GIW/ ABACBS 2019

30TH INTERNATIONAL CONFERENCE ON GENOME INFORMATICS & AUSTRALIAN BIOINFORMATICS AND COMPUTATIONAL BIOLOGY SOCIETY ANNUAL CONFERENCE

WELCOME

2019 marks a very special time in the history of the Australasian Bioinformatics and Computational Biology Society (ABACBS). This is the first time that the annual ABACBS conference has partnered the International Conference on Genome Informatics (GIW). This year, these two conferences will join forces to bring together members from all over Australia, the Asia-Pacific region and the world to enjoy the opportunity to interact and hear fantastic stories about genomics, bioinformatics and computational biology research with an emphasis on how advances in computational and statistical techniques are applied to solve important biological and biomedical problems.

To keep pace with the growing bioinformatics community, the ABACBS conference is launching parallel sessions as well as live streaming of presentations. In addition to subsidising childcare at this year's conference, live streaming reflects our continued commitment to maximise opportunities for researchers in our vibrant community to attend our annual conference.

We would like to thank the ABACBS and GIW program committee co-chairs who have organised an outstanding program covering the themes of genomics and integrative analysis, precision medicine, single-cell analytics, non-human, agricultural, environmental and microbial genomics, proteomics and metabolomics and finally, methods development and reproducibility research. We have eight international and four national keynote presenters, in addition to 36 presentations from GIW, selected from peer-reviewed full paper submissions and 32 presentations from ABACBS selected from peer-reviewed abstracts. We look forward to 12 exciting fast forward talks and two dynamic posters sessions with 170 posters.

We wish to sincerely thank our local organising committee, program committee chairs and representatives from the ABACBS and GIW communities who gave so much of their time to make this conference a reality. We are very grateful to all of our sponsors for their generous support of this conference, in particular our gold sponsors, the NSW Department of Industry and Amazon Web Services.

On behalf of the local organising committee, we look forward to welcoming you to the beautiful campus of Sydney University, on the traditional lands of the Gadigal people of the Eora nation. We hope that you enjoy the conference, the social events and the many wonders that Sydney has to offer.

ABACBS
ABACBS was founded in 2014 and represents over 850 bioinformaticians and computational biologists from across Australia. Our members are a mix of students, academics, researchers, and professionals. The annual conference is one of the highlights for the society and scientific community for face-to-face interactions.

GIW
The Genome Informatics Workshop (GIW) was first held in Tokyo in 1990 and continued annual workshops in Japan until 2000. Since 2001, it has been renamed as the international GIW conference, providing unique opportunities that bridge bioinformatics theory and experiments, academia and industry, and East and West.

Prof Tony Papenfuss
Peter MacCallum Cancer Centre and Walter Eliza Hall Institute, ABACBS Conference Chair

