

## Interactive web application to teach population genetics

The COVID-19 pandemic not only forced educational institutions to shift teaching from face-to-face to online but also had detrimental repercussions on students' mental health, including depression and anxiety. These repercussions ultimately result in deficits in learning, attention, comprehension and retention.

To restore the confidence and abilities of students, it is necessary to develop and adopt new teaching and learning strategies to guarantee the academic progression of the generations of students affected by the pandemic.

Web applications, or simply web apps, are becoming critical resources to improve teaching and learning strategies. Web apps offer a customisable environment that can include interactive activities and visually appealing information. Furthermore, web apps are very accessible tools since all that is needed is a computer with internet access.

This project will develop an interactive web app to complement classes on population genetics at the University of Canberra and as an accompanying learning tool for the R package *dartR*, a genetic analysis platform used to inform conservation.

The objectives of this project go beyond presenting concise and quality information on population genetics. The web app will include exercises based on real-time computer simulations allowing students to explore different population genetic models and manipulate their assumptions and parameters. These simulation exercises will provide a fluid and dynamic presentation of complex population genetics concepts displayed as students move sliders, enter specific values, or click buttons.

Additionally, the web app will include creative game modules such as "Tic-Tac-Toe", "Hangman", and matching games to help students review the knowledge acquired in the different modules. The games could be scored, and the students could only access the next module if they got a specific number of points.

The innovative approach used in this project will engage students, and, as a result, they will more easily understand complex concepts in population genetics. Presenting the course on a web app offers them opportunities to review a concept multiple times.

The project will use the R package Shiny (<https://shiny.rstudio.com>), a platform for building web-based applications.

The capabilities of this approach are exemplified by the project "Book Of Apps for Statistics Teaching" (BOAST), developed by undergraduate students at Penn State University:

<https://shinyapps.science.psu.edu>

As the BOAST project showed, this type of project can be scalable by involving students in developing the web app. In the future, this project could be extended to include workshops, summer camps or a specialised class to teach interested students the skills necessary to extend and improve the web app, such as coding and a deeper understanding of selected population genetic concepts. This approach could be used to develop similar web apps for other subjects and other universities.

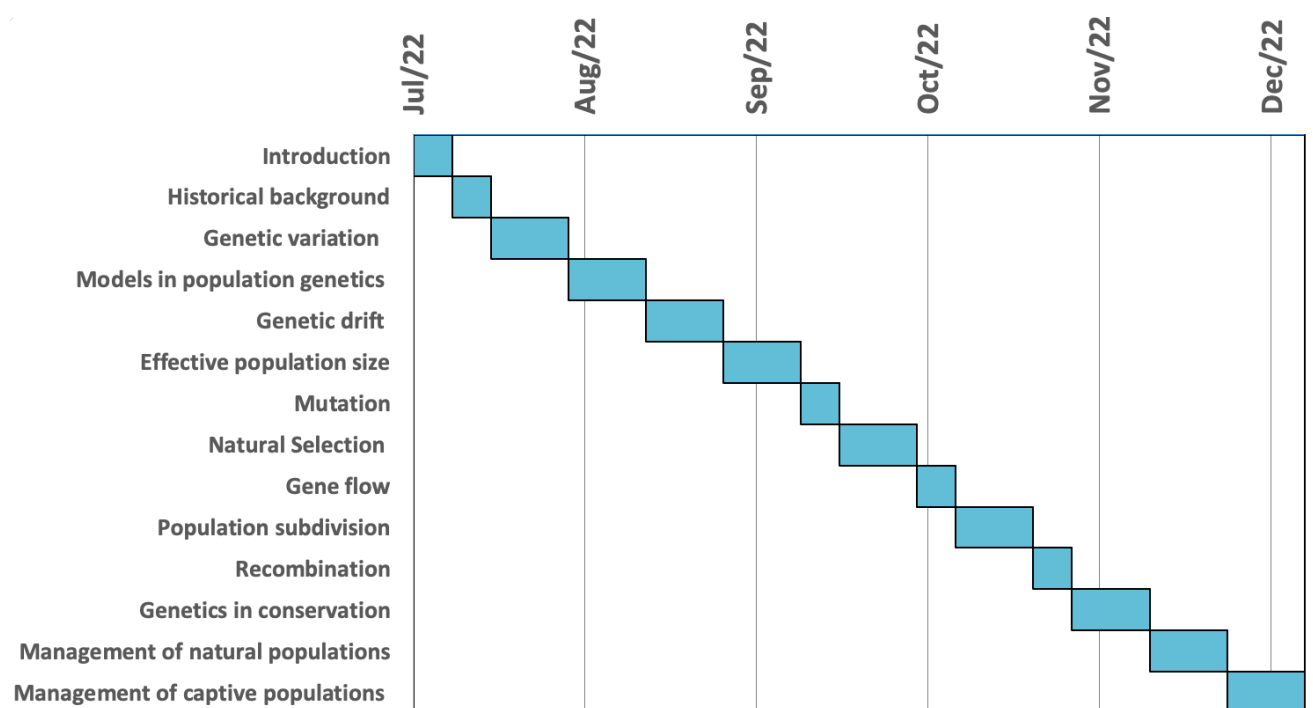
## Budget

The web application will be hosted at [www.shinyapps.io](http://www.shinyapps.io) for ten months using the basic service, which includes 500 active hours per month. The first two months of the project will be used to develop a working webpage. After this period, the web application will be deployed and updated as the different sections are finished.

Dr Mijangos will dedicate 5 hours per week to developing the project for 23 weeks.

Concept	Amount	Units	Cost	Total
Dr Mijangos salary	115	Working hours (including on-cost rates)	\$ 80.24	\$ 9,227.60
Hosting services	10	Monthly fee	\$ 55.01 (\$39 US)	\$ 550.10
<b>Total</b>				<b>\$ 9,777.70</b>

## Timeline



### Capacity of the nominee to deliver the project

The nominee, Dr Luis Mijangos, has a PhD in population genetics from the University of New South Wales. His PhD supervisors, Prof Sherwin, Dr Holleley and Prof Nichols, are recognised leaders in population genetics. During his PhD, Dr Mijangos developed a powerful computer-simulation model to explore theoretical and applied questions.

Dr Mijangos is currently employed at the University of Canberra, developing the R package “dartR”. This software is a new but already established genetic analysis platform used to inform conservation that has been downloaded more than 100,000 times. Dr Mijangos has had a transformational impact on the functionality of dartR and its uptake by a large and growing community. His work resulted in the release of the second version of dartR. In this position, Dr Mijangos has had the opportunity to know up close dartR users' requirements and difficulties in analysing their genetic data.

Dr Mijangos has supported and advised Master's and PhD students at the University of Sydney and the University of Canberra.