# Curriculum Vitae

## Personal Data

| Title | Prof. Dr. |
|---|---|
| First name | Peter F. |
| Name | Stadler |
| Current position | Full Professor of Bioinformatics |
| Current institution(s)/site(s), country | Leipzig University, Germany |
| Identifiers/ORCID | 0000-0002-5016-5191 |

## Qualifications and Career

| Stages | Periods and Details |
|---|---|
| **Degree programme** | 1984 – 1990: Studies at the University of Vienna: Undergraduate degrees (1. Diplom) in Chemistry 1986, Astronomy 1988, Physics 1989, Mathematics 1990 MSc in Chemistry 1988 |
| **Doctorate** | 1988 – 1990: Dissertation at the Institute for Theoretical Chemistry, University of Vienna, Austria (PhD in Chemistry) |
| **Stages of academic/professional career** | |
| Since March 2009: | External Scientific Member of the Max Planck Society, affiliated with the MPI "Mathematics in the Sciences" in Leipzig, Germany |
| Since September 2002: | Full Professor of Bioinformatics, University Leipzig, Germany |
| 1997 – 2002: | Außerordentlicher Universitätsprofessor, University of Vienna, Austria |
| 1994: | Habilitation: Venia Legendi for Theoretical Chemistry, University of Vienna, Austria |
| 1991 – 1994: | Universitätsassistent at the Institute for Theoretical Chemistry and Radiation Chemistry, University of Vienna, Austria |
| 1990 – 1991: | Postdoc at the Department for Biochemical Kinetics, Max Planck, Institute for Bio-Physical Chemistry, Göttingen, Germany |

## Engagement in the Research System

- Co-editor-in-chief:
    - Algorithms for Molecular Biology (together with Burkhart Morgenstern)
    - Theory in Biosciences (together with Jürgen Jost und Manfred Laubichler)
- Editor by:
    - RNA (responsible for bioinformatics/computational biology)
- Member of the Editorial Board by:

- o Advances in Complex Systems
- o Journal of Experimental Zoology
- o BMC Bioinformatics
- o BMC Evolutionary Biology
- o Journal of Bioinformatics and Computational Biology
- o Journal of Systems Chemistry
- o LIFE
- o Mathematics in Computer Science

**Supervision of Researchers in Early Career Phases**

During his career, Peter successfully supervised more than 50 PhD students of which 8 (Steve Hoffmann, Marc Hellmuth, Manja Marz, Sonja J Prohaska, Clara Isabel Bermudez Santana, Maribel Hernández Rosales, Sarah Berkemer, Arli Aditya Parikesit) have a professor position to date.

**Finished Ph.D. students (2019-2023):** Yazbeck, Ali; Scheibe, Patrick; Berkemer, Sarah; Geiß, Manuela, Gärtner, Fabian, Retzlaff, Nancy, Hoffmann, Anne; Sen, Rituparno; Engelhardt, Jan; Saker, Halima; Riverola-Duarte, Lorena; Schaller, David; Rodriguez Fernandez, Angel; Gatter, Thomas; Kühnl, Felix; Leal, Wilmer; Lozada-Chavez, Irma; Nunn, Adam; Velandia Huerto, Cristian Arley;

**Project funded PostDocs (2019-2023):** Gatter, Thomas; Jorge, Natasha; Kehr, Stephanie; Lozada Irma; Santiago Arguello, Anahy; Guillaume, Scholz; Korchmaros, Annachiara

**Scientific Results**

Citations: >71,000, H-Index 113
https://scholar.google.de/citations?user=pVnGRlkAAAAJ&hl=de

**Project relevant Publication List**

1) Dulce I. Valdivia, Manuela Geiß, Marc Hellmuth, Maribel Hernandez Rosales, and Peter F. Stadler. Hierarchical and modularly-minimal vertex colorings. Art Discr. Appl. Math, 6:P2.01, 2023.
2) Grover E. C. Guzman, Peter F. Stadler, and Andre Fujita. Efficient eigenvalue counts for tree-like networks. J. Complex Networks, 10:cnac040, 2022.
3) Guzman, G., Stadler, P., & Fujita, A. (2021). Efficient Laplacian spectral density computations for networks with arbitrary degree distributions. Network Science, 9(3), 312-327. doi:10.1017/nws.2021.10
4) Katharina T. Huber, Marc Hellmuth, Guillaume E. Scholz, and Peter F. Stadler. Injective split systems. Graphs and Combinatorics, 2023. accepted
5) Carsten R. Seemann, Vincent Moulton, Peter F. Stadler, and Marc Hellmuth. Planar median graphs and cubesquare-graphs. Discr. Appl. Math., 331:38–58, 2023.
6) Juan Jos´e Montellano Ballesteros, Anahy Santiago Arguello, and Peter F. Stadler. Hamiltonicity in power graphs of a type of abelian groups. J. Algebraic Comb., 313-328:57, 2023.

**Academic Distinctions**

- Honorary Professor, Faculty of Sciences, U Nacional de Colombia, Bogota since 2018
- Corresponding member of the Austrian Academy of Sciences since 2010.
- Member of the External Faculty of the Santa Fe Institute, New Mexico, 1994-2003, and since 2004.
- Member of the Board of the Biotechnologisch-Biomedizinisches Zentrum (BBZ) of the University Leipzig, since 2003.
- Member of the Board of the Interdisziplinäres Zentrum für Bioinformatik (IZBI), Leipzig, since 2002.
- Member of the Board of the Chemisch Physikalische Gesellschaft in Wien, elected for the periods 2000/2001 and 2001/2002.
- Novartis-Award for Chemistry (Austria) 2002
- Otto-Hahn Medal of the Max Planck Society 1992

Leipzig, 07 July 2023

# CURRICULUM VITAE

**Name:** André Fujita
**Position:** Associate Professor and the Bioinformatics Graduate Program Director
**Affiliation:** Dept. of Computer Science, Institute of Mathematics and Statistics, the University of São Paulo, Brazil
**Address:** Rua do Matão 1010 Bld. C Office 05 – Cidade Universitária – SP, 05508-090, Brazil
**E-mail:** andrefujita@usp.br          **Phone:** +55 11 3091 5177 (office) / +55 11 99784 5995 (mobile)
**Date of birth:** January 19th, 1981.

## 1) EDUCATION

| | | |
|---|---|---|
| **Habilitation** | University of São Paulo | 2016 |
| **Ph.D.** in Bioinformatics | University of São Paulo | 2003 - 2007 |
| Internship | Human Genome Center / University of Tokyo | Jul – Oct 2006 |
| **B.Sc.** in Computer Science | University of São Paulo | 1999 - 2003 |
| Internship | Cell and Molecular Biology Lab. / Dept. of Biochemistry | 2002 - 2003 |

## 2) PROFESSIONAL POSITIONS

| | | |
|---|---|---|
| **Fulbright Fellow**, Dept. of Mathematics & Statistics, Boston University | Mar – May 2022 |
| **Bioinformatics Graduate Program Director**, University of São Paulo | Since Mar 2020 |
| **FAPESP-ERC Fellow**, SGDP Centre, King's College London | Jul – Nov 2019 |
| **Bioinformatics Graduate Program Vice-Director**, University of São Paulo | Mar 2018 - Feb 2020 |
| **Alexander von Humboldt Fellow**, Dept. of Computer Science, Leipzig University | Dec 2018 – Feb 2019 |
| **Alexander von Humboldt Fellow**, Dept. of Computer Science, Leipzig University | Dec 2017 – Feb 2018 |
| **Associate Professor**, Dept. of Computer Science, University of São Paulo | Since Apr 2016 |
| **JICA Fellow**, Cancer Research Institute, Kanazawa University | Dec 2014 – Jan 2015 |
| **Visiting Scientist**, Cancer Research Institute, Kanazawa University | Jan 2014 |
| **Assistant Professor**, Dept. of Computer Science, University of São Paulo | Mar 2011 – Mar 2016 |
| **SPDR Fellow**, Computational Science Research Program, RIKEN | Apr 2009 – Feb 2011 |
| **Postdoc**, Human Genome Center, the University of Tokyo | Nov 2007 – Mar 2009 |

## 3) HONORS, AWARDS, AND FELLOWSHIPS

2023 **Best paper award**, Brazilian Symposium on Bioinformatics
2022 **Latin America Research Award**, Google
2021 **Fulbright Fellowship**, the USA
2021 **Intercontinental Academia Fellowship** – University-Based Institutes for Advanced Study (UBIAS)
2021 **Sigma Xi Nominated Full Membership** – The Scientific Research Honor Society, the USA
2019 **FAPESP-ERC Fellowship**, Brazil – the UK
2018 **Newton Advanced Fellowship**, Newton Fund/Academy of Medical Sciences/Royal Society, the UK
2017 **Alexander von Humboldt Fellowship**, Alexander von Humboldt Foundation, Germany
2017 **Outstanding Scientist Award**, Brazilian Association for Bioinformatics and Computational Biology
2014 **Japan International Cooperation Agency Fellowship**, JICA, Japan
2009 **Special Postdoctoral Researcher (SPDR) Fellowship**, RIKEN, Japan
2009 **Honorable mention**, CAPES Ph.D. theses contest in Biological Sciences, Brazil
2008 **Best Ph.D. thesis award**, Brazilian Society for Computer Science, Brazil
2006 **Japan International Cooperation Agency Fellowship**, JICA, Japan
2003 **Graduate student research fellowship**, CAPES, Brazil
2002 **Undergraduate student research fellowship**, CNPq, Brazil

## 4) PUBLICATION LIST

*Journal articles* (*: indicates the corresponding author)
  1. Farhat LC, Blakey R, Smith GD, **Fujita A**, Shephard E, Stergiakouli E, Tiling K, Eley T, Thapar A, Polanczyk. The association between neurodevelopmental traits, social-environment stressors, co-

occurring emotional dysregulation in children and depression over development: a Bayesian multivariate analysis of two UK population-based longitudinal studies. *The American Journal of Psychiatry*. (in press).

2. Ramos TC, Mourao-Miranda J, **Fujita A**\*. Spectral density-based clustering algorithms for complex networks. *Frontiers in Neuroscience*. **17**: 926321, 2023.

3. Guzman GEC and **Fujita A**\*. A fast algorithm to approximate the spectral density of locally tree-like networks with assortativity. *Journal of Complex Networks*. **11**: cnad005, 2023.

4. Moretti E, Rodrigues AC, Marques B, Totola L, Ferreira C, Brito C, Matos C, da Silva F, Santos R, Lopes L, Moreirra T, Akamine E, Baccala LA, **Fujita A**, Steiner A. Autoregulation of blood flow drives early hypotension in a rat model of systemic inflammation induced by bacterial lipopolysaccharide. *PNAS Nexus*. **2**: pgad014, 2023.

5. Cunha M, Borges AP, Carvalho VJ, **Fujita A**, Castro Junior G. Predicting survival in metastatic non-small cell lung cancer patients with poor ECOG-PS: a single arm prospective study. *Cancer Medicine*. **12**: 5099 - 5109, 2022.

6. Oku A, Barreto C, Bruneri GA, Brockington G, **Fujita A**, Sato JR. Applications of graph theory to the analysis of fNIRS data in hyperscanning paradigms. *Frontiers in Computational Neuroscience*. **16**: 975743, 2022.

7. Guzman GEC, Stadler PF, **Fujita A**\*. Efficient eigenvalue counts for tree-like networks. *Journal of Complex Networks*. **10**: cnac040, 2022.

8. Rius FE, Papaiz DD, Azevedo HFZ, Ayub ALP, Pessoa DO, Oliveira TF, Loureiro APM, Andrade F, **Fujita A**, Reis EM, Mason CE, Jasiulionis MG. Genome-wide promoter methylation profiling in a cellular model of melanoma progression reveals markers of malignancy and metastasis that predict melanoma survival. *Clinical Epigenetics*. **14**: 68, 2022.

9. Guzman GEC, Takahashi DY, **Fujita A**\*. A fast parameter estimator for large complex networks. *Journal of Complex Networks*. **10**: cnac022, 2022.

10. Da Costa DR, **Fujita A**, Sales MR, Szezech Jr JD, Batista AM. Dynamical properties for a tunable circular to polygonal billiard. *Brazilian Journal of Physics*. **52**: 75, 2022.

11. Da Costa DR, **Fujita A**, Batista AM, Sales MR, Szezech Jr JD. Conservative generalized bifurcation diagrams and phase space properties for oval-like billiards. *Chaos, Solitons and Fractals: Nonlinear Science, and Nonequilibrium and Complex Phenomena*. **155**: 111707, 2022.

12. De Siqueira Santos S, **Fujita A**, Matias C. Spectral density of random graphs: convergence properties and application in model fitting. *Journal of Complex Networks*. **9**: cnab041, 2021.

13. Guzman GEC and **Fujita A**\*. Convolution-based linear discriminant analysis for functional data classification. *Information Sciences*. **581**: 469 – 478, 2021.

14. Guzman GEC, Stadler PF, **Fujita A**\*. Efficient Laplacian spectral density computations for networks with arbitrary degree distributions. *Network Science*. **9**: 312 – 327, 2021.

15. Ribeiro AH, Vidal MC, Sato JR, **Fujita A**\*. Granger causality among graphs and application to functional brain connectivity in autism spectrum disorder. *Entropy*. **23**: 1204, 2021.

16. Fernandes PACM, Kinker GS, Navarro BV, Jardim VC, Ribeiro-Paz ED, Córdoba-Moreno MO, Santos-Silva D, Muxel SM, **Fujita A**, Nakaya HI, Buckeridge MS, Markus RP. Melatonin-Index as a biomarker for predicting the distribution of presymptomatic and asymptomatic SARS-CoV-2 carriers. *Melatonin Research*. **4**: 189-205, 2021.

17. **Fujita A**\*, Lira E, de Siqueira Santos S, Soares GE, Bando SY, Takahashi DY. A semi-parametric statistical test to compare complex networks. *Journal of Complex Networks*. **8**: 2, 2020.

18. Wang JYT, Whittle MR, Puga RD, Yambartsev A, **Fujita A**, Nakaya HI. Noninvasive prenatal paternity determination using microhaplotypes: a pilot study. *BMC Medical Genomics*. **13**: 157, 2020.

19. Martins LA, Palmisano G, Cortez M, Kawahara R, de Freitas Balanco JM, **Fujita A**, Alonso BI, Barros-Battesti DM, Braz GRC, Tirloni L, Esteves E, Daffre S, Fogaça AC. The intracellular bacterium Rickettsia rickettsii exerts an inhibitory effect on the apoptosis of tick cells. *Parasites & Vectors*. **13**: 603, 2020.

20. Ambrioli AYO, Zimeo GAM, Arantes APB, **Fujita A**, Sato JR. Potential confounders in the analysis of Brazilian adolescent's health: a combination of machine learning and graph theory. *International Journal of Environmental Research and Public Health*. **17**: 90, 2020.

21. Andrade F, Nakata A, Gotoh N, **Fujita A**\*. Large miRNA survival analysis reveals a prognostic four-biomarker signature for triple-negative breast cancer. *Genetics and Molecular Biology*. **43**: e20180269, 2020.

22. Pereira TF, Levin G, Deocesano-Pereira C, Caodaglio AS, **Fujita A**, Tonso A, Sogayar MC. Fluorescence-based method is more accurate than counting-based methods for plotting growth curves of adherent cells. *BMC Research Notes*. **13**: 57061, 2020.

23. Yancy-Caballero D, Ling LY, Archilha NL, **Fujita A**, Ferreira JE, Driemeier C. Intraparticle connectivity in sugarcane bagasse unveiled by pore network modeling. *BioEnergy Research*. **12**: 546 – 557, 2019.

24. Carvalho VJ, de Siqueira Santos S, **Fujita A**, Buckeridge MS. BioNetStat: a tool for biological networks differential analysis. *Frontiers in Genetics*. 10: 594, 2019.

25. Ramos TC, Balardin JB, Sato JR, **Fujita A\***. Abnormal cortico-cerebellar functional connectivity in autism spectrum disorder. *Frontiers in Systems Neuroscience*. **12**: 74, 2019.

26. Bando SY, Iamashita P, Silva FN, Costa LF, Abe CM, Bertonha FB, Guth BEC, **Fujita A**, Moreira-Filho C. Response to Shiga toxin-producing Escherichia coli-associated hemolytic-uremic syndrome. *Microorganisms*. **7**: 195, 2019.

27. Machado RAC, Schneider H, Deocesano-Pereira C, Lichtenstein F, Andrade F, **Fujita A**, Trombetta-Lima M, Weller M, Bowman-Colin C, Sogayar MC. CHD7 promotes glioblastoma cell motility and invasiveness through transcriptional modulation of an invasion signature. *Scientific Reports*. **9**: 3952, 2019.

28. Rached MR, Coelho V, Marin MLC, Pincerato K, **Fujita A**, Kalil JE, Abrao MS. HLA-G is upregulated in advanced endometriosis. *European Journal of Obstetrics & Gynecology and Reproductive Biology*. **235**: 36-41, 2019.

29. Martins LA, Malossi CD, Galletti MFBM, Ribeiro JM, **Fujita A**, Esteves E, Costa FB, Labruna MB, Dafre S, Fogaça AC. The Transcriptome of the Salivary Glands of Amblyomma aureolatum Reveals the Antimicrobial Peptide Microplusin as an Important Factor for the Tick Protection Against Rickettsia rickettsii Infection. *Frontiers in Physiology*. **10**: 529, 2019.

30. Monteiro AC Muenzner J, Andrade F, Rius FE, Ostalecki C, Geppert C, Agaimy A, Hartmann A, **Fujita A**, Schneider-Stock R, Jasiulionis MG. Gene expression and promoter methylation of angiogenic and lymphangiogenic factors as prognostic markers in melanoma. *Molecular Oncology*. **13**: 1433 – 1449, 2019.

31. Guzman GEC, Vidal MC, Sato JR, **Fujita A\***. Identification of alterations associated with age in the clustering structure of functional brain networks. *PLoS ONE*. **13**: e0195906, 2018.

32. Sato JR, Vidal MC, Siqueira SS, Massirer KB, **Fujita A\***. Complex network measures in autism spectrum disorders. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. **15**: 581 - 587, 2018.

33. Nardelli TR, Vanzela EC, Benedicto KC, Brozzi F, **Fujita A**, Cardozo AK, Eizirik D, Boschero AC, Ortis F. Prolactin protects against cytokine-induced beta cell death by NFkB and JNK inhibition. *Journal of Molecular Endocrinology*. **61**: 25 - 36, 2018.

34. Lobba ARM, Carreira ACO, Cerqueira OLD, **Fujita A**, Deocesano-Pereira C, Osorio CAB, Soares FA, Rameshwar P, Sogayar MC. High CD90 (THY-1) expression positively correlates with cell transformation and worse prognosis in basal-like breast cancer tumors. *PLoS ONE*. **13**: e0199254, 2018.

