

Silas Kieser

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"It always seems impossible until it's done." Nelson Mandela

Professional Highlights:

- Lead Developer of Metagenome Atlas, a pipeline for genome-resolved metagenomics, ranking in the top 10% of most downloaded bioinformatics packages.
- Recipient of an award from the Swiss Bioinformatics Institute for extensive analyses of all public mouse microbiome data.
- Internationally recognized speaker and educator for metagenomics and bioinformatics.

Experience

- Metagenome Researcher *HUG Memory Center, Geneva* Jan 2023 – Current
Data analysis of large clinical trials
- Microbiome data Specialist *Nestlé institute of health science, Lausanne* Sept 2022 – Aug 2023
 - Implementing reproducible pipelines on a HPC cluster
 - Data analysis for clinical trials
- Data analyst *SurvivAI, University of Geneva* June 2022 – Aug 2022
 - Analyzing single-cell data using machine learning algorithms in a start-up setting.
 - **Applying deep-learning model (torch) on many datasets**
 - Implementing reproducible analysis from raw-data to report
- PostDoc *Lab of Prof. Trajkovski, University of Geneva* Sept 2021 – Jul 2022
 - Large scale analysis of public human microbiome data at the sub-species level
 - Spatial-transcriptomics of adipose tissue
 - Supervision of a PhD Student.
- I-teams startup-competition *Translational accelerator, University of Geneva* Sept 2018 – Jan 2019
Public award winner for our project to bring an invention from bench to bedside
- Microbiome data analyst *Nestlé Research, Vers-chez-les-Blanc* Feb 2016 – Feb 2017
Pioneering metagenomics at Nestlé research.

Education

- PhD *Faculty of Medicine, University of Geneva* May 2017 – Aug 2021
Supervisor: Prof. Mirko Trajkovski
 - **Led an international collaboration to develop a computational pipeline**
 - Large-scale analysis and functional modeling of microbiomesGraduate courses: Agile project management | **Cloud computing** | Oncology

Master in Bioengineering EPFL, Lausanne Grade: 5.43/6 Minor in Biocomputing Selected courses: Machine learning Bioinformatics Reinforcement learning Biochemistry Genomics and genetics Entrepreneurship	Sept 2014 – Jan 2017
Bachelor in Life Sciences EPFL, Lausanne Grade: 5.12/6	Sept 2011 – Aug 2014

Skills

Programming Languages.....

Python: 10y experience, daily usage **R:** 2y experience, daily usage
Snakemake-workflow language: expert, 5y experience, frequent usage
Google Cloud, Kubernetes: beginner
Git: 6y experience, daily usage **bash:** daily usage

Languages.....

English: Fluent **German:** Mother tongue
French: Fluent

Selected Talks & Teaching

Invited Speaker European space agency, Noordwijk, the Netherlands	October 2023
Selected workshop ISMB/ECCB 2023 conference, Remote	Jun 2023
Invited speaker Swedish University of Agricultural Science, Uppsala	Dec 2022
3-day online workshop Finnish Centre for Scientific Computing, Remote	Sep 2021
Full-day workshop Swiss Institute of Bioinformatics, Remote I proposed, organized, and taught the online class. The mixed audience of PhD students, professors, and industry researchers gave thoroughly positive feedback.	Dec 2020 + Dec 2021
Teaching assistant EPFL, Lausanne Teaching assistant for 1 st year physics and 3 rd year C++ programming	Sept 2012 – Feb 2015

Selected Publications

- Development a **pipeline for genome-resolved metagenomics in an international collaboration**
 - “ATLAS: a Snakemake workflow for assembly, annotation, and genomic binning of metagenome sequence data”
BMC Bioinformatics, 2020 , (1st author)
 - Part of the top 10% most downloaded bioconda packages
 - Used by start-ups and companies such as Koonkie, and Nestlé
- Large-scale analysis of metagenome-assembled genomes from mice
 - “Comprehensive mouse microbiota genome catalog reveals major difference to its human counterpart”
PLoS Computational Biology, 2022 , (only non-PI author)
- Functional prediction of the microbiome confirmed with metabolomics
 - “Warmth Prevents Bone Loss Through the Gut Microbiota”
Cell Metabolism, 2020 , (2nd author)