



ALL-ATLANTIC OCEAN RESEARCH ALLIANCE

Creating an Atlantic Ocean Community by Implementing
the Galway and Belém Statements

AA-BIOTECMAR Report: Biotech Bioinformatics Tools and Applications Workshop



**BUILDING AN ALL ATLANTIC
OCEAN COMMUNITY**
Implementing the Belém Statement



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ALL-ATLANTIC JOINT PILOT ACTIONS

Following a year-long collaborative process among more than 70 stakeholders at the Atlantic level, the All-Atlantic Ocean Research Alliance Multi-Stakeholder Platform, divided into 5 sub-multi-stakeholders platforms, identified more than 1000 initiatives towards strengthening marine research and innovation collaboration at the Atlantic level, 56 gaps and 79 needs/recommendations to achieve the All-Atlantic Ocean Research Alliance ambition, guided by a total of 20 Strategic Objectives, 20 Operational Objectives, and 10 Key Performance Indicators.

Based on these findings and on the idea of collaboration, alignment, and use of existing resources, they have developed six ambitious and long-term collaborative Joint Pilot Actions:

- [All-Atlantic Training Platform \(AA-TP\)](#)
- [All-Atlantic Aquaculture Technology and Innovation Platform \(AA-ATiP\)](#)
- [All-Atlantic Marine Biotechnology Initiative \(AA-BIOTECMAR\)](#)
- [All-Atlantic Data Enterprise 2030 \(AA-DATA2030\)](#)
- [All-Atlantic Blue Schools Network \(AA-BSN\)](#)
- [All-Atlantic Marine Research Infrastructure Network \(AA-MARINET\)](#)

This report is developed by the **All-Atlantic Marine Biotechnology Initiative (AA-BIOTECMAR)** Joint Pilot Action, that is a collective effort to support the development of new and emerging technologies intended to improve human health, encouraging the sustainable use of marine resources through marine biotechnology and advanced technologies in aquaculture, food production, fisheries management, and environmental monitoring. AA-BIOTECMAR is promoting collaboration among countries of the Belem and Galway statements through workshops and technical visits, identify best methodologies for technology transfer, promote outreach and engage ocean leaders to support the blue growth.

This report is a deliverable in scope of JPA AA-BIOTECMAR, Task 2. BIOTECMAR Training Course aiming to train early career leaders from different countries, particularly from Africa and Latin America on marine biotechnology issues.



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SUMMARY

1. Summary

The AA-BIOTECMAR Training Course: Biotec Bioinformatics Tools and Applications was a collaborative online event for experts, researchers, and stakeholders, focusing on marine microbiomes and related bioinformatics tools. The workshop's primary goal was to promote knowledge sharing and collaboration, in line with the AANChOR project's broader mission of fostering research partnerships across the Atlantic. In marine microbiome research, bioinformatics plays a crucial role in analysing and interpreting large amounts of genetic data obtained from diverse microbial communities. During the training course several topics were covered: microbiome and computational approaches; the role of microbiomes in natural environments and how climate change is altering the biochemical cycle; bioinformatics workflow systems applied to bacterial genomes; technicalities of bioinformatics; importance of pipeline construction and execution, using programming languages; power of metagenomics in conveying taxonomic classification, functional annotation, and genome recovery; mining genomes from metagenomic data; application of genomics to non-cultivable microorganisms; programs to access MAGs for analysis and measurement of metagenomics data; introduction to microbiome and virome data analysis tools; as well as exploration of fungal diversity and work towards algal strain improvement. During the discussion, topics such as the microbiome and the computational approach in research were explored. The application of bioinformatics workflow systems in bacterial genomics was also mentioned, highlighting the power and versatility of metagenomics as a technique that provides taxonomic classification, functional annotation, and genome recovery. In summary, bioinformatics is an indispensable tool that will likely lead to new discoveries and insights into the intricate interactions between marine microorganisms and their surroundings as the field continues to evolve.



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2. Introduction

The Biotec Bioinformatics Tools and Applications Workshop was a two-day online international event held on April 21st and 22nd, 2022 jointly organized by the Federal University of Rio de Janeiro (UFRJ) and the University of Brasilia (UnB), and coordinated by Professor Kruger. The event aimed to present the latest findings in the field of bioinformatics, focusing on marine microbiomes and related bioinformatics tools, and it was attended by 104 participants. The event had six presenters throughout the two days.

