

DTU





**DTU Health Technology
Bioinformatics**

**22126: Next Generation Sequencing Analysis
DTU - January 2024
Gabriel Renaud**

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Who am I?

- PhD in Bioinformatics from Max Planck Institute for Evolutionary Anthropology in Leipzig
- Postdoc at KU
- Associate Professor at DTU in Dec. 2019
- Worked since 2006 with NGS
- slow response: gabre [at] dtu [dot] dk
- fast response: gabriel [dot] reno [at] gmail [dot] com

Who am I?

How to contact me?

- slow response: gabre [at] dtu [dot] dk
- medium response: gabriel [dot] reno [at] gmail [dot] com
- fastest response: Discord

Conflict of interest: none, I do not own any stocks or consulting for
any sequencing company

Who am I?

What keeps me busy:

- Methods for NGS analysis
- Ancient DNA and modern samples
- Large sets of genotypes
- Pangenomes

Looking to do a special project/masters' project dealing with NGS, email me!

Who are we?

- Organizer:
 - Gabriel Renaud
 - Kristoffer Vitting-Seerup
 - Ole Lund
 - Frederikke Pedersen
 - Astrid Saksager
 - Grigorii Nos
 - DTU Bioinformatics
 - Peter Wad Sackett
- DTU Food
 - Pimlapas Leekitecharoenphon (Shinny)
- Copenhagen University:
 - Martin Sikora

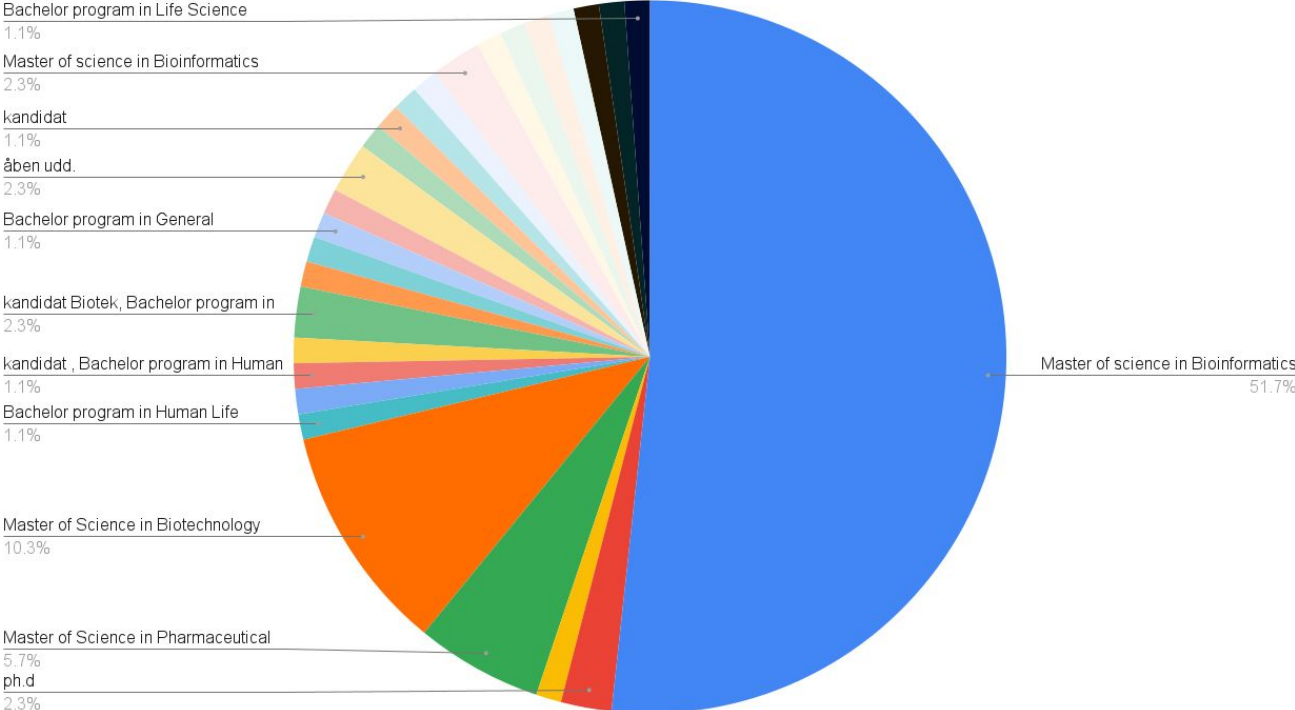
Main teaching assistants

Astrid Saksager
Grigorii Nos

Who are you?

