AMSI BIOINFOSUMMER 2016

A SYMPOSIUM

IN BIOINFORMATICS

The University of Adelaide

28 November to 2 December 2016

AMSI BioInfoSummer 2016 would like to thank the following sponsors for their support:

AMSI BioInfoSummer 2016

Symposium in Bioinformatics

The University of Adelaide
28 November to 2 December 2016

INTRODUCTION

AMSI BioInfoSummer 2016 was held in November at the University of Adelaide, hosted by the School of Mathematical Sciences, with a collaborative effort in organisation from the University of Adelaide, University of South Australia, Flinders University and the South Australian Health and Medical Research Institute (SAHMRI). As one of the Australian Mathematical Sciences Institute's (AMSI) flagship higher-education events, AMSI BioInfoSummer provided bioinformatics training to students, researchers and academics alike, offering something for everyone by aiming to increase all delegates' knowledge and skills in this truly interdisciplinary field.

The symposium was opened by Professor Warren Bebbington (Vice-Chancellor and President, The University of Adelaide), Leanne Harvey (A/g Chief Executive Officer, Australian Research Council) and Professor Terry Speed (Laboratory Head, Walter & Eliza Hall Institute of Medical Research and Chair of the AMSI Scientific Advisory Committee) in the Flentje Lecture Theatre, each addressing the delegation of over 200 with an inviting welcome to the University of Adelaide, AMSI BioInfoSummer and the comprehensive bioinformatics program ahead.

The five-day program, designed for mathematicians, statisticians and biologists, started with an introductory overview on day one followed by four days of specialised content focused on high-dimensional data and multivariate analysis, experimental design and analysis for RNA sequencing, programming for bioinformatics and analysis of long-read (third-generation) data. Each day included a mix of keynote speakers, lectures and hands-on workshop practical sessions, in addition to a variety of program extras.

Featuring 15 national and international keynote speakers including Professor Orly Alter (University of Utah), Professor Simon Anders (Institute for Molecular Medicine, Finland), Dr Jason Chin (Pacific Biosciences), Professor Mingyao Li (University of Pennsylvania) and Professor Xia Yang (University of California, Los Angeles), the organising committee was committed to working towards gender balance throughout the event, and was delighted to have assembled a program of equal gender balance, which attracted a delegation that was similarly equal.

Additional program extras and outreach events were incorporated into the timetable to offer a number of networking and social activities for delegates to maximise their AMSI BioInfoSummer experience. A highlight and extremely popular event was the Poster Talks and Poster Session, which gave presenters the opportunity to spruik their research and share their work in the bioinformatics space with the delegation, in addition to a Women in STEM panel event, COMBINE careers session, public lecture and coding competition.

"AMSI BioInfoSummer 2016 continued a highly successful tradition of collaboration, showcasing the latest in Australian bioinformatics research through specialist lectures and hands-on training workshops. As Director of AMSI, I wish to acknowledge the efforts of Event Director Associate Professor Gary Glonek and the organising committees and lecturers from the University of Adelaide, Flinders University and the University of South Australia in helping coordinate such a successful event.

AMSI BioInfoSummer 2016 was made possible through the efforts of AMSI staff and the generous support of sponsors, participating universities and the Department of Education & Training. On behalf of AMSI, I thank all those involved in AMSI BioInfoSummer 2016 and invite potential partners to join us in supporting future events."

Professor Geoff Prince

Director
Australian Mathematical Sciences Institute

"The program comprised a blend of presentations by leading national and international researchers, and hands-on workshops on bioinformatics programming, providing unique exposure to the field of bioinformatics for delegates from a range of cognate disciplines."

Associate Professor Gary Glonek

AMSI BioInfoSummer 2016 Event Director
The University of Adelaide

PROGRAM

Monday 28 November

Introduction to Biology and Bioinformatics

Code, genetics, and the genetic code, the principles of statistical inference and the basics of sequence-targeted DNA cleavage using restriction enzymes.

Tuesday 29 November

High-Dimensional Data

Analysis and visualisation of high-dimensional data, elucidating gene networks of cardio-metabolic diseases, spectral decompositions and cancer diagnostics.

Wednesday 30 November

RNA-seq Data

Statistical analysis of RNA-seq data from reads to genes to pathways, single-cell sequencing analysis and alternative splicing.

