



2013/14

BioInfoSummer

University of Adelaide
2-6 December 2013

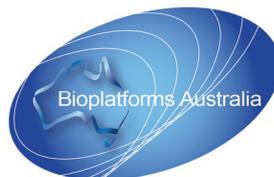
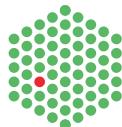


Australian Government
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INTRODUCTION

Championing Bioinformatics to a wider audience

BioinfoSummer is one of the Australian Mathematical Sciences Institute's (AMSI) major annual educational and outreach programs aimed to increase understanding and skill levels in bioinformatics among students and early career researchers. The event runs with the generous support of the European Molecular Biology Laboratory (EMBL) Australia, BioPlatforms Australia and the Department of Education.

BioinfoSummer 2013 was hosted by the School of Mathematical Sciences and the School of Molecular and Biomedical Science at the University of Adelaide.

The program featured:

- Introductory lectures on statistics, biology and bioinformatics
- Keynote talks by leading national and international researchers
- A sequence of hands-on practicals aligned to the daily themes

Speaker	Institution	Country
Prof. Falk Schreiber	Martin Luther University Halle-Wittenberg	Germany
Dr Sylvain Foret	Australian National University	Australia
Dr Stéphane Guindon	The University of Auckland	New Zealand
Dr Joseph Heled	The University of Auckland	New Zealand
Dr Barbara Holland	The University of Tasmania	Australia
Prof. Jeff Leek	Johns Hopkins University	United States
Dr Ville-Petteri Mäkinen	Helsinki University of Technology	Finland
Dr Martin Morgan	Fred Hutchinson Cancer Research Center	United States
Dr Alicia Oshlack	Murdoch Childrens Research Institute	Australia
Prof. Terry Speed	Walter and Eliza Hall Institute of Medical Research	Australia

COMMITTEES

AMSI wishes to acknowledge the generous donation of time and scientific advice of the following committees, without their contribution this event would not be a success.

Organising Committee

- Professor David Adelson, The University of Adelaide (Co-Director)
- Associate Professor Gary Glonek, The University of Adelaide (Co-Director)
- Associate Professor Cathy Abbott, Flinders University
- Dr Ute Baumann, The University of Adelaide
- Dr Stephen Bent, The University of Adelaide
- Simi Henderson, Australian Mathematical Sciences Institute
- Dr Karin Kassahn, The University of Adelaide
- Dr Dan Kortschak, The University of Adelaide
- Dr Lin Liu, University of South Australia
- Dr Bastien Llamas, The University of Adelaide
- Dr Andreas Schreiber, The University of Adelaide
- Dr Julien Soubrier, The University of Adelaide
- Dr Jonathan Tuke, The University of Adelaide
- Dr Nathan Watson-Haigh, The University of Adelaide

BioInfoSummer Committee

- Professor David Adelson, The University of Adelaide
- Dr Conrad Burden, The Australian National University
- Dr Sylvain Foret, James Cook University
- Dr Bruno Gaeta, UNSW Australia
- Associate Professor Gary Glonek, The University of Adelaide
- Simi Henderson, Australian Mathematical Sciences Institute
- Dr Jonathan Keith, Monash University
- Dr Andrew Lonie, VLSCI, University of Melbourne
- Dr David Lovell, CSIRO
- Professor Geoff McLachlan, The University of Queensland
- Professor Stan Miklavcic, University of South Australia
- Professor Geoff Prince, Australian Mathematical Sciences Institute
- Professor Terry Speed, Walter and Eliza Hall Institute of Medical Research (Chair)

FIGHTING CANCER BY THE NUMBERS

Professor Terry Speed inspired attendees with his opening address and keynote presentation *Bioinformatics before, during and after the era of genomics*.

