Informatics team manual of procedures

Ania Tassinari & Caitlin Guccione

2019-07-12

Contents

1 About

This is a manual of operations for the Agios Informatics team. Its puspose is to:

- provide a resource on **best practices** (2)
- aid in setting up effective and reproducible **project workflows** (3)
- promote learning and sharing of **ideas** (4).

2 Best practices

2.1 Reproducible research

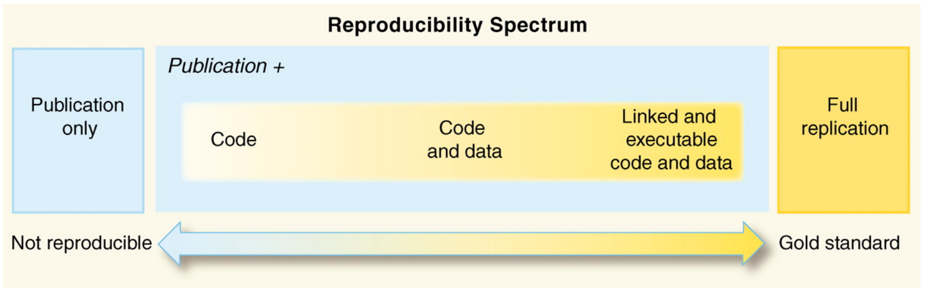
2.1.1 Purpose

1. Improve collaborative analyses:

- make sharing easier
- enable retrieval and interpretation of results long after analysis ended

2. Simplify hand-off to Biostats

3. Improve confidence in our data and results



Source: Peng et al., *Reproducible Research in Computational Science.* Science 2011.

2.1.2 DO's and DON'T's of reproducible research

- DO start with good science
- DON'T do things by hand
  - Was any part of this analysis done by hand?
    * If so, are those parts precisely documented?
    * Does the documentation match reality?
- DON'T point and click
- DO teach a computer
- DO use version control
- DO keep track of your software environment
- DON'T save any output (until it's time to write a paper)
- DO set your seed

Source: Reproducible Research at Coursera

2.2 Version control

2.3 Code guidelines

2.3.1 R

- Tidyverse Style Guide
- Google's R Style Guide

3 Project Workflows

3.1 Using Workflowr

3.1.1 Quick Start

This section is a quick version setting up workflowr, for more clear or specific instructions skip to The Full Guide to Using Workflowr.

3.1.1.1 Set Up

In the `Console` tab of RStudio make sure you are in `(None)` project:

```
install.packages("workflowr")
library("workflowr")
wflow_git_config(user.name = "First Last",
    user.email = "first.last@agios.com")
```

Click here for more specfic details on **set up**

3.1.1.2 Creating Projects

In the `Console` tab,

```
wflow_start("PROJECT_NAME")
wflow_build()
wflow_publish(c("analysis/*.Rmd"),
    "Publish the initial files for PROJECT_NAME")
```

Click here for more specfic details on **creating projects**

3.1.1.3 Connecting to GitLab

In the `Console` tab,

```
wflow_use_gitlab(username = "first.last",
    repository = "PROJECT_NAME",
    domain = "ceres.agios.com")
```

Go to your Agios GitLab and do the following:

- Create a project in GitLab with the same name as the project in RStudio
  - We called our project: PROJECT_NAME
- Scroll down to the push an existing Git repository option
  - Copy everything in the box besides the first line (`cd existing_repo`)
- Make sure you are in PROJECT_NAME directory
  - Paste what you just copied from Git into the `Terminal` tab in RStudio

Click here for more specfic details on connecting to **GitLab**

3.1.1.4 Creating a New File

In the `Console` tab,

```
wflow_open("analysis/NEW_FILE.Rmd")
wflow_build()
wflow_publish(c("analysis/*.Rmd"),
    "Publish the file NEW_FILE")
```

In the `Terminal` tab,

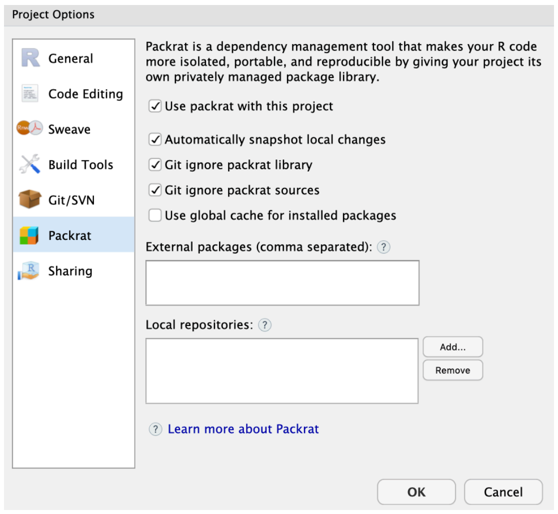
```
git push
```

Click here for more specfic details on **creating new files**

You made it !

