

# **Camous Moslemi**

Bioinformatics Molecular Biology Computer Science

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# **Personality**



# Programming

C/C++ \*\*\*\* Python \*\*\*\* Java \*\*\*\* BASH \*\*\*\* PHP \*\*\*\* R \*\*\* C# \*\*\*\*

# Languages

Danish \*\*\*\*\* English \*\*\*\* French \*\*\*\* Japanese \*\*\*\* German \*\*\*\*

# **Education**

2018-2022	PhD., Bioinformatics	Clinical Immunology, Zealand University Hospital
2013-2018	MSc., Molecular Biology	Aarhus University
1999-2003	BSc., Computer Science	University of Southern Denmark

# Postdoc

Subject

#### Variant Effect Prediction in C3 grasses

- Leverage the latest AI models (EMS, PDS) to predict the effect of 300k induced variants in a population of 900 Brachypodium Distachyon plants.
- Develop in-house LLM models to predict the effects of variants, such as non-coding, for which there is a lack of models, especially plant focused models.
- Developed a pipeline to do VEP in other crops, such as rice, to identify potential targets for back mutation.

### PhD

Subject

#### **Blood type genetics**

- Developed tools for fast reading and processing of plink formatted genetic data.
- Developed an expandable program for generating over 40 blood antigen types.
- Developed a python program for training and deploying Torch AI models for blood type prediction using genetics.
- Used COX regression and Andersen-Gill model analysis in epidemiological analysis of blood types and diseases.
- Found a novel association between COVID-19 infection in the Lewis blood group.

# **Master's Thesis**

Subject Bioinformatics

60 ECTS

- Worked with various tools for gene annotation and gene group generation.
- Developed a sophisticated and flexible tool-set from ground up in C++ for easy analysis of genomics data.
- Developed algorithms for measuring syntentic homogeneity in gene groups for our 200+ rhizobium strains.
- Wrote a suite of R scripts for visualizing genomics data, as well as synteny for a given gene group, plus charting paralogs and synteny for whole strains.
- Performed mixed model heritability and GWAS analysis of rhizobium genome datasets based on gene presence-absence, SNP's and phenotype data.
- Performed DNA extraction and ERIC PCR in order to identify rhizobium strains in various samples.
- Developed algorithms for removing paralogs from rhizobium gene groups.

### **Work Experience**

2023-2025	<b>Postdoc</b> Bioinformatics researcher	Center for Quantita	tive Genetics and Genomics	
	Variant Effect Prediction in	C3 grasses.		
2018-2022	PhD Project Bioinformatics PhD student	- Klinisk Imm	nunologu - Næstved Syghus	
	Genetic prediction of red bl	ood cell types.		
2016-2017	Backend Developer - 1 year of Student programmer	contract	ScienceAtHome.org - AU	
	<ul> <li>Programmed and maintainer Cloud Code</li> <li>Expanded a C# based web f</li> <li>Developed a standalone C- Linux and Windows.</li> <li>Set up Continues Integration ment in the cloud of various</li> <li>Worked with unity.</li> </ul>	ed MongoDB data front-end. ++ development on for automatic k s projects using d	base using Parse and environment for Mac, puild, test and deploy- ocker and github.	
2009-2013	Programmer		Spielo, Moncton, Canada	
	<ul> <li>Programmed, maintained a lottery machines.</li> </ul>	and debugged C-	++ software for video	
2006-2008	Game Developer/Designer	Prog	ressive Media ApS, Aalborg	
	<ul> <li>Developed mobile games us</li> <li>Developed games for the Ni</li> <li>Developed level editors, gar internal use in C# and othe</li> </ul>	sing java. Intendo DS using mes engines and v r languages.	C. various other tools for	

• Wrote design document and made proof-of-concept prototypes for various game project proposals.

## **Skills**

- Mentally well equipped for technical as well as creative thinking which lends itself naturally to scientific analysis and research.
- Strong analytic skills aid in quick problem solving.
- Able to quickly learn new technologies and work methods.
- Efficient and structured worker.
- Conscientious, independent and reliable by nature.
- Great interpersonal skills and a team player.
- Supplements many years of education with many years of work experience in various settings.
- Commands many languages, has both lived and worked overseas, thereby equipped with an international perspective.

### About Me

The primary motivator of my life has always been intellectual curiosity and interest.

Biology, astronomy, computers, video games, literature and movies were some of the things that fascinated me already from a young age. Of these computer science and molecular biology became the subject of my professional focus, while the rest laid claim to my time of leisure.

I have subsequently developed other interests, such as philosophy, fashion and electric engineering. The latter mostly to be able to perform repairs and keep my fragile collection of vintage 80's Japanese computers going.

In my free time I am a volunteer part of the cult movie cinema Slagtehal 3. There I play the role of bartender, cashier, administrator of social media, writer of program texts for upcoming movies and technical wizard for our video and audio equipment.

Finally, I am always equipped with a humorous and easy going attitude towards life and its many challenges.

### **Publications**

Planned	Discovery of novel blood type disease correlations using large pre- scription and genetic datasets Summary Goes Here
In review	A deep learning approach to the genetic prediction of blood group antigens Summary Goes Here
2023	Genetic prediction of 33 blood group antigen types using an exist- ing genotype dataset Summary Goes Here
2022	A large cohort study of the effects of Lewis, ABO , 13 other blood groups, and secretor status on COVID-19 susceptibility, severity, and long COVID-19 Summary Goes Here
2024	Loss of function variant in SMIM1 is associated with reduced energy expenditure and weight gain Summary Goes Here
2020	<b>Symbiosis genes show a unique pattern of introgression and selec- tion within a Rhizobium leguminosarum species complex</b> Summary Goes Here
2019	Syntenizer 3000: Synteny-based analysis of orthologous gene groups Summary Goes Here

## References

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