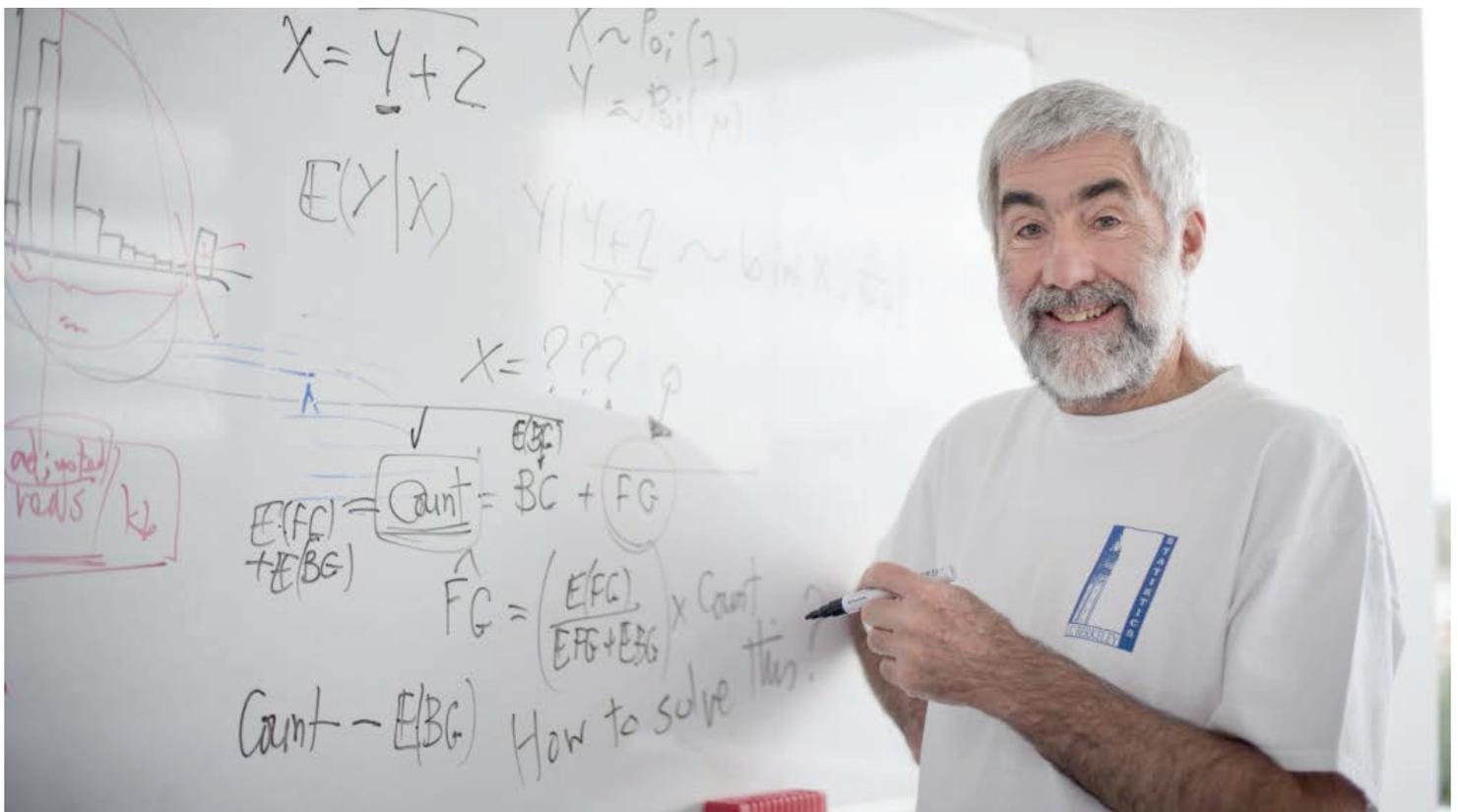
Terry is one of Australia's eminent statisticians and head of Bioinformatics at the Walter and Eliza Hall Institute of Medical Research.

In May 2013 he was elected as a fellow of the Royal Society and in October he was honoured with Australia's highest award for excellence in science – The Prime Minister's Prize for Science, for his contribution to making sense of genomics and related technologies.

Terry doesn't expect to see headlines reading "Statistician cures cancer" any time soon. But he knows that the right mathematics and statistics can help researchers understand the underlying causes of cancer and reduce the need for surgery.

A mathematician and statistician, he has written elegant theoretical papers that almost no-one reads, but he has also testified in court, helped farmers and diamond miners, and given biologists statistical tools to help them cope with the genetic revolution.

Twenty years ago biologists looked at one or two genes in isolation. Today they can track thousands of genes in a single cell, but to understand the results they need tools of the kind that Terry develops.





