Nigel Kurgan

Postdoctoral Research Fellow

Novo Nordisk Foundation Center for Basic Metabolic Research

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Exercise physiologist with expertise in metabolic assays, proteomics, and bioinformatics. I'm interested in combining these approaches to better understand interorgan communication mediated by secreted proteins during exercise and in individuals with metabolic diseases. I am an avid R user for data processing, visualization, communication, reports/dashboards, and am passionate about open and reproducible science.

Current Appointments

Novo Nordisk Foundation Center for Basic Metabolic Research, University of Copenhagen *Copenhagen, Denmark*

Postdoctoral Research Fellow *Sep 2022–Present*

Education

Brock University *St. Catharines, Canada*

Ph.D. Health Biosciences *2022*

- Conferred with Distinction and a Graduate Student Research Excellence Award
- Funded by Scholarships from NSERC (2017-21) and QEII-GSST (2021-2022)
- Thesis: Sclerostin influences body composition adaptations to exercise training

Brock University *St. Catharines, Canada*

M.Sc. Applied Health Sciences *2017*

- Funded by an Ontario Graduate Scholarship
- Thesis: Physical training, inflammation, and bone integrity in elite female rowers

Brock University *St. Catharines, Canada*

B.Sc. Biomedical Sciences *2015*

- Conferred June 2015 with First-Class Standing
- Thesis: Mitochondrial function and phospholipid composition changes in mdx mice skeletal muscle

Research Experience

Universidad San Francisco de Quito *Quito, Ecuador*

Visiting Scientist, Institute of Microbiology *Oct 2021–Present*

- Provide support for the coordination and data analysis of a population-based cohort study in Quito to understand vaccine and infection-induced immunity to SARS-CoV-2
- Support data analyses on the genomic epidemiology and phylogenetics of different SARS-CoV-2 variants circulating in Ecuador

Walter and Eliza Hall Institute of Medical Research *Melbourne, Australia*

Postdoctoral Scientist, Population Health and Immunity Division, Mueller and Robinson Labs *Feb 2019–Present*

- My postdoc work involves the application of a suite of genomic epidemiology approaches to better understand residual and resurgent malaria transmission dynamics in the Asia-Pacific and Americas regions
- Support the field implementation and lead the overall analysis of a 12-month longitudinal cohort study in Papua New Guinea. The aim of this study is to understand the spatiotemporal risk factors for malaria infections in 1000 individuals of all ages residing across four villages on the North Coast of PNG.
- Apply novel genotyping and molecular diagnostic techniques to samples collected from several large-scale epidemiological field studies in Asia-Pacific to identify and track malaria infections over space and time and within individuals. Downstream analysis involves relating genetic data to epidemiological data to better understand spatiotemporal infection dynamics and risk factors
- Outputs: Co-author publications(2), Honors and awards/grants (9), Student/staff supervision (5) PNG

The University of Melbourne *Melbourne, Australia*

Research Fellow in Malaria Population Genetics, Day Lab *May 2018–Feb 2019*

- Applied genomic epidemiology approaches that employed bioinformatic and population genetic methods to better understand the diversity and geographic population structure of *var* genes in Ecuador and Ghana
- Lead the analysis and preparation of manuscripts on the epidemiology and population genetics of malaria in Ecuador and Ghana
- Outputs: Co-author publications (1), Student supervision (1)

Center for Research on Health in Latin America

Quito, Ecuador

Visiting Scientist

Nov 2017–Feb 2018

- I was awarded a JD Smyth Postgraduate Student Travel Award by the Australian Society for Parasitology to support a Researcher Exchange to establish an international research collaboration
- Implemented protocols and novel population genetic analytical methods to examine malaria field samples to better understand malaria transmission patterns in Ecuador
- Trained laboratory staff on molecular genetic protocols and developed analytical skills workshops

