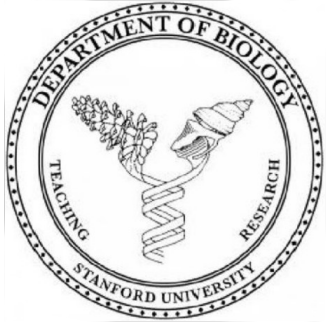
# Remembering what you did: Automated reports with R Markdown

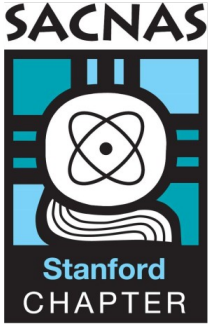
Sur Herrera Paredes

2022-04-23

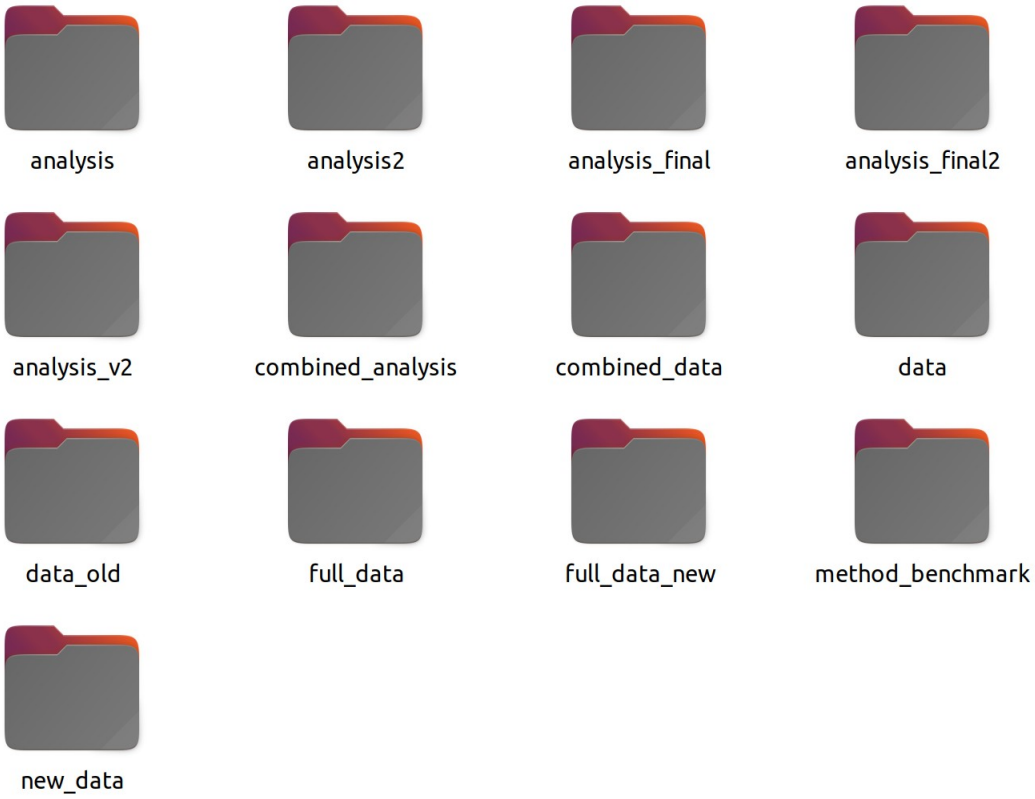
Data management for publishing

Jasper Ridge Biological Preserve

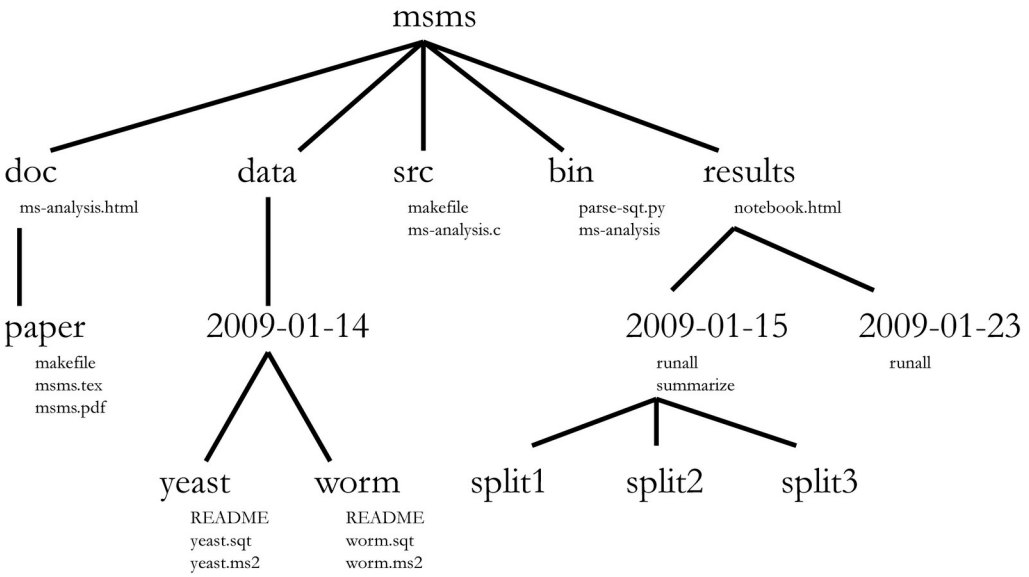




# A (hopefully not) familiar organizational structure



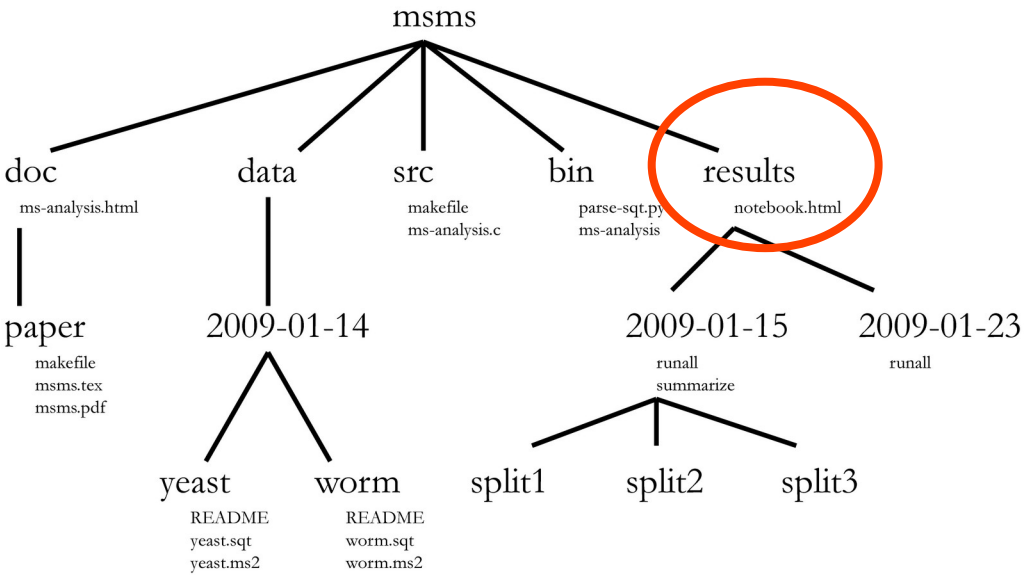
