

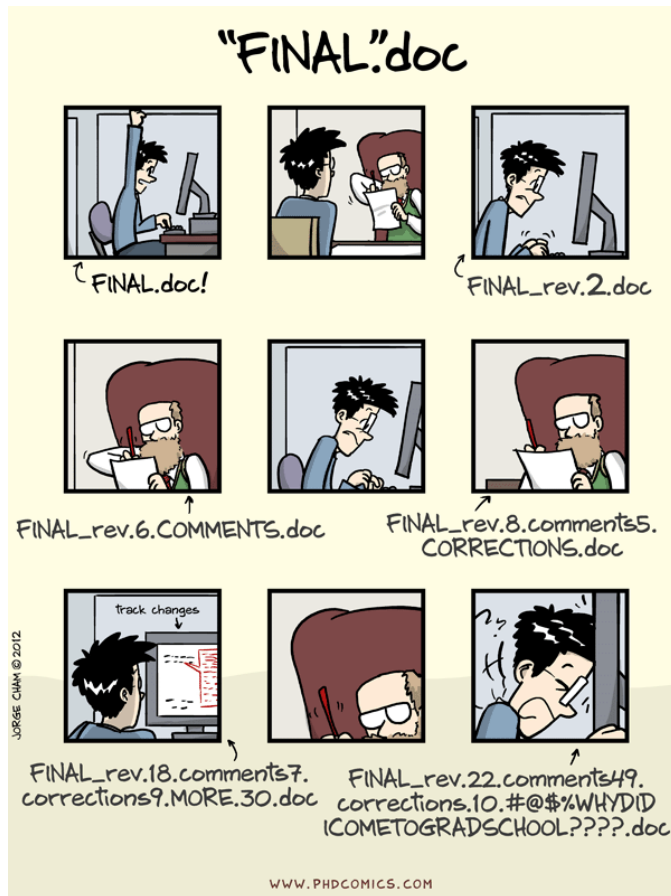


GIT-HUB

What is it for a biologist?



What is Github?



- Website that hosts a **git** server
 - *Git*: Version control system that helps to keep track of programs and files

Based mainly on: <https://swcarpentry.github.io/git-novice/>

What is Github?

■ Website that hosts a git server

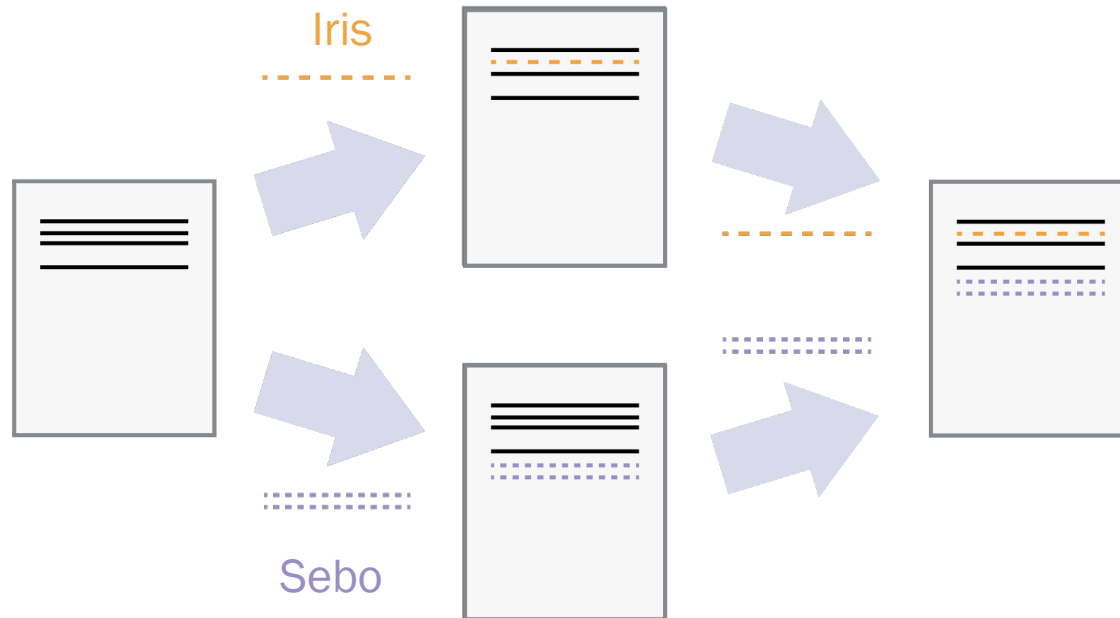
- *Git: Version control system that helps to keep track of programs and files*



Based mainly on: <https://swcarpentry.github.io/git-novice/>

What is Github?

- Website that hosts a **git server**
 - *Git: Version control system that helps to keep track of programs and files*



```
commit 005937fbe2a98fb83f0ade869025dc2636b4dad5 (HEAD -> main)
Author: Vlad Dracula <vlad@tran.sylvan.ia>
Date: Thu Aug 22 10:14:07 2013 -0400
```

Discuss concerns about Mars' climate for Mummy

```
commit 34961b159c27df3b475cfe4415d94a6d1fcd064d
Author: Vlad Dracula <vlad@tran.sylvan.ia>
Date: Thu Aug 22 10:07:21 2013 -0400
```

Add concerns about effects of Mars' moons on Wolfman

```
commit f22b25e3233b4645dabd0d81e651fe074bd8e73b
Author: Vlad Dracula <vlad@tran.sylvan.ia>
Date: Thu Aug 22 09:51:46 2013 -0400
```

Start notes on Mars as a base

```
diff --git a/mars.txt b/mars.txt
index df0654a..315bf3a 100644
--- a/mars.txt
+++ b/mars.txt
@@ -1,2 @@
 Cold and dry, but everything is my favorite color
+The two moons may be a problem for Wolfman
```

Based mainly on: <https://swcarpentry.github.io/git-novice/>

How does it look like?

