



**GeoBio-Center^{LMU}
Report 2016 / 2017**

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Contents

Welcoming note.....	4
Members of the GeoBio-Center ^{LMU}	5
The European Innovative Training Network “Comparative Genomics of Non-Model Invertebrates” (ITN IGNITE)	8
Publications 2016 & 2017.....	16

Welcoming note

Dear Ladies and Gentlemen, dear Colleagues,

I am delighted to present the annual report of the GeoBio-Center for 2016 and 2017. Both years were - again - two successful years for the GeoBio-Center to bring scientists together for collaborative projects, exchange of expertise, and dissemination of knowledge.

The GeoBio-Center co-hosted in 2016 the 17th annual meeting of the *Gesellschaft für Biologische Systematik* (GfBS) and welcomed 160 delegates in the Paleontological Museum Munich, and likewise in 2017 the 15th Annual Meeting of the European Association of Vertebrate Palaeontologists (EVAP). Both meetings were very well received - thanks a lot to all members involved.

Also, the board of the GeoBio-Center changed and we could welcome Prof. Dr. Jochen Heinrichs (LMU Botany) as a new board member after the retirement of Prof. Dr. Günther Heubl.

It is also a great pleasure for me to announce the successful establishment of the Marie Skłodowska-Curie Innovative Training Network (ITN) "IGNITE" at the GeoBio-Center, funded with about 3.8 million Euro by the Horizon 2020 program of the European Commission. The overarching training and research goals of this ITN are to train the next generation of invertebrate genomicists to improve the sampling and analysis of invertebrate genomes from undersampled branches of the invertebrate animal tree of life and to extend the toolbox for their analysis, including the development and deployment of innovative production-level software to go beyond current frontiers of the field. You will find more on this ITN on the following pages.

In this respect, I would like to continue encouraging the members to consider the GeoBio-Center as the host institution for upcoming joint project applications.

For their excellent contributions in the past years, I would like to thank and congratulate all members of the GeoBio-Center - looking forward to continuing working with you!

With the very best regards,

Prof. Dr. Gert Wörheide
Spokesman of the GeoBio-Center^{LMU}



*Prof. Dr. Gert Wörheide
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The European Innovative Training Network “Comparative Genomics of Non-Model Invertebrates” (ITN IGNITE)



The IGNITE consortium with members from 12 European academic and non-academic organisations.

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Project information: <http://www.itn-ignite.eu>

Duration of the project: 01/2018 - 06/2022 (European Union's Horizon 2020 research and innovation program under the Marie Skłodowska-Curie grant agreement No 764840)

Participating organisations:

- Ludwig-Maximilians-Universität München (Germany)
- Centro Interdisciplinar de Investigação Marinha e Ambiental (Portugal)
- European Molecular Biology Laboratory (Germany)
- Université Libre de Bruxelles (Belgium)
- University of Bergen (Norway)
- National University of Ireland Galway (Ireland)
- University of Bristol (UK)
- Heidelberg Institute for Theoretical Studies (Germany)
- Staatliche Naturwissenschaftliche Sammlungen Bayerns (Germany)

- Institut National De La Recherche Agronomique Rennes (France)
- University College London (UK)
- University of Zagreb (Croatia)
- Pensoft Publishers (Bulgaria)
- Queensland Museum (Australia)
- Institut National de Recherche en Informatique et en Automatique (France)
- Institut Pasteur (France)
- Leibniz Supercomputing Centre Munich (Germany)
- Alphabiotoxine (Belgium)
- [Era-7 (Spain) left the consortium due to bankruptcy]

1. Background

The “invertebrates” – animals without a backbone – encompass more than 95% of the planet’s animal biodiversity. They cover all phyla and play crucial roles in the functioning of marine and terrestrial ecosystems, and as providers of essential ecosystem services that positively affect humans and their environments.

However, invertebrates are a surprisingly underexplored reservoir of genetic resources. Genome sequencing across the diversity of animal lineages so far is highly skewed with > 80% of published genomes deriving from vertebrates and arthropods [1]. Especially the content and architecture of genomes of invertebrates, besides well-studied model taxa like *Caenorhabditis elegans* or *Drosophila melanogaster*, remain poorly known or understood.

Invertebrate genomics is a particularly challenging research area due to their sheer diversity of phenotypes and lifestyles. Invertebrates are frequently small, their life history is often unknown, and they are in many cases associated with (microbial) symbionts. Their genomes are typically highly heterozygous and oftentimes contain a high number of repetitive elements, making genome assembly challenging. Hence, “one-size-fits-all” strategies designed for model organisms are difficult or often impossible to apply. The few non-insect/non-model invertebrate genomes already known are tremendously diverse, with sizes ranging between just above 15 Mb in a highly reduced parasitic orthonectid species [2] to over 2.7 Gigabases in cephalopods [3].

A comprehensive understanding of the genomic factors shaping animal complexity and lineage-specific innovations is still lacking due to the patchiness of genome sampling efforts so far. This knowledge is needed to improve our understanding about animal evolution and diversity, their capability to provide ecosystem services and bioproducts of environ-



mental and socio-economic benefit, including the discovery of novel drugs and biomimetic materials in a rapidly changing world.