# Thinking about organization: types of files




- Keep different types of digital objects (e.g. data, code, exectuables, analysi) separate.
- Establish rules for different types of digital objects (i.e. files)
- Be consistent!

Noble, «A quick guide to organizing computational biology projects».

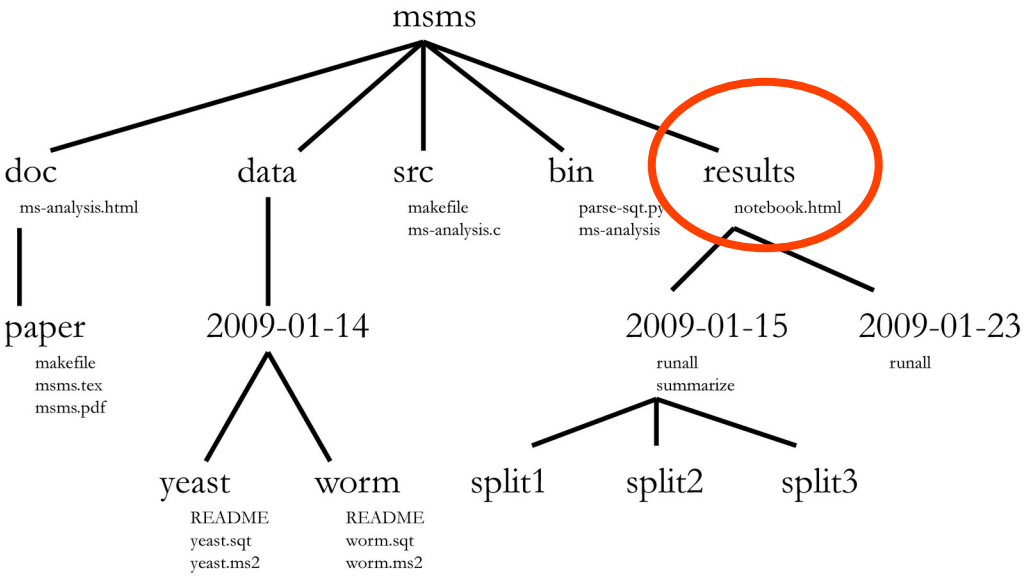
# Thinking about organization: types of files