The screenshot shows the GitHub repository page for `jokergoo/ComplexHeatmap`. The repository is public and has 35 watchers, 193 forks, and 1k stars. The main content area displays a file tree with the following files and their last commit dates:

File	Description	Last Commit
<code>.github</code>	NA is allowed in pch in legend	4 months ago
<code>R</code>	closeCluster	3 days ago
<code>docs</code>	generate documentations by pkgdown	4 years ago
<code>inst</code>	fixed a bug of annotation legends when 'df' is set	7 months ago
<code>man</code>	update	5 days ago
<code>tests</code>	add a new <code>add_points</code> argument in <code>anno_boxplot()</code>	5 months ago
<code>vignettes</code>	<code>draw()</code> stores legend-related configurations	2 years ago
<code>.Rbuildignore</code>	fixed warnings	last year
<code>.gitignore</code>	kmeans-slices are reordered by <code>row_reorder</code> or <code>column_reorder</code>	5 years ago
<code>DESCRIPTION</code>	update	5 days ago
<code>LICENSE</code>	use <code>unitType(, recurse=T)</code> to test absolute units	3 years ago
<code>NAMESPACE</code>	rename to <code>anno_textbox()</code>	9 months ago
<code>NEWS</code>	<code>Legend()</code> : colors are correctly calculated when differences between '...	last month
<code>README.md</code>	update	7 months ago
<code>_pkgdown.yml</code>	use pkgdown to build the doc site	4 years ago
<code>build_pkg_site.R</code>	generate documentations by pkgdown	4 years ago
<code>logo.R</code>	add <code>labels_rot</code> argument to <code>anno_mark()</code>	4 years ago

The right sidebar contains the following information:

- About**: Make Complex Heatmaps. Link: jokergoo.github.io/ComplexHeatmap-r...
- Tags**: `clustering`, `heatmap`, `complex-heatmaps`
- Readme**: View license, Cite this repository
- Stars**: 1k stars
- Watching**: 35 watching
- Forks**: 193 forks
- Contributors**: 18 contributors (10 shown)
- Languages**: R 99.8%, CSS 0.2%

<https://github.com/jokergoo/ComplexHeatmap>

How does it look like?

README.md

Make Complex Heatmaps

R-CMD-check


passing

coverage 67%

rank 47 / 2195

In Bioc

8 years



Complex heatmaps are efficient to visualize associations between different sources of data sets and reveal potential patterns. Here the **ComplexHeatmap** package provides a highly flexible way to arrange multiple heatmaps and supports various annotation graphics.

The **InteractiveComplexHeatmap** package can directly export static complex heatmaps into an interactive Shiny app. Have a try!

Citation

Zuguang Gu, et al., [Complex heatmaps reveal patterns and correlations in multidimensional genomic data](#), Bioinformatics, 2016.

Zuguang Gu. [Complex Heatmap Visualization](#), iMeta, 2022.

Install

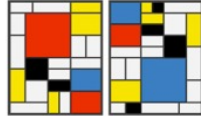
ComplexHeatmap is available on [Bioconductor](#), you can install it by:

```
if (!requireNamespace("BiocManager", quietly=TRUE))
  install.packages("BiocManager")
BiocManager::install("ComplexHeatmap")
```

If you want the latest version, install it directly from GitHub:

```
library(devtools)
```

ComplexHeatmap
Complete Reference



Zuguang Gu

<https://github.com/jokergoo/ComplexHeatmap>

How does it look like?

The screenshot shows the GitHub repository page for `jokergoo/ComplexHeatmap`. The repository is public and has 35 watchers, 193 forks, and 1k stars. The main content area displays a list of files and folders, including `.github`, `R`, `docs`, `inst`, `man`, `tests`, and `vignettes`. A dropdown menu is open, showing options to clone the repository using HTTPS, SSH, or GitHub CLI, or to open it with GitHub Desktop or download it as a ZIP file. The right sidebar contains the 'About' section, which includes the repository's description, a link to the repository's website, and a list of contributors. The 'Languages' section shows that the repository is primarily composed of R code (99.8%) and CSS (0.2%).

Search or jump to... Pull requests Issues Codespaces Marketplace Explore

jokergoo / ComplexHeatmap Public

Watch 35 Fork 193 Star 1k

<> Code Issues 75 Pull requests Discussions Actions Projects Wiki Security Insights

master 5 branches 3 tags

Go to file Add file <> Code

Local Codespaces New

Clone

HTTPS SSH GitHub CLI

git@github.com:jokergoo/ComplexHeatmap.g

Use a password-protected SSH key.

Open with GitHub Desktop

Download ZIP

About

Make Complex Heatmaps

jokergoo.github.io/ComplexHeatmap-r...

