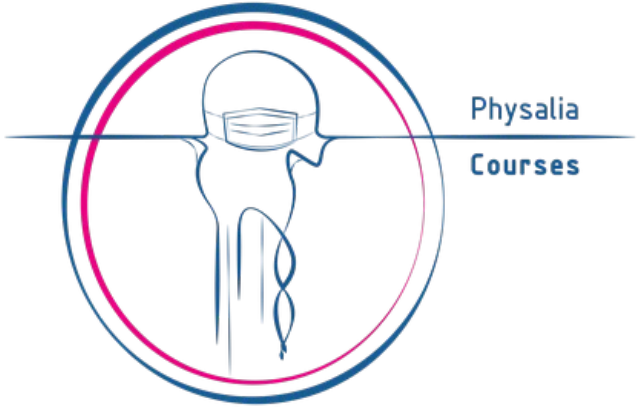



# Course introduction

Population genomic inference from low-coverage whole genome sequencing data

# Course goals

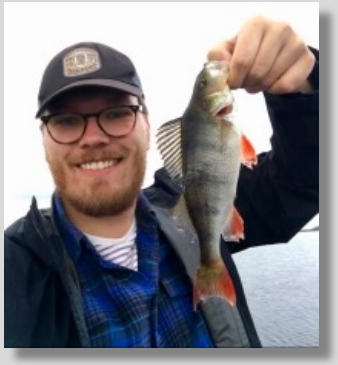
- Understand the power and challenges associated with using low-coverage whole genome sequencing data for population genomic analysis
- Become familiar with all steps involved from sample to inference
- Develop an intuition for the statistical framework implemented in ANGSD and associated programs
- Gain experience with building a bioinformatic pipeline to process low-coverage sequencing data to perform different types of population genomic analyses

# Who we are

Nina Overgaard Therkildsen
Cornell University

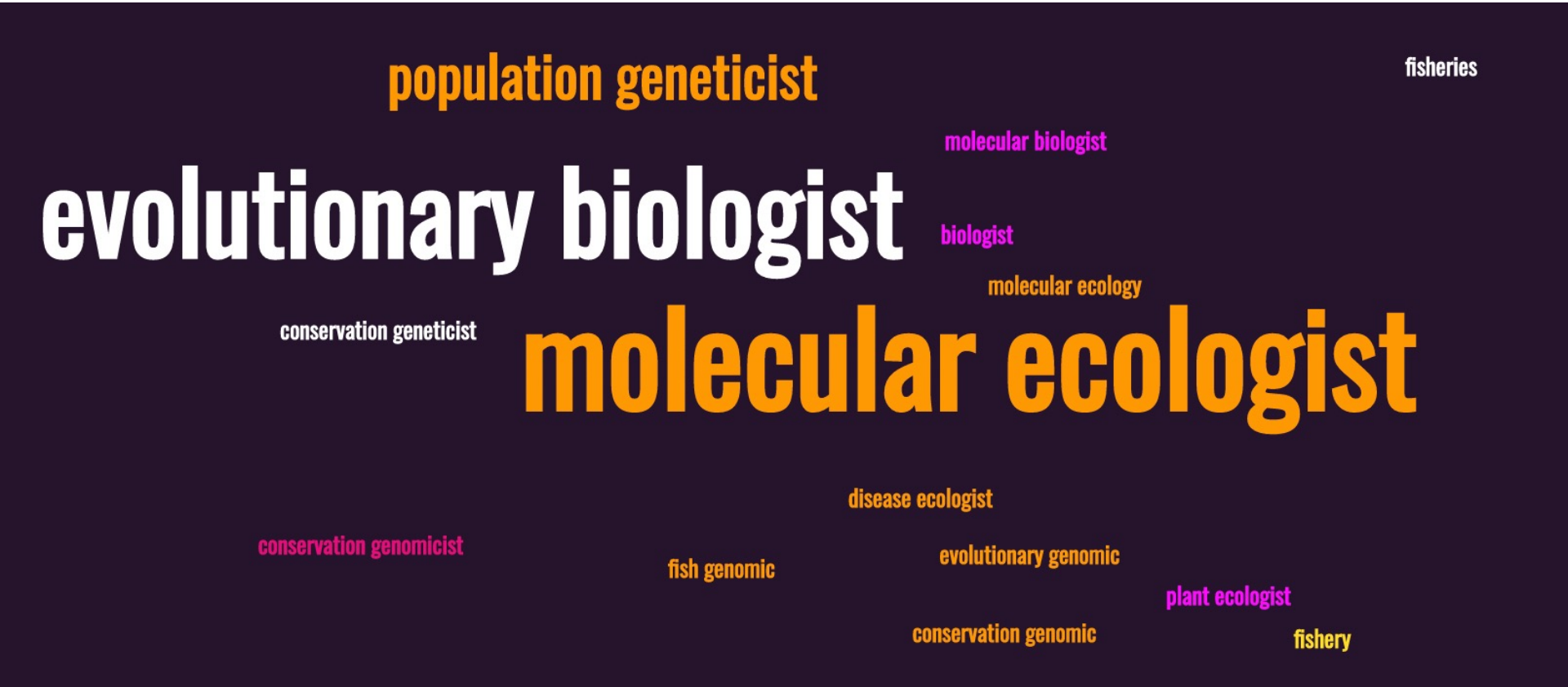
Tyler Linderoth
Michigan State University

