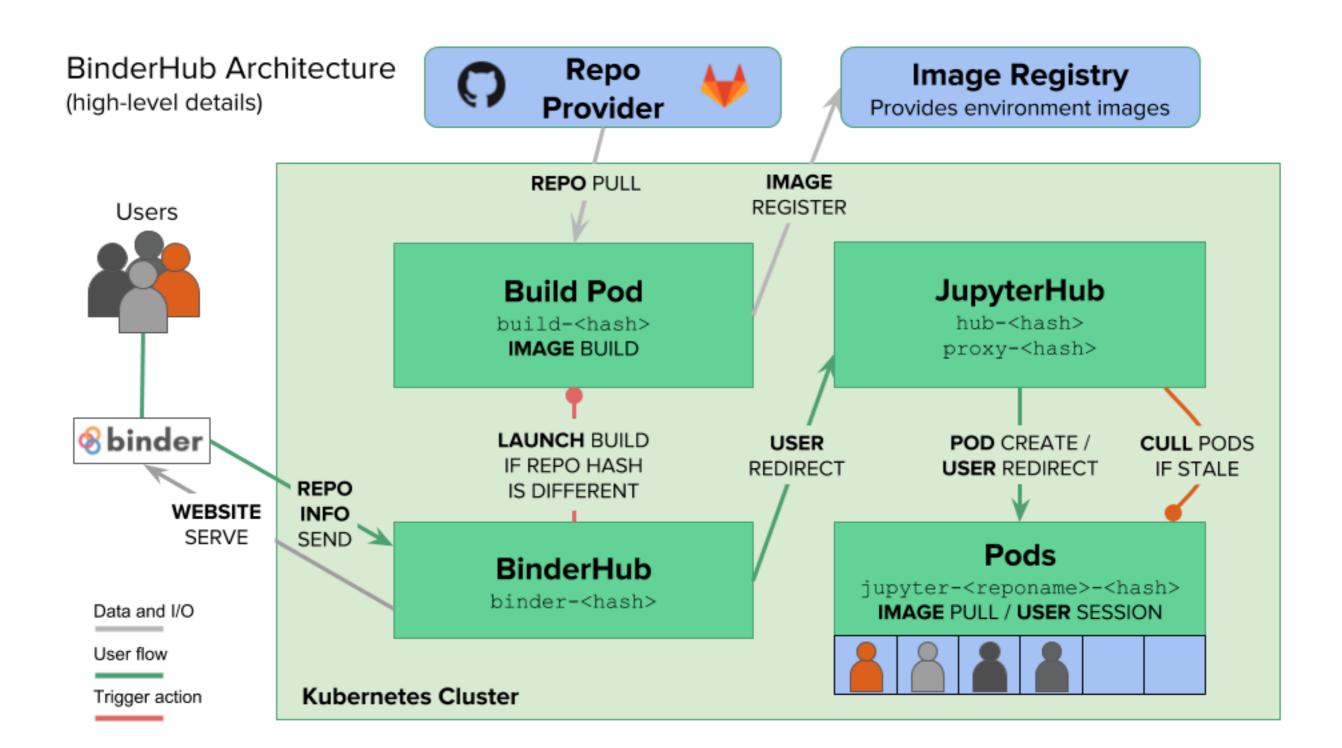
- Binder is powered by BinderHub, which is an opensource tool that deploys the Binder service in the cloud.
- Binder works by pulling a repository that you set up on GitHub into a Docker container.
- Think of a repository as a folder containing your R code, your data, and a few other small bits and pieces - but it sits in the cloud rather than on your computer.



My R code and data files.