The University of Melbourne

Melbourne, Australia

Postgraduate Researcher, Day Lab

Feb 2014–May 2018

- Developed a high-throughput amplicon sequencing genotyping tool and customised computational and analytical methods for characterizing antigenic diversity in *P. falciparum*
- My PhD work involved the generation of microsatellite genotyping and *var* gene illumina sequence data and downstream analysis using population genetic, bioinformatic, phylodynamic and epidemiology approaches to relate parasite diversity data to epidemiological data collected in the field
- Visited our field site in Bongo District, Ghana in 2014 and was directly involved in the field coordination and data collection as part of a cross-sectional survey in Bongo
- Outputs from my PhD: First-author publications (2), Co-author publications (3), Honors and awards (7), Student supervision (1)

New York University of School of Medicine

New York, USA

Research Assistant, Day Lab, Division of Medical Parasitology

Jun 2012–Jan 2014

- Analyzed the molecular epidemiology and population genetics of the *Plasmodium falciparum var* multi-gene family encoding the major variant surface antigen of malaria

New York Blood Center Lindsley F. Kimball Research Institute

New York, USA

Research Intern, Lustigman Lab, Molecular Parasitology

Jul 2011–Aug 2011

- Research project: Polymorphisms in invasion ligand genes from Peruvian, Colombian and Brazilian *Plasmodium falciparum* field isolates
- Identified novel polymorphisms in DNA sequences coding for proteins critical to the invasion process and pathogenicity of *P. falciparum*

Teaching and Supervision

In addition to the formal supervision roles listed below, I am also actively involved in the supervision, mentorship and capacity-building of researcher officers and technical staff in partner institutions in Indonesia, Papua New Guinea and Ecuador. I am also serving on 2 PhD committees at the University of Melbourne.

Guest Lecturer

Quito, Ecuador

Universidad San Francisco de Quito

44531

- Guest lecturer for the Masters of Innovation on COVID-19 epidemiology, variant dynamics and implications for public health in Ecuador

Honours Student Co-Supervisor

Melbourne, Australia

Walter and Eliza Hall Institute of Medical Research

Feb–Dec 2021

- Designed and co-supervised an Honours research project in seroepidemiology for a Biomedical undergraduate student
- Research project: Application of Serological Markers for the Assessment of Spatial Heterogeneity of *Plasmodium vivax* infections in Papua New Guinea

Undergraduate Student Supervisor

Melbourne, Australia

Walter and Eliza Hall Institute of Medical Research

Feb–Dec 2021

- Designed and supervised a six-month research project in genomics (both lab and analytics) for a Biomedical undergraduate student
- Research project: Amplification of six novel markers for *Plasmodium vivax* genotyping by targeted amplicon sequencing

Guest Lecturer

Melbourne, Australia

Nossal Institute for Global Health, University of Melbourne

Oct 2019–Present

- Guest lecturer for the Nossal Institute for Global Health Masters of Public Health on Malaria and Child Health (POPH90086: Global Child Health)

PhD Student Co-Supervisor

Melbourne, Australia

Walter and Eliza Hall Institute of Medical Research

Jul 2019–Present

- Co-supervise a Medical Biology PhD student on *Plasmodium vivax* genomics and bioinformatics
- Research project: The role of transcription and translational regulation in *Plasmodium vivax* sporozoites

PhD Student Co-Supervisor

Melbourne, Australia

Walter and Eliza Hall Institute of Medical Research

Jul 2019–Jun 2021

- Co-supervised a PhD student on *Plasmodium vivax* genomics (both lab and analytics) and population genetics
- Research project: Development of novel genotyping tools for *Plasmodium vivax*

MSc Student Co-Supervisor

Melbourne, Australia

The University of Melbourne

Feb 2018–Dec 2019

- Co-supervised a Genetics MSc student in genetic epidemiology, population genetics and statistical genetics
- Research project: The effects of seasonality on the population genetics of the reservoir of asymptomatic *Plasmodium falciparum* in Bongo District, Ghana

Guest Lecturer

Quito, Ecuador

Universidad de los Hemisferios

43070

- Guest lecturer for the Masters of Entrepreneurship on the topic of Social Impact Business Models and The Artisan Project as a Case Study

Undergraduate Student Supervisor

Melbourne, Australia

The University of Melbourne

Jul 2016–Nov 2016

- Designed and supervised a six-month research project in statistical genetics and genetic epidemiology for a Computational Biology undergraduate student through the Undergraduate Research Opportunities Program scheme
- Research project: Host genetic factors that influence malaria parasitemia in Ghanaian children