clustering heatmap complex-heatmaps

Readme View license Cite this repository 1k stars 35 watching 193 forks

Contributors 18

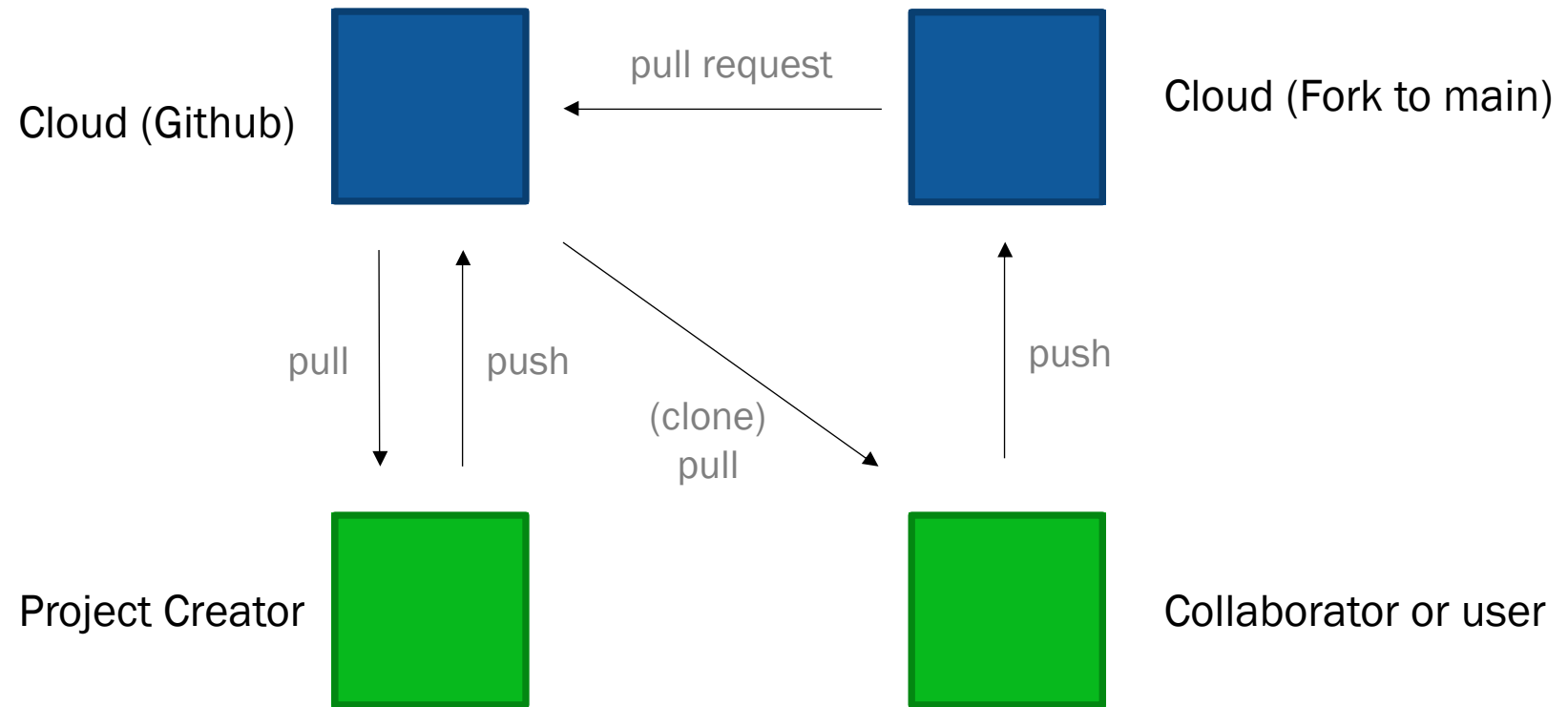
+ 7 contributors

Languages

R 99.8% CSS 0.2%

<https://github.com/jokergoo/ComplexHeatmap>

How does it look like?

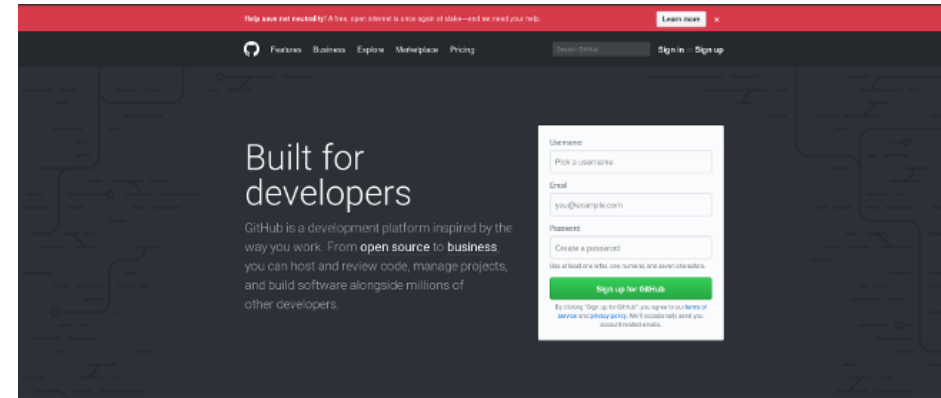


Why is version control important?

- “Unlimited Undo”, with trackable control of changes
- Collaboration
- **FAIR** data: Findability, Accessibility, Interoperability and Reusability
- Publishing
- Open source code
- Portfolio

How can I start?

- Open an account in Github

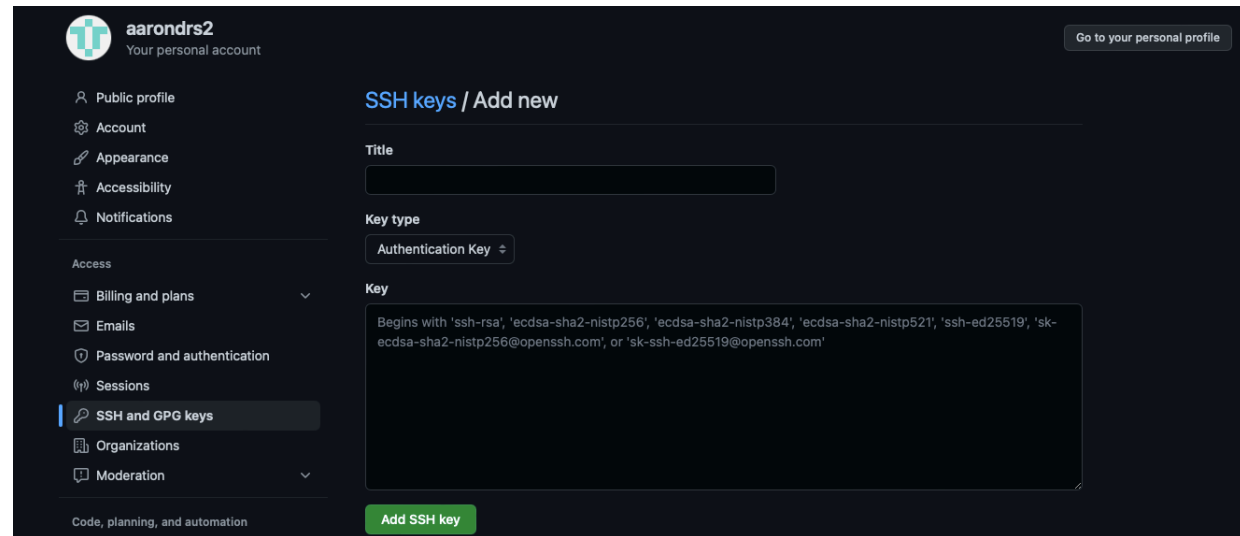


- Setup your account in your local machine:
 - `>git config --global user.name "Aaron Ramirez"`
 - `>git config --global user.email a.d.ramirez.sanchez@umcg.nl`
- In your local machine:
 - *Go to your project folder*
 - `> git init`

READY! (in your local machine)

How do I connect my local project to cloud (remote directory)?