The first day counted with the presence of Dr. Thulani Makhalanyane, Associate Professor of the Department of Biochemistry, Genetics and Microbiology in the University of Pretoria, presenting an introduction to the Southern Ocean microbiomes and the research of his group using bioinformatics approaches. The second guest speaker was Dr. Georgios Papas, Professor at the University of Brasilia in the department of Cell Biology, who covered the bioinformatics workflow systems applied to bacterial genomics. The third guest speaker was Dr. Matt Olm, postdoctoral researcher at Stanford University, who presented his work on genome-resolved population genomics and strain-level comparisons.

The second day of the workshop counted with the presence of Dr. Diogo Tschoeke, Professor at the Biomedical Engineering Program at the Federal University of Rio de Janeiro, presenting an introduction to Metagenomics and the methodology/programs to access Metagenome Assembled Genomes. Afterwards, Dr. Karthik Anantharaman, Assistant Professor in the Department of Bacteriology at the University of Wisconsin-Madison, Dr. Patricia Tran, and Dr. Zhichao Zhou made a presentation on microbial biogeochemical interactions and viruses. Finally, the last speaker, Dr. Andrei Stecca Steinforff, made a presentation on fungal and algal program science and tools. Table 1 shows the presenters, their country and a brief description of their research.

Presenter	Country	Topic of research
Thulani Makhalanyane (University of Pretoria)	South Africa	Elucidating Southern Ocean microbiomes
Georgios Pappas Jr. (University of Brasilia)	Brazil	Introduction to bioinformatics workflow systems applied to bacterial genomics
Matt Olm (Stanford University)	United States of America	Genom-resolved population genomics and strain-level comparisons
Diogo Tschoeke (Federal University of Rio de Janeiro)	Brazil	Mining genomes from Metagenomic data: Introduction and application
Karthik Anantharaman (University of Wisconsin-Madison)	United States of America	Using metagenomics to study microbial biogeochemistry, interactions, and viruses



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Patricia Tran (University of Winconsin-Madison)	United States of America	Using metagenomics to study microbial biogeochemistry, interactions, and viruses
Zhichao Zhou (University of Winconsin-Madison)	United States of America	Using metagenomics to study microbial biogeochemistry, interactions, and viruses
Andrei Stecca Steindorff (Joint Genome Institute)	United States of America	Mycocosm tools for comparative genomics

Table 1: Presenters of the AA-BIOTECMAR Workshop - Biotec Bioinformatic Tools and Applications



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3. Overview

Throughout the workshop, the presenters spoke about different aspects of the bioinformatics and biotechnology when dealing with marine research.

Dr. Thulani Makhalanyane shared his work, giving an introduction of the microbiome and the computational approach that he has been using it in his research. He followed his presentation explaining the role of microbiomics in natural environments and how climate change is changing the biochemical cycle, focusing in four main thematic areas: Microbial processes, adaptation and applications; Microbial ecology; Microbiomics of geographically strategic marine environments; and Human gut microbiomes. He focused his presentation in the Southern Ocean, which is an important regulator of nutrient's transportation across oceans, explaining the typical methods that he implements in his lab:

- When using fix cells as samples, he proceeds to flow cytometry in order to estimate the abundance;
- When using filter and DNA extraction, he can: (a) proceed to 16S rRNA sequencing and then use bioinformatics and statistical analysis; (b) proceed to shotgun sequencing, which demand bioinformatics and statistical analysis for the reconstruction of MAGs (Metagenome-Assembled Genomes), for function annotation and metagenome assembly, such as SPAdes.

Finally, Dr. Thulani showed that there is a smaller effect on early spring phytoplankton bloom on microbial communities due to the constant effect of nutrients, the resilience of the microbiomes, insufficient organic matter and time for niche development.

The second presentation was made by Dr. Georgios Pappas and Felipe Almeida. It was about computational workflows under the theme of "Introduction to bioinformatics workflow systems applied to bacterial genomics". Dr. Pappas presented the workflows from the end-user perspective, directing the conversation for biologists. He explained some technicalities on bioinformatics and highlighted the role of Linux system, as well as Python for modelling, and Conda as an environment management system. Furthermore, he talked about the importance of using frameworks for pipeline construction and execution, using programming languages such as Snakemake, docker and softwares such as Nextflow. He talked about the workflows in bioinformatics. Felipe Almeida spoke about the workflows in Nextflow software.