Laboratory Demonstrator

Melbourne, Australia

The University of Melbourne

Jul 2015–Aug 2017

- Led groups of high school students attending the Victorian Certificate of Education Biology workshops in genetics

Tutor and Teaching Assistant

Colorado, USA

The Colorado College

Sep 2008–May 2012

- Biology Department and Quantitative Reasoning Center, courses included: Introduction to Molecular Genetics, Introduction to Cellular Biology, Advanced Genetics Courses
- Spanish Department, courses included: Beginner, Intermediate and Advanced Spanish and Cultural Context and Written Expression

Leadership, Service & Community Engagement

Manuscript peer-review: Journal of Infectious Diseases (1), PLOS Genetics (1), Malaria Journal (2), International Journal for Parasitology (1), Frontiers in Genetics (1), Infection, Genetics and Evolution (1), Scientific Reports (1)

Panelist: Universidad San Francisco de Quito (Quito, Ecuador) *Jan 2021*

- Panelist on the panel discussion "Lessons learned from COVID-19 variants" (Lecciones aprendidas con variantes COVID-19) hosted by USFQ and national newspaper El Universo

TV interview: Visionarias EC News Program (Quito, Ecuador) *Dec 2021*

- Interview on a national news program on the segment "Omicron - the new variant affecting the globe" (Ómicron - la nueva variante que esta afectando al mundo)

Local Organizing Committee: International Conference on *Plasmodium vivax* research (Melbourne, Australia) *Aug 2021–Present*

President and Co-organizer: R-Ladies Melbourne (Melbourne, Australia) *Aug 2021–Present*

- R-Ladies Melbourne is a non-profit organization aiming to promote gender diversity in the R statistical programming community

Member, Web-based applications working group: Walter and Eliza Hall Institute (Melbourne, Australia) *Jul 2021–Present*

Mentor: CareerTrackers Young Indigenous Women in STEM Academy (Melbourne, Australia) *Dec 2020–Present*

Member, Postdoctoral Association: Walter and Eliza Hall Institute (Melbourne, Australia) *Dec 2020–Present*

Crowdfunding for SARS-CoV-2 serosurveillance in Quito, Ecuador: Collaboration with Ecuadorian Red Cross (Quito, Ecuador) *Sep 2020–Present*

- Led the establishment and provide ongoing support for serosurveillance of SARS-CoV-2 antibodies in blood donors in Ecuador to support COVID-19 epidemiological surveillance. Early in the pandemic, crowdfunding for this initiative raised US$2,500

Consultant Epidemiologist: National COVID-19 Response Emergency Committee in Ecuador (Quito, Ecuador) *Apr–Aug 2020*

Guest Curator: WeAreRLadies Twitter Community (Online) *Feb 2020*

ICEMR Workshop Co-Organizer: Walter and Eliza Hall Institute (Melbourne, Australia) *Sep–Dec 2019*

- Co-organized an ICEMR-funded hands-on workshop to train six malaria-endemic country scientists on amplicon sequencing (AmpSeq) for *Plasmodium falciparum*, a novel and high-resolution genotyping technique that can be used to sensitively discriminate different clones of *Plasmodium* spp. infections

STEM Workshop Co-Leader: It Takes a Spark Melbourne Conference 2019 (Melbourne, Australia) *Sep 2019*

- Co-led the development of a workshop to teach high-school girls epidemiology and R coding skills to solve an outbreak and become a "disease detective". (Materials here)

Discovery Tour Volunteer: Walter and Eliza Hall Institute (Melbourne, Australia) *Jul 2019–Present*

- Volunteer for WEHI Discovery Tours to showcase the malaria research and expose the wider community to medical research

Member, Reconciliation Committee: Walter and Eliza Hall Institute (Melbourne, Australia) *Jun 2019–Present*

- The RC aims to contribute towards reconciliation by working towards 'closing the gap' in life expectancy, disease incidence, and mortality for Aboriginal and Torres Strait Islander Australians

Secretary and Co-organizer: R-Ladies Melbourne (Melbourne, Australia) *Apr–Aug 2021*

