JIM GATHERAL SCHOLARSHIP REPORT 2018-2019

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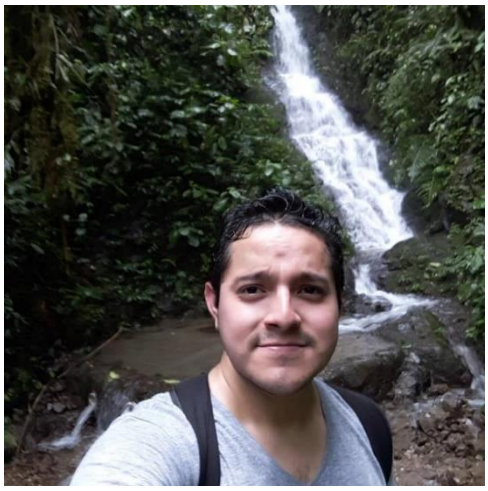
I am from the Yucatan state in southeast Mexico where I graduated from Vet school in 2012. After 2 years of practice with wild fauna, I decided to embark to a research career. My interest on animal and human diseases transmission and control motivated me to undertake the University of Glasgow Quantitative Methods in Biodiversity, Conservation and Epidemiology Masters programme in 2014. In 2016, I started my Doctorate studies with Dr Martin Llewellyn based at the University of Glasgow Institute of Biodiversity, Animal Health and Comparative Medicine.

I applied to the 2018 Jim Gatheral travel scholarship call during the 3rd year of my Doctorate studies to visit the Mathematical and Computational research group – BIOMAC at Los Andes University in Bogota, Colombia leaded by Dr Juan Manuel Cordovez. I was awarded with £3357 to support my travel, visa and living expenses in Colombia for a period of 3 months.



Why did you apply for this travel scholarship?

My research focuses on understanding the population dynamics of main Chagas disease vector, *Rhodnius ecuadoriensis*, in the highlands in southern Ecuador using next generation sequencing molecular techniques and modelling analysis. This disease is caused by a parasite, *Trypanosoma cruzi*, and transmitted by post-biting contamination with faeces of triatomine insects, commonly known as kissing bugs. Approximately 7 million people are infected with Chagas disease, mainly in Latin America, and they frequently present heart, nervous and digestive system pathologies during the latter stages of infection when treatment has little probability to succeed. Until now, domicile vectors eradication has been the most effective intervention to reduce disease burden in endemic countries. However, triatomine domicile adaptation and complex ecology (e.g. sylvatic bugs recolonizing treated human households) jeopardise the current vector control programs. Therefore, molecular and modelling approaches are powerful tools to solve gaps in the knowledge of triatomine bugs populations dynamics. So far in my research, I have gathered the largest triatomine bug single nucleotide polymorphism (SNP) marker set which provided me with high resolution molecular data to differentiate between triatomine bugs populations and test hypothesis of dispersal.

I applied to this scholarship to visit BIOMAC to learn about mathematical techniques that allow to model the factors driving triatomine dispersal in my study area. This model of triatomine dispersal could be useful to inform insecticide spraying programmes. Specifically, I was interested on Agent-

based modelling, a very popular technique used in urban and transport studies and it has become recently used to model disease transmission. Visiting BIOMAC was important because of their expertise in mathematical modelling of Chagas disease systems in South America.

Details of my visit

During the first week in BIOMAC, I was welcomed by Dr Juan Cordovez and his team integrated by a postdoctoral researcher, and several doctorate and master students. We discussed the purpose of my visit and we agreed on a plan to take advantage of this short visit.

Coincidentally during my arrival, the BIOMAC team was planning a field trip to collect triatomine bugs, and bats stools and blood for a project in the Colombian Llanos, a region with high prevalence of Chagas disease (Figures 1 & 2). The reason for this sample collection trip was to obtain epidemiological data about triatomine *T. cruzi* infection and the role bats play as reservoirs of *T. cruzi*. Given that this was a different Chagas disease system to the one I have been studying in southern Ecuador, I decided to join the team.

