HALFDAN RYDBECK

Profile

Expert in applied bioinformatics with 8+ years of experience in providing transparent and reproducible solutions for diverse areas of biological and medical research. Deep knowledge of underlying issues in need of bioinformatics support. Experience includes genetic epidemiology of rare diseases, integrative omics analysis of data from cancer tissue and immune cells, micro array analysis, preprocessing to final analysis of NGS output, sequence alignment and assembly working with non-human genomes from bacteria to fish species and wolf in evolutionary research and finally integrative analysis of proteomics, clinical and brain imaging data. Experience running jobs with queuing systems on high performance clusters.

Objective

To improve biological/medical insight through the development of computational infrastructure and algorithms

Driving forces

Understanding more about life, who we are, and to cure disease

Strengths

I love being creative and come up solutions that wasn't thought of in advance but am also carful that no negative consequences have an impact on anyone else. I work very hard to achieve the intended result which has been decided from the start on time. I am not pretentious. I speak my mind and make it safe for others to do so.



RESEARCH EXPERIENCE

2022 | 2020

Researacher bioinformatics

Core Facilities Bioinformatics vid Sahlgrenska Akademin, Univeristy of Gothenburg

♀ Göteborg, Sweden

• Developed a pipeline of rscripts to perform pathway and correlation network analysis of cord blood plasma proteomics data. Worked with Rstudio and the R package collections Bioconductor and Tidyverse. Reports where generated with R notebooks and the R package Bookdown. Github and GitKraken is used for code version control. Recently applied R packages are DEqMS for differential expression analysis of mass spectrometry data, WGCNA for proteins correlation analysis and ReactomeGSA for pathway analysis



View this CV online with links at https://rpubs.com/halryd/cv

CONTACT

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- halfdanrydbeck.me
- in https://www.linkedin.com
 /in/halfdan rydbeck

LANGUAGE SKILLS

R
Bash
Python
SQL

Made with the R package pagedown.

The source code is available here.

Last updated on 2022-03-22.

2017 2014

Senior engineer bioinformatics

Norwegian Sequencing Center

• University of Oslo. Norway

· Set up server infrastructure for NGS data handling. Manged NGS file servers, user access and data delivery. Examples of downstream analysis: Blasted an exon sequence against multiple assembled fish genomes to look for systematic loss in phylogeny. Analyzed bacterial methylomes, sequenced with Pacbio in, respect to virulens. System setup, user management, data preprocessing, delivery and down stream analysis of Illumina and Pacbio sequence data at the Norwegian DNA sequencing center. Workflow automation with cron and make

2008 2007

Principal engineer

Bioinformatics core facility

Rikshospitalet HF, Norway

- · Microarray gene expression analysis
- · Developing network-based methods to investigate and visualize clinically relevant patterns in data.

2007 2006

Research assistant

Human Genetics division

Children's Hospital of Philadelphia, USA

- · Bash and scripting for data wrangling and testing Solar, Plink, TDT, Merlin, STATA, SAS, R
- · Work primarily done in R Shiny and Javascript (node and d3js).

2005 2004

Senior research assistant

A. I duPont Hospital for Children, USA Dept. of genetic epidemiology

· Used software for genetic linkage and association studies of diseases/syndroms Velocardiofacial Syndrome, ADHD, Neuroblastoma, Osteoporosis, Cornelia de Lange's syndrome and Myopia · Solar, Plink, TDT, Merlin, STATA, SAS, R

2004 2002

Database coordinator

Human Genetics division

Children's Hospital of Philadelphia, USA

· Manged a database for SNP information Progeny2000

♣☐ TEACHING EXPERIENCE

2018 2017

R for reprodicible scientific programming

Software carpentry

Oslo Norway

- · Covered introduction to R language for statistics applications
- · Graduate level class

2018 2017

Version controlling with git and github

Software carpentry

Oslo Norway

- · Topics covered from penalized regression to boosted trees and neural networks
- · Highest level course offered in department

Calmness and exitement are good conditions for teaching and learning

Unix 2018 Oslo Norway Software carpentry 2017 · Covered modern statistical computing algorithms · 4th year PhD level class **EDUCATION** PhD bioinformatics 2012 Oslo, Norway Medical faculty, University of Oslo 2007 • PhD project with thesis title: Integrative epigenome analysis¹. Scripts Sometimes I am almost tireless. developed in R and The Genomic Hyperbrowser was used to study the This means that I fight hard so dependencies and select genes, based on genomic, epigenomic and that the tasks or projects I transcriptomic alterations in samples from osteosarcoma and immune undertake are completed on cells. The gene expression, promoter methylation and DNA copy number time and I do not give up until data were acquired by oligonucleotide microarray technology, and the histone modification data was acquired by technology based on I've achieved the intended result chromatin immune precipitation and next generation sequencing, ChIPseq. Developed and R package for clustering of genomic tracks. · University Graduate Fellow **Master of Science in Bioinformatics** 2001 Oothenburg, Sweden Chalmers University of Technology 2000 1999 Master of Science in Molecular biology **♀** Göteborg/Uppsala, Sweden University of Gothenburg /Uppsala 1993



SELECTED PUBLICATIONS, POSTERS, AND TALKS

2022 2022 The proteome signature of cord blood plasma with high hematopoietic stem and progenitor cell count²

Stem Cell Research

· Authored with Anders K.Nilsson, Annika Thorsell, Sofia Frändberg, Helena Barreto Henriksson, Camilla Hesse, Gunnel Hellgren, Pia Lundgren, AnnHellström

References are available on reauest



- 1: https://www.duo.uio.no/handle/10852/39398?locale attribute=en
- 2: https://www.sciencedirect.com/science/article/pii/S1873506122001015