The last speaker of the first day of the event was Dr. Matt Olm, who gave a presentation about "Genom-resolved population genomics and strain-level comparisons". Dr. Matt affirmed that Metagenomics is a powerful and versatile technique that conveys taxonomic classification, functional annotation and genome recovery. By the means of metagenomics, it is possible to differentiate strain comparisons in microdiversity using PopANI, which stresses the role of bioinformatics and biotechnology in data analysis process. He finished his presentation talking about some practicalities in the field, going from an overview of analysis techniques, such as K-mer based, gene-based and genome-based, how to detect genomes in metagenomes,



how to generate a genome database, dereplicate a genome database and how to run in it inStrain, a program that carries mapping files, which can be used for comparison purposes.

The second day of the workshop started with the presentation of Dr. Diogo Tschoeke, who introduced “Mining genomes from Metagenomic data: Introduction and Application”. Dr. Tschoeke started introducing metagenomics, its definition and overall data of the field, reinforcing the idea that only 10% of microorganisms on the planet have been characterized and described. He explained that metagenomics is also an application of genomics to non-cultivable microorganisms, and that programs to access MAGs are needed to analyse and measure metagenomics data. In order to do so, users can try MetaBAT pipeline for pre-processing, MetaBAT for different calculations.

Dr. Karthik explained the Anantharaman Microbiome Laboratory (AML) work, done at the intersection of the fields of biogeochemistry, microbial and viral systems ecology, and computational biology: 1. The roles of microbes and viruses in driving sulphur metabolism in environmental and human systems; 2. How to use viruses to potentially modulate microbial communities.

Patricia Tran and Zhichao Zhou continued Dr. Karthik’s presentation by introducing the analysis of microbiome and virome data. They introduced the term “Virome” – metagenomes specifically target the viral fraction of the environmental samples. However, the essence of their presentation was to provide information on two main tools “Metabolic” and “Vibrant”, the workflows connected to their usage, as well as their inputs/outputs, and examples of their application. In short: “Metabolic” is a free and open-source tool that enables metabolic and biogeochemical analyses for genomes and microbial communities. It also enables the visualisation of biogeochemical cycling potential and community-scale functional networks. In turn, “Vibrant” - Virus Identification By iterative ANnoTation- identifies bacterial and archaeal (prokaryotic) viruses from metagenomic assemblies and MAGs. In conclusion, Patricia Tran and Zhichao Zhou stated that bioinformatic tools development allows us to explore genomic data. Specifically, “Metabolic-C”, “Metabolic-G” and “Vibrant” focus on the roles of bacteria in biogeochemical cycle.

The last speaker of the event, Dr. Andrei Stecca Steindorff made a presentation on Fungal and Algal program Science and Tools. His presentation was constituted by a first part focused on science, the ongoing bioenergy research in his laboratory, including the exploration of Fungal diversity and the work toward Algal strain improvement; and a second part focused on the tools for Eukaryotic genome annotation pipeline and the Genome portals, namely MycoCosm and Phycocosm.



4. Concluding Remarks

During the workshop different aspects of the bioinformatics and biotechnology when dealing with marine research were approached. The microbiome and the computational approach in research were discussed, as well as the use of bioinformatics workflow systems applied to bacterial genomics. The metagenomics was recognized as a powerful and versatile technique that conveys taxonomic classification, functional annotation and genome recovery. The scientific knowledge exchanged between speakers can improve sequencing data analyses that are already widely performed in partner laboratories. There is the need to improve and increase the use of computational analysis and invest in teaching bioinformatics to students.



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5. Workshop Agenda



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All-Atlantic Ocean Research Alliance

BIOTEC BIOINFORMATICS TOOLS AND APPLICATIONS WORKSHOP

Save the date
APRIL 21 - 22, 2022
Brasília, Brazil Standard Time 9AM - 12AM
ON YOUTUBE CHANNEL: AANchor Workshop
[Youtube AANchor Workshop](#)

SPEAKERS

April 21, 2022


- Thulani P. Makhalanyane (University of Pretoria)
- Georgios Papas (University of Brasilia - UnB)
- Matt Olm (Stanford University)

April 22, 2022

- Diogo Tschoeke (Federal University of Rio de Janeiro)
- Karthik Anantharaman, Patricia Tran, and Zhichao Zhou (University of Wisconsin - Madison)
- Andrei Stecca (Joint Genome Institute - JGI)

