






About

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shiltemann   

Languages

Bilingual Dutch/English
German & French

Skills

Python, C, C++,
Galaxy, Docker, Jekyll

Interests

Bioinformatics, Training, Community Building, Genome Sequencing, Data Analysis, Workflows, Automation, Visualisation, Best Practices, Cancer Research, Microbiome Analysis, Infosec, CTF, Traveling, Hiking, Reading, Puzzles.

Education

Since 2012	Ph.D. candidate in Bioinformatics <i>Bioinformatics for Everybody.</i>	Erasmus Medical Center
2008–2010	M.Sc. Computer Science Specialization in Bioinformatics	LIACS, University of Leiden & TU Delft
2005–2008	B.Sc. Computer Science	LIACS, University of Leiden
2002–2005	B.Sc. course work Physics & Astronomy	University of Leiden
2002	High School (VWO) Specialization in Science & Technology	Alfrink College, Zoetermeer

Work Experience

Current	Erasmus Medical Center, Rotterdam Bioinformatician and Doctoral Researcher <ul style="list-style-type: none"><i>Software Development and Pipeline building</i><i>Training Development and Delivery</i><i>Galaxy System's Administrator</i><i>Microbiota Analysis and Antibiotic Resistance Detection</i><i>Prostate Cancer Analysis</i>	
2010-2012	After's Cool, The Hague Tutor of High School Students. <i>Math, Physics, Chemistry</i>	Tutor of High School Students.
2002-2010	Self-Employed Tutor of High School Students. <i>Math, Physics, Chemistry</i>	

Projects

2018	Clinical Microbiota Analysis Pipeline Development of an analysis pipeline for use in daily clinical diagnostics of sepsis patients for Streeklab Haarlem.	ErasmusMC
2016-18	Galaxy Training Materials Co-developed infrastructure for the collaborative development of Galaxy training materials, as well as development of several training manuals on topic of Metagenomics, Galaxy Development and Visualisation	GalaxyProject

2016	Galaxy CTF	Galaxy Community Conference 2016
	Together with Helena Rasche, built a framework and 28 challenges for a "Capture the Flag" event based on Galaxy. Tasks included exploiting recently patched security bugs within Galaxy, Docker security issues, exploring new Galaxy features, and exploiting common bugs in Galaxy tools. Approximately 16 people participated in the competition. The infrastructure for the competition was released afterwards to allow others to re-use it for educational purposes.	
2016-18	Galaxy Interactive Environment Development	GalaxyProject
	Created Galaxy Interactive Environments (GIEs) for several applications, including Phinch for metagenomic data visualisation and Ethercalc.	
2012-18	Galaxy Tool Development	GalaxyProject
	I have integrated over 100 tools into the Galaxy Tool shed, including Complete Genomics Tools, Mothur for 16S rRNA sequence Analysis, Circos for visualisation, and more. Member of Galaxy's IUC team of tool developers.	

Publications

The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update
Afgan, Enis, Dannon Baker, Bérénice Batut, Marius Van Den Beek, Dave Bouvier, Martin Čech, John Chilton, Dave Clements, Nate Coraor, Björn A Grüning, et al.

Nucleic acids research 46.W1 (2018) W537–W544. Oxford University Press, 2018

ASaiM: a Galaxy-based framework to analyze microbiota data

Batut, Bérénice, Kévin Gravouil, Clémence Defois, Saskia Hiltmann, Jean-François Brugère, Eric Peyretailade, and Pierre Peyret

GigaScience 7.6 (2018) giy057. Oxford University Press, 2018

Community-driven data analysis training for biology

Batut, Bérénice, Saskia Hiltmann, Andrea Bagnacani, Dannon Baker, Vivek Bhardwaj, Clemens Blank, Anthony Bretaudeau, Loraine Guéguen, Martin Čech, John Chilton, et al.

BioRxiv (2018) p. 225680. Cold Spring Harbor Laboratory, 2018

Development and evaluation of a culture-free microbiota profiling platform (MYcrobiota) for clinical diagnostics

Boers, Stefan A, Saskia D Hiltmann, Andrew P Stubbs, Ruud Jansen, and John P Hays

European Journal of Clinical Microbiology & Infectious Diseases 37.6 (2018) pp. 1081–1089. Springer, 2018

Systematically linking tranSMART, Galaxy and EGA for reusing human translational research data

Zhang, Chao, Jochem Bijlard, Christine Staiger, Serena Scollen, David van Enckevort, Youri Hoogstrate, Alexander Senf, Saskia Hiltmann, Susanna Repo, Wibo Pipping, et al.

