

The MRC IEU R-Universe of Mendelian randomization related R packages

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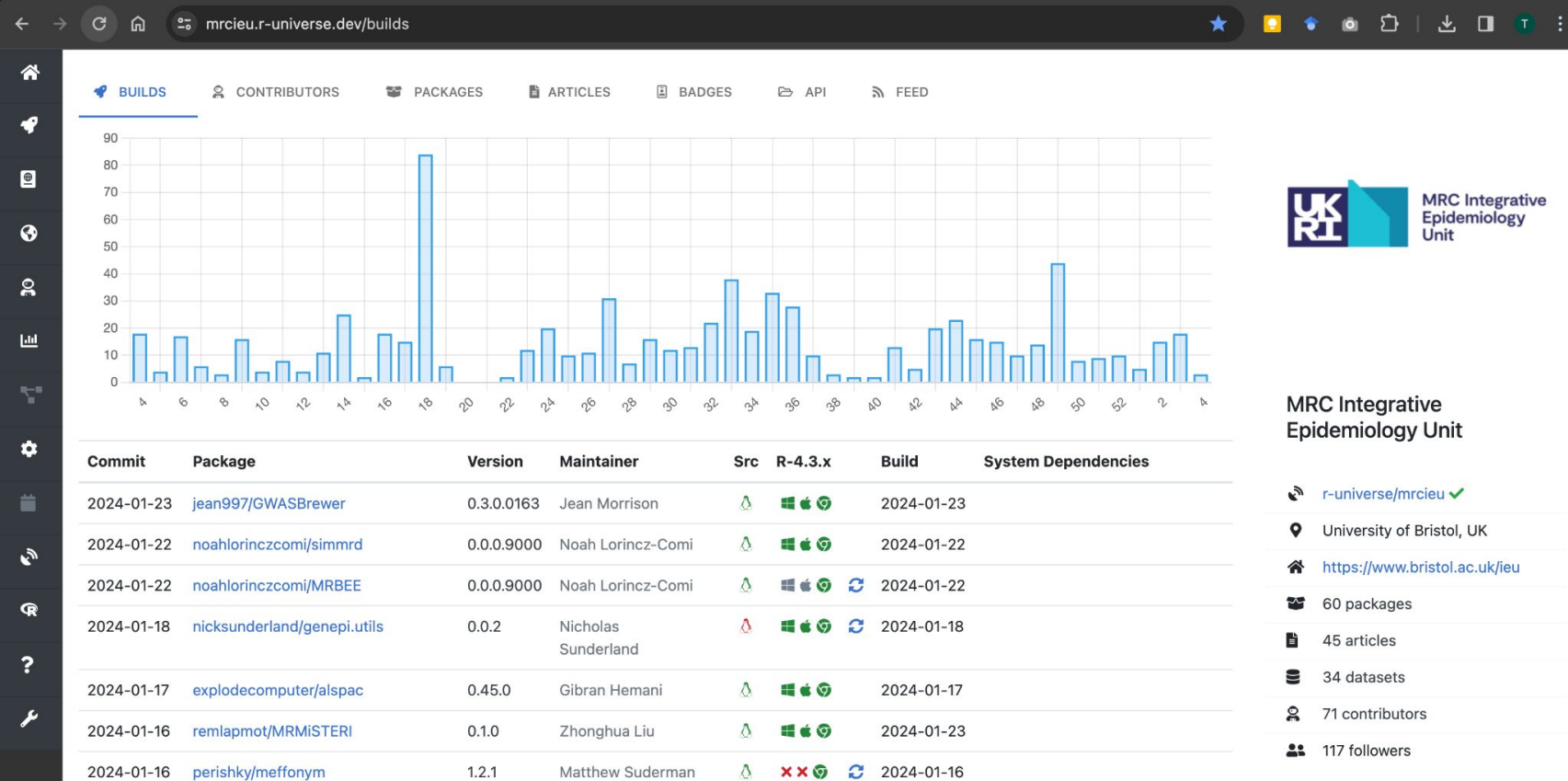


MRC Integrative
Epidemiology
Unit



University of
BRISTOL

<https://mrcieu.r-universe.dev/builds>



MRC Integrative Epidemiology Unit

- [r-universe/mrcieu](#) ✓
- University of Bristol, UK
- <https://www.bristol.ac.uk/ieu>
- 60 packages
- 45 articles
- 34 datasets
- 71 contributors
- 117 followers

mrcieu/TwoSampleMR 0.5.8



TwoSampleMR: Two Sample MR Functions and Interface to MR Base Database

A package for performing Mendelian randomization using GWAS summary data. It uses the IEU GWAS database to obtain data automatically, and a wide range of methods to run the analysis. You can use the MR-Base web app to try out a limited range of the functionality in this package, but for any serious work we strongly recommend using this R package.

Authors: Gibran Hemani [aut, cre], Philip Haycock [aut], Jie Zheng [aut], Tom Gaunt [aut], Ben Elsworth [aut], Tom Palmer [aut]



Gibran Hemani

[TwoSampleMR_0.5.8.tar.gz](#)

[TwoSampleMR_0.5.8.zip](#) (r-4.4) [TwoSampleMR_0.5.8.zip](#) (r-4.3) [TwoSampleMR_0.5.8.zip](#) (r-4.2)

[TwoSampleMR_0.5.8.tgz](#) (r-4.3-any) [TwoSampleMR_0.5.8.tgz](#) (r-4.2-any)

[TwoSampleMR_0.5.8.tar.gz](#) (r-4.3-jammy) ?

[TwoSampleMR_0.5.8.tgz](#) (r-4.3-emscripten) ?