35. Vidal MC, Sato JR, Balardin JB, Takahashi DY, **Fujita A\***. ANOCVA in R: A software to compare clusters between groups and its application to the study of autism spectrum disorder. *Frontiers in Neuroscience*. **11**: 16, 2017.

36. **Fujita A\***, Vidal MC, Takahashi DY. A statistical method to distinguish functional brain networks. *Frontiers in Neuroscience*. **11**: 66, 2017.

37. Martins LA, Galletii MFBM, Ribeiro JM, **Fujita A**, Costa FB, Bruna MB, Daffre S, Fogaça AC. The distinct transcriptional response of the midgut of Amblyomma sculptum and Amblyomma aureolatum ticks to Rickettsia rickettsii correlates to their differences in susceptibility to infection. *Frontiers in Cellular and Infection Microbiology*. **7**: 129, 2017.

38. Esteves E, Maruyama SR, Sakuma R, **Fujita A**, Martins LA, Righi A, Costa FB, Palmisano G, Labruna MB, Sá-Nunes A, Ribeiro JM, Fogaça AC. Analysis of the salivary gland transcriptome of unfed and partially fed Amblyomma sculptum ticks and descriptive proteome of the saliva. *Frontiers in Cellular and Infection Microbiology*. **7**: 476, 2017.

39. Bando SY, Iamashita P, Guth BE, Santos LF, **Fujita A**, Abe CM, Ferreira LR, Moreira-Filho CA. A hemolytic-uremic syndrome-associated strain O113:H21 Shiga toxin-producing Escherichia coli specifically expresses a transcriptional module containing dicA and is related to gene network dysregulation in Caco-2 cells. *PLoS ONE*. **12**: e0189613, 2017.

40. Ribeiro AH, Lotufo P, **Fujita A**, Goulart A, Chor D, Mill JG, Bensenor I, Santos IS. Association between short-term systolic blood pressure variability and carotid intima-media thickness in ELSA-Brasil baseline. *American Journal of Hypertension*. **30**: 954 - 960, 2017.

41. Sato JR, Balardin J, Vidal MC, **Fujita A\***. Identification of segregated regions in the functional brain connectome of autistic patients by a combination of fuzzy spectral clustering and entropy analysis. *Journal of Psychiatry & Neuroscience*. **41**: 124-132, 2016.

42. Fonseca M, Rodrigues AC, Cezar L, **Fujita A**, Soriano F, Steiner A. Spontaneous hypothermia in human sepsis is a transient, self-limiting and non-terminal response. *Journal of Applied Physiology*. **120**: 1394 - 1401, 2016.

43. Kinker GS, Thomas AM, Carvalho VJ, Lima FP, **Fujita A\***. Deletion and low expression of NFKBIA are associated with poor prognosis in lower-grade glioma patients. *Scientific Reports*. **6**: 24160, 2016.

44. Galletti MFBM, **Fujita A**, Rosa RD, Martins L, Soares HS, Labruna MB, Daffre S, Fogaça AC. Virulence genes of Rickettsia rickettsii are differentially modulated by either temperature upshift or blood-feeding in tick midgut and salivary glands. *Parasites & Vectors*. **9**: 331, 2016.

45. **Fujita A\***, Takahashi DY, Balardin JB, Vidal MC, Sato JR. Correlation between graphs with an application to brain network analysis. *Computational Statistics & Data Analysis*. **109**: 76 - 92, 2016.

46. Alexandrino P, Mendonça T, Bautista L, Cherix J, Lozano-Sakalauskas G, **Fujita A**, Ramos Filho E, Long P, Padilla G, Taciro M, Gomez JG, Silva L. Draft genome sequence of the polyhydroxyalkanoate-producing bacterium Burkholderia sacchari LMG 19450 isolated from Brazilian sugarcane plantation soil. *Genome Announcements*. **3**: e00313-15, 2015.

47. Nakata A, Yoshida R, Yamaguchi R, Yamauchi M, Tamada Y, **Fujita A**, Imoto S, Shimamura T, Higuchi T, Nomura M, Kimura T, Nokihara H, Higashiyama M, Kondoh K, Nishihara H, Tojo A, Yano S, Miyano S, Gotoh H. Elevated beta-catenin pathway as a novel target for patients with resistance to EGF receptor targeting drugs. *Scientific Reports*. **5**: 13076, 2015.

48. De Siqueira Santos S, Galatro TFA, Watanabe RA, Oba-Shinjo SM, Marie SKN, **Fujita A\***. CoGA: an R package to identify differentially co-expressed gene sets by analyzing the graph spectra. *PLoS ONE*. **10**: e0135831, 2015.

49. Gomes LR, **Fujita A**, Mott JD, Soares FA, Labriola L, Sogayar MC. RECK is not an independent prognostic marker for breast cancer. *BMC Cancer*. **15**: 660, 2015.

50. Molina E, **Fujita A**, Sogayar MC, Demasi MA. A quantitative and humane tail bleeding assay for efficacy evaluation of antihaemophilic factors in haemophilia A mice. *Haemophilia*. **20**: 392-398, 2014.

51. Rodrigues AC, Machado BS, Florence G, Hamad AP, Sakamoto AC, **Fujita A**, Baccala LA, Amaro Jr E., Sameshima K. Brain network dynamics characterization in epileptic seizures. *The European Physical Journal. Special Topics*. **223**: 2933-2941, 2014.

52. Maciel C, **Fujita A**, Gueroni DI, Ramos AD, Capurro ML, Sa-Nunes, A. Evans blue as a simple method to discriminate mosquitoes feeding choice on small laboratory animals. *PLoS ONE*. **9**: e110551, 2014.

53. Azevedo H, **Fujita A**, Bando SY, Iamashita P, Moreira-Filho CA. Transcriptional network analysis reveals that AT1 and AT2 Angiotensin II receptors are both involved in the regulation of genes essential for glioma progression. *PLoS ONE*. **9**: e110934, 2014.

54. **Fujita A\***, Takahashi DY, Patriota AG, Sato JR. A non-parametric statistical test to compare clusters with applications in functional magnetic resonance imaging data. *Statistics in Medicine*. **33**: 4949-4962, 2014.

55. Sato JR, Takahashi DY, Hoexter MQ, Massirer KB, **Fujita A\***. Measuring network's entropy in ADHD: A new approach to investigate neuropsychiatric disorders. *Neuroimage*. **77**: 44-51, 2013.

56. Galletti MFBM, **Fujita A**, Nishiyama Jr MY, Malossi CD, Pinter A, Soares JF, Daffre S, Labruna MB, Fogaça AC. Natural Blood Feeding and Temperature Shift Modulate the Global Transcriptional Profile of Rickettsia rickettsii Infecting Its Tick Vector. *PLoS ONE*. **8**: e77388, 2013.

57. Halcsik E, Forni MF, **Fujita A**, Verano-Braga T, Jensen ON, Sogayar MC. New insights in osteogenic differentiation revealed by mass spectrometric assessment of phosphorylated substrates in murine skin mesenchymal cells. *BMC Cell Biology*. **14**: 47, 2013.

58. **Fujita A\***, Takahashi DY, Patriota AG. A non-parametric method to estimate the number of clusters. *Computational Statistics & Data Analysis*. **73**: 27-39, 2013.

59. De Siqueira Santos S, Takahashi DY, Nakata A, **Fujita A\***. A comparative study of statistical methods used to identify dependencies between gene expression signals. *Briefings in Bioinformatics*. **15**: 906-918, 2013.

60. Kojima K, Imoto S, Yamaguchi R, **Fujita A**, Yamauchi M, Gotoh N, Miyano S. Identifying regulational alterations in gene regulatory networks by state space representation of vector autoregressive models and variational annealing. *BMC Genomics*. **13**: S6, 2012.

61. Sato JR, **Fujita A**, Hoexter MQ, Rohde LA. Evaluation of Pattern Recognition and Feature Extraction Methods in ADHD Prediction. *Frontiers in Systems Neuroscience*. **6**: 68, 2012.

62. **Fujita A**, Severino P, Kojima K, Sat JR, Patriota AG, Miyano S. Functional clustering of time series gene expression data by Granger causality. *BMC Systems Biology*. **6**: 137, 2012.

63. Takahashi DY, Sato JR, Ferreira CE, **Fujita A\***. Discriminating Different Classes of Biological Networks by Analyzing the Graphs Spectra Distribution. *PLoS ONE*. **7**: e49949, 2012.

64. Nagasaki M, **Fujita A**, Sekiya Y, Saito A, Ikeda E, Li C, Miyano S. XiP: a computational environment to create, extend and share workflows. *Bioinformatics*. **29**: 137-139, 2012.

65. **Fujita A**, Sato JR, Demasi MA, Yamaguchi, R, Shimamura T, Ferreira CE, Sogayar MC, Miyano S. Inferring contagion in regulatory networks. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. **8**: 570-576, 2011.

66. Kasparek T, Thomaz CE, Sato JR, Schwarz D, Janousova E, Marecek R, Prikryl R, Vanicek J, **Fujita A**, Ceskova E. Maximum-uncertainty linear discrimination analysis of first-episode schizophrenia subjects. *Psychiatry Research Neuroimaging*. **191**: 174-181, 2011.

67. Nagasaki M, Saito A, **Fujita A**, Tremmel G, Ueno K, Ikeda Jeong E, Miyano S. Systems biology model repository for macrophage pathway simulation. *Bioinformatics*. **27**: 1591-1593, 2011.

68. Valenzuela JCB, **Fujita A**, Halcsik E, Granjeiro JM, Sogayar JM, Sogayar MC. Unveiling novel genes upregulated by both rhBMP2 and rhBMP7 during early osteoblastic transdifferentiation of C2C12 cells. *BMC Research Notes*. **4**: 370, 2011.

69. **Fujita A**, Sato JR, Kojima K, Gomes LR, Nagasaki M, Sogayar MC, Miyano S. Identification of Granger causality between gene sets. *Journal of Bioinformatics and Computational Biology*. **8**: 679, 2010.

70. Shimamura T, Imoto S, Nagasaki M, Yamauchi M, Yamaguchi R, **Fujita A**, Tamada Y, Gotoh N, Miyano S. Collocation-based sparse estimation for constructing dynamic gene networks. *Genome Informatics*. **24**: 164-178, 2010.

71. **Fujita A**, Nagasaki M, Imoto S, Saito A, Ikeda E, Shimamura T, Yamaguchi R, Hayashizaki Y, Miyano S. Comparison of gene expression profiles produced by CAGE, illumina microarray and Real Time RT-PCR. *Genome Informatics*. **24**: 56-68, 2010.

72. Sato JR, **Fujita A**, Cardoso EF, Thomaz CE, Brammer MJ, Amaro Jr E. Analyzing the connectivity between regions of interest: An approach based on cluster Granger causality for fMRI data analysis. *NeuroImage*. **52**: 1444-1455, 2010.

73. **Fujita A**, Severino P, Sato JR, Miyano S. Granger causality in systems biology: modeling gene networks in time series microarray data using vector autoregressive models. *Lecture Notes in Computer Science*. **6268**: 13-24, 2010.

74. **Fujita A**, Kojima K, Patriota AG, Sato JR, Severino P, Miyano S. A fast and robust statistical test based on Likelihood ratio with Bartlett correction to identify Granger causality between gene sets. *Bioinformatics*. **26**: 2349-2351, 2010.

75. Niida A, Imoto S, Yamaguchi R, Nagasaki M, **Fujita A**, Shimamura T, Miyano S. Model-free unsupervised gene set screening based on information enrichment in expression profiles. *Bioinformatics*. **26**: 3090-3097, 2010.

76. **Fujita A**, Sato JR, Demasi MA, Sogayar MC, Ferreira CE, Miyano S. Comparing Pearson, Spearman and Hoeffding's D measures for gene expression association analysis. *Journal of Bioinformatics and Computational Biology*. **7**: 663, 2009.

77. Sato JR, **Fujita A**, Thomaz CE, Martin MGM, Mourão-Miranda J, Brammer MJ, Amaro Jr E. Evaluating SVM and MLDA in the extraction of discriminant regions for mental state prediction. *NeuroImage*. **46**: 105-114, 2009.

78. Shimamura T, Imoto S, Yamaguchi R, **Fujita A**, Nagasaki M, Miyano S. Recursive regularization for inferring gene networks from time-course gene expression profiles. *BMC Systems Biology*. **3**: 41, 2009.

79. **Fujita A**, Saito JR, Silva FHL, Galvao MC, Sogayar MC, Miyano S. Quality control and reproducibility in DNA microarray experiments. *Genome Informatics*. **23**: 21-31, 2009.

80. **Fujita A**, Patriota AG, Sato JR, Miyano S. The impact of measurement errors in the identification of regulatory networks. *BMC Bioinformatics*. **10**: 412, 2009.

81. **Fujita A**, Sato JR, Festa F, Gomes LR, Oba-Shinjo SM, Nagahashi-Marie SK, Ferreira CE, Sogayar MC. Identification of Col6a1 as a differentially expressed gene in human astrocytomas. *Genetics and Molecular Research*. **7**: 371 - 378, 2008.

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83. **Fujita A**, Sato JR, Garay-Malpartida HM, Sogayar MC, Ferreira CE, Miyano S. Modeling nonlinear gene regulatory networks from time series gene expression data. *Journal of Bioinformatics and Computational Biology*. **6**: 961, 2008.

84. Kojima K, **Fujita A**, Shimamura T, Imoto S, Miyano S. Estimation of nonlinear gene regulatory networks via L1 regularized NVAR from time series gene expression data. *Genome Informatics*. **20**: 37 - 51, 2008.

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88. Sato JR, **Fujita A**, Amaro Jr E, Mourao-Miranda J, Morettin PA, Brammer MJ. DWT-CEM: An algorithm for scale-temporal clustering in fMRI. *Biological Cybernetics*. **97**: 33 - 45, 2007.

89. **Fujita A**, Sato JR, Garay-Malpartida HM, Morettin PA, Sogayar MC, Ferreira CE. Time-varying modeling of gene expression regulatory networks using the wavelet dynamic vector autoregressive method. *Bioinformatics*. **23**: 1623/13-1630, 2007.
90. **Fujita A**, Sato JR, Garay-Malpartida HM, Yamaguchi R, Miyano S, Sogayar MC, Ferreira CE. Modeling gene expression regulatory networks with the sparse vector autoregressive model. *BMC Systems Biology*. **1**: 39, 2007.
91. **Fujita A**, Sato JR, Ferreira CE, Sogayar MC. GEDI: a user-friendly toolbox for analysis of large-scale gene expression data. *BMC Bioinformatics*. **8**: 457, 2007.
92. **Fujita A**, Sato JR, Rodrigues LO, Ferreira CE, Sogayar MC. Evaluating different methods of microarray data normalization. *BMC Bioinformatics*, v. 7, p. 0/469, 2006.
93. **Fujita A**, Massirer KB, Durham AM, Ferreira CE, Sogayar MC. The GATO gene annotation tool for research laboratories. *Brazilian Journal of Medical and Biological Research*. **38**: 1571 - 1574, 2005.

*Book chapters*

1. Guzman GEC, Fatori D, **Fujita A\***. Análise de redes. In: Clarice Gorenstein; Wang Yuan-Pang. (Eds.). Instrumentos de Avaliação em Saúde Mental 2nd edition. Grupo A Educação (in press).
2. Demasi MAA, Carreira ACO, Gomes LR, Lima MT, Lobba ARM, Lojudice FH, Degaki TL, Montor WR, **Fujita A**, Sogayar MC. Genomica funcional em oncologia. In: Paulo Hoff; Artur Katz; Roger Chammas; Vincente Odoni; Yana Novis (Eds.). Tratado de Oncologia. 2nd edition. Rio de Janeiro: Atheneu, 2022.
3. Carvalho VJ, Moreno CC, **Fujita A\***. Computational tools for comparing gene coexpression networks. In: da Silva FAB, Carels N, Trindade dos Santos M, Lopes FJP. (Eds.). Networks in Systems Biology. Computational Biology. Vol. 32. Springer, pp. 19 – 30, 2020.
4. Guzman GCE, Balardin JB, Biazoli Jr CE, Sato JR, **Fujita A\***. Network analysis of neuropsychiatric disorders. In: Joel Faintuch, Salomão Faintuch, Beth Israel Deaconess. (Eds.). Precision medicine for investigators, practitioners and providers. 1ed.: Elsevier/USA, pp. 397 – 408, 2020.
5. Patriota AG, Vidal MC, Jesus DAC, **Fujita A\***. ANOCVA: a non-parametric statistical test to compare clustering structures. In: Fabricio Alves Barbosa da Silva; Nicolas Carels; Floriano Paes Silva Junior. (Eds.). Theoretical and Applied Aspects of Systems Biology. 1ed.: Springer International Publishing, pp. 113 - 125, 2018.
6. De Siqueira Santos S, Takahashi DY, Sato JR, Ferreira CE, **Fujita A\***. Statistical methods in graphs: parameter estimation, model selection, and test. In Matthias Dehmer, Frank Emmert-Streib, Zengqiang Chen, Xueliang Li, Yongtang Shi (Eds). Mathematical foundations and applications of graph entropy. Wiley-VCH Verlag, pp. 183 - 202, 2016.
7. **Fujita A\***, Severino P, Alexandrino PMR, Oliveira FCA, Miyano S. Granger causality for time series gene expression data. In: Ka-Chun Wong (Ed.). Computational Biology and Bioinformatics: Gene Regulation. CRC Press - Taylor & Francis Group, pp. 48 - 65, 2016.
8. Ribeiro AH, Soler JMP, Chaibub-Neto E, **Fujita A\***. Causal Inference and Structure Learning of Genotype-Phenotype Networks Using Genetic Variation. Big Data Analytics in Genomics. 1ed.: Springer International Publishing, pp. 89-143, 2016.
9. **Fujita A\***, Miyano S. A tutorial to identify nonlinear associations in gene expression time series data. In: Etsuko Miyamoto-Sato; Hiroyuki Ohashi; Hirotaka Sasaki; Jun-Ichi Nishikawa; Hiroshi Yanagawa (Eds.). Transcription Factor Regulatory Networks - Methods and Protocols. Springer, pp. 87-95, 2014.
10. Demasi MAA, Carreira ACO, Gomes LR, Lima MT, Lobba ARM, Lojudice FH, Degaki TL, Montor WR, **Fujita A**, Sogayar MC. Genômica funcional em oncologia. In: Paulo Hoff; Artur Katz; Roger Chammas; Vincente Odoni; Yana Novis (Eds.). Tratado de Oncologia. 1st edition. Rio de Janeiro: Atheneu, pp. 505-521, 2013.
11. **Fujita A**, Sato JR, Demasi MAA, Miyano S, Sogayar MC, Ferreira CE. An introduction to time-varying connectivity estimation for gene regulatory networks. In: Frank Emmert-Streib; Matthias Dehmer. (Eds.). Medical Biostatistics for complex diseases. Weinheim, Germany: Wiley VCH Verlag, pp. 205-230, 2010.

