

DTU





**DTU Health Technology  
Bioinformatics**

# Metagenomics and Microbiome Analysis: Introduction to course

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# Menu

- Who are we?
- What is this course about?
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- Exam and evaluation
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- Pre-test

# Course responsible

Gisle Vestergaard

Associate Professor, Section of Bioinformatics



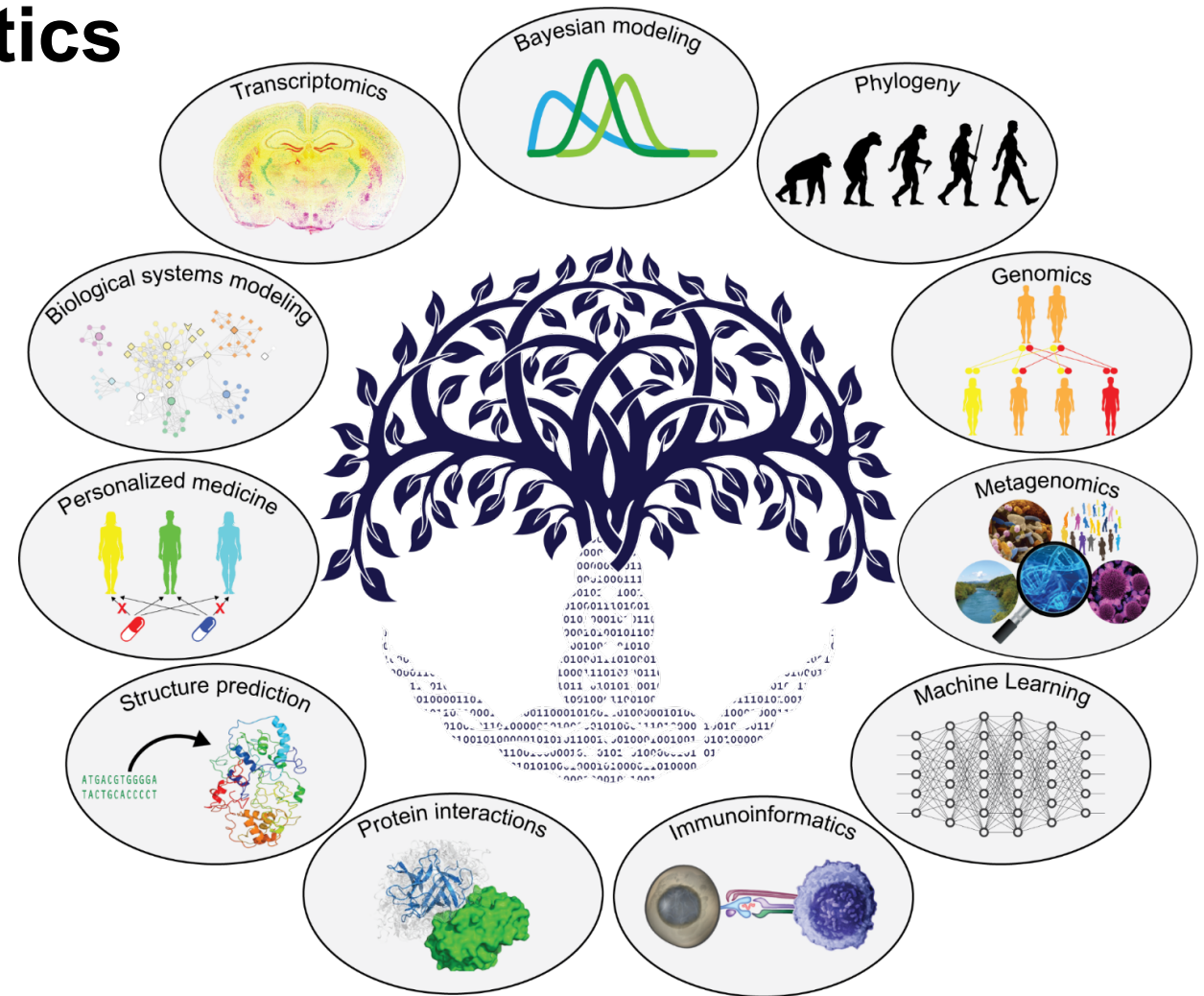
Marlene Danner Dalgaard

Senior researcher, Head of DTU Multi-AssayCore (DMAC)



