Gregorio Alanis-Lobato

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I am a computational biologist using network science, machine learning and data analytics to study complex biological systems and provide data-driven guidance to wet-lab biologists for more informed experimental design. I enjoy working with interdisciplinary teams on the development of ground-breaking solutions to challenging problems.

SKILLSET

Technical		Soft	
Programming/Scripting	R, Python, C/C++, shell, git, Nextflow	Project management	Project planning, staffing, implementation and control. Agile for research with Atlassian.
Data wrangling and analysis	tidyverse, tidymodels, pandas, scikit-learn, igraph, Matplotlib, Gephi, Cytoscape	Team work and leadership	Part of various collaborative projects, supervision of students, conference and event organisation
Web development	JavaScript, HTML, CSS, PHP, Shiny	Creativity and engineering	Development of novel methods to approach complex problems
Databases, HPC, Cloud	SQL, MySQL, Slurm, AWS S3 and EC2, Docker, Singularity	Communication and writing	Presentations in international conferences, publications in scientific journals, teaching
Office suites/Text editors	MS Office, iWork, Markdown, $\text{L\!A\!T\!E\!X}$, vi	Intercultural and interdisciplinary skills	Work with multidisciplinary groups, part of an international team
Operating systems	Linux, macOS, Windows	Languages	Spanish (native), English (fluent), German (B1)

PROFESSIONAL EXPERIENCE

December 2020-Present	**Principal Computational Biologist for Central Nervous System Disease Research and Research Beyond Borders** Boehringer Ingelheim Pharma, Biberach an der Riß, Germany Supervisor: Dr. Stefano Patassini • Leading the Indication Expansion Matrix team, driving the identification and pursuit of new therapeutic opportunities to maximise the potential of the company's compounds. • Automated drug target characterisation. • Development of novel therapeutic concepts in collaboration with CNS scientists. • Data-driven drug target identification based on network propagation and integration of diverse data modalities (e.g. omics, genetics, brain imaging, behavioural data) • Establishment and testing of data processing and analysis pipelines for novel technologies (e.g. spatial omics, AAV capsid screening). • Supervision of one postdoctoral fellows and CRO scientists.

January 2019-December 2020	**Postdoctoral Training Fellow at the Human Embryo and Stem Cell Laboratory** The Francis Crick Institute, London, UK Supervisor: Dr. Kathy Niakan • Integration of diverse omics data and use of machine learning, network science and systems biology for mapping and inspection of the protein networks that regulate the development of the human pre-implantation embryo. • Mapping and analysis of the human pre-implantation embryo proteome. • Estimation of the frequency of CRISPR-Cas9-induced on-target damage in human embryos. • Establishment and standardisation of pipelines for omics data analysis. • Support to other lab members with bioinformatics and statistical analyses. • Responsible for training sessions on statistics and data analysis tools for lab members.
February 2015-December 2018	**Research associate at the Computational Biology and Data Mining Research Group** Johannes Gutenberg Universität, Mainz, Germany Supervisor: Prof. Miguel Andrade • Integration of bio-data, analysis of the latent geometry of the human protein interaction network, bias reduction in protein network datasets, development of bioinformatic web tools. • Postdoc representative at the Institute of Molecular Biology.
July 2014-December 2014	**Research consultant at the KAUST Environmental Epigenetics Programme** Department of Bioscience, King Abdullah University of Science and Technology, Thuwal, Makkah, Saudi Arabia Supervisor: Prof. Valerio Orlando • Systems-based analysis of RNA-Seq and hCAGE data from human skeletal muscle cell differentiation time series. Healthy donors and Duchenne Muscular Distrophy patients were compared with the aim to detect the set of transcripts whose expression over time contributes the most to their differences.
Summer 2013	**Intern at the Centre for Complex Network Research** Department of Physics, Northeastern University, Boston, MA, USA Supervisor: Prof. Albert-László Barabási Project title: *Towards the construction of a reliable genetic interaction map for human* • Explored different data integration approaches for the construction of a reliable human genetic interaction network.
Summer 2010	**Intern at Cisneros Lab** Department of Chemistry, Wayne State University, Detroit, MI, USA Supervisor: Prof. Andrés Cisneros Project title: *Analysis of the impact of P. falciparum's LCRs in protein folding regulation by coarse grained molecular dynamics* • Studied the role of low-complexity regions in the correct folding of *P. falciparum's* proteins by means of molecular dynamics tools such as VMD. These analyses are important for drug design against malaria.
July 2008-July 2009	**Intern at IBM** Service Management Automation, Integrated Technology Delivery, IBM, Mexico City, Mexico • Administered the Server Resource Manager tool in the servers of >5 IBM clients, which allowed IBM to comply with the service level agreement contracted by these clients. • Administered the Virtual Server Administration tool in the servers of a couple of IBM clients, which allowed for remote server administration of IBM software in client machines.
Sept. 2005-July 2008	**Software Developer at the National Paediatric Hospital "Federico Gómez"** Information Systems Department, Mexico City, Mexico • Migrated the database serving the hospital at the time from MS SQL Server 2000 to MS SQL Server 2005. • Developed the Patient Classification System, which improved the attention of the >30,000 patients that visit the hospital annually. • Made walk-in patient attention more efficient by training medical staff in the Classification System. • Provided training to >20 administrative employees and medical staff in Office tools and medical software every 6 months, making them more updated and competent personnel. • Started the development of the current Surgery Scheduling System that serves the >9,000 patients that undergo surgery in the hospital annually.