## 5) GRANTS HELD AS PI

1. CNPq 440245/2022-2. Development of causal models among omics, brain, environment, and executive/language functions in the first 1,000 days. Amount: USD100,000. Period: 2023 – 2026.
2. CAPES-DAAD. Development of efficient statistical tools for networks and their applications to biological data. Amount: USD380,000. Period: 2022 – 2025.

3. Wellcome Leap. Identifying biomarkers and trajectories of typical neurodevelopment in children living in high-risk environments. Amount: USD3,000,000. Period: 2021 – 2024. PI: Guilherme Polanczyk. Co-PI: André Fujita.
4. PRP-USP. Connecting people by heart. Amount: USD54,000. Period: September 2021 – August 2022.
5. FAPESP-eScience 2020/01479-1. Classification of body/mental states for a human-machine interface based on the heart rate variability. Amount: USD45,000. Period: October 2020 – September 2023.
6. FAPESP-UdL 2020/08343-8. Graph/Hypergraph (spectral) analysis to compare metabolic networks of pathogenic Trypanosoma sp. Amount: USD34,000. Period: December 2020 – November 2022.
7. FAPESP-INRIA 2019/22845-9. Computational approaches to explore intra and cross-species interactions and their role in all domains of life. Amount: USD15,000. Period: March 2020 – February 2022.
8. FAPESP 2018/21934-5. Network Statistics: theory, methods, and applications. Amount: USD510,000. Period: May 2019 - April 2024.
9. Academy of Medical Sciences NAF\R1\180002, the UK National Academy. A model-based graph clustering approach for autism stratification. Amount: USD80,000. Period: March 2018 – March 2021.
10. CNPq 303855/2019-3. Productivity fellowship. Amount: USD10,000. Period: 2020 - 2022.
11. CAPES / Alexander von Humboldt Foundation. Statistical methods on graphs. Amount: USD48,000. Period: December 2017 - November 2020.
12. PRP-USP. The use of heart rate variability to construct activity reading and human-machine interfaces. Amount: USD20,000. Period: April 2019 - October 2020.
13. CNPq 304876/2016-0. Productivity fellowship. Amount: USD12,500. Period: 2017 - 2019.
14. FAPESP 2016/13422-9. Statistical methods for graphs with applications in life sciences. Amount: USD46,000. Period: November 2016 – October 2018.
15. FAPESP 2014/09576-5. Development of computational statistical methods to construct, model, and analyze biological networks associated with human diseases. Amount: USD100,000. Period: July 2014 – September 2016.
16. CNPq 304020/2013-3. Productivity fellowship. Amount: USD12,500. Period: 2014 - 2016.
17. CAPES 51/2013 – Academic cooperation network for developing structural and functional genomics tools. (Co-PI). Amount received: USD80,000. Period: 2014 – 2019.
18. CAPES 51/2013 – Development and applications of computational tools in biology: from molecular modeling to translational research. (Co-PI). Amount received: USD35,000. Period: 2014 – 2019.
19. CNPq 473063/2013-1. Pattern recognition in large scale social interactions: the use of non-human primates as a model system. Amount: USD12,500. Period: July 2014 – December 2016.
20. FAPESP 2011/07762-8. Granger causality for sets of time series: development of methodologies for model selection and extensions in the frequency domain with molecular biology and neuroscience applications. Amount: USD86,000. Period: July 2011 – December 2013.
21. CNPq 306319/2010-1. Productivity fellowship. Amount: USD19,000. Period: 2011 - 2013.
22. RIKEN 090042. Development of computational methods for large scale gene regulatory networks: construction and structural analysis. Amount: USD17,000. Period: April 2009 – February 2011.

## 6) LIST OF ONGOING SUPERVISIONS (competitive scholarships between parenthesis)

1. Aline Rodrigues Nunes, Master candidate (CAPES)
2. Bruno Pereira Fazano, undergrad student in Applied Mathematics
3. Caio Matheus Prates Batalha Faria, Ph.D. candidate. Co-advisor (CNPq)
4. Daniel Cunha Oliveira, Ph.D. candidate
5. Daniela Bizinelli, Ph.D. candidate (CAPES)
6. Diego Trindade de Souza, Postdoc (PRP-USP)
7. Eduardo Lira, Ph.D. candidate (CAPES)
8. Eric Tierre A. Rodrigues – Master candidate
9. Grover Enrique Castro Guzman, Postdoc (Wellcome Leap)
10. Heitor Baldo, Ph.D. candidate (CAPES). Co-advisor
11. Henrique Apocalypse, Master candidate (CAPES)
12. Jaqueline Yu Ting Wang, Ph.D. candidate. Co-advisor
13. Leonardo Sanches, Ph.D. candidate. Co-advisor
14. Marcelo Meireles dos Santos, Postdoc (PRP-USP)
15. Mario Muramatsu Junior – Master candidate (FAPESP)
16. Maruan Bakri Ottoni – Master candidate (CAPES)
17. Victor Chavauty Villela – Master candidate (CAPES)

# 7) LIST OF GRADUATED STUDENTS (competitive scholarships between parenthesis)

*Post docs*
1. Daniel de Oliveira Dantas (PRP-USP), 2022 – assistant professor at Federal University of Sergipe
2. Marcos Inacio Severo de Almeida, Postdoc (PRP-USP), 2022 – assistant professor at
Federal University of Goias
3. Rômulo Damasclin Chaves dos Santos (PRP-USP), 2022
4. Diogo Costa (FAPESP), 2021
5. Abner Cardoso Rodrigues Neto (CAPES), 2018 - researcher at
Edmond and Lily Safra International Institute of Neurosciences

*Ph.D. theses*
1. Vinicius Jardim Carvalho (FAPESP), 2023
2. Grover Enrique Castro Guzman (CAPES), 2021
3. Taiane Coelho Ramos (CNPq), 2021 – assistant professor at Fluminense Federal University
With one year internship at University College London, the UK
4. Carlos Eduardo Martins Relvas, 2020 – founder of the start-up DataRisk
5. Maciel Calebe Vidal (CAPES), 2020 - lecturer at Insper Institute
6. Suzana de Siqueira Santos (FAPESP), 2020 – researcher at Getúlio Vargas Foundation
with four months of internship at Sorbonne Université, France
***Best poster award at the 11th International Conference of the AB3C***
7. Gabriela Eleutério Soares (CAPES), 2018 – currently at Talkdesk, Portugal
8. Adèle Helena Ribeiro (CAPES), 2018 – postdoc at Columbia University, the USA
with six months of internship at Princeton University, the USA
***Best poster award at the 14th International Conference of the AB3C***
9. Gustavo Pinto Vilela (FAPESP), 2017 – currently at Amazon.
10. Fernando Cipriano Andrade Oliveira (CAPES), 2017 – lecturer at Loyola University Chicago
with six months of internship at Cincinnati Children's Hospital Medical Center, the USA
11. Abner Cardoso Rodrigues Neto (CAPES), 2016 - researcher at Edmond and Lily Safra International Institute of Neurosciences
***Bioinformatics Graduate Program best Ph.D. thesis***

*Master dissertations*
1. Renata Biaggi Biazzi (CAPES), 2022 – currently a Ph.D. student at Princeton University
2. Daniel Cunha Oliveira, 2021
3. Carlos Enrique Paucar Farfán (CAPES and Hewlett Packard Enterprise), 2021 – currently at BlueShift
4. Vinicius Jardim Carvalho (CAPES), 2018
5. Taiane Coelho Ramos (CAPES), 2017
6. Jaqueline Yu Ting Wang (GENOMIC company), 2017 – currently a researcher at the Human Genome Center – the University of São Paulo
7. Juan Manuel Vidal Garcia (FAPESP), 2016 – currently a Ph.D. student at Prof. Sergio R. Matioli lab – the University of São Paulo.
8. Paulo Moisés Raduan Alexandrino (CNPq), 2016 – currently a Ph.D. student at Max Planck Institute
9. Grover Enrique Castro Guzman (CAPES), 2016
10. Davi Toshio Inada (FAPESP), 2016 – currently a researcher at Butantan Institute
11. Eduardo Cocca Padovani (CAPES), 2015 – currently a Ph.D. student at Prof. Luciano F. Costa lab – the University of São Paulo.
12. Suzana de Siqueira Santos (FAPESP), 2015
***Third place in the XXIII Latin American Contest of Master Thesis***
13. Maciel Calebe Vidal (CAPES), 2014

*Undergraduate students*
1. Camilla de Oliveira Fonseca, undergrad student in Statistics (PRP-USP), 2022
2. Christyan Ossamu Namikuchi, undergrad student in Applied Mathematics (FAPESP), 2022
3. Mayara dos Santos Nascimento, undergrad student in Statistics (PRP-USP), 2022
4. Lasse Rippa, undergrad student in Computer Science, Technische Universität Hamburg (DAAD), 2022
5. Higor Mendes Garcia, undergrad student in Statistics (PRP-USP), 2022
6. João Felipe Lobo Pevidor, undergrad student in Computer Science (PRP-USP), 2022
7. Maximilian Henkel – undergrad student from Universität Tübingen (DAAD), 2021
8. Guilherme Duarte Laurindo de Souza – B.Sc. in Molecular Sciences (PRP-USP), 2021

9. Mario Muramatsu Junior – B.Sc. in Computer Science at State University of São Paulo, 2020
10. Lucas Marques Gasparino – B.Sc. in Computer Science, 2020
11. Ravi do Valle Luz. B.Sc. in Molecular Sciences (FAPESP), 2020
12. Pedro Ivo Nepomuceno. B.Sc. in Computer Science (PIBIC-CNPq), 2016
13. Henrique C. de Souza Rodrigues. B.Sc. in Applied Mathematics with minor in Biological Sciences, 2014
14. Pedro Parik Americano. B.Sc. in Mechatronics Engineering (PIBIC-CNPq), 2013
15. Suzana de Siqueira Santos. B.Sc. in Computer Science (PIBIC-CNPq), 2013
16. Yuri Gomes de Abreu. B.Sc. in Manufacturing Engineering (PRP-USP), 2012
17. Claudivan Ribeiro. B.Sc. in Computer Science, 2011
18. Tiago N. Bombenti. B.Sc. in Computer Science, 2011

## 8) COURSES AND OTHER SERVICES PROVIDED TO STUDENTS AND THE HOME INSTITUTION

- Undergraduate courses: CCM0118 – Computation I for Molecular Scientists, CCM0128 - Computation II for Molecular Scientists, MAC2166 – Introduction to Computer Science for Engineers, MAC0110 – Introduction to Computer Science, MAC0323 – Data Structure, MAC0101 – Integration in the University and Career, MAC0102 – Paths in the Bachelor Course of Computer Science, MAC0323 – Voluntary Community Work, MAC0214 – Extracurricular Activities, MAC0215 – Undergraduate Research.
- Graduate courses: MAC6992 – Introduction to Network Statistics, MAC6937 – Advanced Studies in Connectivity Measures, IBI5048 – Inference of Connectivity and Causal Relations by Multivariate Time Series Analysis in Biological Systems, IBI5030 – Advanced Course of Cell Signaling and Genetic Modulation Networks (joint course with Dr. Ricardo Garcia Corrêa of Sanford-Burnham Medical Research Institute, the USA), MAC5917 – Introduction to Systems Biology, BTC5809 – Systems Biology (Biotechnology course), MAC5710 – Data Structure and Its Manipulation.
- Bioinformatics Graduate Program Director (since 2020)
- Bioinformatics Graduate Program Vice-Director (2018 - 2020)
- Member of several local committees: departmental council (since 2011), computer science graduate program (2012 - 2016), bioinformatics graduate program (since 2011), informatics (since 2011), research (since 2017), congregation (2016 - 2019)
- Bioinformatics Graduate Program Entrance Exam Coordinator (2016 - 2020)
- Bioinformatics Summer Course Coordinator 2013 (*highlighted by the Research Provost as one of the year's best educational events*) and 2022
- Ad hoc committee that designed the eScience track (minor Bioinformatics) for the Computer Science undergraduate course (2013 - 2014).

## 9) MAIN ACHIEVEMENTS AS THE BIOINFORMATICS GRADUATE PROGRAM DIRECTOR

- Due to the COVID-19 pandemic, disciplines started to minister remotely. I capitalized on this infrastructure and proposed and led a national network among all Bioinformatics graduate programs. The purpose is to construct infrastructure to allow students of any program to attend other programs.
- During the Brazilian economic crisis, I led the Bioinformatics committee to get four master's and three Ph.D. additional scholarships for the Bioinformatics Graduate Program. It corresponds to an increase of 50% and 25% of master's and Ph.D. scholarships, respectively.
- We transformed the standard paper-based entrance exam into a digitalized form, which allowed candidates from all over the world to apply remotely. Consequently, the number of applications increased from an average of 60 in the last five years to 138 candidates, i.e., over 100% increase.
- I organized the Bioinformatics committee to be in a proportion of 50/50 women/men. Also, we debate all topics extensively, considering minority groups' opinions. As a consequence, voting became unnecessary. We make all decisions with consensus.

## 10) OTHER PROFESSIONAL ACTIVITIES

- Organization of the 10th IEEE International Conference on e-Science, Workshop on Bioinformatics and Algorithms 2015, 11th International Conference of the AB3C + Brazilian Symposium of Bioinformatics, Workshop on Network Statistics at University College London.
- Presentation of seminars/talks abroad: Argentina (XVIII Congreso Argentino de Bioingeniería), Denmark (The International Statistical Institute World Congress – satellite meeting in Dynamic Statistical Models),

Germany (Max-Planck Institute for the History of Science, Max-Planck Institute for Mathematics in the Sciences, Friedrich-Alexander Universität Erlangen-Nürnberg, Universität Tübingen), Japan (University of Tokyo, Tohoku University, Nagoya University, Kanazawa University, Conference of the International Federation of Classification Societies, International Symposium on Tumor Biology), Slovenia (the University of Primorska, 9th Slovenian International Conference on Graph Theory), the UK (University College London, University of London – Royal Holloway, University of East Anglia), etc.

- Presentation of seminars/talks in Brazil: Federal University of Rio Grande do Norte, Federal University of Rio de Janeiro, State University of São Paulo, State University of Campinas, Federal University of Technology – Paraná, Federal University of Minas Gerais, Oswaldo Cruz Foundation at Rio de Janeiro, Oswaldo Cruz Foundation at Bahia, Catholic University of Goiás, International Institute for Neuroscience of Natal, Insper, etc.
- Habilitation thesis opponent: José Luiz Rybarczyk Filho (State University of São Paulo), Ariane Machado Lima (University of São Paulo), Marcelo Falsarella Carazzolle (State University of Campinas), Renato Vicentini dos Santos (State University of Campinas), Tatiana Teixeira Torres (University of São Paulo).
- Consultations: O Boticário (second largest Brazilian cosmetic company), Cogsign (start-up for health monitoring), IAssist Tecnologia (start-up for early cancer diagnosis using AI).
- Reviewer for funding agencies: BBSRC (the UK), MRC (the UK), The Italian Ministry for Education, University and Research (Italy), University of Piemonte Orientale (Italy), The Romanian National Research Council for Scientific Research (Romania), CONICYT (Chile), FAPESP (Brazil), CNPq (Brazil), and Oswaldo Cruz Foundation (Brazil).
- Reviewer for journals: Bioinformatics, PLoS Computational Biology, BMC Bioinformatics, BMC Systems Biology, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Nucleic Acids Research, NeuroImage, Human Brain Mapping, Computational Statistics & Data Analysis, Statistics in Medicine, Neoplasia, etc.
- Associate Editor for the Springer/Nature journal Network Modeling Analysis in Health Informatics and Bioinformatics (NHIB).

## 11) LANGUAGES

- Portuguese – Native
- English – Advanced
- Spanish – Advanced (D.E.L.E. Spanish Certification C2 level)
- French – Intermediate (D.E.L.F. French Certification B2 level)
- Japanese – Advanced (J.L.P.T. Japanese Certification N1 level)

# Jörg Fallmann

*CV*

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*Germany*
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*0000-0002-4573-9939*
ⓖ *jfallmann*

## Summary

Current position: Postdoctoral Researcher Stadler Lab, Department for Mathematics and Informatics; Background in bioinformatics and molecular biology with focus on RNA and cell biology; 32 peer-reviewed publications; International and interdisciplinary collaborations; Organization of scientific and training events as co- and main organizer; Reviewing experience; Teaching experience in computer science, bioinformatics and molecular biology; Mentoring of 4 PhD students together with Peter F. Stadler and 3 Master Students as (Co-)Supervisor.

## Research Interests

RNA Biology; Gene Expression Regulation; Bioinformatics; High-throughput Data Analysis; FAIR Data Science; Molecular Biology; Biomarker

## Personal Information

Fullname          **Jörg Fallmann, PhD**.

Date of Birth     **26 February 1984**.

Place of Birth    **Vienna**.

Address           **Bioinformatics, University of Leipzig**, *Härtelstr. 16-18*, D-04107 Leipzig, Germany.

Nationality       **Austria**.

Civil Status      **Married, 1 child (*2021)**.

Email             **joerg@fallmann.info**.

Homepage          `https://www.fallmann.info/joerg`.

ORCiD             `https://orcid.org/0000-0002-4573-9939`.

