UMC Utrecht

Mendelian Randomization studies

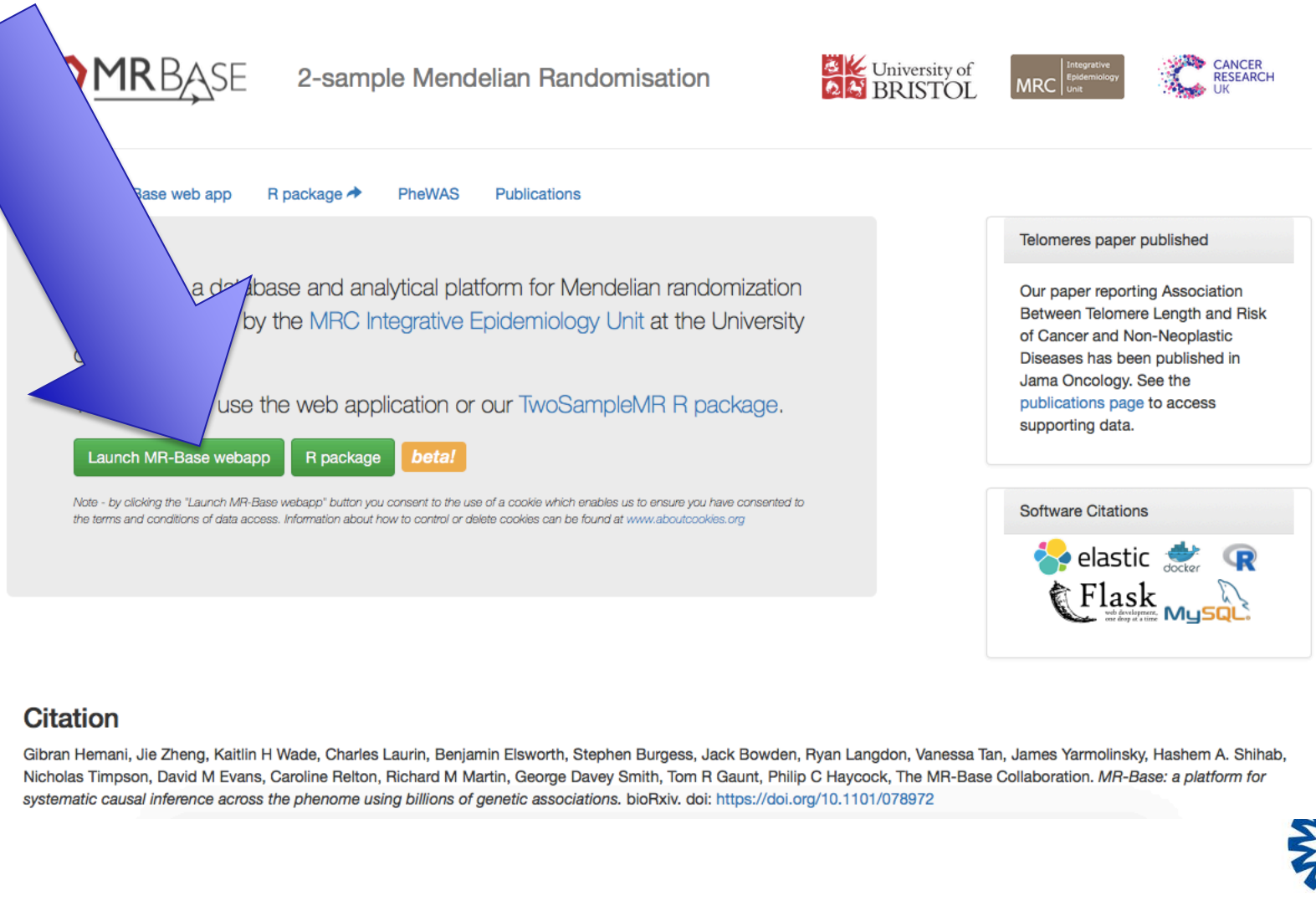
Assignment practical

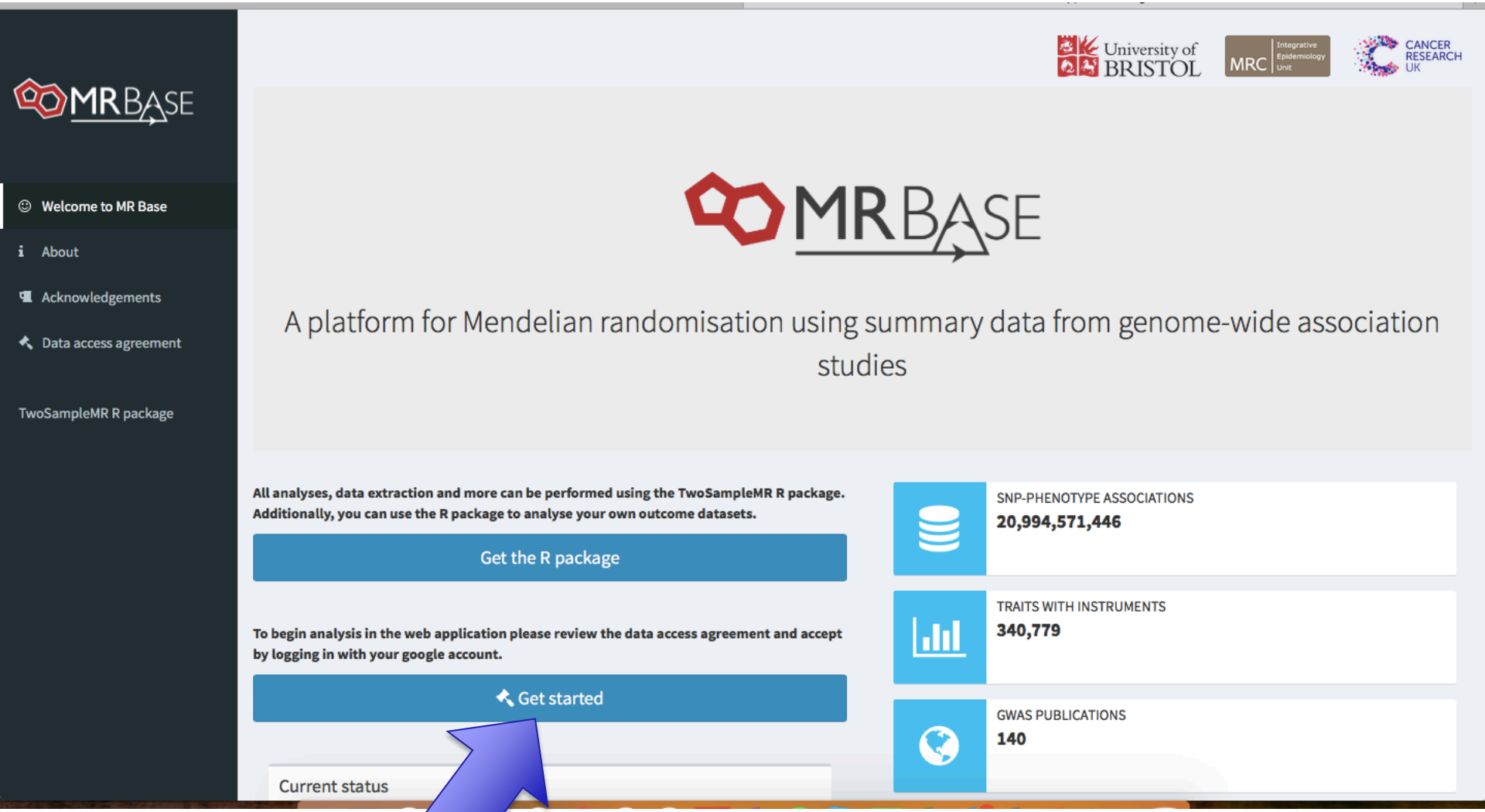
Perform an MR study…

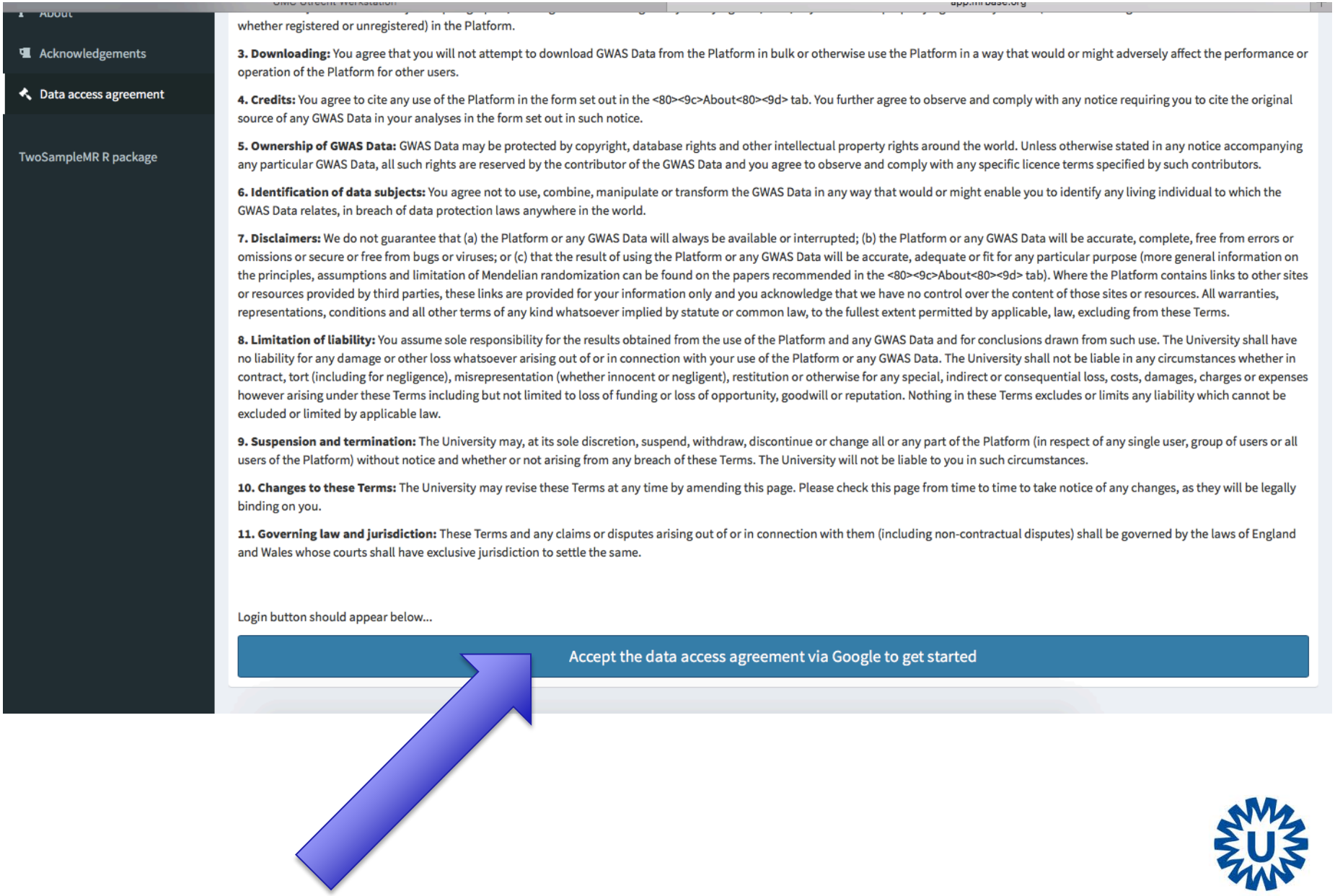
- …wait…what?

- Yes, you can: http://www.mrbase.org/beta/

Start MRBase




MR BASE
Welcome to MR Base
About
Acknowledgements
Data access agreement
TwoSampleMR R package
University of BRISTOL
MRC Integrative Epidemiology Unit
CANCER RESEARCH UK
MR BASE
A platform for Mendelian randomisation using summary data from genome-wide association studies
All analyses, data extraction and more can be performed using the TwoSampleMR R package. Additionally, you can use the R package to analyse your own outcome datasets.
Get the R package
To begin analysis in the web application please review the data access agreement and accept by logging in with your google account.
Get started
Current status
SNP-PHENOTYPE ASSOCIATIONS
20,994,571,446
TRAITS WITH INSTRUMENTS
340,779
GWAS PUBLICATIONS
140