MONDAY 2 DECEMBER

BACKGROUND IN BIOLOGY AND STATISTICS

A general introduction of biology for attendees with mathematics, statistics and computer science backgrounds. A parallel stream was given, covering introductory statistics for participants with a biology background.



TUESDAY 3 DECEMBER

EVOLUTIONARY BIOLOGY

Evolutionary biology is a sub-field of biology concerned with the study of the evolutionary processes that produced the diversity of life on Earth.



WEDNESDAY 4 DECEMBER

SYSTEMS BIOLOGY

Systems biology is a biology-based interdisciplinary field of study that focuses on complex interactions within biological systems, using a holistic approach to biological and biomedical research.



THURSDAY 5 DECEMBER

NEXT GENERATION SEQUENCING

Next generation sequencing is the catch-all term used to describe a number of different modern sequencing technologies that have revolutionised the study of genomics and molecular biology.



FRIDAY 6 DECEMBER

PROGRAMMING FOR BIOINFORMATICS

An overview of some techniques and tools used to perform computations in biological research and create information from data.

“The opportunity to see what type of research is currently happening in Bioinformatics and to network with other young researchers were invaluable opportunities for my career.”



EVENT HIGHLIGHTS

STUDENT TRAVEL AWARDS

EMBL Australia and BioPlatforms annually offer travel support for students to attend the event. This year eight students and early career researchers received travel awards.



OPENING

BioInfoSummer2013 was officially opened by the Executive Dean of the Faculty of Engineering, Computer and Mathematical Sciences, Professor John Beynon.



POSTER COMPETITION & SYMPOSIUM BARBECUE

On Thursday 5 December attendees got the chance to showcase their research with poster presentations. Two participants, Westa Domanova and Reuben Buckley were awarded prizes for the exceptional quality of their posters. After the Poster session participants networked over food and drinks at the symposium BBQ.

CODING COMPETITION

The coding competition set a collection of bioinformatics problems provided by the Rosalind Project, an online platform for learning bioinformatics through problem solving.

Competitors were challenged to solve the problems using whatever programming language (or approach) they wanted, showing their methods. Competitors entered as individuals or as groups to get across the idea that there is a trade-off between team effectiveness and personal glory. The winner was the entrant with the greatest number of solved problems over the course of the workshop.

The winner was a team from the South Australia Cancer Genomics Facility (Katherine Pillman, Paul Wang, Frank Feng and David Lawrence), followed very closely by an individual entrant, Jono Tuke from The University of Adelaide.

PUBLIC LECTURE: EVOLUTION'S MYSTERIES UNRAVELLED WITH GENOMES AND COMPUTERS



PROFESSOR STEVE DONNELLAN
SOUTH AUSTRALIAN MUSEUM

On 3 December Professor Steve Donnellan explored some of South Australian Museum's exciting findings beginning with his adventures in the field and moving onto the application of the latest technologies and the increasingly important contribution of bioinformatics – a pioneering combination of computing, statistics and biology.

Some of the big questions in evolution of life on earth, such as how did life begin, why did sex evolve, how do species form, are starting to be unravelled by the availability of genetic information from entire genomes.

South Australian Museum scientists are currently pursuing major questions in evolution around the globe using the latest genetic technologies. In support of these endeavours, the South Australian Museum has one of the world's largest wildlife tissue collections and state of the art genetics facilities for extracting genetic information from the collection.

The audience's questions during the question time and at the following reception showed a great amount of interest piqued by the lecture.

Speaker Biography

Professor Donnellan is a chief researcher at the South Australian Museum and an affiliate professor in the University of Adelaide's School of Earth & Environmental Sciences. Steve has been researching the origins and evolution of Australia's biodiversity.

His research has taken him on adventurous fieldwork in Australia and to our near north in Indonesia and Papua New Guinea. Steve brought DNA technology into the SA Museum; expanding its capability and cementing it as the leading research museum in Australia.



BIOINFOSUMMER INTERNSHIPS

Since 2012 EMBL Australia and BioPlatforms Australia have supported AMSI internship placements linked to BioInfoSummer. The program builds research-industry partnerships and establishes long-term partnerships in the bioinformatics area.

Under the guidance of an experienced researcher, postgraduate students complete a 4–5 month project with an Australian business. The internships provide access to the vast research expertise in Australia's universities and bring new perspectives and the latest knowledge to a research challenge.

