



# DR. MARIA BEATRIZ WALTER COSTA

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EU permanent resident (Germany)

<https://waltercostamb.github.io/>

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## SUMMARY

Bioinformatician with 15+ years of experience in biological data analysis and interpretation, with strong skills in pipeline development. Proven track record of interdisciplinary collaboration and support of data-driven decisions. Seeking a senior role in the biotechnology industry with real-world impact.

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## WORK EXPERIENCE

### Research Associate (fixed-term contract)

*Friedrich-Schiller University Jena*

Jena, Germany

10/2022 - 09/2025

- Led a project in Microbiology with large-scale data and collaborators (Machine Learning, python)
- Designed and implemented a scalable, reproducible high-throughput pipeline (snakemake, slurm)
- Co-supervised a Doctoral researcher and co-designed a Masters' level course on Big Data analysis
- Regularly presented results to interdisciplinary audiences at national and international conferences

### Research Associate (fixed-term contract)

*University of Leipzig Medical Center*

Leipzig, Germany

02/2020 - 12/2021

- Developed and delivered three applied projects in Laboratory Medicine (Statistics, R, SAP-based data)
- Organized and structured a clinical knowledge dataflow, improving consistency and downstream analysis
- Worked in close collaboration with physicians to support decision-making and improve patient safety

### Consultant (fixed-term contract)

*Brazilian Agricultural Research Corporation (EMBRAPA)/Agroenergy*

Brasília/DF, Brazil

11/2018 - 03/2019

- Designed and executed a project to optimize industrial ethanol production (Bioinformatics, R)
- Worked closely with biologists to support experimental decision-making in engineered strain development

### Research Associate (fixed-term contract)

*University of Leipzig*

Leipzig, Germany

04/2017 - 03/2018

- Led and implemented a project to improve understanding of ncRNA evolution (Bioinformatics, perl)
- Developed and released two tools for ncRNA analysis (Bioinformatics, perl, bash)

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## EDUCATION

### Dr. rer. nat. in Computer Science (*Magna cum laude*)

2013 - 2018

- University of Leipzig, Faculty of Mathematics and Computer Science, Chair of Bioinformatics (Germany)
- Dissertation: "Adaptive Evolution of Long Non-Coding RNAs"

## M. Sc. in Molecular Biology

2010 - 2012

- University of Brasília, Institute of Biological Sciences, Graduation Program of Molecular Biology (Brazil)
- Thesis: "Genetic Variability of anti-DNA antibodies"

## B. Sc. in Biological Sciences (Grade: 4.3/5.0)

2006 - 2010

- University of Brasília, Institute of Biological Sciences (Brazil)

## LANGUAGES

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<b>English</b>	Near-native speaker (C2, Cambridge CPE)
<b>Portuguese</b>	Native speaker (C2)
<b>German</b>	Advanced (C1)
<b>Spanish</b>	Advanced (B2/C1)

## TECHNICAL SKILLS

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<b>Programming</b>	python, R, perl, bash, SQL (mySQL)
<b>Workflow &amp; Automation</b>	Snakemake
<b>Bioinformatics</b>	omics analysis, differential expression, mapping, sequence analysis, alignment, NGS analysis, ncRNAs, annotation, genome assembly, machine learning, software development
<b>Cluster Platforms (user)</b>	Slurm, Sun Grid Engine (SGE)
<b>Version Control</b>	Git, GitHub
<b>Others</b>	Linux, Jupyter Notebook, Latex, Markdown

## MAIN PRODUCTS (FULL LIST ON PERSONAL WEBSITE)

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- **FxTractor**: scalable high-throughput pipeline for feature extraction from microbial genomes  
<https://github.com/MGXlab/FxTractor>
- **SSS-test**: the first tool of the scientific community that detects adaptive selection in ncRNAs  
<https://github.com/waltercostamb/SSS-test>
- **genes-synteny**: tutorial and scripts to visualize gene synteny and homology  
[https://github.com/MGXlab/genes\\_synteny](https://github.com/MGXlab/genes_synteny)

## MAIN SCIENTIFIC PUBLICATIONS (FULL LIST ON PERSONAL WEBSITE)

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- **Walter Costa MB et al.** The Clinical Decision Support System AMPEL for Laboratory Diagnostics: Implementation and Technical Evaluation. *JMIR Med Informatics*, 2021  
<https://medinform.jmir.org/2021/6/e20407>
- **Walter Costa, MB et al.** SSS-Test: A novel test for detecting selection on the secondary structures of non-coding RNAs. *BMC Bioinformatics*, 2019  
<https://doi.org/10.1186/s12859-019-2711-y>