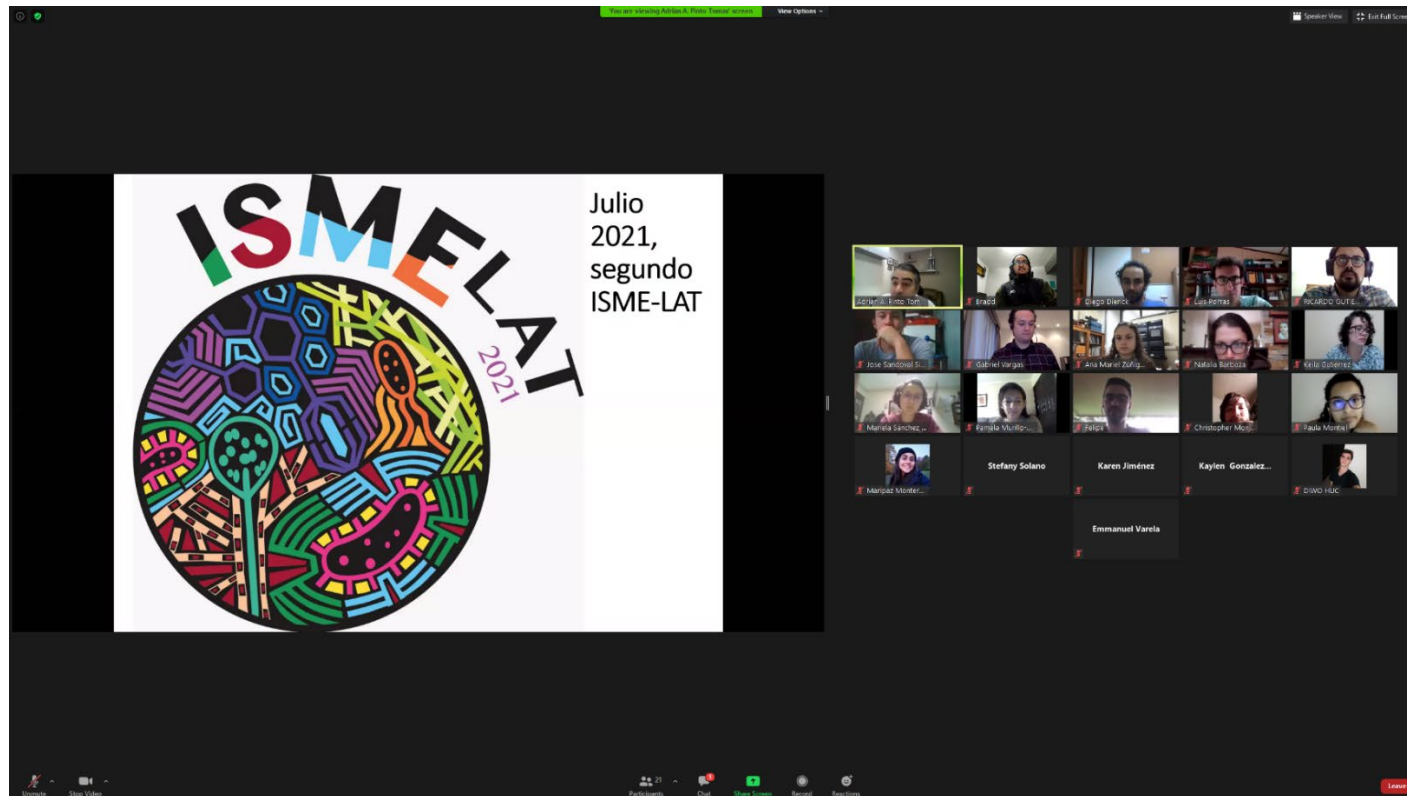UNIVERSIDAD DE COSTA RICA

CIEMIC

Centro de Investigación en **Estructuras Microscópicas**

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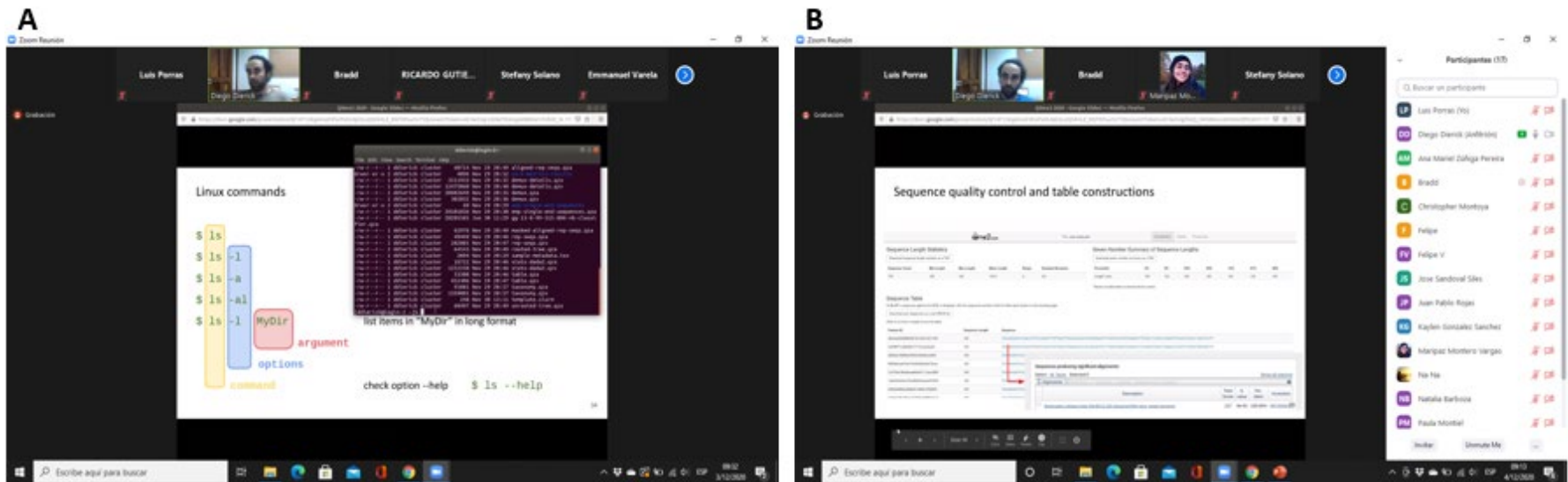
FM Facultad de **Medicina**

Workshop 1: "Introduction to metagenomic analysis in IMG" and "Microbial communities analysis using QIIME2"

Dates: December 2 – 4th, 2020
Mode: Virtual workshop
Capacity: 25 participants.
Hours: 8 am – 3 pm.

Description: During the first day Gabriel Vargas taught introductory concepts related to metagenomics. Besides, he taught different and useful tools clustered in the Integrated Microbial Genomes (IMG) platform to analyze the different genomes and metagenomes uploaded in this platform. On day 2, Diego Dierrick gave introductory concepts of microbial communities and basic microbial data analysis using the software QIIME2. On day 3, the instructors continued the data analysis exercises using QIIME 2 followed by basic visualizations in R commonly employed in microbial community analyses. Scientific literature, QIIME2, R scripts and recorded sessions were provided to all participants.

Instructors: Ph.D. Gabriel Vargas, microbiologist graduated from the University of Chicago, and postdoc in the Department of Bacteriology at the University of Wisconsin-Madison, EEUU (Laboratory of Dr. Cameron Currie). Ph.D. Diego Dierrick, Forestry engineer graduated from Ghent University, and postdoc at the University of Costa Rica.