# Education

| | |
|---|---|
| since 2016 | **Postdoctoral researcher with Prof. Peter F. Stadler**, *Professorship for Bioinformatics, University of Leipzig.* |
| 17.11.2016 | **Ph.D.**, *University of Vienna.* |
| 2012-2016 | **PhD Thesis**, *Institute for theoretical Chemistry, University of Vienna, Group Prof. Ivo Hofacker, 1090 Vienna, Bioinformatical analysis of RNA - protein interactions in AU-rich element mediated decay.* |
| 16.12.2011 | **Mag. rer. nat.**, *University of Vienna*, Graduation with distinction. |
| 2010-2011 | **Master's Thesis**, *Institute for Theoretical Chemistry, University of Vienna, Group Prof. Ivo Hofacker, 1090 Vienna, Investigation and prediction of interactions between AU-rich binding proteins and AU rich elements and the generation of the 'AREsite' webserver.* |
| 2004–2011 | **Undergraduate studies**, *Molecular Biology, University of Vienna.* |
| 1999–2004 | **Federal Training and Research Institute for Industrial Chemistry HBLVA Rosensteingasse**, *1170 Vienna.* |

# Professional Experience

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|---|---|
| 2016-2022 | **Teaching/Assisting**, *Algorithms and Data Structures I+II, RNA Regulation, Advanced Methods in Bioinformatics, Institute for Informatics, University of Leipzig*, 04107 Leipzig. |
| 2012-2015 | **University assistant**, *Institute for Theoretical Chemistry, University of Vienna, 1090 Vienna.* |
| 2009-2010 | **Teaching**, *Max F Perutz Laboratories*, 1030 Vienna, Student assistant in laboratory course: Molecular Biology Techniques. |
| 2008-2008 | **System Administrator**, *Institute for Theoretical Chemistry, University of Vienna, 1090 Vienna*, Administration of workstations, cluster machines and network. |

# Parental leave

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|---|---|
| 01-03,08/2022 | **Paternity leave**. |
| 01-04 2023 | **Part time work 32h (Partnerschaftsmonate)**. |

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# Reviewing

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|---|---|
| Since 2011 | **Manuscripts**, *Bioinformatics, BMC-Bioinformatics, RNA Biology, NAR genomics and bioinformatics, Molecular Biology and Evolution, Protein and Peptide Letters, others..* |
| 2021 | **Review of proposal**, *BSF, US-Israel Binational Science Foundation..* |
| 2017 | **Conference proceedings**, *RECOMB*. |

# Presentations and Posters at Conferences and Seminars

| | |
|---|---|
| 11/2019 | **Talk**, *DAAD Seminar: 'RNA bioinformatics', Sao Paulo, Brazil.* |
| 08/2019 | **Talk**, *Dagstuhl Seminar 19342: 'Advances and Challenges in Protein-RNA Recognition, Regulation and Prediction', Wadern, Germany.* |
| 11/2018 | **Talk**, *DAAD Seminar: 'RNA bioinformatics', Rio de Janeiro, Brazil.* |
| 09/2018 | **Poster**, *German Conference on Bioinformatics: 'The RNA Workbench 2.0.19', Vienna, Austria.* |
| 06/2018 | **Talk**, *IZBI Workshop „Genome Bioinformatics for Health": 'de.NBI, Galaxy and my work', Grimma, Germany.* |
| 2016-2020 | **Poster, annually**, *de.NBI meeting: 'The RNA bioinformatics center Leipzig', Bielefeld/Berlin, Germany.* |
| since 2008 | **Regular talks at seminars almost every year**.<br>○ February: *Winterseminar*, Bled, Slovenia. Organized by TBI Vienna.<br>○ October: *Herbstseminar*, Doubice, Czech Republic. Organized by Bioinformatics Leipzig. |

# List of Courses

| | |
|---|---|
| 01/04/16 - 01/04/23 | **Teaching winter term**, *Algorithms and Data structures I assisting Thomas Gatter, Sven Findeiss and Peter F. Stadler.* |
| 01/04/16 - 01/04/23 | **Teaching summer term**, *Algorithms and Data structures II assisting with Thomas Gatter, Sven Findeiss and Peter F. Stadler.* |
| 01/04/21 - 01/07/21 | **Special Lecture**, *Advanced Methods in Bioinformatics together with Peter F. Stadler.* |
| 01/04/22 - 01/07/22 | **Special Lecture**, *Advanced Methods in Bioinformatics together with Thomas Gatter and Peter F. Stadler.* |

01/04/18 - 01/07/18 **Special Lecture**, *RNA Regulation together with Stephan Bernhart, Stefanie Kehr and Zasha Weinberg.*

01/02/16 - 31/12/22 **Workshops, on-demand**, *NGS Analysis together with the de.NBI team of the RNA bioinformatics center Freiburg.*

09/09/18 - 13/09/18 **Winter school**, *RNA Secondary Structures together with Kevin Lamkiewicz.*

25/09/17 - 29/09/17 **Summer school**, *Computational Genomics and RNA Biology together with Peter F. Stadler and de.NBI RNA bioinformatics center training team.*

## Theses Supervision

2019 - 2022 **Supervision PhD Thesis**, *Cristian Velandia: Workflows for the Large-Scale Assessment of miRNA Evolution together with Peter F. Stadler.*

2018 - 2021 **Supervision PhD Thesis**, *Rituparno Sen: Computational Characterization of Long Non-coding RNAs together with Peter F. Stadler.*

2017 - 2020 **Supervision PhD Thesis**, *Anne Hoffmann: The marvelous world of tRNAs together with Peter F. Stadler.*

2016 - 2019 **Supervision PhD Thesis**, *Ali Yazbeck: Improved Workflows for RNA Homology Search together with Peter F. Stadler.*

2020 **Supervision Master student**, *Robin Goldmann: Modular Analysis of Differential Splicing and Trancript Isoform Quantification using RNA-Seq Data.*

2020 **Supervision Master student**, *Christiane Gärter: RAP: Ribozeq Analysis Pipeline.*

2020 **Co-Supervision Master student**, *Christopher Klapproth: Support vector machine retraining for de novo detection of functional non-coding RNAs, Main supervisor Sven Findeiss.*

## Collaborators

Peter F. Stadler (Bioinformatics, Leipzig University), Zasha Weinberg (Bioinformatics, Leipzig University), Christina Weinberg (Institute for Biochemistry, Leipzig University), Mario Mörl (Institute for Biochemistry, Leipzig University), Heike Betat (Institute for Biochemistry, Leipzig University), Anita Marchfelder (Universität Ulm), Thomas Arendt (Universitätsklinikum Leipzig), Peter Kovacs (Universitätsklinikum Leipzig), Jörg Hackermüller (Helmholtz-Zentrum für Umweltforschung), Kristin Reiche (Fraunhofer IZI), Christian Arnold (EMBL Heidelberg), Matthias Blüher (Universitätsklinikum Leipzig), Rolf Backofen (Universität Freiburg), Julian König (IMB Mainz), Manja Marz (Friedrich-Schiller-Universität Jena), Maria Emilia MT Walter (Universidade de Brasília - UnB), Alexandre Paschoal (Federal University of Technology, Paraná/Brazil), Douglas Domingues (University of São Paulo), Steve Hoffmann (FLI Jena), Christoph Grevelding (Institute for Parasitology, Giessen University)

# Languages

**German**: native
**English**: advanced

# Computer skills

**Programming**: Python, Perl, C++, Bash, JS
**OS**: Linux, Windows
**Misc**: R, Latex, Galaxy, Conda, MySQL

# Publications

ORCiD: https://orcid.org/0000-0002-4573-9939

The annotations [ XX ɡ ] report citation numbers according to Google scholar as of writing, [YY%] estimates my contributions.

## Peer-Reviewed Publications

[1]  V. J. Olzog, L. I. Freist, R. Goldmann, J. Fallmann, and C. E. Weinberg, "Application of RtcB ligase to monitor self-cleaving ribozyme activity by RNA-seq," *Biological Chemistry*, Jan. 2022, ISSN: 1437-4315. DOI: `10.1515/hsz-2021-0408` [20%] [ 2 ɡ ]

[2]  J. Wörtz, V. Smith, J. Fallmann, S. König, T. Thuraisingam, P. Walther, H. Urlaub, P. F. Stadler, T. Allers, F. Hille, and A. Marchfelder, "Cas1 and Fen1 Display Equivalent Functions During Archaeal DNA Repair," *Frontiers in Microbiology*, vol. 13, 2022, ISSN: 1664-302X [10%] [ 1 ɡ ]

[3]  R. M. Chakaroun, L. Massier, A. Heintz-Buschart, N. Said, J. Fallmann, A. Crane, T. Schütz, A. Dietrich, M. Blüher, M. Stumvoll, N. Musat, and P. Kovacs, "Circulating bacterial signature is linked to metabolic disease and shifts with metabolic alleviation after bariatric surgery," *Genome Medicine*, vol. 13, no. 1, p. 105, Jun. 22, 2021, ISSN: 1756-994X. DOI: `10.1186/s13073-021-00919-6` [10%] [ 8 ɡ ]

[4]  T. Gatter, S. von Löhneysen, J. Fallmann, P. Drozdova, T. Hartmann, and P. F. Stadler, "LazyB: Fast and cheap genome assembly," *Algorithms for molecular biology: AMB*, vol. 16, no. 1, p. 8, Jun. 1, 2021, ISSN: 1748-7188. DOI: `10.1186/s13015-021-00186-5`. pmid: `34074310` [10%] [ 2 ɡ ]

[5]  A. Hoffmann, L. Erber, H. Betat, P. F. Stadler, M. Mörl, and J. Fallmann, "Changes of the tRNA Modification Pattern during the Development of Dictyostelium discoideum," *Non-coding RNA*, vol. 7, no. 2, p. 32, May 28, 2021, ISSN: 2311-553X. DOI: `10.3390/ncrna7020032`. pmid: `34071416` [25%] [ 0 ɡ ]

[6]  N. A. N. Jorge, U. Ueberham, M. Knobloch, P. F. Stadler, J. Fallmann, and T. Arendt, "Disturbance of phylogenetic layer-specific adaptation of human brain gene expression in Alzheimer's disease," *Scientific Reports*, vol. 11, no. 1, p. 20 200, Oct. 12, 2021, ISSN: 2045-2322. DOI: `10.1038/s41598-021-99760-5`. pmid: `34642398` [25%] [ 1 ɡ ]

[7]  C. Klapproth, R. Sen, P. F. Stadler, S. Findeiß, and J. Fallmann, "Common Features in lncRNA Annotation and Classification: A Survey," *Non-Coding RNA*, vol. 7, no. 4, p. 77, Dec. 2021, ISSN: 2311-553X. DOI: `10.3390/ncrna7040077` [30%] [ 5 ɡ ]

[8]  E. Parra-Rincón, C. A. Velandia-Huerto, A. Gittenberger, J. Fallmann, T. Gatter, F. D. Brown, P. F. Stadler, and C. I. Bermúdez-Santana, "The Genome of the "Sea Vomit" Didemnum vexillum," *Life*, vol. 11, no. 12, p. 1377, Dec. 2021, ISSN: 2075-1729. DOI: `10.3390/life11121377` [10%] [ 1 ɡ ]

[9]  H. Saker, R. Machné, J. Fallmann, D. B. Murray, A. M. Shahin, and P. F. Stadler, "Weighted Consensus Segmentations," *Computation*, vol. 9, no. 2, p. 17, 2 Feb. 2021. DOI: `10.3390/computation9020017` [20%] [ 0 ɡ ]

[10]  C. A. Velandia-Huerto, J. Fallmann, and P. F. Stadler, "miRNAture—Computational Detection of microRNA Candidates," en, *Genes*, vol. 12, no. 3, p. 348, Mar. 2021, Number: 3 Publisher: Multidisciplinary Digital Publishing Institute. DOI: `10.3390/genes12030348` [30%] [ 2 ɡ ]

[11] L. Erber, A. Hoffmann, J. Fallmann, M. Hagedorn, C. Hammann, P. F. Stadler, H. Betat, S. Prohaska, and M. Mörl, "Unusual Occurrence of Two Bona-Fide CCA-Adding Enzymes in Dictyostelium discoideum," en, *International Journal of Molecular Sciences*, vol. 21, no. 15, p. 5210, Jan. 2020. DOI: 10.3390/ijms21155210 `15%` `4 ᵍ`

[12] S. M. Hoser, A. Hoffmann, A. Meindl, M. Gamper, J. Fallmann, S. H. Bernhart, L. Müller, M. Ploner, M. Misslinger, L. Kremser, H. Lindner, S. Geley, H. Schaal, P. F. Stadler, and A. Huettenhofer, "Intronic tRNAs of mitochondrial origin regulate constitutive and alternative splicing," *Genome Biology*, vol. 21, no. 1, p. 299, Dec. 2020, ISSN: 1474-760X. DOI: 10.1186/s13059-020-02199-6 `15%` `3 ᵍ`

[13] L. Massier, R. Chakaroun, S. Tabei, A. Crane, K. D. Didt, J. Fallmann, M. von Bergen, S.-B. Haange, H. Heyne, M. Stumvoll, M. Gericke, A. Dietrich, M. Blüher, N. Musat, and P. Kovacs, "Adipose tissue derived bacteria are associated with inflammation in obesity and type 2 diabetes," en, *Gut*, gutjnl–2019–320 118, Apr. 2020, ISSN: 0017-5749, 1468-3288. DOI: 10.1136/gutjnl-2019-320118 `10%` `86 ᵍ`

[14] A. Nitsche, C. Arnold, U. Ueberham, K. Reiche, J. Fallmann, J. Hackermüller, F. Horn, P. F. Stadler, and T. Arendt, "Alzheimer-related genes show accelerated evolution," en, *Molecular Psychiatry*, pp. 1–7, Mar. 2020, ISSN: 1476-5578. DOI: 10.1038/s41380-020-0680-1 `10%` `6 ᵍ`

[15] I. Nowak, E. Boratyn, S. Student, S. F. Bernhart, J. Fallmann, M. Durbas, P. F. Stadler, and H. Rokita, "MCPIP1 ribonuclease can bind and cleave AURKA mRNA in MYCN-amplified neuroblastoma cells," *RNA Biology*, vol. 0, no. 0, pp. 1–13, Aug. 2020, ISSN: 1547-6286. DOI: 10.1080/15476286.2020.1804698 `10%` `4 ᵍ`

[16] R. Sen, J. Fallmann, M. E. M. T. Walter, and P. F. Stadler, "Are spliced ncRNA host genes distinct classes of lncRNAs?" *Theory in Biosciences*, vol. 139, no. 4, pp. 349–359, 2020, ISSN: 1431-7613. DOI: 10.1007/s12064-020-00330-6 `20%` `1 ᵍ`

[17] N. Bašić, S. J. Berkemer, J. Fallmann, P. W. Fowler, T. Gatter, T. Pisanski, N. Retzlaff, P. F. Stadler, and S. S. Zemljič, "Convexity Deficit of Benzenoids," en, *Croatica Chemica Acta*, vol. 92, no. 4, pp. 457–466, Nov. 2019, ISSN: 0011-1643. DOI: 10.5562/cca3602 `10%` `3 ᵍ`

[18] L. Erber, A. Hoffmann, J. Fallmann, H. Betat, P. F. Stadler, and M. Mörl, "LOTTE-seq (Long hairpin oligonucleotide based tRNA high-throughput sequencing): Specific selection of tRNAs with 3'-CCA end for high-throughput sequencing," *RNA Biology*, vol. 0, Sep. 2019, ISSN: 1547-6286. DOI: 10.1080/15476286.2019.1664250 `20%` `13 ᵍ`

[19] J. Fallmann, P. Videm, A. Bagnacani, B. Batut, M. A. Doyle, T. Klingstrom, F. Eggenhofer, P. F. Stadler, R. Backofen, and B. Grüning, "The RNA workbench 2.0: next generation RNA data analysis," *Nucleic Acids Research*, May 2019, ISSN: 0305-1048. DOI: 10.1093/nar/gkz353. eprint: http://oup.prod.sis.lan/nar/advance-article-pdf/doi/10.1093/nar/gkz353/28578734/gkz353.pdf `40%` `7 ᵍ`

[20] A. M. Yazbeck, P. F. Stadler, K. Tout, and J. Fallmann, "Automatic curation of large comparative animal MicroRNA datasets," *Bioinformatics*, Apr. 2019, ISSN: 1367-4803. DOI: 10.1093/bioinformatics/btz271. eprint: http://oup.prod.sis.lan/bioinformatics/advance-article-pdf/doi/10.1093/bioinformatics/btz271/28670693/btz271.pdf `35%` `9 ᵍ`

[21] B. Grüning, R. Dale, A. Sjödin, B. A. Chapman, J. Rowe, C. H. Tomkins-Tinch, R. Valieris, and J. Köster, "Bioconda: Sustainable and comprehensive software distribution for the life sciences," En, *Nature Methods*, vol. 15, no. 7, p. 475, Jul. 2018, ISSN: 1548-7105. DOI: 10.1038/s41592-018-0046-7 `10%` `612 ᵍ`

[22] A. Hoffmann, J. Fallmann, E. Vilardo, M. Mörl, P. F. Stadler, and F. Amman, "Accurate mapping of tRNA reads," en, *Bioinformatics*, vol. 34, no. 7, pp. 1116–1124, Apr. 2018, ISSN: 1367-4803. DOI: `10.1093/bioinformatics/btx756` 20% 32 ℊ

[23] L. K. Kutsche, D. M. Gysi, J. Fallmann, K. Lenk, R. Petri, A. Swiersy, S. D. Klapper, K. Pircs, S. Khattak, P. F. Stadler, J. Jakobsson, K. Nowick, and V. Busskamp, "Combined Experimental and System-Level Analyses Reveal the Complex Regulatory Network of miR-124 during Human Neurogenesis," English, *Cell Systems*, vol. 7, no. 4, 438–452.e8, Oct. 2018, ISSN: 2405-4712. DOI: `10.1016/j.cels.2018.08.011` 20% 37 ℊ

[24] F. R. Sutandy, S. Ebersberger, L. Huang, A. Busch, M. Bach, H.-S. Kang, J. Fallmann, D. Maticzka, R. Backofen, P. F. Stadler, K. Zarnack, M. Sattler, S. Legewie, and J. König, "In vitro iCLIP-based modeling uncovers how the splicing factor U2AF2 relies on regulation by cofactors," en, *Genome Research*, vol. 28, no. 5, pp. 699–713, May 2018, ISSN: 1088-9051, 1549-5469. DOI: `10.1101/gr.229757.117` 5% 56 ℊ

[25] R. Backofen, J. Engelhardt, A. Erxleben, J. Fallmann, B. Grüning, U. Ohler, N. Rajewsky, and P. F. Stadler, "RNA-bioinformatics: Tools, Services and Databases for the Analysis of RNA-based Regulation," en, *Journal of Biotechnology*, May 2017, ISSN: 01681656. DOI: `10.1016/j.jbiotec.2017.05.019` 20% 21 ℊ

[26] J. Fallmann, S. Will, J. Engelhardt, B. Grüning, R. Backofen, and P. F. Stadler, "Recent advances in RNA folding," *Journal of Biotechnology*, Bioinformatics Solutions for Big Data Analysis in Life Sciences presented by the German Network for Bioinformatics Infrastructure, vol. 261, pp. 97–104, Nov. 2017, ISSN: 0168-1656. DOI: `10.1016/j.jbiotec.2017.07.007` 60% 69 ℊ

[27] B. A. Grüning, J. Fallmann, D. Yusuf, S. Will, A. Erxleben, F. Eggenhofer, T. Houwaart, B. Batut, P. Videm, A. Bagnacani, M. Wolfien, S. C. Lott, Y. Hoogstrate, W. R. Hess, O. Wolkenhauer, S. Hoffmann, A. Akalin, U. Ohler, P. F. Stadler, and R. Backofen, "The RNA workbench: Best practices for RNA and high-throughput sequencing bioinformatics in Galaxy," en, *Nucleic Acids Research*, Jun. 2017, ISSN: 0305-1048, 1362-4962. DOI: `10.1093/nar/gkx409` 25% 44 ℊ

[28] J. Fallmann, V. Sedlyarov, A. Tanzer, P. Kovarik, and I. L. Hofacker, "AREsite2: An enhanced database for the comprehensive investigation of AU/GU/U-rich elements," *Nucleic Acids Research*, no. Database issue 44, 2016 75% 69 ℊ