You now have a functioning workflowr setup

3.1.1.5 Quick Useful Additions



Packrat is a dependency management tool that makes your R code more isolated, portable, and reproducible by giving your project its own privately managed package library.

☑ Use packrat with this project

☑ Automatically snapshot local changes

☑ Git ignore packrat library

☑ Git ignore packrat sources

☐ Use global cache for installed packages

External packages (comma separated):

Local repositories:

Learn more about Packrat

Figure 1: Showing how to install PackRat into a current project with the suggested selections

3.1.1.6 Adding PackRat

PackRat records or saves the exact package versions that you depend on and stores them in GitLab.

1. Install PackRat

```
install.packages("packrat")
```

2. Add PackRat to Existing Project

   - Go to `Tools`
   - Click on `Project Options`
   - Click `Add PackRat` then check `Use PackRat for this project`
   - Now, check the following boxes (shown in the image below) and tap `OK` *:

- This step may take a while if you have a number of packages you are backing up.

Click here for more specfic details on **PackRat**

3.1.1.6.1 Update Session Information Function

Add the following line to your `_workflowr.yml` file :

```
sessioninfo:"devtools::session_info()"
```

Click here for more specfic details on **Session Info**

3.1.1.6.2 Publish to GitLab without Rebuilding Sites

A quicker way to push to GitLab without rebuilding your website.

1. Edit the Rmd file and save your changes
2. Run one of the following commands (doesn't matter which one you select)
    - `wflow_build()`
        - It doesn't matter if we build other files, they won't be added to git unless we add them in the next step
    - `wflow_build("file.rmd")`
    - Knit the file
3. `wflow_git_commit("file.rmd", "This is your commit message")`
4. Flip into the terminal and run `git push()`

The Full Guide to Using Workflowr

3.1.2 Installation

3.1.2.1 Programs Needed

We are assuming that you already have RStuido and GitLab, for this implementation we are using the RStudio on the new server (hpc.agios.local) which is RStudio version 1.2.1335.1.

If you don't have GitLab you need to have an account set up through Agios. If you don't have the updated RStudio you need to get access to the new server and then use the following link : hpc.agios.local

3.1.2.2 Installing Workflowr

1. Open RStudio and change project in the top right corner to `(None)`

- Make sure you are in your home directory on RStudio as well, thus in the bottom right corner of your screen under `New Folder`, it is labeled `Home` with a small house.

2. In the `Console` tab located in the bottom left hand corner type:

```
install.packages("workflowr")
```

3. Confirm you have access to Workflowr, in the `Console` tab:

```
library("workflowr")
```

3.1.2.3 Configure Git This only needs to be done once per laptop

In the `Console` tab:

```
wflow_git_config(user.name = "First Last",
    user.email = "first.last@agios.com")
```

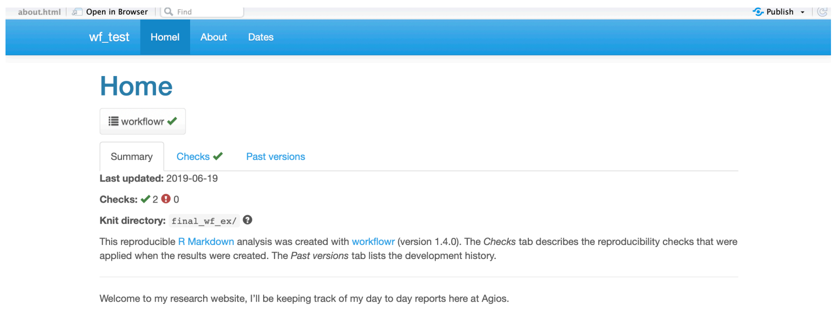
3.1.3 Create Project

3.1.3.1 Start Project

In the `Console` tab:

```
wflow_start("PROJECT_NAME")
```

1. What does `wflow_start` do?
   - Creates a directory that contains all files necessary to start a workflowr project
   - Changes your current directory to PROJECT_NAME
   - Creates a `.git` folder which we will connect to GitLab repository
2. What is the `analysis` folder for?
   - Contains all source R Markdown files (Rmd)
     - Includes: `index.rmd`*
       - Contains no R code but generates `index.html` which eventually runs the entire project
   - Contains `_site.yml`
     - Allows user to edit theme, navigation bar, menus ect.
     - Helpful link to customizing
3. What is the `docs` folder for?



Home

Last updated: 2019-06-19

Checks: ✓ 2 ❗ 0

Knit directory: `final_wf_ex/`

This reproducible R Markdown analysis was created with workflowr (version 1.4.0). The *Checks* tab describes the reproducibility checks that were applied when the results were created. The *Past versions* tab lists the development history.

Welcome to my research website, I'll be keeping track of my day to day reports here at Agios.

