

Gesiele Almeida Barros de Carvalho
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Summary of Skills

- Operational Systems: MacOS and Linux ;
- Programming:
 - Main: Python, SQL, Perl and WDL;
 - Basic Knowledge: R, Ruby, HTML, CSS and Shell script;
- Toolkit for Data Analysis: Jupyter-Notebook, Metabase and RStudio;
- Libraries: Pandas, Numpy, Matplotlib, Seaborn, Boket and Scikit-learn;
- Databases: PostgreSQL, MySQL and MongoDB (basic);
- Version Control System: Git, GitHub and GitLab;
- Good practices with Data Visualization;
- Machine Learning: Linear Regression, Logistic Regression and Clustering (K-means);
- Knowledge in Quality Control: ABNT NBR ISO 15189;
- Agile methodology: Trello and Mondays;
- Pipeline development;
- Biological Data Analysis (Bioinformatics): Genomics (Assembly and Annotation), RNAseq (*De novo* assembly, Quantification, among others), Transposable Elements analysis, miRNAs, among others;
- Intermediary English;
- Good communication skills.

Work History

- 2018-now: Butantan Institute
- 2017-2018: Mendelics Análise Genômica
- 2012– 2016: Genomics and Transposable Elements Lab (GaTE-USP)
- 2009– 2012: Soil Biotechnology Lab (EMBRAPA Soybean)

Education

- PhD in Bioinformatics (IME-USP, 2016);
- Master's Degree in Biotechnology (UEL, 2012);
- Bachelor's Degree in Biological Sciences (UENP, 2009).

Main Publications:

BARROS-CARVALHO, G.A.; LOPES, F.M.; HUNGRIA, M.; VAN SLUYS, M.A. Brazilian-adapted soybean *Bradyrhizobium* strains uncover IS elements with potential impact on biological nitrogen fixation. *FEMS Microbiology Letters*, 2019.

BARROS-CARVALHO G.A.; VAN SLUYS M.A.; LOPES, F.M. An Efficient Approach to Explore and Discriminate Anomalous Regions in Bacterial Genomes Based on Maximum Entropy. *Journal of Computational Biology*, 2017.

HELENA TURANO, FERNANDO GOMES, **GESIELE BARROS-CARVALHO**, RALF LOPES, LOUISE CERDEIRA, LUIS NETTO, ANA GALES, NILTON LINCOPAN. Tn6350, a Novel Transposon Carrying Pyocin S8 Genes Encoding a Bacteriocin with Activity against Carbapenemase-Producing *Pseudomonas aeruginosa*. *Antimicrobial Agents and Chemotherapy*, v. 61, 2017.

BARROS-CARVALHO, G.A.; PASCHOAL, A.R.; MARCELINO-GUIMARÃES, F.C.; HUNGRIA, M. Prediction of potential novel microRNAs in soybean when in symbiosis. *Genetics and Molecular Research*, v. 13, p. 8519-8529, 2014.

BARROS DE CARVALHO, G. A.; BATISTA, J. S.; MARCELINO-GUIMARÃES, F. C.; COSTA DO NASCIMENTO, L.; HUNGRIA, M.. Transcriptional analysis of genes involved in nodulation in soybean roots inoculated with *Bradyrhizobium japonicum* strain CPAC 15. *BMC Genomics*, v. 14, p. 153, 2013.

CARVALHO, GESIELE ALMEIDA BARROS; BATISTA, JESIANE STEFÂNIA SILVA; MARCELINO, FRANCISMAR CORRÊA; HUNGRIA, MARIANGELA. Subtractive library of soybean roots in response to inoculation with *Bradyrhizobium japonicum*. *BBR- Biochemistry and Biotechnology Reports*, v. 1, p. 3-8, 2012.