

# Meeting agenda

9 July, 2020

## Agenda (Thank you, Stefan!)

1. Welcome and why we're meeting (kick-off, getting to know each other and agree on the project).
2. A quick introduction about the project.
3. Introducing everyone and their supposed **role in the project**.
4. Overview of what is already done: [Report from Mark's course](#)
5. Current ideas on how to develop the project and how it will be managed (leading and assisting): **file attached**
6. Questions?

## Minutes of the meeting

### Attendees:

- We can target Genome Biology for this project
- We plan to integrate data from different species: human, rat, mouse, plants
- The idea to have a continuous benchmark is good. There might be a lot of work at beginning, but later it would be easy.
- We could have an R package which could run all the different analysis (wrapper around all tools, which can accept all forms of input)
- We may try to have our own simulations as well
- This benchmark will help researchers to choose the best method for their data
- Here, we will only benchmark methods available for WGBS data