

# SMED 8020

Genetic Epidemiology

**pre-course information and preparations**

# Information regarding SMED8020 spring 2025

Welcome to SMED8020 Genetic Epidemiology 2025.

All teaching will take place on campus at NTNU, and we have chosen Blackboard as the platform to communicate and share course content with you. If any issues arise, please do not hesitate to contact us.

## LECTURES

Lectures will be in person. Recorded lectures from previous years will be made available on Blackboard for you to review them in your own time. We aim to make the lecture notes available a few days prior to the scheduled time to give you time to view them. Questions to the lectures can be asked during the sessions each day and on email and Blackboard.

## ASSIGNMENT:

The assignment will be made available on Blackboard on the first day of the course, **Monday 02.06.2025**. The assignment must be completed by and presented orally on **Thursday 12.06.2025** with a 15 min oral presentation. (Applicable only for those who are taking the course for credits).

## PRACTICALS:

The hands-on work for the course SMED8020 will be done using HUNT Cloud. A separate virtual environment will be set up for the purpose of the course. Here you will access files and analysis-tools.

## HELP DESK (ZOOM):

To troubleshoot any issues with onboarding to HUNT Cloud we will have a live help desk session on **Thursday 22.05.2025 at 10:00-10:30**. The Zoom link will be posted on Blackboard.

## BASH AND R-INTRO SESSION (ZOOM):

If you have little prior experience working in R or the command line, we recommend that you join our introduction session on R and bash. We will have a live session on **Thursday 22.05.2025 at 10:30-11:00**. The Zoom link will be posted on Blackboard.

## Before the course

Before the course we need you to do the following:

### #1 – Setup HUNT Cloud

**\*\*\*Important note!!!** You may need to get admin rights to your computer to complete this setup. Depending on your IT department this might take days to obtain, so important to start the process early.

Every user needs to sign a user agreement – download here:

<https://assets.hdc.ntnu.no/assets/agreements/hunt-cloud-user-agreement.pdf>

LAB NAME: **smmed8020-2025**

LAB LEADER: **Ben Brumpton**

**This must be returned no later than MAY 2. Please send to It will be signed and forwarded to HUNT Cloud.**  
**Cloud.**[\*\*ben.brumpton@ntnu.no\*\*](mailto:ben.brumpton@ntnu.no) **It will be signed and forwarded to HUNT Cloud.**

To be able to set up you account you need the following:

- smartphone
- google authenticator
- signal, on your smartphone (Search for “Signal” in the iOS or Android app stores, or use the links below.
  - [Download and install for iOS here](#)
  - [Download and install for Android here](#)

## **WHEN YOUR USER HAS BEEN CREATED:**

To get started and set-up your account, please follow the instructions (Please allow **two hours** to complete the remaining onboarding steps):

### **Instructions: “HOW TO CONNECT”**

<https://docs.hdc.ntnu.no/do-science/getting-started/>

### **Instructions: “HUNT Workbench installation”**

<https://docs.hdc.ntnu.no/do-science/hunt-workbench/installation/>

Due to the requirement to complete the practicals, we will prioritise the students having signed up for credits. The practicals will be available on github for all students, but the tutoring will be prioritised for those who will receive credits for the course (this year or next).

## **#2 – Pre-course reading**

There are two pre-course readings. Please allow for two **four-hour** sessions to complete the pre-course reading. The articles can be downloaded from NTNU Blackboard.

Uffelmann, E., Huang, Q.Q., Munung, N.S. et al. **Genome-wide association studies**. Nat Rev Methods Primers 1, 59 (2021). <https://doi.org/10.1038/s43586-021-00056-9>

Sanderson, E., Glymour, M.M., Holmes, M.V. et al. **Mendelian randomization**. Nat Rev Methods Primers 2, 6 (2022). <https://doi.org/10.1038/s43586-021-00092-5>

## Recommended preparations

Before the course we recommend that you make sure you are familiar with Linux, PLINK and R. If you have little prior experience working in R or the command line, we recommend that you have a look at the suggested links below.

### BASIC introduction to Linux, PLINK and R:

- Linux: <https://ryanstutorials.net/linuxtutorial/>
- PLINK: [https://www.cog-genomics.org/plink/2.0/general\\_usage](https://www.cog-genomics.org/plink/2.0/general_usage)
- R: <https://www.datacamp.com>
- R: <https://www.statmethods.net/r-tutorial/index.html>

### Contact information:

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