



Anders Gonçalves da Silva, PhD

Senior Bioinformatician | Microbiological Diagnostic Lab Public Health Laboratory

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Employment

Microbiological Diagnostic Unit Public Health Laboratory, The University of Melbourne

Senior Bioinformatician 2018-

Microbiological Diagnostic Unit Public Health Laboratory, The University of Melbourne

Bioinformatician 2015-2018

Ornithology Lab, Monash University

Postdoctoral Researcher 2012-2015

CSIRO Marine and Atmospheric Research

Postdoctoral Fellow 2009-2012

Ecological and Conservation Genomics Lab, University of British Columbia

Postdoctoral Teaching and Research Fellow 2007-2009

Education

Columbia University, PhD Ecology and Evolutionary Biology 2007

Columbia University, MSc Ecology and Evolutionary Biology 2004

Columbia University, MA Conservation Biology 2003

Universidade Estadual de Campinas, BSc Biology 2000

Service and Leadership

Leadership of the AusTrakka Development Team.

Leadership of the MDU PHL Bioinformatics Team.

Leadership of the national CDGN Bioinformatics Working Group.

Leadership of the MDU/DHHS Partnership Grant.

Leadership in AusTrakka (data sharing for public health).

Leadership in development of best practices for accreditation of Bioinformatics software for use in public health.

Leadership in development of national proficiency testing programs for Next Generation Sequencing and Bioinformatics software.

Leadership in development of a national pathogen surveillance platform based on genomic data.

Publications

Journal Articles

2020

- Baines, S. L., A. Gonçalves da Silva, G. P. Carter, et al. (2020). "Complete microbial genomes for public health in Australia and the Southwest Pacific". En. In: *Microb Genom* 6.12.
- Ferdinand, A. S., M. Kelaher, C. R. Lane, et al. (2020). "The Pathogen Genomics in Public Health Surveillance Evaluation (PG-PHASE) Framework: An Implementation Science Approach to Evaluating Pathogen Whole Genome Sequencing in Public Health". In: *Research Square*.
- Gorrie, C. L., A. Gonçalves da Silva, D. J. Ingle, et al. (2020). "Systematic analysis of key parameters for genomics-based real-time detection and tracking of multidrug-resistant bacteria". In: *bioRxiv*.
- Griffiths, E. J., R. E. Timme, A. J. Page, et al. (2020). "The PHA4GE SARS-CoV-2 contextual data specification for open genomic epidemiology". In: *Preprints*.
- Ingle, D. J., P. Andersson, M. Valcanis, et al. (2020). "Prolonged outbreak of multidrug-resistant *Shigella sonnei* harboring blaCTX-M-27 in Victoria, Australia". In: *Antimicrob. Agents Chemother.* 64.12.
- Lane, C. R., J. Brett, M. Schultz, et al. (2020). "Search and Contain: Impact of an integrated genomic and epidemiological surveillance and response program for control of carbapenemase-producing Enterobacterales". In: *Clin. Infect. Dis.*.
- Lau, K. A., A. Gonçalves da Silva, S. A. Ballard, et al. (2020). "Proficiency Testing for bacterial whole genome sequencing in assuring the quality of microbiology diagnostics in clinical and public health laboratories". In: *bioRxiv*.
- Seemann, T., C. R. Lane, N. L. Sherry, et al. (2020). "Tracking the COVID-19 pandemic in Australia using genomics". In: *Nat. Commun.* 11.1, pp. 1-9.

2019

- Gonçalves da Silva, A., W. Barendse, J. Kijas, et al. (2019). "Genomic data suggest environmental drivers of fish population structure in the deep sea: A case study for the orange roughy (*Hoplostethus atlanticus*)". In: *J. Appl. Ecol.* 49. Ed. by M. Coleman, p. 103.
- Jensen, S. O., N. Firth, A. Gonçalves da Silva, et al. (2019). "Remodeling of pSK1 family plasmids and enhanced chlorhexidine tolerance in a dominant hospital lineage of methicillin-resistant *Staphylococcus aureus*". In: *Antimicrob. Agents Chemother.*.
- Lee, J. Y. H., G. P. Carter, S. J. Pidot, et al. (2019). "Mining the Methylome Reveals Extensive Diversity in *Staphylococcus epidermidis* Restriction Modification". En. In: *MBio* 10.6.