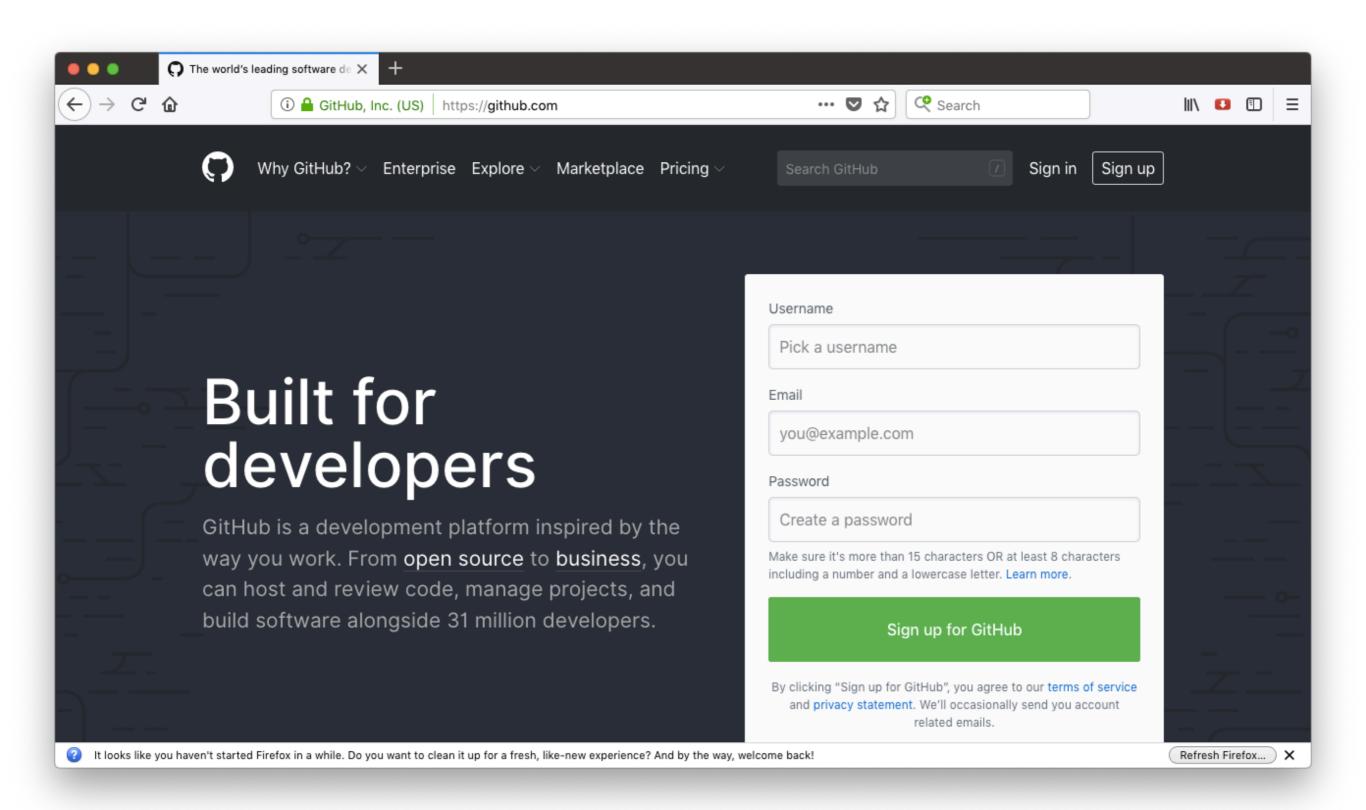
- When I link my GitHub repository to Binder and launch it I then get the following in my web browser.
- This is RStudio running the cloud using my code, my data and the appropriate versions of the packages that I was using when I did the analysis originally!



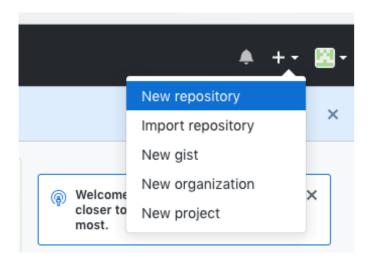


https://binderhub.readthedocs.io/en/latest/index.html

### Step 1 - Set up a GitHub account



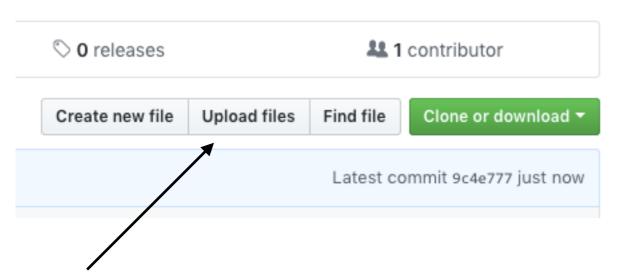
### Step 2 - Create a new repository



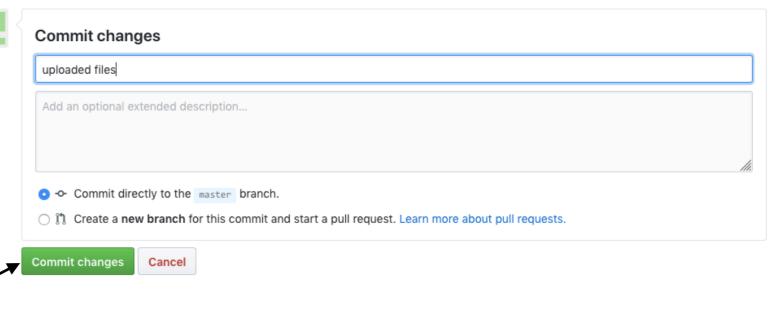
Give it a name, set it to public and tick "Initialise this repository with a README".

