COMBINE

Australian Computational Biology and Bioinformatics Student Society   ISCB REGIONAL *Student* GROUP Australia

Bioinformatics Student Symposium

In-person and virtual conference
28th November 2022
Melbourne

COMBINE 2022 Symposium
Welcome

Welcome to the 2022 COMBINE Symposium.

The COMBINE Symposium is a student-run, non-profit conference that aims to gather a diverse group of students and ECRs who are curious, passionate and eager to learn more about bioinformatics and computational biology. This annual event is an opportunity for students and early career researchers to present their work to peers in a relaxed and supportive environment. All attendees are expected to show respect and courtesy to everyone throughout the conference. The ABACBS code of conduct will apply to the symposium.

We hope you enjoy today's Symposium.

Regards, The 2022 COMBINE Symposium Committee.

2022 COMBINE Symposium Committee

Chairs: Akari Komori and Natalie Charitakis

Committee Members: Himal Shrestha, Tyrone Chen, Neke Ibeh, Michael Harper, Mikhail Dias, Bhavika Kumar, Alanah Grant-St James

For any enquiries please email symposium@combine.org.au.

Symposium Information

Useful links

https://pheedloop.com/ABACBS2022/site/home/

combine-au.slack.com

https://www.combine.org.au/

https://www.abacbs.org/

Follow the #COMBINE22 Symposium on twitter

@combine_au

In-person symposium venue:

Address: Monash Docklands Campus, 750 Collins St, Docklands, VIC

Symposium prizes

- Best session talks (first, second and third places)
- Best poster talks (first, second and third places)
- People's choice for session talk
- People's choice for poster talk
- Best tweet using #COMBINE22

COMBINE 2022 Symposium
Program Overview

The times indicated in the following program are in Sydney, Australia (AEDT) time zone.

9:00 - 9:30   ## Registration

9:30 - 9:45   ## Symposium Welcome
Natalie Charitakis, Akari Komori

9:45 - 10:50   ## Genomics Session
Chairs: Natalie Charitakis and Neke Ibeh
Session talks

10:50 - 11:15   *Morning tea break*

11:15 - 12:00   ## Keynote Address
Chair: Akari Komori
A/Prof. Torsten Seemann, Microbiological Diagnostic Unit, University of Melbourne

12:00 - 1:00   *Lunch*

1:00 - 2:20   ## Transcriptomics Session
Chairs: Himal Shrestha and Tyrone Chen
Session talks

2:20 - 3:00   ## Poster Session *and afternoon tea*

3:00 - 4:20   ## Translational Bioinformatics Session
Chairs: Alanah Grant-St James and Bhavika Kumar
Session talks

4:20 - 4:30   *Afternoon tea break*

4:30 - 5:30   ## Careers Panel Session
Chairs: Neke Ibeh, Bhavika Kumar
Dr. Shila Ghanzafar, Australian Research Council DECRA Fellow - University of Sydney
Prof. Tony Papenfuss, Laboratory Head, Leader - Computational Biology Theme - The Walter and Eliza Hall Institute of Medical Research
Dr. Natalie Twine, Senior Research Scientist - Translational Bioinformatics Group - CSIRO
Dr. Milica Ng Senior Director, Head of Data Science - CSL

5:30 - 6:00   ## Symposium Closing
Chairs: Natalie Charitakis, Akari Komori and Sachintha Wijegunasekara
Prizes announcements
COMBINE Annual report
Closing address

Invited Speakers

Keynote Speaker

A/Prof. Torsten Seemann

Lead Bioinformatician, Microbiological Diagnostics Unit and Head of Austrakka

A/Prof. Torsten Seemann is the lead bioinformatician at the Microbiological Diagnostics Unit, Victoria's leading public health laboratory, and head of Austrakka, Australia's endorsed national pathogen genomics surveillance platform which came to prominence during the COVID-19 pandemic. Part research, part service, Torsten sits at the translational interface between research, public health, and government. He is best known internationally for his software tools for microbial genomics, is an advocate for open science and open source software, and believes in building strong online bioinformatics communities.

Title

Evolution of a bioinformatician.

Abstract

This talk will cover the my bioinformatics career, from a total beginner at the cusp of the next generation sequencing wave, to running national projects like Austrakka which inform real public health decisions. What did I do right? Where did I go wrong? How much of it was pure luck? How has bioinformatics changed over my life? Can you learn anything from my experience? All will be revealed as I take you on a edutainment journey through academia, private consulting, clinical and public health microbiology, and government projects.