- Keep different types of digital objects (e.g. data, code, exectuables, analysi) separate.
- Establish rules for different types of digital objects (i.e. files)
- Be consistent!

Noble, «A quick guide to organizing computational biology projects».

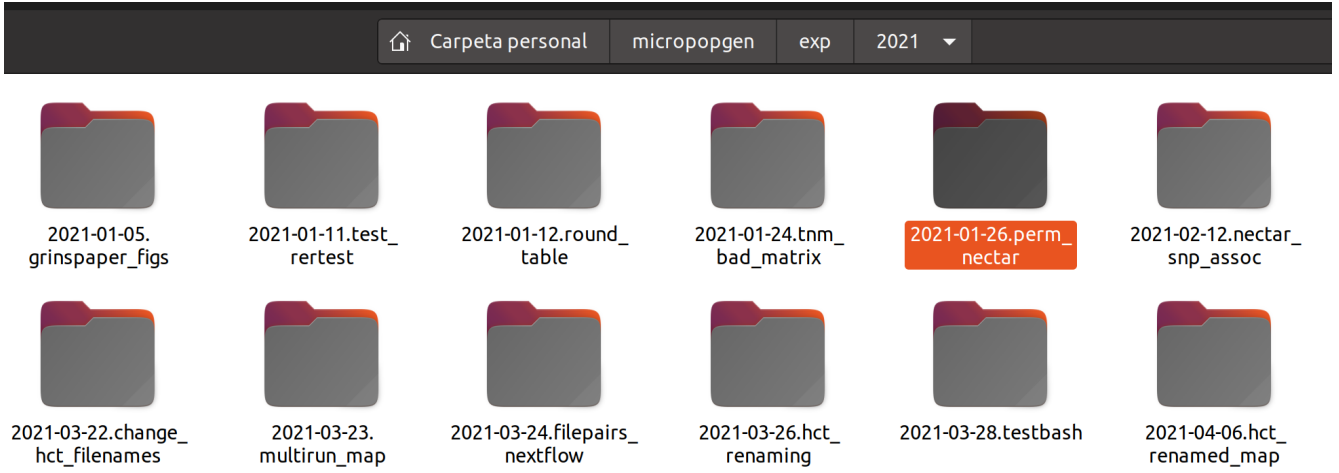
# Organize your analysis chronologically




Noble, «A quick guide to organizing computational biology projects».