Figure 2: An example of a sucessfully built workflowr page

- Contains all HTML files for webpage
  - Note that this file will be empty until we build the project
  - Each HTML file is built from a corresponding Rmd file in the `analysis` folder
- Contains any figures created by Rmd files

4. What about the `data`, `code` and `output` files?
   - These files are there for your use and thus can be deleted if desired

3.1.3.2 Build Project*

In the `Console` tab:

```
wflow_build()
```

1. What does `wflow_build()` do?
   - Builds all the R Markdown files in analysis and saves their HTML in docs
   - Displays the website

Your website should be similar to the image of mine shown below (except with a Publish tab instead of a Dates tab)

3.1.3.3 View Project*

At any time you can view the current site on your local machine by typing in the `Console` tab:

```r
wflow_view()
```

*Shortcut : You can use the knit button to do both of these

3.1.3.4 Publish Website

Currently, our project is simply an HTML file stored on our laptop, publishing the website will make it available online.

In the `Console` tab:

```r
wflow_status()
```

This allows you to view which files are published or unpublished currently.

Now we want to publish our page the command to do so takes three parts

1. c - Stands for commit
2. (“analysis/index.Rmd”, “analysis/about.Rmd”, “analysis/license.Rmd”)
    - A character vector of the Rmd files you want to be published
    - It may be easier to place (”*.Rmd”) here to use all the files
3. “Publish the initial files for PROJECT_NAME” - A commit message to be posted

Overall, `wflow_publish` is a quick and error-free way for us to commit and push all of our Rmd files to our GitLab at once.

In the `Console` tab:

```r
wflow_publish(c("analysis/index.Rmd",
    "analysis/about.Rmd", "analysis/license.Rmd"),
    "Publish the initial files for PROJECT_NAME")
```

3.1.4 Connecting to GitLab

3.1.4.1 Creating a remote repository on GitLab

1. Log in to GitLab and click `New Project`
2. The project name in GitLab has to be the same name as the project name in RStudio: PROJECT_NAME
3. Make sure to save it as `Internal` so everyone at Agios can see it

3.1.4.2 Not working? Do you have an ssh key? *

In order for you to successfully connect to GitLab, you need to have an ssh key linked to your GitLab.

There is a simple guide to doing this on GitLab here so you can simply follow along below and click the link if you get lost.

1. Automatically copy your public key to the clipboard using one of the following commands:

```
# macOS:
pbcopy < ~/.ssh/id_ed25519.pub
# WSL / GNU/Linux (requires the xclip package):
xclip -sel clip < ~/.ssh/id_ed25519.pub
#Git Bash on Windows:
cat ~/.ssh/id_ed25519.pub | clip
```

2. Go back into your GitLab account and click on `Settings` then `SSH Keys` and simply paste there.

- Only need to do this once per laptop or GitLab account

3.1.4.3 Connect RStudio and GitLab

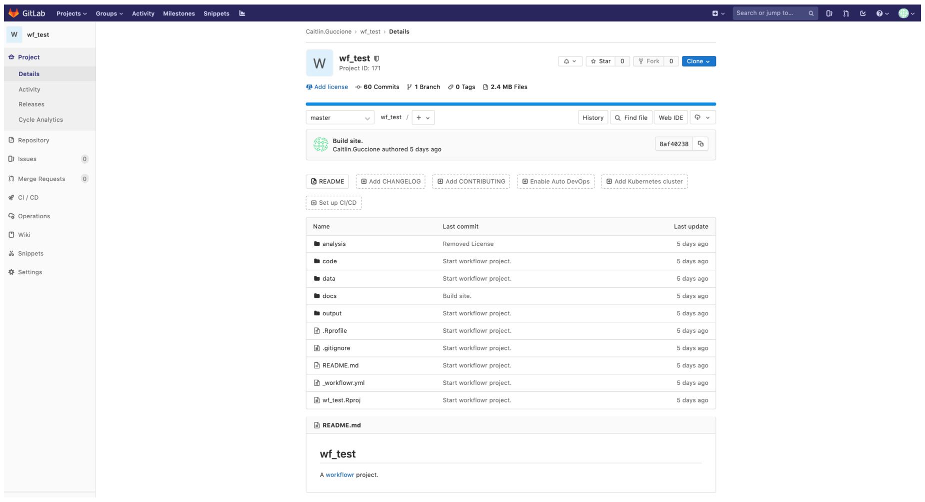
1. Go to RStudio, in `Console` tab, type:

```
wflow_use_gitlab(username = "first.last",
    repository = "PROJECT_NAME",
    domain = "ceres.agios.com")
```

2. Go back to GitLab and scroll down to the `push an existing Git repository` option
    - Copy everything in the box on GitLab besides the first line (`cd existing_repo`), there is an example below of what this should look like.

```
git remote rename origin old-origin
git remote add origin git@ceres.agios.com:Caitlin.Guccione/test-.git
git push -u origin --all
git push -u origin --tags
```

3. Go back into RStudio and in the `Terminal` tab



wf_test
Project ID: 171

Build site.
Caitlin.Guccione authored 5 days ago
8af40238

Name	Last commit	Last update
analysis	Removed License	5 days ago
code	Start workflowr project.	5 days ago
data	Start workflowr project.	5 days ago
docs	Build site.	5 days ago
output	Start workflowr project.	5 days ago
.Rprofile	Start workflowr project.	5 days ago
.gitignore	Start workflowr project.	5 days ago
README.md	Start workflowr project.	5 days ago
_workflowr.yml	Start workflowr project.	5 days ago
wf_test.Rproj	Start workflowr project.	5 days ago

README.md

wf_test

A workflowr project.