[29] M. Hölzer, V. Krähling, F. Amman, E. Barth, S. H. Bernhart, V. A. O. Carmelo, M. Collatz, G. Doose, F. Eggenhofer, J. Ewald, J. Fallmann, L. M. Feldhahn, M. Fricke, J. Gebauer, A. J. Gruber, F. Hufsky, H. Indrischek, S. Kanton, J. Linde, N. Mostajo, R. Ochsenreiter, K. Riege, L. Rivarola-Duarte, A. H. Sahyoun, S. J. SaundeRs, S. E. Seemann, A. Tanzer, B. Vogel, S. Wehner, M. T. Wolfinger, R. Backofen, J. Gorodkin, I. Grosse, I. Hofacker, S. Hoffmann, C. Kaleta, P. F. Stadler, S. Becker, and M. Marz, "Differential transcriptional responses to Ebola and Marburg virus infection in bat and human cells," en, *Scientific Reports*, vol. 6, no. 1, Dec. 2016, ISSN: 2045-2322. DOI: `10.1038/srep34589` 10% 53 ℊ

[30] V. Sedlyarov, J. Fallmann, F. Ebner, J. Huemer, L. Sneezum, M. Ivin, K. Kreiner, A. Tanzer, C. Vogl, I. L. Hofacker, and P. Kovarik, "Tristetraprolin binding site atlas in the macrophage transcriptome reveals a switch for inflammation resolution," en, *Molecular Systems Biology*, vol. 12, no. 5, pp. 868–868, May 2016, ISSN: 1744-4292. DOI: `10.15252/msb.20156628` 35% 61 ℊ

[31] M. T. Wolfinger, J. Fallmann, F. Eggenhofer, and F. Amman, "ViennaNGS: A toolbox for building efficient next-generation sequencing analysis pipelines," *F1000Research*, vol. 4, 2015 30% 36 ℊ

[32] A. R. A. Gruber, J. Fallmann, F. Kratochvill, P. Kovarik, and I. L. Hofacker, "AREsite: A database for the comprehensive investigation of AU-rich elements.," *Nucleic acids research*, vol. 39, no. Database issue, pp. 1–4, Nov. 2011, ISSN: 1362-4962. DOI: `10.1093/nar/gkq990` 50% 183 g

## Submitted Manuscripts or Manuscripts in Preparation

[1] J. Fallmann, R. Goldmann, and P. F. Stadler, "MONSDA: Modular Organizer of Nextflow and Snakemake driven HTS Data Analysis," DOI: `10.31219/osf.io/jeqgr` 70% - g

[2] J. Fallmann, D. Rabsch, R. Backofen, and P. F. Stadler, "RNAmediator: RNA secondary structure as mediator of intermolecular interaction," 40% - g

[3] S. Fuchs, C. Danßmann, F. Klironomos, A. Winkler, A. Szymansky, J. Naderi, J. Fallmann, S. Bernhart, K. Helmsauer, M.-L. Kirchner, P. Mertins, C. Suenkel, J. Toedling, P. Stadler, P. Hundsdoerfer, H. E. Deubzer, A. Künkele, P. Lang, J. Fuchs, A. Eggert, N. Rajewsky, and F. Hertwig, "Defining the landscape of circular RNAs in neuroblastoma unveils a global suppressive function of MYCN," p. 8, 10% - g

## Theses

[1] J. Fallmann, "Bioinformatical Analysis of RNA - Protein Interactions in AU-Rich Element Mediated Decay," Ph.D. dissertation, University of Vienna, 2016. [Online]. Available: `http://othes.univie.ac.at/44276/`

[2] J. Fallmann, "Investigation and Prediction of Interactions between AU-Rich Binding Proteins and AU Rich Elements and the Generation of the AREsite Webserver," M.S. thesis, University of Vienna, 2011. [Online]. Available: `http://othes.univie.ac.at/17132/`

## Public Domain Software packages

[1] Jörg Fallmann, Dominik Rabsch, *RNAmediator*, 2022. [Online]. Available: `https://github.com/jfallmann/RNAmediator`

[2] Jörg Fallmann, Robin Goldmann, *MONSDA: Modular Organizer of Nextflow and Snakemake driven hts Data Analysis*, 2022. [Online]. Available: `https://github.com/jfallmann/MONSDA`

[3] Ali Yazbeck, Jörg Fallmann, Cristian Velandia, *MIRfix*, 2020. [Online]. Available: `https://github.com/Bierinformatik/MIRfix`

[4] Björn Grüning, Jörg Fallmann, Pavankumar Videm, *Galaxy RNA Workbench*, 2020. [Online]. Available: `https://github.com/bgruening/galaxy-rna-workbench`

[5] Cristian Velandia, Jörg Fallmann, *miRNAture*, 2020. [Online]. Available: `https://github.com/Bierinformatik/miRNAture`

[6] Rainer Machné, Jörg Fallmann, *ConsSeg: Weighted Consensus Segmentation in R*, 2020. [Online]. Available: `https://github.com/Bierinformatik/consseg`

[7] Bioconda Team, *Bioconda*, 2018. [Online]. Available: `https://github.com/bioconda/bioconda-recipes`

# CURRICULUM VITAE
## NORA BEIER

## PERSONAL DETAILS

Name:             Nora Beier
Date of birth:    18. September 1987
Place of birth:   Dresden

**Nora Beier**
Prager Straße 31
04315 Leipzig
☎ 0151/ 4044 17 13
✉ nora@bioinf.uni-leipzig.de

## STUDIES

| | |
|---|---|
| 10/2015 – 03/2019 | Hochschule Zittau/Görlitz, Zittau<br>*Field of study:* Molecular biotechnology<br>*Degree:* Bachelor of Science |
| 10/2019 - 05/2022 | University Leipzig<br>*Field of study:* Biochemie<br>*Degree:* Master of Science |
| 10/2019 - 05/2022 | *Field of study:* Bioinformatik<br>*Degree:* Master of Science |
| 01/2023 - | PhD Position Bioinformatics, University Leipzig |

## EDUCATION

| | |
|---|---|
| 09/2014 – 10/2015 | BSZ of economics „Franz Ludwig Gehe" Dresden<br>*advanced technical college certificate* |

## PRACTICAL EXPERIENCE

| | |
|---|---|
| 02/2018 – 07/2018 | University Hospital Jena<br>Institute for Experimental Radiology<br>*Intern for Bachelor Practical Module* |
| 08/2016 – 09/2016 | University Hospital Carl Gustav Carsus Dresden,<br>*Intern facultative* |
| 05/2019 – 09/2019 | Biotechnology Centre TU Dresden,<br>Working group Brankatschk<br>*research assistant* |

## FURTHER TRAINING AND CAREER

| | |
|---|---|
| 10/2015 – 08/2014 | working as a waiter |
| 08/2007 – 07/2009 | BSZ HOGA Schloss Albrechtsberg<br>*Education:* waiter |
| 08/2004 – 07/2006 | Academy for Information and Communication Design<br>*Education:* Technical design assistant |

Leipzig, 10. Dezember 2022

# Curriculum Vitae
Bruno Johann **Schmidt**

## Personal Data

| | |
|---|---|
| **Name** | Bruno Johann Schmidt |
| **Date of Birth** | 30.11.1996 |
| **Place of Birth** | Nordhausen |
| **Address** | Kirschbergstraße 68a, 04155 Leipzig, Deutschland |
| **E-Mail** | bruno@bioinf.uni-leipzig.de |
| **Phone** | +49 152 36867601 |

## Education

| | |
|---|---|
| **since October 2022** | PhD Student, Computer Science, Leipzig University, Supervisor: Peter F. Stadler, Topic: Phylogenetic Networks and Clustering Systems |
| **October 2019 - September 2022** | Bioinformatics, Master of Science, Leipzig University, Final Grade - 1.1 |
| **October 2016 - September 2019** | Computer Science, Bachelor of Science, Leipzig University, Final Grade - 1.8 |
| **August 2007 - July 2015** | A-Levels (Abitur), Staatliches Herder Gymnasium Nordhausen, Final Grade - 1.4 |

# Work Experience

| | |
|---|---|
| **since January 2023** | PhD Position<br>Max Planck Institute for<br>Mathematics in the Sciences,<br>Supervisor: Peter F. Stadler |
| **April 2022 - December 2022** | Research Assistant<br>Leipzig University,<br>Interdisciplinary Center for Bioinformatics IZBI,<br>Supervisor: Peter F. Stadler |
| **January 2020 - December 2022** | Freelance Work,<br>Courage Netzwerk für Demokratieförderung e.V.,<br>Consultant |
| **October 2021 - February 2022** | Student Assistant<br>Leipzig University,<br>Faculty for Bioinformatics<br>Trainer in the module sequence analysis |
| **September 2021 - December 2021** | Student Assistant<br>Leipzig University,<br>Interdisciplinary Centre for Bioinformatics (IZBI) Leipzig<br>Characterization and identification of short non-coding RNAs |
| **May 2021 - August 2021** | Student Assistant<br>Leipzig University,<br>Faculty for Bioinformatics<br>Trainer in the module RNA and protein structures |
| **October 2020 - December 2020** | Student Assistant<br>Leipzig University,<br>Faculty for Mathematics & Computer Science<br>Design and revision of lecture slides for the module algorithms and data structures I |
| **September 2019 - October 2019;**<br>**February 2020 - December 2020** | Student Assistant<br>Helmholtz Centre for Environmental Research,<br>Research Group BioGeoOmics<br>Database administration, automation, workflow design and implementation |
| **October 2019** | Student Assistant<br>Leipzig University,<br>Institute for Applied Informatics (InfAI),<br>Organizational aid at CLARIN<br>Annual Conference 2019 |

## Additional Interests

**Languages**                    German (native),
                                 English (C1)

**Academic Interests**           Comparative Genomics, Phylogeny,
                                 Permutations, Sorting Algorithms,
                                 Graph Theory, Cluster Systems, Metrics

**Technical Know-How**           Python, Java, C, C#, R, bash, HTML, CSS

**Date :** 29.06.2023          **Unterschrift :**

Daniel Yasumasa Takahashi
Brain Institute
Federal University of Rio Grande do Norte
(Jun 2023)

## Personal Information

Address         Instituto do Cérebro, UFRN, Natal, RN -Brazil
Email           takahashiyd@gmail.com, takahashiyd@neuro.ufrn.br
Website         https://ethogenesis.science/

## Positions held

2019 –          Assistant Professor
                Brain Institute
                Federal University of Rio Grande do Norte, Natal, RN Brazil

2015 – 2019     Associate Research Scholar
                Princeton Neuroscience Institute
                Princeton University, Princeton, NJ USA

2010 – 2015     Postdoctoral Research Fellow
                Princeton Neuroscience Institute
                Princeton University, Princeton, NJ USA

2009 - 2010     Postdoctoral Research Fellow
                Institute of Mathematics and Statistics
                Universidade de São Paulo, USP, São Paulo, Brazil

2009 - 2009     Postdoctoral Research Fellow
                Instituto de Matemática Pura e Aplicada, IMPA, São Paulo, Brazil

## Education

2004 - 2009     PhD in Bioinformatics (Theoretical Neuroscience)
                Universidade de São Paulo, USP, Sao Paulo, Brazil
                Universidade de São Paulo
                Thesis: Measures of information flow in neuroscience (advisors: Koichi Sameshima
                and Luiz Antonio Baccalá)

| | |
|---|---|
| 2004 - 2008 | BSc in Applied Mathematics |
| | Universidade de São Paulo, USP, Sao Paulo, Brazil |
| | Senior thesis: Schwartz kernel theorem (advisor: Paulo Domingos Cordaro) |
| | |
| 1998 - 2003 | MD |
| | Universidade de São Paulo, USP, Sao Paulo, Brazil |
| | Graduation thesis: Applying artificial neural network in the diagnosis of Alzheimer's disease (advisor: Koichi Sameshima) |

## Honors and Awards

| | |
|---|---|
| 2018 | Young Investigator Award from Brazilian Association of Bioinformatics and Computation Biology |
| 2018 | Cosyne travel award |
| 2010-2012 | Pew Latin American Fellowship |
| 2009-2010 | FAPESP Fellowship |
| 2007 | Travel Grant Award - 10th Tamagawa-Riken Dynamic Brain Forum |
| 2006 | Best Work Award - I Latin American School on Computational Neuroscience |
| 2004-2008 | CAPES Fellowship |
| 2002 | Oswaldo Cruz Award in medical research – Honorable mention |
| 1998-2003 | CNPq Fellowship |
| 1997 | Bronze medal – Brazilian Mathematical Olympiad |

## In the media

My research findings were covered by several national and international news media:
BBC News, BBC World Service Science in Action Radio, National Geographic News Watch, Daily Mail UK, Decoded Science, The Independent, Wired, io9, Science, Nature, National Public Radio, Deutschlandfunk, Science News, Journal da FAPESP, Estadão.

## Invited talks

2023 –UFABC Mathematics seminar, São Paulo, *Brazil*
2022 – ESI Systems Neuroscience Conference - The ever-changing brain: Through development and evolution, Frankfurt, *Germany*
2022 – Gordon Research Conferences – Neural Mechanism of Acoustic Communication, Massachusetts, *USA*
2022 – CSHL Genetics & Neurobiology of Language, New York, *USA*
2021 – Connecting Brain Lecture Series (Max Planck Institute for Brain Research), *webinar*
2021 – XLIX Escola de Verão em Matemática da UnB, *webinar*

2020 - Seminário de Psicobiologia da UFRN, *webinar*
2020 - Seminar on Probability and Stochastic Process IME-USP, *webinar*
2020 - Probability Webinar IM-UFRJ, *webinar*
2020 - Mathematics and Neurobiology Intertwined, *webinar*
2020 - Dias Probabilísticos no Fundão, UFRJ, Rio de Janeiro, *Brazil*
2019 - ICe House Symposium, UFRN, Natal, *Brazil*
2019 - Brain Institute Seminar, UFRN, Natal, *Brazil*
2019 – Simpósio de Psicobiologia, Natal, *Brazil*
2019 - Neurocolloquium, Tübingen, *Germany*
2019 - InDiQ, Université Paris-Saclay, Orsay, *France*
2019 - LLR seminar, École Polytechnique, Palaiseau, *France*
2019 - Pararel Decision Processing seminar, Princeton University, Princeton, *USA*
2019 - Presidential seminar on Society and Neuroscience, Columbia University, New York, *USA*
2019 - Princeton Neuroscience in-house Seminar, Princeton University, Princeton, *USA*
2018 - Society for Neuroscience Annual Meeting, San Diego, *USA*
2018 - X-meeting 2018, São Paulo, *Brazil*
2018 - Fifty Years of Thermodynamic Formalism, Leiden, *Netherland*
2018 - International Congress of Neuroethology, Brisbane, *Australia*
2018 – Université Paris-Sud, Orsay, *France*
2018 – IMEC, Leuven*, Belgium*
2018 – Psychology Department, Indiana University, Bloomington, *USA*
2018 – LASCON, University of São Paulo, *Brazil*
2017 – SciBr, Boston University, Boston, *USA*
2016 – Marmoset Conference, Tokyo, *Japan*
2016 – Department of Life Sciences, University of Tokyo, Tokyo, *Japan*
2016 – Physics Department, Universidad Autónoma de San Luis Potosí, San Luis Potosí, *Mexico*
2016 – Riken Brain Science Institute, Saitama, *Japan*
2016 – International Congress of Psychology, Yokohama, *Japan*
2016 - Workshop on Evo-Devo of Vocal Learning and Plasticity, Tokyo, *Japan*
2016 - Second Neuromat Workshop, São Paulo, *Brazil*
2016 - Friedrich Miescher Institute for Biomedical Research, Basel, *Switzerland*
2016 – Neuroscience and Social Decision Seminar, Princeton University, *USA*
2015 – Institute of Mathematical Sciences and Computation, USP São Carlos, São Paulo, *Brazil*
2015 – Workshop on Stochastic chains, Hitting Times, Return Times, Long Range Dependence, UFSCAR, São Paulo, *Brazil*
2014 - First Neuromat Workshop, São Paulo, *Brazil*
2014 - Neuroscience and Social Decision Seminar, Princeton University, *USA*
2013 – Workshop on Statistical Methods for Neuronal Data, Paris, *France*
2013 – Department of Mathematics, Laboratoire J.A. Dieudonné, Université de Nice, Nice, *France*
2012 - Annual Meeting of the Pew Biomedical Sciences Programs, Panama, *Panama*
2012 – BRhyCoCo, New York University, *USA*
2012 – IBRG meeting, Princeton University, *USA*
2011 – Workshop on Chains and Systems with Interactions of Variable Range, São Paulo, *Brazil*
2011 – NUMEC Workshop, São Paulo, *Brazil*
2010 – Department of Mathematics, Universidade Federal do Rio de Janeiro, Rio de Janeiro, *Brazil*
2010 – Instituto de Matemática Pura e Aplicada (IMPA), Rio de Janeiro, *Brazil*
2009 - Jorma's Razor I, São Paulo, *Brazil*

2009 – NUMEC Workshop, São Paulo, *Brazil*
2009 – Department of Mathematics, Universitá degli Roma Tre, Rome, *Itali*
2008 – International Brain Research Organization (IBRO)/LARC Conference, Rio de Janeiro, *Brazil*
2006 – CONICYT-INSERM Workshop "Networks in Cognitive Systems", Complex System Institute, Valparaiso, *Chile*


## Reviewer

Ad hoc reviewer for National Science Foundation (NSF)
Ad hoc reviewer for Leakey Foundation Research Grant
Ad hoc reviewer for scientific journals: Science, Nature Communication, Current Biology, Plos Biology, Plos Computational Biology, Animal Behaviour, Open Biology, Biology Letters, IEEE Transactions on Biomedical Engineering, Entropy, Frontiers in Psychology, Scientific Report, Biology Direct, Plos One, Frontiers in Neuroscience, Games, Entropy, Journal of Experimental Biology, Royal Society Open Science, American Journal of Primatology, BMC Biology


## Articles

Google scholar = https://scholar.google.com/citations?user=DyIxrZUAAAAJ&hl=en


*Vocal communication*

Zhang YS, **Takahashi DY**, El Hady A, Ghazanfar AA (2022)
Active neural coordination of motor behaviors with internal states.
*PNAS*, 119 e2201194119

Narayanan DZ, **Takahashi DY**[#], Kelly LM, Hlavaty SI, Huang J, Ghazanfar AA[#] (2022)
Prenatal development of neonatal vocalizations.
*eLife* **11**:e78485.

Varella TT, Zhang YS, **Takahashi DY**[#], & Ghazanfar AA[#] (2022).
A mechanism for punctuating equilibria during mammalian vocal development.
*PLoS computational biology*, *18*(6), e1010173.