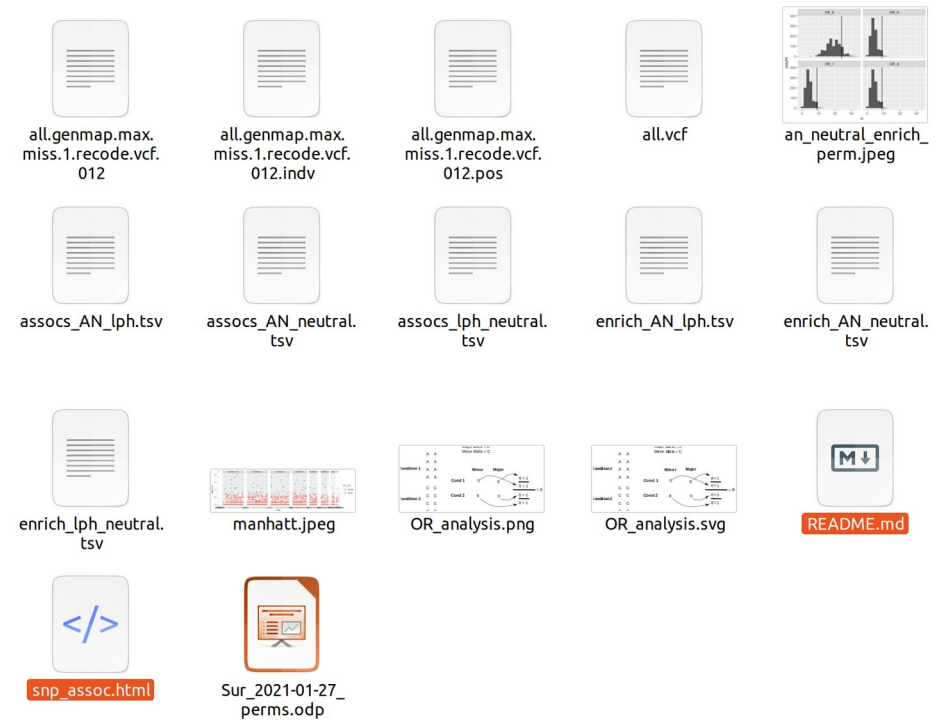
- You never know where your results will take you...yay Science!
- Organizing your results chronologically ensures that you can keep the organization consistent

# Create a digital lab notebook: chronoligical order

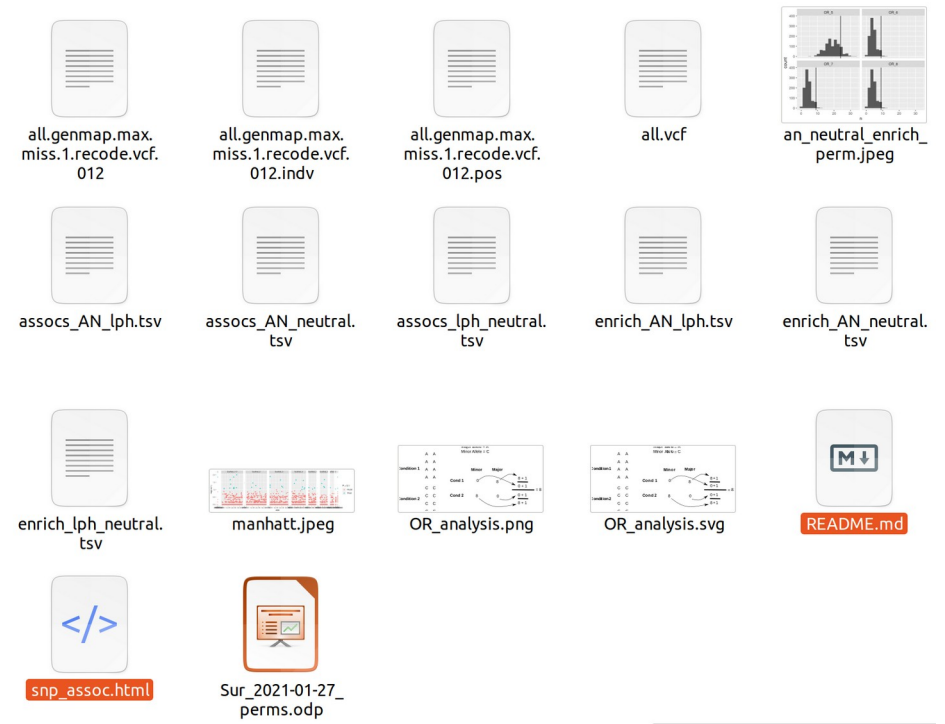



*Don’t forget to add a small informational name to the directory names*

# Create a digital lab notebook: A self-contained record of every analysis



# Create a digital lab notebook: save the code and output together




```
an_neutral <- test_condition_pair(selected_conditions = c("neutral", "AN"),
                                  geno = geno, meta = meta, Perms = Perms)
write_tsv(lph_neutral$assocs, "assocs_AN_neutral.tsv")
write_tsv(lph_neutral$enrich, "enrich_AN_neutral.tsv")
an_neutral
```

