Sina Rüeger

(Genomic) Data Scientist

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Areas of experience

Genome-wide association studies (GWASs)	Creating GWAS pipelines, quality control procedures, GWAS for unconventional endpoints (time-to-event data, proxy cases), rare variant association analysis, summary statistics follow-up methods (colocalization, fine-mapping, causal inference, heritability estimation).
Statistical modelling	Regression modelling techniques, model selection, data dimension reduction, classification, unsupervised clustering.
Data visualisation	Visual representation of concepts and results.
Reproducibility	Version control, workflow automation, documentation with literate programming and best coding practices.
Domain knowledge	Genomics, Parkinson's disease, bariatric surgery, Hepatitis C, Tuberculosis & other infections, solid organ transplantation, multiple sclerosis, human height, critical care patients.
Data sets	Genomic data, brain imaging data, clinical data, questionnaire data, drugbank data.

Employment

Feb-2021 – present	**Data Scientist**, *data42 at Novartis*, Basel, Switzerland.
Sep-2019 – Jan-2021	**Data Analyst / Bioinformatician**, *FinnGen, Institute for Molecular Medicine Finland (FIMM)*, University of Helsinki, Helsinki, Finland. Extending PheWAS with novel statistical genetics methods.
Sep-2018 – Aug-2019	**Postdoctoral Researcher**, *Fellay Lab, Global Health Institute*, EPFL, Lausanne, Switzerland. Analysis of human and pathogen genomes for different infections.
Feb-2013 – Sep-2013	**Internship**, *Statistical Genetics Group, Department of Medical Genetics*, University of Lausanne, Lausanne, Switzerland. Rare genetic variant analysis.
Feb-2012 – Mar–2013	**Biostatistician**, *Division of Biostatistics, ISPMZ (now EBPI)*, University of Zurich, Zurich, Switzerland. Statistical consulting.
Mar-2009 – Jan-2012	**Research Assistant**, *Institute of Data Analysis and Process Design, Zurich University of Applied Sciences*, Winterthur, Switzerland. Statistical modelling for a mix of industry projects.

Education

Oct-2013 – Sep 2018	**PhD in Life Sciences**, *University of Lausanne*, Lausanne, Switzerland, supervised by Prof. Zoltán Kutalik, Statistical Genetics Group, Institute of Social and Preventive Medicine, Lausanne University Hospital (CHUV). **Topic**: Integrative statistical analysis of -omics and genome-wide association studies data.
Feb-2009 – Jun-2011	**Master of Science in Engineering with Specialisation in Information and Communication Technologies**, *Zurich University of Applied Sciences*, Winterthur, Switzerland.
Oct-2005 – Oct-2008	**Bachelor in Engineering, Degree Program in Data Analysis and Process Design**, *Zurich University of Applied Sciences*, Winterthur, Switzerland.

Computing skills

Statistical programming	**R** [highly proficient], **Python** [familiar], **SQL** [familiar]
Genomics tools	**Plink**, **QCTOOL**, **GTCA**, ...
Developer tools	**Unix/Linux**, **git**, **GNU make**
R	Daily used for statistical computing and data visualisation; familiar with the architecture of R, package development and best practices.
Computing experience	Experience using cloud computing / high performance clusters for analysis and storage of large datasets.

Other activities

RStudio Tidyverse Instructor	Certified since July 2020
SatRday Neuchatel 2020	Co-organiser of SatRday Neuchatel in 2020, a one day conference for R users.
R-Ladies community	Founding member and former co-organiser of R-Ladies Lausanne, a bi-monthly R user group. Former community manager of R-Ladies Slack.

Languages

German [native speaker], **English** [fluent, C1], **French** [good command, B1], **Finnish** [beginner]

Awards

Apr-2017	*The 'Human Heredity' Best Student Platform Presentation Award* at the European Mathematical Genetics Meeting in Tartu, Estonia.
Mar-2017	*Poster prize* at the ePerMed Workshop about 'Functional annotation of genome-wide variants' in Lausanne, Switzerland.
May-2016	*Lodewijk Sandkuijl Award* for an outstanding talk in the field of complex genetics and statistical genetics at the European Society of Human Genetics Conference, Barcelona, Spain.

Main publications

Sina Rüeger, Aaron McDaid, and Zoltán Kutalik. Evaluation and application of summary statistic imputation to discover new height-associated loci. *PLOS Genetics*, 14(5):1–32, 05 2018a

Sina Rüeger, Aaron McDaid, and Zoltán Kutalik. Improved imputation of summary statistics for realistic settings. *bioRxiv*, page 203927, 2018b

Sina Rüeger et al. Impact of common risk factors of fibrosis progression in chronic hepatitis C. *Gut*, 64(10):1605–1615, 2015