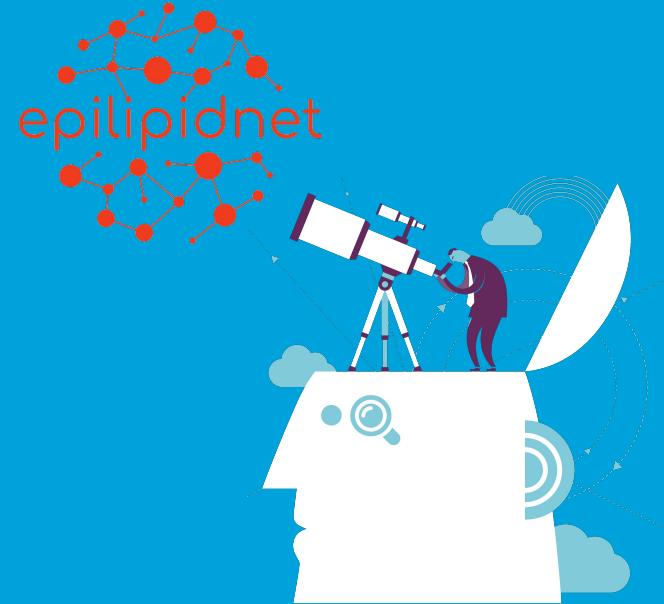


Metabolomics data analysis

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Tuesday March 11, 2025



Hands-on session - GitHub Desktop

The screenshot shows the GitHub Desktop application interface. At the top, there's a menu bar with options: File, Edit, View, Repository, Branch, Help. Below the menu is a header bar with three items: "Current repository Workshop1", "Current branch main", and "Fetch origin Never fetched". The main area is titled "No local changes". It contains a message: "There are no uncommitted changes in this repository. Here are some friendly suggestions for what to do next." Below this message are three cards:

- Open the repository in your external editor**
Select your editor in [Options](#)
Repository menu or **Ctrl + Shift + A** [Open in GNOME Text Editor](#)
- View the files of your repository in your File Manager**
Repository menu or **Ctrl + Shift + F** [Show in your File Manager](#)
- Open the repository page on GitHub in your browser**
Repository menu or **Ctrl + Shift + G** [View on GitHub](#)

At the bottom left, there's a "Summary (required)" field with a user icon, a "Description" field, and a "Commit to main" button.

You should have something that looks like this now!

Hands-on session - GitHub Desktop

The screenshot shows the GitHub Desktop application interface. At the top, there are three dropdown menus: 'Current repository' set to 'Workshop1', 'Current branch' set to 'main', and 'Fetch origin' status 'Never fetched'. Below these are two tabs: 'Changes' (selected) and 'History'. The 'Changes' tab shows one changed file, 'scripts/README.md'. The commit message in the main pane reads:

```
scripts/README.md
@@ -0,0 +1 @@
1 +This folder contains the scripts relevant for this workshop.
```

In the bottom left, a commit history card shows a previous commit by a user named 'Added scripts folder'. The commit message is: "Including a ~~README~~ so we can keep track of the available scripts @susancoort and @mkutmon". There is a placeholder for adding more contributors with 'R+' and a large blue 'Commit to main' button at the bottom.

Hands-on session - GitHub Desktop

Folder we
are working
in



Branch
("version")
we are in

Button to
update local
and online

Hands-on session - GitHub Desktop

The screenshot shows the GitHub Desktop application interface. At the top, there are three main status indicators: "Current repository Workshop1" (highlighted by a blue box), "Current branch main" (highlighted by a pink box), and "Fetch origin Never fetched" (highlighted by a blue box). Below these, the main window displays a commit history with one change: "scripts/README.md". A green box highlights the file name. To the right, a preview of the file content is shown, containing the text: "@@ -0,0 +1 @@\n1 +This folder contains the scripts relevant for this workshop." A red box highlights this preview area. On the left side, a sidebar shows the commit details: "Changes 1" (highlighted by a purple box) and "1 changed file" (highlighted by a green box). A blue box highlights the "scripts/README.md" entry in the list. A pink box highlights the "History" tab. At the bottom, a commit message box shows "Added scripts folder" and "Including a README so we can keep track of the available scripts @susancourt and @mkutmon". A blue box highlights the "Commit to main" button.

Folder we are working in

Number of changes that occurred

Name of changed file(s)

Branch ("version") we are in

Preview of change(s) in selected file

Button to update local and online

Hands-on session - GitHub Desktop

The screenshot shows the GitHub Desktop application interface with several callout boxes highlighting specific features:

- Folder we are working in**: Points to the "Current repository" dropdown showing "Workshop1".
- Number of changes that occurred**: Points to the "Changes 1" indicator.
- Name of changed file(s)**: Points to the "scripts/README.md" file listed under changes.
- Your GitHub account icon :D**: Points to the user icon in the commit history.
- Short name for the change (commit message)**: Points to the commit message "Added scripts folder".
- Longer description for change**: Points to the detailed commit message "Including a README so we can keep track of the available scripts @susancoort and @mkutmon".
- Branch ("version") we are in**: Points to the "Current branch main" dropdown.
- Preview of change(s) in selected file**: Points to the preview pane showing the file content and diff.
- Button to save changes in local git**: Points to the "Commit to main" button.
- Button to update local and online**: Points to the "Fetch origin" button.

Hands-on session - GitHub Desktop

The screenshot shows the GitHub Desktop application interface. At the top, there's a header bar with "Current repository Workshop1" and "Current branch main". To the right of "main", there's a button labeled "Push origin" with a small icon and the text "Last fetched 15 minutes ago". A blue box highlights this "Push origin" button.

No local changes

There are no uncommitted changes in this repository. Here are some friendly suggestions for what to do next.

