

**VOLUME 13 | MAY 2023** 

Advancing Bioinformatics and Allied Disciplines in the Asia & Pacific Region

#### NEWS HIGHLIGHT



**APBioNET ExCo Election 2022-24** 



Viral Genomics and Bioinformatics/SARS-CoV-2 (Asia): From My Eyes



InSyB 2022 Chairman Report

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### **InCoB 2022 Chairman Report**

By: Xin Gao, Ph.D & Mohammad Asif Khan (InCoB 2022 Co-Chairs)

The 21st InCoB took on theme of "Accelerating Innovation to Meet Biological Challenges: The Role of Bioinformatics". The conference was held from the 21st to 23rd November 2022 and organized virtually, for the second time, by the Asia-Pacific Bioinformatics Network (APBioNET) in collaboration with the Computational Bioscience Research Center (CBRC) at King Abdullah University of Science and Technology (KAUST). The conference aimed to bring together researchers, decision makers, educators and scholars from the Asia-Pacific region and beyond for a scientific discourse and exchange on the state-of-the-art in the field, while providing for networking opportunities.

InCoB 2022 successfully attracted 74 registrants, with as many as 66 accepted presentation submissions. Majority were original research manuscripts submitted for publication consideration in as many as 7 partner journals: BMC Genomics, BMC Medical Genomics, BMC Bioinformatics, BMC Molecular and Cell Biology, Journal of Bioinformatics and Computational Biology (JBCB), Quantitative Biology and Frontiers Journals Research Topic Collection.

We thank all the participants, the members of the organizing and scientific committees and we look forward to your continued support in the future.

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### **VOLUME 13 | MAR 2023**

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#### **NEWS HIGHLIGHT**

### APBioNET ExCo Election (2022-24)

By: Nurul Salwanie & Shoba Ranganathan (APBioNET Election Committee)

Every two years, our members gather to vote for a new slate of APBioNET ExCo members. These ExCo members will serve the organization for 2 years, during which they will decide the direction of the organization, and provide the necessary leadership required to make it a success.

At the Annual General Meeting (AGM) during InCoB 2022, held from the 21 – 23 November 2022, the final virtual ballot and the elected ExCo members were announced. This election cycle received 12 candidates, and throughout the online voting of three weeks, 10 candidates were elected as ExCo members. The elected ExCo members then convened to decide the office bearers position. The second voting cycle has decided the following individuals as its office bearers:

- President (Mohammad Asif Khan, University of Doha for Science and Technology, Qatar)
- Vice President (Harpreet Singh, Hans Raj Mahila Maha Vidyalaya Jalandhar, Punjab, India)
- Secretary (Kiyoko F. Kinoshita, Soka University, Japan)
- Treasurer (Yun Zheng, Fudan University)
- Assistant Vice President (Hilyatuz Zahroh, Universitas Yarsi, Indonesia)
- Assistant Secretary (Kubra Kubat, Turkey)
- Assistant Treasurer (Xavier Chee, Malaysia)
- Non-office bearer ExCo Members (Sarinder Kaur, University Malaya, Malaysia; Wisnu Ananta Kusuma, IPB University, Indonesia; and N Latha, Bennet University, India)



Link: https://www.apbionet.org/current-exco-members-2022-2024/

We extend our congratulations and wish the current exco members continued success in the coming term.

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#### **NEWS HIGHLIGHT**

# 6<sup>th</sup> International Symposium on Bioinformatics (InSyB 2022)

By: Didik Huswo Utomo, PhD

The 6th InSyB was held in conjunction with the 3rd BBC Conference. The International Symposium on Bioinformatics (InSyB) bridges the gap between InCoB (International Conference on Bioinformatics) and irregular local APBioNet-supported workshops or training courses. This particular installment witnessed several other highlights - a Memorandum of Understanding between MABBI and APBioNet. The event also accommodated the annual meeting for bioinformaticians in Indonesia and provided a special event for university students to globally spread their ideas or prototypes of their products related to the bioinformatics area. With no doubt, this was one of the most significant bioinformatics events in Indonesia, where we invited researchers to enhance the development of bioinformatics by attending this annual scientific meeting (BBC). There were 39 oral presenters, 1 poster presenter, and 46 abstract submissions. The event received participation from various countries such as Indonesia, India, Malaysia, Morocco, United Arab Emirates, Germany, Senegal, China, Turkey, the United States, Egypt, Bangladesh, Ghana, and Uganda. In the series of conference events, there were also workshops on the topics: Multiomics data integration and visualization; Immunoinformatics screening for the discovery of peptide vaccines; and Machine Learning for Bioinformatics Using Google Colab, and Single-cell RNAseq.



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#### **UPCOMING EVENTS**

Event Name: InCoB 2023

Event type: Conference

**Date**: 12 – 15 November 2023

Venue: Queensland University

of Technology (QUT), Brisbane

Mode: Physical

Website link:

incob.apbionet.org/incob23



Event Name: Asia & Pacific

**Bioinformatics Joint Congress 2024** 

(APBJC 2024)

Event type: Congress

Date: 22 - 25 October 2024

Venue: Okinawa, Japan

Mode: Physical

Website link: Coming soon



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#### **WORKSHOP HIGHLIGHT**

### Viral Genomics and **Bioinformatics/SARS-CoV-2 (Asia):** From My Eyes

By: Li Chuin Chong, Oudamdaniel Yanneth and COG-Train + Wellcome Connecting Science team

The Viral Genomics and Bioinformatics/SARS-CoV-2 (Asia) workshop was jointly hosted by Wellcome Connecting Science and COG-Train team. It was a successful virtual event held from August 22 to 26, 2022. This workshop aimed to develop good educational practices on viral bioinformatics biologists among computational biologists from the Asia region, in order to promote and improve bioinformatics in their institutions. There were 26 selected participants from 12 different countries: Bangladesh, Cambodia, India, Indonesia, Japan, Malaysia, Pakistan, Philippines, Singapore, Thailand, Turkey, and Vietnam.

