

Git & GitHub

Venexia Walker, Winfred Gatua, Yi Liu

Agenda

Part 1: The Basics [Venexia Walker]

Part 2: GitHub Functionality [Winfred Gatua]

Part 3: IEU GitHub organisation [Yi Liu]

Part 1: The Basics

Venexia Walker

What?

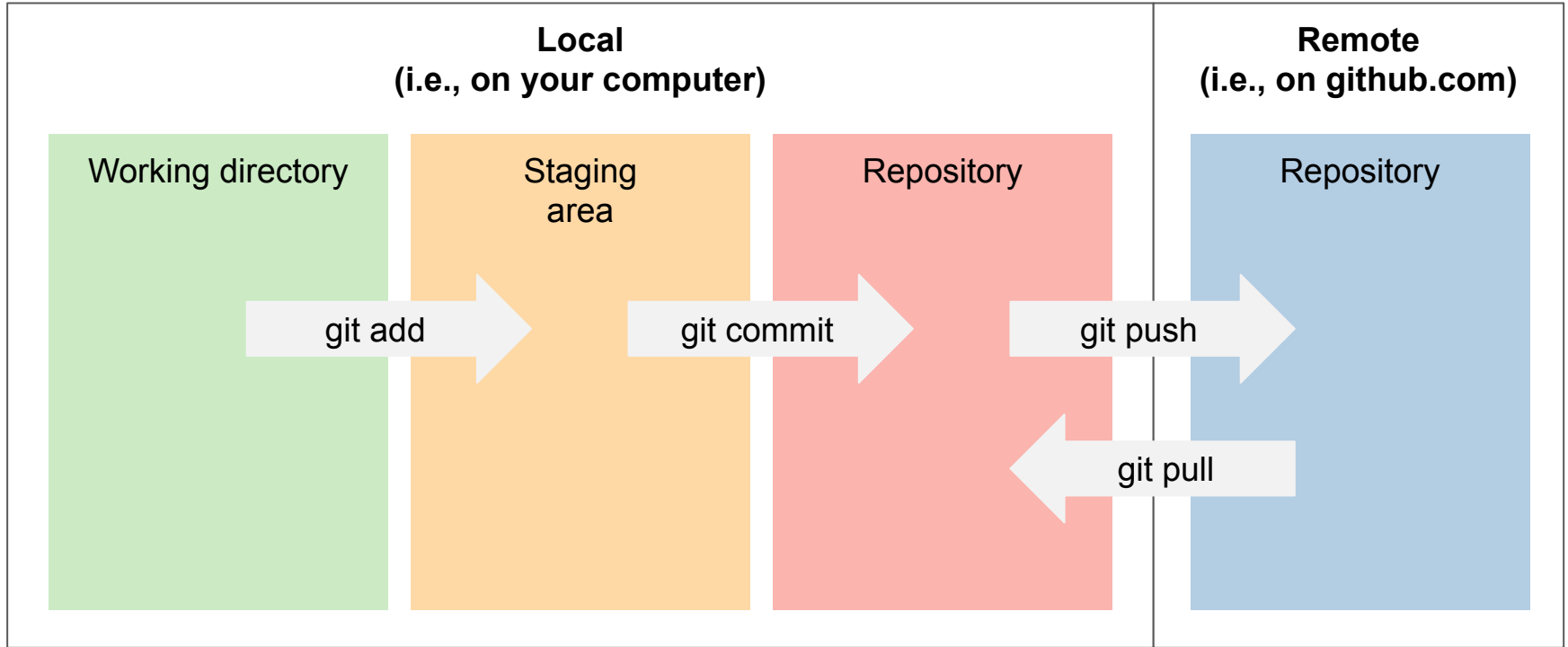
Git is a content tracking software.

GitHub is one online provider of Git.

Alternatives to GitHub include Bitbucket and GitLab.

You can sign up to GitHub for free at <https://github.com/>.

What?



Why?

Reproducible research.

Version control.

Code backup.

Work on code with collaborators.

Personal online code record.

How?

Online using <https://github.com/>

GitHub Desktop

GitHub command line tool (CLI)

Git integration into RStudio
or other software

Online using https://github.com/

The screenshot displays the GitHub web interface for a repository named 'venexia/test'. The top navigation bar includes a search bar, 'Pull requests', 'Issues', 'Codespaces', 'Marketplace', and 'Explore'. Below the repository name, there are buttons for 'Unwatch 1', 'Fork 0', and 'Star 0'. A secondary navigation bar contains 'Code', 'Issues', 'Pull requests', 'Actions', 'Projects', 'Wiki', 'Security', 'Insights', and 'Settings'. The main content area shows a large box with a document icon and the text 'Drag files here to add them to your repository' and 'Or choose your files'. Below this is a 'Commit changes' dialog box with a profile picture, a title, a text input for 'Add files via upload', a larger text area for 'Add an optional extended description...', and two radio button options: 'Commit directly to the main branch.' (selected) and 'Create a new branch for this commit and start a pull request. Learn more about pull requests.'. At the bottom of the dialog are 'Commit changes' and 'Cancel' buttons.