**Takahashi DY**, El Hady A, Zhang YS, Liao DA, Montaldo G, Urban A, Ghazanfar AA (2022)
Social-vocal brain networks in a non-human primate.
bioRxiv 2021.12.01.470701; doi: https://doi.org/10.1101/2021.12.01.470701

Zhang YS, **Takahashi DY**, El Hady A, Liao DA, Ghazanfar AA (2022)
Active neural coordination of motor behaviors with internal states.
bioRxiv 2021.12.10.472142; doi: https://doi.org/10.1101/2021.12.10.472142

Varella TT, Zhang YS, **Takahashi DY**[#], Ghazanfar AA[#] (2022)
A mechanism for punctuating equilibria during mammalian vocal development.
*Plos Computational Biology,* doi: 10.1371/journal.pcbi.1010173

Sliwa J, Mallet M, Christiaens M, **Takahashi DY** (2022)
Neural basis of multi-sensory communication in primates.
*Ethology Ecology & Evolution*, v. 34, 322-43.

Ghazanfar AA, Kelly LM, **Takahashi DY**, Winters S, Terret R, Higham JP (2020)
Domestication phenotype linked to vocal behavior in marmoset monkeys.
*Current Biology,* doi: 10.1016/j.cub.2020.09.049

Zhang YS, **Takahashi DY**, Liao DA, Ghazanfar AA[#] and Elemans CPH[#] (2019)
Vocal state change through laryngeal development.
*Nature Communications*, 10:4592 doi: 10.1038/s41467-019-12588-6

Gustison ML, Borjon JI, **Takahashi DY**[#], Ghazanfar AA[#] (2019)
Vocal and locomotor coordination develops in association with arousal state.
*eLife*, e41853, doi: 10.7554/eLife.41853

Ghazanfar AA, Liao DA, **Takahashi DY** (2019)
Volition and learning in primate vocal behavior.
*Animal Behaviour*, doi: 10.1016/j.anbehav.2019.01.021

Sliwa J, **Takahashi DY**, Shepherd SV (2018)
Mécanismes neuronaux pour la communication chez les primates.
*Revue de Primatologie*, 9, doi: 10.4000/primatologie.2950

**Takahashi DY**[#], Liao DA, Ghazanfar AA[#] (2017)
Vocal learning via social reinforcement by infant marmoset monkeys
*Current Biology*, v. 27, 1844-1852, doi: 10.1016/j.cub.2017.05.004

Teramoto Y, **Takahashi DY**[#], Holmes P[#], Ghazanfar AA[#] (2017)
Vocal development in a Waddington landscape.
*eLife*, 6:e20782. doi: 10.7554/eLife.20782

Borjon JI, **Takahashi DY**[#], Cervantes DC, Ghazanfar AA[#] (2016)
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*Journal of Neurophysiology*, v. 116, 753-764.

**Takahashi DY**, Fenley AR, Ghazanfar AA (2016)
Early development of turn-taking with parents shapes vocal acoustics in infant marmoset monkeys.
*Philosophical Transaction of Royal Society B*, v. 371, doi: 10.1098/rstb.2015.0370

**Takahashi DY**[#], Fenley AR, Teramoto, Y, Narayanan DZ, Borjon JI, Holmes P, Ghazanfar AA[#] (2015)

The developmental dynamics of marmoset monkey vocal production.
*Science,* v. 349, 730-734.

Choi JY, **Takahashi DY**[#], Ghazanfar AA[#] (2015)
Cooperative vocal control in marmoset monkeys via vocal feedback.
*Journal of Neurophysiology*, v. 114, 274-283.

Ghazanfar AA, **Takahashi DY** (2014)
The evolution of speech: vision, rhythm, cooperation.
*Trends in Cognitive Sciences*, v. 18, 543-553.

Ghazafar AA, **Takahashi DY** (2014)
Facial expressions and the evolution of the speech rhythm.
*Journal of Cognitive Neuroscience*, v. 26, 1196-1207

**Takahashi DY**[#], Narayanan DZ, Ghazanfar AA[#] (2013)
Coupled oscillator dynamics of vocal turn-taking in monkeys.
*Current Biology*, v. 23, 2162-2168.

Ghazanfar AA, **Takahashi DY**, Mathur NA, Fitch WT (2012)
Cineradiography of monkey lipsmacking reveals the putative origins of speech dynamics.
*Current Biology*, v. 22, p. 1176-1186.


*Stochastic processes*

Chazottes J-R, Gallo S, **Takahashi DY** (2022)
Gaussian concentration bounds for stochastic chains of unbounded memory.
*Annals of Applied Probability, in press*

Gallo S, Iacobelli G, Ost G, **Takahashi DY** (2021)
Self-Switching Markov Chains: Emerging dominance phenomena.
*Stochastic Processes and their Applications*, v. 143, 254-84.

Gallesco C, **Takahashi DY** (2021)
Mixing rates for potentials of non-summable variations.
*Ergodic Theory and Dynamical System*, doi: 10.1017/etds.2021.65

Gallesco C, Gallo S, **Takahashi DY** (2018)
Dynamic uniqueness for stochastic chains with unbounded memory.
*Stochastic Processes and their Applications*, doi: 10.1016/j.spa.2017.06.004

Gallo S, **Takahashi DY** (2014)
Attractive regular stochastic chains: perfect simulation and phase transition.
*Ergodic Theory and Dynamical System*, v. 34, 1567-1586

Gallesco C, Gallo S, **Takahashi DY** (2014)

Explicit estimates in the Bramson-Kalikow model.
*Nonlinearity*, v. 27, 2281-2296.

Gallo S, Lerasle M, **Takahashi DY** (2013)
Markov approximations of chains of infinite order in the $\bar{d}$-metric.
*Markov Processes and Related Fields*, v. 19, 51-82.


*Statistical methods for connectivity analysis - theory*

Ost G, **Takahashi DY** (2022)
Sparse Markov Models for High-dimensional Inference.
arXiv preprint arXiv:2202.08007

Baccalá LA, **Takahashi DY**, Sameshima, K (2016)
Directed Transfer function: Unified asymptotic theory and some of its implications.
*IEEE Transactions of Biomedical Engineering*, v. 63, 2450-2460.

**Takahashi DY** and Lerasle M (2016)
Sharp oracle inequalities and slope heuristic for specification probabilities estimation in discrete random fields.
*Bernoulli*, v. 22, 325-344.

Sameshima K, **Takahashi DY**, Baccalá LA (2015)
On statistical performance of Granger-causal connectivity estimators.
*Brain informatics*, doi: 10.1007/s40708-015-0015-1

**Takahashi DY**, Galves A, Orlandi E (2015)
Identifying interacting pairs of sites in Ising models on a countable set.
*Brazilian Journal of Probability and Statistics*, v. 29, 443-459.

**Takahashi DY**, Baccalá LA, Sameshima K (2014)
Canonical information flow decomposition among neural structure subsets.
*Frontiers in Neuroinformatics*, doi: 10.3389/fninf.2014.00049 c

Baccalá LA, de Brito CS, **Takahashi DY**, Sameshima K (2013)
Unified asymptotic theory for all partial directed coherence forms.
*Philosophical Transactions of the Royal Society A*, v. 371, 20120158

**Takahashi DY**, Lerasle M (2011)
An oracle approach for interaction neighborhood estimation in random fields.
*Electronic Journal of Statistics*, v. 5, p. 534-571.

**Takahashi DY**, Baccalá LA, Sameshima K (2010)
Information theoretic interpretation of frequency domain connectivity measures.
*Biological Cybernetics*, v.103, p. 463-469.

**Takahashi DY**, Baccalá L, Sameshima K (2008)

Partial directed coherence asymptotics for VAR processes of infinite order.
*International Journal of Bioelectromagnetism*, v. 10, p. 31-36.


**Takahashi DY**, Baccalá LA, Sameshima K (2007)
Connectivity Inference via Partial Directed Coherence.
*Journal of Applied Statistics*, v. 34, p. 1259-1273.



*Statistical methods for connectivity analysis – application*

Guzman GE, **Takahashi DY**, Fujita A (2022)
A fast parameter estimator for large complex networks.
*Journal of Complex Network,* v. 10, doi: 10.1093/comnet/cnac022

Raphaldini B, Teruya AS, Raupp CF, Silva-Dias PL, **Takahashi DY** (2021)
Inference of the topology of geomagnetic field multipole interactions.
*The European Physical Journal Special Topics*, doi: 10.1140/epjs/s11734-021-00201-1

Raphaldini B, Teruya AS, Raupp CF, Silva-Dias PL, **Takahashi DY** (2021)
Information flow between MJO-related waves: a network approach on the wave space.
*The European Physical Journal Special Topics*, doi: 10.1140/epjs/s11734-021-00170-5

Raphaldini B, Teruya AS, Dias PLS, Massaroppe L, **Takahashi DY** (2020)
Stratospheric ozone and QBO interaction with the tropical troposphere on intraseasonal and
interannual time-scales: a wave interaction perspective.
*Earth System Dynamics,* v.12, p.83-101.

Fujita A, Silva EL, Santos SDS, Bando SY, Soares GE, **Takahashi DY** (2019)
A semi-parametric statistical test to compare complex networks.
*Journal of Complex Networks*, cnz028, doi:10.1093/comnet/cnz028

Fujita A, **Takahashi DY**, Balardin JB, Vidal MC, Sato JR (2017)
Correlation between graphs with an application to brain network analysis.
*Computational Statistics & Data Analysis,* v. 109, 76-92

Fujita A, Vidal MC, **Takahashi DY** (2017)
A statistical method to distinguish functional brain networks.
*Frontiers in Neuroscience,* v. 11, doi:10.3389/fnins.2017.00066

Vidal MC, Sato JR, Balardin JB, **Takahashi DY**, Fujita A (2017)
ANOCVA in R: A Software to Compare Clusters between Groups and Its Application to the Study
of Autism Spectrum Disorder.
*Frontiers in Neuroscience,* v. 11, doi:10.3389/fnins.2017.00016

Fujita A, **Takahashi DY**, Patriota AG, Sato JR (2014)

A non-parametric statistical test to compare clusters with applications in functional magnetic resonance imaging data.
*Statistics in Medicine*, v. 33, 4949-4962.

Fujita A, **Takahashi DY**, Patriota A (2014)
A non-parametric method to estimate the number of clusters.
*Computational Statistics and Data Analysis*, v. 73, 27-39.

Santos SS, **Takahashi DY**, Nakata A, Fujita A (2013)
A comparative study of statistical methods used to identify dependencies between gene expression signals.
*Briefing in Bioinformatics*, v. 15, 906-918.

Sato JR., **Takahashi DY**, Hoexeter, MQ, Massirer KM, Fujita A (2013)
Measuring network's entropy in ADHD: A new approach to investigate neuropsychiatric disorders.
*Neuroimage*, v. 77, 44-51.

**Takahashi DY**, Sato JR, Ferreira CE, Fujita A (2012)
Discriminating different classes of biological networks by analyzing the graphs spectra distribution.
*PLoS ONE,* v. 7(12): e49949. doi:10.1371/journal.pone.0049949

Sato JR , **Takahashi DY**, Arcuri SM, Sameshima K, Morettin PA, Baccalá, LA (2009)
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*Human Brain Mapping*, v. 30, 452-461.

Dzirasa K., Ramsey AJ, **Takahashi DY**, Stapleton J, Potes JM, Williams JK, Gainetdinov RR, Sameshima K, Caron MG, Nicolelis MAL (2009)
Hyperdopaminergia and NMDA Receptor Hypofunction Disrupt Neural Phase Signaling.
*The Journal of Neuroscience*, v. 29, 8215-8224.

Sato JR, Felix MM, **Takahashi DY**, Amaro Jr E, Brammer MJ, Morettin PA (2006)
A method to produce evolving functional connectivity maps during the course of an fMRI experiment using wavelet based time-varying Granger causality.
*NeuroImage*, v. 31, 187-196.

Sato JR, **Takahashi DY**, Cardoso EF, Martin MGM, Amaro Jr E, Morettin PA (2006)
Intervention Models in Functional Connectivity Identification Applied to fMRI.
*International Journal of Biomedical Imaging*, doi: 10.1155/IJBI/2006/27483


*Alzheimer disease*

Raicher I, Shimizu M, **Takahashi DY**, Nitrini R, Caramelli P (2008)
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*International Psychogeriatrics*, v. 20, 471-481.

Shimizu M, Raicher I, **Takahashi DY**, Caramelli P, Nitrini R (2008)
Disclosure of the diagnosis of Alzheimer's disease: caregivers' opinions in a Brazilian sample.
*Arquivos de Neuro-Psiquiatria*, v. 66, 625-630.

Raicher I, **Takahashi DY**, Kanda PAM, Nitrini R, Anghinah R (2008)
qEEG spectral peak in Alzheimer's disease: a possible tool for treatment follow-up.
*Dementia & neuropsychologia*, v. 2, 9-12.

Vittielo AP, Ciriaco JG, **Takahashi DY**, Nitrini R, Caramelli P (2007)
Brief cognitive evaluation of patients attended in a general neurological outpatient clinic.
*Arquivos de Neuro-Psiquiatria*, v. 65, 299-303.

Nitrini R, Caramelli P, Herrera E, Castro I, Bahia VS, Anghinah R, Caixeta L, Radanovic M, Charchat-Fichman H, Porto CS, Carthery MT, Hartmann APBJ, Huang N, Smid J, Lima P, **Takahashi DY**, Takada LT (2005)
Mortality from dementia in a community-dwelling Brazilian population.
*International Journal of Geriatric Psychiatry*, v. 20, 247-253.

Nitrini R, Caramelli P, Herrera E, Bahia VS, Caixeta L, Radanovic M, Anghinah R, Charchat-Fichman H, Porto CS, Carthery MT, Hartmann APBJ, Huang N, Smid J, Lima P, Takada LT, **Takahashi DY** (2005)
Incidence of dementia in a community-dwelling Brazilian population.
*Alzheimer Disease and Associated Disorders*, v. 18, 241-246.

Anghinah R, Caramelli P, **Takahashi DY**, Nitrini R, Sameshima K (2005)
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*Arquivos de Neuro-Psiquiatria*, v. 63, 83-86.

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*Arquivos de Neuro-Psiquiatria*, v. 62, 751-755.

*Diagnosis in medicine*

Lopes RI, Nogueira L, Albertotti CJ, **Takahashi DY**, Lopes RN (2008)
Comparison of of virtual cystoscopy and transabdominal ultrasonography with conventional cystoscopy for bladder tumor detection.
*Journal of Endourology*, v. 22, 1725-1729.

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*Revista Brasileira de Hipertenção*, v. 12, 27-32.

Costa GGO, Ctenas BB, **Takahashi DY**, Mion O, Mello JJF, Butugan O (2005)
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*Arquivos de Otorrinolaringorologia*, v. 9, 203-211.

## Book Chapters

Sliwa J, **Takahashi DY**, Shepherd SV (2017)
Neural mechanisms of communication
*In: The Wiley Handbook of Evolutionary Neuroscience*, ed: Shepherd, Wiley-Blackwell, 444-477

Ghazanfar AA, **Takahashi DY** (2016)
The evo-devo of vocal communication: insights from marmoset monkeys
*In: Evolution of nervous systems*, ed: Kaas, Academic Press, 317-324

Santos SS, **Takahashi DY**, Sato JR, Ferreira CE, Fujita A (2016)
Statistical Methods in Graphs: Parameter Estimation, Model Selection, and Hypothesis Test
*Mathematical Foundations and Applications of Graph Entropy*, v. 98, 183-202

**Takahashi DY**, Baccalá LA, Sameshima K (2014)
Information partial directed coherence
*In: Methods in Brain Connectivity Inference through Multivariate Time Series Analysis*, ed: Baccalá, Sameshima. CRC Press, 75-86.

Baccalá LA, **Takahashi DY**, Sameshima K (2014)
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*In: Methods in Brain Connectivity Inference through Multivariate Time Series Analysis*, ed: Baccalá, Sameshima, CRC Press, 113-131.

Baccalá LA, **Takahashi DY**, Sameshima K (2006)
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*In: Handbook of Time Series Analysis* ed: Wilterhalter; Schelter; Timmer, Springer, 411-435.

Sameshima K, **Takahashi DY** (2004)
Métodos Quantitativos em Medicina
*In: Métodos Quantitativos em Medicina* ed: Massad, Ortega, Silveira. Manole, v.1, 493-526.

**Takahashi DY**, Charchat H, Nitrini R, Caramelli P, Sameshima K (2000)
Exploração de redes neurais artificiais no auxílio ao diagnóstico neuropsicológico da doença de Alzheimer.
In: Anais do I congresso de lógica aplicada à tecnologia – LAPTEC 1, Plêiade, v.1, 359-371.

## Articles Published in Peer-Reviewed Proceedings

Biazzi RB, Fujita A, **Takahashi DY** (2021)
Predicting soft robot's locomotion fitness.
Proceedings of the Genetic and Evolutionary Computation Conference Companion 2021, 81-82.

**Takahashi DY**, Narayanan DZ, Ghazanfar AA (2013)
Development of self-monitoring essential for vocal interaction in marmoset monkeys
*ICDL-EPIROB Conference,* doi: 10.1109/DevLrn.2013.6652553

**Takahashi DY**, Narayanan DZ, Ghazanfar AA (2013)
A computational model for vocal exchange dynamics and their development in marmoset monkeys
*ICDL-EPIROB Conference,* doi: 10.1109/DevLrn.2012.6400844

Brito SC, Baccalá LA, **Takahashi DY**, Sameshima K (2010)
Asymptotic behavior of generalized partial directed coherence
*IEEE Engineering in Medicine and Biology Society. Conf.* , v.1, p.1718 - 1721.

**Takahashi DY**, Baccalá LA, Sameshima K (2010)
Frequency domain connectivity: an information theoretic perspective
*IEEE Engineering in Medicine and Biology Society. Conf.* , v.1, p.1726 - 1729.

Baccalá LA, **Takahashi DY**, Sameshima K (2007)
Generalized Partial Directed Coherence
*InternationalConference on Digital Signal Processing*, v.1. p.162 - 166

**Takahashi DY**, Charchat H, Caramelli P, Nitrini R, Sameshima K (2000)
Análise da não-linearidade do modelo diagnóstico neuropsicológico da doença de Alzheimer por redes neurais artificiais
*Anais do VII congresso brasileiro de informática em saúde*

## Comments

**Takahashi DY** (2019)
Vocal learning: shaping by social reinforcement
*Current Biology*, v.29, R125-R127

**Takahashi DY** (2018)
Animal communication: chit-chat in meerkats
*Current Biology*, v.28, R1298-R1300

**Takahashi DY**, Ghazanfar AA (2014)
Vocal communication is multi-sensorimotor coordination within and between individuals
*Behavioral and Brain Sciences*, v.37, 572-573.

# Research Supports

*Current supports*

2022-2025 – CNPq DAAD (co-PI)
Complex random networks

2013-2023 –FAPESP 2013/ 07699-0 (collaborator)
Center for Neuromathematics.