A/Prof Mark Cowley
Children's Cancer Institute, ABACBS co-convenor

Prof Jean Yang
University of Sydney, ABACBS co-convenor

Prof Shoba Ragnanathan
Macquarie University, GIW co-convenor

Prof Jinyan Li
University of Technology Sydney, Australia, GIW co-convenor

ORGANISING COMMITTEE

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PROF. TONY PAPENFUSS

CONFERENCE C0-CHAIRS

PROF. JEAN YANG

A/PROF. MARK COWLEY

PROF. SHOBA RANGANATHAN

PROF. JINYAN LI

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YINGXIN LIN

DR. IGNATIUS PANG

KATARINA STUART

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ROHAN WILLIAMS

HONG-HEE WON

EMILY WONG

KOON HO WONG

LIMSOON WONG

LING-YUN WU

WEI WU

JIANMIN WU

JINBO XU

YOSHIHIRO YAMANISHI

JINN-MOON YANG

PENGYI YANG

WANG YANG

SUNGROH YOON

AIDONG ZHANG

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SHUQIN ZHANG

JINGHUI ZHANG

ZIDING ZHANG

YAOQI ZHOU

SHANDAR AHMAD

TATSUYA AKUTSU

ROLF BACKOFEN

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JINYAN LI

HEE WOONG LIM

BING LIU

TAO LIU

RUIBANG LUO

JESSICA MAR

HIDEO MATSUDA

YOUNG JI NA

JOSE NACHER

KA-LOK NG

RAFAEL IRIZARRY - JOINT PLENARY

Professor Irizarry's work has focused on applications in Genomics. In particular, he has worked on the analysis and signal processing of high-throughput data. He has distinguished himself by disseminating his statistical methodology as open source software shared through the Bioconductor Project, a leading open source and open development software project for the analysis of high-throughput genomic data. His widely downloaded software tools have helped him become one of the most highly cited scientists in his field. Although Professor Irizarry's focus has been in genomics, he is an applied statistician generally interested in read-world problems. During his career he as co-authored papers on a variety of topics including musical sound, infectious diseases, circadian patterns in health, fetal health monitoring, and estimating the effects of Hurricane María in Puerto Rico.

MONA SINGH

Prof. Mona Singh's research is in computational molecular biology, as well as its interface with machine learning and algorithms. Her group is particularly interested in predicting specificity in protein interactions and uncovering how molecular interactions and networks vary across context, organisms and individuals. Mona leverages high-throughput biological datasets in order to develop data-driven algorithms for predicting protein interactions and specificity; foruncovering protein functions via sequences and structures, and for analysing biological networks in order to uncover cellular organization, function, and pathways.

JÜRGEN COX

Jürgen Cox is a research group leader at the Max Planck Institute for Biochemistry in Martinsried where he heads the Lab for Computational Systems Biochemistry. He received his PhD in physics at the Massachusetts Institute of Technology and has since developed MaxQuant, a quantitative proteomics software package designed for analyzing large mass spectrometric data sets. Dr. Cox is the author of numerous peer reviewed publications in the field of data analysis in mass spectrometry and quantitative proteomics.

JOHN MARIONI

Dr John Marioni's group use computational approaches to understand the molecular mechanisms that underlie cell fate decisions. Since cell fate decisions are ultimately made at the single-cell level, this requires assaying molecular characteristics of individual cells. The field of single-cell biology has revolutionised our ability to make such measurements, especially in the area of single-cell transcriptomics. John's group has developed cutting-edge computational methods in this domain and has applied them, with outstanding collaborators, to study cell fate decisions in a variety of contexts, focussing especially on early mammalian development.

ELANA FERTIG

Dr. Fertig runs a hybrid computational and experimental lab in the systems biology of cancer and therapeutic response. Her wet lab develops time course models of therapeutic resistance and performs single cell technology development. Her computational methods blend mathematical modeling and artificial intelligence to determine the biomarkers and molecular mechanisms of therapeutic resistance from multi-platform genomics data. These techniques have broad applicability beyond her resistance models, including notably to the analysis of clinical biospecimens, developmental biology, and neuroscience.

JASON WONG

Dr Jason Wong is an Associate Professor at the University of Hong Kong. He obtained is B.Sc from the University of Sydney and D.Phil from the University of Oxford. His research is in the field of cancer genomics. He has a particular interest in the study of mutational processes in cancer with a focus on understanding the interactions between DNA damage, repair and epigenetic mechanisms in the human genome. His research leverages large cancer genomics datasets making use of computational and statistical methods to uncover novel mutational processes in cancer. He is also interested in the study of the impact of somatic mutations in the non-coding regions of cancer genomes such as the role of cis-regulatory mutations in cancer.

PEI WANG

Prof. Pei Wang's research is in biostatistics and computational biology. Her group focuses on developing statistical and computational methods to address scientific questions based on data from high throughput biology/genetics experiments as well as modern digital health studies. Dr. Wang and her team have developed numerous novel statistical methods for analyzing and integrating various genetic/genomic/proteomic data. In the past decade, Dr. Wang has been actively involved in the NCI funded CPTAC (Clinical Proteomic Tumor Analysis Consortium). Currently, Dr. Wang is the MPI of the national Proteomics and Genomics data analysis center of CPTAC.
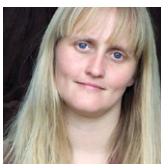
ELAINE HOLMES