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

venexia/test Private Unwatch 1 Fork 0 Star 0

generated from venexia/template

<> Code Issues Pull requests Actions Projects Wiki Security Insights Settings

test /

Drag files here to add them to your repository
Or choose your files

Commit changes

Add files via upload

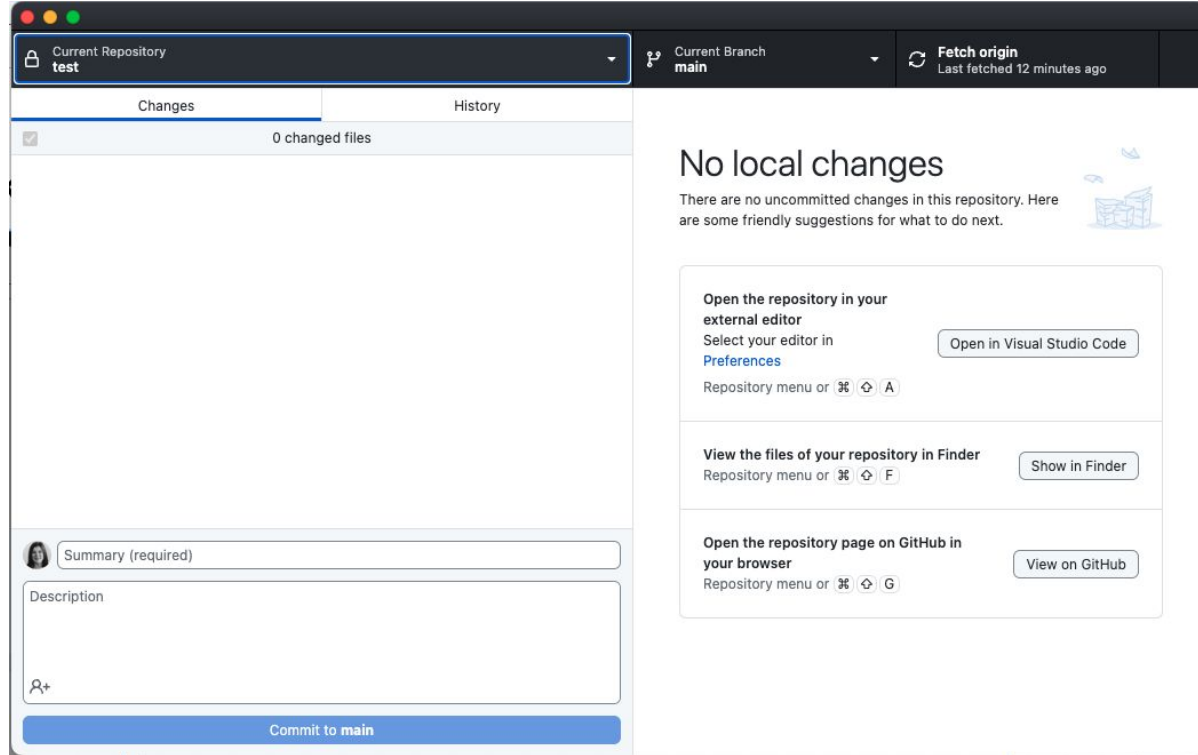
Add an optional extended description...

Commit directly to the `main` branch.

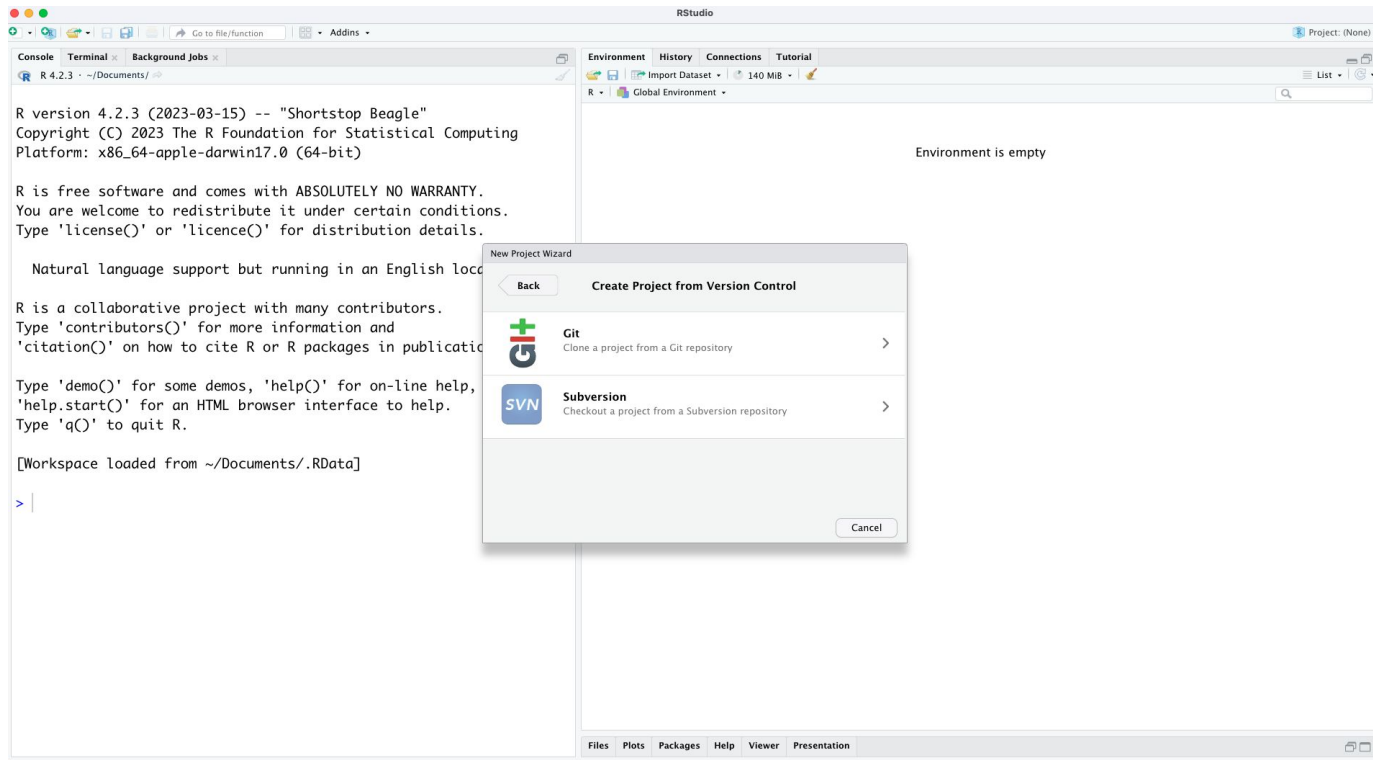
Create a new branch for this commit and start a pull request. [Learn more about pull requests.](#)