#### Create a new repository A repository contains all project files, including the revision history. Repository name \* Owner andrewstewarttest first\_binder Great repository names are short and memorable. Need inspiration? How about probable-funicular? Description (optional) Anyone can see this repository. You choose who can commit. Private You choose who can see and commit to this repository. Initialize this repository with a README This will let you immediately clone the repository to your computer. Skip this step if you're importing an existing repository. Add a license: None ▼ Add .gitignore: None ▼ Create repository

## Step 3 - Upload your R script and data and make your first "Commit"



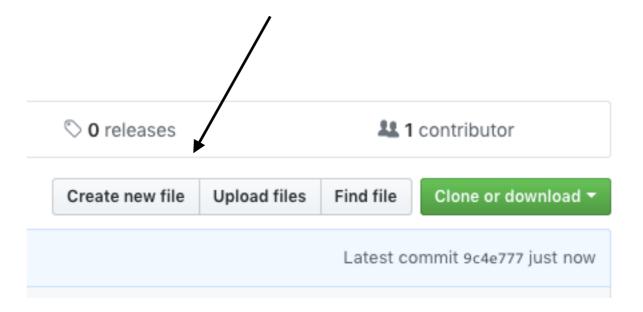
Click here to upload

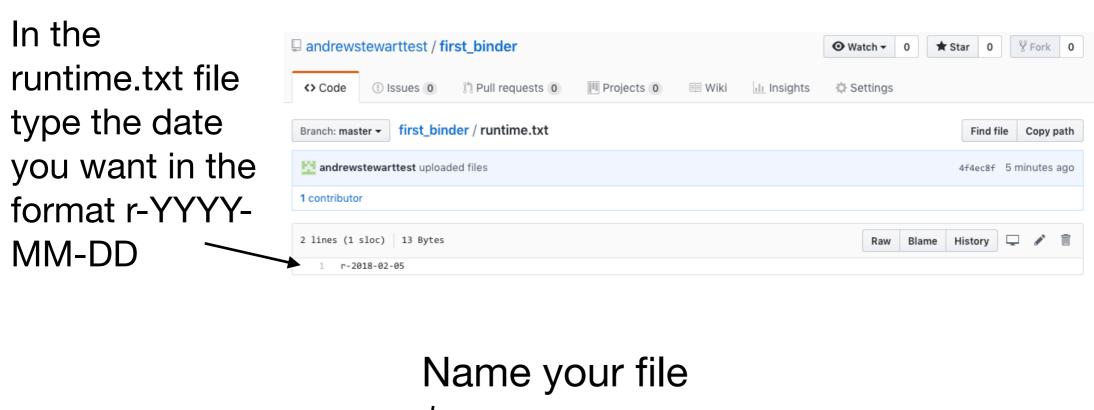


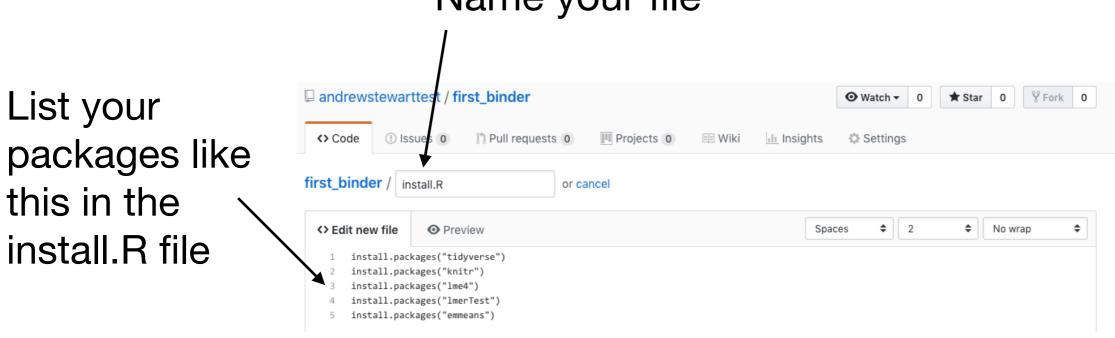
Click here to Commit

## Step 3 - Upload your R script and data and make your first "Commit"

- We need two other files at this point one is called "runtime.txt" and contains the date of R and its associated packages that you want to simulate.
- The other is called "install.R" and contains the list of R packages that need to be installed in order for your script to run.
- To create a new file select "Create new file"