- Push commits to the origin remote**
You have 1 local commit waiting to be pushed to GitHub.
Always available in the toolbar when there are local commits waiting to be pushed or **Ctrl + P**.
Push origin
- Open the repository in your external editor**
Select your editor in [Options](#)
Repository menu or **Ctrl + Shift + A**
Open in GNOME Text Editor
- View the files of your repository in your File Manager**
Repository menu or **Ctrl + Shift + F**
Show in your File Manager
- Open the repository page on GitHub in your browser**
Repository menu or **Ctrl + Shift + G**
View on GitHub

Summary (required)

Description

Commit to main

Committed just now
Added scripts folder

Undo

Button to save changes in local git: Successful!

Button to update local and online:

Pull = Download from online to local files

Push = Upload from local to online files

Steps so far in Terminal:

The screenshot shows a GitHub repository named 'Workshop1' (Public). The repository has 1 branch and 0 tags. The file list includes 'Create tutorials.md', '_layouts', 'assets/css', 'images', 'lectures', and 'pages'. A context menu is open over the 'Create tutorials.md' file, showing options like 'Clone', 'HTTPS', 'SSH', and 'GitHub CLI'. The 'SSH' option is highlighted with a blue box. The URL 'git@github.com:NUTRIOME/Workshop1.git' is also highlighted with a blue box.

Click this button to copy
(select SSH for secure transfer
of data)

```
(base) deniseslenter@deniseslenter-HP-EliteBook-840-G2:~/git/NUTRIOME$ git clone
git@github.com:NUTRIOME/Workshop1.git
(base) deniseslenter@deniseslenter-HP-EliteBook-840-G2:~/git/NUTRIOME/Workshop1/
(base) deniseslenter@deniseslenter-HP-EliteBook-840-G2:~/git/NUTRIOME/Workshop1$ git status
on branch main
Your branch is ahead of 'origin/main' by 1 commit.
  (use "git push" to publish your local commits)
nothing to commit, working tree clean
```

Code to check changes in local
git: Successful!

```
(base) deniseslenter@deniseslenter-HP-EliteBook-840-G2:~/git/NUTRIOME/Workshop1$ git remote set-url origin git@github.com:NUTRIOME/Workshop1.git
(base) deniseslenter@deniseslenter-HP-EliteBook-840-G2:~/git/NUTRIOME/Workshop1$ git push
Warning: the ECDSA host key for 'github.com' differs from the key for the IP address
Offending key for IP in /home/deniseslenter/
Matching host key in /home/deniseslenter/.ssh/
Are you sure you want to continue connecting (yes/no)? yes
Counting objects: 4, done.
Delta compression using up to 4 threads.
Compressing objects: 100% (3/3), done.
Writing objects: 100% (4/4), 448 bytes | 448.00 KiB/s, done.
Total 4 (delta 1), reused 0 (delta 0)
remote: Resolving deltas: 100% (1/1), completed with 1 local object.
To github.com:NUTRIOME/Workshop1.git
  9bie3ea..f1bb9ff main -> main
```

In case you failed previously setting up with SSH like me ;)

<https://docs.github.com/en/get-started/getting-started-with-git/managing-remote-repositories>

Code to update local and online:

git pull = Download from online to local files

git push = Upload from local to online files

Hands-on session - GitHub Desktop

 **Workshop1** Public

 Edit Pins ▾

 Watch (2) ▾

 main ▾

 1 Branch

 0 Tags

 Go to file



Add file ▾

 Code ▾



DeniseSI22 Added scripts folder



f1bb9ff · 25 minutes ago

 172 Commits

Hands-on session - GitHub Desktop

Workshop1 Public

Edit Pins

Watch (2)

main

1 Branch 0 Tags

Go to file

t

Add file

Code

DeniseSI22 Added scripts folder · f1bb9ff · 25 minutes ago · 172 Commits

Note: if you get this message in GitHub Desktop, something in your setup is not correct, ask us for help!

Error



Authentication failed. Some common reasons include:

- You are not logged in to your account: see File > Options.
- You may need to log out and log back in to refresh your token.
- You do not have permission to access this repository.
- The repository is archived on GitHub. Check the repository settings to confirm you are still permitted to push commits.
- If you use SSH authentication, check that your key is added to the ssh-agent and associated with your account.
- If you used username / password authentication, you might need to use a Personal Access Token instead of your account password. Check the documentation of your repository hosting service.

Close

Open options

Hands-on session - GitHub Desktop

The screenshot shows the GitHub Desktop application interface. At the top, it displays the current repository as "desktop", the current branch as "the-end-of-it-all" (PR #15640), and the status as "Pull origin" (last fetched 5 minutes ago). The main area shows a diff for the file "app/src/ui/diff/seamless-diff-switcher.tsx". The left sidebar lists three changes: "3 changed files" (with checkboxes checked) and "Stashed Changes" (empty). The right pane displays the code diff with line numbers and highlights for added and deleted code.

```
.... @@ -19,6 +19,7 @@ import {  
    import { Loading } from '../lib/loading'  
    import { getFileContents, IFileContents  
} from './syntax-highlighting'  
    import { getTextDiffWithBottomDummyHunk  
} from './text-diff-expansion'  
    + import { textDiffEquals } from './diff-h  
    elpers'  
    ...  
    /**  
     * The time (in milliseconds) we allow w  
     hen loading a diff before  
    .... @@ -127,7 +128,7 @@ function isSameDiff(prevDiff: IDiff, newDiff: IDiff) {  
        prevDiff === newDiff ||  
        (isTextDiff(prevDiff) &&  
        isTextDiff(newDiff) &&  
        - prevDiff.text === newDiff.text)  
    )  
    }  
    ....  
    127 128  prevDiff === newDiff ||  
    128 129  (isTextDiff(prevDiff) &&  
    129 130  isTextDiff(newDiff) &&  
    130 131  + textDiffEquals(prevDiff, newDiff))  
    131 132  )  
    132 133  }  
    133 134  ....
```

At the bottom, there is a "Commit to the-end-of-it-all" button.

Join our quiz!