EDUCATION

King Abdullah University of Science and Technology, Thuwal, Saudi Arabia
PhD in Computer Science, 2011-2014
Dissertation title: *Exploitation of complex network topology for link prediction in biological interactomes*
Dissertation advisor: Prof. Timothy Ravasi

King Abdullah University of Science and Technology, Thuwal, Saudi Arabia
MSc in Computer Science, 2009-2010
Research focus: Computational Biosciences

Instituto Politécnico Nacional, Escuela Superior de Cómputo, Mexico City, Mexico
Computer Systems Engineering, 2005-2009
Dissertation title: *Application of self-organising maps to the protein folding problem*
Dissertation advisor: Prof. Jorge Rosas-Trigueros

AWARDS AND RECOGNITIONS

Science
- Academic Excellence Award, King Abdullah University of Science and Technology, (Saudi Arabia, 2013-2014).
- 1st place in the 1st King Abdullah University of Science and Technology Graduate Research Symposium (Saudi Arabia, 2011).
- King Abdullah University of Science and Technology Provost Award (Saudi Arabia, 2009).
- King Abdullah University of Science and Technology Graduate Fellowship Scholarship (Saudi Arabia, 2009).
- Acknowledgement of Academic Excellence in Computer Systems Engineering (Mexico, 2005).
- Winner of the Knowledge Olympiad, lunch with Mexican president at the time (Mexico, 1999).

Athletics
- Gold Medal, Discus Throw, Distrital Olympic Games (Mexico, 2001).
- Silver Medal, Discus Throw, National Olympic Games (Mexico, 1999).

PUBLICATION LIST

Google Scholar Profile: https://scholar.google.de/citations?user=nAGRhSEAAAAJ&hl=en

* Publications in which I am a first co-author.

✉ *Publications in which I am corresponding author.*

Peer-reviewed papers

2024
Zhang, C., Dulinskas, R., Ineichen, C., Greter, A., Sigrist, H., Li, Y., **Alanis-Lobato, G.**, Hengerer, B., Christopher R Pryce, C. R. Chronic stress deficits in reward behaviour co-occur with low nucleus accumbens dopamine activity during reward anticipation specifically. *Communications Biology* 7(1), 966.

✉**Alanis-Lobato, G.**, Bartlett, T. E., Huang, Q., Simon, C. S., McCarthy, A., Elder, K., Snell, P., Christie, L., Niakan, K. K. MICA: a multi-omics method to predict gene regulatory networks in early human embryos. *Life Science Alliance* 7(1).

2023
Fan, W., Jurado-Arjona, J., **Alanis-Lobato, G.**, Péron, S., Berger, C., Andrade-Navarro, M. A., Falk, S., Berninger, B. The transcriptional co-activator Yap1 promotes adult hippocampal neural stem cell activation. *The EMBO Journal* 42(11), e110384.

Madur, L., Ineichen, C., Bergamini, G., Greter, A., Poggi, G., Cuomo-Haymour, N., Sigrist, H., Sych, Y., Paterna, J-C., Bornemann, K., Viollet, C., Fernandez-Albert, F., **Alanis-Lobato, G.**, Hengerer, B., Pryce, C.R. Stress deficits in reward behaviour are associated with and replicated by dysregulated amygdala-nucleus accumbens pathway function in mice. *Communications Biology* 6(1), 422.

