

DTU



22126: Next Generation Sequencing Analysis

DTU - January 2026

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Who am I?

- Undergrad + honours – University of Otago, New Zealand
- PhD in Evolutionary biology – University of Potsdam, Germany
- Postdoc – University of Copenhagen
- Assistant professor – University of Copenhagen
- Associate professor (since Aug. 2025) – DTU

Research interests

- Rise and fall of biodiversity
- Conservation
- Improve study of non-model organisms
- Cross-disciplinary approaches



Key research themes

- **Palaeogenomics (ancient DNA):**
 - Species extinction, adaptation
- **Conservation Genomics**
 - Genomic erosion/rescue
- **Methodological Innovation:**
 - Developing pipelines for low-quality DNA



Study systems

Extinct species



Endangered species

Who are we?

- **DTU**

- Mick Westbury (organiser)
- Mads Hartmann (TA)
- Amanda Gammelby Qvesel (TA)
- Kristoffer Vitting-Seerup
- Rasmus Lykke Marvig

- **University of Copenhagen**

- Martin Sikora
- Juan Rodríguez
- David Duchene
- Luke Holman



Feedback

- My 1st time teaching this course
- Working on improving
- NGS is very broad now, no one masters everything
- Give us feedback
 - Please do the evaluation at DTU Inside

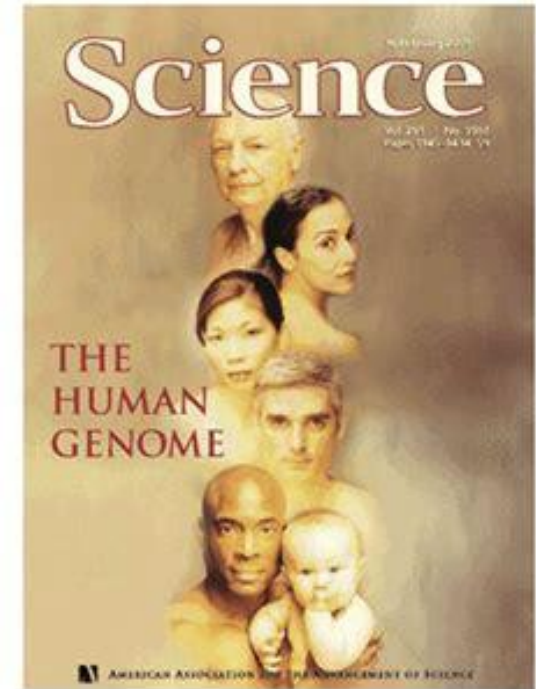
Why we (next generation) sequence?

Why we sequence

- DNA encodes all genetic information
- Differences in DNA explain variation between
 - Individuals
 - Species
 - Diseases
- Sequencing is how we read this information.

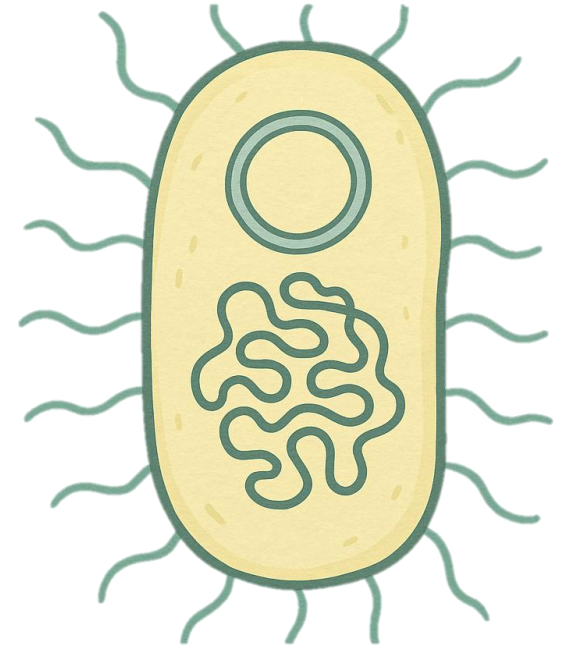
Human genome project (HGP)

- Pre-next generation sequencing
 - Sanger sequencing + BAC clones
- Started 1990
- First draft in 2001
- Completed 2004.
- Cost: ~5.5 billion USD (adjusted)
- Involved 20 research centres
 - 6 countries