This workshop included twelve modules:

- Introduction to Linux
- Linux text processing
- Introduction to NGS sequencing
- NGS data quality control
- Introduction to BASH scripting
- Reference alignment
- Coverage plots and stats
- Consensus and variant calling
- De novo assembly
- Pathogen sequence detection using metagenomics
- Introduction to phylogenetic methods
- SARS-CoV-2 workflows

It is a known fact that viral infections are and important worldwide public health burden; hence, this workshop highlighted the current technologies in the viral identification and surveillance and management of viral diseases. Throughout this workshop, the participants had opportunities to learn the ways to analyze viral genome sequences and interpret the genomic data obtained by high-throughput sequencing, besides a hands-on practice pertaining to SARS-CoV-2 genomic analysis.



Li Chuin Chong (Course participant from Malaysia, currently a

doctoral researcher/Ph.D. candidate at TWINCORE GmbH/Hannover Medical School; former APBioNET Ambassador)

"It was a great pleasure to be a participant in this virtual course. This five-day course was very comprehensive to gain an understanding of the current state-of-the-art techniques and technologies in the field (e.g. next generation sequencing platform and data analysis). The hands-on practice and small group discussions facilitated through breakout rooms were particularly effective in ensuring that participants were able to grasp both the theoretical and technical aspects of the material. Besides getting new knowledge, the organizer provided a great platform to build connections and collaborations by dedicating 15 minutes every day to make acquaintances with fellow participants. It is vital to acknowledge the significance of this towards the establishment and strengthening of bioinformatics network in the Asia & Pacific region.

The sharing of resources, expertise and best practices among researchers and healthcare professionals can greatly enhance the effectiveness and efficiency of viral genomics and bioinformatics research and disease management initiatives, specifically in terms of SARS-CoV-2 and neglected tropical diseases. In light of this, the collaboration between APBioNET and COG-Train/WCS should be strengthened in fostering mutual support and resource sharing, and is crucial for promoting viral bioinformatics research in the Asia & Pacific region. Specifically, the partnership would enable both organizations to share expertise and resources, thus facilitating the advancement of research in this field."

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### **WORKSHOP HIGHLIGHT**

Jorge Batista da Rocha is a South African bioinformatician and holds a PhD from the University of the Witwatersrand. This course made use of a large amount of data and bigdata ready software, all packaged into a virtual machine which would then run on the participants own computer. There are a few concerns when dealing with big data, such as waiting hours or even days for a large download only to have it break when it is just about to finish, or find that it is finished but your files are corrupted. In developing this course, Jorge brought his experience in working in African settings to serve participants who may have similar scenarios with big data - like where electricity connectivity can be uncertain, or where the internet is unreliable and often disconnects. Thus, the course team used a data delivery platform called Globus to share the virtual machine. Globus is able to resume broken download connections, and also will check for file integrity to avoid data corruption.

In terms of expertise, it was vital to Jorge and the COG-Train and Wellcome Connecting Science teams to unite a group of experts from different countries in Asia to develop the content of this course. This strategy enabled the tailoring of the content to be useful and practical to Asian context, and also promoted and intensified the establishment of regional connections and collaborations compared to courses led only by European based educators. Additionally, the team developed the course openly on the GitHub platform. This allowed instructors to configure the code and instructions directly, and for participants to be able to clone, remake, reuse and share their own outputs based on what they learned.

This course had a large number of highly qualified applicants, and it was difficult for the instructors to select a group of only 26 participants who could attend. The organising and instructor teams made sure to choose the best candidates, taking into consideration gender and geographical representation. This added the potential to link up scientists who may not have had the chance to meet and collaborate. The course also included Advanced Learning and Training techniques, which taught skills in developing and delivering training events such as this. Jorge hoped to see participants develop not only their research skills, but also their ability to train others in their networks, which can lead to feedback effect where a community of knowledge sharing can grow.



Jorge Batista da Rocha (Course developer, COG-Train + Wellcome **Connecting Science**)



**Oudamdaniel Yanneth** (Course participant from Cambodia; research biologist at the Pasteur Institute in Cambodia)

"This course was rigorous, yet insightful and enjoyable. Not only were the teaching materials and resources up to date, but the pedagogical method was also fascinating. The best feature was the presentation of the guest lecturers, during which they presented their work, valuable experiences, and the relevance of all the courses we had learned to the actual world. For instance, the courses about metagenomics, phylogenetic, and their great influences in real-world situations, such as during the pandemic.

I learned more than I thought I would about both theory and practice, and I would strongly recommend this course to other people and students who want to learn about bioinformatics. Now that I've picked up a fresh nugget of information and my institution has a sequencing/bioinformatics team, I'm happy to discuss and share my experiences with others so that we may all improve. I also anticipate collaborating with other participants on new projects in the future."

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