




Saskia Hiltemann

Doctoral Researcher, Bioinformatics & Training



About

Laakkade 378
2521 XV, Den Haag
The Netherlands

zaskia@gmail.com ✉
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 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.	Galaxy Community Conference 2016
2016-18	Galaxy Interactive Environment Development Created Galaxy Interactive Environments (GIEs) for several applications, including Phinch for metagenomic data visualisation and Ethercalc.	GalaxyProject
2012-18	Galaxy Tool Development 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.	GalaxyProject

Publications

1. MYcrobiota
2. Training materials
3. Galaxy update
4. ASAIM
5. Chao Zhang, Jochem Bijlard, Christine Staiger, Serena Scollen⁴, David van Enckevort, Youri Hoogstrate, Alexander Senf, **Saskia Hiltemann**, Susanna Repo, Wibo Pipping, Mariska Bierkens, Stefan Payralbe, Bas Stringer, Jaap Heringa, Andrew Stubbs, Luiz Olavo Bonino Da Silva Santos, Jeroen Belien, Ward Weistra, Rita Azevedo, Kees van Bochove, Gerrit Meijer, Jan-Willem Boiten, Jordi Rambla, Remond Fijneman, J. Dylan Spalding, Sanne Abeln. Systematically linking tranSMART, Galaxy and EGA for reusing human translational research data. *F1000Research*. 2017, 6:1488 (doi: 10.12688/f1000research.12168.1).
6. Youri Hoogstrate, Chao Zhang, Alexander Senf, Jochem Bijlard, **Saskia Hiltemann**, David van Enckevort, Susanna Repo, Jaap Heringa, Guido Jenster, Remond J.A. Fijneman, Jan-Willem Boiten, Gerrit A. Meijer, Andrew Stubbs, Jordi Rambla, Dylan Spalding and Sanne Abeln. Integration of EGA secure data access into Galaxy. *F1000Research*. 2016;5:ELIXIR-2841. doi:10.12688/f1000research.10221.1.
7. Hoogstrate Y, Böttcher R, **Hiltemann S**, van der Spek PJ, Jenster G, Stubbs AP. FuMa: reporting overlap in RNA-seq detected fusion genes. *Bioinformatics*. 2016 Apr 15;32(8):1226-8. doi: 10.1093/bioinformatics/btv721.
8. **Hiltemann S**, Jenster G, Trapman J, van der Spek P, Stubbs A. Discriminating somatic and germline mutations in tumor DNA samples without matching normals. *Genome Research*. 2015;25(9):1382-1390. doi:10.1101/gr.183053.114.

9. Moorhouse MJ, van Zessen D, IJspeert H, **Hiltemann S**, Horsman S, van der Spek PJ, van der Burg M, Stubbs AP. ImmunoGlobulin galaxy (IGGalaxy) for simple determination and quantitation of immunoglobulin heavy chain rearrangements from NGS. *BMC Immunology*. 2014;15:59. doi:10.1186/s12865-014-0059-7.
10. **Hiltemann S**, Hoogstrate Y, der Spek P van, Jenster G, Stubbs A. iReport: a generalised Galaxy solution for integrated experimental reporting. *GigaScience*. 2014;3:19. doi:10.1186/2047-217X-3-19.
11. Teles Alves I, Hartjes T, McClellan E, **Hiltemann S**, Böttcher R, Dits N, Temanni MR, Janssen B, van Workum W, van der Spek P, Stubbs A, de Klein A, Eussen B, Trapman J, Jenster G. Next-generation sequencing reveals novel rare fusion events with functional implication in prostate cancer. *Oncogene*. 2015 Jan 29;34(5):568-77. doi: 10.1038/onc.2013.591.
12. **Hiltemann S**, Mei H, de Hollander M, et al. CGtag: complete genomics toolkit and annotation in a cloud-based Galaxy. *GigaScience*. 2014;3:1. doi:10.1186/2047-217X-3-1.
13. Teles Alves I, **Hiltemann S**, Hartjes T, van der Spek P, Stubbs A, Trapman J, Jenster G. Gene fusions by chromothripsis of chromosome 4q in the VCaP prostate cancer cell line. *Hum Genet*. 2013 Jun;132(6):709-13. doi: 10.1007/s00439-013-1308-1.
14. **Hiltemann S**, McClellan EA, van Nijnatten J, Horsman S, Palli I, Teles Alves I, Hartjes T, Trapman J, van der Spek P, Jenster G, Stubbs A. iFUSE: integrated fusion gene explorer. *Bioinformatics*. 2013 Jul 1;29(13):1700-1. doi: 10.1093/bioinformatics/btt252.
15. Stubbs A, McClellan EA, Horsman S, **Hiltemann S**, Palli I, Nouwens S, Koning AHJ, Hoogland F, Reumers J, Heijnsman D, Swagemakers S, Kremer A, Meijerink J, Lambrechts D, van der Spek PJ. Huvariome: a web server resource of whole genome next-generation sequencing allelic frequencies to aid in pathological candidate gene selection. *Journal of Clinical Bioinformatics*. 2012;2:19. doi:10.1186/2043-9113-2-19.

Training