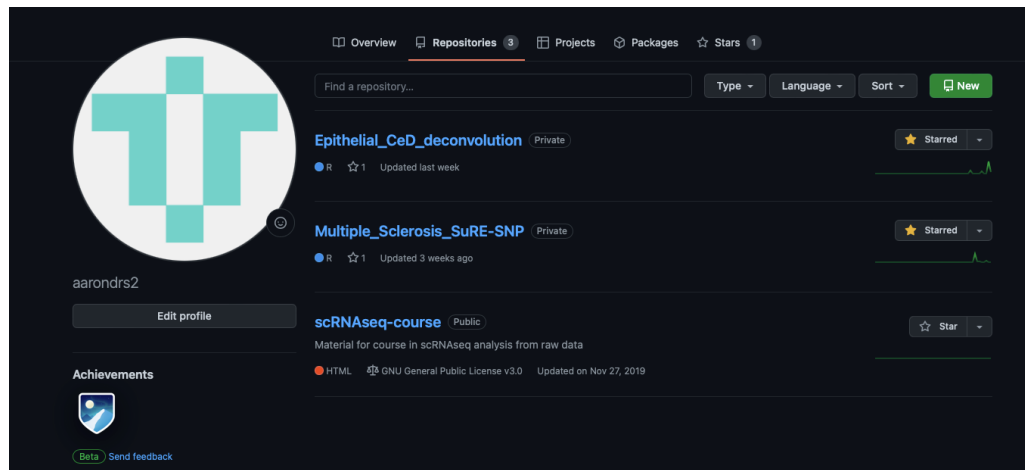
- Get credentials of identification in your local machine (SSH keys)
 - `ls -al ~/.ssh` #To verify whether they already exist, otherwise check link
- Share the **PUBLIC** key to Github
 - In Github, go to settings > SSH and GPG keys >> New SSH key



<https://swcarpentry.github.io/git-novice/07-github/index.html>

How do I connect my local project to cloud (remote directory)?

- Start a new repository in your Github account



Create a new repository

A repository contains all project files, including the revision history. Already have a project repository elsewhere? [Import a repository.](#)

Owner * **Repository name ***

aarondrs2 /

Great repository names are short and memorable. Need inspiration? How about **sturdy-barnacle**?

Description (optional)

☐ **Public**
Anyone on the internet can see this repository. You choose who can commit.

☒ **Private**
You choose who can see and commit to this repository.

Initialize this repository with:
Skip this step if you're importing an existing repository.

☐ **Add a README file**
This is where you can write a long description for your project. [Learn more.](#)

Add .gitignore
Choose which files not to track from a list of templates. [Learn more.](#)

.gitignore template: None

Choose a license
A license tells others what they can and can't do with your code. [Learn more.](#)

License: None

ⓘ You are creating a private repository in your personal account.

Create repository

How do I connect my local project to cloud (remote directory)?

- Get the link from your project (in SSH)

The screenshot shows a GitHub repository page for 'aarondrs2 / Epithelial_CeD_deconvolution'. The repository is private. The navigation bar includes links for Code, Issues, Pull requests, Actions, Projects, Security, Insights, and Settings. The repository has 1 branch (main) and 0 tags. The file list shows the following files and their descriptions:

File	Description
data	Heatmap plots and clusters u
output	Removed Y chromosomes
src	Added a description in READM
.gitignore	.DS_Store banished!
Epithelial_CeD_deconvolution.Rproj	Start of project
README.md	Modified root Readme with ex
run_analysis.R	Start of project

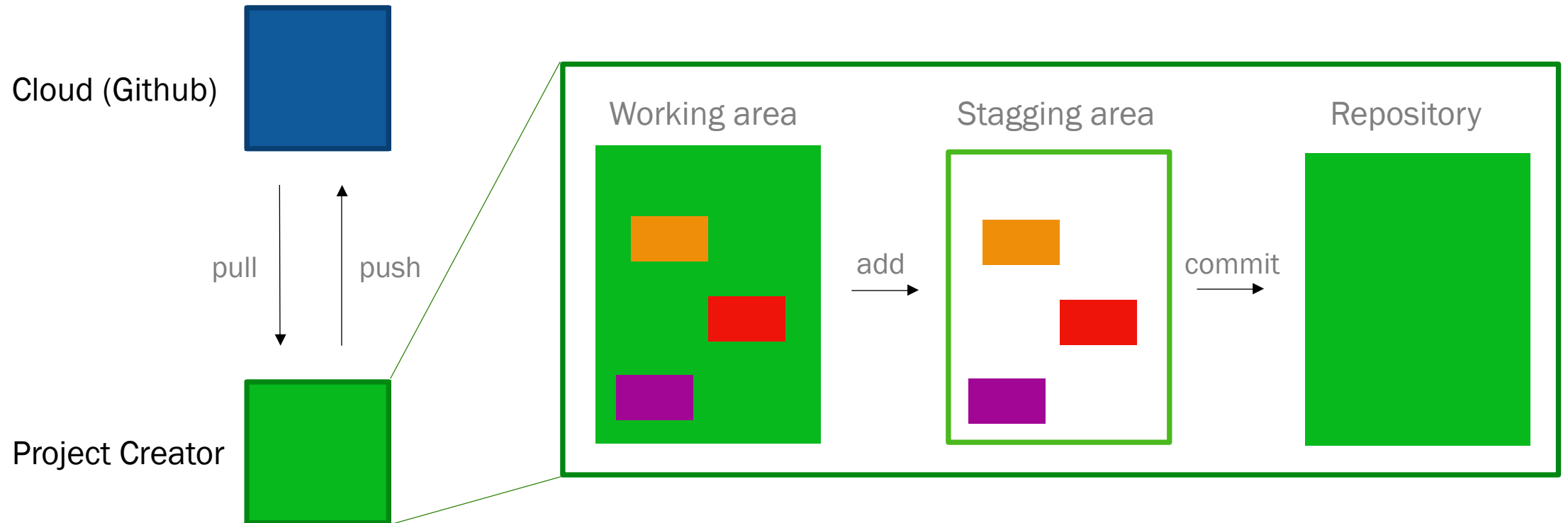
The 'Code' dropdown menu is open, showing options for cloning the repository. The 'SSH' option is selected, and the SSH link is displayed: `git@github.com:aarondrs2/Epithelial_CeD_`. The menu also includes options for 'Open with GitHub Desktop' and 'Download ZIP'.