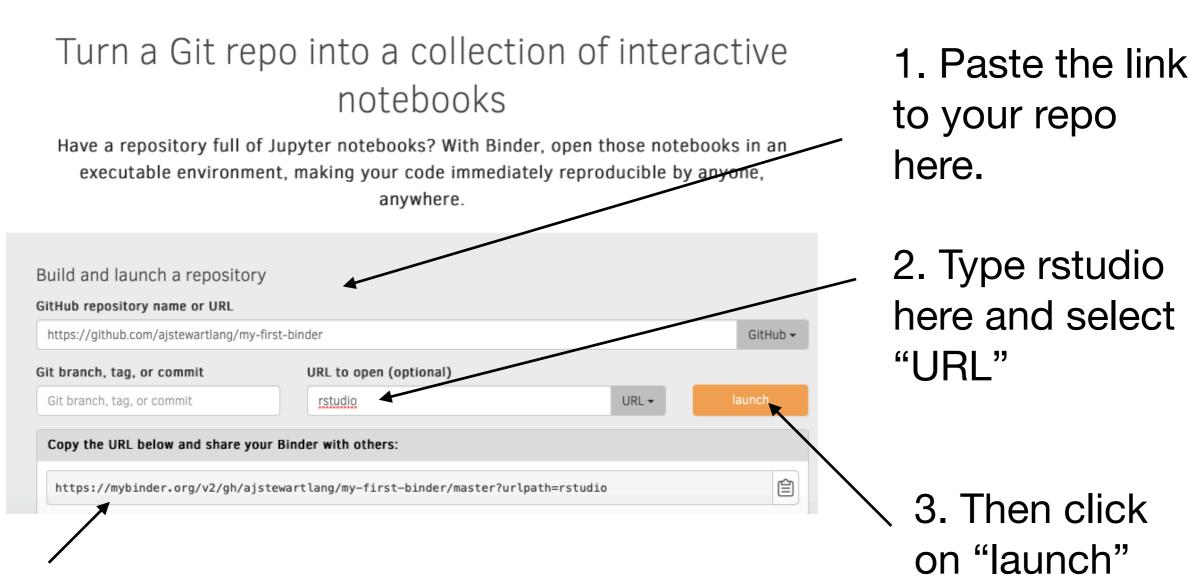




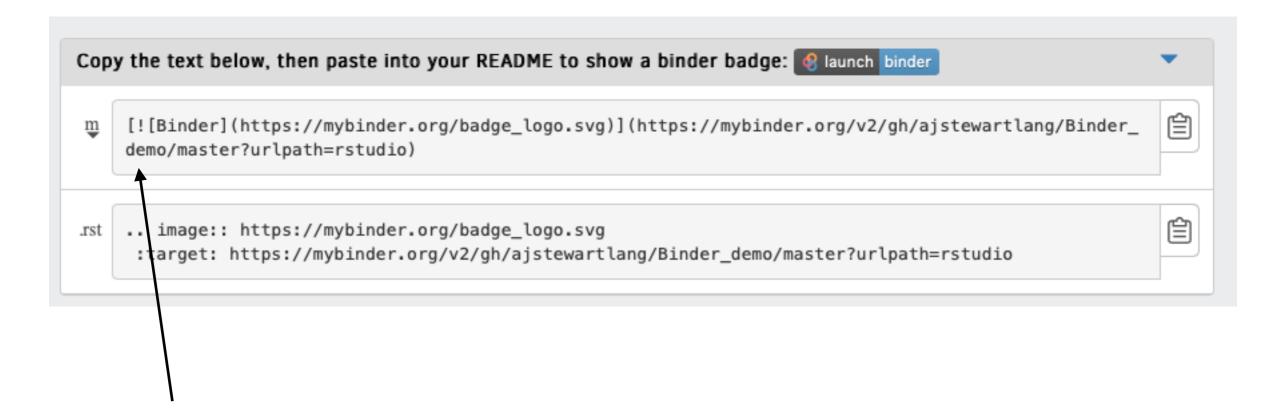
Don't forget to click "Commit" after you've created each file!