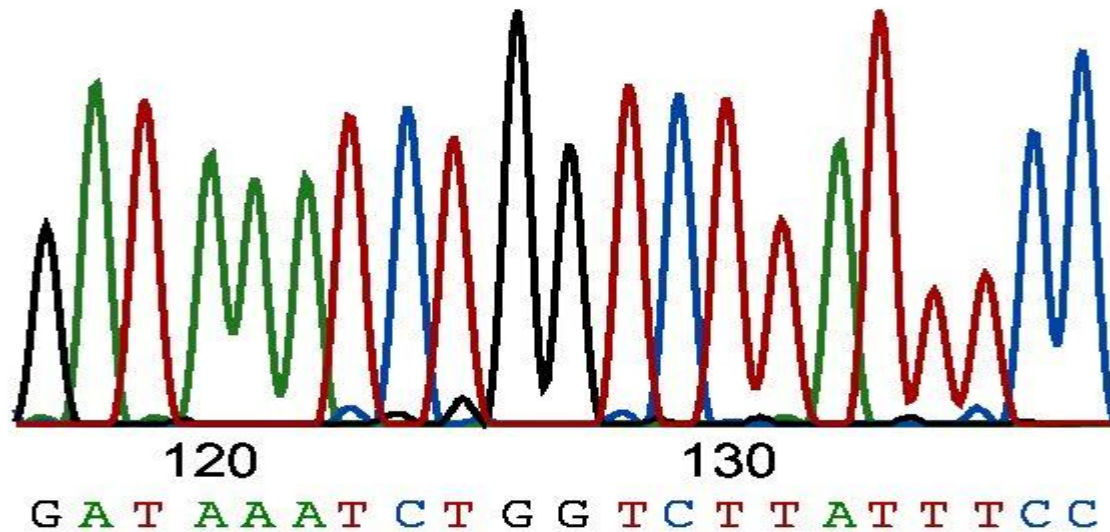
HGP – long DNA problem

- Human genome is ~3.2 billion bases long
- Challenge: How to break DNA, sequence the pieces, and reconstruct the original genome?
- BAC (Bacterial Artificial chromosomes)
- Break into long fragments
 - Break long into smaller
 - Insert to bacteria and clone
 - Sequence plasmids



HGP – long DNA problem

- Technology of the time ~700-1,000bp
 - Sanger sequencing
 - 3.2 million single sequencing reactions = \$\$\$



HGP - shotgun sequencing


- Developed at scale by Celera Genomics during the HGP
- Randomly fragmenting DNA into small pieces and
- Assembling them with overlaps.
- First demonstration of high-throughput
- Shotgun sequencing introduced
 - Massive parallelization
 - Volume over accuracy
 - Ideas that directly led to NGS



First NGS genome

Article | [Open access](#) | Published: 13 December 2009

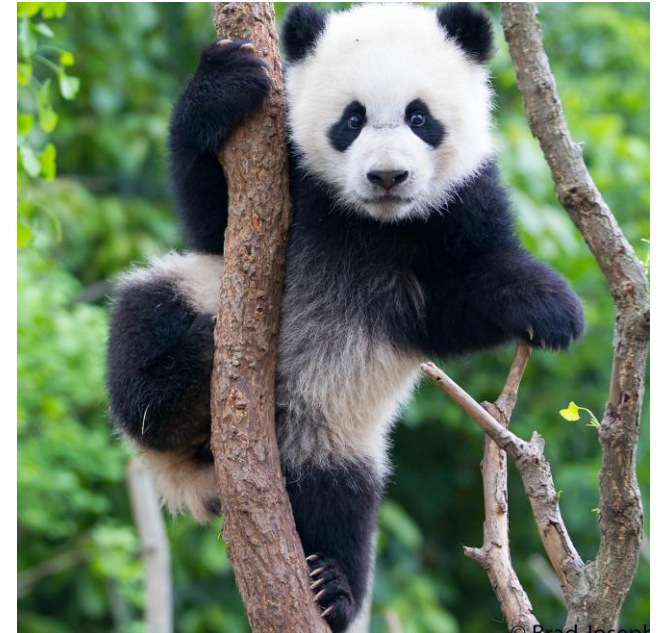
The sequence and *de novo* assembly of the giant panda genome

[Ruiqiang Li](#), [Wei Fan](#), [Geng Tian](#), [Hongmei Zhu](#), [Lin He](#), [Jing Cai](#), [Quanfei Huang](#), [Qingle Cai](#), [Bo Li](#), [Yinqi Bai](#), [Zhihe Zhang](#), [Yaping Zhang](#), [Wen Wang](#), [Jun Li](#), [Fuwen Wei](#), [Heng Li](#), [Min Jian](#), [Jianwen Li](#), [Zhaolei Zhang](#), [Rasmus Nielsen](#), [Dawei Li](#), [Wanjun Gu](#), [Zhentao Yang](#), [Zhaoling Xuan](#), ... [Jun Wang](#) 