This unexpected field work experience provided me with a better understanding of the different Chagas disease transmission cycles and the interactions between the different agents in the disease transmission pathway. I was very satisfied to be able to go to the field and observe at first-hand what we usually epidemiologist/modellers only imagine in our computational analyses.

Figure 2 From left to right: tent used for camping during the field trip, chicken trap used to capture triatomine bugs directly from palm trees and a well-deserved meal with the Colombian field work gang.

Figure 1 Different species of bats captured during the field trip. Bats play an important role as reservoirs of many infectious disease such as rabies and Chagas disease.

After the field trip, I focused on having weekly meetings with the BIOMAC group to design the propose model. During those meetings there was always a group member presenting updates of their work or just talk about different mathematical approaches. During my visit I met different senior researchers and postdoctoral and master students. Dr Jose Arteaga is a physicist working in different projects using mathematical theory (Figure 3) such as time series and Monte Carlo simulations. I met Carlos Bravo, a doctoral student working on a model to predict snake-bite accidents and antiserum distribution, a very prevalent problem in Colombia. I also met master's students (Figure 4) Juan Umaña and Norma Forero, they both work within the Chagas disease system. Juan works with domicile and sylvatic vector-host interactions, and Norma is modelling the role that bats play on disease transmission. Their advice for my modelling work and their friendship made this a worthy experience which I am sure it will translate in future collaborations.

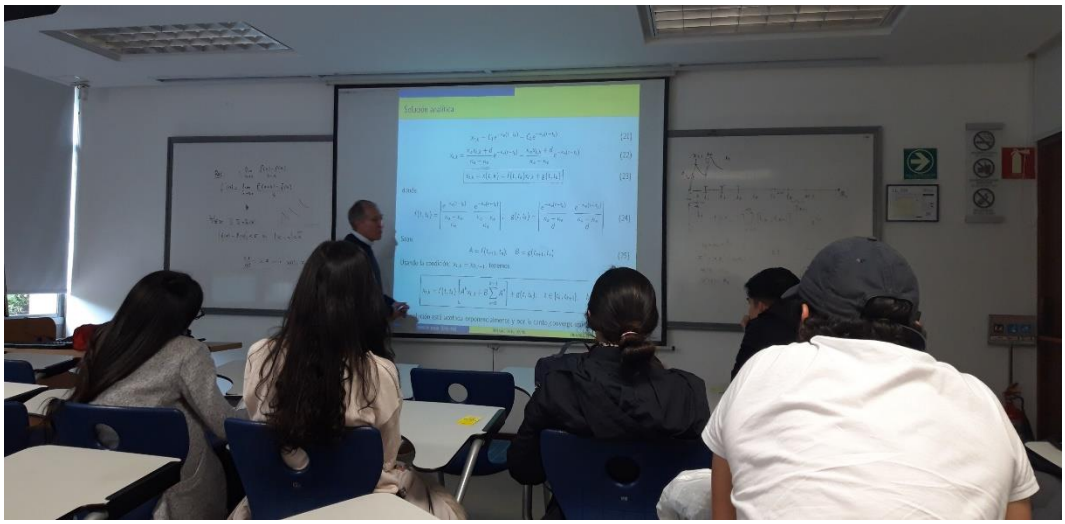


Figure 3 Dr Jose Arteaga explaining time series modelling and Monte Carlo simulations during a BIOMAC weekly meeting.

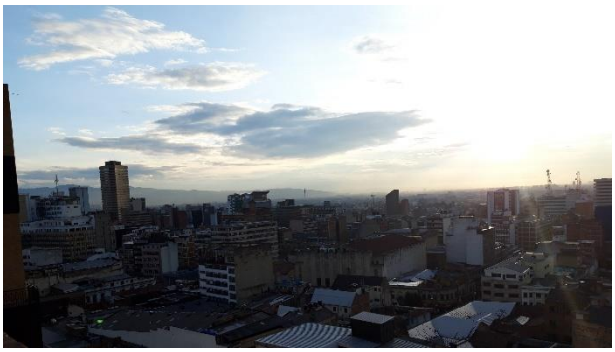


Figure 4 Pictures from left to right: Juan Umaña and Norma Forero, two early career researchers from Los Andes University in Bogota, Colombia. Credits: Ana Maria Rudas. View of Bogota city centre in a chilly evening.

