

Jonas Falck

BIOINFORMATICS - DATA ANALYSIS

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Skills

IT skills

- **r/bioconductor:** tidyverse, biomaRt, ggplot2, caret, data.table, grid, shiny
- **python:** pandas, matplotlib, scikit-learn, django, SQLAlchemy, flask, jinja2
- **productivity:** shell scripting, regex
- **database:** SQL, elasticsearch
- **operating systems:** linux, windows, macOS
- **version control:** git
- **container and virtualization:** docker, virtualbox, qemu
- **webserver:** nginx, shiny

Data science/Machine learning

- **supervised:** linear regression, knn, decision trees
- **unsupervised:** HCA, PCA, kmeans
- **statistics:** parametric and non-parametric methods
- **visualization:** publication ready plots, development of custom visualizations using grid
- **datatypes:** bed, bigWig, 2bit, fasta, fastq, vcf

Languages

- **English:** fluent
- **Dutch:** fluent (nt2)
- **German:** native

Experience

Identification and ranking of p63 binding sites putatively involved in the etiology of non-syndromic cleft lip with or without cleft palate

Nijmegen, Netherlands

RADBOD UNIVERSITY MEDICAL CENTER NIJMEGEN RUNMC, HUMAN GENETICS

2015-2016

- In-silico prediction and in-vitro validation of clinically relevant transcription factor binding sites using an integrative multiomics approach.
- Took ownership of a wetwork research project and pioneered bioinformatical research in a solely wetwork focused lab, teaching myself the necessary bioinformatic skills.
- Development of a pipeline to integrate publicly available and in-house multi-omics data (Chip-seq, SNP, GWAS, conservation, linkage disequilibrium), to generate reproducible results.
- Effective communication and presentation of bioinformatical methods and results to researches with no bioinformatical expertise.

CTCF-motif directionality controls CTCF-mediated chromatin interactions and correlates with topological domain structure

Nijmegen, Netherlands

CENTER FOR MOLECULAR AND BIOMOLECULAR INFORMATICS CMBI, COMPARATIVE GENOMICS

2016

- Drove and transformed a loosely defined, explorative research project into a hypothesis driven project resulting in a publication (see writing).
- Hypothesis generation by leveraging multi-omics datasets describing different dimensionalities of the genome, ranging 1D (sequence), 2D (ChIP-Seq), and 3D data (ChIA-PET, Hi-C).
- Hypothesis testing by applying parametric and non-parametric methods, randomization, as well as modeling of chromatin loops.
- Applying unsupervised machine learning techniques e.g. PCA, HCA as well as a multitude of visualizations for data exploration.

Logistics employee

Beuningen, Netherlands

QUANTORE

2018 - now

- Using warehouse management software to analyse erroneous orders and to troubleshoot and provide technical support to co-workers.
- Solving problems independently or to communicate issues with the superiors.
- Ensuring customer satisfaction by quality controlling orders.

Extracurricular Activity

Machine Learning

Grade: 87%

STANFORD UNIVERSITY, ONLINE

- 11 week course covering go to methods applied in supervised and unsupervised learning, regularization and how to tackle problems like bias and overfitting.
- Certificate of accomplishment: <https://tinyurl.com/4ww44jm7>

Computing for Data Analysis

Grade: 97%

JOHN HOPKINS UNIVERSITY, ONLINE

- This course covered the basics of data analysis and visualization in R in a medical context.
- Certificate of accomplishment: <https://tinyurl.com/ym9rd5dc>

Full stack web development

2012-2015

SELF-TAUGHT

- Setup and administration of headless Linux systems.
- Applied SQL-like databases and the NoSQL database elasticsearch in a website environment.
- Used python model-view-controller frameworks django and flask + SQLAlchemy.
- Applied caching technology like memcached and redis to speed up website performance.
- Learned html, css, templating and javascript for front-end use.

Education

Radboud University

Nijmegen, Netherlands

M.S. IN MEDICAL BIOLOGY

2015 -

Radboud University

Nijmegen, Netherlands

B.S. IN MEDICAL BIOLOGY

2012 - 2015

Writing

CTCF-mediated chromatin loops enclose inducible gene regulatory domains

BMC Genomics

MARTIN OTI, JONAS FALCK, MARTIJN A. HUYNEN & HUIQING ZHOU

March 2016, BMC Genomics; 17:252

- Available here: <https://doi.org/f8vnsg>

CTCF-motif directionality controls CTCT-mediated chromatin interactions and correlates with topological domain structure

Master Internship

COMPARATIVE GENOMICS, CENTER FOR MOLECULAR AND BIOMOLECULAR INFORMATICS NIJMEGEN

2016

- Available here: <https://tinyurl.com/2p9hekax>

Identification, ranking and testing of p63 binding sites putatively involved in the etiology of non-syndromic cleft lip with or without cleft palate

Master Internship

HUMAN GENETICS, UNIVERSITY MEDICAL CENTER NIJMEGEN

2016

- Available here: <https://tinyurl.com/259vt5zk>