Students awarded internship placements in 2012 presented their projects at BioInfoSummer 2013.



Milica Ng and supervisor Dr Matt Ritchie

SUCCESS STORIES

Sori Kang and VLSCI

Sori's project was set in the context of bioinformatics tool development for human cancer genomics. The general area of research is human cancer genomics, with special emphasis on the application of high throughput DNA sequencing.



Sori Kang and Milica Ng

Milica Ng and CSL

Milica used her skills and diverse background in computer science, mathematics and engineering to help establish an innovative way to store and analyse biological data collected by CSL. In the future, this will strengthen CSL's ability to quickly and reliably select appropriate drug targets for a variety of important human health conditions.

INTRODUCING THE SPEAKERS

Dr Alicia Oshlack on the size of the genome

Your genome is your personal DNA sequence. DNA is a really long molecule that we represent with a string of letters which can be one of four types: A, T, G or C. The human genome has about 3 billion of these 'letters'.

Now let me give you a feel for how big this really is. Imagine Tolstoy's very thick novel *War and Peace*. It has around 3 million letters in it, so the human genome has as many letters as 1,000 copies of *War and Peace*. If you were to pile this many copies of the paperback novel on top of each other you would form a stack about as high as an 18-storey building.

There are a lot of letters in that stack and a lot of information that we are trying to understand. A genetic disease is like having a typo in one of those copies of *War and Peace*.

In order to achieve this we have to shatter the DNA into millions of small pieces and then we can sequence these fragments simultaneously.

So this is like taking our 18-storey stack of *War and Peace* books, ripping out all the pages, shredding them into pieces that only contain a few hundred letters and simultaneously 'reading' the letters on each tiny piece of paper.

As a result we have a huge pile of all the words and letters, but the trick is to try and put them back together correctly to make the original books. This can be quite a hard task and is really a computational and statistical challenge. You cannot do this by hand; you cannot even do this with an Excel spreadsheet!

My job as a bioinformatician is to work with these data computationally and statistically in order to make sense of the DNA and understand what it means. We try and find the 'typo' in the genome that is related to disease. I see my job as the interface between our ability to generate data and our ability to understand what it is telling us about biology.

Dr Alicia Oshlack is Head of Bioinformatics at the Murdoch Childrens Research Institute and an NHMRC Career Development Fellow.

You can find out more about Dr Alicia Oshlack – astrophysicist turned bioinformatician here – www.mathsofplanetearth.org.au/alicia-oshlack



“Bioinformatics is an exciting, fascinating and high-paced field that has real potential to make a difference to people.”

INTRODUCING THE SPEAKERS

Dr Ville-Petteri Mäkinen – computational engineer turned bioinformatician

A computational engineer by training, Ville has always been drawn to the boundary between biology and engineering. And he's applied this passion to analysing large datasets, establishing connections between our genes and clinical disease.

At the time of the interview Ville was a post doc at UCLA he has now brought his systems biology approach to Adelaide, as EMBL Australia Group Leader at the Heart Health research theme at the South Australian Health and Medical Research Institute (SAHMRI).

Dr Ville-Petteri Mäkinen talked to Stéphanie Pradier about the complications associated with diabetes, and how taking into account both macroscopic and microscopic biomarkers the links between type one diabetes, kidney disease and glaucoma can be better understood.

Watch the interview – www.mathsofplanetearth.org.au/ville-makinen



DR VILLE MAIKINEN
UNIVERSITY OF CALIFORNIA, LA

“The merging of statistics, biology and medicine is the way forward. The way to, hopefully, discover new cures and prevent diseases”

- Dr Ville-Petteri Mäkinen

Dr Stephane Guindon – biologist turned computational evolutionist

Stephane Guindon is a lecturer at The University of Auckland and the creator of the widely popular software PhyML for running maximum likelihood phylogenetic analyses.

Dr Guindon talked to us about his path — through the South of France — to bioinformatics and explains how, through his research, he witnesses natural selection everyday seeing differences at the DNA level that are not observable at the protein level.

Highlighting the increasingly critical role of computer scientists, mathematicians and statisticians in biology - while these skills have always been important the advent of high-powered computing will see the bonds between these disciplines strengthen and the importance of these skills grow exponentially.

