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MIGUEL L. GRAU

PERSONAL STATEMENT

I am a bioinformatic researcher working at the Disease Ecology and Evolutionary Genetics group, in the Department of Microbiology at Monash University. My main task consists in the analysis of Next Generation Sequencing data, especially focused in the evolution aspects of pathogens.

I design pipelines to solve a huge variety of questions. These tasks include the use of illumina/ionTorrent/pacbio/nanopore data to perform new assemblies, within host population analysis (iSNV), phylogenetics, virus-host interactions studies, analysis of factors affecting transmission of pathogens (bottlenecks), identification of positive selection, among others.

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

EDUCATION & CERTIFICATION

CLOUD SYSTEMS AND SERVICES. SPECIALIZATION. UNIVERSITAT OBERTA DE CATALUNYA. 2019-PRESENT.

Cloud computing. IaaS: AWS, Azure, Google, etc. PaaS (Heroku) & SaaS. DevOps (Docker).
Encloud computing & security.

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. UNIVERSITAT JAUME I. 2012-2013

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

PROGRAMING COURSE. ADVANCED JAVA. UNIVERSITAT JAUME I. 2012

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

PROGRAMING COURSE. PHP. UNIVERSITAT JAUME I. 2009

JOB EXPERIENCES

TECHNICAL OFFICER. BIOINFORMATICS. DEPARTMENT OF MICROBIOLOGY AT MONASH UNIVERSITY. AUSTRALIA.

2017 – Present

Pipelines design for NGS data, especially focused in the evolution aspects of pathogens, for the [Disease Ecology and Evolutionary Genetics lab.](#)

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

2013 – 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

- *D. Vijaykrishna, Y.M. Deng, M.L. Grau, M. Kay, A. Suttie, P. Dussart, I.G. Barr, E.A. Klaason.* Genomic diversity of influenza A H7N4 virus in Cambodian poultry. 2019. Submitted
- *M. Linster, C. Donato, M. G Mah, M.L. Grau, J. G Low, E.E. Ooi, Y.C.F. Su, G. JD Smith, D. Vijaykrishnaa.* Genetic diversity of respiratory enteroviruses and rhinoviruses in febrile adults, Singapore 2007–2013. 2019. Submitted
- *M.A. Techer, R.V. Rane, M.L. Grau, J. M. K. Roberts, S.T. Sullivan, I. Liachko, A.K. Childers, J.D. Evans, A.S. Mikheyev.* Genomic analyses of sibling honey bee ectoparasitic mite species show divergent strategies of adaptation. bioRxiv 2019 Jan doi: 10.1101/512988
- *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>
- *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

CONTRIBUTIONS

- *M. Helmkamp, 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. Helmkamp, 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

CONFERENCES

11TH ANNUAL CENTERS OF EXCELLENCE FOR INFLUENZA RESEARCH AND SURVEILLANCE (CEIRS) NETWORK MEETING. NEW YORK, USA. 2018. (POSTER PRESENTATION).

REFERENCES

PROF. VIJAYKRISHNA DHANASEKARAN

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PROF. FRANCISCO FABREGAT

Group of Photovoltaic and Optoelectronic Devices, University Jaume I. Spain.
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