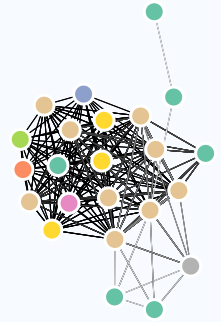


# HALFDAN RYDBECK

Recently developed a pipeline of rscripts to perform pathway and correlation network analysis of cord blood plasma proteomics data<sup>1</sup>. Developed pipelines for automatic preprocessing and delivery of Illumina and Pacbio DNA sequencing output. 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. PhD project<sup>2</sup>. Developed an R package for clustering of genomic tracks. Scripts developed in R and The Genomic Hyperbrowser<sup>3</sup> 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.



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

## EDUCATION

2012  
|  
2007

### PhD bioinformatics

Medical faculty, University of Oslo

Oslo, Norway

- Thesis title: Integrative epigenome analysis
- courses mostly statistics (30p)
- Analysed gene expression, promoter methylation, histone occupancy and copynumber variation data with R and The Genomic Hyperbrowser. 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 /University of Uppsala

Göteborg/Uppsala, Sweden

## RESEARCH EXPERIENCE

present  
|  
2020

### Researcher bioinformatics

Core Facilities Bioinformatics vid Sahlgrenska Akademien, University of Gothenburg

Göteborg, Sweden

- Working with Rstudio and the R package collections Bioconductor and Tidyverse. Reports are generated with R notebooks and the R package Bookdown. Github and GitKraken is used for code version control. Recently applied R packages are DESeqMS 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](https://twitter.com/hrydbeck)

🌐 [github.com/halryd](https://github.com/halryd)

🔗 [shorturl.at/xIP78](https://shorturl.at/xIP78)

in <https://www.linkedin.com/in/halldan-rydbeck>

## LANGUAGE SKILLS

R

Bash

Python

SQL

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

The source code is available on [github.com/halryd/cv](https://github.com/halryd/cv).

Last updated on 2021-09-11.

- 2017  
|  
2014

●

**Senior engineer bioinformatics**  
 Norwegian Sequencing Center
 

📍 University of Oslo, Norway

  - 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
 

📍 A. I duPont 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

- 2020

●

**R for reproducible scientific programming**  
[Software carpentry](#)

📍 Oslo Norway
- 2020

●

**Version controlling with git and github**  
 Software carpentry
 

📍 Oslo Norway
- 2018

●

**Unix**  
 Software carpentry
 

📍 Oslo Norway

I like when teaching and learning is relaxing and joyfull