

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

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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, Daffre 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, Galletti 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, Sato 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. Kasperek T, Thomaz CE, Sato JR, Schwarz D, Janousova E, Marecek R, Prikrýl 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.
82. Sato JR, da Graça MMM, **Fujita A**, Mourão-Miranda J, Brammer MJ, Amaro Jr E. An fMRI normative database for connectivity networks using one-class support vector machines. *Human Brain Mapping*. **30**: 1068-1076, 2008.
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.
85. Hatanaka Y, Nagasaki M, Yamaguchi Rui, Obayashi T, Numata K, **Fujita A**, Shimamura T, Tamada Y, Imoto S, Kinoshita K, Nakai K, Miyano S. A novel strategy to search conserved transcriptional factor binding sites among coexpressing genes in human. *Genome Informatics*. **20**: 212 - 221, 2008.
86. Sato JR, Thomaz CE, Cardoso E, **Fujita A**, Martin M, Amaro Jr E. Hyperplane navigation: A method to set individual scores in fMRI group datasets. *NeuroImage*. **42**: 1473 - 1480, 2008.
87. **Fujita A**, Gomes LR, Sato JR, Yamaguchi R, Thomaz CE, Sogayar MC, Miyano S. Multivariate gene expression analysis reveals functional connectivity changes between normal/tumoral prostates. *BMC Systems Biology*. **2**: 106, 2008.
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. Genômica 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. Mاتيoli 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)