Thursday 1 December

Long-Read (Third Generation) Sequencing Data

Recent progress in long-read genome assembly, the koala genome with long reads, single-molecule real-time sequencing, and integrating long reads with short reads.

Friday 2 December

Programming for Bioinformatics

Exploration of big multi-omics data sets beyond DESeq2, computing with k-mers and writing using bioinformatics software that people will use and cite.

TALKS

| TITLE	SPEAKER
Codes, genetics and the genetic code	Professor Terry Speed, The Walter and Eliza Hall Institute of Medical Research
EMBL Australia Bioinformatics Resource (EMBL–ABR)	Dr Philippa Griffin, Victorian Life Sciences Computation Initiative (VLSCI) & The University of Melbourne
Cancer diagnostics and prognostics from comparative spectral decompositions of patient-matched genomic profiles	Associate Professor Orly Alter, The University of Utah
Analysis and visualisation of high-dimensional data using molecular networks	Dr Melissa Davis, The Walter and Eliza Hall Institute of Medical Research
Elucidating gene networks of cardiometabolic diseases via systems genomics	Associate Professor Xia Yang, University of California, Los Angeles
Statistical issues in single-cell RNA sequencing analysis	Associate Professor Mingyao Li, University of Pennsylvania
Statistical analysis of RNA-seq data: from reads to genes to pathways	Professor Gordon Smyth, The Walter & Eliza Hall institute of Medical Research
Alternative splicing: one cell's trash is another's treasure	Dr Katherine Pillman, The University of South Australia & The University of Adelaide
Recent progress in long-read genome assembly: theory, practice and future challenges	Dr Jason Chin, Pacific Biosciences
The SMRT way to sequence a genome: adventures in PacBio sequencing	Dr Richard Edwards, The University of New South Wales
Sequencing the koala genome with long reads	Dr Denis O'Meally, University of the Sunshine Coast
Why I love k-mers, and why you should too	Dr Thomas Conway, IBM Research Australia & The University of Melbourne
Exploration of big multi-omics data sets, and comparative analysis beyond DESeq2	Dr Simon Anders, Institute for Molecular Medicine Finland, University of Helsinki
How to write bioinformatics software that people will use and cite	Associate Professor Torsten Seemann, The University of Melbourne

WORKSHOPS

| TITLE	WORKSHOP LEADER/S
Wet lab introductory session	Professor David Adelson, The University of Adelaide
Introduction to statistics session	Associate Professor Gary Glonek, The University of Adelaide Professor Jean Yang, The University of Sydney
High-dimension data computing lab	Associate Professor Ville-Petteri Mäkinen, The University of Adelaide Dr Melissa Davis, The Walter and Eliza Hall Institute of Medical Research
RNA-seq data computing lab	Dr Katherine Pillman, The University of South Australia & The University of Adelaide
Integrating long reads with short reads computing lab	Professor David Adelson, The University of Adelaide
Genomics in python computing lab	Dr Paul Wang, SA Pathology & The University of Adelaide Dave Lawrence, Centre for Cancer Biology
Graphics in r computing lab	Stephen Pederson, The University of Adelaide
k-mer manipulation with python computing lab	Dr Thomas Conway, IBM Research Australia & The University of Melbourne

PARTICIPANT BREAKDOWN

UNIVERSITY/INSTITUTION

|	
Australian Wine Research Institute	1
Centre For Cancer Biology	3
Children's Medical Research Institute	1
Curtin University of Technology	1
Deakin University	1
Edith Cowan University	1
Flinders University	25
Ghent University (Belgium)	1
Macquarie University	2
Millennium Science	1
Monash University	4
Murdoch Children's Research Institute	1
University of Ghana (Ghana)	1
Pacific Biosciences (USA)	1
The University of Adelaide	101
The University of Melbourne	10
The University of New South Wales	4
The University of Queensland	5
The University of Sydney	8
University of California, Los Angeles (USA)	1
University of Helsinki (Finland)	1
University of Pennsylvania (USA)	1
University of South Australia	19
University of Tasmania	2
University of Technology Sydney	3
University of the Sunshine Coast	1
University of Utah (USA)	2
Victoria University	1
Walter & Eliza Hall Institute of Medical Research	2
West Gippsland Veterinary Centre	1
TOTAL	**206**
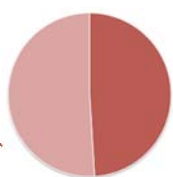
GENDER

