DR. MARKUS MEIER

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PROFILE

- Well-versed software developer and data engineer from Germany with a PhD in bioinformatics and intensive experience working with C++ and Python in machine learning
- Accomplished alumnus of the Ludwig Maximilian University of Munich and the Max Planck Institute for Biophysical Chemistry; strong skills in mathematics and computational biology
- Enthusiastic, assertive and resilient team player, delivering innovative solutions; exceptional interest in state-of-the-art machine learning; proficient English language skills

MeierMark.github.io Github.com/MeierMark Linkedin.com/in/MeierMark13

PROFESSIONAL EXPERIENCE

Since 05.2018

Research Engineer for Artificial Intelligence in Robotics
Magazino GmbH, Munich (Germany)

- Project: “Multi-Robot Coordination in Warehouses”
  - Improvement of the existing single-robot system by including the positions of the other robots in path planning
  - Design of a holistic “Multi-Robot Coordination System”

09.2017 – 02.2018

Software Engineer
Sulzer GmbH, Munich (Germany)

- Project: “International Volume Planning”
  - Maintenance of Java EE projects; implementation of FUBAs
  - Customization of planning GUI; access permission adjustments for market planners; introduction to Big Data via Hadoop

01.2017 – 08.2017

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

- Project: PEnG Motif – Motif discovery tool in DNA sequences
  - Detects statistically over-represented motifs in DNA sequences
  - Written in C++, Python, R

▾ 07.2014 – 12.2016

Scientific Assistant / PhD Student
Max-Planck Institute for Biophysical Chemistry, Göttingen (Germany)
Research group of Dr. Johannes Soeding

- Project: Pdom – Protein domain predictor based on Bayesian statistics
  - Decomposes the complete protein sequence space into domains (structurally and functionally conserved building blocks)
  - Written in C++, Python
- Project: “Diversity-enriched Protein Database of Hidden Markov Models for HHblits”
  - Designed and implemented an efficient compression scheme for multiple sequence alignments
  - Boosted protein homology detection sensitivity of HHblits

07.2012 - 06.2014

Scientific Assistant, / PhD Student

Gene Center at the Ludwig Maximilians University, Munich (Germany)

Research Group of Dr. Johannes Soeding

- Project: „Coordinated the Maintenance and Improvement of HHsuite"
    - Moved the project repository from a local SVN to GitHub
    - Modernizing and optimizing legacy (spaghetti) C++ code; refactoring the build pipeline with cmake; HPC parallelization (Open MPI & OpenMP)

EDUCATION

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

ADVANCED TRAINING & CERTIFICATIONS

Since 10.2018	Udacity – Deep Reinforcement Learning Nanodegree
03.2018	Udacity – Artificial Intelligence Nanodegree
11.2017	Udacity – Deep Learning Nanodegree Foundation
09.2017	Coursera – Applied Data Science with Python Specialization
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

LANGUAGES & ADDITIONAL QUALIFICATIONS

German	Native speaker	
English	Proficient knowledge	
IT Skills	Expert knowledge:	C++, Python, Data Science
	Intermediate knowledge:	Machine Learning, Deep Learning, AI engineering
Awards	2nd, 1st and 2nd Prize in the Federal Mathematics Competition in 2003, 2002 and 2001, Bavarian State Ministry of Education	