## Step 5 - Now we need to link our repote to Binder (mybinder.org)





4. This is the URL to share with others.



 Paste this code into your GitHub repo README.md you'll then be able to click on the 'launch binder' button in your repository to launch the actual binder once it has been built - makes it easy for others to go from you GitHub repo to your code running in Binder.

### Once you click 'Launch'...

```
Build logs

Build logs

trying URL 'https://mran.microsoft.com/snapshot/2018-02-05/src/contrib/scales_0.5.0.tar.gz'
Content type 'application/octet-stream' length 59867 bytes (58 KB)

trying URL 'https://mran.microsoft.com/snapshot/2018-02-05/src/contrib/lazyeval_0.2.1.tar.gz'
Content type 'application/octet-stream' length 80150 bytes (78 KB)

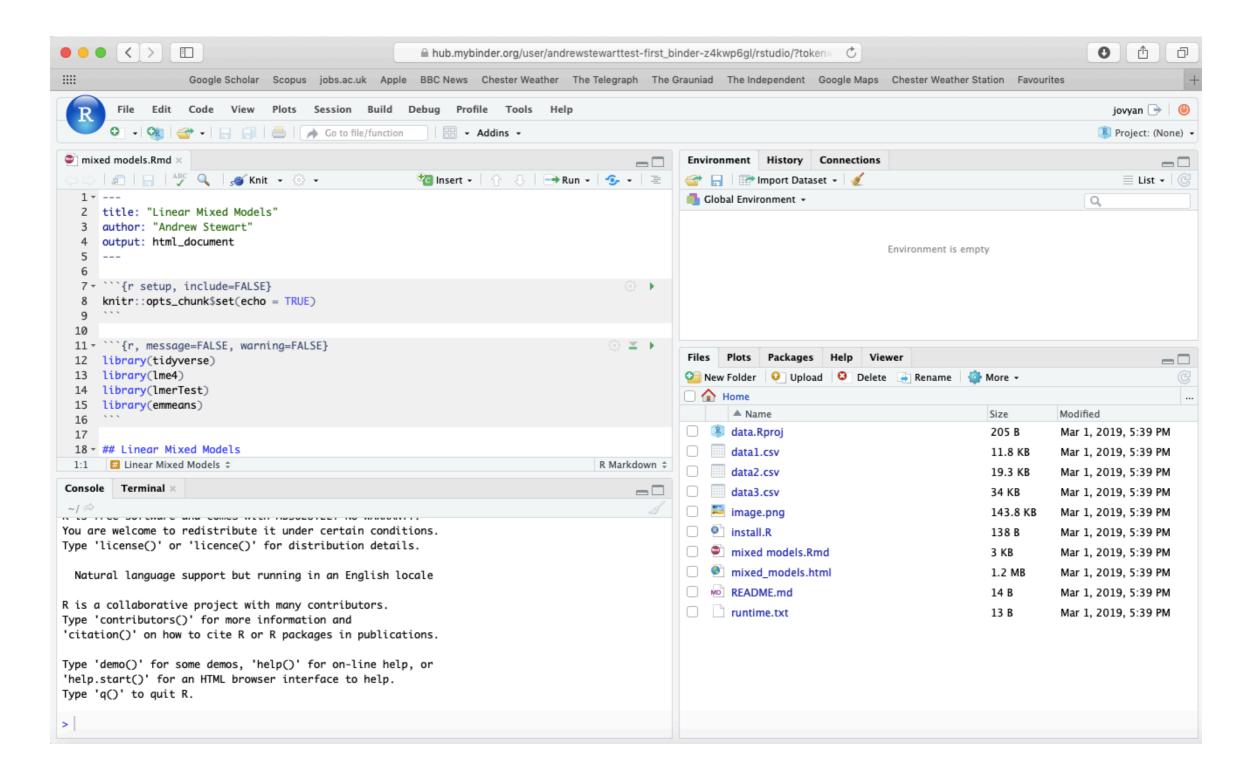
trying URL 'https://mran.microsoft.com/snapshot/2018-02-05/src/contrib/lazyeval_0.2.1.tar.gz'
Content type 'application/octet-stream' length 80150 bytes (78 KB)

trying URL 'https://mran.microsoft.com/snapshot/2018-02-05/src/contrib/cellranger_1.1.0.tar.gz'
Content type 'application/octet-stream' length 63857 bytes (62 KB)
```

You can check the progress of the build by clicking on the "Build logs" bar.