- R-Ladies Melbourne is a non-profit organization aiming to promote gender diversity in the R statistical programming community

Committee Chair, Annual Conference: Australian Centre for Excellence in Malaria Elimination (Australia) *Mar–Oct 2019*

Volunteer, Annual Conference Committee: Australian Society for Parasitology (Melbourne, Australia) *Aug–Sep 2018*

Social Impact Entrepreneur: Melbourne Accelerator Program (Melbourne, Australia) *Sep 2016–Feb 2017*

- Selected to represent The Artisan Project (at the time I was CEO) in the MAP Social Velocity six-month competitive entry program for early stage social impact start-ups

Entrepreneur: European Innovation Academy (Nice, France) *Jul 2016*

- Selected as one of four students to represent University of Melbourne at EIA, the world's largest extreme accelerator program for tech and digital innovations

Campaign Manager: Ecuadorian Research and Entrepreneurship Network (Melbourne, Australia) *Apr 2016*

- As president of EREN at the time, I co-managed a large-scale fundraising campaign across Australia to raise relief funds in response to the 7.8-magnitude earthquake in Ecuador (total amount raised: A$17,963)

Open House Volunteer: Bio21 Institute (Melbourne, Australia) *Jul 2015–Jul 2018*

- Showcased our malaria research to members of the wider community at the Bio21 Open House events

Co-Organizer: ResBaz Ecuador (Quito, Ecuador) *Feb 2015–Feb 2016*

- The Research Bazaar is a worldwide festival promoting the digital literacy emerging at the centre of modern research. I was co-organizer of the first ResBaz in the Americas in 2015 and 2016

Additional training and professional development

2021 **Short course: Multiple imputation** (Victorian Centre for Biostatistics)
2021 **RStudio Diversity Scholar Workshops** (RStudio)
2018 **Certification "Teaching Skills for Graduate Researchers"** (University of Melbourne)
2017 **Winter School in Mathematical Biology** (Institute for Molecular Science, The University of Queensland)
2015 **Short course: Spatial mapping and GIS skills** (University of Melbourne)
2015 **UOM subject: Epidemiology 1** (University of Melbourne)
2015 **UOM subject: Biostatistics 1** (University of Melbourne)
2015 **UOM subject: Linear and Logistic Regression** (University of Melbourne)

Skills

Laboratory	Analytical	Programming	Software/Tools
DNA extraction	Epidemiological database curation/management	R (advanced)	Git/Github
PCR/qPCR	Univariate/multivariate data analysis	Rstudio	REDCap
Illumina amplicon sequencing	Population genetics	RMarkdown	LaTeX
PacBio long-read sequencing	Genome-wide analyses	SLURM/high-performance computing	CSS
Whole-genome sequencing	Reproducible research	STATA	HTML

Awards and Funding

2023-25 **NSERC Postdoctoral Fellowship** (University of Copenhagen): Awarded 90,000 CAD to study mechanisms of tissue crosstalk mediated by extracellular vesicles

2022 **Distinguished Graduate Student** (Brock University): Awarded 100 CAD for being the most distinguished graduate from my graduate program

2021 **CSEP Graduate Student Oral Presentation Finalist** (CSEP Conference): Awarded 250 CAD for being selected as a finalist for best graduate student oral presentation

2020-21 **QEII Graduate Scholarship in Science and Technology** (Brock University): Awarded a 15,000 CAD scholarship for my Ph.D. work

2020 **Jack M Miller Excellence in Research** (Brock University): Awarded 1,341 CAD in recognition for my excellence in researc

2017-19 **NSERC Postgraduate Scholarship – Doctoral** (Brock University): Awarded 63,000 CAD to study bone-secreted proteins during exercise

2017-19 **Dean of Graduate Studies Excellence Scholarship** (Brock University): Awarded 21,000 CAD for my academic excellence

2017 **Dean of Graduate Studies Entrance Scholarship – Doctoral** (Brock University): Awarded 2,000 CAD for my academic excellence

2016-17 **Ontario Graduate Scholarship – Masters** (Brock University): Awarded 15,000 CAD to study bone health in elite female rowers