January 2024

Background



Feedback

- My 5th time! 3rd time in person.
- We are still improving
- It is very difficult to keep up with new tech...
- NGS is very broad now, no one masters everything
- Please give us feedback !
 - Please do the evaluation at DTU Inside



Why are we here?

nature communications

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Article | [Open access](#) | [Published: 05 January 2023](#)

Germline *TP53* mutations undergo copy number gain years prior to tumor diagnosis

[Nicholas Light](#), [Mehdi Layeghifard](#), [Ayush Attery](#), [Vallijah Subasri](#), [Matthew Zatzman](#), [Nathaniel D. Anderson](#), [Rupal Hatkar](#), [Sasha Blay](#), [David Chen](#), [Ana Novokmet](#), [Fabio Fuligni](#), [James Tran](#), [Richard de Borja](#), [Himanshi Agarwal](#), [Larissa Waldman](#), [Lisa M. Abegglen](#), [Daniel Albertson](#), [Jonathan L. Finlay](#), [Jordan R. Hansford](#), [Sam Behjati](#), [Anita Villani](#), [Moritz Gerstung](#), [Ludmil B. Alexandrov](#), [Gino R. Somers](#), [Joshua D. Schiffman](#), [Varda Rotter](#), [David Malkin](#)  & [Adam Shlien](#)  [— Show fewer authors](#)

[Nature Communications](#) **14**, Article number: 77 (2023) | [Cite this article](#)

5754 Accesses | 3 Citations | 198 Altmetric | [Metrics](#)

Findings:

In people with Li-Fraumeni syndrome (a genetic condition that increases cancer risk), genetic mutations, occur early and are common in tumors, many years before cancer is diagnosed.

Published: 03 Jan 2023

Why are we here?

FASTQ files were aligned to the hg19 reference genome using BWA-mem (v0.78). Duplicates were marked with Picard (v1.1.08), and base recalibration and realignment was performed using GATK (v2.8.1). Merged in silico bulk sequencing BAMs were generated by processing together all WGS FASTQ files from multiple regions to generate a single BAM file for each tumor. BAM files generated from individual tumor regions as well as in silico merged BAMs were processed for variant calling and filtering as described below. Substitution and indel calls were made using MuTect2 from GATK (v3.4.0). Structural variants (deletions, duplications, inversions and translocations) were called using delly²⁹ with a minimum of 4 discordant reads in the tumor required to call each SV (v0.7.1). Clonal and subclonal CNVs were called using Battenberg v3.2.2. All mutation calls (SNVs and SVs) were filtered as previously described using in house pipelines³⁰. To reiterate, we required a minimum depth of 10X in the tumor and normal with 0 reads supporting the variant in the matched normal.

Why are we here?

“Around 2 a.m. on Jan. 5, after working over 40 hours straight, Dr. Zhang and his team at the Shanghai Public Health Clinical Center sequenced the unknown virus on the NovaSeq™ 6000 System. They published its genome on **Jan. 10th 2020.**”

<https://www.illumina.com/company/news-center/blog/2020-in-genomics.html>



Yong-Zhen Zhang

Why are we here?

“... Moderna’s mRNA-1273, which reported a 94.5 percent efficacy rate on November 16, had been designed by **January 13th 2020**. This was just **two days** after the genetic sequence had been made public

...

It was completed [...] **more than a week before** the first confirmed coronavirus case in the United States.”



Yong-Zhen Zhang

<https://nymag.com/intelligencer/2020/12/moderna-covid-19-vaccine-design.html>

Not a wet lab course...



...it's a computational one



Tips

Tip: Do not memorize the name of the tools/procedure, they come and go



Tips

Tip: Understand the problem and how various tools work

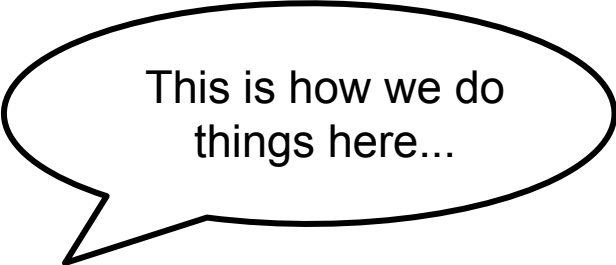


Tips for NGS in general

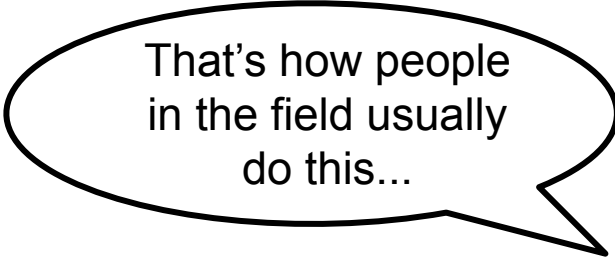
- New tools or procedures get released all the time
- The best tool/format/pipeline in 2024 may not be the best in 2034
- Understand how they work, in which cases they perform well

