

Computational Science: Bioinformatics

Research Group for Biomedical Informatics & Centre for Bioinformatics

16 August 2022

Torbjørn Rognes
Department of Informatics, UiO
torognes@ifi.uio.no



UiO • University of Oslo

Computational Science at IFI

Study programme (master):

- Computational Science (CS)

Study programme options at IFI:

- CS: Bioinformatics
- CS: Imaging and Biomedical Computing

ML Research groups:

- BMI – Biomedical informatics
(Biomedisinsk informatikk)
- DSB – Digital Signal Processing and Image Analysis
(Digital signalbehandling og bildeanalyse)

Centre:

- SBI – Centre for Bioinformatics

Scientific staff at BMI & SBI

Please contact any of the scientific staff if you are interested in a master thesis within bioinformatics.



**Torbjørn
Rognes**
BMI leader &
Professor



**Ole Christian
Lingjærde**
Professor



**Geir Kjetil
Sandve**
Professor



**Rolf
Skotheim**
Professor
(20%)



**Knut
Liestøl**
Professor
emeritus



**Eivind
Hovig**
SBI leader &
Professor
(70%)



**Trine B.
Rounge**
Assoc. prof
SBI



**Lex
Nederbragt**
Senior lecturer
SBI (30%)



**Jonas
Paulsen**
Assoc. prof
SBI



**Oleksandr
Frei**
Assoc. prof
SBI



**Jon K.
Lærdahl**
Assoc. prof
SBI (20%)

Postdocs, PhD students & Engineers



Chakravarthi
Kanduri



Ivar
Grytten



Knut D.
Rand



Enrico
Riccardi



Paula
Istvan



Bayram Cevdet
Akdeniz



Christian D.
Bope



Jeanne
Chèneby



Einar
Birkeland



Jean-Marc
Costanzi



Milena
Pavlovic



Cecile
Bucher-Johansen



Lonneke
Scheffer



Sumana
Kalyanasundaram



Ghadi S.
Al Hajj



Jonas Meier
Strømme



Ekaterina
Avershina



Maja
Jacobsen



Sveinung
Gundersen



Morten
Johansen



Nazeefa
Fatima



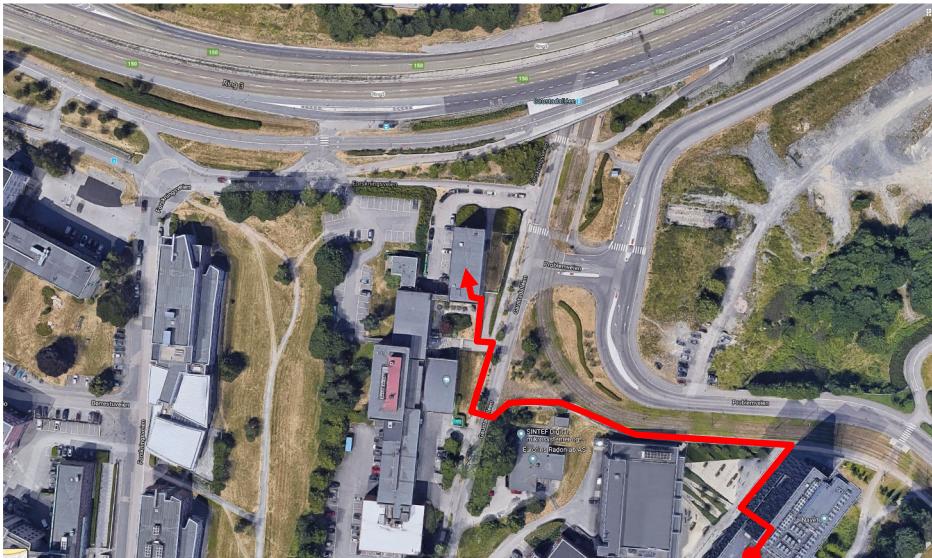
Jushua
Baskaran



Lev
Mozhaev

Where are we located?

Floors 1 and 2 in the former NEMKO building, Gaustadalléen 30, D



BMI/SBI

What is bioinformatics?

An interdisciplinary subject:

Computer science/maths/statistics + biology/medicine

Definition: Bioinformatics is the development and use of computational and mathematical methods to gather, process and interpret molecular biological data.

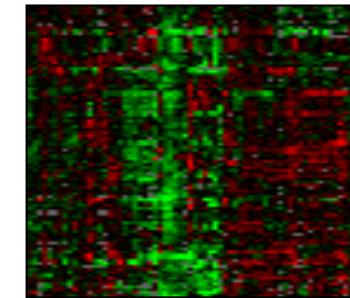
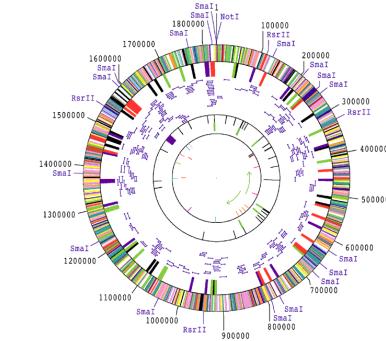
Aim of research: To increase our understanding of biological mechanisms while developing better theories and methods in computer science and statistics.