2022
Gurbuz, O., **Alanis-Lobato, G.**, Picart-Armada, S., Sun, M., Haslinger, C., Lawless, N., Fernandez-Albert, F. Knowledge Graphs for Indication Expansion: An Explainable Target-Disease Prediction Method. *Front. Genet.* 13 (814093).

2021   Bower, O. J., McCarthy, A., Lea, R. A., **Alanis-Lobato, G.**, Zohren, J., Gerri, C., Turner, J. M. A. & Niakan, K. K. Generating CRISPR-Cas9-mediated null mutations and screening targeting efficiency in human pluripotent stem cells. *Current Protocols* 1(8), e232.

Alanis-Lobato, G., Zohren, J., McCarthy, A., Fogarty, N. M. E., Kubikova, N., Hardman, E., Greco, M., Wells, D., Turner, J. M. A. & Niakan, K. K. Frequent loss of heterozygosity in CRISPR-Cas9-edited early human embryos. *PNAS* 118 (22), e2004832117.

2020   Gerri, C., McCarthy A., **Alanis-Lobato, G.**, Demtschenko, A., Bruneau, A., Loubersac, S., Fogarty, N. M. E., Hampshire, D., Elder, K., Snell, P., Christie, L., David, L., Van de Velde, H., Fouladi-Nashta, A. A. & Niakan, K. K. Initiation of a conserved trophectoderm program in human, cow and mouse embryos. *Nature* 587, 443-447.

Kastano, K., Erdös, G., Mier, P., **Alanis-Lobato, G.**, Promponas, V. J., Dosztányi, Z. & Andrade-Navarro, M. A. Evolutionary study of disorder in protein sequences. *Biomolecules* 10, 1413.

✉**Alanis-Lobato, G.**, Möllmann, J. S., Schaefer, M. & Andrade-Navarro, M. A. MIPPIE: the mouse integrated protein–protein interaction reference. *Database* 2020, baaa035.

Dallago, C., Goldberg, T., Andrade-Navarro, M. A., **Alanis-Lobato, G.** & Rost, B. Visualizing human protein-protein interactions and subcellular localizations on cell images through CellMap. *Current Protocols in Bioinformatics* 69(1), e97.

Laidou, S., **Alanis-Lobato, G.**, Pribyl, J., Raskó, T., Tichy, B., Mikulasek, K., Tsagiopoulou, M., Oppelt, J., Kastrinaki, G., Lefaki, M., Singh, M., Zink, A., Chondrogianni, N., Psomopoulos, F., Prigione, A., Ivics, Z., Pospisilova, S., Skladal, P., Izsvák, Z., Andrade-Navarro, M. A. & Petrakis, S. Nuclear inclusions of pathogenic ataxin-1 induce oxidative stress and perturb the protein synthesis machinery. *Redox Biology* 101458.

Wamaitha, S., Grybel, K., **Alanis-Lobato, G.**, Gerri, C., Ogushi, S., McCarthy, A., Mahadevaiah, S., Healy, L., Lea, R., Molina-Arcas, M., Devito, L., Elder, K., Snell, P., Christie, L., Downward, J., Turner, J. & Niakan, K. K. IGF1-mediated human embryonic stem cell self-renewal recapitulates the embryonic niche. *Nature Communications* 11, 764.

Della Valle, F., Thimma, M. P., Caiazzo, M., Pulcrano, S., Celii, M., Adroub, S., Liu, P., **Alanis-Lobato, G.**, Broccoli, V. & Orlando, V. Transdifferentiation of mouse embryonic fibroblasts into dopaminergic neurons reactivates LINE-1 repetitive elements. *Stem Cell Reports* 14(1), 60-74.

2019   Geiß, C., **Alanis-Lobato, G.**, Andrade-Navarro, M. A., Régnier-Vigouroux, A. Assessing the reliability of gene expression measurements in very-low-numbers of human monocyte-derived macrophages. *Sci. Rep.* 9, 17908.

*El Amrani, K., **Alanis-Lobato, G.**, Mah, N., Kurtz, A. & Andrade-Navarro, M. A. Detection of condition-specific marker genes from RNA-seq data with MGFR. *PeerJ* 7, e6970.