2016-17 **Dean of Graduate Studies Excellence Scholarship – Masters** (Brock University): Awarded 2,500 CAD for my academic excellence

2016 **CSEP Poster Award Finalist** (CSEP Conference): Selected as a finalist for best poster

2016 **Dean of Graduate Studies Spring Research Fellowship** (Brock University): Awarded 4,000 CAD for my academic excellence

2015-16 **Dean of Graduate Studies Entrance Scholarship** (Brock University): Awarded 2,500 CAD for my academic excellence

2015 **Graduate Studies Fellowship** (Brock University): Awarded 7,000 CAD to study the bone response to acute exercise

2012-14 **Brock Returning Scholars Award/Deans Honour List** (Brock University): Awarded 1,500 CAD for my academic excellence

2010 **Brock Entrance Scholars Award** (Brock University): Awarded 2,500 CAD for my academic excellence

Publications

*indicates equal contribution

2022

Charnaud, S., Munro, J., Semenec, L., Mazhari, R., Brewster, J., Bourke, C., **Ruybal-Pesántez, S.**, James, R., Lautu-Gumal, D., Karunajeewa, H., & Mueller, I. (2022, *accepted*). *PacBio long-read amplicon sequencing for scalable high-resolution population allele typing of the complex CYP2D6 locus*. Communications Biology.

Ruybal-Pesántez, S., Tiedje, K. E., Pilosof, S., Tonkin-Hill, G., He, Q., Rask, T. S., Amenga-Etego, L., Oduro, A. R., Koram, K. A., Pascual, M., & Day, K. P. (2022). *Age-specific patterns of DBLa var diversity can explain why residents of high malaria transmission areas remain susceptible to Plasmodium falciparum blood stage infection throughout life.* International Journal for Parasitology. https://doi.org/10.1016/j.ijpara.2021.12.001

- This work was featured on the Herminthology #WomenBehindTheWork initiative

Feng, Q., Tiedje, K. E., **Ruybal-Pesántez, S.**, Tonkin-Hill, G., Duffy, M. F., Day, K. P., Shim, H., & Chan, Y. (2022). *An accurate method for identifying recent recombinants from unaligned sequences.* Bioinformatics. https://doi.org/10.1093/bioinformatics/btac012

2021

Ruybal-Pesántez, S., Sáenz, F., Deed, S. L., Johnson, E. K., Larremore, D. B., Vera-Arias, C. A., Tiedje, K. E. & Day, K. P. (2021, *preprint*). *Clinical malaria incidence following an outbreak in Ecuador was predominantly associated with Plasmodium falciparum with recombinant variant antigen gene repertoires.* medRxiv. https://doi.org/10.1101/2021.04.12.21255093

Mazhari, R., **Ruybal-Pesántez, S.**, Angrisano, F., Kiernan-Walker, N., Hyslop, S., Longley, R. J., Bourke, C., Chen, C., Williamson, D. A., Robinson, L. J., Mueller, I., & Eriksson, E. M. (2021). *SARS-CoV-2 Multi-Antigen Serology Assay*. Methods and Protocols, 4(4), 72. https://doi.org/10.3390/mps4040072

Argyropoulos, D. C.* , **Ruybal-Pesántez, S.*** , Deed, S. L., Oduro, A. R., Dadzie, S. K., Appawu, M. A., Asoala, V., Pascual, M., Koram, K. A., Day, K. P., & Tiedje, K. E. (2021). *The impact of indoor residual spraying on Plasmodium falciparum microsatellite variation in an area of high seasonal malaria transmission in Ghana, West Africa*. Molecular Ecology, 30(16), 3974–3992. https://doi.org/10.1111/mec.16029

- This work was chosen by the editors to be featured in the Molecular Ecology blog

Tonkin-Hill, G., **Ruybal-Pesántez, S.**, Tiedje, K. E., Rougeron, V., Duffy, M. F., Zakeri, S., Pumpaibool, T., Harnyuttanakorn, P., Branch, O. H., Ruiz-Mesía, L., Rask, T. S., Prugnolle, F., Papenfuss, A. T., Chan, Y., & Day, K. P. (2021). *Evolutionary analyses of the major variant surface antigen-encoding genes reveal population structure of Plasmodium falciparum within and between continents*. PLOS Genetics, 17(2), e1009269. https://doi.org/10.1371/journal.pgen.1009269