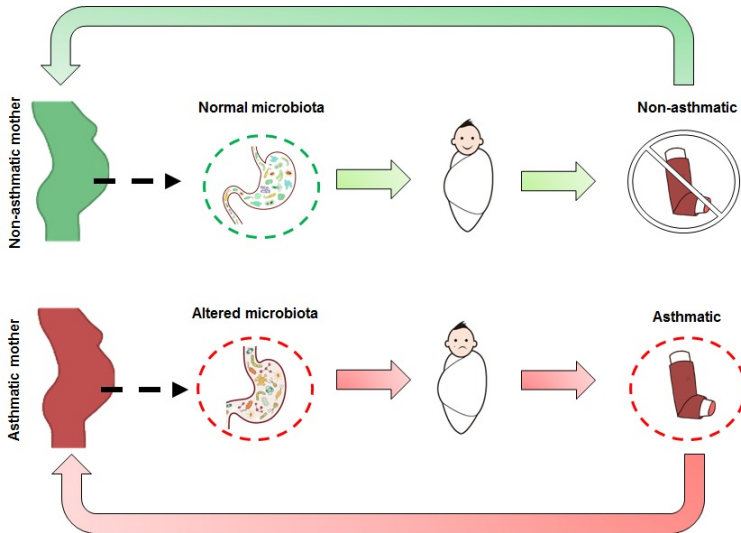
# Section of Bioinformatics

Solving biological problems using a wide variety of state-of-the-art informatics solutions



# Who am I?

- PhD in Biochemistry from Copenhagen University
- Postdoc at Helmholtz Zentrum München on a Humboldt Research Fellowship
- Assistant Professor at Copenhagen University in 2018
- Associate Professor at DTU in 2019
- Taught NGS in München and at Copenhagen University
- Head of studies for the MSc degree in Bioinformatics and Systems Biology



# Who are we?

- MSc in Molecular Biology and Chemistry
- PhD in Human Biology: Testicular Cancer
- Senior Researcher, Head of DMAC: Multiassay Core Facility
- 6th year course responsible



# Who are you?

- 30 Participants
- Master students
  - Bioinformatics and Systems Biology
  - Biotechnology
  - Quantitative biology
  - Mathematical Modelling and Computation
- Quite a lot of externals

WHO  
ARE  
YOU?



# Feedback

- Sixth time course is running
- Second time I am course responsible
- We are still improving
- Please give us feedback !
  - Please do the evaluation at DTU Inside



# Learning objectives

- Explain the concept of metagenomics and its applications opposed to single genomics
- Discuss a possible metagenomics experimental design; from sampling to sequencing
- Explain basic metagenomic data generation
- Explain the advantages and limitations of microbiome data
- Perform basic metagenomics analysis
- Explain the basic principles of microbiome ecology
- Explain the basic principles of quantitative count based data analysis
- Perform basic quantitative count based data analysis
- Perform calculations of basic ecological measures
- Present project work orally and on a poster

# Course material

- No text book required
- Material will be distributed during the course on DTU Inside and the [homepage](#)
- You will also find recommended reading and supplementary information on the homepage



# Online learning, recommended reading and supplementary information

Will NOT be part of the curriculum

Great recent overview paper: "Best practices for analysing microbiomes"

<https://www.nature.com/articles/s41579-018-0029-9.pdf>

Coursera course: "Gut Check: Exploring Your Microbiome"

<https://www.coursera.org/learn/microbiome>

- Videos, reading and quizzes





# YOUR microbial metagenomic study

- Today design this years microbial metagenomic study
- Limitations have to be considered: time limitation, effect, cohort size, feasibility
- Collect samples until next weeks laboratory exercise
- Previous years this has always been a students stool used for an intervention study EXCEPT last year!

