Curriculum vitae

Name: André Fujita (ORCID: 0000-0002-7756-7051)
Position: Associate Professor and Coordinator of the Bioinformatics Graduate Program
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/Training

2016	Habilitation	University of São Paulo

2003 – 2007   Ph.D. in Bioinformatics   University of São Paulo
Internship in the Human Genome Center, the University of Tokyo (JICA Scholarship)
CAPES Scholarship
Best Ph.D. thesis award, Brazilian Society for Computer Science
Honorable mention in Biological Sciences, CAPES Ph.D. theses contest

1999 – 2003   B.Sc. in Computer Science   University of São Paulo
Internship in the Cell and Molecular Biology Lab. – Dept. of Biochemistry
CNPq Scholarship

2) Languages

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

3) Professional positions held

1. Since Mar 2020: Coordinator of the Bioinformatics Graduate Program, University of São Paulo.
2. Jul – Nov 2019: FAPESP-ERC Fellow, Social Genetic & Developmental Psychiatry Centre, King's College London.
3. Mar 2018 - Mar 2020: Vice-coordinator of the Bioinformatics Graduate Program, University of São Paulo.
4. Dec 2018 – Feb 2019: Alexander von Humboldt Fellow, Dept. of Computer Science, Leipzig University.
5. Dec 2017 – Feb 2018: Alexander von Humboldt Fellow, Dept. of Computer Science, Leipzig University.
6. Since Apr 2016: Associate Professor at the Dept. of Computer Science, University of São Paulo.
7. Dec 2014 – Jan 2015: JICA Fellow at the Cancer Research Institute, Kanazawa University.
8. Jan 2014: Visiting Scientist at the Cancer Research Institute, Kanazawa University.
9. Mar 2011 – Mar 2016: Assistant Professor at the Dept. of Computer Science, University of São Paulo.
10. Apr 2009 – Feb 2011: Special Postdoctoral Researcher, Computational Science Research Program, RIKEN.
11. Nov 2007 – Mar 2009: Postdoc at the Human Genome Center, the University of Tokyo.

4) Professional honors, awards, and fellowships

2021   Intercontinental Academia Fellow, University-Based Institutes for Advanced Study (UBIAS)
2021   Fulbright Fellowship, 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 Program Fellowship, RIKEN, Japan
2009   Honorable mention, CAPES Ph.D. theses contest in Biological Sciences, Brazil
2008   Best Ph.D. thesis award in Computer Science, Brazilian Society for Computer Science, Brazil
2006   Japan International Cooperation Agency (JICA) Fellowship, JICA, Japan

5) Publication list

Journal articles (*: indicates the corresponding author)

1. 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.

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

3. 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.

4. 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.

5. 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.

6. 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.

7. 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.

8. 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.

9. Jardim VC, Siqueira SS, **Fujita A**, Buckeridge MS. BioNetStat: a tool for biological networks differential analysis. *Frontiers in Genetics*. 10: 594, 2019.

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

11. 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.

12. 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.

13. 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.

14. 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.

15. 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.

16. 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.

17. 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.

18. 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.

19. 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.

20. 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.

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

22. 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.

23. 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.

24. 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.

25. 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.

26. 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.

27. 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.

28. 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.

29. 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.

30. **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.

31. 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.

32. 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.

33. Santos SS, 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.

34. 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.

35. 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.

36. 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.

37. 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.

38. 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.

39. **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.

40. 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.

41. 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.

42. 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.

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

44. Siqueira SS, 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.

45. 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.

46. 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.

47. **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.

48. 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.

49. 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.

50. **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.

51. 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.

52. 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.

53. 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.

54. **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.

55. 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.

56. **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.

57. 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.

58. **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.

59. **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.

60. 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.

61. **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.

62. 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.

63. 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.

64. **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.

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

66. **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.

67. 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.

68. **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.

69. 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.

70. 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.

71. 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.

72. **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.

73. 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.

74. **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.

75. **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.

76. **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.

77. **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.

78. **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. 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.

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 (in press).

3. 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.

4. 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.

5. Siqueira SS, 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.

6. **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.

7. 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.

8. **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.

9. 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.

10. **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.

6) Courses taught and other services provided to students and the home institution

1. 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, MAC0213 - Voluntary Community Work, MAC0214 - Extracurricular Activities, MAC0215 - Undergraduate Research.

2. Graduate courses: 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.

3. Coordinator of the Bioinformatics Graduate Program (since 2020)

4. Vice-coordinator of the Bioinformatics graduate program (2018 - 2020)

5. 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)

6. Coordinator of the Bioinformatics Entrance Exam (2016 - 2020)

7. Coordinator of the Bioinformatics Summer Course 2013 (*highlighted by the Research Dean as one of the year's best educational events*)

8. The team member that designed the eScience track (minor Bioinformatics) for the Computer Science undergraduate course (2013 - 2014).