Figure 3: Example of a Workflowr connection on GitLab

- Make sure you are in the PROJECT_NAME repo
- Paste the above commands we got from GitLab

4. Return to GitLab to ensure your entire project exists there

3.1.5 Adding New Files

3.1.5.1 Creating New Files

Make sure you are inside the PROJECT_NAME project inside RStudio

In `Console` tab type:

```
wflow_open("analysis/NEW_FILE.Rmd")
```

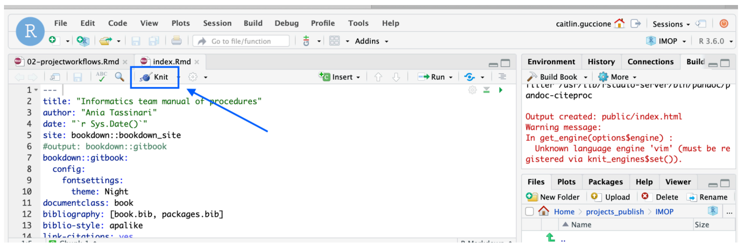
- This command creates a new Rmd file and then opens it for your convenience.

If we now want to see the HTML version of our file then we have two options:

1. In `Console` tab type:

```
wflow_build()
```

- You can add specific files to this command or simply leave it empty



```
---
title: "Informatics team manual of procedures"
author: "Ania Tassinari"
date: "`r Sys.Date()`"
site: bookdown::bookdown_site
#output: bookdown::gitbook
bookdown::gitbook:
  config:
    fontsettings:
      theme: Night
documentclass: book
bibliography: [book.bib, packages.bib]
biblio-style: apalike
```

```
andoc-citeproc

Output created: public/index.html
Warning message:
In get_engine(options$engine) :
  Unknown language engine 'vim' (must be re
gistered via knit_engines$set()).
```

Figure 4: Display of where the Knit button is located in RStudio

- This produces a small view of your website right on RStudio

2. Press the 'Knit' button in RStudio as shown below:

- This produces a large web version of your current HTML file

These steps will simply change the local HTML file, but in order to make this public and add it to GitLab, we need to update our changes.

3.1.5.2 Update your Changes

1. Check the status to see what needs to be updated, in the `Console` tab, type:

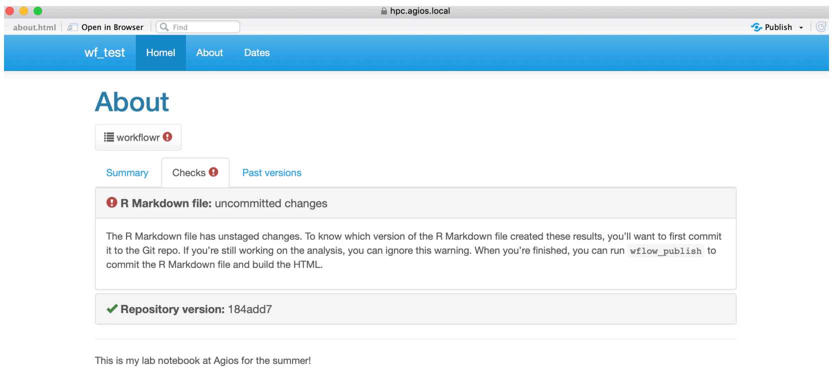
```
wflow_status()
```

This can also be done by looking at the red checks on the workflowr section of your live page as shown below:

2. Make the appropriate HTML files public and updated, in the `Console` tab, type:

```
wflow_publish(c("analysis/index.Rmd",
    "analysis/NEW_FILE.Rmd"), "Add my first file")
```

- This is the same format found on the **Publish Website** tab of this page and so you can customize it in the same way



About

R Markdown file: uncommitted changes

The R Markdown file has unstaged changes. To know which version of the R Markdown file created these results, you'll want to first commit it to the Git repo. If you're still working on the analysis, you can ignore this warning. When you're finished, you can run `wflow_publish` to commit the R Markdown file and build the HTML.

✓ **Repository version:** 184add7

This is my lab notebook at Agios for the summer!

Figure 5: A demenstration of a live Workflowr page

There is one exception to this and it's when you want to make updates to the `_site.yml` file found in the `analysis` folder. This file controls the style on the top of every page of your website. In this case, you want to update all HTML files even though their Rmd files aren't changed.