Prof. Holmes heads the Division of Computational and Systems Medicine and is Professor of Chemical Biology at Imperial College, London, UK. She has over 20 years experience in metabolomic technology and its applications. Her focus is on metabolic biomarkers in personalised healthcare and population studies, affecting cardiovascular, neuroscience and infectious disease. She has spearheaded metabolome-wide association study (MWAS) in molecular epidemiology, linking hypertension, diet and metabolic profiles and characterized gut microbiome host metabolic interactions in colorectal cancer, obesity and IBD. She also has developed chemometric and statistical methods for Omics data analysis.

DAVID LYNN

Prof. Lynn is Director of the Computational & Systems Biology Program at SAHMRI (1 of the 16 Programs/Divisions at SAHMRI); Professor at Flinders University College of Medicine & Public Health; and an EMBL Australia Group Leader in the SAHMRI Microbiome & Host Health Program. He leads a multidisciplinary team of computational and experimental researchers, which currently includes 4 postdoctoral fellows, 1 research officer, 2 PhD and 2 Honours students. Under his leadership, his team has developed advanced capacity in systems biology and employs computational, in vitro, and preclinical models, coupled with clinical cohorts (such as his NHMRC-funded Antibiotics and Immune Responses trial) to investigate the regulation of complex systems, with a particular focus on the immune system and cancer. He is particularly interested in the role the microbiota plays in modulating the immune system in different contexts. Prof. Lynn is also an international leader in computational biology and bioinformatics. He was awarded the 2018 Australian Bioinformatics and Computational Biology Society Mid-Career Researcher Award and his computational resources, such as InnateDB.com, are used by tens of thousands of researchers globally. He was a principal investigator on the PRIMES project, a European Commission funded cancer systems biology project to map the EGFR protein interaction network in colorectal cancer cells. He has published >70 peer-reviewed articles to date (50 last 10 years; 25 as corresponding author). These articles are cited >5,800 times (Google Scholar) and include recent senior author publications in Nature Communications (2019), Cell Systems (2018), and Cell Host Microbe (2018). In the last 5 years, he has supported his team by building an international network of collaborators and as a CI on externally-funded projects worth >$20 million (directly receiving >$3 million) including from The NHMRC (3 CIA; 1 CID), European Commission, MRFF, and Cancer Australia.

DENIS BAUER

Dr Denis Bauer is an internationally recognised expert in machine learning, specifically in processing big genomic data to help unlock the secrets in the human DNA. Her achievements include developing open-source, cloud-based bioinformatics solutions used by 10,000 researchers annually. She is on advisory committees for bringing genomics into the clinical practice and is frequently invited as keynote speaker at heavyweight medical and IT conferences including International Conference on Bioinformatics Jakarta '19, Amazon Web Services Summit '19, International conference on Frontotemporal Dementia '18, and Open Data Science Conference India '18. She has 40 peer-reviewed publications (19 as first or senior author, h-index 17) and her achievements have been featured in international press such as GenomeWeb, ZDNet, Computer World, the Australian Financial Review, CIO Magazine and the AWS Jeff Barr blog. To date, she has attracted more than $31M as chief instigator to further health research and digital applications.

CLAIRE WADE

Claire Wade began her career in quantitative genetics before making the leap to genomics in 2002 when she began a position with the Whitehead Institute for Biomedical Research at Massachusetts Institute of Technology. The genomics group at the Whitehead later became one of the founding groups of what is now the Broad Institute. While in the USA, Claire worked on several mammalian genome projects including the mouse, dog and horse (for which she was the lead researcher).Claire's research interests include unravelling the secrets of genome biology using next generation sequencing. She studies the application of new genomic technologies to improve our understanding of diseases and behavioural traits in domestic animals and wildlife and our understanding of the links between DNA and phenotype in general. Projects currently underway are as diverse as finding genes underlying canine separation anxiety and working dog performance, improving captive animal management using new genetic resources, and better understanding the genomics of behaviour.