Invited Speakers

Careers Panel

Dr. Shila Ghanzafar - Australian Research Council DECRA Fellow - University of Sydney

Dr. Shila Ghanzafar completed her undergraduate and PhD studies in statistics and statistical bioinformatics at The University of Sydney, before completing a Royal Society Newton International Fellowship at The University of Cambridge under the mentorship of Dr. John Marioni in Computational Biology. Recently, she became one of the first grantees of the Chan Zuckerberg Initiative Data Insights program. Dr. Ghanzafar's interests are in developing statistical bioinformatics and biomedical data science approaches for the meaningful integration of complex and high dimensional biological datasets. She is an expert in statistical and computational analysis of spatial transcriptomics and single cell RNA-seq data.

Dr. Natalie Twine - Senior Research Scientist - Translational Bioinformatics Group - CSIRO

Dr. Natalie Twine is a Senior Research Scientist and leads the Genome Insights team within CSIRO's Transformational Bioinformatics Group. She is a recognised expert in the domains of translational genomics and genetics, cloud-computing, and bioinformatics. Dr. Twine's research achievements include 29 peer-reviewed publications (H-index of 17, >1700 citations) and >$12M in funding. Her work is featured in the high impact journal Cell Neuron (2018) and in media outlets such as Australian Financial Review (2019) and GenomeWeb (2020). Dr. Twine leads the development of cutting-edge digital products which leverage new technologies in genomics, cloud computing, and machine learning. These products deliver translational impact in the fields of precision medicine and digital health across academic, government, and commercial sectors. She collaborates broadly, both nationally and internationally.

Dr. Milica Ng - Senior Director, Head of Data Science - CSL

Dr. Milica Ng is a Data Science professional with achievements in biomedical R&D, entrepreneurship, international IT management consulting, and software engineering. Since 2013, Milica has worked for CSL, a leading global biotech company headquartered in Melbourne, employing almost 30,000 people in more than 30 countries. She is responsible for delivering state-of-the-art data analytics capabilities in Bioinformatics, Biostatistics, Image Analytics, Molecular Systems Modelling, Data Management & Engineering, and AI/ML. Prior to that she completed her PhD at the University of Melbourne, developing new mathematical models in Metabolic Engineering. She also has extensive experience as an international IT management consultant and has completed a Master's in Engineering in Information and Communications Technology at the University of Adelaide, including 2/3rds of an MBA.

Prof. Tony Papenfuss - Laboratory Head, Leader - Computational Biology Theme - The Walter and Eliza Hall Institute of Medical Research

Tony is a laboratory head and the Computational Biology Theme Leader at the Walter and Eliza Hall Institute of Medical Research. He uses mathematics, statistics and computation to understand how cancers are initiated and evolve as they progress and in response to therapy. This involves the development of novel computational methods to analyse genomics, transcriptomics and other omics data. His laboratory has developed some of the leading methods for identification and characterisation of genomic rearrangements in cancer and applied these to understand melanoma evolution and the role of circular chromosomes in cancers. He was the founding President of the Australian Bioinformatics and Computational Biology Society (2014-2018).

COMBINE 2022 Symposium
Detailed Program

Symposium Welcome - 9:30am - 9:45am

AEDT

Chairs: Natalie Charitakis, Akari Komori

9:30 - 9:45

Acknowledgement of Country
Welcome to COMBINE 2022

Genomics Session - 9:45am - 10:50am

Chairs: Natalie Charitakis and Neke Ibeh

9:50 - 10:05 Modelling Systematic Inter-Replicate Bias in the Integration of ChIP-seq experiments
Oliver Hughes

10:05 - 10:20 Distinguishing transcriptional and genetic heterogeneity in metastatic prostate cancer
Sirui Weng

10:20 - 10:35 Hybrid Sequencing of Staphylococcus aureus from Chronic Rhinosinusitis Patients Reveals Widespread Beta-Lactamase Carrying Plasmids Associated with Compensatory Chromosomal Mutations in Virulence Genes
George Bouras

10:35 - 10:50 Automating discovery of tandem duplications in cancer
Briana Robson

Morning Tea Break 10:50am - 11:15am

Keynote address - 11:15am - 12:00pm

11:15 - 12:00 *Chair:* Akari Komori

A/Prof. Torsten Seemann, Microbiological Diagnostic Unit, University of Melbourne
Title: Evolution of a bioinformatician

Lunch 12:00pm - 1:00pm

Transcriptomics Session - 1:00pm - 2:20pm

Chairs: Himal Shrestha and Tyrone Chen

1:05 - 1:20   Building an RNA-seq subtype classifier for T-cell acute lymphoblastic leukaemia
Allen Gu

1:20 - 1:35   Cytocipher detects significantly different populations of cells in single cell RNA-seq data
Brad Balderson

1:35 - 1:50   A computational framework to detect ceRNA cross-talks in pan-cancer studies
Yi-Wen Hsiao