Join at menti.com | use code **6634 3857**

Mentimeter

Instructions

Go to

www.menti.com

Enter the code

6634 3857



Or use QR code

Hands-on session - GitHub Desktop



DeniseSI22 / Workshop1

Type ⌘ to search



Button to
save changes
in online git

Code Pull requests Actions

Projects Wiki Security Insights Settings

Files

main + Q

Go to file t

- _layouts
- assets
- images
- lectures
- pages
- scripts

Folder we
are working
in

Workshop1 / scripts / README.md in main

Cancel changes

Commit changes...

Edit Preview

Spaces 2 Soft wrap

```
1 This folder contains the scripts relevant for this workshop.  
2  
3 Contents:  
4 - metabolomics processing script (DIY)  
5 - metabolomics processing script (with answers)  
6
```

Hands-on



DeniseSI22 / Workshop1

Code Pull requests Actions

Files

main + Q

Go to file t

- > _layouts
- > assets
- > images
- > lectures
- > pages
- > scripts

README.md

.gitignore

LICENSE

README.md

_config.yml

index.md

Folder we are working in

Commit changes

X

Commit message

Added contents list

Extended description

Currently has two examples, to be linked to actual content.

Commit directly to the main branch

Create a **new branch** for this commit and start a pull request [Learn more about pull requests](#)

Button to save changes in online git

| > | + | - | 0 | n | e | profile

Cancel changes Commit changes...

Spaces 2 Soft wrap

Branch ("version") we are in

Cancel

Commit changes

Hands-on session - GitHub Desktop



Workshop1 Public

forked from [NUTRIOME/Workshop1](#)

Pin

Watch 0

To request a merge from our content to the original one (Pull Request or PR)

main ▾

1 Branch 0 Tags

Go to file

t

Add file ▾

Code ▾

This branch is 1 commit ahead of

NUTRIOME/Workshop1:main .

Contribute ▾

Sync fork ▾



DeniseSI22 Added contents list



dec57b7 · now



173 Commits

To check for updates from our version to the original one

Hands-on session - GitHub Desktop



Workshop1

Public

forked from [NUTRIOME/Workshop1](#)

Pin

Watch 0

To request a merge from our content to the original one (Pull Request or PR)

main

1 Branch 0 Tags

Go to file

t

Add file

Code

This branch is 1 commit ahead of

NUTRIOME/Workshop1:main .

Contribute

Sync fork



DeniseSI22 Added contents list

dec57b7 · now



173 Commits

To check for updates from our version to the original one

No ‘upstream’ changes

This branch is 1 commit ahead of NUTRIOME/Workshop1:main .

Contribute Sync fork

This branch is not behind the upstream NUTRIOME/Workshop1:main

DeniseSI22 Added contents list

_layouts Update default.html

assets/css Update style.scss

images Add files via upload

lectures Add files via upload

pages Create tutorials.md

scripts Added contents list

.gitignore Update .gitignore

ONE ‘upstream’ change

This branch is 1 commit ahead of, 1 commit behind NUTRIOME/Workshop1:main .

Contribute Sync fork

This branch is out-of-date

Update branch to merge the latest changes from the upstream repository into this branch.

Discard 1 commit to make this branch match the upstream repository. 1 commit will be removed from this branch.

Learn more about syncing a fork

DeniseSI22 Added contents list

_layouts Update default.html

assets/css Update style.scss

images Add files via upload

lectures Add files via upload

pages Create tutorials.md

scripts Added contents list

.gitignore Update .gitignore

Discard 1 commit

Update branch

This branch is 2 commits ahead of NUTRIOME/Workshop1:main .

‘upstream’ change integrated in fork

Hands-on session - GitHub Desktop

Comparing changes

Choose two branches to see what's changed or to start a new pull request. If you need to, you can also compare across forks or learn more about diff comparisons.

base repository: NUTRIOME/Workshop1 ▾ base: main ▾ ... head repository: DeniseSI22/Workshop1 ▾ compare: main ▾ Able to merge. These branches can be automatically merged.

Discuss and review the changes in this comparison with others. [Learn about pull requests](#)

Create pull request

2 commits 1 file changed 1 contributor

Commits on May 27, 2024

Added contents list ···
DeniseSI22 committed 11 minutes ago
Merge branch 'NUTRIOME:main' into main
DeniseSI22 committed 5 minutes ago

Showing 1 changed file with 4 additions and 0 deletions.

scripts/README.md

00 -1 +1,5 00

This folder contains the scripts relevant for this workshop.

```
1 This folder contains the scripts relevant for this workshop.
```

DeniseSI22 added 2 commits 14 minutes ago

Added contents list ···
Merge branch 'NUTRIOME:main' into main

DeniseSI22 merged commit 2808dcf into NUTRIOME:main now

Pull request closed

If you wish, you can delete this fork of **NUTRIOME/Workshop1** in the [settings](#).

DeniseSI22 added 2 commits 13 minutes ago

Added contents list ···
Merge branch 'NUTRIOME:main' into main

Add more commits by pushing to the [main](#) branch on **DeniseSI22/Workshop1**.

This branch has not been deployed
No deployments

This branch has no conflicts with the base branch
Merging can be performed automatically.

Merge pull request ▾ or view [command line instructions](#).