+ Show authors

[Nature](#) **463**, 311–317 (2010) | [Cite this article](#)

93k Accesses | **1038** Citations | **175** Altmetric | [Metrics](#)

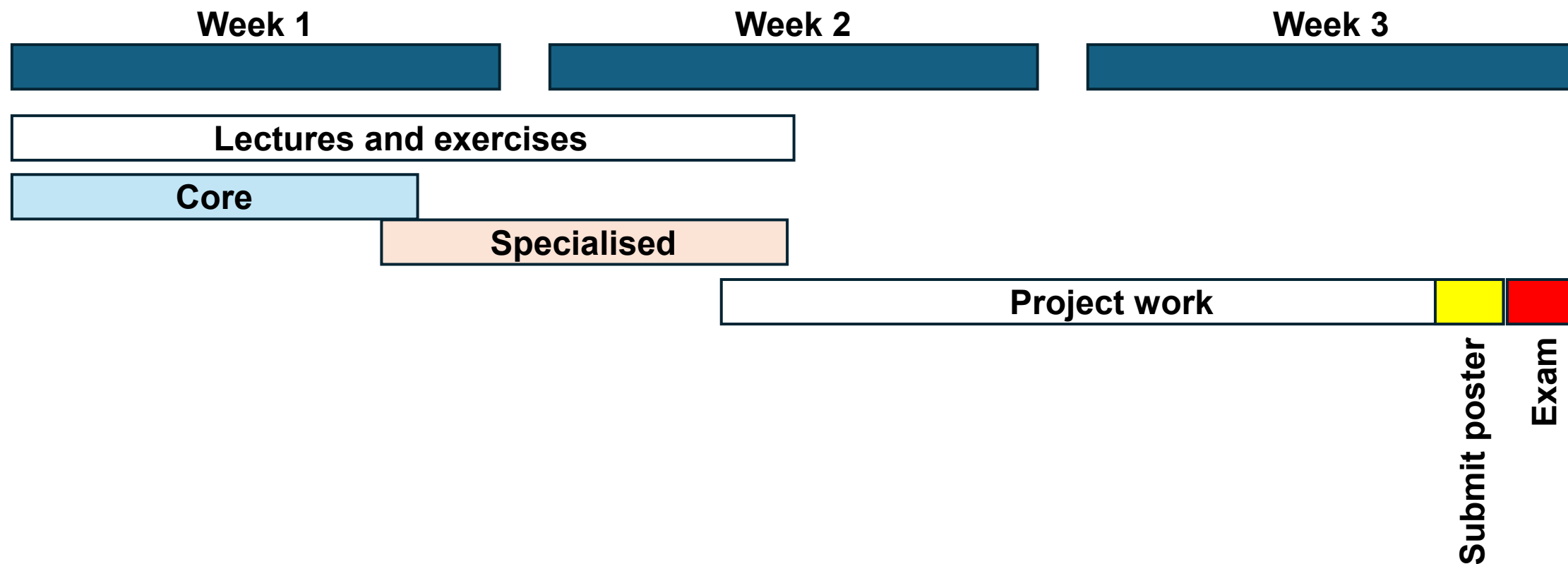


Why sequencing matters today

- Rapid outbreak response
- Cancer profiling and precision oncology
- Rare disease diagnostics
- Prenatal cell-free DNA screening
- Microbiome and ecosystem studies
- Evolution, population genomics, phylogenomics

Course information

Course overview



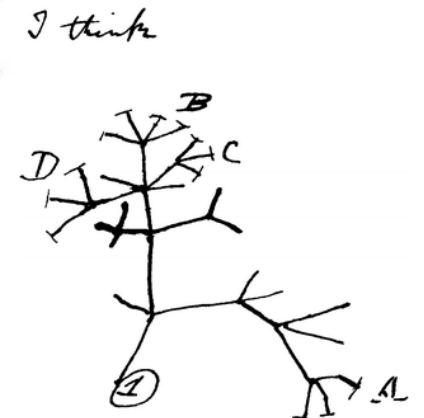
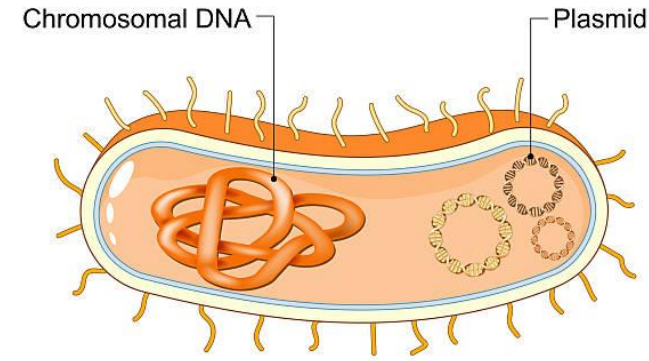
Upcoming course topics