The virtual workshop had 25 participants in total. Most of them were students and researchers/professionals from the University of Cost Rica (74 %), the Costa Rican Institute of Technology (4 %), the National University of Costa Rica (4 %), the National Center for Biotechnology Innovations (4 %), and the Banana National Coorporation (8 %). In this virtual workshop, we also had the participation of an international researcher from the University of El Salvador. Participants are interested in areas such as microbial ecology, host-microbiome interactions, plant protection, molecular biology, and bioinformatics. Based on the workshop's survey, we received positive records and feedback from the participants. In a 10 base evaluation we received records above 8.

The activity was satisfactorily completed during december 2 – 4th, 2020 (Figure 1 and 2).

ISME

Figure 1. Introduction to ISME and invitation to latinamerican ISME congress 2021 during Day 1 by Dr. Adrián Pinto Tomás, Ph.D.

Figure 2. QIIME2 sessions during day 2 (A) and day 3 (B) of the first virtual workshop taught by Diego Dierrick, Ph.D.

Workshop 2: "Introduction to phylogenomic analysis"

Dates: December 14 – 16th, 2020
Mode: Virtual workshop hired to Physalia. ISME funds were requested to support this event.
Capacity: 20 participants.
Hours: 9 am – 11 am (GMT -6).

Description: The workshop consisted in the use of the bioinformatic tool BEAST2, useful for phylogenetic and phylogenomic analyses. During the first day María Martínez did an introduction to BEAST2 and developed basic exercises using this tool. In the second day, María Martínez continued with some Bayesian inference methods employing BEAST, for example, Bayesian Skyline Plot and the Extended Bayesian Skyline Plot (EBSP). Besides, two practical sessions were conducted. In the third day, the instructor explained the MultiTypeTree package included in BEAST for Bayesian inference models and taught how to use Babette package that allows to run BEAUti2, BEAST and Tracer in the free software R. This session included two practical sessions as well.

During the afternoons, support sessions were programmed by the organizers, to clarify doubts or problems students had during the morning sessions. All workshop's sessions were recorded and given to the participants, as well as their corresponding digital participant's certificate (provided by Carlo Pecoraro from Physalia courses).

Instructor: Ph.D. María Martínez Agüero is a biologist who developed her Ph.D. in population genetics and evolutionary biology in the Pontificia Universidad Javeriana, Colombia.

The virtual workshop application reached 72 participants, however only 20 participants were chosen for this activity. Most of them are principal investigatores, one is a postdoc, and professionals from the University of Cost Rica (60 %), the Costa Rican Institute of Technology (5 %), the National University of Costa Rica (1 %), the National Center of High Technology – CENAT (10 %), and the University of Wisconsin-Madison (5%). In this virtual workshop, we also had the participation of two international participants from the University of Antioquia (Colombia) and the San Carlos University of Guatemala. Participants are interested in areas such as microbial ecology (bacteria, fungi, parasites, nematodes), genetic population of plants and animals, and molecular biology. Based on the workshop's survey, we received positive records and feedback from the participants. In a 1-10 scale. we received records above 8 in our evaluations.

ISME

The activity was satisfactorily completed during december 14 – 16th, 2020 (Figure 3 and 4).