Hands-on session - GitHub Desktop

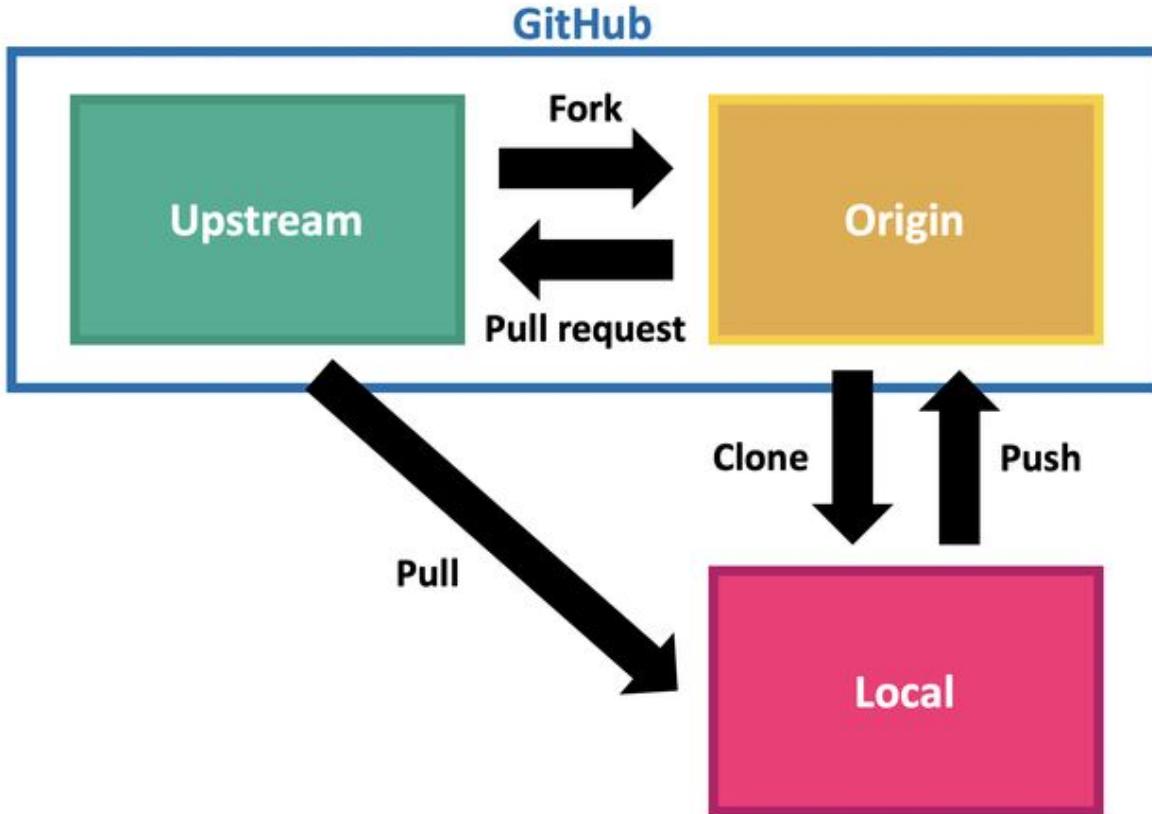


Image from: <https://anujf0510.medium.com/the-guide-to-git-terminology-bbae2a3d8af5> and <https://medium.com/@vishwasacharya/github-desktop-vs-command-line-choose-the-right-tool-for-you-feb58c3f0e30>

Hands-on session - Adding GitHub to Rstudio

Step 1: Have Rstudio installed

Step 2: Open Rstudio

Step 3: Select File/New Project (top left menu) ;



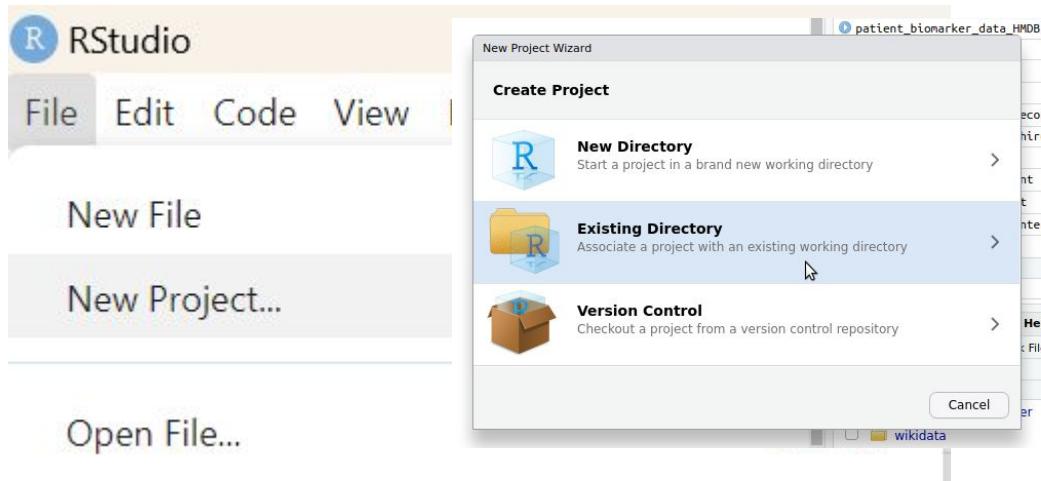
- Existing Directory
- Browse
- Find location of folder from GitHub called

Hands-on session - Adding GitHub to Rstudio

Step 1: Have Rstudio installed

Step 2: Open Rstudio

Step 3: Select File/New Project (top left menu) ;



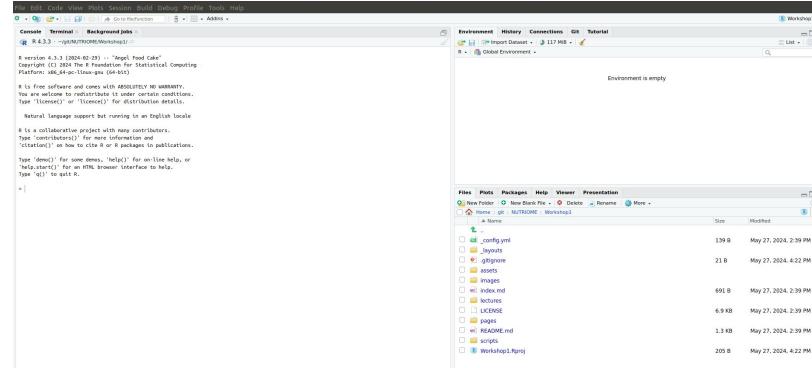
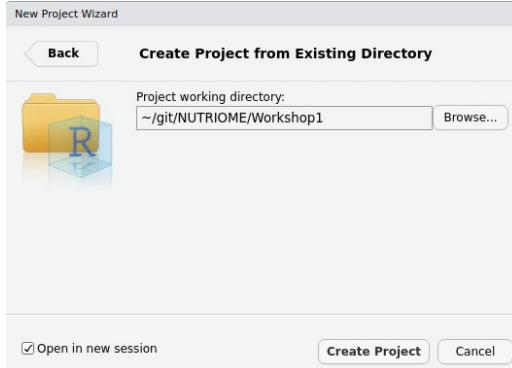
- Existing Directory
- Browse
- Find location of folder from GitHub called

Hands-on session - Adding GitHub to Rstudio

Step 4: Select the top folder (PETcourseMetabolomics)

Step 5: Check if ‘Project working Directory’ is similar to printscreen below!

