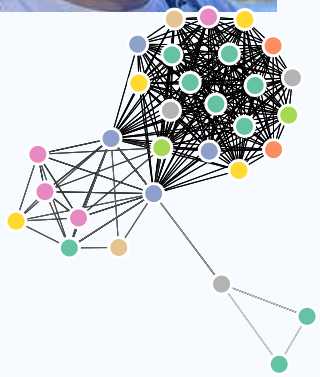
HALFDAN RYDBECK



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, microarray 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. Focused on keeping at the forefront of the latest within computational omics analysis. I seek to understand the healthcare environment and external trends. Emotional intelligence, strong communication, great teammate. My collegues say about me that I am hardworking, joyful and problemsolving.

Objective

AstraZeneca aims to find treatments for a range of diseases that poses interesting challanges from an omics and bioinformatics perspective and appears to have an excellent fleet of researchers and gold standard resources to back up the effort. Within this stimulating environment I would like to contribute with reproducible bioinformatics piplines and fine tuned algorithms for AI and by sharing skills with collegues.

Relevant competences

- transcriptomics and proteomics
- Integrative cancer omics analysis
- NGS preprocessing and analysis
- shell, (Python), R, git, Github, Nextflow, Docker
- scientific communication and writing
- project management

Recommendations

"Halfdan has shown both analytical and technical skills in his work. He has also shown an ability to work independently and with the eagerness and persistence required for attaining results. I am convinced that Halfdan will be well prepared and suited for works in the biomedical field. Therefore it is a pleasure to recommend him" Professor Dan Röhme, cmb-genetics University of Gothenburg

Halfdan did a "very good job as a senior engineer at NSC and is a responsible and pleasant person to work with" Professor Kjetil Sigurd Jakobssen, founder of Norwegin DNA Sequencing Center

CONTACT

hrydbeck@gmail.com

00 (46) 76 1860773

Lenas väg 1, 43994 Onsala

hrydbeck

github.com/hrydbeck

halfdanrydbeck.me

https://www.linkedin.com/in/halfdan rydbeck

*Made with the R package **pagedown**.*

*The source code is available **here**.*

RESEARCH EXPERIENCE

2022 | 2020

Researacher bioinformatics

Sahlgrenska ac., 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

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

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

2005 | 2004

Senior research assistant

Dept. of genetic epidemiology — Nemours Hospital for Children, USA

- 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

EDUCATION

2012 | 2007

PhD bioinformatics

Oslo, Norway

Medical faculty, University of Oslo

- PhD project with thesis title: Integrative epigenome analysis[7]. Scripts developed in R and The Genomic Hyperbrowser was used to study the dependencies and select genes, based on genomic, epigenomic and transcriptomic alterations in samples from osteosarcoma and immune cells. The gene expression, promoter methylation and DNA copy number data were acquired by oligonucleotide microarray technology, and the histone modification data was acquired by technology based on chromatin immune precipitation and next generation sequencing, ChIP-seq.
- Developed and R package for clustering of genomic tracks.

2001 | 2000

Master of Science in Bioinformatics

Gothenburg, Sweden

Chalmers University of Technology

1999 | 1993

Master of Science in Molecular biology

University of Gothenburg /Uppsala

Göteborg/Uppsala, Sweden

TEACHING EXPERIENCE

2018 | 2017

R for reprodicible scientific programming

Oslo Norway

Software carpentry

2018 | 2017

Version controlling with git and github

Oslo Norway

Software carpentry

2018 | 2017

Unix

Oslo Norway

Software carpentry

SELECTED PUBLICATIONS, POSTERS, AND TALKS

When feeling exited by the topic yet being calm and focused good learning can take place

https://www.researchgate.net/profile/Halfdan_Rydbeck; ORCID identification number: 0000-0003-1606-38420000

2022

The proteome signature of cord blood plasma with high hematopoietic stem and progenitor cell count[2]

Stem Cell Research

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

2015

ClusTrack: Feature Extraction and Similarity Measures for Clustering of Genome-Wide Data Sets[3]

Plos One

- Authored with Geir Kjetil Sandve, Egil Ferkingstad and Eivind Hovig

2010

The Genomic HyperBrowser: inferential genomics at the sequence level[4]

Genome biology

- Authored with Geir K Sandve, Sveinung Gundersen, Ingrid K Glad, Lars Holden, Marit Holden, Knut Liestøl, Trevor Clancy, Egil Ferkingstad, Morten Johansen, Vegard Nygaard, Eivind Tøstesen, Arnoldo Frigessi & Eivind Hovig

SPECIAL COMPETENCES

Preprocessing of NGS output

FASTQC, Cutadapt, MultiQC etc.

Downstream analysis of NGS output

Transcriptomics, proteomics, integragive cancer omics, gene centric(DEG), GO and pathway centric, correlation module centric, cluster computing

Programming

R, Unix shell, Python

Reproducibility

git, Github, Docker, Nextflow

Other

Project management, scientific communication and writing

LANGUAGES

Swedish (native)

English (native)

Norwegian (good)

References are available on request:

PEDAGOGIC EXPERIENCE

Tutoring PhD students

LINKS

1: https://www.duo.uio.no/handle/10852/39398?locale attribute=en
2: https://www.sciencedirect.com/science/article/pii/S1873506122001015
3: https://www.researchgate.net/publication/277618279_ClusTrack_Feature
_Extraction_and_Similarity_Measures_for_Clustering_of_Genome Wide_Data_Sets
4: https://link.springer.com/article/10.1186/gb 2010 11 12 r121