Nicolas Lou
UC Berkeley

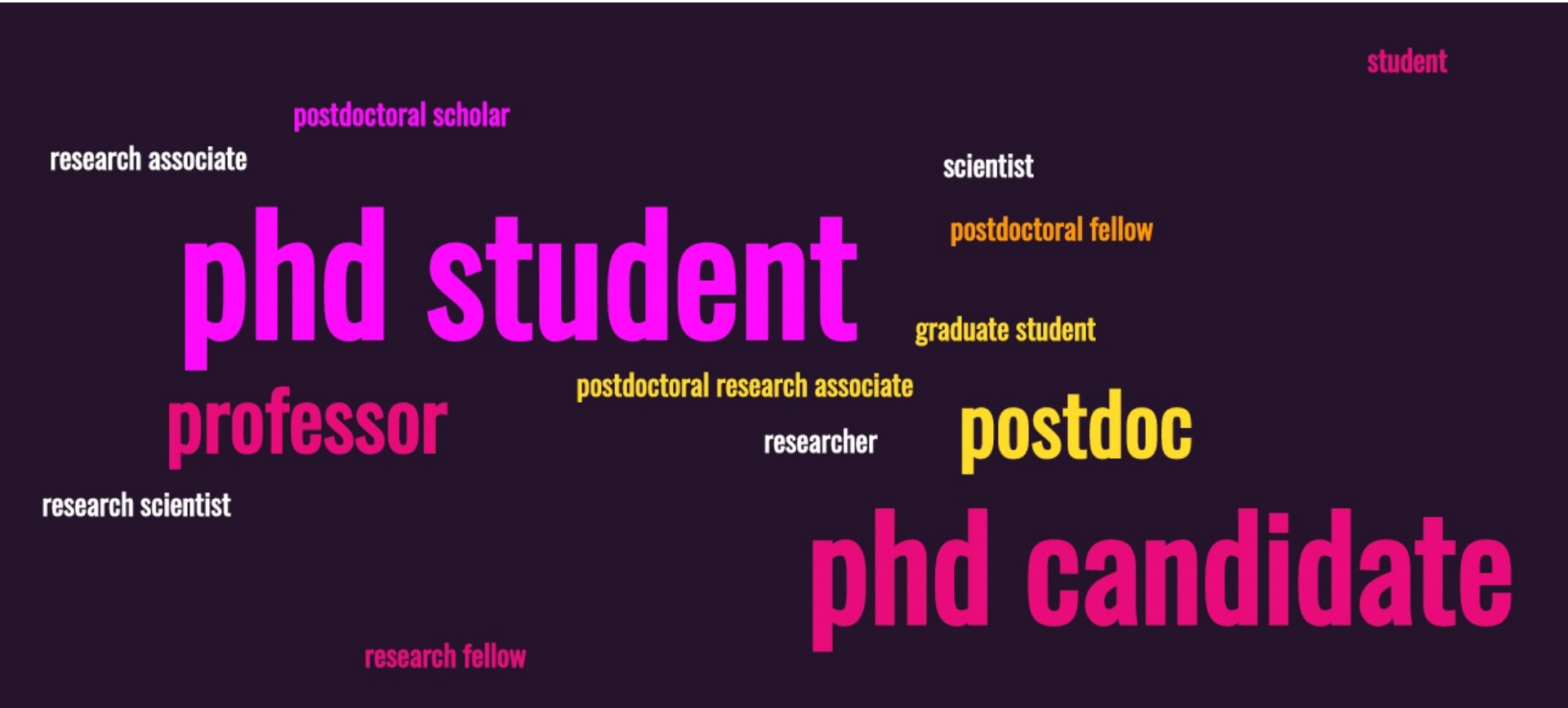


Arne Jacobs
University of Glasgow

# Who you are


population geneticist
fisheries
molecular biologist
evolutionary biologist
biologist
molecular ecology
conservation geneticist
molecular ecologist
disease ecologist
conservation genomicist
fish genomic
evolutionary genomic
plant ecologist
conservation genomic
fishery

# Who you are


student
postdoctoral scholar
research associate
scientist
phd student
postdoctoral fellow