Step 6: Click → Create Project



Break time!?

Hands-on session - Adding GitHub to Rstudio

Section where code is executed (after the >) in console (also note 'Terminal' as second option)

```
R version 4.3.3 (2024-02-29) -- "Angel Food Cake"
Copyright (C) 2024 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

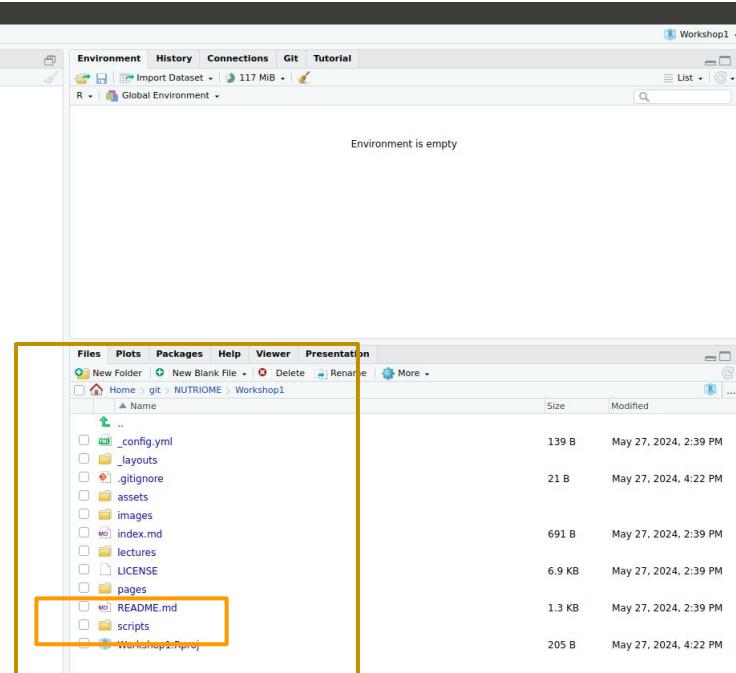
Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.
```

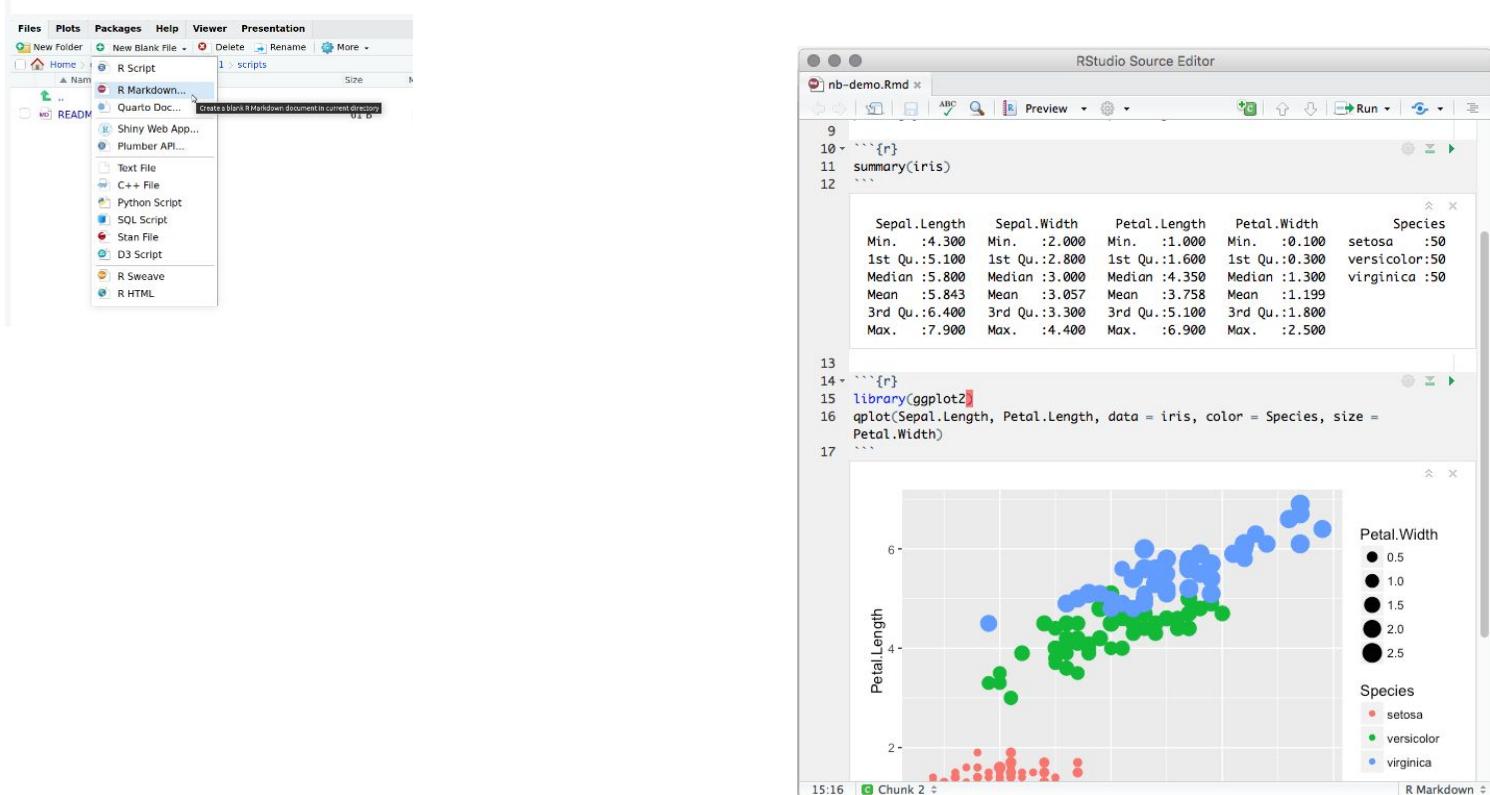
Currently loaded version of R (check this for potential compatibility issues!)