Methods: Machine learning, statistics, graphs, algorithms, visualisation, parallelisation, efficient data structures, ...

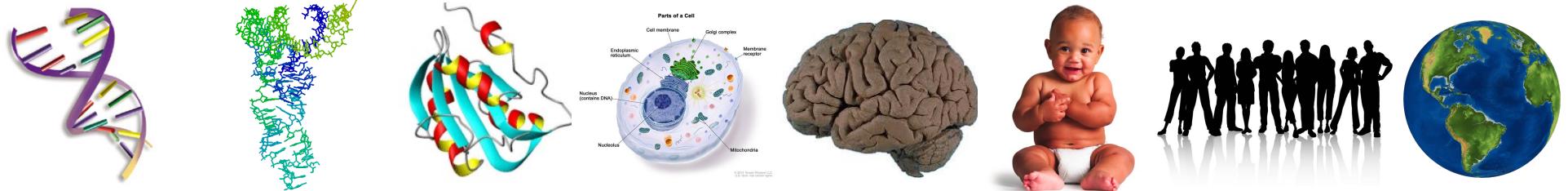
Data: Genomes, genes, DNA, RNA, proteins, immune receptors, gene expression levels, 3D molecular structures, cells, organisms, populations, gene variants and mutations, patient info, ...

P13051|UNG_HUMAN/1-313
P12887|UNG_YEAST/1-359
P12295|UNG_ECOLI/1-229
P16769|UL114_HCMVA/1-250

144 K D V K V V I L G O D P Y H G P N Q A H G L C F S V Q R P V P P P P S L E N I Y K E L S T D E D F V H 195
152 N K V K V V I L G O D P Y H G P N Q A H G L A F S V K P P T P A P P S L K N I Y K E L K Q E Y P D F V E 203
54 G D V K V V I L G O D P Y H G P G Q A H G L A F S V R P G I A I P P S L L N M Y K E L E N T I P G F T R 105
81 E Q V R V V I V G O D P Y C D - G S A S G L A F G T L A G R P P P P S L N N V F R E L A R T V D G F Q R 131



Bioinformatics at many levels



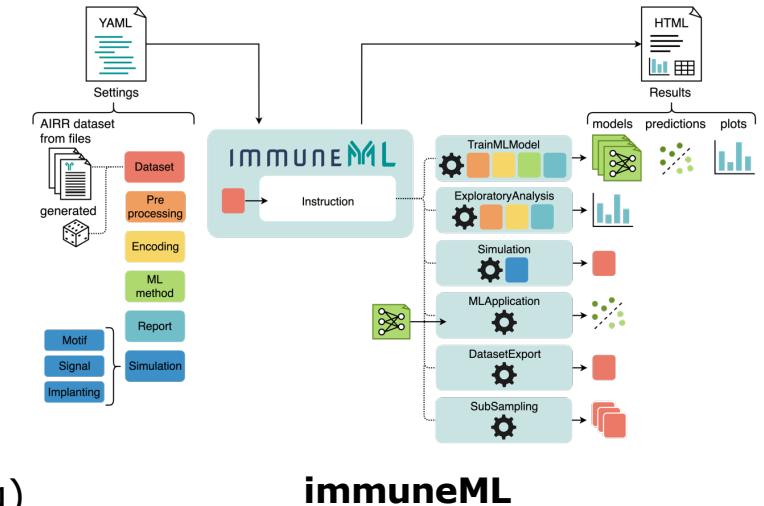
DNA	RNA	Protein	Cell	Organ	Individual	Population	Biosphere
Genomics	Transcript-omics	Proteomics	System biology	Neuro-informatics	Precision medicine	Population genetics	Metagenomics
Genome assembly	RNomics	Structural biology	Cell simulation	Organ modelling/simulation	Variant detection	Epidemiology	Evolutionary biology
Genefinding	Microarrays	Drug design	Metabolism studies				Phylogenomics
Annotation	RNA-folding	MS analysis					
"Read mapping"	RNA-seq	Binding site analysis		Meta-genomics			
ChIP-Seq	Structure biology	Interaction networks		Cancer genomics			

Main research areas of BMI/SBI

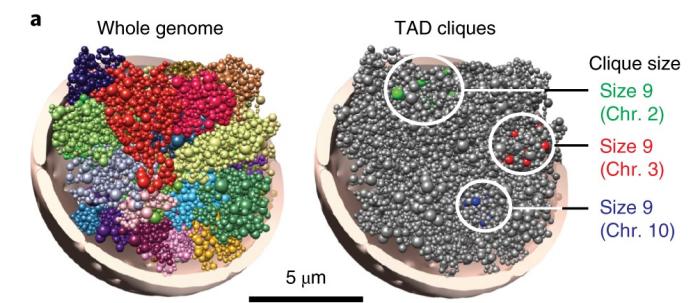
Advanced use and development of new methods and tools in computer science and statistics to analyse molecular data