2018   Härtner, F., Andrade-Navarro, M. A. & ✉**Alanis-Lobato, G.** Geometric characterisation of disease modules. *Applied Network Science* 3(10).

✉**Alanis-Lobato, G.**, Mier, P. & Andrade-Navarro, M. A. The latent geometry of the human protein interaction network. *Bioinformatics* 34(16), 2826-2834.

2017   Hildebrandt, A., **Alanis-Lobato, G.**, Voigt, A., Zarnack, K., Andrade-Navarro, M. A., Beli, P. & König, J. Interaction profiling of RNA-binding ubiquitin ligases reveals a link between posttranscriptional regulation and the ubiquitin system. *Sci. Rep.* 7, 16582.

Mier, P., **Alanis-Lobato, G.** & Andrade-Navarro, M. Context characterization of amino acid homorepeats using evolution, position and order. *Proteins: Structure, Function, and Bioinformatics* 85(4) 709-719.

Mier, P., **Alanis-Lobato, G.** & Andrade-Navarro, M. Protein-protein interactions can be predicted using coiled coil co-evolution patterns. *Journal of Theoretical Biology* 412, 198-203.

Alanis-Lobato, G., Andrade-Navarro, M. & Schaefer, M. HIPPIE v2.0: enhancing meaningfulness and reliability of protein-protein interaction networks. *Nucleic Acids Research* 45(D1) D408-D414.

2016   ✉**Alanis-Lobato, G.**, Mier, P. & Andrade-Navarro, M. Manifold learning and maximum likelihood estimation for hyperbolic network embedding. *Applied Network Science* 1(10).

✉**Alanis-Lobato, G.** & Andrade-Navarro, M. Distance distribution between complex network nodes in hyperbolic space. *Complex Systems* 25(3), 223-236.

✉**Alanis-Lobato, G.**, Mier, P. & Andrade-Navarro, M. Efficient embedding of complex networks to hyperbolic space via their Laplacian. *Sci. Rep.* 6, 30108.

2015 *,✉**Alanis-Lobato, G.**, Cannistraci, C.V., Eriksson, A., Manica, A. & Ravasi, T. Highlighting nonlinear patterns in population genetics datasets. *Sci. Rep.* 5, 8140*.*

2013 **Alanis-Lobato, G.,** Cannistraci, C.V. & Ravasi, T. Exploitation of genetic interaction network topology for the prediction of epistatic behavior. *Genomics* 102(4), 202-208.

*Cannistraci, C.V., **Alanis-Lobato, G.** & Ravasi, T. Minimum curvilinearity to enhance topological prediction of protein interactions by network embedding. *Bioinformatics* 29, i199-i209.

*Cannistraci, C.V., **Alanis-Lobato, G.** & Ravasi, T. From link-prediction in brain connectomes and protein interactomes to the local-community-paradigm in complex networks. *Sci. Rep.* 3, 1613.

Book chapters

2020 **Alanis-Lobato, G.** & Schaefer, M. Generation and interpretation of context-specific human protein-protein interaction networks with HIPPIE. *Chapter in the book Protein-Protein Interaction Networks* 2074, 135-144.

Reviews & editorials

2018 ✉**Alanis-Lobato, G.** & Petrakis, S. Protein interaction networks and disease: highlights of the 3rd Challenges in Computational Biology Meeting. *Genomics and Computational Biology* 4(1), e100056.

2015 ✉**Alanis-Lobato, G.**, Mining protein interactomes to improve their reliability and support the advancement of network medicine. *Front. Genet.* 6(296)*.*

Pre-prints and others

2024 Menchero, S., Barrington, C., **Alanis-Lobato, G.**, Varsally, W., Niakan, K. K., Turner, J. M. A. Marsupial single-cell transcriptomics provides an atlas of developmental heterochrony. *bioRxiv* 2024.05.26.595746, https://doi.org/10.1101/2024.05.26.595746

2017 ✉**Alanis-Lobato, G.** & Andrade-Navarro, M. A reliable and unbiased human protein network with the disparity filter. *bioRxiv* 207761, https://doi.org/10.1101/207761

2014 **Alanis-Lobato, G.,** Cannistraci, C.V. & Ravasi, T. Exploring the Genetics Underlying Autoimmune Diseases with Network Analysis and Link Prediction. *Proceedings of the MECBME 2014*, 167-170.