- If Binder can find an image that you've built previously, it will simply launch that.
- If you've made changes to your GitHub repo, it will rebuild the Docker image and create a new Binder.
- Either way, once Binder launches you get the following in your browser (even on mobile devices so you can even R away on your phone)...

### And then...

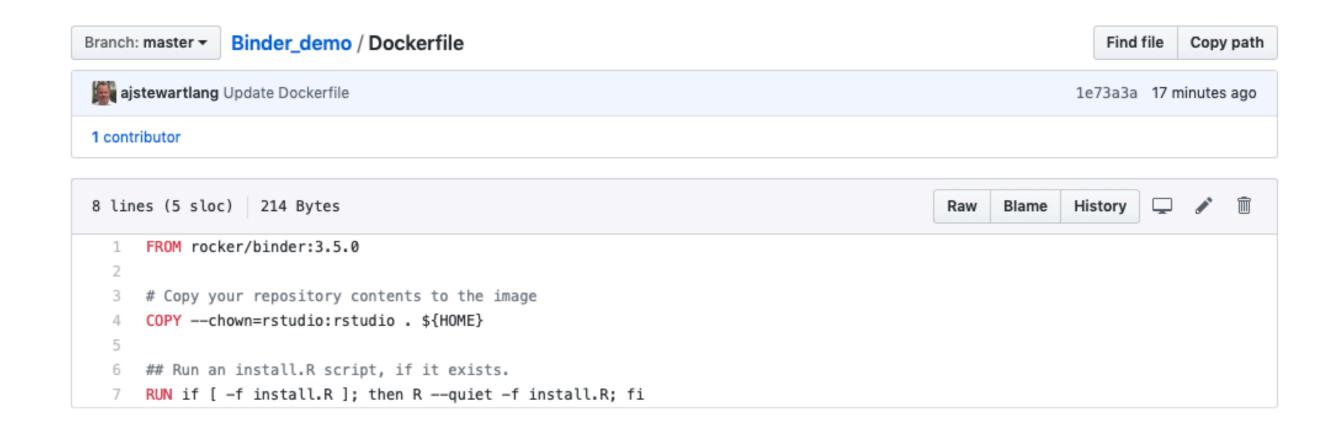


### Speeding things up...

- You can create a Dockerfile in your GitHub repo which allows a pre-built version of R to be run in Binder (thus saving time) - note that not all packages are in these prebuilds and runtime.txt is ignored via this route.
- Create a new file called "Dockerfile" and paste in the following code:

```
# Copy your repository contents to the image
COPY --chown=rstudio:rstudio . ${HOME}

## Run an install.R script, if it exists.
RUN if [ -f install.R ]; then R --quiet -f install.R; fi
```



Click on 'commit' and then build your Binder as normal...

### A few other things...

- Installing the entire Tidyverse in a Binder can take a long time better to install only the packages you use (e.g., ggplot2, dplyr, readr etc.) this will also ensure the packages are consistent with the date in your runtime.txt file.
- Even with just a couple of packages it can take ~15 minutes or so for your Binder to be built.
- Some R packages need system-level packages to also be installed - you can do that via an additional apt.txt file which lists those packages - this is used by apt-install to install those packages from the Ubuntu apt repository.

### A few other things...

- At the moment, you can't change the version of R that runs on Binder (currently set to 3.4.4.) so need to go down the Rocker route but be aware that you may not get the right version of the packages that you want...
- Something to think about if you're using set.seed() and sample() in R 3.6 - if so, consider using (e.g.) RNGversion("3.5.3") for pre-3.6 reproducibility.
- You can close your laptop if Binder is taking too long the image and your Binder will continue to be built in the Cloud. And it's always a good excuse for another coffee...

### For Ultimate Reproducibility

- Make sure you have updated all your packages before you run your script.
- Build your Binder and specify the day your ran your analysis in the runtime.txt file
- Don't use pre-built Dockerfiles (as these likely won't have the same package versions that you are using).
- Patience while your Binder builds...

### Slides

http://ajstewartlang.github.io/Binder\_slides.pdf

## My step-by-step guide (including an example R script if you don't have one)

https://hackmd.io/gO3cehAVSpuCB2EDEvepzg?view