ESRs gathering in a poster session during a network-wide training event.

Although recent advances in sequencing technologies and bioinformatics, coupled with increasing computing power, pandered the analysis of a larger diversity of non-model invertebrate genomes, the greatest challenge is the paradigm shift from generating increasingly large amounts of sequence data to delivering high-quality analyses. Consequently, the next generation of scientists needs to be trained to analyse a considerably larger diversity of high-quality animal genomes, especially from phyla that were neglected until now.

Europe is home to significant world-leading expertise in invertebrate genomics, but research and training efforts in invertebrate genomics have, until recently, been uncoordinated across the continent. The Innovative Training Network “Comparative Genomics of Non-Model Invertebrates” (ITN IGNITE), funded through the Marie Skłodowska-Curie Actions of the European Horizon 2020 framework program, has begun to fill this gap. IGNITE bundles the expertise of 13 lead investigators (“beneficiaries”) across Europe to jointly train 15 internationally recruited Early-Stage Researchers (ESRs) in all aspects of genomics, to further our understanding of invertebrate genome diversity and evolution and to excellently prepare them for the job market both in academia and industry.

2. Objective and training goals

IGNITE’s overarching research goals are to improve the sampling and analysis of invertebrate genomes, especially from undersampled branches of the animal tree of life, and to extend the toolbox for their analysis, including the development and deployment of innovative production-level software beyond the current state-of-the-art.



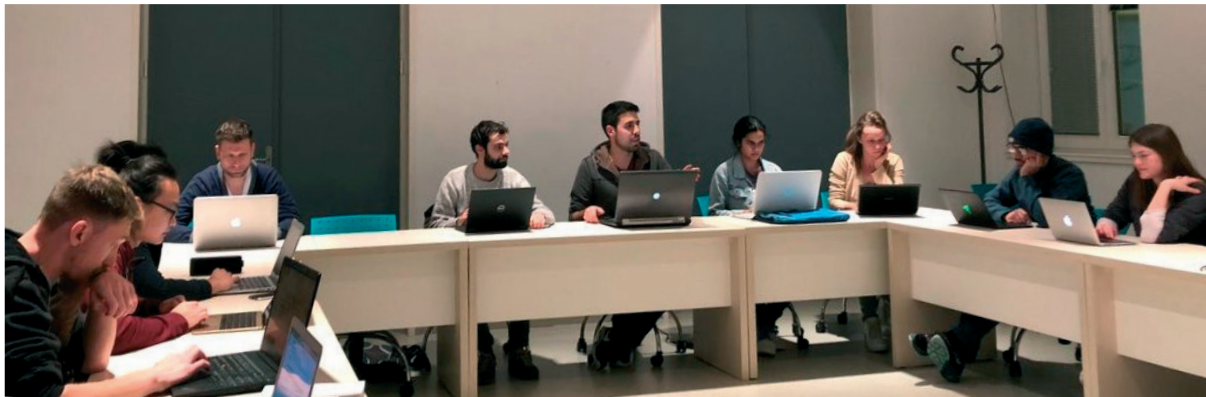
IGNITE ESRs and the project manager during the student-organised bioinformatics workshop at the Mediterranean institute for Life Sciences (MedILS) in Split (Croatia)

IGNITE's core training objectives are:

1. to convey broad interdisciplinary knowledge in organismal biology, animal physiology, ecology, biogeography, evolution, and genomics;
2. to provide the technical laboratory skills required for genomics;
3. to impart technical computing skills in programming and bioinformatic pipeline development;
4. to build experience in effective dissemination and communication of results to target audiences; and
5. to provide young researchers with a unique set of relevant academic and non-academic transferable skills to enhance human resource development and entrepreneurship; and
6. to establish a strong and long-lasting European and international network in invertebrate genomics.

These training objectives are being reached by means of three levels of training.

First, ESRs receive in-depth local training-by-research through individual scientific doctoral projects and through participation in complementary skills and scientific course-level training offered at each of the beneficiaries' institutions. The 15 individual research projects revolve around four broad topics: i) Function – genomes and the organism, ii) Ecology – genomes in the environment [4], iii) Evolution – genomes through Earth's history [5], iv) Bioinformatics – new tools to study genomes and to publish genomic data [6-8].



Second, in so-called yearly “network-wide training events” (NTEs, a sort of summer schools), inter/multidisciplinary, intersectoral, and transferable-skill training is provided to the whole group of ESRs by different beneficiaries (depending on topic) and/or external trainers. Four such NTEs have been performed in the course of the project:

IGNITE ESRs poring over a coding exercise during the student-organised bioinformatics workshop.