In that case, use this,

```
wflow_publish("analysis/_site.yml",
    "Change the theme", republish = TRUE)
```

3. Push the final changes to GitLab

As we did previously in the `Publish Website`, in the `Terminal` tab, type:

```
git push
```

3.1.5.3 Adding Workflowr to New File

If you want the workflowr setup which is found on all the other pages, then replace the — part of the file with the following code:

```
            ---
            title: "Home"
            site: workflowr::wflow_site
            output:
              workflowr::wflow_html:
                toc: false
            editor_options:
              chunk_output_type: console
            ---
```

You made it !

You now have a functioning workflowr setup

3.1.6 Quick Additions to Improve your Workflowr

3.1.6.1 Adding PackRat

PackRat records or saves the exact package versions that you depend on and stores them in GitLab.

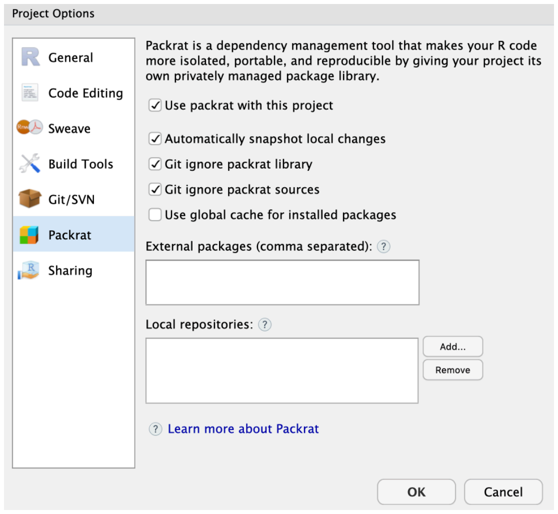
1. Install PackRat

```r
install.packages("packrat")
```

2. Add PackRat to Existing Project

   - Go to `Tools`
   - Click on `Project Options`
   - Click `Add PackRat` then check `Use PackRat for this project`
   - Now, check the following boxes (shown in the image below) and tap `OK` *:

- This step may take a while if you have a number of packages you are backing up.



Packrat is a dependency management tool that makes your R code more isolated, portable, and reproducible by giving your project its own privately managed package library.

- ✓ Use packrat with this project
- ✓ Automatically snapshot local changes
- ✓ Git ignore packrat library
- ✓ Git ignore packrat sources
- ☐ Use global cache for installed packages

External packages (comma separated):

Local repositories:

- This step may take a while if you have a large amount of packages you want to back up

3. A panel called PackRat will now appear under packages
    - It will automatically notify you if packrat has a package that you don't and then prompt you to download it
4. It also gives you the option to clean un-used packages so that packrat doesn't get too cluttered

3.1.6.2 Update Session Information Function

The following steps simply add more information to your `Session Info` button found at the bottom of your workflowr. For more information about how to further customize the `Session Info` output click here

Add the following line to your `_workflowr.yml` file :

```
sessioninfo:"devtools::session_info()"
```

3.1.6.3 Publish to GitLab without Rebuilding Sites

A quicker way to push to GitLab without rebuilding your website.

1. Edit the Rmd file and save your changes
2. Run one of the following commands (doesn't matter which one you select)
    - `wflow_build()`
        - It doesn't matter if we build other files, they won't be added to git unless we add them in the next step
    - `wflow_build("file.rmd")`
    - Knit the file
3. `wflow_git_commit("file.rmd", "This is your commit message")`
4. Flip into the terminal and run `git push()`

3.1.7 Create a LIVE Shareable Webpage

Below are a few ways to share your project with others.

3.1.7.1 A Simple Trick

This is the simplest way to share your workflowr page at the moment. In the future, we are hoping to have a cleaner way to do so.

1. Have the new user clone your page on GitLab
2. Open the `docs` folder
3. Click on the `index.html` file

3.1.7.2 GitLab Pages

GitLab Pages isn't currently available on Agio's GitLab. As soon as it is, we will add updates on how to simply set-up and share GitLab pages. If you would like to experiment with GitHub pages you may do so on your personal GitHub account, once GitLab pages are up and running they should behave in almost the same way.

3.1.7.3 Beaker Browser

Beaker Browser is a simple way to deploy a webpage from your computer without a server. We attempted to use Beaker Browser though we found it had a few setbacks and that other methods may be simpler. If you want to try it out for yourself, the link above is very straightforward.

The comparison above between GitLab pages and Beaker Browser:

GitLab Pages	Beaker Browser
Slightly complex setup	Simpler setup
Automatically updates changes, since it's already linked to Git	Not a clear path to Git and thus must manually update changes
Well documented	Little documentation
Easy to share internally through GitLab	Have to download Beaker in order to view the webpage

3.1.8 Styling the Webpage

3.1.8.1 Helpful Links

If you already have an idea of what you would like to change, below are a few very helpful resources filled with information:

- This resource is a great place to start because it has all basics of Rmd syntax and I used it as a cheat sheet along the way.
  - Rmd Cheat Sheet
- This is an entire book all about Rmd and how to use it. I found it rather lengthy but very helpful.
  - Rmd Thorough Guide
- If something isn't quite working right you may have run into a workflowr issue in which cause their FAQ's page is helpful.
  - Workflowr FAQ's

3.1.8.2 Changing the Theme

Changing the theme modifies the overall appearance of the webpage and is a quick and easy way to spice up the page.

