



Anders Gonçalves da Silva, PhD

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Employment

BC Centre for Disease Control Public Health Laboratory, BC Centre for Disease Control

Consultant 2020-

Department of Microbiology and Immunology, The University of Melbourne

Senior Academic Research Fellow in Public Health Bioinformatics 2018-

Department of Microbiology and Immunology, The University of Melbourne

Academic Research Fellow in Public Health Bioinformatics 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 - USA, PhD Ecology and Evolutionary Biology 2007

Columbia University - USA, MSc Ecology and Evolutionary Biology 2004

Columbia University - USA, MA Conservation Biology 2003

Universidade Estadual de Campinas - Brazil, BSc Biology 2000

Service and Leadership

Leadership of Public Health Alliance for Genomic Epidemiology (PHAGE)

Leadership in PulseNet International (liaison for Australia)

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

2021

Ferdinand, A. S., M. Kelaher, C. R. Lane, et al. (2021). "An implementation science approach to evaluating pathogen whole genome sequencing in public health". En. In: *Genome medicine* 13.1, p. 121.

Gorrie, C. L., A. Gonçalves da Silva, D. J. Ingle, et al. (2021). "Key parameters for genomics-based real-time detection and tracking of multidrug-resistant bacteria: a systematic analysis". En. In: *The Lancet Microbe*.

Ingle, D. J., R. L. Ambrose, S. L. Baines, et al. (2021). "Evolutionary dynamics of multidrug resistant *Salmonella enterica* serovar 4,[5],12:i:- in Australia". En. In: *Nature communications* 12.1, p. 4786.

Lane, C. R., N. L. Sherry, A. F. Porter, et al. (2021). "Genomics-informed responses in the elimination of COVID-19 in Victoria, Australia: an observational, genomic epidemiological study". En. In: *The Lancet. Public health* 6.8, pp. e547-e556.

Lau, K. A., A. Gonçalves da Silva, T. Theis, et al. (2021). "Proficiency testing for bacterial whole genome sequencing in assuring the quality of microbiology diagnostics in clinical and public health laboratories". En. In: *Pathology*.

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: *Microbial genomics* 6.12.

Gonçalves da Silva, A., W. Barendse, J. Kijas, et al. (2020). "Genomic data suggest environmental drivers of fish population structure in the deep sea: A case study for the orange roughy (*Hoplostethus atlanticus*)". En. In: *The Journal of applied ecology* 57.2. Ed. by M. Coleman, pp. 296-306.

Griffiths, E. J., R. E. Timme, A. J. Page, et al. (2020). "The PHA4GE SARS-CoV-2 contextual data specification for open Genomic Epidemiology". En.

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: *Antimicrobial agents and chemotherapy* 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". En. In: *Clinical infectious diseases: an official publication of the Infectious Diseases Society of America*.

Seemann, T., C. R. Lane, N. L. Sherry, et al. (2020). "Tracking the COVID-19 pandemic in Australia using genomics". En. In: *Nature communications* 11.1, p. 4376.

2019

Baines, S. L., S. O. Jensen, N. Firth, et al. (2019). "Remodeling of pSK1 family plasmids and enhanced chlorhexidine tolerance in a dominant hospital lineage of methicillin-resistant *Staphylococcus aureus*". In: *Antimicrobial agents and chemotherapy* 63.5, pp. e02356-18.

Bojang, A., S. L. Baines, L. Donovan, et al. (2019). "Genomic investigation of *Staphylococcus aureus* recovered from Gambian women and newborns following an oral dose of intra-partum azithromycin". En. In: *The Journal of antimicrobial chemotherapy* 74.11, pp. 3170-3178.

Eastwood, J. R., L. Peacock, M. L. Hall, et al. (2019). "Persistent low avian malaria in a tropical species despite high community prevalence". In: *International journal for parasitology. Parasites and wildlife* 8, pp. 88-93.

Ingle, D. J., M. Easton, M. Valcanis, et al. (2019). "Co-circulation of multidrug-resistant *Shigella* among men who have sex with men in Australia". In: *Clinical infectious diseases: an official publication of the Infectious Diseases Society of America* 69.9, pp. 1535-1544.

Ingle, D. J., A. Gonçalves da Silva, M. Valcanis, et al. (2019). "Emergence and divergence of major lineages of Shiga-toxin-producing *Escherichia coli* in Australia". En. In: *Microbial genomics* 5.5.

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: *Antimicrobial agents and chemotherapy*.

Lamb, A. M., A. Gonçalves da Silva, L. Joseph, et al. (2019). "Pleistocene-dated biogeographic barriers drove divergence within the Australo-Papuan region in a sex-specific manner: an example in a widespread Australian songbird". En. In: *Heredity* 123.5, pp. 608-621.

Lee, J. Y. H., G. P. Carter, S. J. Pidot, et al. (2019a). "Mining the Methylome Reveals Extensive Diversity in *Staphylococcus epidermidis* Restriction Modification". En. In: *mBio* 10.6.

——— (2019b). "Mining the Methylome Reveals Extensive Diversity in *Staphylococcus epidermidis* Restriction Modification". In: *mBio* 10.6.

Mu, A., J. C. Kwong, N. S. Isles, et al. (2019). "Reconstruction of the Genomes of Drug-Resistant Pathogens for Outbreak Investigation through Metagenomic Sequencing". En. In: *mSphere* 4.1, pp. e00529-18.