7) Main achievements as the Coordinator of the Bioinformatics Graduate Program (since March 2020)

1. Due to the COVID-19 pandemic, disciplines started to minister remotely. We capitalized on this infrastructure, and I 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.

2. During the Brazilian economic crisis, I led the Bioinformatics committee to get two master's and one Ph.D. additional scholarship for the Bioinformatics Graduate Program. It corresponds to an increase of 25% and 8% of master's and Ph.D. scholarships, respectively. I am currently negotiating with a private company to obtain six to eight additional scholarships.

3. 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 this semester from an average of 60 in the last five years to 138 candidates, i.e., over 100% increase.

4. I organized the Bioinformatics committee to be in a proportion of 50/50 females/males. Also, we debate all topics extensively, taking into account minority groups' opinions. As a consequence, voting became unnecessary. All decisions are made with consensus.

8) Other professional activities, such as workshops, seminars, and consultations

1. 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.

2. 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), Japan (University of Tokyo, Tohoku 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.

3. 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, Catholic University of Goiás, International Institute for Neuroscience of Natal, etc.

4. Consultations: O Boticário (second largest Brazilian cosmetic company), Cogsign (start-up for health monitoring), IAssist Tecnologia (start-up for early cancer diagnosis using AI)

5. 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).

6. Associate Editor: Network Modeling Analysis in Health Informatics and Bioinformatics (Springer/Nature)

7. Reviewer for journals: Bioinformatics, PLoS Computational Biology, BMC Bioinformatics, BMC Systems Biology, IEEE/ACM TCBB, Nucleic Acids Research, NeuroImage, Human Brain Mapping, Computational Statistics & Data Analysis, Statistics in Medicine, Neoplasia, etc.

9) Research grants (only as PI)

1. FAPESP-eScience 2020/01479-1. Classification of body/mental states for a human-machine interface based on the heart rate variability. Amount: R$217,925 + USD$12,943. Period: October 2020 – September 2023.

2. FAPESP-UdL 2020/08343-8. Graph/Hypergraph (spectral) analysis to compare metabolic networks of pathogenic Trypanosoma sp. Amount: R$119,887 + USD$5,750. Period: December 2020 – November 2022.

3. FAPESP-INRIA 2019/22845-9. Computational approaches to explore intra and cross-species interactions and their role in all domains of life. Amount: approx. USD$17,000. Period: March 2020 – February 2022.

4. FAPESP 2018/21934-5. Network Statistics: theory, methods, and applications. Amount: approx. R$1,800,000. Period: May 2019 - April 2024 (includes two co-PIs and dozens of research associates).

5. Academy of Medical Sciences, the UK National Academy. A model-based graph clustering approach for autism stratification. Amount: £61,814. Period: March 2018 – March 2021.

6. CNPq 303855/2019-3. Productivity fellowship. Amount: approx. R$39,600. Period: 2020 - 2022.

7. CAPES / Alexander von Humboldt Foundation. Statistical methods on graphs. Amount: approx. €43,500. Period: December 2017 - November 2020.

8. PRP-USP. The use of cardiac frequency variability to construct activity reading and human-machine interfaces. Amount: approx. R$75,000. Period: April 2019 - October 2020.

9. CNPq 304876/2016-0. Productivity fellowship. Amount: approx. R$39,600. Period: 2017 - 2019.

10. FAPESP 2016/13422-9. Statistical methods for graphs with applications in life sciences. Amount: R$181,866. Period: November 2016 – October 2018.

11. FAPESP 2014/09576-5. Development of computational statistical methods to construct, model, and analyze biological networks associated with human diseases. Amount: R$248,903 + USD$18,000. Period: July 2014 – September 2016.

12. CNPq 304020/2013-3. Productivity fellowship. Amount: approx. R$39,600. Period: 2014 - 2016.

13. CAPES 51/2013 – Academic cooperation network for developing tools for structural and functional genomics. (Co-PI). Amount received: R$232,800. Period: 2014 – 2019.

14. CAPES 51/2013 – Development and applications of computational tools in biology: from molecular modeling to translational research. (Co-PI). Amount received: R$105,600. Period: 2014 – 2019.

15. CNPq 473063/2013-1. Pattern recognition in large scale social interactions: the use of non-human primates as a model system. Amount: R$39,655. Period: July 2014 – December 2016.

16. 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: R$108,681 + USD$34,500. Period: July 2011 – December 2013.