1:50 - 2:05   Characterising gene co-expression changes facilitating the loss of features of multicellularity driving Prostate Cancer progression
Mikhail Dias

2:05 - 2:20   Deciphering heterogeneous patient-derived bulk RNA-seq data using single-sample pathway perturbation analysis and cell-type deconvolution
Wenjun Liu

Poster Session 2:20pm - 3:00pm

Systematic construction of phylogenetic trees enriched with experimental properties
Sebastian Porras

Empirical tokenisation of genomic data and data-free deep-learning model evaluation
Tyrone Chen

Benchmarking long-read RNA-sequencing analysis tools using in silico mixtures
Xueyi Dong

Quantifying native RNA integrity from nanopore sequencing
Aditya Sethi

Single-cell RNA-seq analysis of amniotic fluid: a unique approach for studying foetal development
Calandra Grima

Disparities in Spatially Variable Gene Calling Highlight the Need for Benchmarking Methods in Spatially Resolved Transcriptomics
Natalie Charitakis

Multiomics profiling of lung transplant recipients identifies molecular signatures linked to chronic lung allograft dysfunction
Giulia Iacono

Theoretical prediction of potential molecular mechanisms of Simiao Pills against hyperuricemia: A computational modeling and screening study
Hong Li

Synergistic mechanisms of herbal compounds from Toujie Quwen Granules against the main protease of SARS-CoV-2: a structure-based multi-ligand molecular modelling study
Hong Li

Functional analysis of the stable phosphoproteome reveals cancer vulnerabilities
Di Xiao

Developing methodology to scan public databases using recount3 to identify potential fusion genes
Caitlin Page

A computational model for gene regulatory networks in early kidney development
Adeline Trieu

Finding novel transcripts in bulk and single cell cancer transcriptomics datasets through data analysis of both short and long read RNA sequencing
Michael Nakai

Translational Bioinformatics Session - 3:00pm - 4:20pm

Chairs: Alanah Grant-St James and Bhavika Kumar

3:05 - 3:20 **Identifying cellular interactions and communication in multiplexed in situ imaging data through cell state analysis**
Sourish Iyengar

3:20 - 3:35 **Environment-dependent trajectory inference (ENTRAIN) to determine the extra-cellular signals that specify cell fate**
Wunna Kyaw

3:35 - 3:50 **Multi-omic Profiling Uncovers Molecular Controls in Early Cerebral Brain Organoid Differentiation**
Carissa Chen

3:50 - 4:05 **Developing a user interface for sharing federated genomic and phenotypic data using the Beacon v2 protocol**
Ricky Nguyen

4:05 - 4:20 **Inference of ancestral protein properties in phylogenetic gene trees**
Sam Davis

Afternoon Tea Break 4:20pm - 4:30pm

Careers Panel Session - 4:30pm - 5:30pm

4:30 - 5:30 *Chair:* Neke Ibeh, Bhavika Kumar

Dr. Shila Ghanzafar Australian Research Council DECRA Fellow - University of Sydney
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Symposium Closing - 5:30pm - 6:00pm

5:30 - 6:00 *Chairs:* Natalie Charitakis, Akari Komori and Sachintha Wijegunasekara

Prizes announcements
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COMBINE 2022 Symposium
COVID Safety Statement

Australia is currently experiencing another surge in **COVID-19** cases and we are monitoring the situation. The latest Victorian government regulations do not require masks to be worn indoors, however we strongly recommend you wear a mask at ABACBS and all satellite meetings and workshops, in particular when social distancing can not be maintained.

Surgical Masks and **hand sanitiser** will be available throughout the conference venue. **Free Rapid Antigen Tests (RATS) and N95 style masks** will be also available at the registration desk.

What to do if you are unwell

- **Do not attend** the conference in person.
- All registered participants of ABACBS, COMBINE and BioCAsia have the option of virtual attendance.
- Perform a **Rapid Antigen Test (RAT)**. Free RATs can be obtained from the registration desk.

What to do if you have COVID-19

- Positive RATs can be registered with the state government at https://www.coronavirus.vic.gov.au/report-your-rapid-antigen-test-result
- Although state government regulations no longer require isolation, do not attend the conference if you are currently positive, have tested positive within the prior 7 days, or are still symptomatics from a COVID infection.
- If you need assistance, such as delivery of food or medical supplies to a hotel room, please email covid@abacbs.org and we will support you to isolate and receive the medical help you need.
- If you test positive within 48 hours of attending the conference, please inform us by emailing covid@abacbs.org so we can notify close contacts. Communication will be kept confidential.

Any questions or concerns regarding COVID-19 can be sent to covid@abacbs.org.