Commit changes Cancel

GitHub desktop



Git integration into RStudio or other software



Github command line tool (CLI)



```
$ gh pr status
```

Current branch

```
There is no pull request associated with [develop]
```

Created by you

```
#1011 Update readme [readme-fix]  
- Checks pending - Review required
```

Requesting a code review from you

```
#1015 Improve error handling [better-error-handling]  
✓ Checks passing + Changes requested
```

Summary

Something is better than nothing - if you use Git in anyway, that is great! 🎉

You will get into a horrible Git mess at some point. Don't panic. Backup everything somewhere else before you do anything radical like force a git push or git pull.

There is lots of help out there - the [documentation](#) is a great place to start.

Part 2: Github Functionality

Winfred Gatua

README

This is a useful place to highlight relevant project information, such as:

- How to use the repository
- How to access the relevant data
- Supplementary material for a project
- Project abstract and authors

A README.md file in the repository will automatically be rendered and the Markdown format means markdown links, tables, etc. can be included.

Example: <https://github.com/venexia/repurposing-antihypertensives-dementia>

.gitignore

This hidden file tells Git what it should not track.

Try to keep your sensitive data in a specific directory and add the whole directory to the .gitignore. Alternatively, specific files can be added to the .gitignore.

Maintain directory structure by ignoring the directory, except a README.md:

```
raw/*  
!raw/README.md
```

Git history

Everytime you commit something to Git, it is recorded in the Git history.

When you make a repository public, the history of the repository when it was private is shared.

If sensitive data has been accidentally included at any point, you can use tools, such as [BFG Repo-Cleaner](#), to remove that part of the history. Worst case scenario: you can delete your repository but this will mean losing all your other history.

Relative file paths

Avoid including absolute file paths in your code for security.

The easiest way to do this is to use relative paths - for example, “raw/data.txt” rather than “E:/venexia/phd/project/raw/data.txt”. You would then just need to set your working directory as “E:/venexia/phd/project/” before running anything.

If you are using RStudio, use the project functionality. An RStudio project will open where you left off in your working directory meaning you only ever need relative file paths.