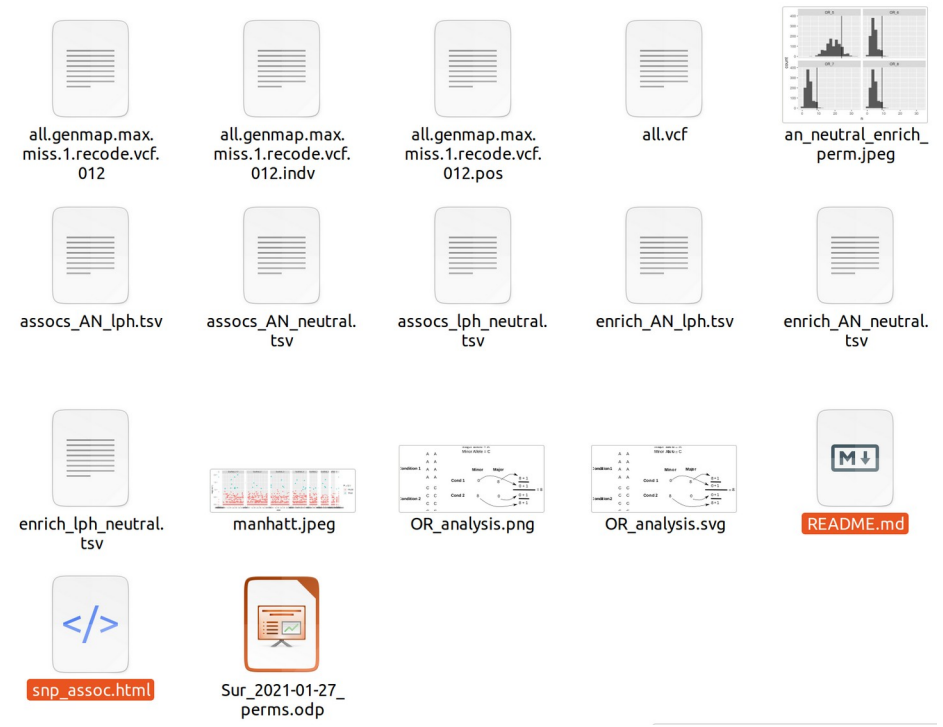
```
## $assocs
## # A tibble: 26,317 x 7
##    snp    major_c1 minor_c1 major_c2 minor_c2 OR.lap       P
##    <chr>     <dbl>    <dbl>    <dbl>    <dbl>  <dbl>   <dbl>
##  1 X11989        8        0        4        4  9     0.00999
##  2 X19677        0        8        4        4  0.111 0.0130
##  3 X10423        8        0        4        4  9     0.0140
##  4 X13824        8        0        4        4  9     0.0140
##  5 X19445        8        0        4        4  9     0.0140
##  6 X1627         0        8        4        4  0.111 0.0210
##  7 X7805         0        8        4        4  0.111 0.0210
##  8 X22988        8        0        5        3  6     0.0220
##  9 X2992         8        0        5        3  6     0.0220
## 10 X3263         3        5        0        8  6     0.0240
## # … with 26,307 more rows
##
## $enrich
## # A tibble: 8 x 2
##   OR.thres  pval
##      <int> <dbl>
## 1        1 0.23
## 2        2 0.212
## 3        3 0.673
## 4        4 0.106
## 5        5 0.106
## 6        6 0.007
## 7        7 0.007
## 8        8 0.007
```

```
an_lph <- test_condition_pair(selected_conditions = c("AN", "lpH"),
                              geno = geno, meta = meta, Perms = Perms)
write_tsv(lph_neutral$assocs, "assocs_AN_lph.tsv")
write_tsv(lph_neutral$enrich, "enrich_AN_lph.tsv")
an_lph
```

```
## $assocs
## # A tibble: 26,317 x 7
##    snp    major_c1 minor_c1 major_c2 minor_c2 OR.lap       P
##    <chr>     <dbl>    <dbl>    <dbl>    <dbl>  <dbl>   <dbl>
##  1 X14333        6        2        0        8 21.    0.00300
##  2 X14565        4        4        8        0  0.111 0.00899
##  3 X22988        4        4        8        0  0.111 0.0110
##  4 X2992         4        4        8        0  0.111 0.0110
##  5 X3282         4        4        8        0  0.111 0.0110
##  6 X3219         4        4        8        0  0.111 0.0130
##  7 X13824        5        3        8        0  0.167 0.0250
##  8 X16220        8        0        5        3  6     0.0250
##  9 X19445        5        3        8        0  0.167 0.0250
## 10 X13756        8        0        5        3  6     0.0350
## # … with 26,307 more rows
##
```

