

Simo Kitanovski

Personal Data

Name Simo Kitanovski
Address Siepenstraße 1
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Phone +49 178 6812100
Date/Place of Birth 24.05.1987 in Tetovo, Macedonia
Nationality macedonian

Academic Qualifications

Jun 2015– **Doctoral studies**
University Duisburg-Essen, Essen
Degree: PhD
Thesis: Computational identification and characterization of genotype-phenotype associations

Apr 2012–Jun 2015 **Graduate studies in Applied Computer Science**
University Duisburg-Essen, Duisburg
Degree: M.Sc.
Thesis: Statistical Learning of Genotype-Phenotype Associations with Phylogenetic Correction

Oct 2006–Jun 2011 **Undergraduate studies in Computer Engineering**
University Duisburg-Essen, Duisburg
Degree: B.Sc.
Thesis: Activity Recognition in Smart Homes using Ambient Sensor Technology.

Aug 2002–Jun 2006 **Gymnasium Yahya Kemal**
Skopje, Macedonia

Aug 1994–Aug 2002 **Primary School Goce Delcev**
Tetovo, Macedonia

Work Experience

- May 2014–Jun 2015 **Research Assistant**, *Centre for Medical Biotechnology, University Duisburg-Essen, Essen.*
- Jul 2011–Sep 2013 **Research Assistant**, *Fraunhofer Institute, Intelligent Room and Building Systems, Duisburg.*
- Mar 2010–Jun 2010 **Internship**, *Fraunhofer Institute, Intelligent Room and Building Systems, Duisburg.*

Publications, Software and Conferences

Publications

Kitanovski S, Hoffmann D. (2020) IgGeneUsage: differential gene usage in immune repertoires. *Bioinformatics*, btaa174

Tucci FA, **Kitanovski S**, Johansson P, Klein-Hitpass L, Kahraman A, Dürig J, Hoffmann D, Küppers R. (2018) Biased IGH VDJ gene repertoire and clonal expansions in B cells of chronically hepatitis C virus-infected individuals. *Blood, The Journal of the American Society of Hematology*, 131, 546–557

Software

R-package (Bioconductor) IgGeneUsage: a tool for differential gene usage in immune repertoires. <https://bioconductor.org/packages/IgGeneUsage/>.

R-package (Bioconductor) genphen: a tool for quantification of associations between genotypes and phenotypes in genome wide association studies (GWAS) with Bayesian inference and statistical learning. <https://bioconductor.org/packages/genphen/>.

Conferences

- Mar 2018 Decoding genotype-phenotype associations with genphen (poster presentation: 28th Annual Meeting of the Society for Virology, Würzburg, Germany)
- Mar 2018 HTSeq analyses of B cell receptor repertoires (poster presentation at: 28th Annual Meeting of the Society for Virology, Würzburg, Germany)
- Jan 2018 HTSeq analyses of genetic diversity of cellular repertoires in oncological contexts (poster presentation at: 1st Essen Translational Oncology Symposium (ETOS), Essen, Germany)
- Sep 2017 genphen: A tool for quantification of genotype-phenotype associations using statistical learning techniques and Bayesian inference (poster presentation at: Molecular Basis of Life, Bochum, Germany)
- Oct 2016 Decoding genotype-phenotype associations with genphen (poster presentation at: Collaborative Research Center TRR60, Shanghai, People's Republic of China)

Skills

IT

Programming	R, Java, Julia, NesC, C, Prolog, C#
Development Environments	RStudio, Eclipse EE/PDE, MS Visual Studio, NetBeans
Databases	MySQL, SQLite
Other Skills	version control (Git/CVS/Subversion), modeling (UML), OSGi, JDBC, MS-Office/Libre Office, graphics software (Gimp, Inkscape), reporting software (Markdown, TeX), interactive application development (Shiny)
Operating Systems	Linux/Unix, Windows Vista/7

Big Data Analysis

Probabilistic modeling	Regression analyses with (multilevel) probabilistic models for Bayes inference with Stan and JAGS
Machine Learning	Supervised (random forest, support vector machine, convolutional neural networks) and unsupervised machine learning
High-Throughput Sequencing Data	<ul style="list-style-type: none">• B/T-cell receptor repertoire analysis: quality control, clonality determination, model-based characterization of clonal structures and repertoire features• GWAS: variant-calling, genetic association analysis with hierarchical models for Bayes inference• RNA-Seq: quality control, transcript abundance inference, differential (gene) expression• ChIP-Seq: quality control, alignment, peak calling, chromatin-state discovery (ChromHMM), integrated ChIP/RNA-Seq data analysis• Downstream analyses: functional (gene ontology, pathway) enrichment, network-based protein-protein interaction analysis

Languages

Macedonian	mother tongue
English	fluent
Serbo-croatian	fluent
German	basic
Turkish	basic