[TwoSampleMR.pdf](#) | [TwoSampleMR.html](#) ✨

[TwoSampleMR/json](#) (API)

[NEWS](#)

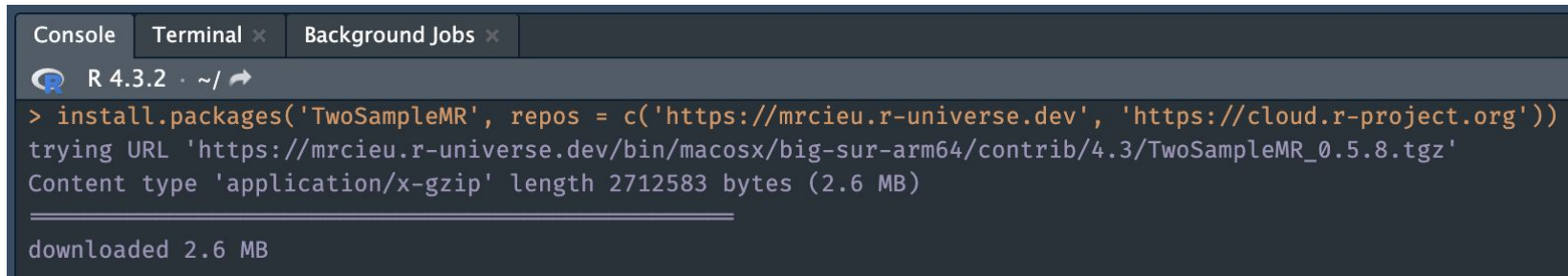
```
# Install TwoSampleMR in R:
```

```
install.packages('TwoSampleMR', repos = c('https://mrcieu.r-universe.dev', 'https://cloud.r-project.org'))
```



Installation code

- Windows and macOS users



```
Console Terminal x Background Jobs x
R 4.3.2 · ~/ ↵
> install.packages('TwoSampleMR', repos = c('https://mrcieu.r-universe.dev', 'https://cloud.r-project.org'))
trying URL 'https://mrcieu.r-universe.dev/bin/macosx/big-sur-arm64/contrib/4.3/TwoSampleMR_0.5.8.tgz'
Content type 'application/x-gzip' length 2712583 bytes (2.6 MB)
downloaded 2.6 MB
```

- Ubuntu Linux and WebR instructions

<https://github.com/MRCIEU/mrcieu.r-universe.dev#readme>

Vignettes and helpfiles

Exposure data

Gibran Hemani

Rendered from `exposure.Rmd` using `knitr::rmarkdown` on 2024-01-15 06:02:44.

Harmonise data

Gibran Hemani

Rendered from `harmonise.Rmd` using `knitr::rmarkdown` on 2024-01-15 06:02:44.

Introduction

Gibran Hemani

Rendered from `introduction.Rmd` using `knitr::rmarkdown` on 2024-01-15 06:02:44.

Major changes to the IEU GWAS resources for 2020

Rendered from `gwas2020.Rmd` using `knitr::rmarkdown` on 2024-01-15 06:02:44.

Outcome data

Gibran Hemani

Rendered from `outcome.Rmd` using `knitr::rmarkdown` on 2024-01-15 06:02:44.

Perform MR

Gibran Hemani and Philip Haycock

Rendered from `perform_mr.Rmd` using `knitr::rmarkdown` on 2024-01-15 06:02:44.

Reference manual

Help page	Topics
TwoSampleMR: Two Sample MR functions and interface to MR Base database	TwoSampleMR-package TwoSampleMR twosamplemr
Add meta data to extracted data	add_metadata
Estimate r-square of each association	add_rsq
Estimate allele frequency from SNP	allele_frequency
Get list of studies with available GWAS summary statistics through API	available_outcomes
Perform LD clumping on SNP data	clump_data
Combine all mr results	combine_all_mrresults
Combine data	combine_data
Obtain 2x2 contingency table from marginal parameters and odds ratio	contingency
Convert outcome data to exposure data	convert_outcome_to_exposure
Convert TwoSampleMR format to MendelianRandomization format	dat_to_MRInput
Convert dat to RadialMR format	dat_to_RadialMR
List of parameters for use with MR functions	default_parameters
Perform MR Steiger test of directionality	directionality_test

Installing R packages can be painful 🤕

- ***Sorry*** to everyone who has ever had to build TwoSampleMR and its dependencies from source 🙄
- The pain can be real on Linux ... many packages require additional system libraries ... `sudo apt-get install ...`
- (Well known) CRAN provides binary R packages for Windows and macOS (Intel and Apple Silicon)
- (Less well known) Public Posit Package Manager provides binary R packages for various Linux distros ... but the packages need to be on CRAN
- Some other efforts r2u, bspm, PPAs etc.

rOpenSci R-Universe <https://r-universe.dev/>

- CRAN like system for R packages on GitHub, GitLab, ...
- No `devtools::check()` requirements
 - Requirements: file structure and DESCRIPTION file are correct (... some packages fail this!)
- Added MRC IEU R packages ... that I have seen ... tell me about more
- Started adding MR and MR related packages from other authors
 - Got carried away ... currently 60 packages
 - Have sent several pull requests to fix some broken packages
- How up-to-date is this? ... Refreshed every hour (occasionally wait till overnight)

Summary

- MRC IEU R-Universe makes GitHub R packages available in binary form (for the first time)
- Satisfied users



liaofengnan commented 2 weeks ago via email 

Thank you for your help! It really work!



yangj6688 commented on Oct 11, 2023

Thanks a lot, the code works.



- Gives an overview of available methods for MR
- Please let me know about additional R packages