

André Fonseca

FULL NAME: ANDRÉ LUÍS FONSECA FAUSTINO

POSITION: COMPUTATIONAL BIOLOGIST

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Summary

Bioinformatician with broad expertise in transcriptome analysis, cancer research, and NGS data integration. Currently, working with prioritization of tumor antigens vaccines, and transcriptional regulation of the MHC region in diseases. Furthermore, proficient in system administration, machine learning algorithms, and the development of bioinformatics tools. Experienced in mentoring and training small teams of bioinformaticians and biomedical researches.

Education

Federal University of Rio Grande do Norte - UFRN

PH.D. IN BIOINFORMATICS

2016 - 2018

- **Thesis:** Bioinformatics applications to prognosis and cancer treatment: Studies on tumor markers, immunotherapy, and drug response. **Supervised by:** Sandro José de Souza

Federal University of Pará - UFPA

M.SC. IN GENETICS AND MOLECULAR BIOLOGY

2014 - 2016

- **Dissertation:** Identification of tumor pathways based on next-generation data: A systems biology perspective. **Supervised by:** Sandro José de Souza

Federal University of Rio Grande do Norte - UFRN

B.SC. IN BIOLOGY

2009 - 2013

Research Experience

Evolutionary Genomics Laboratory, University of São Paulo - USP

POSTDOC RESEARCH ASSOCIATE

August 2019 - Present

- **Project:** Transcriptional regulation of the MHC region across human populations and diseases. **Supervised by:** Diogo Meyer - NIH Grant

BioME, Federal University of Rio Grande do Norte - UFRN

POSTDOC RESEARCH ASSOCIATE

2018 - 2019

- **Project:** Application of bioinformatics approaches to understand immune-response mediated by cancer/testis antigens in melanoma patients. **Supervised by:** Sandro José de Souza

Ludwig Institute, University of California - San Diego - UCSD

VISITING SCHOLAR

2017 - 2018

- Attended a short-term internship as a visiting scholar (Ph.D. student) at Ludwig Institute. **Supervised by:** Richard Kolodner

LBMG - Federal University of Rio Grande do Norte - UFRN

SCIENTIFIC INTERNSHIP

2009 - 2013

- Long-term internship in bioinformatics associated with DNA Repair and metagenomics. **Supervised by:** Lucymara Fassarella Agnez-Lima

Publications

ARTICLES

1. ★ Coelho, A. C. M. F. ; **Fonseca, André L.** ; 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**, *IN PRESS* - MGNM-D-19-00391R4, 11 feb 2020.
2. Dantas, T.; Silva, V. L.; **Fonseca, A. L.**; Morais, A. A. D.; Signoretti, A.; Figuerola, W. B. "Bio-DIA: A web-based tool for data and algorithms integration". **bioRxiv.org - the preprint server for Biology**, 19 dec. 2019.