CONTRIBUTED TALKS AND POSTERS

Alanis-Lobato, G., Zohren, J., McCarthy, A., Fogarty, N. M. E., Kubikova, N., Hardman, E., Greco, M., Wells, D., Turner, J. M. A. & Niakan, K. K. Frequent loss of heterozygosity in CRISPR-Cas9-edited early human embryos. Genome Engineering Seminar Series at Harvard Medical School (remote), October 2021 (Talk).

Alanis-Lobato, G., Bartlett, T. & Niakan, K. K. *Multiomics-based inference of cell type-specific regulatory networks in early human embryos.* Complex Network Conference (remote), Madrid, Spain, December 2020 (Poster).

Härtner, F., Andrade-Navarro, M. & **Alanis-Lobato, G.** *Geometric characterisation of disease modules.* NetMed18, Paris, France, June 2018 (Talk).

Alanis-Lobato, G. & Andrade-Navarro, M. *A reliable and unbiased human protein network with the disparity filter.* Joint Boehringer Ingelheim Research Beyond Borders-IMB Symposium, Mainz, Germany, November 2017 (Talk).

Alanis-Lobato, G., Mier, P. & Andrade-Navarro, M. *GAPI: A web tool for the geometric analysis of the human protein interactome.* Mapping Complexity, Foundations and Applications of Network Geometry, Barcelona, Spain, November 2017 (Talk).

Alanis-Lobato, G., Mier, P. & Andrade-Navarro, M. *The latent geometry of the human protein interaction network.* NetSci-X, Tel Aviv, Israel, January 2017 (Talk).

Alanis-Lobato, G., Mier, P. & Andrade-Navarro, M. *Efficient hyperbolic embedding of complex networks via the spectral decomposition of their Laplacian.* 7th International Workshop on Complex Networks, Dijon, France, March 2016 (Talk).

Alanis-Lobato, G., Cannistraci, C.V. & Ravasi, T. *Exploring the Genetics Underlying Autoimmune Diseases with Network Analysis and Link Prediction.* Middle East Conference on Biomedical Engineering 2014, Doha, Qatar, February 2014 (Talk).

Alanis-Lobato, G., Cannistraci, C.V. & Ravasi, T. *Learning new biology from GWAS by means of network analysis and link prediction.* Human Genome Meeting 2013, Singapore, April 2013 (Poster).

Alanis-Lobato, G., Cannistraci, C.V. & Ravasi, T. *A novel graph dissimilarity index for prediction of genetic interactions.* European Conference in Computational Biology (ECCB) 2012, Basel, Switzerland, September 2012 (Poster).

Alanis-Lobato, G., Cannistraci, C.V. & Ravasi, T. *Prediction of genetic interactions using network topology.* Intelligent Systems for Molecular Biology (ISMB) 2012, Long Beach, CA, USA, July 2012 (Poster).

Cannistraci, C.V., **Alanis-Lobato, G.** & Ravasi, T. *Minimum curvilinearity to address high-throughput protein-protein interaction experiments.* ISMB/ECCB 2011, Vienna, Austria, July, 2011 (Poster).

Cannistraci, C.V., **Alanis-Lobato, G.** & Ravasi, T. *Minimum curvilinearity to address high-throughput protein-protein interaction experiments.* King Fahd University of Petroleum and Minerals Graduate Seminar, Dhahran, Saudi Arabia, May 2011 (Talk).

Cannistraci, C.V., **Alanis-Lobato, G.** & Ravasi, T. *Minimum curvilinearity to address high-throughput protein-protein interaction experiments.* 1st KAUST Graduate Research Symposium, Thuwal, Saudi Arabia, May 2011 (Talk).

Alanis-Lobato, G. T. *Self-organising maps applied to protein structure classification.* ECCB 2010, Ghent, Belgium, September 2010 (Poster).

Alanis-Lobato, G., Rodriguez-Garibay, G. & Rosas-Trigueros, J. *Self-organising maps applied to protein structure prediction.* USA-Mexico Workshop in Biological Chemistry, Mexico City, Mexico, March 2009 (Poster).