*Completed supports*
2016-2018 - FAPESP 2016/13422-9 (collaborator)
Statistical methods on graphs applied in life science.

2014-2016 – CNPq 462064/2014-0 (collaborator)
Finitary coding and chains of long memory

2012-2014 – USP project (collaborator)
Mathematics, computation, language, and the brain

2012-2014 – CNPq 480108/2012-9 (collaborator)
Stochastic modeling of the brain activity

2008-2009 – FAPESP 2008/08171-0 (PI)
Modeling neuronal population by interactive particle system of variable length interaction

## BIOGRAPHICAL SKETCH

NAME: Bizinelli, Daniela

POSITION TITLE: PhD student

ORCID: https://orcid.org/0000-0001-5815-8423

### A. Personal Statement

I graduated with a degree in Pharmacy at Herminio Ometto University Center (2019), where I was recognized as the best student of the undergraduate course and received the Paulo Minami award granted by the Regional Pharmacy Council (CRF-SP). I recently completed a Master's Degree in Oncology, investigating oncogenic signaling pathways modulators in colon cancer liver metastasis using computational strategies. With my Master's project and other research collaborations, I have developed skills in data integration, manipulation, analysis, and visualization, not limited to, but focused on transcriptomics, proteomics, and DNA methylation. Also, my recent experience at Vejle Hospital (University of Southern Denmark) as a guest student taught me even more about how to apply my knowledge to different projects and collaborate with translational research, keeping up with wet lab activities and linking it with in silico analysis. Currently, I am a PhD student in the Interunit Bioinformatics Graduate Program at the University of São Paulo (USP).

### B. Education/Training

| Institution and Location | Degree | Completion Date MM/YYYY | Field of Study |
|---|---|---|---|
| Herminio Ometto University Center, Araras, São Paulo, Brazil | Graduate | 12/2019 | Pharmacy |
| A.C.Camargo Cancer Center, São Paulo, Brazil | M.Sc. | 08/2022 | Oncology |
| University of Southern Denmark, Vejle, Denmark | Intership | 10/2022 | Bioinformatics |
| University of São Paulo, São Paulo, Brazil | Ph.D. | Expected 01/2027 | Bioinformatics |

### C. Additional Training

| | Year | Title | Event/Local |
|---|---|---|---|
| **Mini-course (online)** | 2021 | Understanding the Most Out of Differential Gene Expression from Scratch. | 16th international conference of the AB3C – X-Meeting XPerience 2021. |
| **Extension course (online)** | 2021 | Mass Spectrometry Applied to Metabolomic, Proteomic and Lipidomic Analysis. | Federal University of São Paulo – UNIFESP, São Paulo, Brazil. |
| **International course (online)** | 2020 | Computational Systems Biology of Cancer 3$^{rd}$ Edition. | Institut Curie, Paris. |
| **Mini-course** | 2019 | R software. | Herminio Ometto University Center, São Paulo, Brazil. |

**D. Poster Presentation and Invited Talks**

**Bizinelli, D.**, Klug, K.K., Macedo, K.T., Varella, N., dos Santos,G.O., Labate, M.T.V., Labate, C.A., Camillo, C.M.C., Marchi, F.A. (2023, June). An integrative approach to explore promises targets identifies potential signaling modulators in drug-resistant colon cancer liver metastasis [Poster presentation]. X-Meeting / BSB 2023.
**Bizinelli, D.**, Marchi, F.A., Fujita A. (2023, June). Deciphering oncogenic signaling networks and cellular co-localization profiles by spatial transcriptomics data [Poster presentation]. X-Meeting / BSB 2023.

**Bizinelli, D.**, Oyama, K.T., Silva, V.S., Mello, C.A.L., Olivieri, E.H.R., Mota, L.D.C, Andrade, M.B., Martins Jr., D.C., Barbosa, P.N.V.P., Rogatto, S.R., Marchi, F.A. (2021, October). A multi-omic integrative approach to explore vulnerabilities in drug-resistant colon tumors and hit oncogenic signaling modulators [Online poster presentation]. 16th international conference of the AB3C – X-Meeting XPerience 2021.

**Bizinelli, D.**, Oyama, K.T., Silva, V.S., Mello, C.A.L., Olivieri, E.H.R., Mota, L.D.C, Andrade, M.B., Barbosa, P.N.V.P., Marchi, F.A. (2021, September). A machine learning-based strategy exploring multiomic data identifies oncogenic signaling modulators in drug-resistant colon cancer [Online project presentation]. GENETICS 2021 - Brazilian Congress of Genetics.

**Bizinelli, D.**, Oyama, K.T., Marchi, F.A. (2021, June). Identification of Oncogenic Signaling Modulators in Metastatic Colon Tumors [Online poster presentation]. Next Frontiers to Cure Cancer 2021.

**Bizinelli, D.**, Marchi, F.A. (2021, January). Protegenomic investigation of oncogenic signaling modulators associated with mutational status in patients with metastatic colon cancer [Online poster presentation]. Scientific Meeting of A.C.Camargo Cancer Center, São Paulo, Brazil.

**Bizinelli, D.** (2020, October). Oncogenetics [Invited talk]. Herminio Ometto University Center, Araras, São Paulo, Brazil.

**Bizinelli, D.**, Santos, N.T.H., Faldoni, F.L.C., Navarro, F.F. (2019, October). In vitro functional assays of Cacti-Nea effect on human breast adenocarcinoma [Poster presentation]. Herminio Ometto University Center, Araras, São Paulo, Brazil.

**Bizinelli, D.**, Santos, N.T.H., Faldoni, F.L.C., Navarro, F.F. (2019, September). In vitro evaluation of cell viability and betalains quantification of nutraceutical Cacti-Nea [Poster presentation]. FeSBE Annual Meeting, Campos do Jordão Convention Center, São Paulo, Brazil.

**E. Academic Awards**

| Year | Honors | Event/Local |
|---|---|---|
| 2021 | Honorable Mention Award for poster presentation in the "omics" category (online). Project: "*A multi-omic integrative approach to explore vulnerabilities in drug-resistant colon tumors and hit oncogenic signaling modulators*". | 16th international conference of the AB3C – X-Meeting XPerience 2021. |
| 2021 | Darcy Fontoura de Almeida Award for best project presented in the "genomics and bioinformatics" category (online). Project: "*A machine learning-based strategy exploring multiomic data identifies oncogenic signaling modulators in drug-resistant colon cancer*". | GENETICS 2021 - 66th Brazilian Congress of Genetics. |
| 2021 | Finalist in the poster presentation section (online). Project: "*Proteogenomic investigation of oncogenic signaling* | Scientific Meeting of A.C.Camargo Cancer Center, São Paulo, Brazil. |

| | | |
|---|---|---|
| | *modulators associated with mutational status in patients with metastatic colon cancer*". | |
| 2020 | Finalist (co-author) in the poster presentation section. Project: "*Oncogenic signaling modulation by the activity of enhancers and promoters in colon cancer microenvironment with immune-responsive and non-responsive genomic profile*". | Scientific Meeting of A.C.Camargo Cancer Center, São Paulo, Brazil. |
| 2020 | Paulo Minami Award for best student in Pharmacy degree, from January 2015 to December 2019, granted by the Regional Pharmacy Council of São Paulo (CRF-SP). | Herminio Ometto University Center, Araras, São Paulo, Brazil. |
| 2019 | Award for poster presentation. Project: "*In vitro functional assays of Cacti-Nea effect on human breast adenocarcinoma*". | 13th Scientific Initiation Congress PIBIC-CNPq at Herminio Ometto University Center, Araras, São Paulo, Brazil. |

## F. Peer-reviewed Publications

[Under review – #BIOPHA-D-23-03921] Calanca N, Noronha Francisco AL, **Bizinelli D**, Kuasne H, Camargo Barros Filho M, Campos Troncarelli Flores B, Antonio Lopes Pinto C, Aparecida Rainho C, Botelho Pereira Soares M, Albuquerque Marchi F, Kowalski LP, Regina Rogatto S. DNA methylation-based depiction of the immune microenvironment and immune-associated long non-coding RNAs in oral cavity squamous cell carcinomas. *Biomed. Pharmacother.*

**Bizinelli D**, Flores Navarro F, Lima Costa Faldoni F. Maca Root (*Lepidium meyenii*) Extract Increases the Expression of MMP-1 and Stimulates Migration of Triple-Negative Breast Cancer Cells. *Nutr Cancer*. 2022;74(1):346-356. doi:10.1080/01635581.2021.1882511

## G. Other Contributions to Science

**Collaborator student** in the project "*Heterogeneity of oncogenic signaling associated with colon cancer metastases resistant to systemic therapy: Investigation by proteogenomics and modeling of complex networks*" (FAPESP Regular Grant #2019/20414-0), with Dr. Fabio Albuquerque Marchi as principal researcher.
I was part of the project during my Master's degree and was responsible for patient screening and collection of their biological samples. One of the hypotheses of my master's project was associated with this grant, where I was responsible for bioinformatic analysis trying to identify modulators in several oncogenic signaling pathway. We hope that our findings can impact the personalization of treatment for patients with colon cancer liver metastasis allowing new therapy modalities that can improve survival.

**Collaboration** in the project "*Diagnostic strategies for tuberculosis and identification of the complex microbiome associated with disease development and progression*", with Dr. Patricia Pintor dos Reis as principal researcher (São Paulo State University - UNESP, Botucatu, São Paulo, Brazil).
In this project, our aim was to identify potential molecular signatures that could characterize patients with latent and active disease, which would have a great impact on the care of patients with tuberculosis and would allow the development of efficient and lower cost prognostic strategies. For this, I participated in data integration analysis to apply the results in a machine learning algorithm.

**Collaboration** in the project "*Identification of miRNAs profile in mucoepidermoid carcinoma cells*", with Dr. Cláudia Malheiros Coutinho Camillo as principal researcher (A.C.Camargo Cancer Center, São Paulo, Brazil).
I was responsible for data manipulation, analysis, and visualization, conducting statistical tests to verify differences in miRNAs profiles between groups of salivary tumor samples with different clinical characteristics and treatments.

# Jaqueline Yu Ting Wang

Sao Paulo SP, Brazil
jaqueytw@gmail.com
+55 11 97648 8734
linkedin.com/in/jaqueline-wang

## PROFESSIONAL SUMMARY

Versatile and creative professional positioned to excel within a role requiring organization, attention to details and multidisciplinary knowledge. Well-versed in Perl programming language, shell scripting and R.

## PROFESSIONAL EXPERIENCE

The Human Genome and Stem Cell Research Center (HUG-CELL), Sao Paulo, BR
***Bioinformatics specialist***, Dec 2017 - present
Create pipelines to process and analyze NGS data, support the research in completing assigned experiments and team leader of bioinformatics group.

- Highly skilled in the use of technology for research purposes. Become competent in Bash, SQL, R and Perl programming languages.
- Very experienced in the processing of human sequencing data, including whole genome sequencing (WGS).

## PUBLICATIONS

- Wang, J.Y.T., Whittle, M.R., Puga, R.D. et al. Noninvasive prenatal paternity determination using microhaplotypes: a pilot study. BMC Med Genomics 13, 157 (2020). https://doi.org/10.1186/s12920-020-00806-w
- Naslavsky, M.S., Scliar, M.O., Yamamoto, G.L., Wang, J.Y.T. et al. Whole-genome sequencing of 1,171 elderly admixed individuals from Brazil. Nat Commun 13, 1004 (2022). https://doi.org/10.1038/s41467-022-28648-3
- Fu, J.M., Satterstrom, F.K., Peng, M. et al. Rare coding variation provides insight into the genetic architecture and phenotypic context of autism. Nat Genet 54, 1320–1331 (2022). https://doi.org/10.1038/s41588-022-01104-0
- Castelli, E.C., De Castro, M.V., Naslavsky, M.S. et al. MUC22, HLA-A, and HLA-DOB variants and COVID-19 in resilient super-agers from Brazil. Frontiers in Immunology 13, 1 (2022). https://doi.org/10.3389/fimmu.2022.975918
- Teles e Silva, A.L., Glaser, T., Griesi-Oliveira, K. et al. Rare CACNA1H and RELN variants interact through mTORC1 pathway in oligogenic autism spectrum disorder. Transl Psychiatry 12, 234 (2022). https://doi.org/10.1038/s41398-022-01997-9
- De Castro, M.V., Santos, K.S., Apostolico J.S. et al. Recurrence of COVID-19 associated with reduced T-cell responses in a monozygotic twin pair. Open Biology 12, 210240 (2022). https://doi.org/10.1098/rsob.210240

- Castelli, E.C., de Almeida, B.S., Muniz, Y.C.N. et al. HLA-G genetic diversity and evolutive aspects in worldwide populations. Sci Rep 11, 23070 (2021). https://doi.org/10.1038/s41598-021-02106-4
- Costa, C.I.S., Silva Montenegro, E.M., Sarrei, M. et al. Copy number variations in a Brazilian cohort with autism spectrum disorders highlight the contribution of cell adhesion genes. Clin Genet 101(1), 134-141 (2021). https://doi.org/10.1111/cge.14072
- Alvizi, L., Brito, L.A., Kobayashi, G.S. et al. m ir152 hypomethylation as a mechanism for non-syndromic cleft lip and palate. Epigenetics 17(13), 2278-2295 (2022). https://doi.org/10.1080/15592294.2022.2115606
- Souza, L., Gurgel-Giannetti, J., Sampaio, G. et al. Limb girdle muscular dystrophies. Neuromuscular disorders 30, S91-S92 (2020). https://doi.org/10.1016/j.nmd.2020.08.157
- Borges, J.B., Oliveira, V.F., Ferreira, G.M. et al. Genomics, epigenomics and pharmacogenomics of familial hypercholesterolemia (FHBGEP): A study protocol. Res Social Adm Pharm 17(7), 1347-1355 (2021). https://doi.org/10.1016/j.sapharm.2020.10.007
- Souza, L.S., Almeida, C.F., Yamamoto, G.L. el al. Manifesting carriers of X-linked myotubular myopathy: Genetic modifiers modulating the phenotype. Neurology Genetics 6(5), e513 (2020). https://doi.org/10.1212/NXG.0000000000000513
- Martins Trevisan, C., Naslavsky, M.S., Monfardini, F. el al. Variants in the Kisspeptin-GnRH Pathway Modulate the Hormonal Profile and Reproductive Outcomes. DNA and cell biology 39(6), 1012–1022 (2020). https://doi.org/10.1089/dna.2019.5165
- Naslavsky, M.S., Scliar, M.O., Nunes, K. et al. Biased pathogenic assertions of loss of function variants challenge molecular diagnosis of admixed individuals. American journal of medical genetics. Part C, Seminars in medical genetics 187(3), 357-363 (2021). https://doi.org/10.1002/ajmg.c.31931
- Bride, L., Naslavsky, M., Yamamoto, G.L. el al. TCF7L2 rs7903146 polymorphism association with diabetes and obesity in an elderly cohort from Brazil. PeerJ 9, e11349 (2021). https://doi.org/10.7717/peerj.11349
- Castelli, E.C., de Castro, M.V., Naslavsky, M.S. el al. MHC Variants Associated With Symptomatic Versus Asymptomatic SARS-CoV-2 Infection in Highly Exposed Individuals. Frontiers in immunology 12, 742881 (2021). https://doi.org/10.3389/fimmu.2021.742881

**EDUCATION**

**PhD. in Bioinformatics**, January 2023 - Present
UNIVERSITY OF SAO PAULO, Sao Paulo, BR
Modules included: "The post genomics era, tools and approaches in bioinformatics" and Human Molecular Genetics and Genomics.

**MSc. in Bioinformatics**, 2015 - 2017
UNIVERSITY OF SAO PAULO, Sao Paulo, BR
Modules included: Introduction to Systems Biology, Algorithms in Bioinformatics, Introduction to Computing for Bioinformatics and Database for Bioinformatics.
Dissertation title: Noninvasive prenatal paternity determination by microhaplotypes.

**Multi Professional Expertise in Oncology**, 2015
INSTITUTO ISRAELITA DE ENSINO E PESQUISA ALBERT EINSTEIN, Sao Paulo, BR
Modules included: Conceptual Bases and Diagnostic Tools Applied to Oncology, Cancer Treatment Modalities and Management in Oncology, Oncological Diseases: Solid Tumors and Haematological, Palliative Care and Symptom Control.

**BSc. in Physics and Biomolecular Sciences**, 2007 - 2011
UNIVERSITY OF SAO PAULO, Sao Paulo, BR
The BSc. in Physical and Biomolecular Sciences is based on a molecular approach to biological phenomena, through which knowledge and methods are used from physics, molecular biology and biochemistry. The students also learn about problem diagnosis, molecular modeling, in addition to computational simulations of various types of systems. Such acquired knowledge is integrated with specific biotech applications, such as design and modeling of pharmaceutical drugs, genetic engineering and protein engineering, biomaterials, nanobiotechnology and bioinformatics.

**Scientific initiation in a Laboratory**, 2011
UNIVERSITY OF SAO PAULO, Sao Paulo, BR
The objective of the study was to learn more about Multilocus Sequencing Type (MLST), a technique for epidemiological analysis of Vancomycin-Resistant Enterococci. In order to type *Enterococcus faecalis*, PCR, and its purification products were used along with analysis of sequencing through software Vector NTi (Invitrogen) and the exploration of MLST website to look for alleles and STs numbers for the isolates.

**Teacher assistant of Physic-Chemistry**, 2011
UNIVERSITY OF SAO PAULO, Sao Paulo, BR
Assisted teachers by helping students with general questions, classroom assignments, laboratory activities, and lab reports.


## LANGUAGES

Portuguese (native)
English (bilingual oral and written fluency)
French (proficient)
Chinese - Mandarin (oral)

# Curriculum Vitae

## Identification:

Name: Leonardo Sanches
Address: Av. Prof. Lineu Prestes, 748, Laboratory 1812 - Butantã, São Paulo - SP, 05508-900
Email: leonardo2.sanches@usp.br
Lattes iD: http://lattes.cnpq.br/1796879990589201

## Summary:

Biologist with a degree from the University of São Paulo (USP) and a background in scientific research. Completed undergraduate research and a master's degree at the Ecology and Evolution Laboratory of the Butantan Institute, focusing on antimicrobial peptides from snakes. Driven by a strong interest in bioinformatics, I shifted my focus to cancer genomics. Currently pursuing a Ph.D. in Biochemistry at the Genomics and Gene Expression in Cancer Laboratory of the Institute of Chemistry at USP, with a research project exploring the functionality of cancer-associated long non-coding RNAs (lncRNAs) through co-expression network analysis. I am highly motivated, eager to learn and study new techniques, and committed to contributing to the advancement of knowledge in the field.