How do I connect my local project to cloud (remote directory)?

- While in your local project folder:
 - `git remote add origin git@github.com:aarondrs2/Epithelial_CeD_deconvolution.git`
 - `git branch -M main`
 - `git push -u origin main`
- Verify that it worked:
 - `git remote -v`

```
(base) Aaron-MacPro:Epithelial_CeD_deconvolution RamirezSanAD$ git remote -v
origin  git@github.com:aarondrs2/Epithelial_CeD_deconvolution.git (fetch)
origin  git@github.com:aarondrs2/Epithelial_CeD_deconvolution.git (push)
```

How to use the triforce?



How to use the triforce?

#Adding a file

git add FILE





#Committing new changes

git commit -m ""

#Pushing new changes to GitHub

git push -u origin main

```
(base) Aaron-MacPro:Epithelial_CeD_deconvolution RamirezSanAD$ touch src/example.txt
(base) Aaron-MacPro:Epithelial_CeD_deconvolution RamirezSanAD$ git add src/example.txt
(base) Aaron-MacPro:Epithelial_CeD_deconvolution RamirezSanAD$ git commit -m "Added example file"
[main 05e0347] Added example file
1 file changed, 0 insertions(+), 0 deletions(-)
create mode 100644 src/example.txt
(base) Aaron-MacPro:Epithelial_CeD_deconvolution RamirezSanAD$ git push -u origin main
```

 20_decon-eQTL.sh	Modifications to eQTL scripts	last week
 21_Processing_decon-eQTL_tables.R	Modifications to eQTL scripts	last week
 README.md	Added a description in README of src	last week
 example.txt	Added example file	1 minute ago

Collaborating?

- Invite collaborator to your repository

The screenshot shows the GitHub repository settings for 'aarondrs2 / Epithelial_CeD_deconvolution' (Private). The 'Settings' tab is selected, and the 'Collaborators' sub-tab is active. The left sidebar lists various repository settings: General, Access, Code and automation, Security, and more. The main content area is titled 'Who has access' and shows two access types: 'PRIVATE REPOSITORY' (locked) and 'DIRECT ACCESS' (unlocked). Under 'DIRECT ACCESS', it states '1 has access to this repository. 1 collaborator.' and provides a 'Manage' link. Below this is the 'Manage access' section, which includes a 'Select all' checkbox, a search bar labeled 'Find a collaborator...', and a list of collaborators. One collaborator, 'IrisHJonkers', is listed with a 'Remove' button next to their name.

Who has access

PRIVATE REPOSITORY (locked icon)
Only those with access to this repository can view it.
[Manage](#)

DIRECT ACCESS (unlocked icon)
1 has access to this repository. 1 collaborator.
[Manage](#)

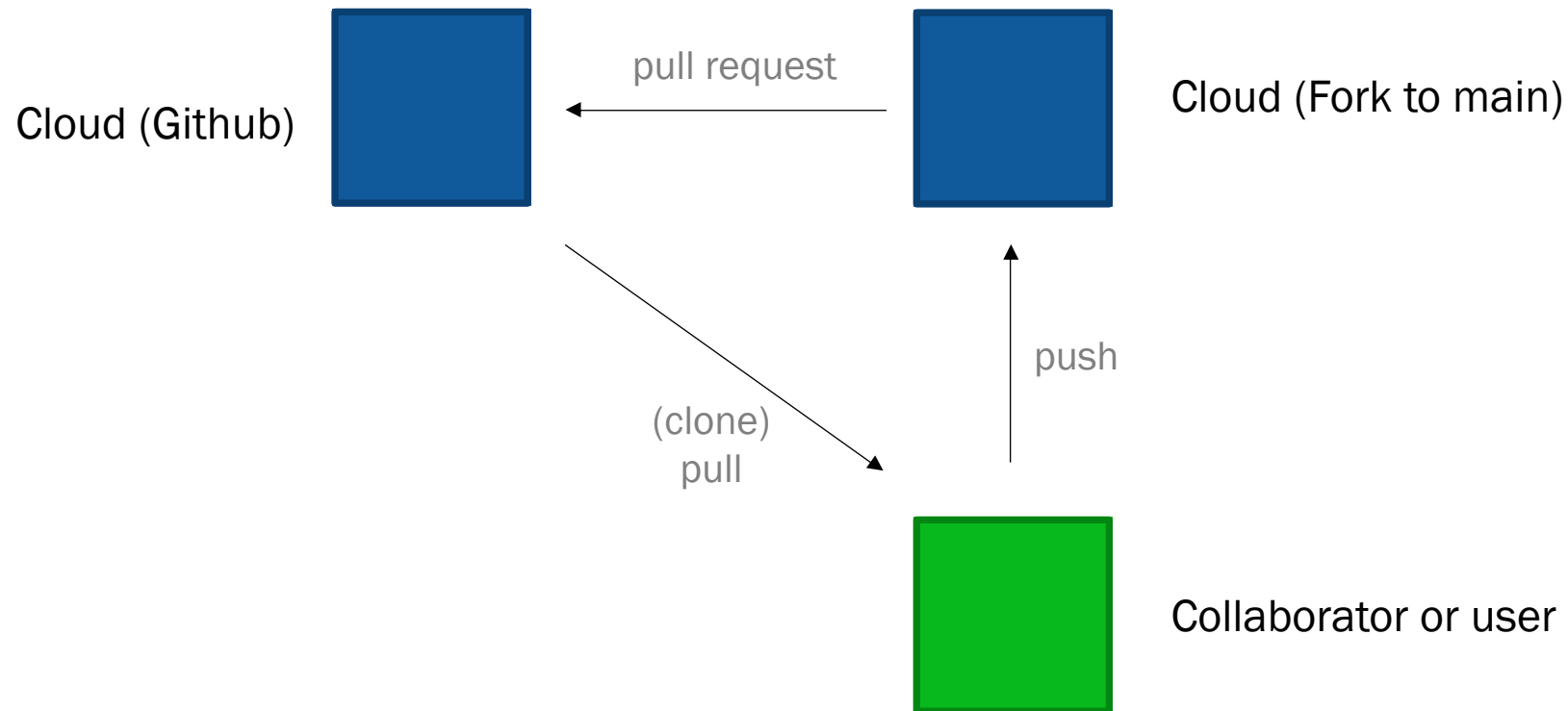
Manage access [Add people](#)