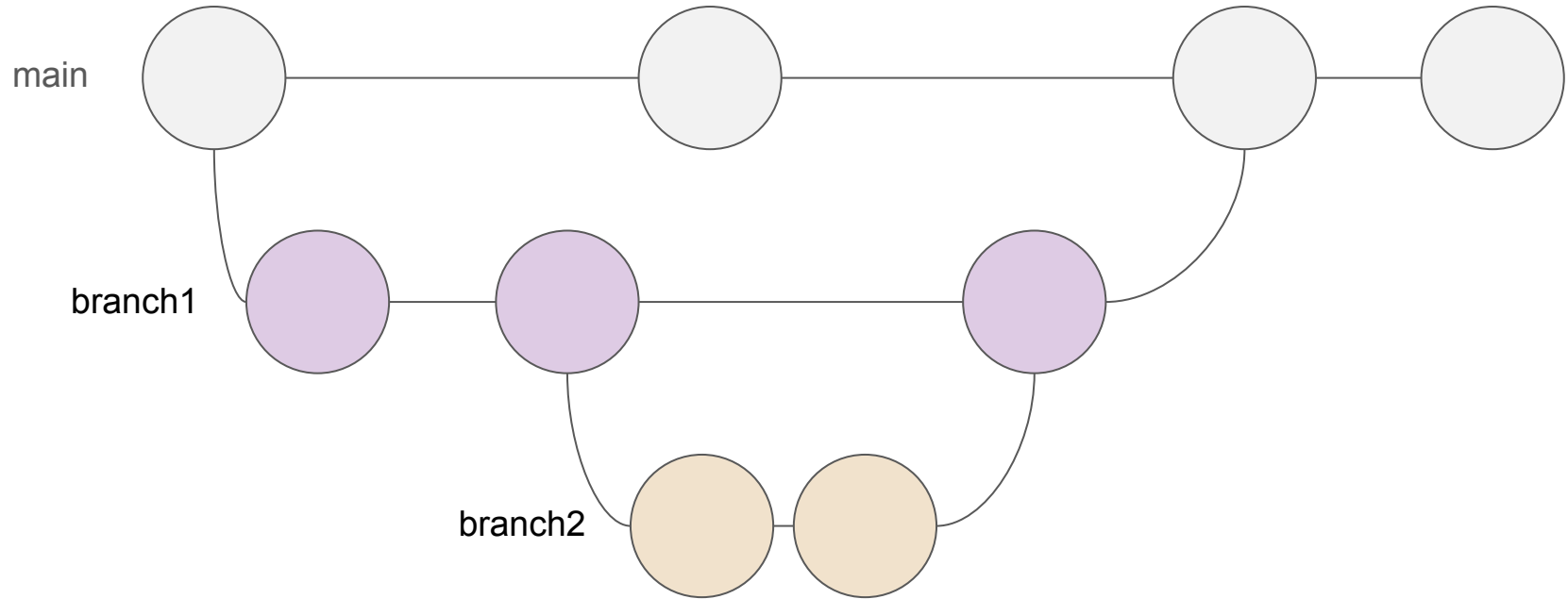
Templates

You can create project templates that can be used when you setup new repositories or you use other people's templates,

To create a template, make a new repository with your preferred setup, then online go to 'Settings > Template repository'.

Example: <https://github.com/venexia/template>

Branches and pull requests



Make a branch

Online

Click branch selector on repository main page
Type branch name
Click 'Create branch'

GitHub Desktop

Click 'Current Branch > New Branch'
Type branch name
Click 'Create Branch'

GitHub CLI

```
git checkout -b branch_name  
first time: git push --set-upstream origin branch_name  
once setup: git push -u origin branch_name
```

Other useful commands:

```
git branch -a
```

Git integration

In RStudio Git tab, click Git logo
Type branch name
Click 'Create'

Make a pull request

Pull requests are used to merge a branch.


The request is made online by clicking 'Pull requests > New pull request' and selecting the relevant branch.

Pull requests allow you to compare what has changed since the branch was made - this is useful for you and can be used by teams for code review.

The request will highlight merge conflicts.

Basic formatting syntax

1. <https://commonmark.org/help/>
2. [Markdown cheatsheet](#)

Type	Or	... to Get
<code>*Italic*</code>	<code>_Italic_</code>	<i>Italic</i>
<code>**Bold**</code>	<code>__Bold__</code>	Bold
<code># Heading 1</code>	Heading 1 =====	Heading 1
<code>## Heading 2</code>	Heading 2 -----	Heading 2
<code>[Link](http://a.com)</code>	<code>[Link][1]</code> : <code>[1]: http://b.org</code>	Link
<code>![Image](http://url/a.png)</code>	<code>![Image][1]</code> : <code>[1]: http://url/b.jpg</code>	
<code>> Blockquote</code>		<div style="border-left: 1px solid gray; padding-left: 10px;">Blockquote</div>
<code>* List</code> <code>* List</code> <code>* List</code>	<code>- List</code> <code>- List</code> <code>- List</code>	<ul style="list-style-type: none">• List• List• List

Summary

Create, assign and manage issues

Default branch is the Master - you can switch or add branches here

README is automatically rendered when you visit any repo

Settings - add collaborators

Make your own copy of the entire repository

Get all the files from the web to your computer

Create a new file

Upload files

The screenshot shows the GitHub interface for a repository named 'Stroke_brain_bloodeQTLs' by user 'winfrednyoroka'. The repository is private and has 4 branches and 0 tags. The main branch is 'main'. A merge pull request #3 is visible. The file list includes: Figures, Results_31_05_2022, Scripts, .gitignore, LICENSE, and README.md. The README.md content is displayed below the file list, stating the aim: 'To elucidate shared genetic aetiology between stroke and select CVD and neurological disorders.' The right sidebar shows repository statistics: 0 stars, 1 watching, 0 forks, and 0 releases. A 'Code' button is highlighted in green. A red arrow points to the 'Code' button, and another red arrow points to the 'Add file' button, which has a dropdown menu open showing 'Create new file' and 'Upload files' options. Red arrows also point from text boxes to various parts of the interface: 'Settings' (top right), 'Issues' (top left), 'main' branch (left), 'README.md' (bottom left), and 'About' (right sidebar).

Part 3: IEU GitHub organisation

Yi Liu

https://github.com/MRCIEU

github.com/MRCIEU

Search or jump to...

Pull requests Issues Codespaces Marketplace Explore

MRC Integrative Epidemiology Unit

63 followers University of Bristol, UK http://www.bristol.ac.uk/ieu

Unfollow

Overview Repositories 171 Projects 6 Packages Teams 21 People 170

README.md


MRC Integrative Epidemiology Unit

Home About MRC IEU software browser Detail

Welcome to MRC Integrative Epidemiology Unit GitHub pages.

The MRC Integrative Epidemiology Unit at the University of Bristol (IEU) conducts some of the UK's most advanced population health science research. It uses genetics, population data and experimental interventions to look for the underlying causes of chronic disease.