After several meetings with the BIOMAC team, we concluded that my data was not suitable for an agent-based modelling. The main reason was agent-based models require of a well-known system to parameterise different relationships between the agents. If I were to build an agent-based model full of assumptions and not actual measured parameters within my system, then the outcomes from this model would be assumptions with no meaningful information. Therefore, after this visit and with a clearer understanding of what an agent-based model requires, I decided to change my modelling approach to landscape/environmental genomics modelling. Now, I am working on testing the correlation of my genomic dataset (triatomine diversity) to different landscape variables such as the elevation, road networks, land use, and environmental variables such as rain, temperature and humidity which may be playing a role on triatomine dispersal from sylvatic to domicile habitats (Figure 5). I will compare between clustering triatomine samples by locality, and habitat type (sylvatic and domicile). In addition, I am using two top analysing frameworks in landscape/environmental genomics modelling, generalised linear mixed-effects modelling and genetic-environment association analyses.

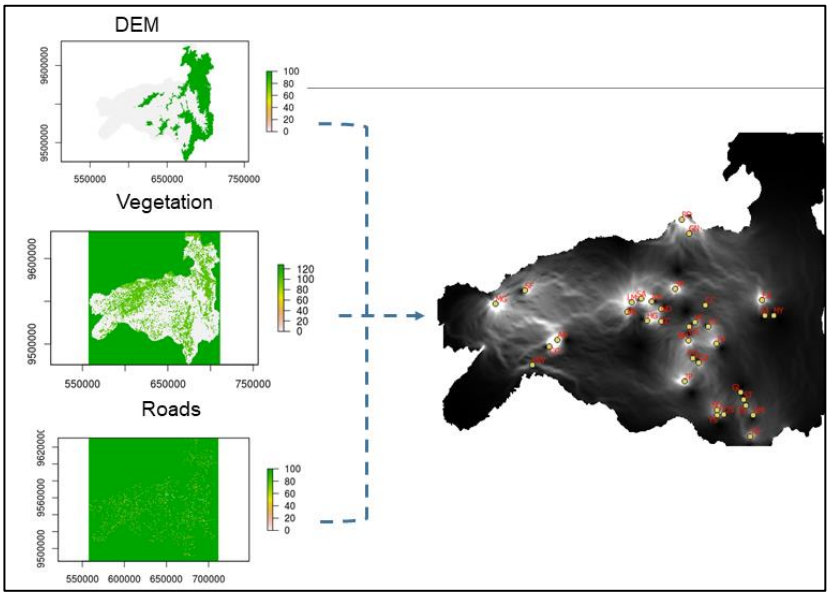


Figure 5 Landscape genomic modelling approach. Three landscape variables are combined into a resistance surface (black map) to uncover the population pairs with most connectivity (white areas on the map are the most connected). This map tells us which households and communities should be insecticide-sprayed together to avoid recolonization.

Impact of the Travel Scholarship

My visit to Los Andes University and BIOMAC was key to decide on the best direction for modelling with the available data. More importantly, the exhaustive discussions about what I need to build an agent-based model provided me with plans to collect information such as social interviews to understand people movements, *R. ecuadoriensis* hosts abundance and other factors involve in disease transmission. It is likely those ideas will be the core for future fellowship applications which can be done in collaboration with BIOMAC/Los Andes University members. I am sure this collaboration would not be possible without my visit to Los Andes University in Bogota, Colombia. This collaboration is key for my current research given the need of diverse mathematical approaches to understand the data that epidemiologist like me collect in the field. Starting collaboration with one of the top Universities in Colombia will bring enormous advantages in my career as tropical disease epidemiologist.