☐ Select all Type ▾

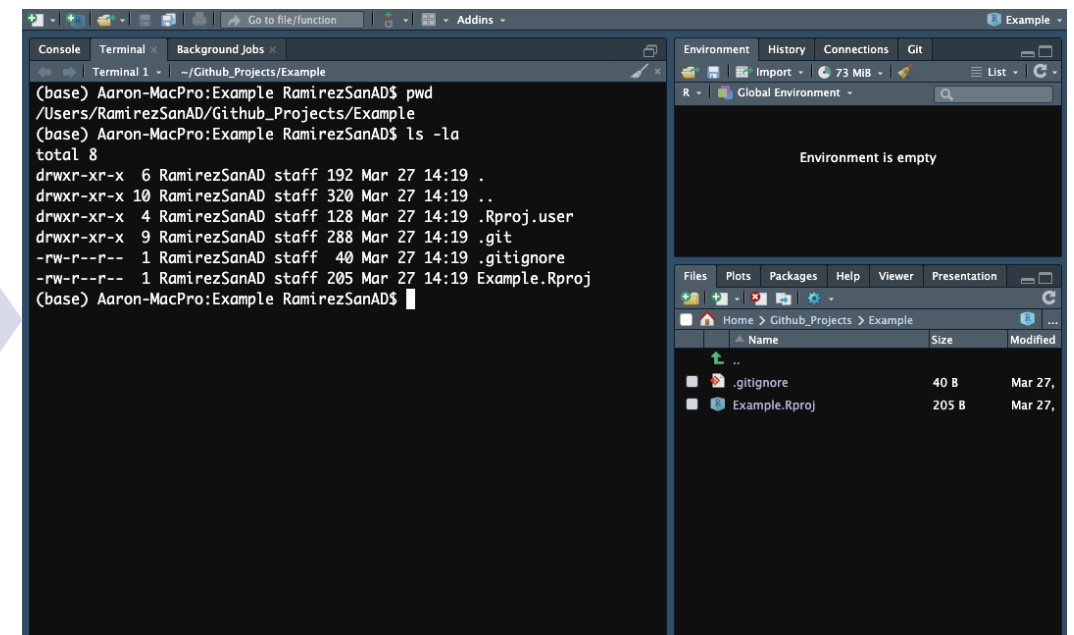
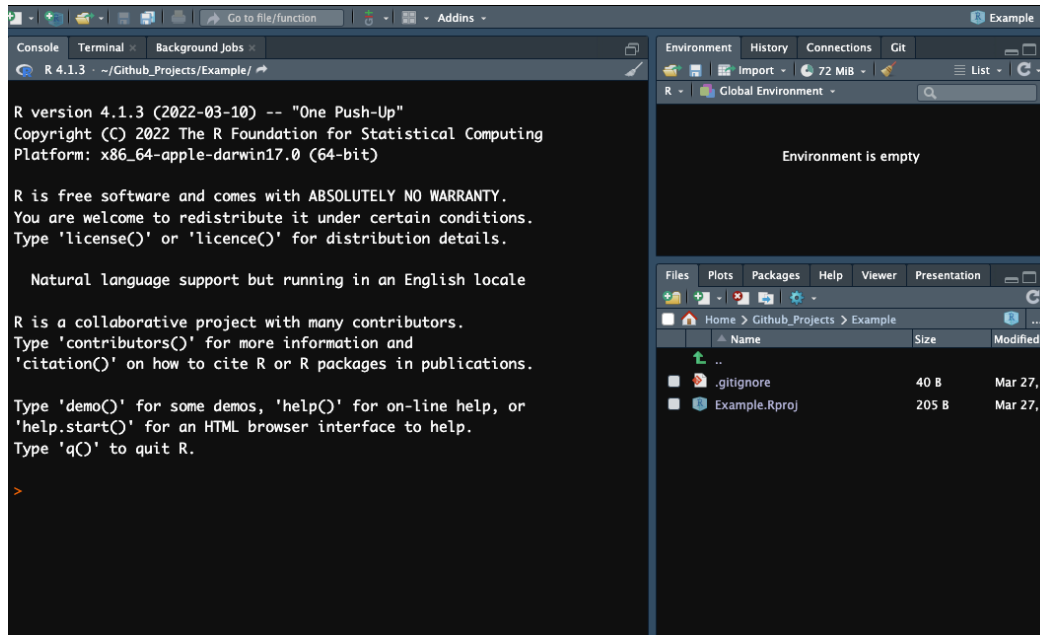
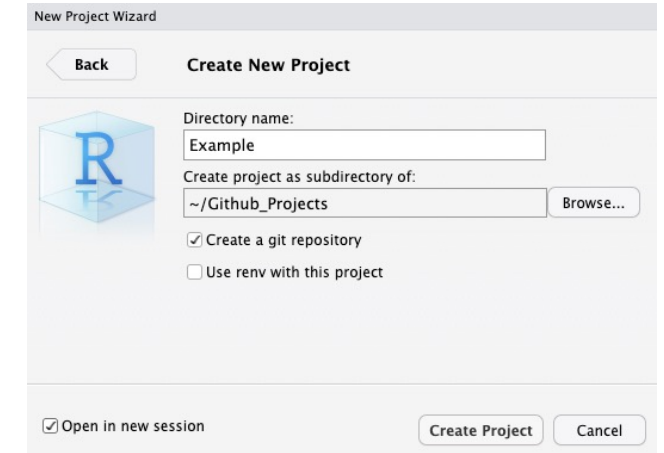
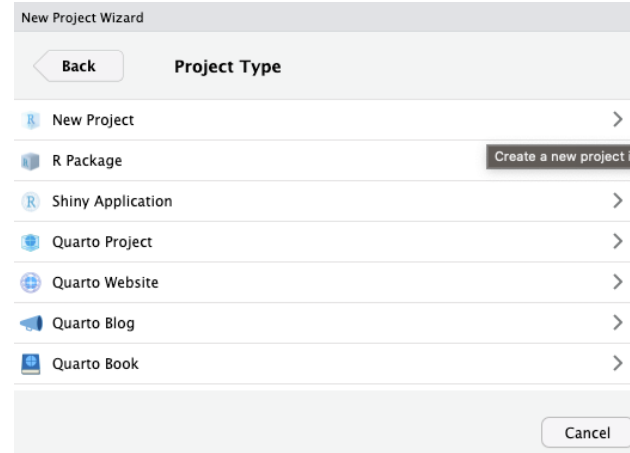
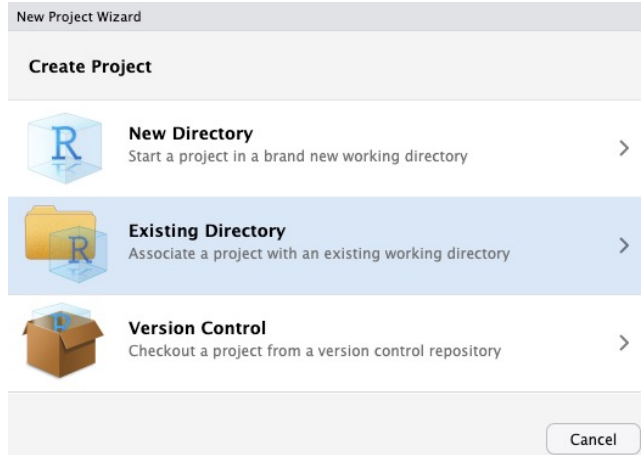
☐ **IrisHJonkers**
Collaborator [Remove](#)

