Jaqueline Yu Ting Wang

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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)