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

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Experience

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

03/2019–08/2019   **Computational Scientist**, *German Center for Neurodegenerative Diseases (DZNE), Bioinformatics*, Tuebingen
- o Whole genome assembly with second and third generation sequencing data
- o Single Nucleotide Polymorphism and structural variant detection for various projects
- o Scripting of different bioinformatic analysis pipelines, e.g. for MicroRNA-Seq, CAGE-Seq data or enrichment analysis
- o Explorative analysis of clinical bulk and Single-Cell RNA-Seq data, e.g. differential expression analysis, pathway regulation analysis and marker gene detection
- o Administration and maintenance of the group internal database
- o 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
- o MD-Simulations with GROMACS and PyMOL
- o Conception of a RESTful API for ArangoDB
- o 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