

# Saskia Hiltemann

Post-Doctoral Researcher, Bioinformatics & Education



## About

De Carpentierstraat 24  
2595HL, Den Haag  
The Netherlands

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shiltemann   

## Languages

Bilingual Dutch/English  
German & French

## Skills

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

## Interests

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

## Education

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|------------|---|--|
| Since 2021 | <b>Post-doctoral Researcher</b>   | Erasmus Medical Center                 |
|            | <i>Focus on Microbiology Research, Federated Data Analysis, FAIR principles, Open Science, Software Development and Bioinformatics Education.</i> |  |
| 2012-2020  | <b>Ph.D. Researcher, Bioinformatician</b>   | Erasmus Medical Center                 |
|            | <i>Focus on cancer analysis, metagenomics research. Galaxy tool and training development.</i>   |  |
| 2008-2010  | <b>M.Sc.</b>  | LIACS, University of Leiden & TU Delft |
|            | Computer Science<br>Specialization in Bioinformatics  |  |
| 2005-2008  | <b>B.Sc.</b>  | LIACS, University of Leiden            |
|            | Computer Science  |  |
| 2002-2005  | <b>B.Sc. course work</b>  | University of Leiden                   |
|            | Physics & Astronomy   |  |
| 2002       | <b>High School (VWO)</b>  | Alfrink College, Zoetermeer            |
|            | Specialization in Science & Technology  |  |

## Work Experience

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|-----------|---|
| Current   | <b>Erasmus Medical Center, Rotterdam</b>  |
|           | Post-doctoral Researcher & Bioinformatician   |
|           | <ul style="list-style-type: none"><li>• Training, Outreach &amp; Dissemination</li><li>• Federated Data Analysis Infrastructure Development</li><li>• FAIR data analysis</li><li>• Education &amp; Curriculum Development</li><li>• Antibiotic Resistance Detection</li></ul> |
| 2016-2021 | <b>Erasmus Medical Center, Rotterdam</b>  |
|           | Ph.D. Candidate   |
|           | <ul style="list-style-type: none"><li>• Software Development and Pipeline building</li><li>• Training Development and Delivery</li><li>• Galaxy System's Administrator</li><li>• Microbiota Analysis and Antibiotic Resistance Detection</li></ul>                            |
| 2012-2016 | <b>Erasmus Medical Center, Rotterdam</b>  |
|           | Junior Researcher & Bioinformatician  |
|           | <ul style="list-style-type: none"><li>• Software Development and Pipeline building</li><li>• Galaxy System's Administrator</li><li>• Prostate Cancer Analysis</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

2020-2023	<b>Gallantries Project, Coordinator</b> Continuation of the Gallantries pilot project, development of bioinformatics curricula for higher education and training workshop.	ErasmusMC, Erasmus+ KA203 grant
2019-2023	<b>CINECA project Training &amp; Dissemination WP co-lead</b> CINECA (Common Infrastructure for National Cohorts in Europe, Canada, and Africa) aims at creating a global infrastructure for federated data analysis. I Co-lead the Training & Dissemination workpackage, and am involved in the Clinical Applications WP.	ErasmusMC, Horizon2020 grant
2019	<b>Gallantries Pilot Project</b> Lesson development combining Galaxy training with Carpentries-style R lessons. Scalable delivery of training via a series of hybrid-style workshops.	ErasmusMC, Mozilla mini-grant
2018	<b>Clinical Microbiota Analysis Pipeline</b> Development of a user-friendly analysis pipeline for 16S taxonomic profiling for use in daily clinical diagnostics of patients for Streeklab Haarlem.	ErasmusMC
Since 2016	<b>GTN: Galaxy Training Materials Infrastructure</b> Co-founder of the GTN infrastructure for the collaborative development of Galaxy training materials. Community building efforts to ensure utility for educators. Development of several tutorials on the topics of Metagenomics, Sequence Analysis, 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
Since 2016	<b>Galaxy Interactive Environment Development</b> Created Galaxy Interactive Environments (GIEs) for several applications, including Phinch for metagenomic data visualisation and Ethercalc.	GalaxyProject
2012-2015	<b>Prostate Cancer Analysis</b> Development of analysis tools and workflows for variant analysis in cancer, including fusion gene detection and impact analysis, and identification of somatic variants without normal samples.	ErasmusMC
Since 2012	<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 that develop and ensure adherence to best-practices and FAIR principles.	GalaxyProject

## Publications

### Fostering accessible online education using Galaxy as an e-learning platform

Saskia Hiltemann, Beatriz Serrano-Solano, Patricia M. Palagi, Melanie C. Föll, Cristóbal Gallardo-Alba, Anika Erxleben, Helena Rasche, Saskia Hiltemann, Matthias Fahrner, Mark J. Dunning, Marcel H. Schulz, Beáta Scholtz, Dave Clements, Anton Nekrutenko, Bérénice Batut, and Björn A. Grüning