- **Day 1 (core)**
 - Basics of NGS
 - Unix introduction
 - First look at data
- **Day 2 (core)**
 - Data basics and preprocessing
 - Alignments



Upcoming course topics

- **Day 5 (specialised)**
 - 3D genomics
 - Ancient DNA
- **Day 6 (specialised)**
 - Microbial genomics
- **Day 7 (specialised)**
 - Phylogenomics



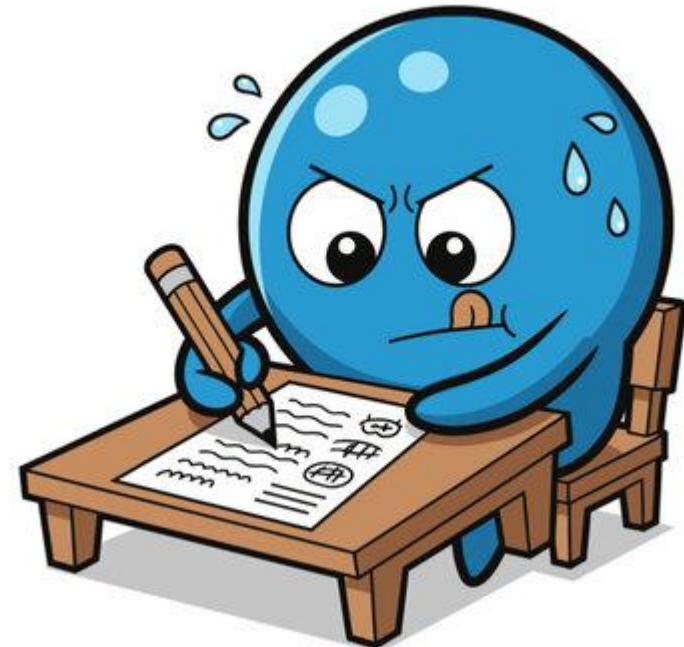
Upcoming course topics

- **Day 8**
 - Metabarcoding (**specialised**)
 - Project introduction
- **Days 9-13**
 - Project work