F1000Research 6 (2017). Faculty of 1000 Ltd, 2017

Integration of EGA secure data access into Galaxy

Dylan, D, Youri Hoogstrate, C Chao, A Alexander, J Jochem, Saskia Hiltemann, David van Enckevort, S Susanna, J Jaap, Guido Jenster, et al.

F1000Research 5 (2016). 2016

Integration of EGA secure data access into Galaxy

Hoogstrate, Youri, Chao Zhang, Alexander Senf, Jochem Bijlard, Saskia Hiltemann, David van Enckevort, Susanna Repo, Jaap Heringa, Guido Jenster, Remond JA Fijneman, et al.

F1000Research 5 (2016). Faculty of 1000 Ltd, 2016

Next-generation sequencing reveals novel rare fusion events with functional implication in prostate cancer

Alves, I Teles, Thomas Hartjes, Elizabeth McClellan, Saskia Hiltemann, René Böttcher, Natasja Dits, MR Temanni, Bart Janssen, W Van Workum, Peter van der Spek, et al.

Oncogene 34.5 (2015) p. 568. Nature Publishing Group, 2015

Discriminating somatic and germline mutations in tumor DNA samples without matching normals

Hiltemann, Saskia, Guido Jenster, Jan Trapman, Peter van der Spek, and Andrew Stubbs

Genome research (2015). Cold Spring Harbor Lab, 2015

FuMa: reporting overlap in RNA-seq detected fusion genes

Hoogstrate, Youri, René Böttcher, Saskia Hiltemann, Peter J van der Spek, Guido Jenster, and Andrew P Stubbs

Bioinformatics 32.8 (2015) pp. 1226–1228. Oxford University Press, 2015

iReport: a generalised Galaxy solution for integrated experimental reporting

Hiltemann, Saskia, Youri Hoogstrate, Peter Van der Spek, Guido Jenster, and Andrew Stubbs

GigaScience 3.1 (2014) p. 19. BioMed Central, 2014

CGtag: complete genomics toolkit and annotation in a cloud-based Galaxy

Hiltemann, Saskia, Hailiang Mei, Mattias de Hollander, Ivo Palli, Peter van der Spek, Guido Jenster, and Andrew Stubbs

GigaScience 3.1 (2014) p. 1. BioMed Central, 2014

ImmunoGlobulin galaxy (IGGalaxy) for simple determination and quantitation of immunoglobulin heavy chain rearrangements from NGS

Moorhouse, Michael J, David van Zessen, Hanna IJspeert, Saskia Hiltemann, Sebastian Horsman, Peter J van der Spek, Mirjam van der Burg, and Andrew P Stubbs

BMC immunology 15.1 (2014) p. 59. BioMed Central, 2014

Gene fusions by chromothripsis of chromosome 5q in the VCaP prostate cancer cell line

Alves, Inês Teles, Saskia Hiltemann, Thomas Hartjes, Peter van der Spek, Andrew Stubbs, Jan Trapman, and Guido Jenster

Human genetics 132.6 (2013) pp. 709–713. Springer, 2013

iFUSE: integrated fusion gene explorer

Hiltemann, Saskia, Elizabeth A McClellan, Jos van Nijnatten, Sebastiaan Horsman, Ivo Palli, Ines Teles Alves, Thomas Hartjes, Jan Trapman, Peter van der Spek, Guido Jenster, et al.

Bioinformatics 29.13 (2013) pp. 1700–1701. Oxford University Press, 2013

Huvariome: a web server resource of whole genome next-generation sequencing allelic frequencies to aid in pathological candidate gene selection

Stubbs, Andrew, Elizabeth A McClellan, Sebastiaan Horsman, Saskia D Hiltemann, Ivo Palli, Stephan Nouwens, Anton HJ Koning, Frits Hoogland, Joke Reumers, Daphne Heijnsman, et al.

Training