1. Go into your `analysis/_site.yml` file
2. Underneath `ouput` add `theme = cerulean` as shown below:

    - The cerulean theme matches Agios colors

```
output:theme:cerulean
```

3. Choose your theme

    - The following themes are available : "default", "cerulean", "journal", "flatly", "darkly", "readable", "spacelab", "united", "cosmo", "lumen", "paper", "sandstone", "simplex", "yeti"
    - You can view how they look here: Themes

4. Preview your theme using,

```
wflow_build()
```

5. Update your website by running,

    - This will rebuild every HTML file even if their corresponding Rmd file hasn't been updated

```
wflow_publish("analysis/_site.yml",
    "Change the theme", republish = TRUE)
```

The following website will also walk you through changing the theme: Themes Overview

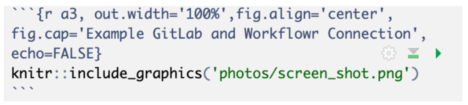
3.1.8.3 Adding Photos

Although this may seem like a simple task, it is a bit challenging since we are using Workflowr

1. Create a `photos` folder inside the `docs` folder and add your photo there:

```
dir.create("docs/photos")
```

2. Include the following command wherever you want your graphic to appear:



~~~~
```{r a3, out.width='100%',fig.align='center',
fig.cap='Example GitLab and Workflowr Connection',
echo=FALSE}
knitr::include_graphics('photos/screen_shot.png')
```
~~~~

```
+ Adjusting `out.width` changes the size of the photo
```

3. View the images on the webpage

```r
wflow_build()
```

4. Add to GitLab

   - We need to push the actual photo to GitLab using `wflow_git_commit` and then we can use `wflow_publish` to automatically push the rest of the files to GitLab

```r
wflow_git_commit("docs/assets/external.png",
    "Add external image of ...")
wflow_publish()
```

3.1.8.4 Blogdown

Blogdown is another way that you can customize your workflowr page more easily. It is a combination of the well known blogdown and workflowr.

You can clone the following repo on GitHub if you want to try it out: Blogdown/Workflowr Repo

---

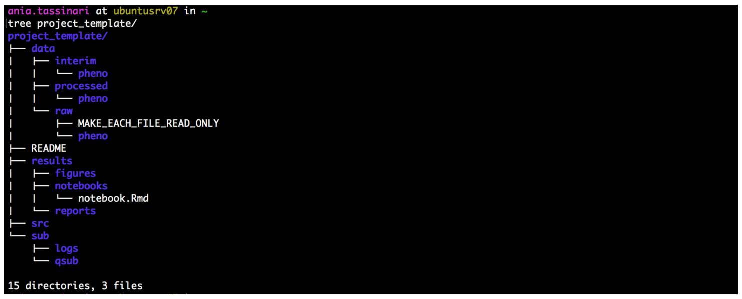
3.2 Set Up Workflow and Executing

3.2.1 Create a folder for your *newproject*

Come up with a project structure you like and stick with it.

3.2.1.1 Copy from a previously created template folder

Use `cp -r project_template newproject`, where `project_template` has structure:



```
ania.tassinari at ubuntusrv07 in ~
tree project_template/
project_template/
├── data
|   ├── interim
|   |   └── pheno
|   ├── processed
|   |   └── pheno
|   └── raw
|       ├── MAKE_EACH_FILE_READ_ONLY
|       └── pheno
├── README
├── results
|   ├── figures
|   ├── notebooks
|   |   └── notebook.Rmd
|   └── reports
├── src
└── sub
    ├── logs
    └── qsub

15 directories, 3 files
```

3.2.1.2 Use a `bash` script

Call `./setup_project.sh newproject`, where `setup_project.sh` is:

Don't forget! - Fill project README - Adapt structure to project needs - Exclude data and other large files from git using `.gitignore` (see next section) - Make files in `data/raw` read-only with `chmod -w`

Project organization ideas: http://projecttemplate.net/getting_started.html Packaging data analytical work reproducibly using R (and friends) R workflow fun Cookiecutter Data Science

3.2.2 Set up a repository for your code on Agios' secure GitLab

Create a new project at http://ceres.agios.com (Mark P. can help)

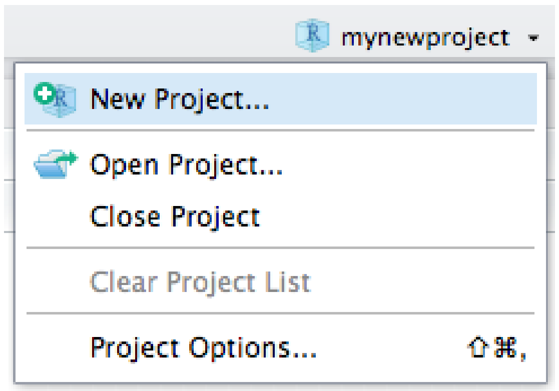
3.2.3 Set up a repository for your code locally and link to GitLab

