

# Practical I

Thursday/Friday, 26/27 January 2023, 2pm – 5pm

Department of Biology, University of Oxford

# Demonstrators/Instructors



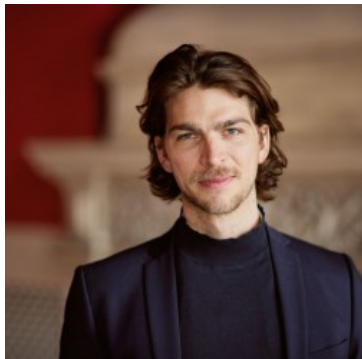
Sumali, (she/her)

Main research: Equity in disease transmission and statistical inference



Rhys, (he/him)

Main research: Genomic epidemiology and sampling biases



Moritz, (he/him)

Main research: Spatio-temporal dynamics of infectious diseases

- About infectious disease surveillance data
- How to analyse case count data using the R-package 'EpiEstim'
  - Specifically estimating the time varying reproduction number  $R_t$



# How are we learning today?

- There are handouts on Canvas with questions and example code
- We take a break after ca. 1 ½ hours for about 15 minutes and you can also take your own short breaks during the session
- Raise your hand should you need assistance or have specific questions
- At the end we will have a short 15-minute wrap up session
- Early next week we will give you access to model answers and you can email us with any questions after as well

# R-Markdown: a quick intro

- Format for writing reproducible and dynamic reports within R
- To create an R-markdown open R Studio click on “File” > “New File” > “R Markdown”
- In the editor window you can add code, text and formatting through the Markdown language e.g. # = headings or - = bullet points
- To insert code, you can use the {r} and ' syntax to create code chunks e.g. `'''{r} x <- 5`
- These chunks can be run independently or be knitted together in the desired format to create a PDF or HTML