Male	101
Female	105
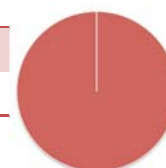
ATSI STATUS

Yes	2	1%
No	204	99%
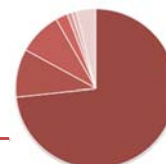
STATE/TERRITORY

SA	151	73%
VIC	20	10%
NSW	18	9%
QLD	5	2%
WA	2	1%
TAS	2	1%
INTERNATIONAL	8	4%
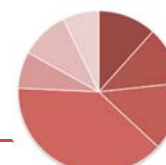
ACADEMIC STATUS

Undergraduate	24	12%
Honours	24	12%
Masters	28	14%
PhD	80	38%
Early-Career Researcher	15	7%
Academic	20	10%
Other	15	7%
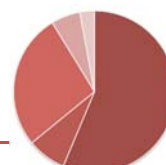
RESIDENCY STATUS

Australian Citizen	116	56%	Not an Australian Resident	12	6%
Permanent Resident	16	8%	Other	6	3%
Student Visa	56	27%			

GRANTS

AMSI Travel Grants

AMSI Travel Grants are offered to support AMSI Member student travel and accommodation to attend flagship higher-education events. AMSI BioInfoSummer 2016 grants were funded by the Australian Mathematical Sciences Institute, the Australian Government's Department of Education & Training and the University of Adelaide, and were determined on a competitive basis.

In 2016, AMSI Travel Grants were awarded to seven students, each from different AMSI Member Universities across Australia:

- Michael Gotama, The University of New South Wales
- Oliver Kulinski, The University of Tasmania
- Nishanthi Raveendran, Macquarie University
- Moeen Riaz, The University of Melbourne
- Anup Shah, The University of Queensland
- Alex Tokolyi, Monash University
- Abdul Zreika, The University of Sydney

CHOOSEMATHS Grants

CHOOSEMATHS Grants are designed to offer full or partial support for Australian female mathematical sciences students and early-career researchers to participate in the AMSI higher-education programs and/or assist with caring responsibilities. The BHP Billiton Foundation, as an initiative of the CHOOSEMATHS program, funded these grants to help females build and extend mathematical skills and professional networks.

In 2016, seven female students and two early-career researchers were awarded a CHOOSEMATHS Grant from five AMSI Member Universities:

- Alysha De Livera, The University of Melbourne
- Mary Dillon, The University of Melbourne
- Xiaochen Fan, The University of Sydney
- Daniela Gaio, University of Technology Sydney
- Anna Kretzschmar, University of Technology Sydney
- Yingxin Lin, The University of Sydney
- Loan Nguyen, The University of Queensland
- Julia Shore, The University of Tasmania
- Letitia Sng, The University of Sydney

PROGRAM EXTRAS

Welcome Lunch and Reception

The University of Adelaide hosted two welcome events this year, an informal lunch following Professor Terry Speed's opening keynote talk and a formal cocktail reception at the end of day one. These events were a great opportunity for the event coordinators to register and check in with the large delegation throughout the day, and enabled some professional and social networking between attendees as well!

Women in Science, Technology, Engineering & Mathematics Lunch

Hosted by the AMSI BioInfoSummer in conjunction with the Australian Mathematical Society's (AustMS) Women in Mathematics Special Interest Group (WIMSIG), the event provided an active forum of discussion focused on highlighting the contribution of women in science, technology, engineering and mathematics (STEM), raising awareness about issues for women, and promoting career pathways.

This lunchtime panel discussion and networking event attracted over 85 people attending from the AMSI BioInfoSummer delegation. The panel included:

- **Chair:** Associate Professor Alicia Oshlack (Head of Bioinformatics, Murdoch Children's Research Institute)
- Professor Tanya Monro (Deputy Vice Chancellor: Research and Innovation, University of South Australia)
- Professor Julie Owens (Pro-Vice Chancellor: Research Strategy, The University of Adelaide)
- Associate Professor Lesley Ward (AustMS Women in Mathematics Special Interest Group Chair & Associate Professor of Mathematics, University of South Australia)

Public Lecture

Professor Claire Wade (The University of Sydney) presented a public lecture at the University of Adelaide's Flentje Lecture Theatre, engaging a broad audience of over 100 with the core themes of the AMSI BioInfoSummer 2016 program through her talk "Learning More of Diseases and Behaviours Using Amazing Dog Genetic Models".