Tips for NGS in general

- Read benchmarking papers and reviews
- Beware of:

A black-outlined speech bubble pointing towards the bottom-left.

This is how we do things here...

A black-outlined speech bubble pointing towards the bottom-right.

That's how people in the field usually do this...

The shell terminal

```
gabriele@desktop: ~/mp  
gabriele@desktop:~/mp$ sudo view MD021.bam | head -n 20  
00034:78:HHNH88BXX:1:1124:12149:10 10 mref 1 250  
00034:78:HHNH88BXX:1:1124:12149:10 10 mref 1 250  
00034:78:HHNH88BXX:1:1124:12149:10 10 mref 1 250  
00034:78:HHNH88BXX:1:1124:12149:10 10 mref 1 250  
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00034:78:HHNH88BXX:1:1124:12149:10 10 mref 1 250  
00034:78:HHNH88BXX:1:1124:12149:10 10 mref 1 250
```

- Available on various platforms



Mac OS

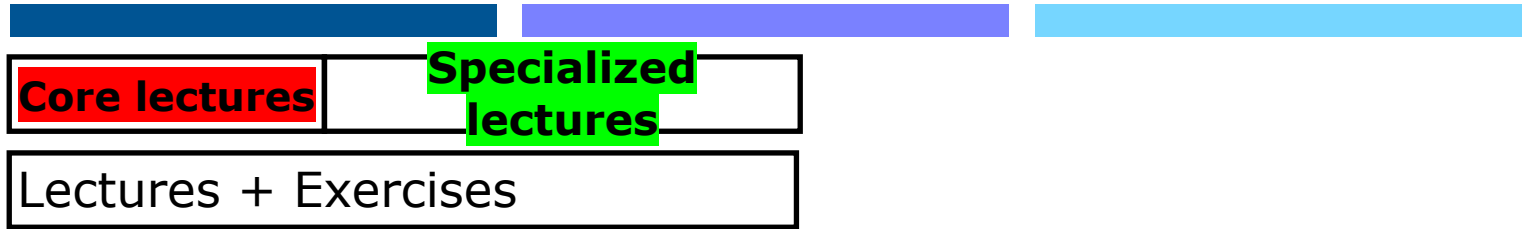


Why the shell terminal

- They can be pipelined, i.e. analyzing 100 files in windowed mode is a pain ...
- Alternative approaches: Galaxy, CLC-wokbench, Geneious

Course structure

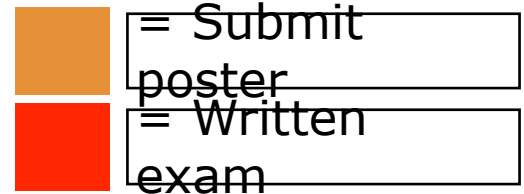
- 3 weeks, 2 tracks



Date: 2n
d

10th

18th 19th



Course breakdown I

- Tuesday 2nd January
 - Introduction NGS technology
 - Unix and first look at data
- Wednesday 3rd January
 - Data basics & preprocessing
 - Alignment
 - Reminder about Bayesian