- This work was chosen by the editors to be featured with an accompanying Perspectives piece

2020

Narh, C. A., Ghansah, A., Duffy, M. F., **Ruybal-Pesántez, S.**, Onwona, C. O., Oduro, A. R., Koram, K. A., Day, K. P.* , & Tiedje, K. E.* (2020). *Evolution of antimalarial drug resistance markers in the reservoir of Plasmodium falciparum infections in the Upper East Region of Ghana*. The Journal of Infectious Diseases. https://doi.org/10.1093/infdis/jiaa286

2019

Pilosof, S., He, Q., Tiedje, K. E., **Ruybal-Pesántez, S.**, Day, K. P., & Pascual, M. (2019). *Competition for hosts modulates vast antigenic diversity to generate persistent strain structure in Plasmodium falciparum.* PLOS Biology, 17(6), e3000336. https://doi.org/10.1371/journal.pbio.3000336

2018

He, Q., Pilosof, S., Tiedje, K. E., **Ruybal-Pesántez, S.**, Artzy-Randrup, Y., Baskerville, E. B., Day, K. P., & Pascual, M. (2018). *Networks of genetic similarity reveal non-neutral processes shape strain structure in Plasmodium falciparum*. Nature Communications, 9(1), 1817. https://doi.org/10.1038/s41467-018-04219-3

Rorick, M. M., Artzy-Randrup, Y., **Ruybal-Pesántez, S.**, Tiedje, K. E., Rask, T. S., Oduro, A., Ghansah, A., Koram, K., Day, K. P., & Pascual, M. (2018). *Signatures of competition and strain structure within the major blood-stage antigen of Plasmodium falciparum in a local community in Ghana*. Ecology and Evolution, 8(7), 3574–3588. https://doi.org/10.1002/ece3.3803

2017

Ruybal-Pesántez, S., Tiedje, K. E., Rorick, M. M., Amenga-Etego, L., Ghansah, A., Oduro, A. R., Koram, K. A., & Day, K. P. (2017). *Lack of Geospatial Population Structure Yet Significant Linkage Disequilibrium in the Reservoir of Plasmodium falciparum in Bongo District, Ghana*. The American Journal of Tropical Medicine and Hygiene, 97(4), 1180–1189. https://doi.org/10.4269/ajtmh.17-0119

Ruybal-Pesántez, S.* , Tiedje, K. E.* , Tonkin-Hill, G., Rask, T. S., Kamya, M. R., Greenhouse, B., Dorsey, G., Duffy, M. F., & Day, K. P. (2017). *Population genomics of virulence genes of Plasmodium falciparum in clinical isolates from Uganda*. Scientific Reports, 7(1), 11810. https://doi.org/10.1038/s41598-017-11814-9

Digital tools

For other non-traditional academic contributions, I have also developed several `R Shiny` web applications to support COVID-19 surveillance efforts and `R flexdashboard` for real-time updates and data visualization of both programmatic/operational aspects and preliminary epidemiological trends as part of the coordination of population-based field studies. Check out my GitHub

CovidClassifyR

Shazia Ruybal-Pesántez *Sep 2021*

- This Shiny web application was developed to support COVID-19 serosurveillance in Papua New Guinea enabling classification of unknown samples as recently exposed to SARS-CoV-2. This tool makes the downstream processing, quality control and interpretation of the raw data generated from a validated COVID-19 serological assay (Mazhari et al 2020) accessible to all researchers without the need for a specialist background in statistical methods and advanced programming. Funding was provided by a COVID-19 Digital Grant, media release

COVID-19 VaccinationScore

Raúl Fernández, Shazia Ruybal-Pesántez, Esteban Ortíz *Feb 2021*

- This Shiny web application was developed during the initial vaccine roll-out in Ecuador to help individuals better understand their "priority status" to receive their COVID-19 vaccine. An algorithm was applied to calculate a priority score based on an individuals answers to a set of questions on socioeconomic status, occupation, exposure, risk behavior, comorbidities, etc. Newspaper article (in Spanish)

Serosurveillance of COVID-19 in Ecuadorian blood donors dashboard (not open-source)

Shazia Ruybal-Pesántez *Jun 2020*

- This R flexdashboard was developed to support COVID-19 serosurveillance in Ecuadorian blood donors in collaboration with the Ecuadorian Red Cross National Blood Bank as part of the emergency response to COVID-19 (active early in the pandemic, June 2020-Dec 2020). This dashboard presented anonymized and aggregated data generated from monthly screening of blood donation samples to visualize seroprevalence trends. Due to confidentiality and internal permissions at ERC this tool is not publicly available.

