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**IMPRS for Biology and Computation**  
Max-Planck-Institut für molekulare Genetik  
Innestr. 63–73  
14195 Berlin

February 2, 2019

Dear Sir or Madam:

I am writing to apply for a position in your doctoral program. I have recently completed my master's thesis in bioinformatics at the Ludwig-Maximilians-Universität and Technical University of Munich and expect to receive the final grade by March 2019.

During my studies in the field of bioinformatics, I could familiarize myself with a wide array of computational methods enabling modern biological research. I am proficient in statistical analysis using R and Python with a focus on the evaluation of biochemical and genomic data such as next generation sequencing and differential expression analysis as well as the biological reasoning behind them. Additionally, I could gain insights on the modeling and prediction of molecules, components and processes not only on a cellular level but also in the context of systems biology. Thanks to my exceptional performance during my studies, I was awarded a membership in best.in.tum, which is a promotion program of the Technical University's Department of Informatics for the best 2% of students.

During my time in Munich, I started working at the Center for Human Genetics and Laboratory Diagnostics (MVZ), where I continue to be employed to this day. My work there allowed me to gain experience with the application of NGS in a diagnostic setting, especially in the area of rare diseases. In this interdisciplinary setting where I work at the intersection of multiple disciplines, including genomics, physiology and computer science, I was introduced to best practices for the evaluation of high-throughput data and applied my acquired knowledge directly to real clinical information. In addition to working with already established techniques, I was tasked with improving on the analysis pipeline. This included the development of applications enabling and simplifying the integration of multiple data preparation and analysis tools as well as the implementation of efficient, domain-specific evaluation methods.

My current research is conducted as part of the Multiple Integration of Data Annotation Study (MIDAS), which is performed by the MVZ in tandem with the TUM School of Medicine. MIDAS explores the possibility of optimizing the diagnostic evaluation of high-throughput data when dealing with rare diseases by integrating additional data sets with the results of already established NGS analyses. This project provided the context of my master's thesis *Syndrome Prediction by Phenotype Similarity and Its Application to Neurodevelopmental Disorders*, which involves the development of a system aiding in the diagnosis of rare diseases by identifying patients similar to each other.

My work in diagnostics has led me to take an interest in the effects genetic variants have on their associated biological processes and affected individuals' health. Upon reading about your research I was very excited about the opportunity to contribute to the knowledge I have been applying in the last years. Thank you for considering my application. I am looking forward to hearing from you.

Yours sincerely,

**Daniel Schmitz**

# Daniel Schmitz

## Curriculum Vitae

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Date of Birth May 3<sup>rd</sup>, 1995

Place of Birth Berlin

### Education

since 2017 **M.Sc. Bioinformatics**, *Ludwig-Maximilians-Universität and Technical University of Munich*, Graduation in early 2019.

2013–2017 **B.Sc. Bioinformatics**, *Ludwig-Maximilians-Universität and Technical University of Munich*, Grade: 1.6.

2005–2013 **Abitur**, *Friedrich-Schiller-Gymnasium Königs Wusterhausen*, Grade: 1.0.

#### Master's Thesis

Title *Syndrome Prediction by Phenotype Similarity and Its Application to Neurodevelopmental Disorders*

Supervisors Professor Dimitrij Frishman, Chair of Bioinformatics, TUM

Dr. Sebastian H. Eck, Center for Human Genetics and Laboratory Diagnostics

Description I developed a system assisting geneticists in identifying developmental disorders using phenotypic annotations. Annotations are based on terms from the Human Phenotype Ontology. Suggestions are made by comparing each new case to patients with an already existing diagnosis.

### Practical Experience

#### Vocational

since 2014 **Software Developer/Student Employee**, *Center for Human Genetics and Laboratory Diagnostics*, Planegg.

Assisted in performing genetic analyses in a diagnostic setting focusing on rare diseases and neurodevelopmental disorders and developed software improving their outcomes and lowering their costs.

Detailed Achievements:

- Supported general diagnostic NGS analyses
- Improved downstream analysis by implementing efficient statistical methods
- Developed applications streamlining the analytic workflow by simplifying the integration of multiple diagnostic tools and databases
- Designed and implemented software for the Multiple Integration of Data Annotation Study, exploring the evaluation of NGS data in a diagnostic setting by integrating data from multiple sources.

## Voluntary

since 2017 **Head of Membership Administration, Verein für Corpsstudentische Geschichtsforschung e.V.**

Management of the membership database of a German society concerned with academic history counting 1,100 members.

## Awards

2018 **Member of best.in.tum.**

Promotion program for the top 2% of students at the TUM Department of Informatics

## Publications

- [1] E Bounda Ndinga, SH Eck, R Brumm, Schmuck M, Schmitz D, Rost I, and Klein HG. *MIDAS GPMS: A flexible gene panel management system*. Poster at ESHG. Milan, 2018.
- [2] Brumm R, Eck SH, Ebert B, Vogl I, Schmitz D, Küçük S, Rath S, Hasselbacher V, Sofeso C, Busse B, Chahrokh-Zadeh S, Marschall C, Mayer K, Rost I, and Klein HG. *A software tool for data Integration in a diagnostic laboratory*. Poster at Genome Informatics. Cold Spring Harbor, NY, 2015.

## Programming & Data Analysis Skills

Basic Rust

Intermediate Perl, UNIX shell

Advanced Java, R, Python, SQL, Microsoft Excel, L<sup>A</sup>T<sub>E</sub>X

## Languages

**German** Mothertongue

**English** Fluent

**Spanish** Intermediate

**French** Basic

## References

**Prof. Dr. Volker Heun**

LFE Bioinformatik  
Institut für Informatik  
Ludwig-Maximilians-Universität  
Amalienstr. 17  
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**Dr. Sebastian Eck**

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**Hayim Malkhasy**

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