Collaborating?

- Now this person can modify/add/remove files
- A good practice is that this person works in a “fork”, so main project person can review the code before committing in the main repository



Rstudio and GitHub



Rstudio and GitHub

- Follow the steps to setup a **remote project**
 - *Start a new repository in Github (it should be empty)*
 - *Copy the link SSH*
 - *Run in the terminal of Rstudio (it should be in the project folder, verify with `pwd`)*
 - `git remote add origin git@github.com:aarondrs2/Example.git`
 - *READY*

Not discussed here

- How to "undo" and go to a previous version
- How to explore changes done to files (diff & checkout)
- How to ignore files (.gitignore)
- How to create an SSH key
- How to set up a fork
- How to review and accept "pull requests"
- How to resolve conflicts
- How to add licensing

Precautions

- Better to add and commit small changes at the time
- If working with someone else, always “pull” before starting, in order to have the most updated version
- Use “forks” when collaborating with someone
- You can ignore folders in your project, useful for results that are going to change a lot, since they may require from a lot of memory to keep track
- **ALWAYS DOBLE, TRIPLE CHECK YOU ARE NOT ADDING/COMMITTING/PUSHING CONFIDENTIAL DATA** (specially if you decided to add a full folder, using correctly .gitignore may also make it very hard to do this error)

PROJECT ORGANIZATION

Data analysis



Why to organize project analysis?

■ Do you remember?

symptoms does not correlate with mucosal healing [Leonard 2017 JPGN]. Lastly, novel biomarkers could help to monitor the efficiency of drugs in patients with the gluten free diet, but also to explore heterogeneity in treatment response.

Thus, the search for novel biomarkers is necessary to improve early diagnosis, to decrease diagnostic burden and to follow adherence to and disease development after initiating GFD. Ideally, these markers should be detectable in material that can be obtained in a non-invasive manner and the test should be easy and quick to perform and interpret. Here we will review potential molecular biomarker tests for CeD, beyond the currently used serological markers. We will mainly focus on recent advances in non-invasive biomarkers that can be measured in blood, urine or feces, which might augment and improve diagnostics and follow-up of celiac disease. We will also summarize recent studies on the immunopathology of CeD as well, as these studies also uncovered potential novel biomarkers.

CeD Immunopathology (Aaron - read by Ineke)

Being classified as a 'complex disease' the pathophysiology of CeD involves a combination of environmental, genetic and perhaps also microbial factors factors.
The most important environmental factor involved in CeD is gluten exposure [Solid &

Sebo Withoff Deleted: new
Sebo Withoff explain
Sebo Withoff Deleted: in drug development
Sebo Withoff GFD and/or novel drugs?
Sebo Withoff Deleted: in celiac disease and predi
Sebo Withoff Moved (insertion) [1]
Iris Jonkers Deleted: ...o improve early
Sebo Withoff Deleted: continues,
Iris Jonkers Deleted: especially finding those tha
Sebo Withoff Deleted: gaps of conventional
Sebo Withoff Formatted
Sebo Withoff Deleted: chnique
Iris Jonkers It's a very nice paragraph with a
I.L. Tan We moved move the part about
I.L. Tan Marcado como resuelto
I.L. Tan Reabierio
Sebo Withoff Formatted
Sebo Withoff Deleted:
Sebo Withoff Deleted: is to explore ...otential
Iris Jonkers I think the intro and explanation of
I.L. Tan Tried to adress this more clearly in
Sebo Withoff Deleted: could
Sebo Withoff Formatted