Watch the interview – www.mathsofplanetearth.org.au/dr-stephane-guindon-biologist-turned-computational-evolutionist

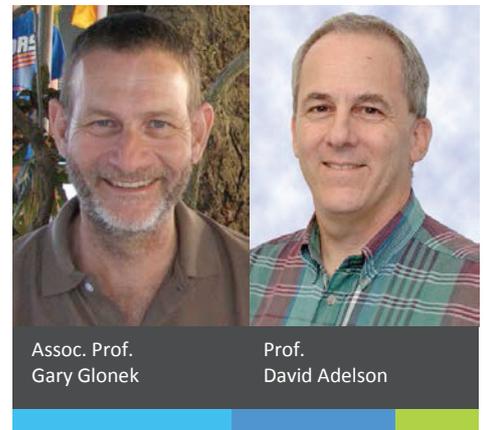


DR STÉPHANE GUINDON
THE UNIVERSITY OF AUCKLAND

DIRECTOR'S REPORT

The BioinfoSummer 2013 program featured an outstanding array of Australian and international keynote speakers including the 2013 Prime Minister's Prize for Science recipient, Professor Terry Speed, Dr Martin Morgan from the Fred Hutchinson Cancer Research Center, Professor Jeff Leek from Johns Hopkins University, Professor Falk Schreiber from Martin Luther University Halle-Wittenberg and Dr Alicia Oshlack, Head of Bioinformatics at the Murdoch Children's Research Institute.

The conference opened on the Monday with a keynote address by Terry Speed giving a unique perspective on the development of bioinformatics before, during



and after the era of genomics. Introductory sessions on Statistics for Biologists and Biology and Bioinformatics set the scene for the rest of the week. The day finished with a keynote address from Barbara Holland of the University of Tasmania on phylogenetic methods, followed by a reception in the Atrium of the Ingkarni Wardli Building.

The themes for the four major days of the symposium were evolutionary biology, systems biology, next generation sequencing and programming for bioinformatics. The program for each day comprised a blend of lectures from invited and local speakers as well as hands-on practical computing sessions. The daily prize for the best question led to very stimulating discussions in the question times. A bioinformatics programming competition run throughout the week generated great interest and many impressive entries.

On the Tuesday evening, Professor Stephen Donnellan, Chief Researcher at the South Australian Museum, presented a public lecture on "Evolution's mysteries unravelled with genomes and computers". Steve's lecture showing how the latest genetic technologies are being used to address fundamental questions such as how did life begin, why did sex evolve and how do species form, was very well attended and generated much interesting discussion in the question time and reception that followed.

The Thursday afternoon poster session gave delegates the chance to showcase their own research. The posters were of very high quality with prizes going to Westa Domanova and Reuben Buckley. Following the poster session, participants adjourned to the atrium of the Ingkarni Wardli Building to enjoy a barbecue.

The organisers are very grateful to the many staff and students who contributed to the smooth running and success of this event and for especially the tireless efforts of Imelda Leavy and Simi Henderson.

*Associate Professor Gary Glonek, The University of Adelaide
Professor David Adelson, The University of Adelaide*

"In my opinion, this year was the most successful, not just in the large numbers that came along, but in the reach to different fields of science."

- Terry Speed, recipient of the 2013 Prime Minister's Prize for Science

STUDENT PROFILE

Biostatisticians unravelling the data

A love for numbers has allowed Shila Ghazanfar to see her country and to explore the statistical minute workings of the human body. Born and bred in Western Sydney, Shila completed all her schooling in Parramatta.

A first generation Australian, born to immigrant Afghani parents, Shila has become the first in her family to complete a university degree. In high school, she enjoyed both chemistry and mathematics, but it was during her Bachelor of Science (Advanced Mathematics) degree at the University of Sydney that she discovered her love of statistics: a love that she pursued into an honours year.

“When I was introduced to Dr Jean Yang I told her that I wanted to work with lots of data; and she told me she had more data than you could poke a stick at. So I began my honours project with her in the realm of statistical bioinformatics.”

Shila hadn't studied any biology since high school so she had a little brushing up to do: “I set out to learn as much about biology as I could before my research project started. This way I would be better able to find, and interpret, the statistical characteristics that result from biological experiments.”