3. Machado, K.C.T.; Fortuin, S.; Tomazella, G.G.; **Fonseca, A. L.**; Warren, R. M.; Wiker, H. G.; De Souza, S. J.; De Souza, G. A. "On the impact of the pangenome and annotation discrepancies while building protein sequence databases for bacteria proteogenomics". **Frontiers in Microbiology**, 2019.
4. Pinheiro, Daniele Maria Lopes; De Oliveira, Ana Helena Sales; Coutinho, Leonam Gomes; Fontes, Fabrícia Lima; De Medeiros Oliveira, Rayssa Karla; Oliveira, Thais Teixeira; **Faustino, André Luís Fonseca**; Lira da Silva, Vandeclecio; De Melo Campos, Julliane Tamara Araújo; Lajus, Tirzah Braz Petta; De Souza, Sandro José; Agnez-Lima, Lucymara Fassarella. "Resveratrol decreases the expression of genes involved in inflammation through transcriptional regulation". **Free Radical and Medicine**, v. 130, p. 8-22, 2019.
5. ★ **Fonseca, André L.**; Da Silva, Vandeclecio; Fonseca, Marbella; Da Silva, Thayna; Coelho, Ana; Kroll, José; De Souza, Jorge; Stransky, Beatriz; De Souza, Gustavo; De Souza, Sandro. "Genome-wide identification of cancer/testis genes and their association with prognosis in a pan-cancer analysis". **Oncotarget**, v. 8, p. 92966-92977, 2017.
6. Putnam, C. D.; Srivatsan, A.; Nene, R. V.; Martinez, S. L.; Clotfelter, S. P.; Bell, S. N.; Somach, S. B.; Souza, J. S.; **Fonseca, André L. F.**; Souza, S. J.; Kolodner, Richard D. "A genetic network that suppresses genome rearrangements in *Saccharomyces cerevisiae* and contains defects in cancers". **Nature Communications**, v. 7, p. 11256, 2016.
7. **Fonseca, André L.**; Da Silva, Vandeclecio L.; Da Fonsêca, Marbella M.; Meira, Isabella T. J.; Da Silva, Thayná E.; Kroll, José E.; Ribeiro-Dos-Santos, André M.; Freitas, Cléber R.; Furtado, Raimundo; De Souza, Jorge E.; Stransky, Beatriz; De Souza, Sandro J. "Bioinformatics Analysis of the Human Surfaceome Reveals New Targets for a Variety of Tumor Types". **International Journal of Genomics**, v. 2016, p. 1-7, 2016.
8. **Fonseca, Andre L.**; Gubitoso, M. D.; Reis, M. S.; De Souza, Sandro J.; Barrera, J. "A new approach for identification of cancer related pathways using protein networks and genomic data". **Cancer Informatics**, v. 14, p. 139, 2016.
9. ★ **Fonseca, André L.**; De Souza, Jorge E. S.; Valieris, Renan; Carraro, Dirce M.; Wang, Jean Y. J.; Kolodner, Richard D.; De Souza, Sandro J. "S-Score: A Scoring System for the Identification and Prioritization of Predicted Cancer Genes". **Plos One**, v. 9, p. e94147, 2014.
10. Pacchioni, Ralfo G.; Carvalho, Fabíola M.; Thompson, Claudia E.; **Faustino, André L. F.**; Nicolini, Fernanda; pereira, tatiana s.; Silva, Rita C. B.; Cantão, Mauricio E.; Gerber, Alexandra; Vasconcelos, Ana T. R.; Agnez-lima, Lucymara F. "Taxonomic and functional profiles of soil samples from Atlantic forest and Caatinga biomes in northeastern Brazil". **MicrobiologyOpen**, v. 3, p. n/a-n/a, 2014.

BOOK CHAPTERS

1. Kroll, J. E.; **Fonseca, Andre L. F.**; Souza, S. J. "Post-genomic Approaches in Cancer and NanoMedicine". 1. ed. **River Publishers**, 2015.

POSTER PRESENTATIONS

1. ★ **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**, 2019.
2. **Fonseca, A. L.**; De Souza, S. J.; Wang, J. Y. J. "An association between RNA-binding proteins expression and drug response in TP53 genotypes". **Third North and Northeast Bioinformatics Symposium**, 2018.
3. ★ **Fonseca, A. L.**; De Souza, S. J. "SurvSign: an interactive R package for cohort stratification and survival analysis". **Systems Biology - 9th IUPAP International Conference on Biological Physics**, 2017.
4. Silva, V. L.; **Fonseca, A. L.**; Da Fonsêca, Marbella M.; Da Silva, Thayna E.; Coelho, Ana. C.; Kroll, José E.; De Souza, Jorge E.S.; Stransky, Beatriz; De Souza, Gustavo Antonio; De Souza, S. J. "Genome-wide identification of cancer/testis genes and their association with prognosis in a pan-cancer analysis". **Systems Biology - 9th IUPAP International Conference on Biological Physics**, 2017.
5. **Fonseca, A. L.**; De Souza, Sandro J. "An intuitive network-based approach to investigate clinical features among breast cancer subtypes". **12th International Conference of the Brazilian Association for Bioinformatics and Computational Biology - X-Meeting**, 2016.

