

# 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 colleagues say about me that I am hardworking, joyful and problemsolving.

## Objective

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

## Driving forces

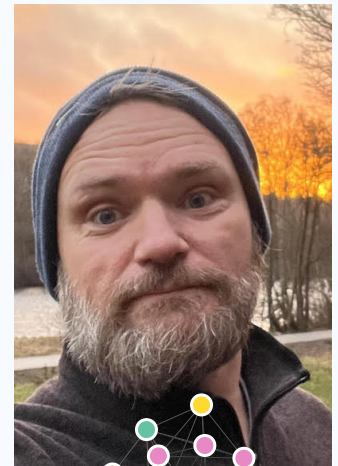
The increased understanding of life, who we are, and the curation of diseases

## Strengths

I love being creative and come up solutions that wasn't thought of in advance but am also careful 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.

## Relevant competences

\* NGS preprocessing and analysis \* scientific communication and writing \* Dynamic



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



## RESEARCH EXPERIENCE

2022  
|  
2020



### Researcher bioinformatics



Sahlgrenska ac., University 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 were 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](mailto:hrydbeck@gmail.com)

🐦 [hrydbeck](#)

📄 [github.com/hrydbeck](https://github.com/hrydbeck)

🔗 [halfdanrydbeck.me](https://halfdanrydbeck.me)










in <https://www.linkedin.com>

/in/halfdan rydbeck

Made with the R package [pagedown](#).







The source code is available [here](#).

Last updated on 2022-03-25.

- 2017  
|  
2014
- **Senior engineer bioinformatics**  
 Norwegian Sequencing Center  University of Oslo, Norway
    - Set up server infrastructure for NGS data handling. Managed 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
    - Managed a database for SNP information Progeny2000



## TEACHING EXPERIENCE

- 2018  
|  
2017
- **R for reproducible scientific programming**  
 Software carpentry  Oslo Norway
    - Set up server infrastructure for NGS data handling. Managed NGS file servers, user access and data delivery.
- 2018  
|  
2017
- **Version controlling with git and github**  
 Software carpentry  Oslo Norway
    - Set up server infrastructure for NGS data handling. Managed NGS file servers, user access and data delivery.
- 2018  
|  
2017
- **Unix**  
 Software carpentry  Oslo Norway
    - Set up server infrastructure for NGS data handling. Managed NGS file servers, user access and data delivery.

Calmness and excitement are essential prerequisites for good teaching and learning



## EDUCATION

2012  
|  
2007



### PhD bioinformatics



Medical faculty, University of Oslo

📍 Oslo, Norway

- PhD project with thesis title: Integrative epigenome analysis<sup>1</sup>. 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 an R package for clustering of genomic tracks.

2001  
|  
2000



### Master of Science in Bioinformatics



Chalmers University of Technology

📍 Gothenburg, Sweden

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*



## SELECTED PUBLICATIONS, POSTERS, AND TALKS

2022



### The proteome signature of cord blood plasma with high hematopoietic stem and progenitor cell count<sup>2</sup>

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<sup>3</sup>

Plos One

2010



### The Genomic HyperBrowser: inferential genomics at the sequence level<sup>4</sup>

Genome biology

[https://www.researchgate.net/profile/Halfdan\\_Rydbeck](https://www.researchgate.net/profile/Halfdan_Rydbeck); ORCID identification number: 0000-0003-1606-38420000



## SPECIAL COMPETENCES

References are available on request

- **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<sup>1</sup>**

## 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](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](https://link.springer.com/article/10.1186/gb_2010_11_12_r121)
- 5: [https://pgec2021.schlieplab.org/PGEC2021\\_Program.pdf](https://pgec2021.schlieplab.org/PGEC2021_Program.pdf)