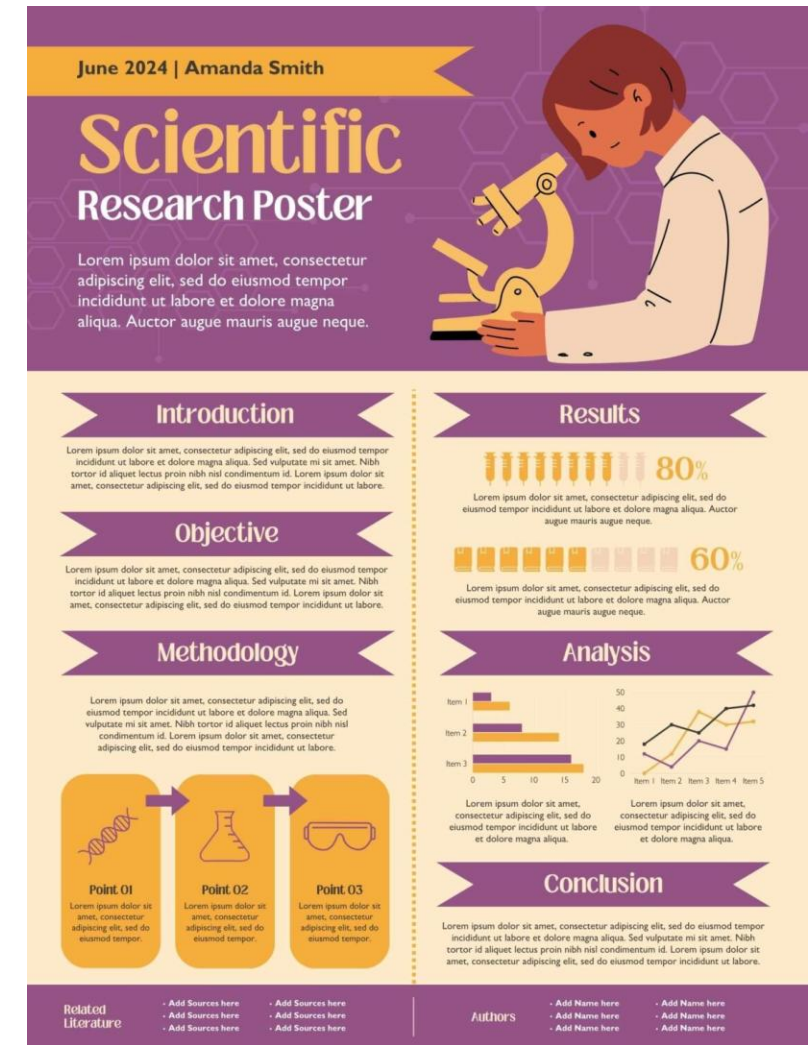
Upcoming course topics

- **Day 14**
 - Project hand-in
- **Day 15**
 - Written exam



Projects

- Analyse an empirical dataset
- Present results as a poster
- 5-6 per group
- You can find a dataset on SRA/ENA
- Empirical data
 - Recreate a previous study
 - Use your own data if group agrees
- Do **not** analyse very large datasets
 - Time + resources = limited

