DR. MARKUS MEIER

Stauffenbergring 1 | 37075 Göttingen
meiermark13@gmail.com | +49 176 922 620 93

Experience

since 01.2017

Max-Planck Institute for Biophysical Chemistry, Göttingen, Germany
Research group of Dr. Johannes Soeding
Postdoc in Computational Biology

"PEnG Motif - A motif discovery tool in DNA sequences"
- Detects statistically over-represented motifs in DNA sequences
- Written in C++, Python, R

▼ 07.2014 – 12.2016

Max-Planck Institute for Biophysical Chemistry, Göttingen, Germany
Research group of Dr. Johannes Soeding
Scientific Assistant, Ph.D. student

"Pdom – A protein domain predictor based on Bayesian statistics"
- Decomposes the complete protein sequence space into domains (structurally und functionally conserved building blocks)
- Written in C++, Python
- Built a web server with nginx, Django, PostgreSQL, celery, redis, d3 and docker to visualize the domain predictions

"Diversity-enriched Protein Database of Hidden Markov Models for HHblits"
- Boosted protein homology detection sensitivity of HHblits
- Designed and implemented an efficient compression scheme for multiple sequence alignments

07.2012 – 06.2014

Gene Center at the Ludwig Maximilians University, Munich, Germany
Research group of Dr. Johannes Soeding
Scientific Assistant, Ph.D. student

"Coordinated the Maintenance and Improvement of HHsuite"
- Moved the project repository from a local SVN to GitHub
- Modernizing legacy (spaghetti) C++ code
- Refactoring the build pipeline with cmake
- Parallelization for HPC (Open MPI and OpenMP)
- Support scripts for a new protein structure format (mmcif)

Technical Skills

Expert	C++, Java, Python, Javascript, Data Science
Intermediate	HTML5, CSS3, Amazon AWS EC2
Beginner	R, C#, Hadoop

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Education

07.2012 – 12.2016	**Ludwig Maximilians University - Munich, Germany** **Doctor of Natural Sciences (Grade: 1.0)** • Doctor thesis: "Decomposing Protein Sequence Space into Domains"
▼ 04.2011 – 06.2012	**Ludwig Maximilians University &** **Technical University - Munich, Germany** **Master of Science: Bioinformatics (Grade: 1.2)** • Master thesis: "Introduction of Protein Sequence-Structure Scores in HHsearch"
▼ 10.2007 – 05.2011	**Ludwig Maximilians University &** **Technical University - Munich, Germany** **Bachelor of Science: Bioinformatics (Grade: 2.0)**

Certificates

06.2017	Udacity – Front-End Web-Developer Nanodegree
03.2017	Coursera – Charting & Data Representation in Python by University of Michigan
12.2016	Coursera – Plotting, Introduction to Data Science in Python by University of Michigan

Hobbies

Board Games, Pen and Paper Role-Playing Games, Aikido, Tai Chi

Profiles

meiermark.github.io   github.com/meiermark   linkedin.com/in/meiermark13

Göttingen, 19.06.2017

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