

Curriculum Vitae

Waldemar Reusch, Marienbader Str. 6/1, 70372 Stuttgart
+49 178 133 90 24, waldemar.reusch@googlemail.com

Skills

Core skills

Design and development of desktop and web applications, focused on life-sciences and devoted to clean, sustainable architecture, future-proof technologies and usability, covering every lifecycle phase from application development to testing, deployment, system administration and every layer between database design and user interface.

Software, programming languages and technologies

docker, Linux, git, pandas, jupyter notebooks VSCode, Eclipse, Oracle DB, VSCode, PyCharm, Glassfish, Maven, HTCondor, SVN, Firebird DB, Vim, Jenkins, Gitlab, Adobe Creative Suite, Firebug, Jira, Confluence, tensorflow, celery, AWS

Python, Java, JavaScript, HTML5, CSS3, Bash, SQL, PHP

devops, Domain Driven Design, Object Oriented Design, JEE, REST, (R)DBMS, functional programming, reactive programming, CI/CD, Scrum, Grid Engines, datascience

Spoken languages

German native proficiency

English professional working proficiency

Russian, Swedish elementary proficiency

Work Experience

Software Engineer and IT Allrounder

since March 2015

Insilico Biotechnology AG
Stuttgart, Germany

Developing a machine learning pipeline to create customized predictive hybrid models for the analysis of bioprocess performance and various optimization scenarios.

Developing enterprise grade software for the design and simulation of metabolic network models, quantitative comparison of bioprocess performance and feed media optimization.

Contribution of software engineering expertise throughout the software development lifecycle, from requirements, through design and implementation to deployment and in all layers between database, middleware, grid engine and user interface.

Maintenance and administration of IT infrastructure including multiple testing and deployment machines running CentOS and SUSE Linux, Oracle 11g database, the CI pipeline, an HTCondor compute cluster and containerized applications on premise and using AWS.

Internship

May 2013 - Jul 2013
(3 months)

Insilico Biotechnology AG
Stuttgart, Germany

Developing a genome-scale metabolic flux model of an antibiotics producing bacteria including extensive literature and database research and modelling with proprietary software.

Research Assistant

Nov 2012 - Apr 2013

Institute of Technical Biochemistry
University of Stuttgart, Germany

Development of an User Interface for the novel enzyme sequence-structure-function database BioCatNet using PHP, HTML, CSS and JavaScript.

Research Assistant

Jan 2011 - Jun 2011

Department of Physics, Chemistry and Biology
Linköping University, Sweden

Gene Expression Analysis of the late flowering gene in the common pea *Pisum sativum*. Working with PCR/rtPCR machines, DNA/RNA-extraction kits and Gelelektrophoresis.

Education

Certified Java EE Workshop

March 2017

PC College, Stuttgart
Enterprise Java Beans 3.1, Session- and MD Beans, CDI, JPA, Lifecycle

Dipl. Biologe, t.o.
technically oriented Biology diploma

Oct 2007 - Nov 2014

University of Stuttgart, Germany
Focus: Bioinformatics, Biophysics

Jan 2011 - Jun 2011

Linköping University, Sweden
Focus: Neuroscience, Gene Expression

Diploma Thesis

Development of a novel Protein Database System for Sequence-Structure-Function Relationships: BioCatNet

Oct 2013 - Dec 2014

Institute of technical Biochemistry
University of Stuttgart, Germany

Development of a bioinformatic data warehouse application including middleware, API and UI, capable of holding and managing protein sequence, structure and function information, using PHP, Perl, HTML, CSS and JavaScript. The system is publicly available for scientific use on <https://biocatnet.de>

Maintanance and administration of IT infrastructure including Apache HTTP and Firebird database servers on Debian Linux machines.

Student Research Paper

Analyse thermokinetischer Potential-Strom-Kennlinien an einem Modell von *Escherichia coli*

Oct 2011 - Jun 2012

Institute for System Dynamics
University of Stuttgart, Germany

Assessing the predictive quality of the novel modelling technique *Thermokinetic Modelling* through automated simulations, using Mathematica, R and bash scripts on a Linux system.