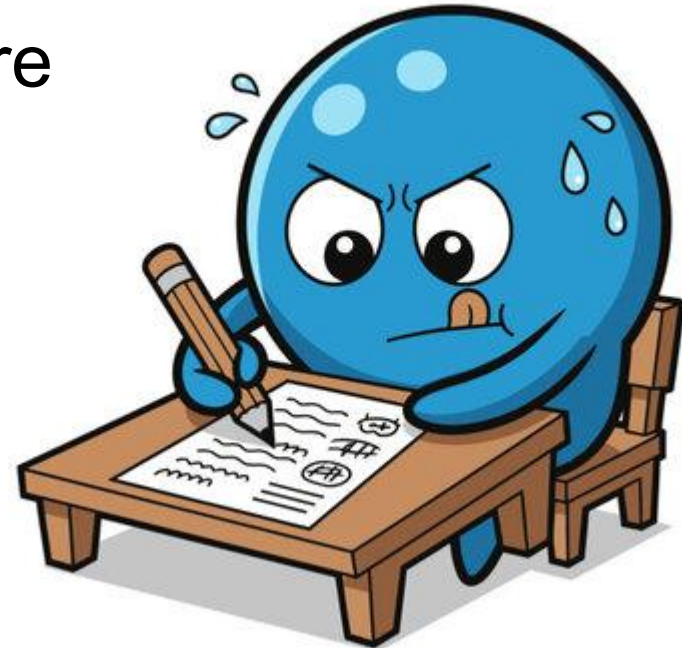


Projects

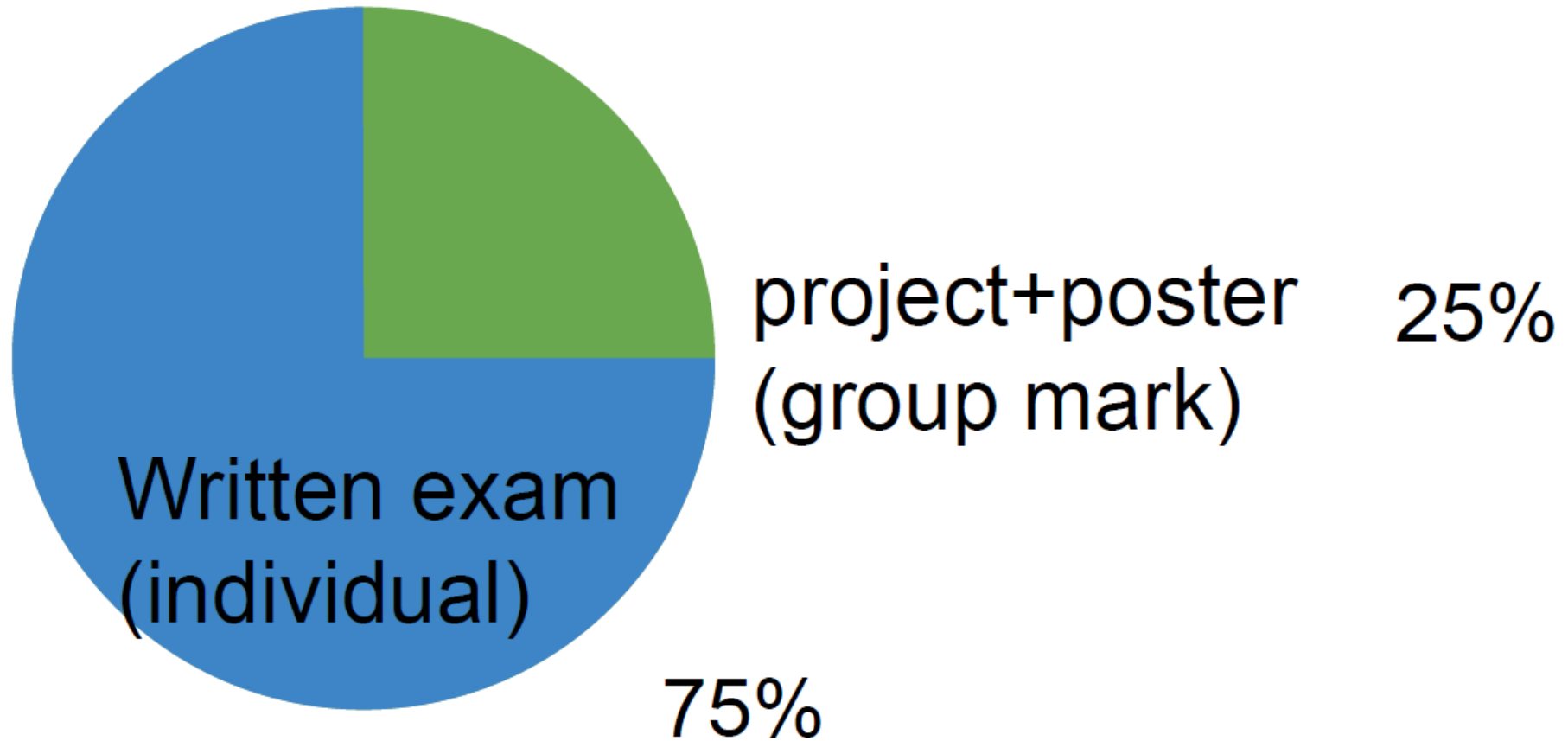
- Each project group will create a poster
- The goal of the project is:
 - Do not memorise
 - Understand what you are doing during the project
 - Understand the concepts taught in class
 - Learn NGS from firsthand experience
- Please send the PDF **before noon on Thursday the 22nd January**

Written Exam

- You cannot write the exam if you have not submitted the poster
- Multiple choice exam
- Focuses on the core lectures
- One basic question per specialised lecture
- Euroteq = oral exam



Marking scheme



Points to remember

- Understand principles of the analysis
- The exercises will be useful for your projects and hopefully later
- You don't need to do all the exercises
 - However, the core lectures are important

Points to remember

- Have an exercise buddy and do them as a team
 - On each individuals' laptop
 - Everyone learns the command-line
- Ask questions at any time!
- You get the solutions for the exercises but **do not copy-paste!!**
- You will not get to copy-paste for the project
- Read the **error message**

Cloud/HPC computing

- Pupil cluster
 - 5 nodes
- Be careful with disk space
- Limited computational power
- Need software installed?
 - Ask me!

Server	Full host name	CPUs	RAM
pupil1	pupil1.healthtech.dtu.dk	40	252G
pupil2	pupil2.healthtech.dtu.dk	24	110G
pupil3	pupil3.healthtech.dtu.dk	24	94G
pupil4	pupil4.healthtech.dtu.dk	48	126G
pupil5	pupil5.healthtech.dtu.dk	48	126G

Course webpage

- Course program, slides, handouts, exercises etc.
- https://teaching.healthtech.dtu.dk/22126/index.php/Program_2026
- The course page is a repository for you

Discord

- Chat with others during off-hours. Create channels!
- Please use your real name
- <https://discord.gg/mgFJxM3W>

Tips

- Do not memorise definitions
 - understand concepts
- The core lectures are especially crucial
- Do not memorise software names
- Understand what you are doing
 - inspect the input
 - inspect the output
 - play with parameters
- Read the error messages

Learning objectives

- Are you able to:
 - work in group and delegate tasks?
 - set realistic objectives?
 - use the command line?
 - understand the strength and weakness of each tool?
 - explain key steps in a critical manner?

Any Questions?