Even though Shila finds her studies exceptionally challenging at times, she really enjoys her research. It has enabled her to form collaborations — and friendships — with researchers and students at many Australian institutes, organisations and universities. And she has travelled all over Australia: “Before I began my PhD I had never been on a plane,” Shila remarked. “Now I have travelled to Adelaide, the Gold Coast and Melbourne on several occasions to attend academic workshops and events.”

At AMSI's BioInfoSummer Shila was impressed, inspired and excited by the national and international speakers. She said that the most valuable aspect of the event was making lasting connections with other postgraduate students and researchers.

“Collaborations across disciplines is where the potential to solve some of the world's biggest, and — in my case — smallest, problems lies.”

Shila isn't all about the numbers though; she enjoys playing squash, speaking French, cheering on her Western Sydney Wanderers and belly dancing.

Her studies coupled with attendance at events like BioInfoSummer have equipped Shila with the skills needed to statistically model and analyse genomic data.

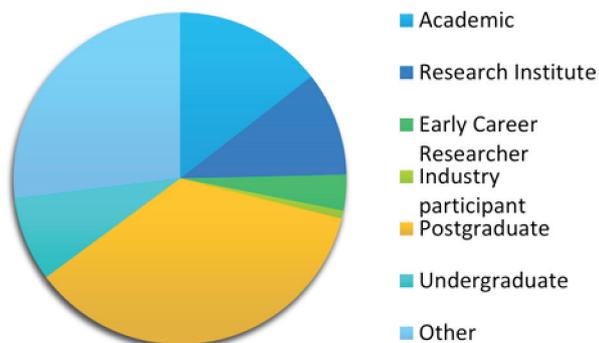
Shila's passion for numbers has allowed her to become a detective; to derive and extract meaning from data. The data Shila extracts meaning from (using her statistical and mathematical skills) allows us to explore the DNA, proteins and RNA of organisms, how they function, evolve and interact to help find more effective treatments for cancer.



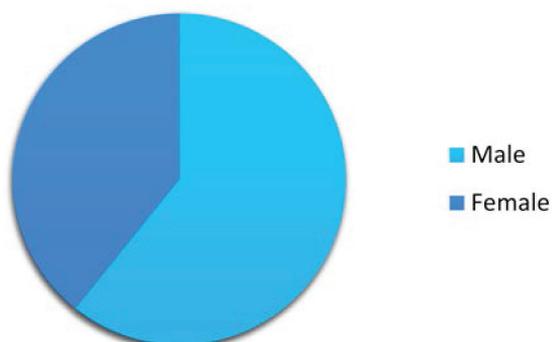
SHILA GHAZANFAR
THE UNIVERSITY OF SYDNEY

PARTICIPANTS

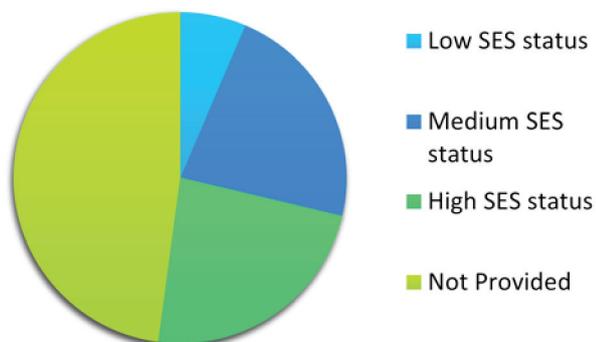
BREAKDOWN BY ENROLMENT STATUS



BREAKDOWN BY GENDER



BREAKDOWN BY SES STATUS



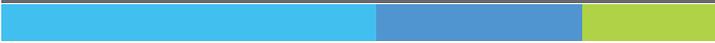
BREAKDOWN BY UNIVERSITY/ORGANISATION

Australian Centre for Plant Functional Genomics	1
Australian National University	1
Centenary Institute	1
Centre for Cancer Biology	1
Charles Darwin University	2
Children's Medical Research Institute	1
Central Queensland University	1
Deakin University	4
Fred Hutchinson Cancer Research Center	1
Johns Hopkins University	1
La Trobe University	2
Martin Luther University Halle-Wittenberg	1
Monash University	7
Murdoch Childrens Research Institute	1
NICTA	1
RMIT University	10
SA Pathology	7
The Australian Wine Research Institute	1
The Flinders University of South Australia	18
The University of Adelaide	89
The University of Auckland	2
The University of Melbourne	4
The University of New South Wales	2
The University of Queensland	2
The University of South Australia	8
The University of Southern Queensland	1
The University of Sydney	6
The University of Tasmania	1
The University of Technology, Sydney	1
The University of Western Australia	1
The Walter and Eliza Hall Institute of Medical Research	3
University of Malaya	2
Not Provided	4
Total	188

