

MIGUEL L. GRAU

PERSONAL STATEMENT

I am a bioinformatic researcher working at Okinawa Institute of Science and Technology in Japan during the last four years. My main task consisted in the analysis of Next Generation Sequencing data, especially focused in the evolution aspects.

I design pipelines to solve a huge variety of ecological questions. These tasks include the use of illumina/pacbio data to perform new assemblies, transcriptome analysis/annotation, SNPs population genomics studies, phylogenetics, analysis of positive selection genes, mitochondrial genomes and proteins analysis across distinct related species, among others.

The pipelines make use of multiple software tools, as well as our own libraries and scripts, using mainly (and not only) Python and R.

EDUCATION & CERTIFICATION

MASTER OF SCIENCE IN BIOINFORMATICS & BIOSTATISTICS. UNIVERSITY OF BARCELONA. 2014-2016.

Computational Genomics, Omics data analysis, Regression analysis, Statistical inference, Molecular and Structural biology, Multivariate analysis, Functional genomics, Computer programming, R, Python.

BSC IN COMPUTER SYSTEMS ENGINEERING. COMPUTER SCIENCE. UNIVERSITAT JAUME I. 2017-2011

Advanced programming, Design of databases, Data structure, Advanced mathematics, Statistics.

SPECIALIZATION PROGRAMING COURSE IN IOS (200H). UNIVERSITAT JAUME I. 2012-2013

Advanced programming, Design of databases, Data structure, Advanced mathematics, Statistics.

PROGRAMING COURSE. ADVANCED JAVA (80H). UNIVERSITAT JAUME I. 2012

Java Server Pages (JSP), XML, Servlets, DB access with JDBC.

PROGRAMING COURSE. PHP (40H). UNIVERSITAT JAUME I. 2009

JOB EXPERIENCES

RESEARCH TECHNICIAN. BIOINFORMATICS. OKINAWA INSTITUTE OF SCIENCE AND TECHNOLOGY. JAPAN.

2013 – July 2017

Build pipelines to analyze NGS data for the [Ecology and Evolution Unit](#).

**RESEARCH TECHNICIAN. GROUP OF PHOTOVOLTAIC AND OPTOELECTRONIC DEVICES.
UNIVERSITY JAUME I. SPAIN**

2010 – 2013

Java desktop applications, Design of web-tools for characterization of photovoltaic cells. Technical support for researchers, #C external libraries developing.

FELLOWSHIP. LAB TECHNICIAN. DEPARTMENT OF PHYSICS. UNIVERSITY JAUME I. SPAIN

2009 – 2010

Java applets.

PUBLICATIONS

- *S.D. Aird, N.J da Silva, L. Qiu, A. Villar-Briones, V. Aparecida Saddi, M. Pires de Campos Telles, M.L. Grau and A.S. Mikheyev.* Coralsnake Venomics: Analyses of Venom Gland Transcriptomes and Proteomes of Six Brazilian Taxa. *Toxins* 2017 Jun 8;9(6). pii: E187. doi: 10.3390/toxins9060187
- *A.S. Mikheyev, A. Zwick, M.J.L. Magrath, M.L. Grau, L. Qiu, Y.N. Su, D. Yeates.* Museum genomics confirms that the Lord Howe Island stick insect survived extinction. *Current Biology*. Oct 2017. doi: <http://dx.doi.org/10.1016/j.cub.2017.08.058>

CONTRIBUTIONS

- *M. Helmkampf, A.S. Mikheyev, Y. Kang, J. Fewell and J. Gadau.* Gene expression and variation in social aggression by queens of the harvester ant *Pogonomyrmex californicus*. *Molecular Ecology*, 25: 3716–3730, 2016
- *C. Morandin, M.M.Y. Tin, S. Abril, C. Gómez, L. Pontieri, M. Schiøtt, L. Sundström, K. Tsuji, J.S. Pedersen, H. Helanterä and A.S. Mikheyev.* Comparative transcriptomics reveals the conserved building blocks involved in parallel evolution of diverse phenotypic traits in ants. *Genome Biology* 17:43, 2016
- *G. Fischer, F.L. Azorsa, F.H. Garcia, A.S. Mikheyev, E.P. Economo.* Two new phragmotic ant species from Africa: morphology and next-generation sequencing solve a caste association problem in the genus *Carebara* Westwood. *ZooKeys* 525: 77-105, 2015
- *C.R. Smith S. Helms Cahan, C. Kemena, S.G. Brady, W. Yang, E. Bronberg-Bauer, T. Eriksson, J. Gadau, M. Helmkampf, D. Gotzek, M. O. Miyakawa, A.V. Suarez and A.S. Mikheyev,* How do genomes create novel phenotypes? Insights from the loss of the worker caste in ant social parasites, *Molecular Biology and Evolution*, 32: 2919-2931, 2015
- *M.M.Y. Tin, F.E. Rheindt, E. Cros and A.S. Mikheyev,* Degenerate adaptor sequences for detecting PCR duplicates in reduced representation sequencing data improve genotype calling accuracy. *Molecular Ecology Resources*. 15:2 329-336, 2015.

- *A.S. Mikheyev and M.M.Y. Tin. A first look at the Oxford Nanopore MinION sequencer. Molecular Ecology Resources. 14: 1097–1102. 2014*

REFERENCES

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