EDUARDO EYRAS

Eduardo Eyras did a PhD in Mathematics (University of Groningen, The Netherlands, 1999) and a Marie Curie postdoc at the Centre for Mathematical Sciences at the University of Cambridge, UK (1999-2001). In 2001, he joined the Informatics Division of the Sanger Institute (2001-2004), where he contributed to the development of the Ensembl gene prediction pipeline, developed one of the first computational methods to predict alternative splicing variants, and contributed to the landmark papers of the mouse, rat, chicken and cow genomes. In 2005 he became ICREA Research Professor, and since then his research has focused on the development of computational tools and Machine Learning methods to study RNA biology and disease. In 2007 he was awarded Young Investigator grant from the European Network on Alternative Splicing (EURASNET), and in 2013 he was a visiting professor at the University of Toronto. In 2019 he was appointed EMBL Australia Group Leader and Professor at the John Curtin School of Medical Research of the Australian National University.

MONDAY DECEMBER 9

REGISTRATION 13:30 ONWARDS (CHARLES PERKINS CENTRE)

SESSION 1. 15:15 (CPC)

TUESDAY DECEMBER 10

SESSION 2. PLENARY LECTURES 9:00-10:50 (WALLACE THEATRE)

MORNING TEA 10:50-11:20 (CPC)

SESSION 3. PARALLEL SESSIONS 11:20-12:20 (CPC)

LUNCH AGM & POSTER SESSION A 12:20 - 14:15 (CPC)

SESSION 4. PARALLEL SESSIONS & FAST FORWARD TALKS 14:15-15:45 (CPC)

FAST FORWARD TALKS 15:15-15:45 (CPC)

AFTERNOON TEA 13:45-15:15 (CPC)

SESSION 5. PLENARY LECTURES 16:15-17:55 (WT)

GIW/ABACBS CONFERENCE DINNER (THE GRANDSTAND, SYDNEY UNIVERSITY)

WEDNESDAY DECEMBER 11

SESSION 6. PLENARY LECTURES 9:00-10:50 (WT)
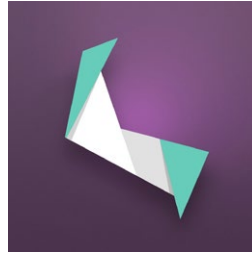
MORNING TEA 10:50-11:20 (CPC)

SESSION 7. PARALLEL SESSIONS 11:20-12:20 (CPC)

LUNCH & POSTER SESSION B 12:20-13:30 (CPC)

SESSION 8. PARALLEL SESSIONS 13:30-14:45 (CPC)

AFTERNOON TEA 14:45-15:15 (CPC)

SESSION 9. PLENARY LECTURES CLOSING SESSION & ABACBS CONFERENCE AWARDS 15:15-17:00 (WT)

eventee will have the most up-to date program and is the only place where we have all of the poster abstracts and presenters.

We encourage all delegates to download the **eventee App from the Google Play, or Apple iTunes Store.**

The event name is **GIW/ABACBS-2019**, or scan this QR code using the eventee app on your mobile device.

Poster and Talk Judging using eventee App
This year we will be crowd-sourcing the judging of poster and parallel conference presentations. Using the Eeventee app, we ask you to vote for every talk that you hear and every poster presenter that you interact with, so we can determine the peoples choice awards at the end of the conference

LOCATION

The Joint GIW/ABACBS 2019 Conference will be held at **The University of Sydney**, at the heart of Sydney – one of the most vibrant metropolitan cities of Australia. The University of Sydney is conveniently located just 10 minutes away from the central business district of Sydney. There are many hotels around the University, with easy access to restaurants, local transportation and tourist attractions.

The conference venue is at **The University of Sydney**, with the Plenary sessions held at the **Wallace Theatre** and the Parallel and Poster sessions held at the **Charles Perkins Centre**. The two locations are around three mins walking distance apart.

GOLD

NSW GOVERNMENT

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REGISTRATION
You can register in the foyer of the Charles Perkins Centre from 1:30 pm, Monday 9 December.

