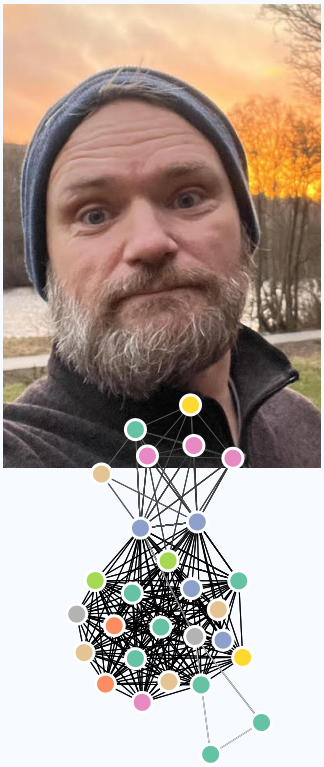
HALFDAN RYDBECK



Profile

TF 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

To contribute to improved biological/medical insight through the develpment of supporting computational infrastructure and algorithms

Driving forces

The increased understanding of life, who we are, and the curation of diseases

Strengths

Dynamic and 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.

Relevant competences

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* NGS preprocessing and analysis * scientific communication and writing
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View this CV online with links at https://rpubs.com/halryd/cv_hr_2022_04_30_Clinical_Application_Consultant_NGS_themo_fisher

RESEARCH EXPERIENCE

2022 | 2020

Researacher bioinformatics

Göteborg, Sweden

Sahlgrenska ac., Univeristy of Gothenburg

- 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

CONTACT

hrydbeck@gmail.com
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.

Last updated on 2022-03-26.

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

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

TEACHING EXPERIENCE

2018 | 2017

R for reprodicible scientific programming

Software carpentry — Oslo Norway

2018 | 2017

Version controlling with git and github

Software carpentry — Oslo Norway

2018 | 2017

Unix

Software carpentry — Oslo Norway

Calmness and exitement are essential prerequistes for good teaching and learning

EDUCATION

2012 | 2007

PhD bioinformatics

Oslo, Norway

Medical faculty, University of Oslo

- PhD project with thesis title: Integrative epigenome analysis[1]. 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

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*

SELECTED PUBLICATIONS, POSTERS, AND TALKS

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

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

SPECIAL COMPETENCES

- **Preprocessing of NGS output**
  FASTQC, etc
- **Downstream analysis of NGS output**
  Gene centric(DEG), GO and pathway centric, correlation module centric
- **Programming**
  R, shell, Python
- **Version control**
  git,Github

LANGUAGES

- **Swedish (native)**
- **English (native)**
- **Norwegian (good)**

CONFERENCE PARTICIPATION

- **Pangenomes Evolution and Computation**[5]

PEDAGOGIC EXPERIENCE

- **Tutoring PhD students**

LINKS

References are available on request

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
5: https://pgec2021.schlieplab.org/PGEC2021 Program.pdf