Overall, my postgraduate experience in this very active research centre in Los Andes University, the Biomedical faculty, was satisfying as I met numerous early career researchers working from neuroscience to nanoparticles for medical applications. Visiting a different research group helped me to feel more confident in different research settings and learn to work in teams with people from a different background from the one I have experienced in Glasgow. I am still maintaining communication with Dr Cordovez and his team while I am finishing with the landscape/modelling analyses.

In terms of my personal experience, being away in such a contrasting country allowed me to learn many things about the Colombian culture and history. I visited the famous Gold museum with a huge collection of gold ancient pieces from the original indigenous people in Colombia. One of my favourite experiences was trying the Colombian cuisine and having freshly made “tinto” (how coffee is called in Colombia) in one of the many artisanal coffee shops. In my free time, I self-funded a trip to one of the most well-preserved and protected natural gems in Colombia, the Tayrona National Park. Home of the most incredible fauna where the indigenous Tayrona people still live by one of the most beautiful Caribbean white-sand beaches (Figure 6). Thanks to the Jim Gatheral Travel Scholarship I was able to have a fantastic experience which will remain during the rest of my research career and personal life.

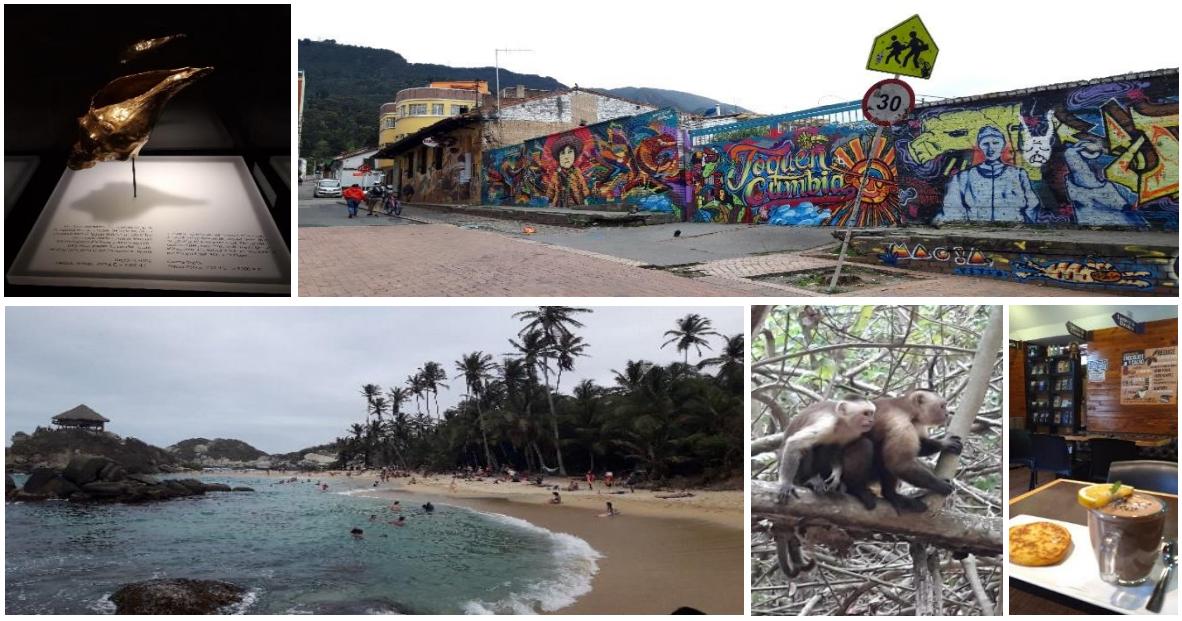


Figure 6 Pictures from left to right and top to bottom: Gold shell at the Gold museum in Bogota, street in Bogota city centre, beach at Tayrona National Park, monkey family at Tayrona National Park, Colombian arepa and hot cocoa.