# Wet lab exercise

- 2 days of laboratory work at Room 006 in Building 208 and Laboratory Room 001 also in Building 208
- Sampling, purification and extraction of DNA, QC
- Library preparation and sequencing
- Don't worry if you lack wet-lab experience!!



# Exams & grading

- Group work with individual exams
  - Each group of 3-4 people will present their poster for about 15 minutes
  - Each member of the group will be examined individually about course objectives and the project for 5-15 minutes
- 2 hour written exam without aids





# Oral exam / Group work

- Group work with individual exams
  - Each group of 3-4 people will present their poster for about 15 minutes
  - Each member of the group will be examined individually about course objectives and the project for 5-15 minutes
- You will have the chance to assign the groups of 3-4 people
- Questions?

≈50%

# Written exam

- 2 hours written exam without help
- Questions?

≈ 50%

# Deliverables

- See program webpage for overview and dates
- Quizzes and assignments are not graded but important when planning recap sessions
- Questions?

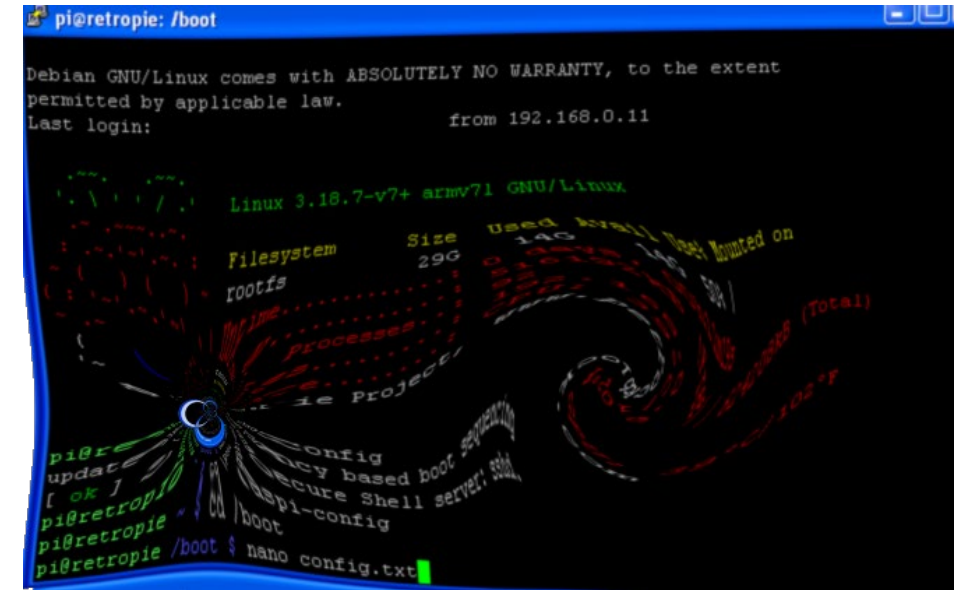
Deliverable	Date	Description
I	02/09-2020	Class Room presentation in groups: Intervention study
II	09/09-2020	Hand-in: Lab protocol Powersoil Kit
III	16/09-2020	Hand-in: Lab protocol Nextflex DNaseq kit
IV	28/09-2020	Hand-in: Sequencing technology report
V	30/09-2020	Class Room Quiz: NGS I
VI	28/10-2020	Class Room Quiz: NGS I+II & Quantitative metagenomics I+II

# Cloud computing

- The course has moved to the Cloud!
- Danish National Supercomputer for Life Science (Computerome) located at DTU Risø
- 16048 cores, 92 Tb RAM an 3Pb storage
- We have 2 nodes via virtual machines
  - Each has +20 cores and 128 Gb RAM