Professor Wade, who began her career in quantitative genetics before making the leap to genomics, discussed DNA sequencing from canine whole-genome sequences and canine high-density genotyping that has been assisting the mapping of disease and behaviour phenotypes in the dog, which is known to lead to learning more of human biology too!

COMBINE Careers Session

A panel and networking session at the Austral Hotel showcased and highlighted career opportunities in bioinformatics and provided a forum for discussion about different pathways to approximately 100 students and early-career researchers. Hosted by COMBINE (the student-run organisation for researchers in computational biology, bioinformatics and related fields) and Stephen Pederson (Bioinformatics Centre Coordinator at the University of Adelaide), the event featured a panel with diverse backgrounds who shared their stories, gave some advice and answered questions throughout the night:

- Dr Philippa Griffin (Victorian Life Sciences Computation Initiative, The University of Melbourne)
- Associate Professor David Lynn (South Australian Health and Medical Research Institute [SAHMRI] & Flinders University)
- Dr Katherine Pillman (The University of South Australia & The University of Adelaide)
- Dr Niharika Sharma (The Australian Centre for Plant Functional Genomics)
- Dr Rick Tearle (The University of Adelaide)
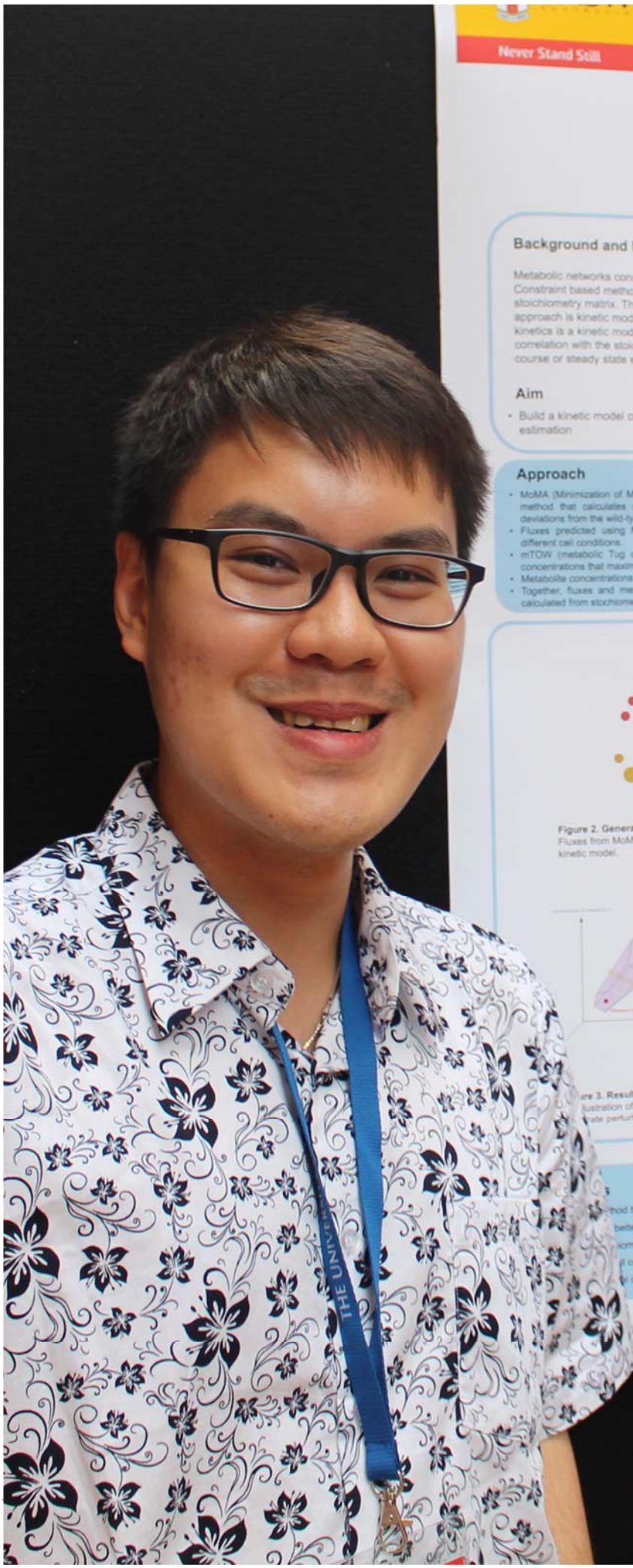
methodology