About
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Data access agreement
TwoSampleMR R package
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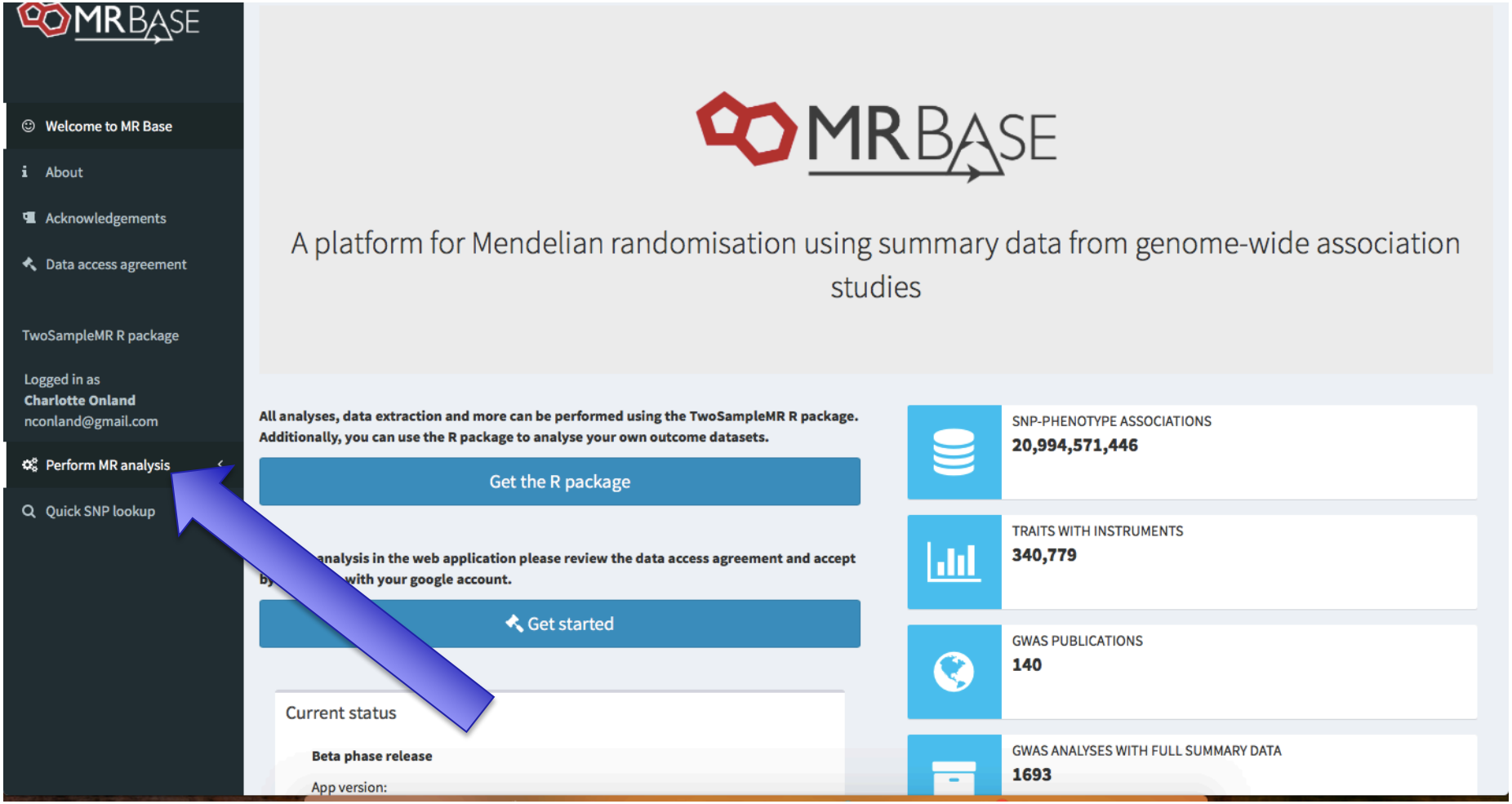
Accept the data access agreement via Google to get started


MR BASE
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Logged in as
Charlotte Onland
nconland@gmail.com
Perform MR analysis
Quick SNP lookup
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GWAS ANALYSES WITH FULL SUMMARY DATA
1693

Perform a MR study…: assignment

- Choose your favourite exposure (e.g. BMI, height, CRP, ….)
  - What should you check for?
  - You can use data from MRBase GWAS, but also upload your own list of SNPs
  - What information do you need on the SNPs if you want to upload your own data for the exposure?
  - We start with 1 variant (use literature to identify 1, and check NHGRI-EPIC-GWAS upload)
    - What should you take into account?
      - Cis/trans
      - Effect size

Perform MR study

- Choose outcome: CHD
  - Check which data you will use
  - What should you take into consideration?
    - Sample size
    - Ethnicity
    - Date
    - Evt. Sex. Etc.

Perform an MR

- After you selected the exposure and outcome
- Click on “Run MR”
- Then you need to make some choices:
  - LD
  - Use of Proxies (incl. value of r2)
  - Allow palandromic SNPs
    - What is a planadromic SNP
    - What should the MAF threshold be and why?
    - Allele harmonization
    - Select methods

- Now click on “Perform MR analysis”
- You will see the results
- Please answer the questions on the next page
- You can use different databases to help answer your questions (apart from the results)
  - For instance: http://www.phenoscanner.medschl.cam.ac.uk/

- Explain in your own words what you see
- Whay do the different methods tell you?
- What do the different plots tell you?
- Do the MR assumtions hold? Please, explain
  - SNP associated with exposure (strong instrument?)
  - No association with confounders
  - Only association with outcome through the exposure
- Is there evidence for pleiotropy?
- Write down the answer to your research question based on the results

- Now take multiple variants
  - Find the lastest GWAS on the exposure you chose
  - Answer the same questions

If you have time

- Try the R-package MendelianRandomization by Stephen Burgess
  - Easy to use
  - Need your data ready
  - Read the manual to understand what you datafiles should look like
- Try the two sample MR package by….