2018

- Baines, S. L., S. O. Jensen, N. Firth, et al. (2018). "Remodelling of pSK1 Family Plasmids and Enhanced Chlorhexidine Tolerance in Methicillin-Resistant *Staphylococcus aureus*". In: *bioRxiv*, p. 457838.

- Carter, G. P., M. B. Schultz, S. L. Baines, et al. (2018). "Topical antibiotic use coselects for the carriage of mobile genetic elements conferring resistance to unrelated antimicrobials in *Staphylococcus aureus*". In: *Antimicrobial agents and chemotherapy* 62.2, pp. e02000-17.
- Carter, G. P., J. E. Ussher, A. Gonçalves da Silva, et al. (2018). "Genomic Analysis of Multiresistant *Staphylococcus capitis* Associated with Neonatal Sepsis". In: *Antimicrobial agents and chemotherapy* 62.11, pp. e00898-18.
- Giulieri, S. G., S. L. Baines, R. Guerillot, et al. (2018). "Genomic exploration of sequential clinical isolates reveals a distinctive molecular signature of persistent *Staphylococcus aureus* bacteraemia". In: *Genome medicine* 10.1, p. 65.
- Giulieri, S., S. Baines, R. Guerillot, et al. (2018). "Genomic Exploration of Within-Host Microevolution Reveals a Distinctive Molecular Signature of Persistent *Staphylococcus aureus* Bacteraemia". In: *bioRxiv*, p. 273904.
- Guérillot, R., A. Gonçalves da Silva, I. Monk, et al. (2018). "Convergent Evolution Driven by Rifampin Exacerbates the Global Burden of Drug-Resistant *Staphylococcus aureus*". In: *mSphere* 3.1, pp. e00550-17.
- Guérillot, R., L. Li, S. Baines, et al. (2018). "Comprehensive antibiotic-linked mutation assessment by resistance mutation sequencing (RM-seq)". In: *Genome medicine* 10.1, p. 63.
- Herrisse, M., J. L. Porter, R. Guerillot, et al. (2018). "The Φ BT1 large serine recombinase catalyzes DNA integration at pseudo-attB sites in the genus *Nocardia*". In: *PeerJ* 6, p. e4784.
- Kwong, J. C., C. R. Lane, F. Romanes, et al. (2018). "Translating genomics into practice for real-time surveillance and response to carbapenemase-producing Enterobacteriaceae: evidence from a complex multi-institutional KPC outbreak". In: *PeerJ* 6, p. e4210.
- Lee, J. Y., I. R. Monk, A. Gonçalves da Silva, et al. (2018). "Global spread of three multidrug-resistant lineages of *Staphylococcus epidermidis*". In: *Nature microbiology* 3.10, p. 1175.
- Lee, R. S., A. Gonçalves da Silva, S. L. Baines, et al. (2018). "The changing landscape of vancomycin-resistant *Enterococcus faecium* in Australia: a population-level genomic study". In: *Journal of Antimicrobial Chemotherapy*, p. dky331. DOI: 10.1093/jac/dky331.
- Pidot, S. J., W. Gao, A. H. Buultjens, et al. (2018). "Increasing tolerance of hospital *Enterococcus faecium* to handwash alcohols". In: *Science translational medicine* 10.452, p. eaar6115.

2017

- Buultjens, A. H., K. Y. Chua, S. L. Baines, et al. (2017). "A supervised statistical learning approach for accurate *Legionella pneumophila* source attribution during outbreaks". In: *Applied and environmental microbiology*, pp. AEM-01482.
- Gonçalves da Silva, A., S. L. Baines, G. P. Carter, et al. (2017). "A phylogenomic framework for assessing the global emergence and evolution of clonal complex 398 methicillin-resistant *Staphylococcus aureus*". In: *Microbial Genomics* 3.1.
- Jacques-Hamilton, R., M. L. Hall, W. A. Buttemer, et al. (2017). "Personality and innate immune defenses in a wild bird: Evidence for the pace-of-life hypothesis". In: *Hormones and behavior* 88, pp. 31-40.

Kpeli, G., A. H. Buultjens, S. Giulieri, et al. (2017). "Genomic analysis of ST88 community-acquired methicillin resistant *Staphylococcus aureus* in Ghana". In: *PeerJ* 5, p. e3047.

