




# Saskia Hiltemann

Doctoral Researcher, Bioinformatics & Training



## About

Laakkade 378  
2521 XV, Den Haag  
The Netherlands

zazkia@gmail.com ✉  
shiltemann   

## Languages

Bilingual Dutch/English  
German & French

## Skills

Python, C, C++, UNIX,  
Galaxy, Docker, Jekyll,  
LaTeX

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

## Work Experience

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

## Projects

2018	<b>Clinical Microbiota Analysis Pipeline</b> Development of an analysis pipeline for use in daily clinical diagnostics of sepsis patients for Streeklab Haarlem.	ErasmusMC
2016-2018	<b>Galaxy Training Materials</b> 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	<b>Galaxy CTF</b> 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
2016-2018	<b>Galaxy Interactive Environment Development</b> Created Galaxy Interactive Environments (GIEs) for several applications, including Phinch for metagenomic data visualisation and Ethercalc.	GalaxyProject
2012-2018	<b>Galaxy Tool Development</b> 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

The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2018 update  
Enis Afgan, 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

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

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

Community-driven data analysis training for biology

Bérénice Batut, Saskia Hiltemann, 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

Stefan A Boers, Saskia D Hiltemann, 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

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

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

Integration of EGA secure data access into Galaxy

D Dylan, 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

Youri Hoogstrate, 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

I Teles Alves, 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

Saskia Hiltemann, 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

Youri Hoogstrate, 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

Saskia Hiltemann, 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

Saskia Hiltemann, 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

Michael J Moorhouse, 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

Inês Teles Alves, 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

Saskia Hiltemann, 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

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

*Journal of clinical bioinformatics* 2.1 (2012) p. 19. BioMed Central, 2012