17. CNPq 306319/2010-1. Productivity fellowship. Amount: approx. R$39,600. Period: 2011 - 2013.

18. RIKEN 090042. Development of computational methods for large scale gene regulatory networks: construction and structural analysis. Amount: approx. USD$18,000. Period: April 2009 – February 2011.

10) **List of ongoing supervisions (competitive scholarships between parenthesis)**

1. Arthur Prado de Fazio – undergrad student in Computer Science
2. Caio Matheus Prates Batalha Faria, Ph.D. candidate. Co-advisor (CNPq)
3. Carlos Enrique Paucar Farfán, Master candidate (CAPES and Hewlett Packard Enterprise)
4. Daniel Cunha Oliveira, Master candidate. Co-advisor.
5. Diego Trindade de Souza, Postdoc
6. Diogo Ricardo da Costa, Postdoc (FAPESP)
7. Eduardo Lira, Ph.D. candidate (CAPES)
8. Grover Enrique Castro Guzman – Ph.D. candidate (CAPES)
9. Guilherme D. L. de Souza - undergrad student in Molecular Sciences (PRP-USP)
10. Heitor Baldo – Ph.D. candidate (CAPES). Co-advisor
11. Mario Muramatsu Junior – undergrad student in Computer Science
12. Nicolle Floriani Paust – undergrad student in Engineering
13. Renata Biaggi Biazzi, Master candidate (CAPES)
14. Victor Chavauty Villela – Master candidate.
15. Vinicius Godoi Fernandes – Ph.D. candidate. Co-advisor
16. Vinicius Jardim Carvalho – Ph.D. candidate (FAPESP)

11) **List of graduated students (competitive scholarships between parenthesis)**

Ph.D. theses

1. Taiane Coelho Ramos, 2021 – she will start a postdoc at Fluminense Federal University soon
2. Carlos Eduardo Martins Relvas, 2020 – founder of the start-up DataRisk
3. Maciel Calebe Vidal (CAPES), 2020 - currently a lecturer at Insper Institute
4. Suzana de Siqueira Santos (FAPESP), 2020 – currently a 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
5. Gabriela Eleutério Soares (CAPES), 2018 – currently at Talkdesk, Portugal
6. Adèle Helena Ribeiro (CAPES), 2018 – currently a 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
7. Gustavo Pinto Vilela (FAPESP), 2017 – currently at Amazon.
8. Fernando Cipriano Andrade Oliveira (CAPES), 2017 – currently a lecturer at Loyola University Chicago
   with six months of internship at Cincinnati Children's Hospital Medical Center, the USA
9. Abner Cardoso Rodrigues Neto (CAPES), 2016 - currently a researcher at Edmond and Lily Safra International Institute of Neurosciences
   Best Ph.D. thesis of the Bioinformatics Graduate Program

Master dissertations

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

Undergraduate students

1. Lucas Marques Gasparino – B.Sc. in Computer Science, 2020
2. Ravi do Valle Luz. B.Sc. in Molecular Sciences (FAPESP), 2020
3. Pedro Ivo Nepomuceno. B.Sc. in Computer Science (PIBIC-CNPq), 2016
4. Henrique C. de Souza Rodrigues. B.Sc. in Applied Mathematics with minor in Biological Sciences, 2014
5. Pedro Parik Americano. B.Sc. in Mechatronics Engineering (PIBIC-CNPq), 2013
6. Suzana de Siqueira Santos. B.Sc. in Computer Science (PIBIC-CNPq), 2013
7. Yuri Gomes de Abreu. B.Sc. in Manufacturing Engineering (PRP-USP), 2012.
8. Claudivan Ribeiro. B.Sc. in Computer Science, 2011
9. Tiago N. Bombenti. B.Sc. in Computer Science, 2011.

12) **International network and relations**

1. Prof. Eric Kolaczyk, Boston University (the USA)
   Fulbright Fellowship host
2. Prof. Gunter Schumann, King's College London (the UK)
   FAPESP-ERC Fellowship host
3. Prof. Janaina Mourao-Miranda, University College London (the UK)
   Newton Advanced Fellowship host
4. Prof. Marie-France Sagot, Université Claude Bernard (Lyon 1) (France)
   Co-PI of joint projects (FAPESP-INRIA 2019/22845-9 and FAPESP-UdL 2020/08343-8)
5. Prof. Masao Nagasaki, Kyoto University (Japan)
   Collaborator
6. Prof. Noriko Gotoh, Kanazawa University (Japan)
   JICA Fellowship host
7. Prof. Peter Stadler, Universität Leipzig (Germany)
   Alexander von Humboldt Fellowship host
8. Prof. Satoru Miyano, Tokyo Medical and Dental University – M&D Data Science Center (Japan)
   Postdoc advisor when he was at the University of Tokyo and SPDR host at RIKEN