Researchers at the MRC IEU have created a range of openly available software tools based on research methods developed within the unit.



momentary assessment
Mendelian randomization
Phenome Scan
EpiGraphDB
Genetics
EWAS
Data integration
MR-pheWAS
Data mining
proteomics
Literature mining
OpenGWAS
Text embedding
Text mining
Machine learning
smoking
MR-Base
DNA methylation
Evidence integration
Phenotypes
EWAS Catalog
Visualization
Illumina Beadchip
metabonomics
microbiomics

View as: Public -
You are viewing the README and pinned repositories as a public user.

People



View all

Top languages

- R
- Python
- HTML
- Jupyter Notebook
- Shell

Most used topics

- bioinformatics
- gwas
- vcf
- graph-database
- summary-statistics

MRC Integrative Epidemiology Unit

Overview Repositories 171 Projects 6 Packages Teams 21 People 170

Find a repository... Type Language Sort

New repository

mrcieu.github.io (Private)
MRC IEU GitHub pages
Jupyter Notebook 5 1 0 0 Updated 1 minute ago

uptime (Public)
Use uptime to monitor web platform status
uptime-monitor status-page uptime
JSON MIT 0 0 0 Updated 19 hours ago

temppo (Public)
Text mining for mechanism prioritisation
mesh-terms
Python GPL-3.0 1 5 0 0 Updated 3 days ago

gwasglue2 (Public)
Connecting GWAS summary data to analytical tools
R 1 13 0 0 Updated 3 days ago

bp-drug-mr (Public)
Multi-ancestry MR of blood pressure drug targets
HTML 1 1 0 0 Updated 3 days ago

epigenetics-journal-club (Public)
Repository for the IEU epigenetics journal club papers, presentations and scripts

Become a member (if you aren't already)

Some of the community repos require you to be a member of the MRCIEU_internal team to access



IEU data management Mailbox










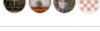








Contact

Request access

 ieu-datamanagement@bristol.ac.uk

 ieu-datamanagement@bristol.ac.uk

21 teams in the MRCIEU organization		Visibility ▾	Members ▾
Developers		20 members	0 teams
epigraphdb EpiGraphDB a database and platform for health data science		9 members	0 teams
External analysts		1 member	0 teams
FATHMM		2 members	0 teams
Genetic epi tutors Tutors for genetic epi practicals		40 members	0 teams
godmc-analysts GoDMC analysis		55 members	0 teams
GoDMC2 GoDMC 2 analysis		16 members	0 teams
gwas_vcf_format Team for developing standard storage format for GWAS summary stats		6 members	0 teams
ieup4 IEU programme 4		23 members	0 teams
it-services Members from IT services		4 members	0 teams
MELODI		3 members	0 teams
MRBase		20 members	0 teams
MRCIEU_internal Internal members of MRC IEU		109 members	0 teams
MVP analysts		5 members	0 teams
OracleCloud Team for Oracle Cloud development work		2 members	0 teams
PhenoSpD A method to estimate phenotypic correlation and multiple testing correction f...		2 members	0 teams
SoftwareCoordination			

IEU GitHub Pages

- Showcase the software, coding, and data science side of IEU research
- Showcase and promote your software!
 - R packages: very many!
 - Processing and application pipelines
 - MELODI-presto
 - MendelVar
 - Applications (web / command line / GUI)
 - MR dictionary
 - MELODI-presto
 - EpiGraphDB (web, API)
 - OpenGWAS (web, API)
 - Big software projects
 - OpenGWAS
 - EpiGraphDB

Welcome to MRC Integrative Epidemiology Unit GitHub pages.

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Researchers at the MRC IEU have created a range of openly available software tools based on research methods developed within the unit.

Key research topics highlighted in the word cloud include: Mendelian randomization, EpiGraphDB, DNA methylation, Text mining, Literature mining, Regression, OpenGWAS, Deep learning, Visualization, Evidence integration, Machine learning, Text embeddings, GWAS, MR-pheWAS, RCT, Data mining, Phenome-Scan, Genetics, EWAS, Natural language processing, Data integration, VQTL, Proteomics, Phenotypes, Missing-not-at-random, MR-Base, Variance, Missing outcomes, EWAS Catalog, and Text embedding.

MRC Integrative Epidemiology Unit

Home About MRC IEU software browser Details Wiki

Annotated Semantic Queries
Natural language query interface to the EpiGraphDB platform.
[View what's new] [View GitHub]

EpiGraphDB Graph Database
Neo4j graph database of the EpiGraphDB platform.
[View what's new] [View GitHub]

EpiGraphDB R package
R package for EpiGraphDB.
[View what's new] [View GitHub]

epigraphdbpy
Python package for EpiGraphDB.
[View what's new]

EpiViz
R package and shiny web app for the production of error plots to display results from large epidemiological analyses.
[View what's new] [View GitHub]

EpiGraphDB WebUI
EpiGraphDB platform web application.
[View what's new] [View GitHub]

EWAS Catalog
The MRC IEU centre of excellence in association studies.
[View what's new]

The EWAS Catalog
A database of associations from EWAS summary datasets, for querying or download.
[View what's new]

