Tristan Kast

Curriculum Vitae

Education

10/2016– 02/2019	**Master of Science**, *Eberhard Karls Universitaet*, Tuebingen, Bioinformatics ○ Relevant Courses: Machine Learning for Health, Graph Databases, Data Visualization, Advanced Web-Development, Software-Quality ○ Thesis: Evaluation of a Hybrid-Assembly Pipeline for Structure Variant Detection, Supervisors: Prof. Dr. Daniel Huson, Prof. Dr. Peter Heutink
03/2018	**Bioinformatic Tools Practical Course**, *Eberhard Karls Universitaet*, Tuebingen ○ Pipeline construction in Python and Bash ○ Sequence assembly, Short & long read alignment (Bowtie2 and Tablet) ○ Taxonomic analysis & functional analysis of metagenomic data ○ Applied technologies: Python, R, Bash, Git, matplotlib
08/2018	**Integrated Bioinformatics Practical Course**, *Eberhard Karls Universitaet*, Tuebingen ○ Integration and unification of data from different sources and of different structure ○ Genotype - Phenotype centered analysis ○ Explorative & Machine Learning supported analysis and data visualization ○ Applied technologies: Python, dplyr, pandas, scipy, statsmodels, matplotlib, seaborn
04/2012– 03/2016	**Bachelor of Science**, *Eberhard Karls Universitaet*, Tuebingen, Bioinformatics ○ Relevant Courses: Computer Science I, II & III, Mathematics I, II & III, Software Development, Algorithms, Stochastic, Computational Immunomics ○ Thesis: Analysis of the 16S Mikrobiom of the human Gut, Supervisor: Prof. Dr. Daniel Huson

Experience

Since 02/2020 **Software Engineer**, *Max Planck Unit for the Science of Pathogenes*, Berlin
- Data analysis in the context of sequence bioinformatics on complex biological data
- Conception, maintenance and implementation of new features for the institutes database service, e.g. interactive plots
- Applied technologies: Python, Javascript, Flask, Vue.js, MongoDB, Axios

03/2019–08/2019 **Computational Scientist**, *German Center for Neurodegenerative Diseases (DZNE), Bioinformatics*, Tuebingen
- Whole genome assembly with second and third generation sequencing data
- Single Nucleotide Polymorphism and structural variant detection for various projects
- Scripting of different bioinformatic analysis pipelines, e.g. for MicroRNA-Seq, CAGE-Seq data or enrichment analysis
- Explorative analysis of clinical bulk and Single-Cell RNA-Seq data, e.g. differential expression analysis, pathway regulation analysis and marker gene detection
- Administration and maintenance of the group internal database
- Applied technologies: Python, R, Docker, Nextflow, Snakemake, Bash, Ubuntu, CentOS, SQL, Git, dplyr, pandas, numpy, DeSeq2, EdgeR, Kanban, Machine Learning, Groovy

04/2017–03/2018 **Research Assistant**, *Eberhard Karls Universitaet, Applied Bioinformatics Group*, Tuebingen
- MD-Simulations with GROMACS and PyMOL
- Conception of a RESTful API for ArangoDB
- Applied technologies: Git, GROMACS, PyMol, SQL, JavaScript, Java, Python, Flask

Languages

Native German
Fluent English

Skills

Certificates Machine Learning by Stanford University on Coursera (Octave/MatLab)
Nextflow

Advanced MacOSX, Linux Ubuntu and CentOS, Docker, Nextflow, Python, JavaScript, R, Latex, Git, Flask, Django, SQL (MySQL, PostgreSQL), NoSQL(MongoDB), HTML + CSS

Basic Windows, Java, PyMol, GROMACS, KNIME, iOS, MATLAB/Octave, Android, Swift, Snakemake, Tableau, C++

Interests

Sports Freeletics, Scuba diving, Skiing & Snowboarding, Hiking, Bouldern
Lifestyle Cooking, Traveling (Travels lasting several months in South-East Asia & Latin America)
Hobby Projects Web and mobile application for BodyWeight-Training and progress visualization
Voluntary work Ronald McDonald House Tuebingen, Cooking Team