■ Know imagine this for a full project

scripts	26 July 2022 at 12:45
20211224-PreventCD-getting_metadata_countmatrix_after_rebuttal.R	26 July 2022 at 12:45
scRNAseq_CeD_script_importing_data_VADRS.R	19 July 2022 at 15:34
20211224-PreventCD-getting_metadata_countmatrix.R	22 February 2022 at 17:04
20200312-Fig1-UMAPplots_for_Rebuttal_R1_gluten_intervention.R	10 February 2022 at 19:47
20200312-Fig1-UMAPplot_of_PreventCD-v1_modifiedforgettingFigures.R	26 January 2022 at 13:13
20210428-MAKINGDEGcombinationfroclassification-v5.R	15 July 2021 at 10:12
20201208-MAKINGDEGcombinationfroclassification-v4.R	17 March 2021 at 11:34
20200317-Fig2-Freqplot_of_PreventCD-v2.R	20 January 2021 at 10:09
20200312-Fig1-UMAPplot_of_PreventCD-v1.R	20 January 2021 at 10:09
20201208-MAKINGDEGcombinationfroclassification-v3.R	8 December 2020 at 15:35
20200128-MAKINGDEGcombinationfroclassification-new.R	30 November 2020 at 12:56
20200128-MAKINGDEGcombinationfroclassification-old.R	30 November 2020 at 12:53
fishertestvNov.R	26 August 2020 at 21:37
20200318-Fig3-UpSetplot_DEG_PreventCD-v1.R	20 March 2020 at 13:38
20200128-MAKINGDEGcombinationfroclassification.R	18 March 2020 at 15:57
20200317-Fig2-Freqplot_of_PreventCD-v1.R	18 March 2020 at 13:51
20191205-PreventCD-Tcellsubsets-Seurat.R	17 March 2020 at 15:13
2019Dec-CheckingGenesinCD4.R	17 March 2020 at 15:12
CreatingViolinplotsV1.R	17 March 2020 at 15:08
20191220-CD4cells-proportions.R	3 February 2020 at 11:17
facet_nested.R	24 January 2020 at 10:42
20191112-PreventCD-Tcellsubsets-Seurat.R	20 November 2019 at 16:01
Novscript-not-sure.R	1 November 2019 at 14:04
NewHeatmapUsingggplot.R	1 November 2019 at 14:04
MakingFreqplotsPerCTVNov.R	1 November 2019 at 13:59
MakingUMAPplotswithDEGvNov.R	1 November 2019 at 13:59
MakingUMAPplotswithDEG.R	4 October 2019 at 14:55
QuickCheckOfCeDGenes.R	4 October 2019 at 14:53
MakingTablewithDEGv2.R	26 September 2019 at 14:24
MAKINGDEgenes.bulklike.newcolor.R	26 September 2019 at 14:24
CreatingUMAPplots.R	18 September 2019 at 14:07
MakingFreqplotsPerCT.R	17 September 2019 at 13:07
Concordance2.R	9 September 2019 at 14:20
UpSetplots.R	9 September 2019 at 14:19
Concordance.Donorwise.Bulklike2.2.R	9 September 2019 at 14:19
MakingTablewithDEG.R	9 September 2019 at 14:18
MAKINGDEgenes.bulklike.R	9 September 2019 at 14:17
crazyhigh.R	2 September 2019 at 17:01
Concordance.Donorwise.Bulklike2.R	23 August 2019 at 11:24
Concordance.Donorwise.Bulklike1.R	21 August 2019 at 14:43

How can I start?

- With a clear outline of your project
 - *What is your goal?*
 - *What is your input?*
 - *What is your final result?*
 - *How is your plan of analysis?*
 - *Are your analysis independent from each other?*
 - *Do you expect results to be dynamic?*

One example

▼ data	31 January 2023 at 11:48	--	Folder
.gitignore	18 January 2023 at 13:22	Zero bytes	Document
> processed	16 March 2023 at 13:40	--	Folder
> raw	20 March 2023 at 14:18	--	Folder
> tmp	18 January 2023 at 13:22	--	Folder
Epithelial_CeD_deconvolution.Rproj	Today at 13:47	205 bytes	R Project
▼ output	19 February 2023 at 16:13	--	Folder
.gitignore	18 January 2023 at 13:22	Zero bytes	Document
> objects	19 February 2023 at 18:45	--	Folder
> plots	17 March 2023 at 17:46	--	Folder
> tables	16 March 2023 at 15:10	--	Folder
> tmp	18 January 2023 at 13:23	--	Folder
README.md	20 February 2023 at 12:00	7 KB	Markdo...cument
run_analysis.R	18 January 2023 at 12:48	Zero bytes	Rez Source
▼ src	Today at 14:07	--	Folder
.gitignore	18 January 2023 at 13:22	Zero bytes	Document
00_Formatting_count_matrix.R	18 February 2023 at 12:15	811 bytes	Rez Source
00_Formatting_metadata.R	18 February 2023 at 12:50	2 KB	Rez Source
00_Template.R	18 February 2023 at 11:15	166 bytes	Rez Source
01_DifExpAnalysis_DESeq.R	19 February 2023 at 14:51	5 KB	Rez Source
02_Enrichment_analysis.R	17 March 2023 at 12:13	5 KB	Rez Source
03_Enrichment_plots.R	17 March 2023 at 12:17	4 KB	Rez Source
04_ZeroVar_count_matrix.R	19 February 2023 at 15:06	901 bytes	Rez Source
05_Heatmaps_and_clusters.R	17 March 2023 at 13:37	8 KB	Rez Source

HOW WE CAN BENEFIT?

Immunogenetics group



Work in private and release in public?

- Start projects in private access with personal accounts
- Once in submission process, clone repository or copy final freeze in a open repository belonging to the Group
 - *This should be the repository used in the manuscript*
- New changes done should occur in Group repository (rebuttal, bug fixing)