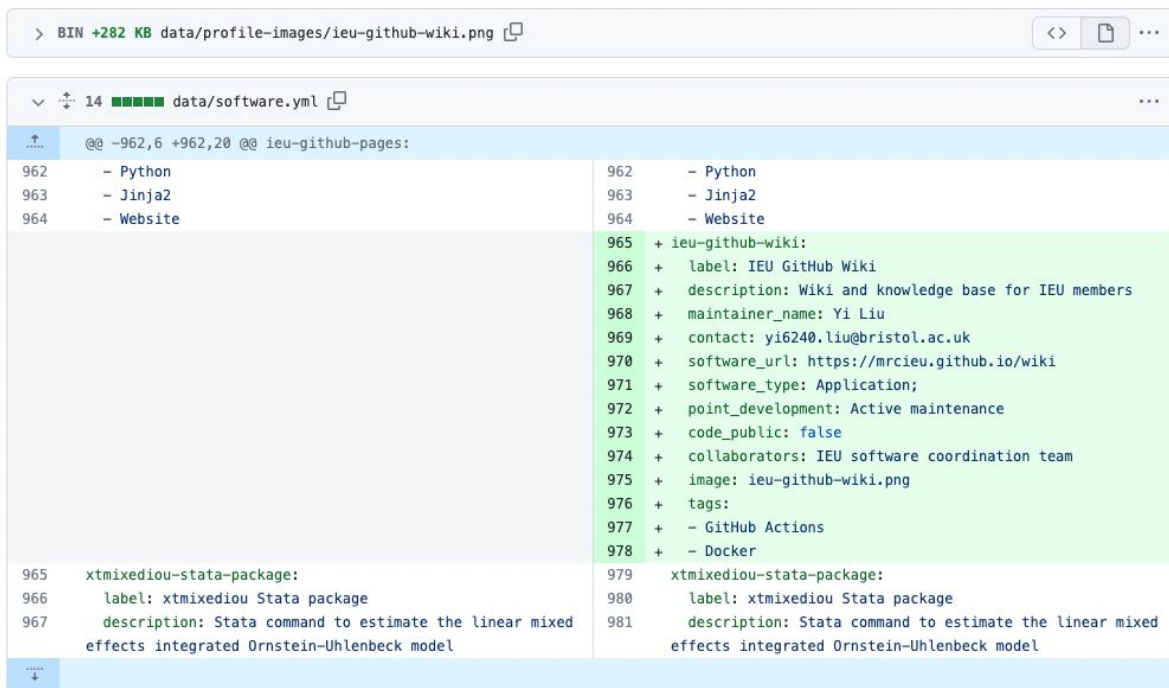
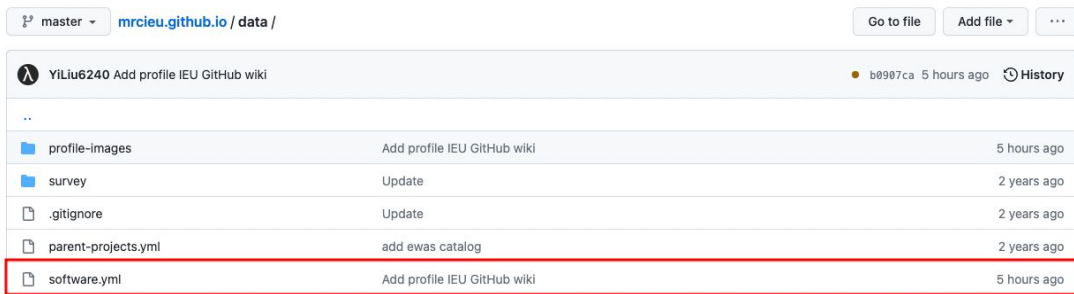
ewaff
R package for performing epigenome-wide association studies (EWAS).
[View what's new]

geograbi
A tool for efficiently grabbing usable metadata and experiment data off GED.
[View what's new]

FATHMM

How to contribute

1. By making a pull request:
 - add an entry to the software.yml
2. Make suggestions on the repo's issues



See further details on the README

See results

Submit / update your software!

MRC Integrative Epidemiology Unit

Home About **MRC IEU software browser** Details Wiki ↻ ↵

MRC IEU software browser

wiki

all API Active development Active maintenance Analytical and/or data processing pipeline Android Studio Application Artistic License 2.0 Bash Bootstrap-vue C++ DNA methylation Data integration Data mining Database Deep learning Dictionary Django Docker EWAS EWAS Catalog Early prototype Elasticsearch EpiGraphDB Evidence integration FastAPI Flask GPL-3 GPLv3 GWAS Gene Expression Omnibus Genetics GitHub Actions Graph database Heteroscedasticity Hugo Illumina Beadchip Interaction effect Java Jinja2 Literature mining MIT MR-Base MR-pheWAS Machine learning Mendelian randomization Metabolomics Methodology Missing outcomes Missing-not-at-random Multilevel models Natural language processing Neo4j None OpenGWAS Phenome Scan Phenotypes PySam Python R RCT Regression Shiny Snakemake Software package Stata Systematic review Terraform Text embedding Text embeddings Text mining The EWAS Catalog Variables Variance Visualization Vue Vue.js WDL Web app Web service Website XML htr metabolomics microbiomics momentary assessment proteomics smoking systematic review vQTL