Kwong, J. C., C. Lane, F. Romanes, et al. (2017). "Real-time genomic and epidemiological investigation of a multi-institution outbreak of KPC-producing Enterobacteriaceae: a translational study". In: *BioRxiv*, p. 175950.

Mu, A., J. C. Kwong, N. S. Isles, et al. (2017). "Genome reconstruction and characterisation of extensively drug-resistant bacterial pathogens through direct metagenomic sequencing of human faeces". In: *bioRxiv*, p. 153874.

Staples, M., R. Graham, V. Hicks, et al. (2017). "Discovery of *Streptococcus pneumoniae* serogroup 35 variants in Australian patients". In: *Clinical Microbiology and Infection* 23.7, pp. 476-479.

Williamson, D. A., S. L. Baines, G. P. Carter, et al. (2017). "Genomic insights into a sustained national outbreak of *Yersinia pseudotuberculosis*". In: *Genome biology and evolution* 8.12, pp. 3806-3814.

Zozaya-Valdés, E., J. L. Porter, J. Coventry, et al. (2017). "A target-specific assay for rapid and quantitative detection of *Mycobacterium chimaera* DNA". In: *Journal of clinical microbiology*, pp. JCM-00197.

2016

Harrisson, K. A., A. Pavlova, A. Gonçalves da Silva, et al. (2016). "Scope for genetic rescue of an endangered subspecies through re-establishing natural gene flow with another subspecies". In: *Molecular ecology* 25.6, pp. 1242-1258.

Kwong, J. C., A. Gonçalves da Silva, K. Dyet, et al. (2016). "NGMASTER: in silico multi-antigen sequence typing for *Neisseria gonorrhoeae*". In: *Microbial Genomics* 2.8.

2015

Edelaar, P., S. Roques, E. A. Hobson, et al. (2015). "Shared genetic diversity across the global invasive range of the monk parakeet suggests a common restricted geographic origin and the possibility of convergent selection". In: *Molecular ecology* 24.9, pp. 2164-2176.

Gonçalves da Silva, A., S. A. Appleyard, and J. Upston (2015). "Establishing the evolutionary compatibility of potential sources of colonizers for overfished stocks: a population genomics approach". In: *Molecular ecology* 24.3, pp. 564-579.

Gonçalves da Silva, A., W. Barendse, J. W. Kijas, et al. (2015). "SNP discovery in nonmodel organisms: strand bias and base-substitution errors reduce conversion rates". In: *Molecular ecology resources* 15.4, pp. 723-736.

2014

Pinho, G. M., A. Gonçalves da Silva, T. Hrbek, et al. (2014). "Kinship and Social Behavior of Lowland Tapirs (*Tapirus terrestris*) in a Central Amazon Landscape". In: *PloS one* 9.3, p. e92507.

2013

Gonçalves da Silva, A., A. Campos-Arceiz, and M. S. Zavada (2013). *On tapir ecology, evolution and conservation: what we know and future perspectives part II*.

2012

Gonçalves da Silva, A., I. C. Cunha, W. S. Santos, et al. (2012). "Gene flow networks among American *Aedes aegypti* populations". In: *Evolutionary Applications* 5.7, pp. 664-676.

2011

Gonçalves da Silva, A. and M. A. Russello (2011). "iRel: software for implementing pairwise relatedness estimators and evaluating their performance". In: *Conservation Genetics Resources* 3.1, pp. 69-71.

2010

De Thoisy, B., A. Gonçalves da Silva, M. Ruiz-García, et al. (2010). "Population history, phylogeography, and conservation genetics of the last Neotropical mega-herbivore, the lowland tapir (*Tapirus terrestris*)". In: *BMC evolutionary biology* 10.1, p. 278.

Gonçalves da Silva, A., J. R. Eberhard, T. F. Wright, et al. (2010). "Genetic evidence for high propagule pressure and long-distance dispersal in monk parakeet (*Myiopsitta monachus*) invasive populations". In: *Molecular ecology* 19.16, pp. 3336-3350.

Gonçalves da Silva, A., S. Kolokotronis, and D. Wharton (2010). "Modeling the eradication of invasive mammals using the sterile male technique". In: *Biological Invasions* 12.4, pp. 751-759.

Gonçalves da Silva, A., K. E. Williams, S. L. Kirk, et al. (2010). "Isolation and characterization of microsatellite loci in two species-at-risk in British Columbia: Great Basin spadefoot (*Spea intermontana*) and Western painted turtle (*Chrysemys picta bellii*)". In: *Conservation Genetics Resources* 2.1, pp. 37-40.