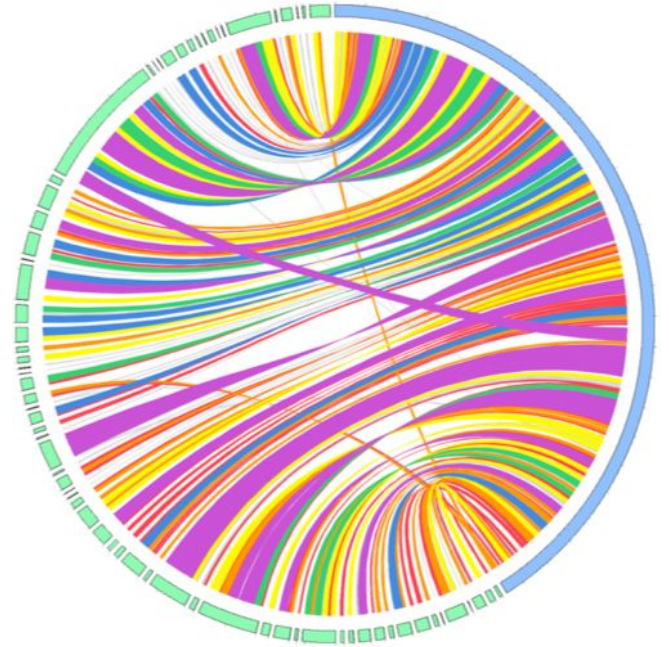
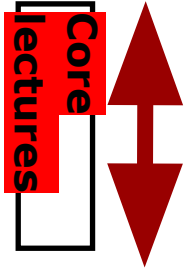


Core
lectures

Course breakdown II

- Thursday 4th January
 - Alignment processing
 - Genotyping
 - *de novo* assembly

- Friday 5th January
 - Ancient DNA
 - RNASeq



Course breakdown III

- Monday 8th January
 - Long read technologies
 - Recap test (after lunch)
 - Finish exercises
- Tuesday 9th January
 - Metagenomics
- Wednesday 10th January
 - Genomic Epidemiology
 - Group formation project

Course breakdown IV

- Thursday 11th January
 - Cancer-seq
 - Project work
 - Individual group talks
- Friday, 12th January
 - Project work
- Monday 13th - Thursday 17th
 - Project work
- Thursday 18th
 - Submit 1 page poster
- Friday 19th
 - Written Exam



Projects

- Try to analyze an empirical dataset and present results on poster
- 4-6 pr. group
- You can find a dataset on SRA/ENA
- You can use your own data if everyone in the group agrees **and** it can be presented on a poster
- Do **not** analyze very large datasets (time, resources)
- 2024: You have 2 days, a weekend and a week to finish



download+align data here!!

Points to remember

- **Understand** principles of the analysis
- The exercises will be useful for your projects and hopefully also later
- You don't need to do all the exercises but the ones from the core lectures are important
- Have an exercise buddy and do them as a team, preferably on each individuals laptop so everyone gets to learn the command-line
- Please **just ask** questions at any time !

Points to remember

- You get the solutions for the exercises but **do not copy-paste!!**
- You will not get to copy-paste for the project

Cloud computing

- Pupil cluster
- We have 3 nodes
 - pupil1 40 cores 252G RAM
 - pupil2 24 cores 110G RAM
 - pupil3 24 cores 94G RAM
- Be careful with disk space
- Limited computational power
- If you want software installed, ask me!



Poster

- Each group will create a poster
- The goal of the project is:
 - Do not memorize, **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 18th

