PERSONAL DATA

I am a mathematician and engineer with a background in machine learning and data science. I work for FarGen, the Faroe Genome Project, where I study the genetic variation in the Faroese population through exome sequencing data and genealogical records. The goal of these studies is to understand the structure of the population, and the distribution of coding variants that may have clinical significance. I'm also in charge of developing our computing environment, the FarGen HTC Cluster.

EDUCATION

2018 – current: PhD candidate, "Elucidating the Genetic Variation within the Faroese Population", University of the Faroe Islands

2017: Master of Science in Engineering in Mathematical Modelling and Computation, Technical University of Denmark

2015: Bachelor of Science in Engineering in Mathematics and Technology, Technical University of Denmark

ACADEMIC POSITIONS

2018 – current: PhD candidate at the Genetic Biobank of the Faroe Islands

2017 – 2018: Bioinformatician at the Genetic Biobank of the Faroe Islands

2015-2017: Intern at RaRe Technologies

2015: Student assistant at FractureCode Corporation

2012: Teaching assistant at the Technical University of the Faroe Islands

RESEARCH INTERESTS/COORDINATION

TEACHING & SUPERVISING

2020: Supervision, "*Linked-reads: Improving and benchmarking of variant calling pipeline*", master's thesis by Elisabet Thomsen

2019: Teaching, "R for Statistics", https://olavurmortensen.github.io/r-for-statistics/, PhD course

Supervision, "Barcode contamination in Linked-reads", course project by Elisabet Thomsen

INTERNATIONAL RELATIONS AND/OR ACTIVITIES

PUBLICATIONS

2020. Johansen M, Svenstrup K**, Mortensen Ó,** Andorsdóttir G, Á Steig B, Joensen P, Hansen T, Petersen MS. Amyotrophic lateral sclerosis in the Faroe Islands - a genealogical study. Amyotroph Lateral Scler Frontotemporal Degener. 2020:1-5. doi: 10.1080/21678421.2020.1813311.

2019: **Mortensen, Ó**., Lydersen, L. N., Apol, K. D., Andorsdóttir, G., Steig, B., & Gregersen, N. O. (2019). *Using dried blood spot samples from a trio for linked-read whole-exome sequencing*. European Journal of Human Genetics. Eur J Hum Genet. 2019 ;27(6):980-988. doi: 10.1038/s41431-019-0343-3https://doi.org/10.1038/s41431-019-0343-3