Research projects

- ML for Immune receptor repertoire analysis + Genome statistics and visualisation (GK Sandve)
- Cancer genomics (OC Lingjærde)
- Cancer sequencing & Precision medicine (E Hovig)
- Microbiome bioinformatics and efficient sequence comparison (T Rognes)
- Microbiomes and cancer (T Rounge)
- Modelling of 3D organisation of DNA in the nucleus (J Paulsen)
- Genome heterogeneity in cancer (RI Skotheim)
- Genome assembly and representation (AJ Nederbragt)
- Genetics of Psychiatric Disorders (O Frei)
- Medical statistics in cancer biology (K Liestøl)



immuneML



DNA 3D organisation

Major collaborators and partners

- Oslo University Hospital (adjunct positions)
- OsloMet
- Akershus University Hospital (Ahus)
- Cancer Registry of Norway
- Big Insight (SFI)
- KG Jebsen Celiac Disease Research Centre
- Centre for Computational Inference in Evolutionary Life Science (CELS) ("Endringsmiljø" / Strategic Research Initiative)
- PharmaTox ("Endringsmiljø" / Strategic Research Initiative)



CS Programme structure

4. semester	Master's thesis	Master's thesis	Master's thesis	
3. semester	Master's thesis	Master's thesis	Master's thesis	Alt: 10 credits elective course
2. semester	<u>IN4200 – High-Performance Computing and Numerical Projects /</u> Mandatory course	Elective course	Elective course	Alt: 10 credits master thesis
1. semester	<u>FYS-STK4155 – Applied Data Analysis and Machine Learning /</u> Mandatory course + HSE courses	<u>MAT4110 – Introduction to Numerical Analysis /</u> Elective course	Elective course	
	10 ECTS credits	10 ECTS credits	10 ECTS credits	

Mandatory, 2 out of these 3 courses:

- IN4200 – High-Performance Computing and Numerical Projects
- FYS-STK4155 – Applied Data Analysis and Machine Learning
- MAT4110 – Introduction to Numerical Analysis

Recommended elective courses

CS: Bioinformatics

- IN4030 – Introduction to bioinformatics (spring)
- IN4050 – Introduction to artificial intelligence and machine learning (spring)
Be aware of 3 credits overlap between FYS-STK4155 and IN4050, usually solved by a small special curriculum.
- IN-BIOS5000 – Genome Sequencing Technologies, Assembly, Variant Calling and Statistical Genomics (autumn 2022)
- BIOS-IN5410 – Bioinformatics for Molecular Biology (autumn)

Other relevant courses

- IN4020 – Database systems (spring)
- IN4110 – Problem solving with high level languages (autumn)
- IN4120 – Search technology (autumn)
- IN5050 – Programming Heterogeneous Multi-Core Architectures (spring)
- IN5320 – Development in Platform Ecosystems (autumn)
- IN5400 – Machine Learning for Image Analysis (spring)
- IN5490 – Advanced Topics in Artificial Intelligence for Intelligent Systems (autumn)
- IN-STK5000 – Adaptive methods for data-based decision making (autumn)
- BIOS-IN5010 – Computational physiology (summer)
- STK4051 Computational Statistics (spring)
- STK-IN4300 – Statistical Learning Methods in Data Science (autumn)
- TEK5020 – Pattern recognition (autumn)
- MEDFL5155 – Introduction to statistics and bioinformatics for the analysis of large-scale biological data (autumn, 5 credits)

Please see the Centre for Bioinformatics' studies page:

<https://www.mn.uio.no/sbi/english/studies/>

Master thesis at BMI/SBI

- Look for available master projects on website:
<https://www.mn.uio.no/ifi/english/research/groups/bmi/master-projects/>
- Presentation of new projects in September/October
- Contact potential supervisors
- Usually 60 credits (0+10+20+30 credits in each semester)
- Make contact early!

Deadlines:

- 1 December 2022: Study plan, select project and supervisor
- 1 June 2023: Essay
- 15 May 2024: Master thesis

Master theses submitted 2020-2022

- Tool to remove specific organisms from microbiome sequencing data (2022)
- A Web Application for MirMachine, a MicroRNA Annotation Tool (2022)
- An assessment of methods for determining and visualizing differential Hi-C contact maps (2022)
- Developing a Toolset for 3D Genome Visualisation and Analysis (2022)
- Comparing Artificial Neural Networks and Microbial Genome Representation Methods for Taxonomic Classification (2021)
- Developing a pipeline for deep analysis of cancer causing genes in the gut microbiome (2021)
- Interpretability of convolutional neural networks when applied to receptor sequence data (2020)
- Algorithms for exploring heterogeneity in prostate cancer patients from RNA-seq data (2020)

Buddy

- Behnoosh Ashrafi
- behnoosh.ashrafi@fys.uio.no
- Buddy for all CS-students at IFI (both CS:Bioinformatics & CS:Imaging and biomedical computing)
- She started as a student at CS:Bioinformatics 1 year ago.