6. **Fonseca, A. L.**; Ribeiro-Dos-Santos, A. M. ; Silva, V. L. ; Moreira, F. C. ; Assumpcao, C. ; Burbano, R. ; Assumpcao, P. ; De Souza, Sandro J. ; RIBEIRO-DOS-SANTOS, A. "An extended approach for small RNA analysis: prospecting and characterization of piRNA diversity". **60° Brazilian Genetics Conference (SBG)**, 2014.
7. **Faustino, A. L. F.**; Carvalho, F. M. ; Nicolini, F.; Agnez-Lima, L. F. "Genomic integrity in metagenomic libraries from distinct Brazilian biomes". **8th International Conference of the Brazilian Association for Bioinformatics and Computational Biology - X-meeting**, 2012.
8. **Faustino, A. L. F.**; Araujo, J. J. P. ; Lima, J. P. M. S. ; Carvalho, F. M. ; Nicolini, F. ; Pereira, T. S.; AGNEZ-LIMA, L. F. "MANGABA: Metagenomic ANnotation and storaGe datABase". **7th International Conference of the Brazilian Association for Bioinformatics and Computational Biology - X-Meeting**, 2011.
9. Silva, R. C. B. ; Melo, A. J ; **Faustino, A. L. F.**; Medeiros, L. A. ; Coutinho, L. G. ; Fontinele, D. C. S. S. "Functional characterization of a new DNA repair enzyme from metagenomic library". **International Workshop on Genomics of Health and Diseases**, 2011.

Honors & Awards

GRANT AND SCHOLARSHIP

- 2017 **Scholarship**, Brazilian doctoral exchange program - CAPES/PDSE
- 2016 **Scholarship**, Full Ph.D. degree - UFRN
- 2014 **Scholarship**, Full Master degree - UFPA
- 2009 **Scholarship**, Undergraduate scientific program - UFRN

ACADEMY AWARDS

- 2011 **Best poster**, Functional characterization of a new DNA Repair enzyme from metagenomic library

Teaching and Mentoring Experience

University of São Paulo - USP

ASSISTANT PROFESSOR

2010

- Lectured a Scientific Writing class in Biomedical Institute graduate program at USP.

University of California San Diego - UCSD

TUTORING ASSISTANT

2017

- Hired as Tutoring Assistant into "Bioinformatics Applications to Human Disease" class (MED263) at UCSD.

Federal University of Rio Grande do Norte - UFRN

GRADUATE MENTOR

2016

- Served as a mentor to students during the undergraduate internship, helping them to conclude their final paper.

Federal University of Paraíba - UFPB

COURSE INSTRUCTOR

2016

- Lectured a short-term course in R to undergraduate students, covering: programming fundamentals, data manipulation, and visualization.

Federal University of Rio Grande do Norte - UFRN

TUTORING ASSISTANT

2014 - 2018

- Invited to teach hands-on courses of R and Linux in IT and Engineering schools at UFRN.

Teaching Interests: Bioinformatics, NGS Analysis, Systems Biology, Introduction to Python, R for Data Scientists, Evolution, Cancer and Molecular Biology, and Genetics.

Professional Experience

DUNA Bioinformatics

BIOINFORMATICS ASSISTANT

2018 - 2019

- Worked as a bioinformatician consultant, project manager and pipeline developer.
- Developed a pipeline to predict and prioritize tumor antigens using RNA-Seq data in several cancer types.

- Worked with cancer research, NGS data processing and integration, database administration, and query optimization into multidimensional data in i2Bio.

Qualifications and Skills

TECHNICAL SKILLS

PYTHON PROGRAMMING

Experience: 5 years

- Has advanced level in Python: web scraping, parallel programming, system administration, pipeline organization (snakemake), and modules development.
- Moderate expertise with Jupyter, Pandas, Scikit, Seaborn and other Anaconda packages.

R PROGRAMMING

Experience: 4 years

- Has upper-intermediate level in R: data manipulation, statistical analysis, and visualization using Tidyverse (dplyr, ggplot2, broom, readr) and Bioconductor packages (DESeq2, Limma, WGCNA and clusterProfiler).
- In-house R package development to analyse, filtering and plotting genomics data.
- Developing web applications using R Shiny to clinicians and other biomedical professionals.

OTHERS TECHNOLOGIES

Experience: 2-4 years

- Moderate expertise with machine-learning approaches, such as classification (Random Forest) and clustering methods (k-Means and Hierarchical clusterization).
- Linux and containerized system administration using Docker and Kubernetes.
- Database administration using SQL and NoSQL technologies, such as MariaDB and MongoDB.
- Other programming languages: Perl, Shell scripting, GO and C++

LANGUAGE

ENGLISH

Fluency

- Finished an advanced English course, also including a language exchange at San Diego.

SPANISH

Intermediate

PORTUGUESE

Native Speaker

References

Sandro José de Souza

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FULL PROFESSOR AT UFRN

Diogo Meyer

Contact: diogomeyer@usp.br

FULL PROFESSOR AT UFRN

Lucymara Fassarella Agnez-Lima

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FULL PROFESSOR AT UFRN