Folder structure (according to GitHub Repository)



Folder with the Scripts
(double click to unfold and show content)

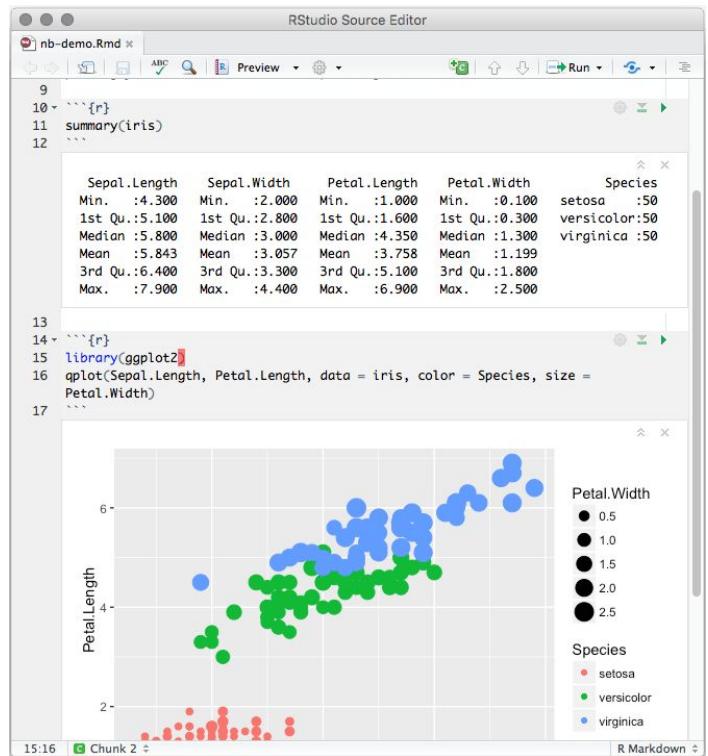
Hands-on session - Adding GitHub to Rstudio



Hands-on session - Adding GitHub to Rstudio

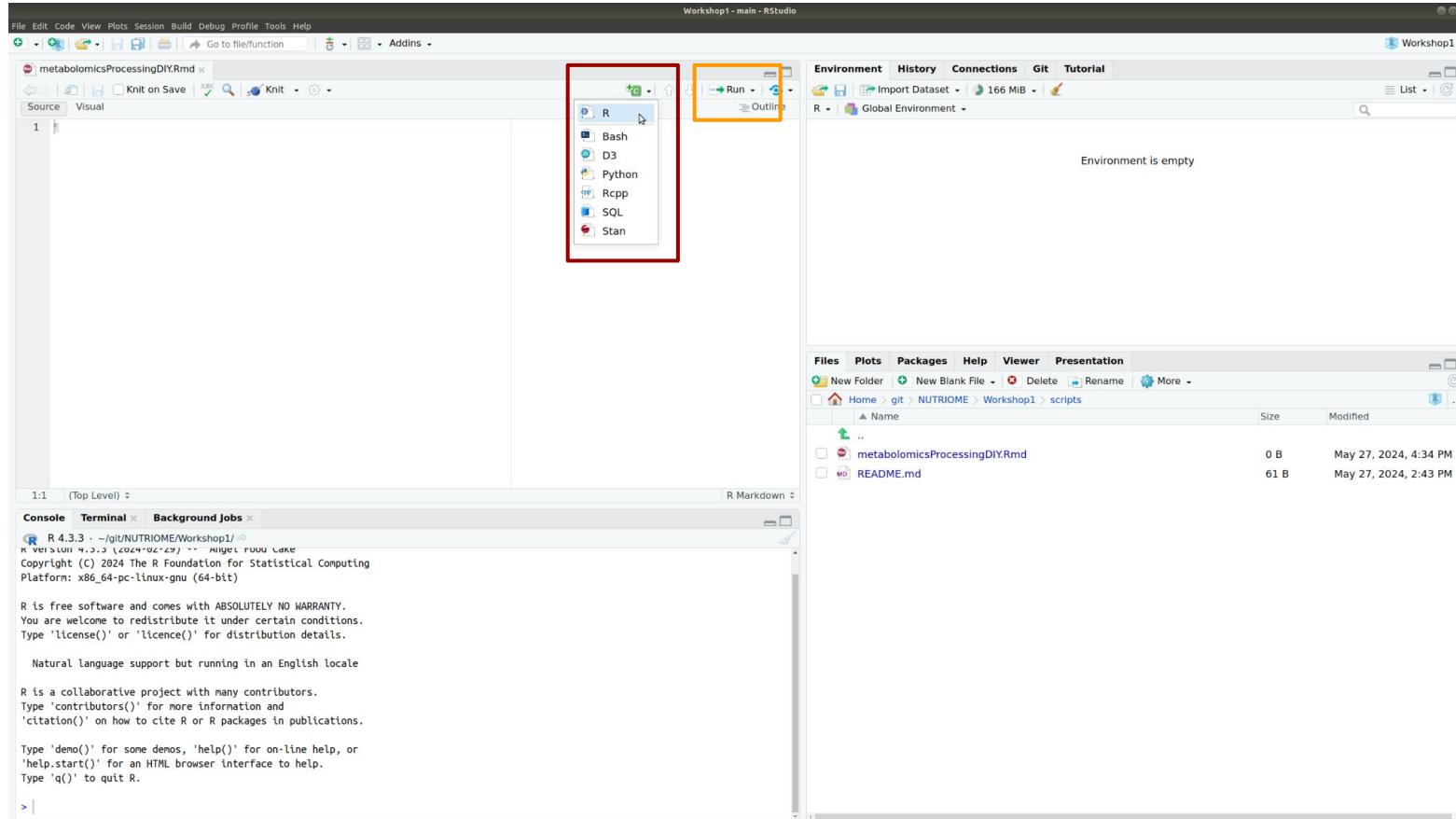
The screenshot shows the RStudio interface with GitHub integration. A green box highlights the 'Source' tab in the top-left corner of the main workspace. Another green box highlights the 'scripts' folder in the 'File Explorer' sidebar.

