

Dr. Dmitriy Drichel
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Summary

Freelance data scientist with an interdisciplinary background in physics, bioinformatics, biostatistics, genomics, and epidemiology. Focused on data science, cloud, and software development, with applications in biotech, life science, and pharmaceutical industries. Over twelve years of experience analyzing and integrating complex data sets as well as developing, testing, and deploying software applications and analysis pipelines. Co-author of 40 scientific publications on genomics.

Key Skills and Interests

- Genomics, transcriptomics, epigenomics, flow cytometry
- Machine learning, statistics, and big data analytics
- Software development (Python, C/C++, R, Perl, awk, bash)
- Exploratory and predictive analytics, modeling, and simulation
- High-performance computing, big data processing
- System integration, analysis pipelines
- Cloud architectures, 8x AWS certified
- Infrastructure as code (AWS CloudFormation), containerization (docker)
- Communicating results, documentation, reporting, visualization

Work Experience

Feb 2023-current

Freelance Senior Data Scientist at Boehringer Ingelheim (BI-X)

Development, testing, benchmarking and documentation of data processing workflows for large-scale genome-wide association studies of structural genomic variants

- Oxford Nanopore and NGS sequencing, microarray genotyping
- AWS, HPC, exploratory and predictive analytics, imputation
- Development of R and python applications
- Documentation and scientific writing

Jun 2021-Jul 2022

Freelance Data Scientist at Merck KgaA

Development, testing, and benchmarking of data processing workflows for large-scale oncological studies on a proprietary AWS-based platform.

- Germline and somatic variant calling, performance evaluation
- AWS, Genedata Profiler, Data Lake, APIs, Rstudio, Gitlab
- Python, R, data acquisition, integration, and simulation

Feb 2020-Jun 2021

Freelance Data Scientist at Boehringer Ingelheim (BI-X)

Development, implementation, and evaluation of a genomics/transcriptomics data processing pipeline on AWS. Requirements- and data engineering, data analysis, software development.

- Oxford Nanopore, PacBio, Illumina NGS, microarray technology
- AWS, Python, R, high-performance computing
- DevOps, CI/CD
- Development of novel algorithms and statistical methodologies

Feb-Nov 2019 **Freelance Application Developer at Miltenyi Biotec**

Development of python applications for custom flow cytometry analysis on embedded systems. Improvement and implementation of unsupervised machine learning methods.

- Python, pandas, scikit-learn, Jupyter
- Git, SVN, Jenkins

Jan-May 2019 **Freelance IT Consultant at Jahnes GmbH**

Requirements engineering for implementation of a third-party supervised machine learning model in a leading German bank. Data engineering, model optimization, exploratory and descriptive analysis.

- SQL, Python, pandas, scikit-learn, matplotlib, Jupyter
- Risk analysis, consumer loans

2015-2021 **Postdoc at Cologne Center for Genomics (CCG), University of Cologne**

Development of analysis software for big genomic data sets. Development of novel statistical methodology and algorithms, management of small teams, writing scientific publications and grant applications.

- C/C++, Python, Perl, R
- Epidemiological studies, GWAS, NGS, scientific writing
- Big data analysis, high-performance computing
- Teaching assistant (statistical genetics, population genetics)

2010-2015 **Research associate at the**

German Center for Neurodegenerative Diseases (DZNE), Bonn

Development of application software for analysis of big biological data. Development and evaluation of novel statistical methodology, high-performance computing, scientific writing.

- C/C++, Python, OpenMP
- Evaluation and optimization of data processing pipelines, GWAS, NGS
- Large-scale simulations of biological data sets

2006-2010 **Teaching assistant at Institute for Theoretical Physics, Leibniz University Hannover and Institute for Physiology, Hannover Medical School**

Academic Education

2016 PhD in Epidemiology at the University Clinic Bonn, thesis:

Association Analysis of Rare Genomic Variants

2003-2010 Studies of physics (focus on mathematical and statistical physics) at the Leibniz University of Hannover, diploma thesis at the Institute for Theoretical Physics (ITP):

Logarithmic Conformal Field Theory with Supersymmetry

2007-2008 Studies of mathematics and physics at the National University of Ireland, Maynooth, and Trinity College, Dublin

Certifications

Dec 2022	AWS Certified Security - Specialty
Dec 2022	AWS Certified Developer - Associate
Dec 2022	AWS Certified Database - Specialty
Nov 2022	AWS Certified Solutions Architect - Professional
Oct 2022	AWS Certified Data Analytics - Specialty
Sep 2022	AWS Certified Machine Learning - Specialty
Aug 2022	AWS Certified Solutions Architect - Associate
Jun 2022	AWS Certified Cloud Practitioner

Personal Details

Languages: German, English, Russian
Nationality: German

Top 5 Publications

- [1] George Kanoungi, Michael Nothnagel, Tim Becker, **Dmitriy Drichel** "The exhaustive genomic scan approach, with an application to rare-variant association analysis" *European Journal of Human Genetics*. 2020 May 15:1-9.
- [2] Isabel Spier, Martin Kerick, **Dmitriy Drichel**, Sukanya Horpaopan, Janine Altmüller, Andreas Laner, Stefanie Holzapfel et al. "Exome sequencing identifies potential novel candidate genes in patients with unexplained colorectal adenomatous polyposis." *Familial cancer* 15, no. 2 (2016): 281-288.
- [3] Stefanie Heilmann, **Dmitriy Drichel**, Jordi Clarimon, Victoria Fernández, André Lacour, Holger Wagner, Mathias Thelen, Isabel Hernández, Juan Fortea, Montserrat Alegret, et al. "PLD3 in non-familial Alzheimer's disease". *Nature* 520.7545 (2015), E3–E5.
- [4] Isabel Spier, **Dmitriy Drichel**, Martin Kerick, Jutta Kirfel, Sukanya Horpaopan, Andreas Laner, Stefanie Holzapfel, Sophia Peters, Ronja Adam, Bixiao Zhao, et al. "Low-level APC mutational mosaicism is the underlying cause in a substantial fraction of unexplained colorectal adenomatous polyposis cases". *Journal of medical genetics* 53.3 (2016), pp. 172–1.
- [5] **Dmitriy Drichel**, Christine Herold, Andre Lacour, Alfredo Ramirez, Frank Jessen, Wolfgang Maier, Markus M. Noethen, Markus Leber, Tatsiana Vaitsiakhovich, and Tim Becker. "Rare Variant Testing of Imputed Data: An Analysis Pipeline Typified." *Human Heredity* 78.3-4 (Dec. 2014).