CONFERENCES ORGANISED/CHAIRED

November 2017   *3rd Challenges in Computational Biology - Protein Interaction Networks and Disease*, Johannes Gutenberg Universität, Mainz, Germany
Organisers: Prof. Miguel Andrade-Navarro; **Gregorio Alanis-Lobato, PhD**; Jean-Fred Fontaine, PhD; Spyros Petrakis, PhD

February 2014   *Middle East Conference on Biomedical Engineering 2014*, Hilton, Doha, Qatar
Chair of Bioinformatics and Systems Biology Session

January 2013   *Workshop in network theory and paradigms in complex networks*, King Abdullah University of Science and Technology, Saudi Arabia
Invited speakers: Prof. Marián Boguñá (University of Barcelona), Prof. Jesper Tegnér (Karolinska Institute) and Dr. Carlo V. Cannistraci (King Abdullah University of Science and Technology)
Organisers: **Gregorio Alanis-Lobato, MSc**; Prof. Timothy Ravasi; Prof. David Keyes

TEACHING

Johannes Gutenberg Universität *2016, 2017, 2018*   Responsible for the *Network Biology* and *Data Wrangling with R* sessions of the master-level course *Proteinbiochemie und Bioinformatik* taught by Prof. Miguel Andrade-Navarro (~30 students).

Johannes Gutenberg Universität *2017*   Responsible for the *Network Biology* session of the postgraduate-level course *Einführung in die Bioinformatik* taught by Prof. Susanne Gerber (~20 students).

Johannes Gutenberg Universität *2017, 2018*   Teaching assistant at the *Protein Structure* sessions of the undergraduate-level course *Biostatistik und Bioinformatik* taught by Prof. Miguel Andrade-Navarro (~120 students).

SUPERVISION

Dhananjay Bhaskar
Yale University
Sep 2023-Aug 2024

- Yale-Boehringer Ingelheim Biomedical Data Science Postdoctoral Fellow
- Geometric deep learning on knowledge graphs for Indication Expansion

Zhe Sun
Yale University
Apr 2020-Aug 2024

- Yale-Boehringer Ingelheim Biomedical Data Science Postdoctoral Fellow
- Prediction of phenotypic outcomes based on the integration of brain imaging, omics and genetics data with statistical models.

David Lingard
University of Warwick
Jul-Sep 2020

- Summer student
- An interactive web resource of gene expression in the human pre-implantation embryo
- Currently an undergraduate student at the University of Warwick

Jannik Möllman
Johannes Gutenberg
Universität
Sep-Dec 2018

- Undergraduate student
- Prediction of signal transduction pathways by navigation of the multi-layer protein-protein interactome
- Currently a master student of Bioinformatics at the Johannes Gutenberg Universität

Alexandra Pogorelskaya
Johannes Gutenberg
Universität
Summer 2018

- Summer student
- Assessment of the relationship between high gene ontology semantic similarities and human protein-protein interactions
- Currently a master student of Bioengineering and Bioinformatics at the Lomonosov Moscow State University

Franziska Härtner
Johannes Gutenberg
Universität
Oct 2016-May 2018

- Master student
- Geometric characterisation of disease modules
- Currently a bioinformatician at the Institute of Medical Biostatistics, Epidemiology and Informatics, Mainz

Abel Hodelin-Hernández
Johannes Gutenberg
Universität
Apr-Oct 2017

- Undergraduate student
- Network geometry and machine learning to predict protein interaction effects
- Currently a bioinformatician at the Universitätsmedizin Mainz

EXTERNAL FUNDING

2020   *British Society for Cell Biology.* Summer vacation studentship to host David Lingard (University of Warwick). £2000 to develop the 8-week project entitled *An interactive web resource of gene expression in the human pre-implantation embryo.*

REFERENCES

Prof. Kathy K. Niakan
Mary Marshall and Arthur Walton Professor of Reproductive Physiology
Director, Centre for Trophoblast Research
Chair, Strategic Research Initiative in Reproduction
Physiological Laboratory, Downing Street, Cambridge CB2 3EG, UK
e-mail: kkn21@cam.ac.uk

Prof. Miguel Andrade Navarro
Professor, Faculty of Biology
Head of the Computational Biology and Data Mining Research Group
Johannes Gutenberg Universität and Institute of Molecular Biology, Mainz, Germany
e-mail: andrade@uni-mainz.de

Prof. Timothy Ravasi
Professor, Marine Sciences
Head of the Marine Climate Change Unit
Okinawa Institute of Science and Technology, Okinawa, Japan
e-mail: timothy.ravasi@oist.jp