Free Registration

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6. Attendance List

Participants - Biotec Bioinformatics Tools and Applications Workshop			
1	Fabiano Thompson	35	Kazeem Adekunle Alayande
2	Larissa Pereira Gonçalves	36	Marcelo Soares
3	Elise Maria De Oliveira Albino	37	Luana Serra
4	Felipe Medeiros	38	João Guilherme Bochnia Küster
5	Talita Fernandes Nunes	39	Tayná Frederico
6	Luisa Coutinho Coelho	40	Gabrielle Rosa Silva
7	Matheus Fernandes Marques De Oliveira	41	Jessica Fernandes De Sousa
8	Fernanda Abreu	42	Julianna Peixoto
9	Daniel Leal Fagundes	43	Ricardo Kruger
10	Giovanna Esperidiao Dos Santos Pereira	44	Rodrigo José Bezerra De Siqueira
11	Gil Amaro Da Silva	45	Raul Alcântara Teixeira Lima
12	Sara Navarrete Bohi Goulart	46	Jacques Fouche
13	Vitória Pinheiro Balestrini	47	Jersom Henrique De Souza
14	Hannah Kaufmann Mattsson	48	Otávio Henrique Bezerra Pinto
15	Tooba Varasteh	49	Philippe De Castro Lins
16	Camille Victoria Leal	50	Rafael Da Silva Oliveira
17	Bianca De Sousa Alcântara	51	Jéssica Pinheiro Silva
18	Mayanne Aline Maia De Freitas	52	Caio Felipe Freire De Sousa
19	Raquel Diniz	53	Anderson Miguel Teixeira Feitosa
20	Olavo Da Silva Júnior	54	Patrick Romano
21	Pooja Sharma	55	Mónica Carrera
22	Caíque Martinez Neves	56	Vitória Saiki Rocha
23	Diogo Figueiredo	57	Carla Simone Vizzotto
24	Paulo Daniel Dourado E Silva	58	Alenna Crystiene Lima Farias De Sousa
25	Saurabh Kumar	59	Bruno Moreira Rosa
26	Marilize Le Roes-Hill	60	Patricia Tran
27	Luisa Dan Favilla	61	Isabel Cristina Cunha Ferreira
28	Grace Okuthe	62	Rafael Icaro Matos Vieira
29	Raeesa Bhikhoo	63	Pedro Henrique Dias Pereira
30	Abram Mahlatsi	64	João Lucas Da Silva Correia
31	Refilwe Mabeo	65	Alana Da Silva Santos
32	Mariska Kleyn	66	Maria Eduarda Chaves Ribeiro
33	Ouattara Koffi Nouho	67	Luísa Costa
34	Kabelo Stenger	68	Irvin Bryan Machado Ferraz



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70	Isabel Cristina Gomes Teixeira	88	Raquel Correia Gonçalves
71	Victoria Botella Baena	89	Donel Martins Bueno
72	Maria Frojan	90	Carla Patrícia Pereira Alves
73	Gonzalo Andres Farinango Vallejos	91	Adriana Ferreira Lima
74	Tallita Tavares	92	Kárita Cristine Rodrigues Dos Santos
75	Ana Carolina Campos Batista	93	Vinicius De Carvalho Ferreira De Lima
76	Luís Henrique Scarparo Pandolfo	94	Pedro Henrique Costa Da Paz
77	Pedro Leonardo Carvalho De Lima	95	Adekunle Raimi
78	Mayna Da Silveira Gomide	96	Deidre Van Wyk
79	Antonio Marcio Barbosa Junior	97	Lucca Albino
80	Matheus De Castro Leitão	98	Maria Efigênia Pereira
81	Cintia Marques Coelho	99	Osvaldo Bonifácio
82	Andrea Farinango Vallejos	100	Amanda Amaral
83	Gabriela Dos Santos Martins Ferreira	101	Júlia Alves Luz
84	Daniella Maria Da Silva	102	Luana Bianca Silva Dantas
85	Triveni A G	103	Ana González Abril
86	Suresh Kumar Mendem	104	Cristiane Thompson



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AA-BIOTECMAR Contact Details

Main contact: Fabiano Thompson

Email: fabianothompson1@gmail.com

Web: <https://allatlanticocean.org/jointaction/all-atlantic-marine-biotechnology-initiative>

All-Atlantic Ocean Contact Details

Coordination: FCT – Fundação para a Ciência e a Tecnologia

Email: info@allatlanticocean.org

Web: <http://www.AllatlAnticOcean.org/>

Twitter: **@AllAtlanticO**

Facebook: **@AllAtlanticOcean**

YouTube: **All-Atlantic Ocean Research Alliance**



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