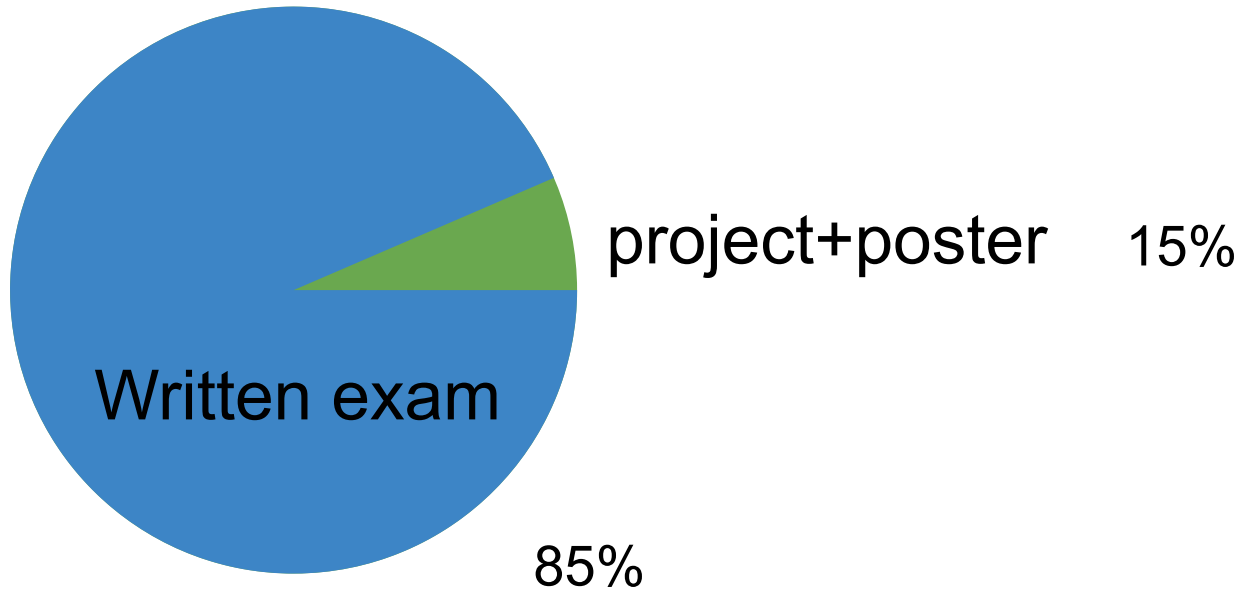
Written Exam

- **You cannot write the exam if you have not submitted the poster**
- Multiple choice exam
- Focuses on the core lectures
- Will have 1 very basic question per specialized lecture

Tips for this class

- Do not memorize definitions, **understand** concepts
- The core lectures are especially crucial
- The final exam is an oral one which will evaluate your understanding, not whether you can parroting definitions
- Do the exercises (esp. the first 3 days).
- Understand what you are doing:
 - inspect the input
 - inspect the output
 - play with parameters

Marking scheme



Disclaimer

- Sequencing technologies change very rapidly!
- We will dive into many areas and you will not learn to master everything
- However, we hope that the building blocks we provide will allow you to see new opportunities

Disclaimer

- We will talk about old techs, working with NGS means working with older datasets from previous studies



source: Dall-E

Be adventurous!

You do not have the ability to do anything
destructive

The worst that can happen is that you lose
your own data

Course webpage

- Course program, slides, handouts, exercises etc.
- <http://teaching.healthtech.dtu.dk/22126>
- We want the course page to be a repository for you!

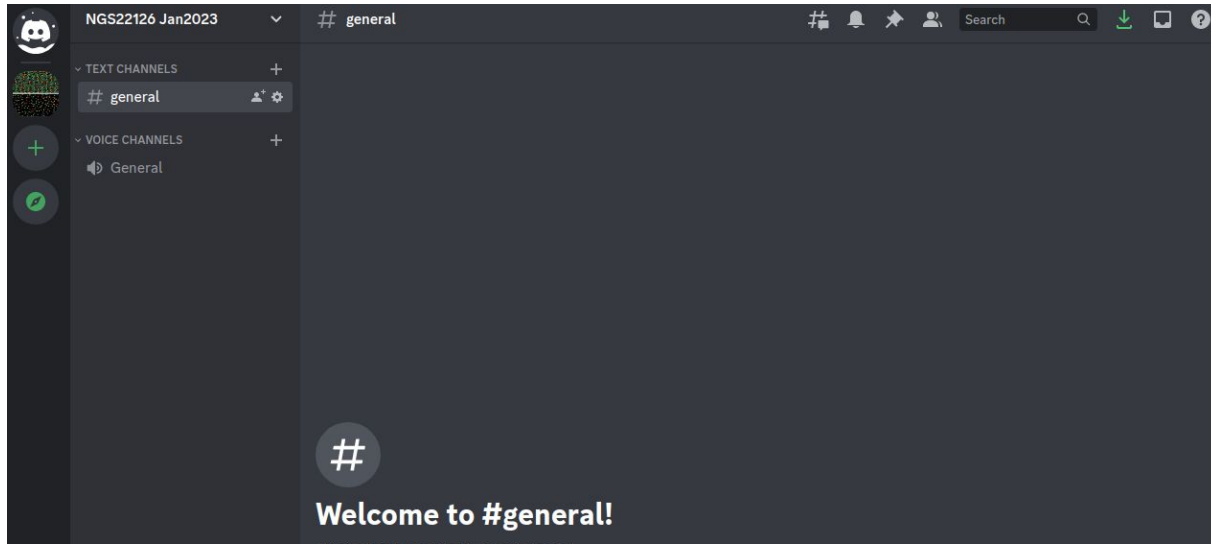
Discord

- Chat with others during off-hours. Create channels!
- Please use your real name:

Jan Jansen



n00b_0wner_18



Reading + wifi

- There are no textbooks for the course, it changes too rapidly
- Wireless networks
 - Use “dtu” and your dtu/campusnet login to get access to wireless
 - Eduroam

Pre-test

- Test your knowledge before we start
- Not used for grading or exam
- Used to understand where you are and what you need