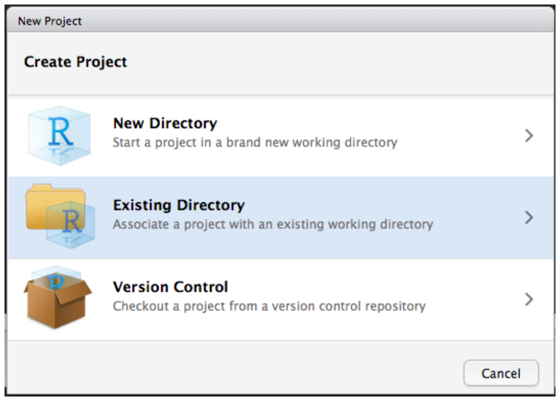
In your *newproject* folder on command line execute (modify user name):

```
git add .
git commit -am 'initial commit'
git remote add origin git@ceres.agios.com:User.Name/newproject.git
git push -u origin master
```

3.2.4 Set up an R project in RStudio

Choose Existing Directory (*newproject*)





New Directory
Start a project in a brand new working directory

Existing Directory
Associate a project with an existing working directory

Version Control
Checkout a project from a version control repository

3.2.5 Analysis in R and RStudio

Data:

- Raw data:
  - If accessed from the web, include url, description, and date accessed in README
- Processed:
  - Processed data should be named so it is easy to see which script generated the data
    - Can add file descriptions to `filename.README` and place processing script in the same directory as data (works well for preprocessing steps, like alignments, etc)
  - Processed data should be tidy

Code:

- Place (almost) all intermediate scripts in `newproject/src/`
- Any chunks of code frequently reused in the analysis should be converted into functions, saved in `newproject/src/functions.R`, and sourced in scripts, notebooks and reports.

- Use Google's R Style Guide or The tidyverse styleguide to format your code and make it easier to read (if need be run code through formatR)

Figures:

- Exploratory:

  - Don't have to be pretty
  - Can be embedded in report/notebook
- Final:
  - Should be polished and saved in `newproject/results/figures/`

Scripts:

- Raw:
  - May be less commented (but comments help you!)
  - May be multiple versions
  - May include analyses that are later discarded
- Final:
  - Clearly commented
  - Small comments liberally - what, when, why, how
  - Bigger commented blocks for whole sections
  - Include processing details
  - Only analyses that appear in the final write-up

Notebooks and reports:

- R markdown files can be used to generate reproducible reports
- Text and R code are integrated
- Notebooks:
  - intermediate
  - may use one per day or one per subanalysis
  - documents all atempts
- Reports:
  - final methods and results only
  - good for sharing

Adapted from: Reproducible Research at Coursera

3.2.6 Version control in git and GitLab

Adopt a branching workflow appropriate for the project and team size, and stick to it.

gitforsmallteams

Reprinted from: Git workflow for small teams. Link currently is password protected.

`git` and `git-workflow` resources: Learn git Git branching model GitFlow

3.2.7 Keeping track of enviroment

Use `devtools::session_info()`

or `sessionInfo()`

or `docker` with `rrtools`

4 Toolbox

4.1 Command Line Tools

4.1.1 Bioinformatics

4.1.1.1 Get average read length from a `.bam` file

```
samtools view sorted.bam | head -n 1000000 | cut -f 10 | perl -ne 'chomp;print length($_) .
```

4.1.2 Docker

4.1.2.1 Basic commands

Here are a few helpful commands for working with `docker` images docker ps -a # Lists containers (and tells you which images they are spun from) docker images # Lists images
docker rm # Removes a container

docker rmi # Removes an image # Will fail if there is a running instance of that image i.e. container

docker rmi -f # Forces removal of image even if it is referenced in multiple repositories, # i.e. same image id given multiple names/tags # Will still fail if there is a docker container referencing image

4.1.2.2 Pruning

```
# remove dangling images
docker rmi $(docker images --filter "dangling=true" -q --no-trunc)

# find other untagged images (with possible children) (<none>:<none>)
docker images -a | grep "none" | awk '{print $3}'

# try removing them
docker rmi $(docker images -a | grep "none" | awk '{print $3}')
```

```
# if any left because of clingy children, get __parent.ID__ (ID of untagged image) and then
# example: docker inspect --format='{{.Id}} {{.Parent}}' $(docker images --filter since=14a
docker inspect --format='{{.Id}} {{.Parent}}' $(docker images --filter since=__parent.id__

# then remove listed __children.id__ one by one
# example: docker rmi 382096f13260254f3c472bf63f063b8ecbc2d4cc06fe7a940d6fbd4636ef77b1
docker rmi __child.id__
```