graduate student
postdoctoral research associate
professor
researcher
postdoc
research scientist
phd candidate
research fellow

# Where are you?

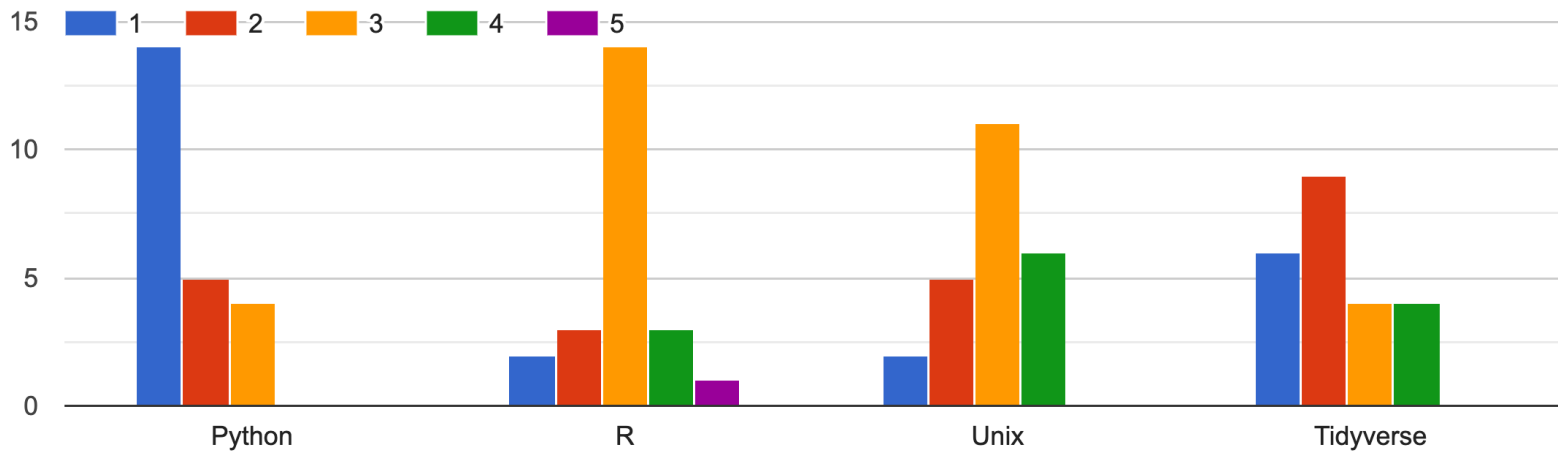
- Please indicate your location on this map https://www.google.com/maps/d/edit?mid=1Q9YlwYz3jvwenA9TUMlaNavSB495h4A&usp=sharing

# Round of introductions

- Please share
  - Your name and current affiliations
  - What kind of organism(s) you work on
  - Why you’re interested in this course

