MARIUS EISELE

BIOINFORMATICIAN

Tenerife, Spain

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WORK EXPERIENCE

Bioinformatician of the MOMENTUM project (CSIC) December 2024 – present
Instituto de Productos Naturales y Agrobiología (IPNA, CSIC), Tenerife (Spain)

Population genetics and metabarcoding data analysis, with a focus on improving currently used algorithms for diversity estimations using different AI approaches.

Bioinformatician of the Horizon Europe's Biodiversity December 2023 – October 2024
Genomics Europe (BGE) project
Instituto de Productos Naturales y Agrobiología (IPNA, CSIC), Tenerife (Spain)

Development of a metabarcoding data analysis pipeline with optimal denoising based on the benchmarking of different denoising tools. A large dataset of whole organism community DNA (wocDNA) of arthropod samples was used to assess the performance of each denoising tool.

Bioinformatician May 2022 – November 2023
Genetikum, Neu-Ulm (Germany)

Optimization of an in-house NGS sequencing pipeline. Developed websites to accelerate disease-causing variant identification. In charge of quality control and access to sequencing data

January 2021 – June 2021
Research assistant
Algorithms of Bioinformatics at the University of Tübingen, Tübingen (Germany)

Metagenome assembly of long-read sequencing data with different command-line tools

September 2020 – December 2020
& November 2022 – April 2023
Internship & Master's thesis
Computomics, Tübingen (Germany)

Plant genetics and breeding. Statistical overview of large datasets and visualization of genetic distances with interactive plots. Exploration of pangenome graph generation tools to determine genetic diversity

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PUBLICATIONS & REPORTS

2024

Eisele, M. H., Roslin T., Ovaskainen O., Furneaux B., Emerson B. & Andujar C. (in prep.) Benchmarking metabarcode sequence denoisers for improved community diversity estimates from bulk samples. Target Journal: Methods in Ecology and Evoluation

Eisele, M. H., Emerson B. & Andujar C. (2024) Milestone Report of Task 8.5 (work package 8) of the BGE project, focused on the benchmarking results of the metabarcode sequence denoisers

2022

Madrigal-Mora, S., Eisele, M. H., & Espinoza, M. (2022). Do reef fish assemblages benefit from a marine protected area in the north Pacific coast of Costa Rica?. Environmental Biology of Fishes, 105(5), 541–559.

2021

Eisele, M. H., & Kappelmann-Fenzl, M. (2021). Ngs technologies. In Next Generation Sequencing and Data Analysis (pp. 47–58). Cham: Springer International Publishing.

2020

Eisele, M. H., Madrigal-Mora, S., & Espinoza, M. (2021). Drivers of reef fish assemblages in an upwelling region from the Eastern Tropical Pacific Ocean. Journal of Fish Biology, 98(4), 1074–1090.

EDUCATION

Master of Science (MSc) in Bioinformatics   2020–2022

Eberhard Karls Universität Tübingen, Germany

Degree in MSc Bioinformatics with a focus on (meta–)genomics, statistics, bioinformatics tools and programming. The master's thesis was about the exploration of pangenome graph generation tools to accurately determine genetic diversity of *Cannabis sativa*

Master of Science (MSc) in Life Science Informatics   2019 - 2020

Deggendorf Institute of Technology (DIT), Germany

Credits of the MSc in Life Science Informatics, centering around the analysis and visualization of next–generation sequencing (NGS) data, sequencing technologies, data structures and data mining

Exchange program   2016 - 2017

Universidad de Costa Rica (UCR), Costa Rica

Strong focus on zoology and ecology of aquatic ecosystems

Bachelor of Science (BSc) in Biology   2014 - 2019

Universität Ulm, Germany

Degree in BSc Biology with a focus on ecology and biostatistics. In my bachelor thesis I explored the effects that (a–)biotic factors have on fish assemblages in different marine protected areas in the Pacific coast of Costa Rica

CONFERENCE ATTENDANCE & PRESENTATIONS

International Barcode of Life Conference (iBOL) September 3–6, 2024   Presenter and Attendee

European Conference on Computational Biology (ECCB) July 23–27, 2023   Attendee

SKILLS

Programming languages   **Microsoft Office**

Python, R, Bash, PHP, JS   Excel, Word, Teams

LANGUAGES

German   **Spanish**   **English**   **Japanese**

native   fluent   fluent   novice speaker

VOLUNTEERING

TedX DIT   2019 - 2020

Head of the curation team

ESN DIT   2019 - 2020

Organizing events for international students

Mediator   2008 - 2010

Solving disputes between students in the secondary school