Gonçalves da Silva, A., D. R. Lalonde, V. Quse, et al. (2010). "Genetic approaches refine ex situ Lowland Tapir (*Tapirus terrestris*) conservation". In: *Journal of heredity* 101.5, pp. 581-590.

Reports

Gonçalves da Silva, A., S. Appleyard, and J. Upston. *Orange roughy (*Hoplostethus atlanticus*) population genetic structure in Tasmania, Australia*. Tech. rep. CSIRO, Australia, 2012.

Gonçalves da Silva, A., D. Williamson, T. Seemann, et al. *Data sharing to improve decision making in public health: a case for Australian Public Health Laboratories*. Tech. rep. Public Health Laboratories Network, 2017.

Hayes, K. R., N. Beebe, J. Dambacher, et al. *Risk assessment for controlling mosquito vectors with engineered nucleases, Part I: sterile male construct*. Tech. rep. CSIRO, Australia. Report to the Foundation for the National Institutes of Health and the Bill and Melinda Gates Foundation, 2015.

Book Chapters

Gonçalves da Silva, A. "Measuring Natural Selection". In: *Bioinformatics Methods in Molecular Biology*. Ed. by J. M. Keith. Springer, 2017, p. 315-347.

Recent Conference Presentations

Gonçalves da Silva, A., T. Seemann, D. A. Williamson, et al. "AusTrakka: Enabling Data Sharing for Surveillance - or Why Your Parents Were Right". In: *ASM Conference on Rapid Applied Microbial Next-Generation Sequencing and Bioinformatic Pipelines*. Ed. by J. Gardy and D. MacCannell. 2018.

Students

PhD

Sara Zufan — Department of Microbiology and Immunology, The University of Melbourne

Courtney Lane — Department of Microbiology and Immunology, The University of Melbourne

Andrew Buultjens — Department of Microbiology and Immunology, The University of Melbourne [Completed]

MSc

Andre Tan — Faculty of Science, The University of Melbourne [Completed]

Gabriela Pinho — Instituto Nacional de Pesquisas da Amazônia [Completed]

Honours

Tiffany Miller-Scott — School of Biological Sciences, Monash University [Completed]

Teaching

Workshops

Genomic Epidemiology of Infectious Diseases. McGill Summer Institute in Infectious Diseases & Global Health 2018

Genomic Epidemiology of Infectious Diseases. McGill Summer Institute in Infectious Diseases & Global Health 2017

Introductory Course in Public Health Microbial Genomics 2017

Introductory Course in Public Health Microbial Genomics 2016

Australian Pathogen Bioinformatics Symposium (ANU) 2014

Population and landscape genomics workshop (ANU) 2014

Units

BINF90002: Elements of Bioinformatics (Lecturer) - The University of Melbourne 2017

BIOL 203: Introduction to Ecology (Instructor) – University of British Columbia 2009

GEOG 213: Introduction to Environmental Issues (Instructor) – University of British Columbia 2008

Grants

Gonçalves da Silva A. Population genomics of orange roughy in Tasmania. South East Trawl Fishing Industry Association/CSIRO – AUD 132,000.00 (2011-2012).

Gonçalves da Silva A. (co-PI with M Russello). Conservation of Amazonian tapirs. National Geographic Society Conservation Fund – USD 20,000.00 (2007-2009).

Gonçalves da Silva A. (co-PI with M Russello). Conservation of Amazonian tapirs. The Rufford Foundation Small Grants – GBP 5,000.00 (2007-2009).

Gonçalves da Silva A. Landscape and conservation genetics of mammals in the Brazilian Atlantic Forest. The Rufford Foundation Small Grants – GBP 5,000.00 (2004-2006).

Gonçalves da Silva A. Landscape and conservation genetics of mammals in the Brazilian Atlantic Forest. Disney Worldwide Emergency Conservation Fund – USD 3,500 (2005).

Gonçalves da Silva A. Landscape and conservation genetics of mammals in the Brazilian Atlantic Forest. American Society of Mammalogists –USD 1,500 (2003).

Gonçalves da Silva A. Landscape and conservation genetics of mammals in the Brazilian Atlantic Forest. The Explorer's Club Exploration Grant – USD 1,000 (2003).