VENUE
There are two venues this year, located at The University of Sydney, approximately three mins walking distance apart.

1. Plenary sessions:
Wallace Theatre (A21)
Western Avenue. The University Of Sydney NSW 2006

2. Parallel & Poster sessions:
Charles Perkins Centre (D17)
John Hopkins Drive. The University Of Sydney NSW 2006

• **Getting there** If travelling by road, take the University of Sydney Western Ave entrance off Paramatta Road; the Wallace Theatre will be on your left. Casual parking is available at the University at a rate of $4 per hour. If travelling by public transport, the nearest stations are Central (~ 30 min walk to the venue), and Redfern (~ 25 min walk). Buses run from Central Station to the University of Sydney along Paramatta Road; ask the driver to drop you at the Western Ave / Ross St gate.

CONFERENCE DINNER
Dinner will be held on Tuesday December 10 at 6.15pm at The Grandstand Restaurant & Function Centre, Blackburn Oval Road, opposite the Charles Perkins Centre. There will be a two-course dinner with a dessert buffet and is sponsored by the Kinghorn Centre for Clinical Genomics, Garvan Institute of Medical Research.

INSTRUCTIONS FOR SPEAKERS
• **Ratio** The maximum aspect ratio of slides is 16:9.

• **Formats** It is preferable for the slides to be in one of the following formats: PowerPoint, PDF or Google Slide.

• **Start times** Speakers are required to be present 10 minutes prior to the start of session in the respective presentation hall to to upload their presentation slides. The session's chair will be present to collect the slides for the talks.

• **Talk duration** International Keynotes (40 minutes), National Keynotes (30 minutes), and Parallel session talks (GIW Papers and ABACBS Talks) (15 minutes). All indicated times are inclusive of time for questions. All speakers are encouraged to keep their talk within the allocated time limit due to tight schedules.

• **Speakers in parallel sessions** Please introduce your name and affiliation to the session chair, so that they can introduce you appropriately at the start of your talk. Each parallel session talk has been allocated 12 minutes for the presentation followed by three minutes for questions.

• **Social Media** If you do not want your work to be photographed, discussed, or shared on social media, please indicate this clearly at the start of your talk.

POSTER DISPLAY
• **Size** Posters have a maximum size of A0 in the portrait orientation.

• **Locations** Poster boards will be located in CPC Dry Lab 1.3, right next to the parallel session room CPC dry lab 1.2
Poster Number 1 - 85 will present their poster during the first Poster Session (10 December lunch time 12:20 - 2:15 pm)
Poster Number 86 - 170 will present their poster during the second Poster Session (11 December lunch time 12:20 - 1:30 pm)

Note: *Please look around on all the poster boards for your poster number as the numbers may be shifted or moved out of consecutive order to accommodate multiple posters presented by the same presenter.*

• **Presenters with multiple posters** There will be allocation of consecutive poster numbers each marked with an asterisk. We will arrange these poster numbers so that they are side-by-side in the same row in the same poster session.

• **Timings** Poster must be mounted in the morning prior to the start of each poster session. All posters must be de-mounted immediately at the close of each poster session. Posters that are not taken down after each poster session will be placed in unattended pile(s). It is the responsibility of the poster presenter to collect their posters at the end of each session.

• **Social Media** If you would not like your poster to be shared on social media(s), please affix a Post-it note or similar next to your poster to indicate this clearly to the audience.

WIFI ACCESS
Username: LakeGuest
Password: 39011047
Eduroam is available.

CHILDCARE
A pop-up childcare at has been contracted to Abracadabra Childcare Services for children under 7 years old - a short walk from the conference venue at Sancta Sophia College. Parents will need to provide any sleeping mats, toys and activities will be provided. Catering arrangements are yet t be confirmed. Please note registration for this care is now closed.

Children aged 5-15 can attend the School Holiday Sports Camps at the University of Sydney Sports and Aquatic Centre. For more information go to https://www.susf.com.au/kids-camps--programs.html

STREAMING
Please refer to the website for more information.

TWITTER HANDLE
#ABACBSGIW19