New 'Markdown' file create in File Explorer and in top left menu



<https://bookdown.org/yihui/rmarkdown/notebook.html>

Hands-on session - Adding GitHub to Rstudio



Button to add a new section of code (code 'chunk')

Button to run your code (or section of it, click small arrow)

Hands-on session - First programming tasks

```
metabolomicsProcessingDIY.Rmd x
Source Visual
3 author:-
4   - "DeniseSL22"
5   - "YourGithubUserName"
6 date: "17/05/24"
7 output:-
8   md_document:-
9     variant: markdown_github
10 always_allow_html: true
11
12 ## Introduction
13 In this section of the workflow, we will obtain the metabolomics data and apply filtering options, to create a dataset ready for further statistical and pathway analysis (on Thursday).
14
15 ## First, we setup the required libraries to get started.
16 ````{r setup, warning=FALSE, message=FALSE}
17 # check if libraries are already installed > otherwise install it
18 if(!requireNamespace("BiocManager", quietly = TRUE)) install.packages("BiocManager", repos = "http://cran.us.r-project.org")
19 if(!"dplyr" %in% installed.packages()) BiocManager::install("dplyr")
20 if(!"stringr" %in% installed.packages()) install.packages("stringr")
21 # load libraries
22 library(dplyr)
23 library(stringr)
24 ````
```

Make sure to have the following content in your Code chunk (select the correct file) and click 'Run' (or the green arrow in the chunk)!

Add your own GitHub User name to the metadata at the top iso 'YourGitHubUserName'

Save the file (locally) and check your GitHub Desktop

Hands-on session - First programming tasks

Console Terminal × Background Jobs ×

R 4.3.3 · ~/git/NUTRIOME/Workshop1/ ↗

Natural language support but running in an English locale

R is a collaborative project with many contributors.

Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.

Type 'q()' to quit R.

```
> # check if libraries are already installed > otherwise install it
> if(!requireNamespace("BiocManager", quietly = TRUE)) install.packages("BiocManager", repos = "http://cran.us.r-project.org")
> if(!"dplyr" %in% installed.packages()) BiocManager::install("dplyr")
> if(!"stringr" %in% installed.packages()){install.packages("stringr")}
> #load libraries
> library(dplyr)
> library(stringr)
> |
```

Check the console; if everything looks okay (see Figure on the left, text should be blue and end with >).

In case of errors (red text**), ask for help!

** Note:
installing libraries might also create red text, so not always an error!

Commit your username
change to your own fork, and
Push!

Hands-on session - First programming tasks

1. Download the metabolomics data:

**Load the data
in R**

2. Add the following steps to the script (see Figure on the right).

Please try yourself first;
you will learn the most
from that!

Answers are in the
following slides, and
will be made available
on Github (in a
separate script after the
workshop).

Read the data:

Download
'readxl' package

Load the 'readxl'
package

Read the first,
second or third
tab of the file

Make a copy of
the data as
backup in R

These two steps are given in the script :)

Hands-on session - First programming tasks

1. Download the metabolomics data:
Load the data in R

2. Add the following steps to the script (see Figure on the right).

Please try yourself first; you will learn the most from that!

Answers are in the following slides, and will be made available on Github (in a separate script after the workshop).

Read the data:

Download
'readxl' package

```
install.packages("readxl")
```

Load the 'readxl'
package

```
library("readxl")
```

Read the first,
second or third
tab of the file

These two steps are given in the script :)

Make a copy of
the data as
backup in R

Hands-on session - First programming tasks

1. Download the metabolomics data:

Load the data in R

2. Add the following steps to the script (see Figure on the right).

Please try yourself first; you will learn the most from that!

Answers are in the following slides, and will be made available on Github (in a separate script after the workshop).

Read the data:

Download 'readxl' package

```
install.packages("readxl")
```

Load the 'readxl' package

```
library("readxl")
```

Read the first, second or third tab of the file

```
header <- read_excel(destfile, 3, range = "A1:Z1", col_names = FALSE)
metabolomicsData <- read_excel(destfile, 3, skip = 1)
colnames(metabolomicsData)[1:4] <- header[1:4] # renaming the first 4 columns, since we had double headers.
```

Make a copy of the data as backup in R

```
metabolomicsDataCopy <- metabolomicsData
```

Hands-on session - First programming tasks

The screenshot shows an RStudio interface. On the left is a data grid titled 'metabolomicsData' containing 55 rows of metabolomics data. The columns include Sample number, Compound, Timepoint, Dose, CheBI ID, and several numerical values. On the right is the Global Environment pane, which lists objects like 'first_line', 'header', 'metabolomicsData' (highlighted in blue), 'metabolomicsDataCopy', 'response', and 'destfile'. Below the environment pane is a file browser showing a folder structure under 'GitHub > PETcourseMetabolomics'.

Again, ask for help in case of errors/issues/question :)

Click on the **dataframe name** you used to inspect the metabolomics data

Loaded 'dataframes'
including number of
rows (obs.) and
columns (variables)

Loaded 'variables' including
their values. Can also be a
list of values and other data
types!

Hands-on session - First programming tasks

Column names

Dataframe name

Search Box to explore data

Sample number in Dataframe

Sample name in dataset

No data measured (NA or NaN) → Not zero!