MRC IEU Wiki

Links and resources

Home

Data management

Links and resources

Scripting

Software development

Articles

Best practices in coding styles

Code Testing

Creating team files from pink software browser

Installing a specific version of R on a Linux server using Conda

Mounting a network drive on Linux

R software examples

Using Biomake

Using Docker

Using Emacs

Table of contents

University links

MRC IEU

- The IEU Intranet (internal) - extensive resources for training in epidemiology - MRC IEU software browser
- MRC IEU homepage and coding
- Code clinic: Teams link - Go here to get lots of peer support and for recorded videos from past sessions

HPC help

- ACRC page
- ACRC HPC docs (internal)

External resources

The University of Edinburgh - Data Science Training in Health & Bioscience

<https://edcarp.github.io/Ed-DASH/>

Ed-DASH is a Data Science training programme for Health and Biosciences. The team has developed workshops using The Carpentries platform on the following topics. See workshops for dates and registration details. All workshops will be delivered remotely.

- List of upcoming workshop sessions: <https://edcarp.github.io/Ed-DASH/workshops.html>

Maintainer(s): Yi Liu

contact: [yi6240.liu\[at\]bristol.ac.uk](mailto:yi6240.liu[at]bristol.ac.uk)

Collaborator(s): IEU software coordination team

Software URL: <https://mrcieu.github.io/wiki>

MRC Integrative Epidemiology Unit

IEU GitHub Wiki

Wiki and knowledge base for IEU members

MRC IEU Wiki

Search

MRC IEU Wiki

Home

Data management

Links and resources

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Maintainer(s): Yi Liu

contact: [yi6240.liu\[at\]bristol.ac.uk](mailto:yi6240.liu[at]bristol.ac.uk)

Collaborator(s): IEU software coordination team

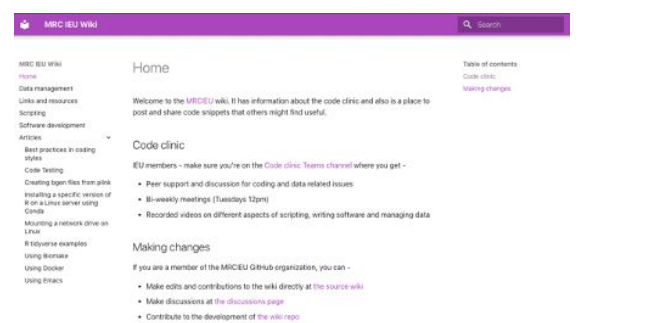
Software URL: <https://mrcieu.github.io/wiki>

IEU software projects

- Annotated Semantic Queries
- API for MRC-IEU OpenGWAS
- BESIDEMR R package
- bpbounds R package
- bpbounds Stata package
- cofunnel Stata package
- DataWatch
- dmrff
- dnamacr
- EpiGraphDB
- EpiViz
- ewaff
- FATHMM
- geograbi
- GLU R package
- GWAS of trait variance
- gwas2vcf
- IEU GitHub Pages
- IEU GitHub Wiki
- iPVs
- ivonesamplemr Stata packag
- medrxiv
- meffil
- MELODI
- MELODI-Presto

IEU wiki

- Curated knowledge base and wiki for IEU (GitHub) members
- Wiki site
- source wiki



The screenshot shows the top portion of the MRC IEU Wiki website. At the top right is a search bar. On the left is a navigation menu with categories like 'MRC IEU Wiki', 'Data management', 'Links and resources', 'Scripting', 'Software development', and 'ARTICLES'. The main content area is titled 'Home' and contains a welcome message, a 'Code clinic' section with a list of activities, and a 'Making changes' section with instructions for members. On the right side, there are links for 'Table of contents', 'Code clinic', and 'Making changes'.

Home

YILKJ240 edited this page on Jan 16 - 12 revisions

Welcome to the MRCIEU wiki. You are looking at the internal source wiki (on the public facing site this page will be replaced by "SITE_README"). This wiki is aimed at building a curated knowledge base for IEU members to share knowledge.

As a member of the MRCIEU GitHub organization, you can

- Make edits and additions to the wiki directly at the [source wiki](#)
- Make discussions at the [discussions page](#)
- Contribute to the development of the [wiki repo](#)

Making changes

NOTE: The following covers steps to make changes to the content pages of the wiki site. If you are hoping to make changes to the wiki site itself (i.e. to the repo's code), you should consult the [documentation of the wiki repo](#).

- Creating a new page: On this wiki page click 'New page'
 - Give the page a title, at the top of the body of the page put something like "Author: Your Name. (if you want to claim ownership), and then just write the snippet and relevant info below in Markdown format.
- To edit an existing page: simply go to a page and click on edit.
- Once you save the page the GitHub Actions will automatically update the <https://mrcieugithub.io/wiki> website. There's nothing else you need to do.

NOTE: Aside from some exceptions (including this one), EVERY visible page on this source wiki will be visible on the public facing <https://mrcieugithub.io/wiki> site. So please do not add information that might be sensitive or confidential (e.g. server address, patient information etc).