## Areas of Expertise:

- Bioinformatics
- Biochemistry / Molecular Biology

## Skills:

- Co-expression network analysis
- Transcriptomics analysis using RNA-seq data
- Bioinformatics tools and pipelines
- Python programming
- R programming
- Linux and Bash scripting
- Genomic data visualization
- Genetics
- Philogeny Analysis
- Molecular biology techniques

## Languages:

- English: Proficient in comprehension, reasonable speaking and writing skills.
- Portuguese: Proficient in comprehension, speaking, reading, and writing.
- Spanish: Proficient in comprehension, reasonable speaking, reading, and basic writing skills.

## Education:

**2021 - Present**

Ph.D. in Biochemistry (CAPES Grade 6) University of São Paulo (USP), Brazil Title: Exploring Cancer-Associated lncRNAs Functionality through Co-expression Networks Analysis Advisor: Eduardo Moraes do

Rego Reis Scholarship: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Brazil

**2020 (Interrupted)**

Ph.D. interrupted in 2021 in Bioinformatics (CAPES Grade 4) University of São Paulo (USP), Brazil Advisor: Eduardo Moraes Rego Reis Interruption year: 2021

**2015 - 2017**

Master's Degree in Toxinology (CAPES Grade 5) Instituto Butantan (IBU), Brazil Title: Expression of B-defensins in the snake Bothrops jararaca Year of Completion: 2017 Advisor: Nancy Oguiura Scholarship: Coordenação de Aperfeiçoamento de Pessoal de Nível Superior (CAPES), Brazil

**2009 - 2014**

Bachelor's Degree in Biological Sciences University of São Paulo (USP), Brazil Title: Interaction of crotamine, a myotoxin from rattlesnake venom, with artificial membranes Advisor: Nancy Oguiura

## Scientific Production:

1. OGUIURA, NANCY ; SANCHES, LEONARDO ; DUARTE, PRISCILA V. ; SULCA-LÓPEZ, MARCOS A. ; MACHINI, MARIA TERÊSA . Past, Present, and Future of Naturally Occurring Antimicrobials Related to Snake Venoms. ANIMALS, v. 13, p. 744, 2023.

2. VALENTE, RICHARD HEMMI ; LUNA, MILENE SCHMIDT ; DE OLIVEIRA, URSULA CASTRO ; NISHIYAMA-JUNIOR, MILTON YUTAKA ; JUNQUEIRA-DE-AZEVEDO, INÁCIO DE LOIOLA ; PORTES-JUNIOR, JOSÉ ANTONIO ; CLISSA, PATRICIA BIANCA ; VIANA, LUCIANA GODOY ; SANCHES, LEONARDO ; MOURA-DA-SILVA, ANA MARIA ; PERALES, JONAS ; YAMANOUYE, NORMA . Bothrops jararaca accessory venom gland is an ancillary source of toxins to the snake. Journal of Proteomics, v. 177, p. 137-147, 2018.

3. VIALA, VINCENT LOUIS ; HILDEBRAND, DIANA ; FUCASE, TAMARA MIECO ; SCIANI, JULIANA MOZER ; PREZOTTO-NETO, JOSÉ PEDRO ; RIEDNER, MARIA ; SANCHES, LEONARDO ; NISHIMURA, PAULA JULIANA ; OGUIURA, NANCY ; PIMENTA, DANIEL CARVALHO ; SCHLÜTER, HARTMUT ; BETZEL, CHRISTIAN ; ARNI, RAGHUVIR KRISHNASWAMI ; SPENCER, PATRICK JACK . Proteomic analysis of the rare Uracoan rattlesnake Crotalus vegrandis venom: Evidence of a broad arsenal of toxins. TOXICON, v. 107, p. 234-251, 2015.

4. COSTA, BRUNO A. ; SANCHES, LEONARDO ; GOMIDE, ANDREZA BARBOSA ; BIZERRA, FERNANDO ; DAL MAS, CAROLINE ; OLIVEIRA, EDUARDO B. ; PEREZ, KATIA REGINA ; ITRI, ROSANGELA ; OGUIURA, NANCY ; HAYASHI, MIRIAN A. F. . Interaction of the Rattlesnake Toxin Crotamine with Model Membranes. JOURNAL OF PHYSICAL CHEMISTRY B, v. 118, p. 5471-5479, 2014.

## Additional Education:

**2023**

6th Researchers School at Campus USP São Carlos (14 hours), University of São Paulo (USP) (online course)

**2021**

Bioinformatics for Biologists: An Introduction to Linux, Bash Scripting (15 hours), Wellcome Genome Campus (online course)

**2020**

Introduction to Genomic Technologies (6 hours), Johns Hopkins University (online course)
Python for Genomic Data Science (8 hours), Johns Hopkins University (online course)
Genomic Data Science with Galaxy (8 hours), Johns Hopkins University (online course)
R Programming (57 hours), Johns Hopkins University (online course)

**2018**

Summer Course Workshop in Bioinformatics (8 hours), University of São Paulo
Summer Course in Bioinformatics (40 hours), University of São Paulo

2017 Annual Biosafety Course (8 hours), Instituto Butantan
Introduction to the R Language - hands-on (32 hours), Instituto Butantan

**2016**

Theoretical and Practical Fundamentals of Phylogenetic Systematics (40 hours), Instituto Butantan
Endnote Workshop - reference management tool (7 hours), Instituto Butantan

**2015**

Basic Concepts for the Study of Toxinology (30 hours), Instituto Butantan

**2012**

Biochemistry of Venoms (4 hours), University of São Paulo

**2011**

Apoptosis, Checkpoints, and Cancer (12 hours), University of São Paulo
Reptile Terrarium (4 hours), University of São Paulo

**2010**

Human Evolution: Molecular vs. Paleontological (12 hours), University of São Paulo
Forensic Entomology (12 hours), University of São Paulo

## Presentations:

LACEN: An R Package for lncRNAs Functional Annotation Using Co-Expression Networks. SBBq. 2022.(Conference Presentation).

LACEN: An R Package for lncRNAs Functional Annotation Using Co-Expression Networks. I Simpósio dos Pós-Graduandos da Bioquímica. 2022. (Symposium Presentation).

Expression of B-defensins in Bothrops jararaca snake. 2017. (Conference Presentation).

Expressão de beta-defensinas na serpente Bothrops jararaca. 2016. (Symposium Presentation).

Expressão de B-defensinas na serpente Bothrops jararaca. 2016. (Seminar Presentation).

Interaction of the Rattlesnake Toxin Crotamine with Model Membranes. 2014. (Other Presentation).

Interação da crotamina com vesículas unilamelares gigantes. 2014. (Seminar Presentation).

Interaction of crotamine with giant unilamellar vesicles. 2013. (Conference Presentation).

Interação de crotamina com vesículas unilamelares gigantes. 2012. (Conference Presentation).

## Participation in Events, Congresses, Exhibitions, and Fairs:

FEBRACE. Evaluator at FEBRACE. 2023. (Fair).

FEBRACE. Evaluator at FEBRACE. 2022. (Fair).

I Simpósio dos Pós-Graduandos da Bioquímica. 2022. (Symposium).

SBBq. 2022. (Congress).

FEBRACE. Evaluator at FEBRACE. 2020. (Fair).

FEBRACE. Evaluator at FEBRACE. 2019. (Fair).

XIV Congresso Brasileiro de Toxinologia. Expression of B-defensins in Bothrops jararaca snake. 2017. (Congress).

Simpósio da Pós-Graduação em Toxinologia do Instituto Butantan. Expressão de beta-defensinas na serpente Bothrops jararaca. 2016. (Symposium).

Reunião Científica Anual do Instituto Butantan. Interaction of Crotamine with giant unilamellar vesicles. 2014. (Other).

Seminários do Laboratório de Ecologia e Evolução do Instituto Butantan. Interação da crotamina com vesículas unilamelares gigantes. 2014. (Seminar).

Reunião Científica Anual do Instituto Butantan. Interaction of Crotamine with giant unilamellar vesicles. 2013. (Meeting).

XI Congress of the Pan American Section of the International Society on Toxinology. Interaction of Crotamine with giant unilamellar vesicles. 2013. (Congress).

Reunião Científica Anual do Instituto Butantã. Interaction of Crotamine with giant unilamellar vesicles. 2012. (Meeting).

Reunión y Taller Científico Técnico de la Red Iberoamericana CYTED. Interação de crotamina com vesículas unilamelares gigantes. 2012. (Other).

Seminários do Laboratório de Ecologia e Evolução do Instituto Butantan. Interaction of Crotamine with giant unilamellar vesicles. 2012. (Seminar).

Workshop on Synthetic Biology and Robotics. 2011. (Other).

# Caio Matheus Prates Batalha Faria

## Rua Valson Lopes, 70, apartment 56B, São Paulo, São Paulo, Brazil
## caio.batalha@yahoo.com.br
## +55 13 9-9756-9757

A final year PhD candidate with a research background in molecular biology and systems biology. My main research interests are in the biology of aging and systems biology fields.

## Education

### University of São Paulo (ongoing)

PhD

Used a systems biology approach, particularly network science and causal discovery, to analyze age-related patterns in gene expression data of humans during aging, and find potential candidate genes for interventions aimed at modulating age related alterations. Currently writing thesis. Joint supervisors: Professor Nadja Cristhina de Souza Pinto, Department of Biochemistry, Chemistry Institute (University of São Paulo), and Professor André Fujita, Institute of Mathematics and Statistics (University of São Paulo).

### University of São Paulo (2018)

MsC

Explored the relationship between the mTOR protein, a known modulator of longevity in model organisms, and DNA repair, using molecular biology techniques. Supervisor: Professor Nadja Cristhina de Souza Pinto, Department of Biochemistry, Chemistry Institute (University of São Paulo).

### Federal University of the ABC (2013)

BSc Industrial Engineering

BSc Science and Technology

Joint BSc, with high interdisciplinary content, focusing on STEM, with a few credits in humanities.

### Federal Institute of Cubatão (2008)

High school.

## Teaching/supervising experience

### Teaching assistant, University of São Paulo

- Teching assistant 3 times for the Experimental Biochemistry course and 2 times for the Molecular Biology course
- Assisting with programme development and student assessment
- Assisting in wet lab experiments and bioinformatics assignments
- Delivering teaching sessions

## Guest lecturer, MSc Health Sciences, Albert Einstein Hospital - São Paulo

- Delivered lectures on the "Aspects of the Research on Aging" course by invitation for 3 years
- Student assessment

## Molecular biology summer school lecturer, University of São Paulo (2017)

- Coordinating summer school programme
- Devising and delivering interactive wet lab experiments

## Publications

- Alencar RR, Batalha CMPF, Freire TS, de Souza-Pinto NC. Enzymology of mitochondrial DNA repair. Enzymes. 2019;45:257-287. doi: 10.1016/bs.enz.2019.06.002.
- Batalha CMPF, Vercesi AE, Souza-Pinto NC. The Many Roles Mitochondria Play in Mammalian Aging. Antioxid Redox Signal. 2022 May;36(13-15):824-843. doi: 10.1089/ars.2021.0074.
- Welsh H, Batalha CMPF, Li W, Mpye KL, Souza-Pinto NC, Naslavsky MS, Parra EJ. A systematic evaluation of normalization methods and probe replicability using infinium EPIC methylation data. Clin Epigenetics. 2023 Mar 11;15(1):41. doi: 10.1186/s13148-023-01459-z.
- Batalha CMPF, Fujita A, de Souza-Pinto NC. Combination of differential expression and co-expression network analyses identify novel conserved age-associated changes among different tissues. bioRxiv 2023.05.26.542445; doi: https://doi.org/10.1101/2023.05.26.542445.
- Rowies FT, Batalha CMPF, Nakahara TS, Malnic B, de Souza-Pinto NC. Expression of DNA repair genes is modulated during differentiation of olfactory sensory neurons. bioRxiv 2023.04.06.535865; doi: https://doi.org/10.1101/2023.04.06.535865.

## Research skills

- Application of systems biology and bioinformatics techniques: differential expression analysis, network science, causal discovery, mendelian randomization, enrichment analysis, differential methylation analysis, linear models (simple and mixed), genome alignment, among others.

- Application of wet lab molecular biology and biochemistry techniques: western blot, RT-PCR, enzyme assays, Searhorse analyzer, flow cytometry, cell culture, mitochondria isolation, agarose DNA electrophoresis, among others.
- Programing languages: R and Python.

**Other qualifications**

- English (fluent)
- Spanish (intermediate)

**Employment**

**Consultant, KPMG Structured Finance, São Paulo (2012-2014)**

- Structuring projected finances of infrastructure projects
- Market research for infrastructure projects
- Business valuation
- Other types of financial modeling

**Intern, Novelis/Aditya Birla, São Paulo (2011-2012)**

- Market research
- Writing a monthly newsletter about the Brazilian market in some specific sectors of interest of the company
- Prospecting engineering companies

**Name:** Diego Trindade de Souza

Institute for Technological Research
Av. Prof. Almeida Prado, 532
Cidade  Universitária
05508-901 - São Paulo, SP - Brasil
Email: diegotsouza@ipt.br

## 1.- Training

| Year | Title or activity | Institution |
|------|-------------------|-------------|
| 2008 | Undergraduate<br><br>**Biological Sciences** | Instituto Superior de Educação Anísio Teixeira, Universidade Estadual de Minas Gerais. |
| 2012 | Master's Degree<br><br>**Biotechnology** | Centro de Ciências da Saúde, Universidade Federal do Espírito Santo. |
| 2016 | PhD<br><br>**Bioinformatics** | Instituto de Biociências, Universidade de São Paulo. |

## 2.- Professional history

2022 to present - Full Researcher - Institute for Technological Research - Artificial Intelligence and Analytics Section

> The focus of this work is on developing a solution for a sustainable way to store enterprise data by storing data on DNA. Collaborating to develop, build, and validate bioinformatics tools.

2021 to present - Post-doctorate - Dept. of Computer Science - IME USP

> I am developing a post-doctoral internship at the Institute of Mathematics and Statistics at USP. In it I will focus on the implementation of machine learning techniques that will allow us to identify, from the heart rate variability signal, if or how individuals can distinctly affect each other's physiological states and emotional experiences in the absence of direct communication while playing a game.

2016 to 2020 - Post-doctorate - Dept. Botany - IB USP; Fellow CAPES and FAPESP

> Between the years 2016 and 2018, I was responsible for developing a web query application for RNAseq and MS/MS data of *Araucaria angustifolia* embryogenesis produced by the lab. This application allows the laboratory users a simplified way to search the information available in the database, besides allowing some analysis (for example, sequence alignment

and differential expression analysis).    This study has generated one paper (in submission) and 4 abstracts published in international conferences (that can be seen in the Lattes Curriculum).

Between the years 2018 and 2020, I was responsible for developing and integrating computational tools for transcriptome analysis of *Piper* species.    Using Python and integration with the [Arabidopsis Information Resource](#) and [Kyoto Encyclopedia of Genes and Genomes](#) databases, it was possible to identify which genes and their molecular functions were being regulated during chemically mediated multitrophic (plant-insect-parasite) interactions.    This study generated an abstract published in international conferences (that can be seen in the Lattes Curriculum).

2013 to 2016- Post-graduation (PhD) - Dept. of Genetics and Evolutionary Biology - IB USP, FAPESP Fellow

This study consisted in the implementation of methodologies and computational resources that allowed us to model the origin of more recent proteins, based on two aspects: (i) detecting their origin from exon shuffling (as a molecular mechanism, manifested by the formation of new architectures from pre-existing domains) and (ii) detecting their origin from ancestral genes, evidenced by Position-Specific Scoring Matrix created by PSI-BLAST software, and corroborated by structural overlap analysis with common topologies. The programming languages Perl, Python and R, and the database management platform MySQL were used for this.    In addition to integration with several biological databases, including: [Uniprot](#), [Pfam](#), [Gene Ontology](#).    This study generated 4 abstracts published in international congresses (that can be seen in the Lattes Curriculum).

2010 to 2012- Post-graduation (MSc) - CCS - UFES - FAPES; CAPES Scholarship

Study that evaluated the changes in gene expression of yeast subjected to high hydrostatic pressure in order to identify the molecular targets responsible for this adaptation. Using R and the integration with the [Saccharomyces Genome Database](#), it was possible to identify which genes and their molecular functions were being regulated during the high hydrostatic pressure stress suffered by yeast in fermentation vats.    This study generated two papers, listed below, and 3 abstracts published in international conferences (that can be seen in the Lattes Curriculum).

2009 to 2010 - Basic Education Teacher - Elementary School II - Discipline: Sciences. City Hall of Contagem, PMC, Brazil

2007 to 2008 - Trainee and Scientific Initiation scholarship holder -Department of Biochemistry and Immunology -UFMG

## 3.- List of most relevant research results

3.1. **Souza, Diego T**.; Elbl, Paula M. ; Rosado, Daniele ; De Oliveira, Leandro F.; Navarro, Bruno V.; Matioli, Sergio R.; I. S. Floh, Eny . Building an embryo: an auxin gene toolkit for zygotic and somatic embryogenesis in Brazilian pine. GENE, v. 00, p. 146168, 2022.

3.2. Navarro, B.V., Elbl, P., de Oliveira, L.F., Piovezani, A.R., Dos Santos, A. L. W., **Souza, D.T**., et al. Cell-to-cell trafficking patterns in cell lines of Araucaria angustifolia (Brazilian pine) with contrasting embryogenic potential. Plant Cell Tiss Organ Cult (2021). https://doi.org/10.1007/s11240-021-02166-4

3.3. Bravim, Fernanda; Lippman, Soyeon I. ; Silva, Lucas F. ; **Souza, Diego T**.; Fernandes, A. Alberto R. ; Masuda, Claudio A. ; Broach, James R. ; Fernandes, Patricia M. B. . High hydrostatic pressure activates gene expression that leads to ethanol production enhancement in a Saccharomyces cerevisiae distillery strain. Applied Microbiology and Biotechnology, v. online, p. 1-15, 2012.

3.4. BRAVIM, F.; Silva, Lucas F.; **SOUZA, D. T**.; LIPPMAN, S.; BROACH, J. R.; Fernandes, A. Alberto R. ; Fernandes, Patricia M. B. . High Hydrostatic Pressure Activates Transcription Factors Involved in Saccharomyces cerevisiae Stress Tolerance. Current Pharmaceutical Biotechnology (Print), v. 13, p. 2712, 2012.

**4.- Other Publications**

4.1. Matioli, Sergio Russo; **Souza, Diego Trindade.** Introduction to Bioinformatics. 1st Edition. Campinas: Unicamp, 2021.

**5.- Quantitative indicators.**

Publications in periodicals with selective editorial policy: 5

Number of citations: 15 (ISI), 22 (Scopus), 44 (Google)

**6-Link**

Lattes resume: http://lattes.cnpq.br/6114507020608659

MyResearcherID (ISI): http://www.researcherid.com/rid/D-2473-2013

MyCitations (Google Scholar): https://scholar.google.com.br/citations?user=ijZcyb0AAAAJ

Linkedin: https://www.linkedin.com/in/diego-trindade-de-souza-746685116/