*PLOS Computational Biology* (2021). 2021

### ASaiM-MT: a validated and optimized ASaiM workflow for metatranscriptomics analysis within Galaxy framework

Subina Mehta, Marie Crane, Emma Leith, Bérénice Batut, Saskia Hiltemann, Magnus Ø Arntzen, Benoit J. Kunath, Phillip B. Pope, Francesco Delogu, Ray Sajulga, Praveen Kumar, James E. Johnson, Timothy J. Griffin, and Pratik D. Jagtap

*10 (Apr. 2021) p. 103. F1000 Research Ltd, 2021*

### Comparison of Illumina versus Nanopore 16S rRNA Gene Sequencing of the Human Nasal Microbiota

Astrid P. Heikema, Deborah Horst-Kreft, Stefan A. Boers, Rick Jansen, Saskia D. Hiltemann, Willem de Koning, Robert Kraaij, Maria A. J. de Ridder, Chantal B. van Houten, Louis J. Bont, Andrew P. Stubbs, and John P. Hays

*11.9 (Sept. 2020) p. 1105. MDPI AG, 2020*

### NanoGalaxy: Nanopore long-read sequencing data analysis in Galaxy

Saskia Hiltemann, Willem de Koning, Milad Miladi, Saskia Hiltemann, Astrid Heikema, John P Hays, Stephan Flemming, Marius van den Beek, Dana A Mustafa, Rolf Backofen, Björn Grüning, and Andrew P Stubbs

*GigaScience* (2020). 2020

### Galactic Circos: User-friendly Circos plots within the Galaxy platform

Saskia Hiltemann, Helena Rasche, and Saskia Hiltemann

*GigaScience* (2020). 2020

### 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

*37.6 (Mar. 2018) pp. 1081–1089. Springer Science and Business Media LLC, 2018*

### Galaxy mothur Toolset (GmT): a user-friendly application for 16S rRNA gene sequencing analysis using mothur

Saskia D Hiltemann, Stefan A Boers, Peter J van der Spek, Ruud Jansen, John P Hays, and Andrew P Stubbs

*GigaScience* (Dec. 2018). *Oxford University Press (OUP)*, 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, Dave Clements, Olivia Doppelt-Azeroual, Anika Erxleben, Mallory Freeberg, Simon Gladman, Youri Hoogstrate, Hans-Rudolf Hotz, Torsten Houwaart, Pratik Jagtap, Delphine Larivière, Gildas Le Corguillé, Thomas Manke, Fabien Mareuil, Fidel Ramírez, Devon Ryan, Florian Sigloch, Nicola Soranzo, Joachim Wolff, Pavankumar Videm, Markus Wolfien, Aisanjiang Wubuli, Dilmurat Yusuf, Rolf Backofen, James Taylor, Anton Nekrutenko, and Björn Grüning

*(Nov. 2017). Cold Spring Harbor Laboratory, 2017*

### Systematically linking tranSMART, Galaxy and EGA for reusing human translational research data [version 1; referees: 2 approved]

Saskia Hiltemann, Chao Zhang, Jochem Bijlard, Christine Staiger, Serena Scollen, 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, and Sanne Abeln

(2017). 2017

Integration of EGA secure data access into Galaxy [version 1; referees: 2 approved]

Youri Hoogstrate, C Zhang, A Senf, J Bijlard, S Hiltemann, D van Enckevort, S Repo, J Heringa, G Jenster, R J.A. Fijneman, JW Boiten, G A. Meijer, A Stubbs, J Rambla, D Spalding, and S Abeln

F1000Research 5.2841 (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 J.A. Fijneman, Jan-Willem Boiten, Gerrit A. Meijer, Andrew Stubbs, Jordi Rambla, Dylan Spalding, and Sanne Abeln

F1000Research 5 (Dec. 2016) p. 2841. F1000 Research, 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) pp. 568–577. 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 25.9 (2015) pp. 1382–1390. 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 (2015) btv721. Oxford Univ Press, 2015

iReport: a generalised Galaxy solution for integrated experimental reporting.

Saskia Hiltemann, Youri Hoogstrate, Peter van v. der Spek, Guido Jenster, and Andrew Stubbs

GigaScience 3 (2014). 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 Nijmegen, Sebastiaan Horsman, Ivo Palli, Ines Teles Alves, Thomas Hartjes, Jan Trapman, Peter van der Spek, Guido Jenster, et al.

Bioinformatics (2013) *btt252*. Oxford Univ 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 Heijman, et al.

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

Multi-coloured Cellular Automata

Saskia Hiltemann

Bachelor thesis, Erasmus Universiteit, Rotterdam, Netherlands (2008). 2008