ICEMR weekly dashboard (not open-source)

Shazia Ruybal-Pesántez *Mar 2020*

- This R flexdashboard was developed to support the ICEMR field teams in Madang, Papua New Guinea (active during the entire longitudinal cohort study March 2020 until Sep 2021). This dashboard was updated weekly and presented operational data (e.g. follow-up rates in each field site) that could be used by the team to plan field activies and identify any areas for improvement as well as preliminary epidemiological trends (e.g. RDT positivity, prevalence of fever). As this tool was meant for internal use within the ICEMR project, it is not publicly available.

processqpcR

Shazia Ruybal-Pesántez *In development*

- This Shiny web application is in development to support laboratory researchers with little to no programming skills with a tool for downstream processing of raw data generated from several qPCR machines (e.g. Lightcyler480, Quantstudio, etc). Functions will include automatic matching of sample IDs using a user-supplied 96-well or 384-well plate map, quantification of unknown samples using the assay standard curve/positive controls (e.g. to detect malaria-positive samples) and some preliminary visualizations of the data.

Selected presentations

I have participated in oral and poster presentations at 18 conferences (13 international, 5 national; 6 travel awards).

2021 **Understanding the factors underlying malaria resurgence in East Sepik, Papua New Guinea: a preliminary analysis**, Invited to speak at the Australian Centre for Excellence in Malaria Elimination webinar series. See recording

2021 **rstudio::global(2021) %>% filter(workshops == "diversity scholars") %>% summarize()**, Presented at the R-Ladies Melbourne meet-up, slides

2018 **Why are adults still infected in malaria-endemic areas? Insights from the epidemiology of *P. falciparum var* genes**, Oral presentation at the annual meeting of the American Society of Tropical Medicine and Hygiene, New Orleans, USA

2018 **Maintenance of the parasite reservoir in Ghana: parasite diversity and the epidemiology of *P. falciparum var* genes**, Invited to speak at the London School of Hygiene and Tropical Medicine Malaria Centre seminar series in London, UK

2017 **Why is it difficult to control malaria? (¿Por qué es dificil controlar la malaria?)**, Invited to speak at the University of San Francisco of Quito (USFQ) Faculty of Biological and Environmental Sciences seminar series in Quito, Ecuador

2017 ***Var* code: a new molecular epidemiology tool for monitoring *Plasmodium falciparum* in a high transmission area of Ghana, West Africa**, Selected to participate in the Young Investigator Award Poster Session of the American Society of Tropical Medicine and Hygiene, Atlanta, USA

About me

I am half Ecuadorian and half American, born in The Netherlands, I am fluent in English and Spanish (beginner French and Dutch), and grew up overseas in several countries in Africa and Latin America: Ecuador, Tanzania, Guatemala, and Honduras. I am an Australian Permanent Resident and have been living in Melbourne, Australia since 2014 when I moved to pursue my PhD. Apart from my research, I am highly committed to furthering health and development initiatives, particularly in my home country of Ecuador. From early 2016 until the COVID-19 pandemic, I was CEO and co-founder of the The Artisan Project, a social enterprise that worked hand in hand with talented indigenous artisans in Ecuador. We used fashion as a tool to create income-generating opportunities, particularly for indigenous women, and impulse social impact and innovation. During the COVID-19 pandemic I was actively involved as a consultant epidemiologist providing analyses on case and testing trends, importation dynamics, Reff calculations, among others, to the Ecuadorian National COVID-19 Emergency Response committee - most of this work remains unpublished due to competing political agendas and turnover of public health officials.