Sherry, N. L., C. R. Lane, J. C. Kwong, et al. (2019). "Genomics for Molecular Epidemiology and Detecting Transmission of Carbapenemase-Producing Enterobacterales in Victoria, Australia, 2012 to 2016". En. In: *Journal of clinical microbiology* 57.9, pp. e00573-19.

Tan, A., T. Seemann, J. A. Lacey, et al. (2019). *emmtyper*.

2018

Buultjens, A., J. Kwong, A. Gonçalves da Silva, et al. (2018). *legsta: In silico Legionella pneumophila Sequence Based Typing*.

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*". En. In: *Antimicrobial agents and chemotherapy* 62.2.

Giulieri, S. G., S. L. Baines, R. Guerillot, et al. (2018a). "Genomic exploration of sequential clinical isolates reveals a distinctive molecular signature of persistent *Staphylococcus aureus* bacteraemia". En. In: *Genome medicine* 10.1, p. 65.

—— (2018b). "Genomic exploration of sequential clinical isolates reveals a distinctive molecular signature of persistent *Staphylococcus aureus* bacteraemia". En. In: *Genome medicine* 10.1, p. 65.

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*". En. In: *mSphere* 3.1, pp. e00550-17.

Herisse, 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*". En. 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". En. In: *PeerJ* 6, p. e4210.

Kwong, J., K. A. Horan, A. Gonçalves da Silva, et al. (2018a). *_meningotype: In silico serotyping, finotyping and Bexsero antigen sequence typing of _Neisseria meningitidis_*.

Kwong, J., K. Horan, A. Gonçalves da Silva, et al. (2018b). *_lissero: In silico serotype prediction for _Listeria monocytogenes_*.

Lee, J. Y. H., I. R. Monk, A. Gonçalves da Silva, et al. (2018). "Global spread of three multidrug-resistant lineages of *Staphylococcus epidermidis*". En. In: *Nature microbiology* 3.10, pp. 1175-1185.

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". En. In: *The Journal of antimicrobial chemotherapy* 73.12, pp. 3268-3278.

Lee, R. S., T. Seemann, H. Heffernan, et al. (2018). "Genomic epidemiology and antimicrobial resistance of *Neisseria gonorrhoeae* in New Zealand". En. In: *The Journal of antimicrobial chemotherapy* 73.2, pp. 353-364.

Pidot, S. J., W. Gao, A. H. Buultjens, et al. (2018). "Increasing tolerance of hospital *Enterococcus faecium* to handwash alcohols". En. In: *Science translational medicine* 10.452.

Seemann, T., J. Kwong, S. Gladman, et al. (2018). *Shovill: Faster SPAdes assembly of Illumina reads*.

2017

Buultjens, A. H., K. Y. L. Chua, S. L. Baines, et al. (2017). "A Supervised Statistical Learning Approach for Accurate *Legionella pneumophila* Source Attribution during Outbreaks". En. In: *Applied and environmental microbiology* 83.21.

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*". En. In: *Microbial genomics* 3.1, p. e000105.

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". En. 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". En. In: *PeerJ* 5, p. e3047.

Staples, M., R. M. A. Graham, V. Hicks, et al. (2017). "Discovery of *Streptococcus pneumoniae* serogroup 35 variants in Australian patients". En. In: *Clinical microbiology and infection: the official publication of the European Society of Clinical Microbiology and Infectious Diseases*.

Zozaya-Valdés, E., J. L. Porter, J. Coventry, et al. (2017). "Target-Specific Assay for Rapid and Quantitative Detection of *Mycobacterium chimaera* DNA". En. In: *Journal of clinical microbiology* 55.6, pp. 1847-1856.

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". En. 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.

Williamson, D. A., S. L. Baines, G. P. Carter, et al. (2016). "Genomic Insights into a Sustained National Outbreak of *Yersinia pseudotuberculosis*". En. In: *Genome biology and evolution* 8.12, pp. 3806-3814.

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". En. 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". En. 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". En. 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". En. 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". In: *Integrative zoology* 8.1, pp. 1-3.

2012

Gonçalves da Silva, A., A. Campos-Arceiz, and M. S. Zavada (2012). "On tapir ecology, evolution and conservation: what we know and future perspectives-part I". In: *Integrative zoology* 7.4, pp. 329-330.

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

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

Real-time Combined Genomic and Epidemiological Monitoring of COVID-19 in British Columbia. MSFHR - (2020-2022)	
AusTrakka: real-time pathogen genomics surveillance. Commonwealth Department of Health - AUD \$1,160,000 (2020-2022).	
AusTrakka: real-time pathogen genomics surveillance. Victorian State Government - AUD 800,000 (2020-2022).	
Tracking COVID-19 using genomics. MRFF - AUD 3,270,000 (2020-2022)	
PPHAGE: Precision Public Health in Australia through Integrated Pathogen Genomics - NHMRC AUD 2,000,000 (2020-2025)	
Population genomics of orange roughy in Tasmania. South East Trawl Fishing Industry Association/CSIRO – AUD 132,000.00 (2011-2012).	
Conservation of Amazonian tapirs. National Geographic Society Conservation Fund – USD 20,000.00 (2007-2009).	
Conservation of Amazonian tapirs. The Rufford Foundation Small Grants – GBP 5,000.00 (2007-2009).	
Landscape and conservation genetics of mammals in the Brazilian Atlantic Forest. The Rufford Foundation Small Grants – GBP 5,000.00 (2004-2006).	
Landscape and conservation genetics of mammals in the Brazilian Atlantic Forest. Disney Worldwide Emergency Conservation Fund – USD 3,500 (2005).	

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

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