4.1.3 File system

4.1.3.1 List top 5 largest files

```
du -a /path/to/my/dir/ | sort -n -r | head -n 5
```

Example:

```
du -a /bin | sort -n -r | head -n 5
```

4.1.3.2 List files in a folder separated by delimeter

```
ls -1 /path/to/my/dir/ | paste -sd "," -
```

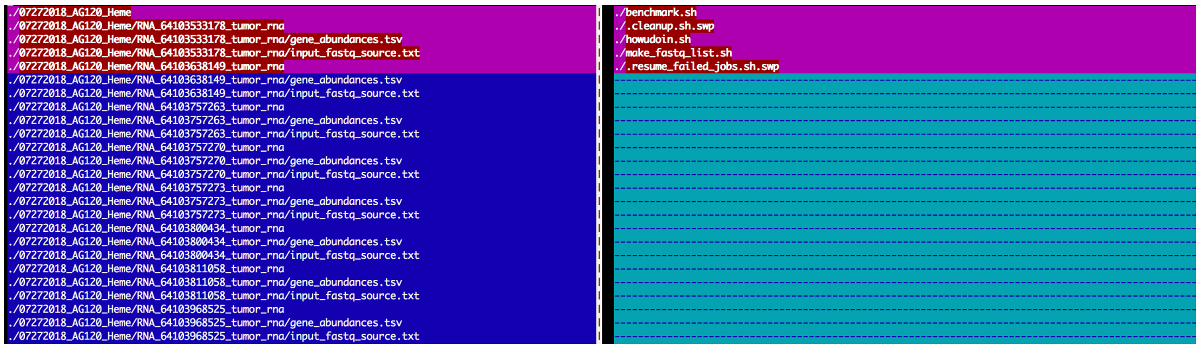
Example:

```
ls -1 /bin | paste -sd "," -
```

4.1.3.3 Compare structure of two directories

```
vimdiff <(cd dir1; find . | sort) <(cd dir2; find . | sort)
```

Example:



```
./07272018_AG120_Heme
./07272018_AG120_Heme/RNA_64103533178_tumor_rna
./07272018_AG120_Heme/RNA_64103533178_tumor_rna/gene_abundances.tsv
./07272018_AG120_Heme/RNA_64103533178_tumor_rna/input_fastq_source.txt
./07272018_AG120_Heme/RNA_64103638149_tumor_rna
./07272018_AG120_Heme/RNA_64103638149_tumor_rna/gene_abundances.tsv
./07272018_AG120_Heme/RNA_64103638149_tumor_rna/input_fastq_source.txt
./07272018_AG120_Heme/RNA_64103757263_tumor_rna
./07272018_AG120_Heme/RNA_64103757263_tumor_rna/gene_abundances.tsv
./07272018_AG120_Heme/RNA_64103757263_tumor_rna/input_fastq_source.txt
./07272018_AG120_Heme/RNA_64103757270_tumor_rna
./07272018_AG120_Heme/RNA_64103757270_tumor_rna/gene_abundances.tsv
./07272018_AG120_Heme/RNA_64103757270_tumor_rna/input_fastq_source.txt
./07272018_AG120_Heme/RNA_64103757273_tumor_rna
./07272018_AG120_Heme/RNA_64103757273_tumor_rna/gene_abundances.tsv
./07272018_AG120_Heme/RNA_64103757273_tumor_rna/input_fastq_source.txt
./07272018_AG120_Heme/RNA_64103800434_tumor_rna
./07272018_AG120_Heme/RNA_64103800434_tumor_rna/gene_abundances.tsv
./07272018_AG120_Heme/RNA_64103800434_tumor_rna/input_fastq_source.txt
./07272018_AG120_Heme/RNA_64103811058_tumor_rna
./07272018_AG120_Heme/RNA_64103811058_tumor_rna/gene_abundances.tsv
./07272018_AG120_Heme/RNA_64103811058_tumor_rna/input_fastq_source.txt
./07272018_AG120_Heme/RNA_64103968525_tumor_rna
./07272018_AG120_Heme/RNA_64103968525_tumor_rna/gene_abundances.tsv
./07272018_AG120_Heme/RNA_64103968525_tumor_rna/input_fastq_source.txt
```

```
./benchmark.sh
./.cleanup.sh.swp
./howudoin.sh
./make_fastq_list.sh
./.resume_failed_jobs.sh.swp
```

4.1.4 Sun Grid Engine

4.1.4.1 Deprioritize jobs queued on SGE

```
qalter -p -100 {jobid1..jobidn}
```

4.1.5 vim

4.1.5.1 Repeat content of line in new column

```
# repeat content of line
# a
# b
# c
# becomes
# a = C.a
# b = C.b
# c = C.c
:%s/.*/& = C.&
```

4.2 R

4.2.1 Heatmaps

4.2.2 Addition

```
x <- 3
y <- 4
z <- x + y
z
```

```
## [1] 7
```

4.3 python

4.4 perl

4.4.0.1 Get number of lines in a file

```perl
open(my $input, "-|", "wc -l < $fastqs");
my $rc = <$input>;
if ($rc =~ /(\d+)/) {
    print $rc;
}
```