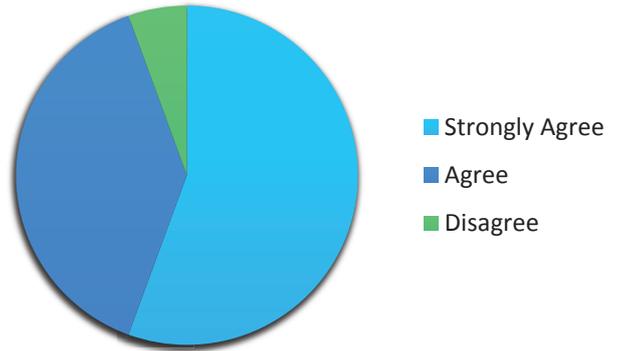
ABORIGINAL AND TORRES STRAIT ISLANDER PARTICIPATION

Number of Aboriginal and Torres Strait Islander participants: 2

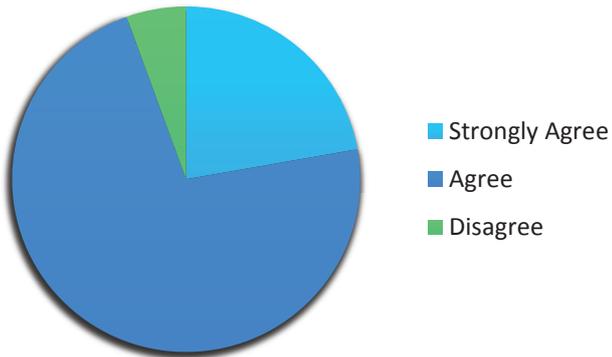
EVENT FEEDBACK



THE PRESENTATIONS WERE PROFESSIONAL AND ENGAGING



THE CONTENT PRESENTED WAS RELEVANT TO MY NEEDS



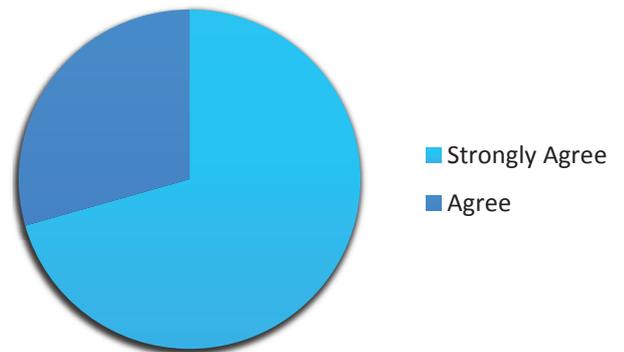
"... Awesome and engaging speakers and an opportunity to meet great early, middle or long career researchers.

- Luis Arriola

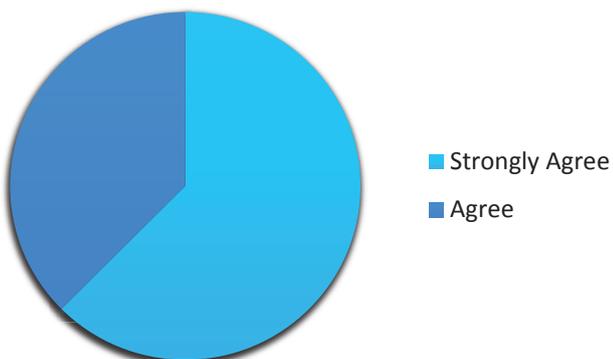
"It was great event with knowledgeable guest speakers and good opportunities to network. "

- Magdalena Budzinska

I WOULD RECOMMEND BIOINFOSUMMER TO MY COLLEAGUES & FRIENDS



I FOUND THE SOCIAL EVENTS A GOOD OPPORTUNITY TO NETWORK



"Great introduction to bioinformatics for the more statistical or mathematically inclined"

- Brock Hermans

Australian Mathematical Sciences Institute

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