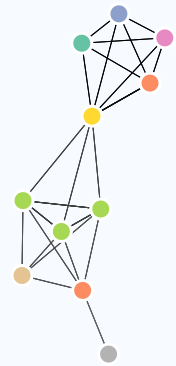


HALFDAN RYDBECK

Profile

Recently developed a pipeline¹ of rscripts to perform pathway and correlation network analysis of cord blood plasma proteomics data. 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 project². Developed an R package for clustering of genomic tracks. Scripts developed in R and The Genomic Hyperbrowser³ 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>



RESEARCH EXPERIENCE

2022
|
2020



Researcher bioinformatics

Core Facilities Bioinformatics vid Sahlgrenska Akademien, University of Gothenburg

📍 Göteborg, Sweden

- 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 DESeqMS 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

- System setup, user management, data preprocessing, delivery and down stream analysis of Illumina and Pacbio sequence data at the Norwegian DNA sequencing center. Work

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.

CONTACT

✉ hrydbeck@gmail.com

🐦 [hrydbeck](https://twitter.com/hrydbeck)

🔗 github.com/hrydbeck

🔗 halfdanrydbeck.me

in https://www.linkedin.com/in/halfdan_rydbeck

LANGUAGE SKILLS



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

The source code is available on github.com/hstryder/cv.

Last updated on 2022-03-19.

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

📍 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

- Managed a database for SNP information Progeny2000



TEACHING EXPERIENCE

2018
|
2017



R for reproducible scientific programming

Software carpentry

📍 Oslo Norway

- Covered introduction to R language for statistics applications
- Graduate level class

2018
|
2017



Version controlling with git and github

Software carpentry

📍 Oslo Norway

- Topics covered from penalized regression to boosted trees and neural networks
- Highest level course offered in department

2018
|
2017



Unix

Software carpentry

📍 Oslo Norway

- Covered modern statistical computing algorithms
- 4th year PhD level class

I like when teaching and learning is relaxing and joyfull



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.
- University Graduate Fellow

Sometimes I am almost tireless. This means that I fight hard so that the tasks or projects I undertake are completed on time and I do not give up until I've achieved the intended result

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



SELECTED PUBLICATIONS, POSTERS, AND TALKS

2022
|
2022



The proteome signature of cord blood plasma with high hematopoietic stem and progenitor cell count⁴

Stem Cell Research

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

References are available upon request



LINKS

- 1: <https://github.com/halryd/Neored>
- 2: <https://www.duo.uio.no/handle/10852/39398?locale=attribute=en>
- 3: <https://hyperbrowser.uio.no/hb/#!/mode=basic>
- 4: <https://www.sciencedirect.com/science/article/pii/S1873506122001015>