# Why shell terminal?



```
pi@retropie: /boot
Debian GNU/Linux comes with ABSOLUTELY NO WARRANTY, to the extent
permitted by applicable law.
Last login:                from 192.168.0.11

Linux 3.18.7-v7+ armv7l GNU/Linux
Filesystem      Size  Used  Avail  Mounted on
rootfs          29G   14G   14G
Processes
ie Project
config
secure based boot server
aspi-config
/boot
pi@retropie /boot $ nano config.txt
```

- The command-line is not as dangerous as it looks...trust us!
- Almost all tools for NGS analysis are command line only
- Generally more efficient/flexible, you can play around with the tools/data
- They can be pipelined, ie. analyzing 100 files in windowed mode is a pain ...
- Alternative approaches: Galaxy, CLC-workbench, Geneious

# Course essentials

- Course homepage:
  - [https://teaching.healthtech.dtu.dk/22136/index.php/22136:Course\\_plan\\_autumn\\_2020](https://teaching.healthtech.dtu.dk/22136/index.php/22136:Course_plan_autumn_2020)
- Teaching Wednesdays in Room 162, Building 210, EXCEPT:
  - Week 2 & 3 wet lab exercises at Room 162 in Building 210 and Laboratory Room 001 in Building 208
- Form groups for project work to begin 21.10.2020
- Poster exam 02.12.2020
- Written exam 18.12.2020

# Course advice

- Use the cloud servers on other days than Wednesday
- Learn principles of how to analyse metagenomics data
- Use principles for your project
  - This includes formulating a project that can be answered with the time, tools and data you have available
- Use the cloud servers for group analysis and coordinate data heavy analysis across all groups (no need for all groups to perform assembly of the same data)
- Form groups with people from other backgrounds...diversity IS an advantage
- Use the cloud servers on other days than Wednesday
- ...and again please feel free to answer questions and give us feedback!!

# Course breakdown – Week 1



- Course introduction
- Pre-test
- General introduction to metagenomics
- Introduction to course study design
- Agreement on course study...YOUR study!



# Course breakdown – Week 2 & 3

W1

W2-W3

W4

W9

W9-W13

- Sample purification
- DNA isolation
- Quality control
- Fragmentation
- Create sequencing library



# Course breakdown – Week 4

W1

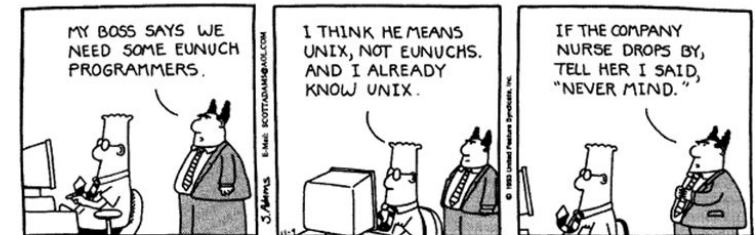
W2-W3

W4

W9

W9-W13

- Introduction to UNIX
- Log on to Computerome
- Introduction to Next-Generation Sequencing
- Next-Generation Sequencing basics



# Course breakdown – Week 5-9



- R
- 16s rRNA analysis
- Quantitative metagenomics
- De novo assembly & Binning
- Human gut microbiome
- Association studies
- Group formation and project formulation

## Course breakdown – Week 9-13



- Group work on projects

# Course breakdown – Exams



- Oral presentation of project posters
  - Group work, 3-4 per group, and present results on a poster
  - Try to form diverse groups in terms of skills
  - Analyse your own data!
  - Supplement with existing data (e.g. MetaHIT, SRA...)
  - Don't run too large datasets (computational and time restrictions)

# Pre-test

- 10 min individually
- Discuss in plenum and summarize
- Not used for grading, it will give us an idea of your level