This report covers the two first workshops as previously defined: one targeted for beginners and the second one for an intermediate level audience. The third workshop will be developed next February based on the skills obtained from the workshop "Introduction to phylogenomic analysis". This workshop will be developed by the GISiHM group.
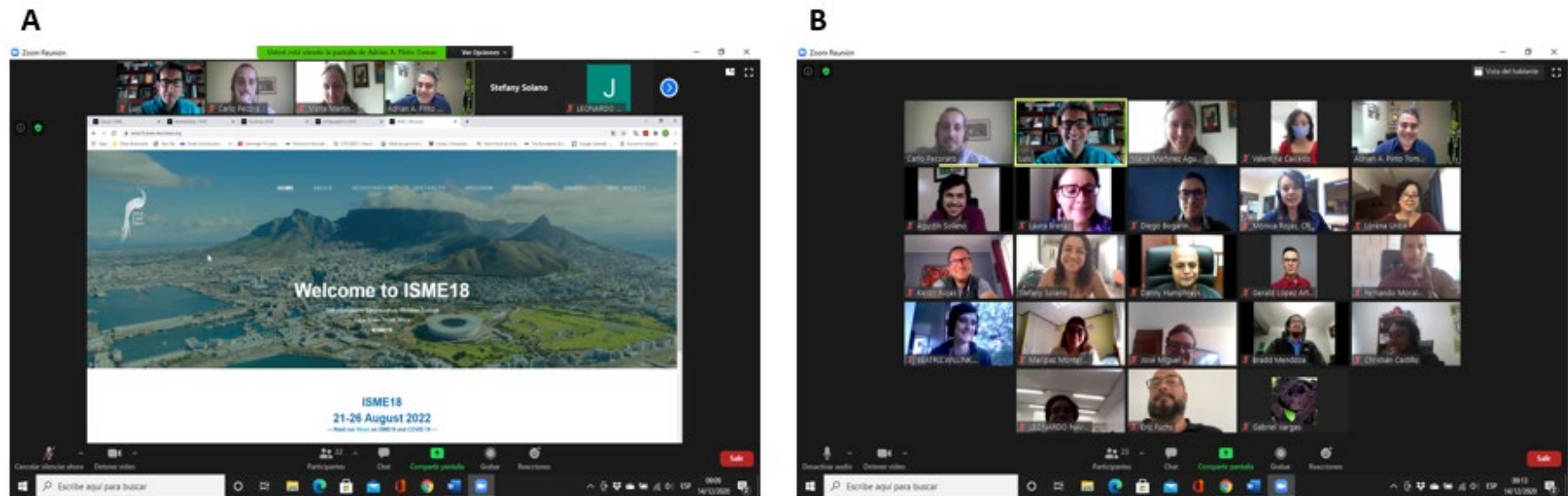
Figure 3. Introduction to ISME and invitation to ISME congress in South Africa 2022 during Day 1 by Dr. Adrián Pinto Tomás, Ph.D. (A). Participants from the virtual workshop in the Zoom session (B).
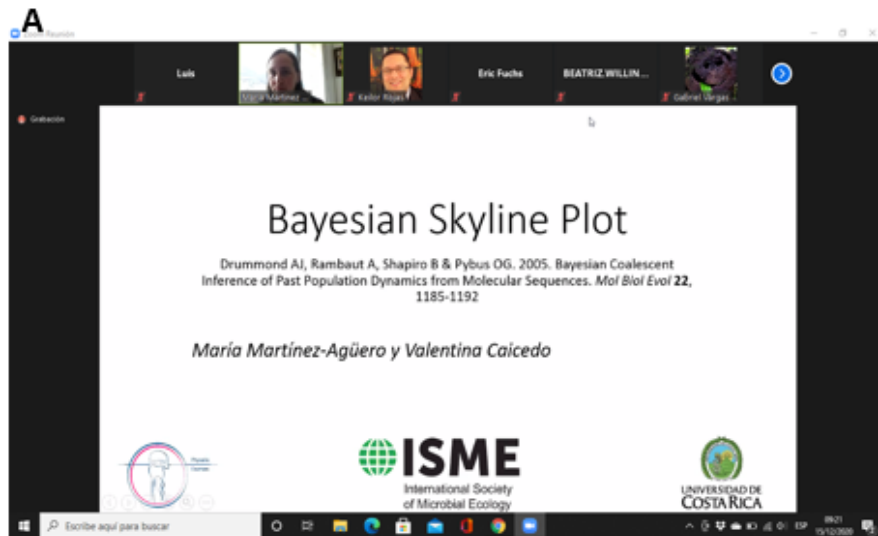
Figure 4. Bayesian Skyline Plot session during the second workshop's day (A) and the IcyTree tool for phylogenetic tree visualizations explained in the last day by María Martínez Agüero, Ph.D.

Invitation to the workshops: "Introduction to metagenomic analysis in IMG" and "Microbial communities analysis using QIIME2".

Invitation to the workshop: "Introduction to phylogenomic analysis"