

# 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. I am innovative and have general drive to find solution to technological problems. In my thesis project for MS in molecular biology I worked with cloning of a tumor suppressor gene. I seek to understand the healthcare environment and external trends. I have emotional intelligence, strong communication skills and am a great teammate. I am 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. My colleagues say about me that I am hardworking, joyful and problemsolving.

## Objective

To use my scientific expertise to contribute to the efforts of the pharmaceutical industry towards the curation of disease. To take part in fulfilling the promises of genome editing.

## Relevant competences

- Using bioinformatic tools and databases to identify novel proteins based on available target class information – and novel DNA nucleases or DNA modifying enzymes for genome editing applications.
- scientific communication and writing
- project management



## RESEARCH EXPERIENCE

2022  
|  
2020

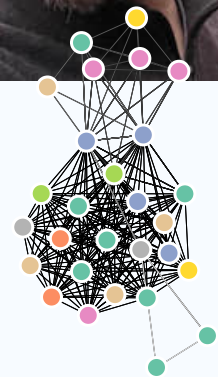
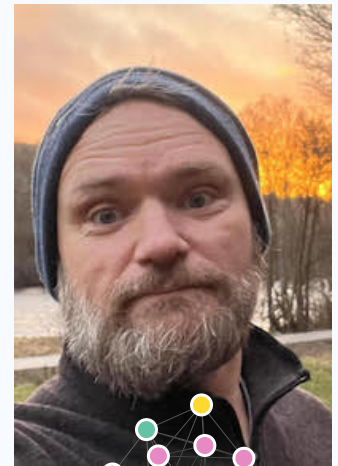
### Researcher bioinformatics



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



View as html: [https://rpubs.com/halryd/cv\\_2022\\_04\\_17\\_Sen\\_Sci\\_Mol\\_Bio\\_Bioinf\\_AZ](https://rpubs.com/halryd/cv_2022_04_17_Sen_Sci_Mol_Bio_Bioinf_AZ)

## CONTACT

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☎ 00 (46) 76 1860773

🐦 [hrydbeck](#)











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

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







in <https://www.linkedin.com/in/halrydbeck>  
*halrydbeck R package*  
[pagedown.](#)

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

Last updated on 2022-04-16.

- 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
- 2018  
|  
2017
- Version controlling with git and github**  
 Software carpentry  Oslo Norway
- 2018  
|  
2017
- Unix**  
 Software carpentry  Oslo Norway

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, founder of Norwegian DNA Sequencing Center*



## 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, Ann Hellström

2015



### ClusTrack: Feature Extraction and Similarity Measures for Clustering of Genome-Wide Data Sets<sup>3</sup>

Plos One

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

2010



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

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, Arnaldo Frigessi & Eivind Hovig

[https://www.researchgate.net/profile/Halfdan\\_Rydbeck](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

References are available on request



## LANGUAGES

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



## CONFERENCE PARTICIPATION

- **Pangenomes Evolution and Computation<sup>5</sup>**



## PEDAGOGIC EXPERIENCE

- **Tutoring PhD students**



## LINKS

- 1: [https://www.duo.uio.no/handle/10852/39398?locale\\_attribute=en](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)