	Sample number	Compound	Timepoint	Dose	CheBI ID	15570	16414	17895	171154	16523	1
1	9001	Daunorubicin	T144	Therapeutic	NA	1.0743243	0.8107843	0.8435871	0.8251928	0.4965157	
2	9002	Daunorubicin	T144	Therapeutic	NA	1.1891892	0.8137255	0.8519291	0.8251928	0.6167247	
3	9003	Daunorubicin	T144	Therapeutic	NA	1.5472973	0.8382353	0.8018770	0.8431877	0.8641115	
4	9004	Daunorubicin	T144	Toxic	NA	1.0202703	0.8284314	0.8748697	0.8174807	0.8797909	
5	9005	Daunorubicin	T144	Toxic	NA	1.4797297	0.8460784	0.8800834	0.8200514	0.8362369	
6	9006	Daunorubicin	T144	Toxic	NA	1.1418919	0.8303922	0.8623566	0.8149100	0.8397213	
7	DAU72H	Daunorubicin	72hr	Blank Inc.	NA	1.0000000	1.0000000	1.0000000	1.0000000	1.0000000	
8	9010	Fluorouracil	T144	Therapeutic	NA	0.8479532	0.7774510	0.7607843	0.8184143	0.6666667	
9	9011	Fluorouracil	T144	Therapeutic	NA	0.9356725	0.7480392	0.7411765	0.7774936	0.6175711	
10	9012	Fluorouracil	T144	Therapeutic	NA	0.8830409	0.7637255	0.7313725	0.7723785	0.6072351	
11	9016	Fluorouracil	T144	Toxic	NA	2.9356725	0.8225490	0.7764706	0.8132992	1.1421189	
12	9017	Fluorouracil	T144	Toxic	NA	7.6608197	0.8008627	0.8106079	0.7070540	2.5271218	

Showing 1 to 12 of 55 entries, 45 total columns

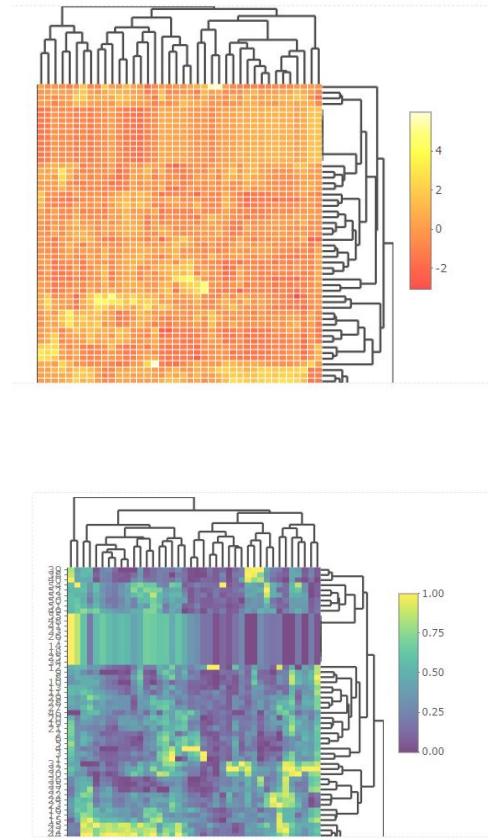
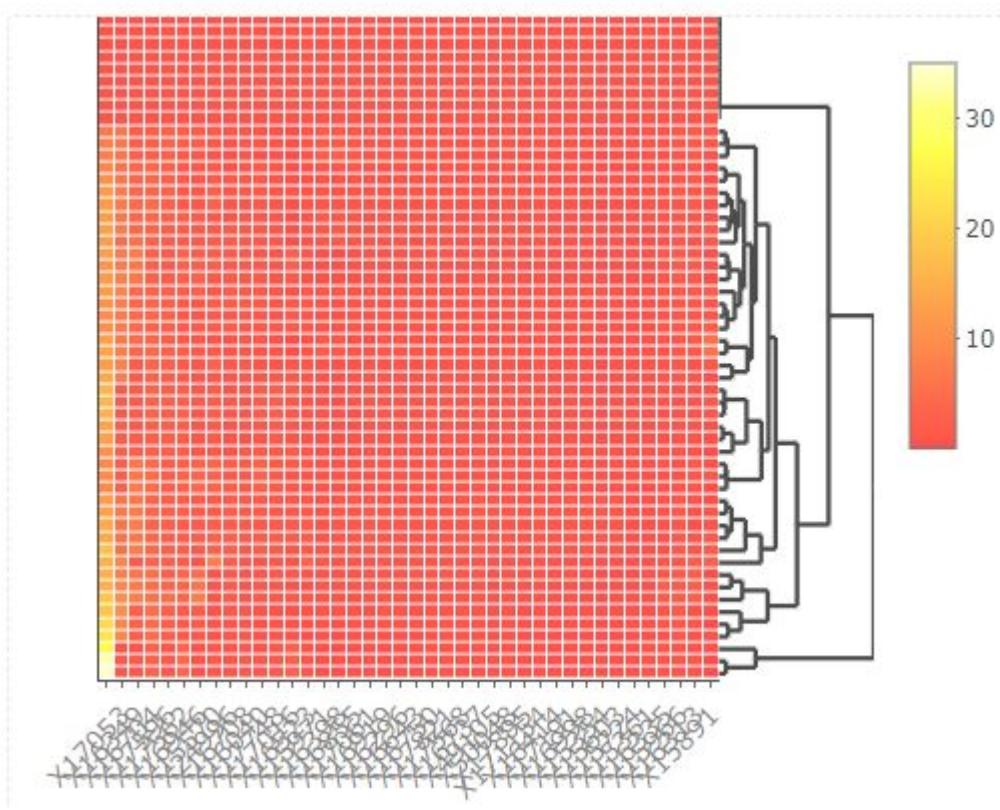
Console Terminal × Background Jobs ×

Hands-on session - Second task

1. Make sure all data is captured as numbers (numeric!)
Otherwise the data is not read correctly by the heatmap functions
2. Visualize all information in a heatmap
Regular, scaled, and normalized

Hands-on session - Second tasks

Do you see
anything
important
pop-up
here?



Hands-on session - Third tasks: Transposing the data and performing a basic Fold Change calculation on them

Execute the steps in the script and answer the questions.

Cytoscape session

For now, manual.

Script will be added in answers.

If time permits:

Analyze the other chemical compounds, by adapting the script.

Visualize the data in a different pathway

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