# From the pre-course survey

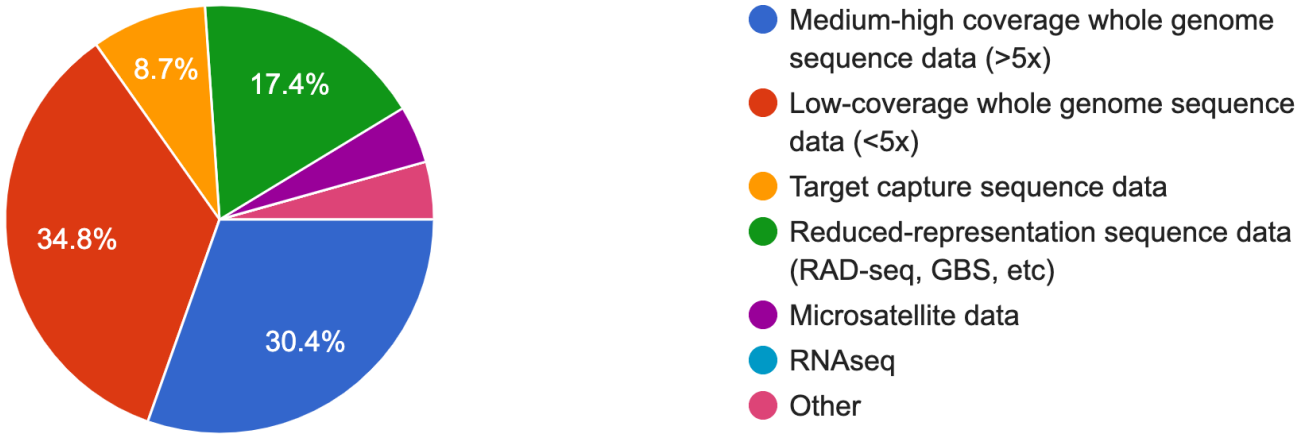
3. Rate your familiarity with the following on a scale of 1 (beginner)-5 (wizard):



# From the pre-course survey

Which of the following data types do you work with

23 responses




Graphic: https://allarewelcomehere.us/

# Code of Conduct

- We are dedicated to providing a **welcoming and supportive environment for everyone**, regardless of background, identity and prior experience. Everyone in this course will be coming from a different place with different experiences and expectations. We will not tolerate any form of language or behavior used to exclude, intimidate, or cause discomfort. This applies to all course participants (instructor, students, guests). In order to foster a positive and professional learning environment, we encourage the following kinds of behaviors

# Behaviors we encourage

- Use welcoming and inclusive language
- Be respectful of different viewpoints and experiences
- Show courtesy and respect towards others
- Help each other - you may well learn something or reinforce your own skills in the process

# Approximate daily schedule

| Berlin time | US eastern | Activity |
|---|---|---|
| 14 – 15.15 | 8 - 9.15 | Session 1 |
| | | BREAK |
| 15.30 – 16.45 | 9.30 -10.45 | Session 2 |
| | | BREAK |
| 17.15 – 18.30 | 11.15 - 12.30 | Session 3 |
| | | BREAK |
| 18.45 - 20 | 12.45 - 2 | Session 4 |

# Course schedule

- Day 1
  - Welcome!
  - Introduction to low-coverage whole genome sequencing
  - From sample to fastq
  - From fastq to bam

- Day 2
  - Recap on exercises from day1
  - Genotype likelihoods
  - SNP calling
  - Allele calling

# Course schedule

- Day 3
  - Linkage disequilibrium
  - Population structure (PCA and admixture analysis)

- Day 4
  - The site frequency spectrum (1d and 2d)
  - Fst and diversity statistics
  - Overview of other applications and future perspective

# Daily practicals

- Will be available in a GitHub repo that you can keep accessing after the course
- Will work in breakout rooms
- Indicate your breakout room preference each day
  - Quiet room (everyone works independently)
  - Semi-quiet room (people mostly work independently, but can ask each other questions)
  - Collaborative room (you work through the exercises together)
- Ask questions!

# Make sure you have access to the server

- If you haven’t logged on already, please do that during one of the breaks today so we can help or troubleshoot if there are issues

# What we will not have time to cover

- Genotype – phenotype association
- Imputation
- Methods specific to ancient DNA
- Structural variant detection

# Course goals

- Understand the power and challenges associated with using low-coverage whole genome sequencing data for population genomic analysis
- Become familiar with all steps involved from sample to inference
- Develop an intuition for the statistical framework implemented in ANGSD and associated programs
- Gain experience with building a bioinformatic pipeline to process low-coverage sequencing data to perform different types of population genomic analyses