Differences between the source wiki and the public wiki website

- Terminology
 - The repo of the wiki site is <https://github.com/MRCIEU/wiki>

Pages (11)
Find a page...
Home
Making changes
Differences between the source wiki and the public wiki website
Technicals
Best practices in coding styles
Code Testing
Creating bgen files from plink
Data management
Installing a specific version of R on ...
Links and resources
Mounting a network drive on Linux
R tidyverse examples
Scripting
SITE_README
Software development
Using Biomake
Using Docker
Using Emacs

How to contribute

The screenshot shows the GitHub interface for the repository `MRCIEU/wiki`. The `Wiki` tab is highlighted with a red box. The repository is private and has 59 unwatchers, 1 fork, and 0 stars. The main branch is `main` with 3 branches and 0 tags. The commit history table is as follows:

Commit	Message	Time
YiLiu6240	Update todo	59 commits
d71f7a5	Fix actions/checkout to v3 instead of master	3 months ago
	Refactor processing logics	3 months ago
	Add missing shebang line	3 months ago
	Overhaul structure	3 months ago
	Minor fixes	3 months ago
	Update todo	3 months ago
	Overhaul structure	3 months ago
	Refactor processing logics	3 months ago
	Add links and resources to top level	3 months ago

The `README.md` file content is:

Wiki for MRC IEU users

This is the code repository of [MRCIEU's GitHub wiki site](#), where the [wiki of this repo](#) is served as the page content of the rendered site.

- If you want to make changes to the wiki's content, please check the [documentation here](#).
- If you want to make changes to the wiki site itself, please continue reading the docs.

The sidebar on the right shows repository statistics: `MRCIEU GitHub Wiki`, [mrcieu.github.io/wiki](#), 0 stars, 59 watching, and 1 fork. It also lists 5 contributors and a language usage chart:

Language	Percentage
Shell	55.0%
Makefile	38.6%
Dockerfile	6.4%

How to contribute

The screenshot shows the GitHub Wiki page for MRCIEU. The page title is "Home" and it was last edited by YiLiu6240 on Jan 16 with 12 revisions. The main content area contains a welcome message and a list of contribution instructions. A red box highlights the "Making changes" section, which includes a note about content vs. site changes and a list of steps for creating and editing pages. Below this is a section titled "Differences between the source wiki and the public wiki". On the right side, there is a sidebar with a "Pages" list containing 15 items, including "Home", "Best practices in coding styles", "Code Testing", "Creating bgen files from plink", "Data management", "Installing a specific version of R on ...", "Links and resources", "Mounting a network drive on Linux", "R tidyverse examples", "Scripting", and "SITE_README".

MRCIEU / wiki Private

Unwatch 59 Fork 1 Star 0

<> Code Issues Pull requests Discussions Actions Wiki Security Insights Settings

Home

YiLiu6240 edited this page on Jan 16 · 12 revisions

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- Make discussions at [the discussions page](#)
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Making changes

NOTE: The following covers steps to make changes to the *content pages of the wiki site*. If you are hoping to make changes to the *wiki site itself* (i.e. to the the repo's code), you should consult [the documentation of the wiki repo](#).

- Creating a new page: On this wiki page click 'New page'
 - Give the page a title, at the top of the body of the page put something like `Author: Your Name` (if you want to claim ownership), and then just write the snippet and relevant info below in Markdown format.
- To edit an existing page: simply go to a page and click on edit.
- Once you save the page the Github Actions will automatically update the <https://mrcieu.github.io/wiki/> website. There's nothing else you need to do.

NOTE: Aside from some exceptions (including this one), **EVERY** visible page on this source wiki will be visible on the public facing <https://mrcieu.github.io/wiki/> site. So please do not add information that might be **sensitive or confidential** (e.g. server address, patient information etc).

Differences between the **source wiki** and the **public wiki**

Pages 15

Find a page...

- ▾ Home
 - Making changes
 - Differences between the source wiki and the public wiki website
 - Technicals
- Best practices in coding styles
- Code Testing
- Creating bgen files from plink
- Data management
- Installing a specific version of R on ...
- Links and resources
- Mounting a network drive on Linux
- R tidyverse examples
- Scripting
- SITE_README

See results

Editing Best practices in coding styles

Page history [New page](#) [Delete page](#)

Best practices in coding styles

Write Preview

h1 h2 h3 **B** *i* <> Edit mode: [Markdown](#)

Best practices in coding styles

Author: Yi Liu

Maintaining a good and consistent coding style is important in the sense that it improves the **readability** of your code.

Coding styles

Below are some of the commonly practiced coding styles in various programming languages:

- [R: tidyverse style](https://style.tidyverse.org/)
- [R: google](https://google.github.io/styleguide/)
- [Python: PEP8](https://peps.python.org/pep-0008/)
- [Python: google](https://google.github.io/styleguide/pyguide.html)
- [Shell: google](https://google.github.io/styleguide/shellguide.html)

Formatters

Attach files by dragging & dropping, selecting or pasting them.

Edit message

Write a small message here explaining this change. (Optional)

MRC IEU Wiki

[Home](#)

[Data management](#)

[Links and resources](#)

[Scripting](#)

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Best practices in coding styles

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Maintaining a good and consistent coding style is important in the sense that it improves the **readability** of your code.

Coding styles

Below are some of the commonly practiced coding styles in various programming languages:

- [R: tidyverse style](#)
- [R: google](#)
- [Python: PEP8](#)
- [Python: google](#)
- [Shell: google](#)

Formatters

There are formatters in many programming languages that support formatting your code into a consistent style.

- [R: formatR](#)
- [Python: black](#)
- [Web development \(js/ts, html, css\): prettier](#)