Jonas **Falck**

Web-Development - Data-Analysis - Bioinformatics

Holzstraße 1, 44869, Bochum, Germany

(+31) 655707314 | jonas@falcken.de | joe-nas.github.io | joe-nas

Skills

IT skills	• **operating systems:** linux 10+ years (Arch, Debian based), Windows, macOS • **version control:** git • **Productivity and Office:** Shell scripting, Regex, LaTeX, Markdown, Pandoc • **container and virtualization:** docker, qemu, wsl
Web-Development	• **Languages:** Java, JavaScript, Python • **Frameworks and Libraries:** Spring-Boot, JUnit, Mockito, React, Next.js, Django, Flask, Testcontainers • **Databases:** SQL, MongoDB • **Other web related skills:** REST, HTML, tailwindcss • **Web servers:** nginx, shiny
Data science/Machine learning	• **Languages:** R/bioconductor, Python, Bash • **Frameworks and libraries:** tidyverse, caret, biomaRt, grid, shiny, scikit-learn, pandas, numpy • **visualization:** publication ready plots, development of custom visualizations using grid, ggplot2, seaborn, matplotlib, plotly, shiny • **supervised:** linear regression, knn, decision trees, random forests • **unsupervised:** HCA, PCA, kmeans • **statistics:** parametric and non-parametric methods
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

Radboud 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, transforming it into bioinformatical research, 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. haplotplotR: http://tinyurl.com/4cjw7s5h
- 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 an 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 - 2022*

- Using warehouse management software to analyze 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.

Software

Iron Delirium™ - The Workout Tracker that no one asked for *Backend@github, Frontend@github*

Jonas Falck

- My current toy project Iron Delirium™ is a workout tracker that allows users to track their workouts and progress over time. Users can create an account, log in using google and github oauth to log their workouts. Workouts can be edited and deleted, and users can view their workout history. Iron Delirium™ is built around a REST API which is implemented using Spring-Boot/Security in the backend and Next.js/next-auth in the frontend. The Data is stored in a MongoDB database.

haploplotR: Visualizing linkage disequilibrium from 1000 genomes data *haploplotR@github*

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- HaploplotR is a project that provides a tool for visualizing linkage disequilibrium patterns in human populations using data from the 1000 Genomes Project. HaploplotR uses haplotype data from the 1000 Genomes Project to generate LD plots, which show patterns of correlation between alleles at different loci across the genome. These plots can help researchers to identify regions of the genome that are associated with particular traits or diseases.

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/f8vngs

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

Education

Radboud University *Nijmegen, Netherlands*

M.S. in Medical Biology *2015 - dropout*

Radboud University *Nijmegen, Netherlands*

B.S. in Medical Biology *2012 - 2015*

Certificates & Trainings

2014 **Machine Learning**, Stanford University, Online
2022 **Intro to Machine Learning**, Kaggle.com, Machine-Learning Community
2022 **Pandas**, Kaggle.com, Machine-Learning Community
2022 **Feature Engineering**, Kaggle.com, Machine-Learning Community
2022 **Data Visualization**, Kaggle.com, Machine-Learning Community
2013 **Computing for Data Analysis**, John Hopkins University, Online
2023 **Nextflow and nf-core community training**, Seqera.io, Online
2023 **The Complete JavaScript Course 2023: From Zero to Expert!**, Udemy, Online
2023 **Node.js, Express, MongoDB & More**, Udemy, Online
2023 **Testing Spring Boot App with JUnit, Mockito & Testcontainers**, Udemy, Online
2023 **Master Spring Boot 3 & Spring Framework 6 with Java**, Udemy, Online
2023 **Java 17 Masterclass: Start Coding in 2023**, Udemy, Online