*That's where that table came from*

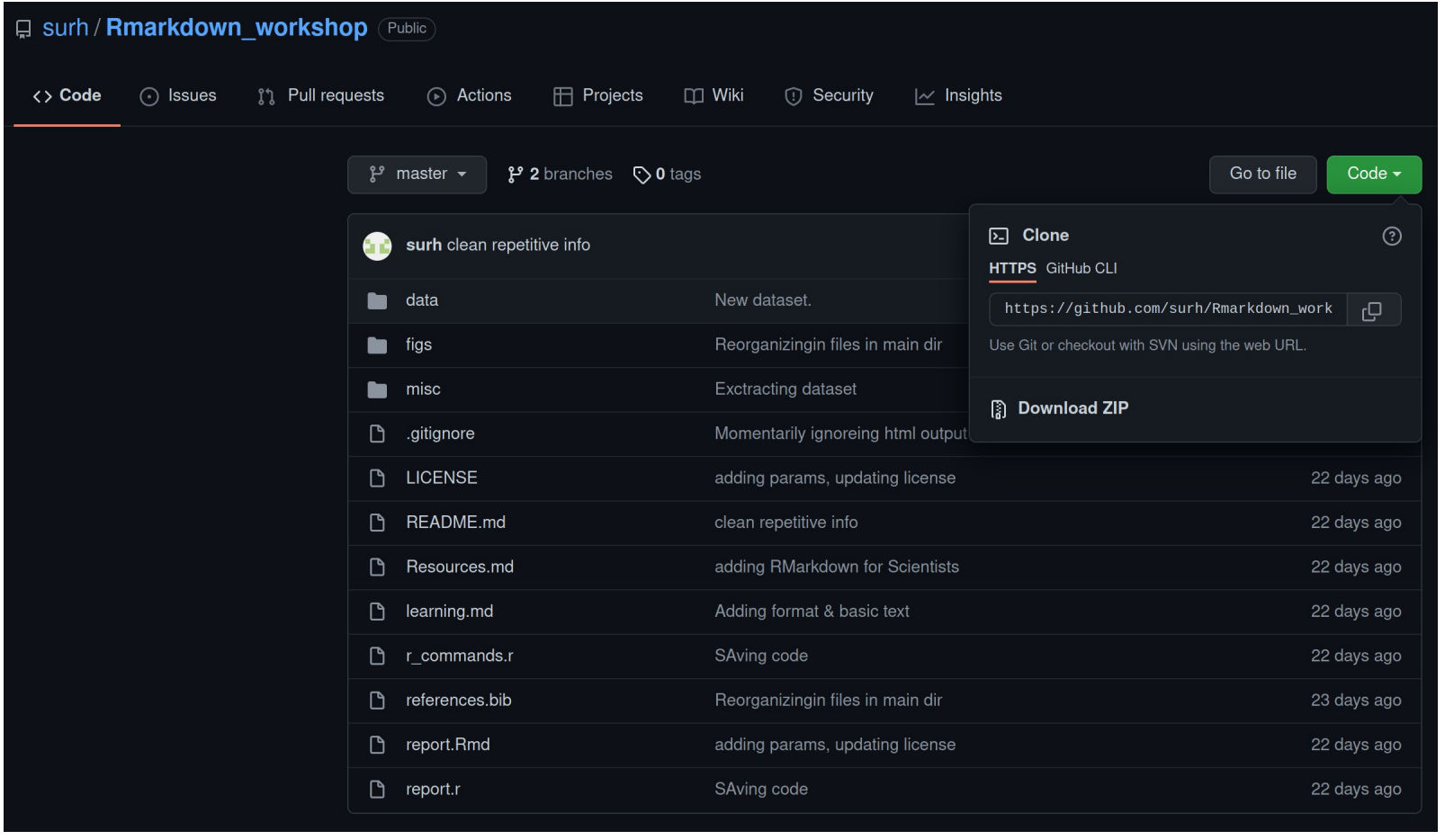
# Create a digital lab notebook: the README is your notebook




*In the wet lab nothing is more important than having a lab notebook. The same is true in the dry lab*

# Create a digital lab notebook: a simple approach

- Organize analysis chronologically
- Add a simple tag to each analysis directory
- Save the code together with the output that it produced.
- Keep a README inside every analysis
- Recreate don’t overwrite




**https://github.com/surh/Rmarkdown_workshop**