- The first IGNITE Network-Training Event (NTE-1) took place at the Mediterranean Institute for Life Sciences (MedILS) in Split, Croatia, in summer 2018. The event provided the first opportunity to gather all the participants of IGNITE, Principal Investigators (PIs), Early Stage Researchers (ESRs) and collaborators. A combination of lectures and practical hands-on experience provided a base knowledge to all the participants. As part of the activities, the ESRs had the opportunity to collect samples (i.e. planktons and sea organisms) and perform molecular biology experiments instructed by some of the PIs. A series of lectures were presented by PIs and external scientists, in which they outlined the main challenges in the field. ESRs further received training in complementary skills, including teamwork, communication, diversity and time management.
- NTE-2 took place in Spring 2019 at the Observatoire Océanologique de Banyuls-sur-mer (France). Lecturers and instructors for this event came from six different countries to teach ESRs in diverse genomics-related topics: genome assembly, deep learning in genomics, automatic and manual annotation of genomes, omics data integration. In addition, multiple complementary skills topics were on the agenda, including gender dimension in research, research integrity, data ownership and open science. During the event, ESRs had the opportunity to present the first results during a poster session.
- NTE-3 was held in summer 2019 in a hotel up the hills in Zagreb (Croatia). The theory dominated event included lectures by PIs on statistics in R and general statistical principles, evaluation of genome quality, genome annotation, transcriptomics including real-life examples, metagenomics, comparative genomics, and

available computational resources for ESR projects. Two external speakers, Tomislav Domazet-Lošo and Momir Futo, provided insights on phylostratigraphy, and the external expert advisor Jose Lopez (Nova Southeastern University, USA) enlightened the IGNITE consortium on the activities of the Global Invertebrate Genomics Alliance (GIGA) and other genomic initiatives around the world. The event again included a poster session with impressive results from ESRs. Each ESR also gave a short talk to present her/his background. The event was complemented by a general discussion on best practises in scientific communication, including tips on scientific writing. NTE-3 was also the official mid-term review meeting by the European Commission, attended by the Project Officer responsible for the ITN from Brussels.

- Due to the impacts of the Covid-19 pandemic, NTE-4 was held as an online-only event in early 2021. Scientific lectures by PIs included various topics: systematic errors in phylogenetics, comparative phylogenomics of non-bilaterian animals, evolutionary genomics & biotechnology, phylogenetics & molecular evolution, biogeography, evolutionary assembly of the neuronal machinery, and evolution of haplosclerid sponges. Prof. John Hooper, an international authority on sponges (phylum Porifera) and emeritus Professor of the IGNITE partner organisation Queensland Museum (Australia), talked about his research and career as a taxonomist. A Q&A session on phylogenetics was then led by Prof. Alexandros Stamatakis, who had recorded and shared several lectures on the subject with IGNITE ESRs during part I of NTE-4 in Sept. 2020. Prof. Denis Tagu and Dr. Anthony Bretaudeau from INRAE presented their project on citizen science for manual annotation of genomes. The external expert advisors Prof. Toni Gabaldón (CRG Centre for Genomic Regulation, Barcelona) and Jose Lopez, lectured on “comparative genomics” and “genetics and microbiome of the model sponge *Cynachyrella*”, respectively. Mariya Dimitrova, ESR-15 from the SME Pensoft (Bulgaria), gave two presentations about her research on the linking of biodiversity data and the publication of omics data in omics data papers. Finally, two half-day sessions were reserved for a practical scientific writing tutorial provided by an external expert.

In addition to NTEs, a “bioinformatics workshop” was self-organised by the ESRs. In this workshop (in Dec. 2018 in Split), the ESRs took advantage of their diverse backgrounds in bioinformatics and applied computer sciences. The “student-teach-student” workshop helped establish basic and advanced bioinformatics skills, especially for those ESRs without prior experience in this field. Topics included bash scripting, programming in R and Python, and sequence assembly. Within a week full of classes, lectures, and networking, students had the great opportunity to develop bioinformatics skills, exchange experience and share

research ideas. Lectures and hands-on exercises from the workshop are openly available at: <https://itn-ignite.github.io/ESRs-Programming-and-Bioinformatics-Workshop/>.

The third level of training are interdisciplinary and/or intersectoral secondments, where each ESR carried out topical work related to his/her doctoral project in another beneficiaries' lab for a period of normally one month, rounding up the training program.

3. Impact on science and society

Well-trained genomicists are in increasing demand in universities, research institutions, as well as in software, biomedical, and pharmaceutical industries. Through their excellent interdisciplinary and intersectoral training spanning from biology to bioinformatics and computer science, IGNITEs graduates will be in a prime position to take up leadership roles in both academia and industry in order to drive the complex changes needed to advance the sustainability of our knowledge-based society and economy. Genomics and bioinformatics are still to a large extent male-dominated fields and IGNITE aspires to train a more inclusive generation of scientists. IGNITE is fully devoted to FAIR (Findable, Accessible, Interoperable, Reusable) data and open science principles and promotes, through various measures and activities, gender equality and diversity.

4. Outlook

Although the IGNITE program goes a long way in training the next generation of highly skilled genomicists, large international endeavours such as the Earth Biogenome Project (EBP) or the European Reference Genome Atlas (ERGA) initiative call for additional in-depth coordinated and focused training programs in genomics. The training measures implemented and experiences made in IGNITE may serve as a template for the future development of such training programs.

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