

Andre FONSECA

Bioinformatician | Data Scientist

+1 (832) 872 9090 3433 West Dallas Street, Houston, 77019 @ oandrefonseca@gmail.com oandrefonseca oandrefonseca

I am a bioinformatician with solid expertise in bulk and single-cell transcriptome analysis, tumor immunology, machine learning, and data integration. Currently, I am working on tumor antigen discovery, T-cell cross-reactivity prediction, and single-cell TCR analysis. During my career, I was involved in training small teams of bioinformaticians and biomedical researchers. Furthermore, I am experienced in system administration and software development. As a professional, I would like to bring value and push forward the discovery of new products and treatments against cancer and other human diseases.

Please, check out the url [X](#).

SCIENTIFIC SKILLS

Cancer Biology	Pan-cancer analysis and Survival signature prediction - Paper: 1 , 2 , 3
T-cell and Tumor immunology	Cross-reactivity prediction, and Tumor immunoprofiling analysis - Paper: 4 , 6
Antigen discovery	Neoantigens and Tumor-associated antigens prioritization - Paper: 5 , 6
Single-cell and Bulk Transcriptomics	Cell annotation, TCR Repertoire, Gene expression profiling, and Splicing alternative analysis - Paper: 7 , Code: 1
Pipeline Development	Tumor antigen prediction, and Proteomics screening - Paper: 5 , 8 , Code: 2

TECHNICAL SKILLS

Programming	Python, R, Shell-script, Perl, JavaScript and GO
Package development	R, Shiny, and Steamlit - Code: 1
Machine/Deep Learning	Scikit-learn, and TensorFlow - Code: 2
Transcriptomics	Seurat, DeSeq2, SUPPA2, Monocle3, Immunarch, GLIPH2, MIXCR - Code: 3
Database	MariaDB and MongoDB
Versioning and DevOps	Git, Travis, and CircleCI
OS and System Administration	Ubuntu Server, CentOS, and Slurm
Pipeline management	Snakemake, CWL, Docker, Docker Compose, and Kubernetes
Documentation	Mkdocs, LaTeX, Roxygen2, and pkgdown

EDUCATION

2020 - 2020	Certificated in Data Science - Machine Learning, Awari School
2016 - 2018	Ph.D. in Bioinformatics, Federal University of Rio Grande do Norte
2014 - 2016	M.Sc. in Genetics and Molecular Biology, Federal University of Pará
2009 - 2013	B.Sc. in Biology, Federal University of Rio Grande do Norte

PROFESSIONAL EXPERIENCE

April 2021 Present	Postdoctoral Researcher, UNIVERSITY OF HOUSTON, Texas Project: Predicting T-cell cross-reactivity to mitigate off-target toxicity risk on immunotherapy Cross-reactivity Tumor immunology TCR Repertoire Antigen discovery Single-cell Transcriptomics
September 2019 April 2021	Postdoctoral Researcher, UNIVERISTY OF SAO PAULO, Sao Paulo Project: Characterizing transcriptional regulation of the major histocompatibility complex (MHC) region across human populations and diseases Immunogenetics eQTL Chromatin Regulation Topological-associated Domains Super-Enhancers
November 2018 June 2019	Bioinformatics Assistant, DUNA BIOINFORMATICS, Rio Grande do Norte Project: Pipeline development to prioritize tumor-associated antigens for vaccine design Tumor immunology R package development Antigen discovery Binding-affinity prediction Population coverage

November 2017
April 2018

Visiting Researcher, UNIVERSITY OF CALIFORNIA - SAN DIEGO, California

Project: Investigating chromosome instability and DNA repair genes in pan-cancer cohorts

➤ Hired as **Tutoring Assistant** into “Bioinformatics Applications to Human Disease” class (MED263) at University of California - San Diego - Code: **1**

Genome Instability

DNA Repair

Bulk Transcriptomics

Survival Analysis

+ SOFT SKILLS

- Passionate
- Problem-solving mind
- Team-player and collaborative person
- Curious and lifelong learner

LANGUAGES

Portuguese	●	●	●	●	●
English	●	●	●	●	○
Spanish	●	●	●	○	○

📄 PUBLICATIONS AND POSTERS

- 2022 Tarabini, R. F.; Rigo, M. M.; **Fonseca, A. F.**; Rubin, F., Bellé, R.; Kavrakli, L. E.; Ferreto, T. C.; Antunes, D.A.; Souza, A. P. D. “Large-Scale Structure-Based Screening of Potential T Cell Cross-Reactivities Involving Peptide-Targets From BCG Vaccine and SARS-CoV-2”. **Frontiers Immunology**
- 2021 ★**Fonseca, A. F.**; Antunes, D.A. “Crossdome: An R package to measure cross-reactivity risk on the sequence-space”. **Center for Nuclear Receptors and Cell Signaling Symposium**
- 2020 ★Coelho, A. C. M. F. ; **Fonseca, A. F.** ; Martins, D. L. ; Cunha, L. M. ; Lins, P. B. R. ; De Souza, S. J. “neoANT-HILL: an integrated tool for identification of potential neoantigens”. **BMC Medical Genomics**
- 2019 ★**Fonseca, A. L.**; Coelho, A. C. M. F.; De Souza, S. J. “A bioinformatics approach to cancer vaccines prioritization based on cancer-testis antigens in melanoma”. **15th International Conference of the Brazilian Association for Bioinformatics and Computational Biology - X-Meeting.**
- 2017 ★**Fonseca, A. F.**; Silva, V.; Fonseca, M.; Silva, T. ; Coelho, A.; Kroll, J.; Souza, J.; Stransky, B.; Souza, G.; Souza, S. J. “Genome-wide identification of cancer/testis genes and their association with prognosis in a pan-cancer analysis”. **Oncotarget**
- 2016 Putnam, C. D.; Srivatsan, A.; Nene, R. V.; Martinez, S. L.; Clotfelter, S. P.; Bell, S. N.; Somach, S. B.; Souza, J. S.; **Fonseca, A. L. F.**; Souza, S. J.; Kolodner, R. D. “A genetic network that suppresses genome rearrangements in *Saccharomyces cerevisiae* and contains defects in cancers”. **Nature Communications**
- 2015 Kroll, J. E. ; **Fonseca, Andre L. F.**; Souza, S. J. “Alternative splicing and cancer - Post-genomic Approaches in Cancer and NanoMedicine”. **River Publishers**

For more publications: [Google Scholar](#)