Author: Michael Gotama
Supervisor: Dr Bruno Gaeta

Background and Motivation

Metabolic networks consisting of hundreds to thousands of reactions cannot be understood by intuition alone. Constraint based methodologies are commonly used to gain insight into these networks as all they require is the stoichiometry matrix. The problem in this approach is that the dynamics of the system cannot be elucidated. Another approach is kinetic modelling that can provide insight into the model's dynamics but requires a lot of parameters. Linlog kinetics is a kinetic model that can be built based on stoichiometry data due to the simplicity of its parameters and their correlation with the stoichiometry. Prediction of the elasticity of this type of models can be improved by using time course or steady state experimental data.

Aim

- Build a kinetic model of an organism by a Bayes-linlog approach combining flux prediction with metabolite concentration estimation

Approach

- MoMA (Minimization of Metabolic Adjustment) is a quadratic programming optimization method that calculates reaction fluxes in a knockout model based on minimizing deviations from the wild-type model
- Fluxes predicted using MoMA can be used to predict metabolite concentrations in different cell conditions
- mTOW (metabolic Tug of War) is a constraint-based method for finding metabolite concentrations that maximize enzyme efficiency and minimize metabolite load
- Metabolite concentrations predicted using mTOW are correlated with experimental data
- Together, fluxes and metabolite concentrations can be used to refine the elasticities calculated from stoichiometry

Results

- The fluxes predicted using MoMA around 0.8
- The mTOW 95% confidence interval 0.62
- Concentration predictions for some are improved using the Bayes-linlog
- Most elasticities calculated using the using COPASI

Methodology and Results

MOMA   >   mTOW   >   Bayes' estimator   >

Figure 2. General outline of the Bayes-linlog kinetic model construction
Fluxes from MoMA are used in mTOW. Both fluxes and metabolite concentrations are balanced using stoichiometry data to estimate a kinetic model.

Figure 3. Results of simulations against experimental data
Illustration of the mTOW-MoMA feasible solution. (2) Metabolites predicted from mTOW. (3) Balancing elasticity using prior from rate perturbation

References

1. Smallbone, K from nothing modelling. F
2. Segre, D., Vi perturbed metabolic (2002)
3. Tepper, N a Balance betwe Metabolite Levels

method that generates the elasticity from balancing a stoichiometry prior and the likelihood from better in predicting the changes in internal metabolite concentrations compared to the linlog stoichiometry alone. Although the simulations data generated from MoMA and mTOW were could provide some informative values as shown by the Pearson correlation of predicted data.

Poster Competition: Poster Talks & Poster Session

Sixteen delegates submitted a poster abstract prior to the symposium and participated in the poster competition, which included two components: Poster Talks and the Poster Session. A panel of judges determined winners for Best Poster and Best Student Poster.

The lunchtime Poster Talks gave presenters the opportunity to spruik their research poster in 120 seconds or less to highlight their work in bioinformatics to the delegation.

The evening Poster Session gave delegates the opportunity to have a closer look at each poster, with the creators available to discuss their research one-on-one or in small groups.

Best Poster

Katherine Aiello (The University of Utah)

"Platform-Independent Genome-Wide Pattern of DNA Copy-Number Alterations Predicting Astrocytoma Survival and Response to Treatment Revealed by the GSVD Formulated as a Comparative Spectral Decomposition"

Best Student Poster

Riaz Moeen (The University of Melbourne)

"Uncovering the pharmacogenetic basis of age-related macular degeneration using a next-generation sequencing approach"

Symposium BBQ Dinner

An informal BBQ was held following the Poster Session in the Ingkarni Wardli Atrium at the University of Adelaide. This was a casual affair, encouraging the delegation to attend the Poster Session to get a closer look at each research poster and discuss the research with poster creators. Congenial discussions of the posters continued over the BBQ dinner and drinks, with over 115 attendees enjoying the event. This dinner was also an opportunity for attendees to socialise, relax and reflect on their AMSI BioInfoSummer experience.

Coding Competition

This year's algorithms and data-structures coding competition attracted 16 entrants, a combination of individuals and teams, who undertook the challenge of finding solutions to a set of ROSALIND bioinformatics problems during the symposium. This event was coordinated by Dan Kortschak (The University of Adelaide) who declared the competition winner with the greatest increase in their problem point score at the end of the week to be Dr Michael Roach (Australian Wine Research Institute).
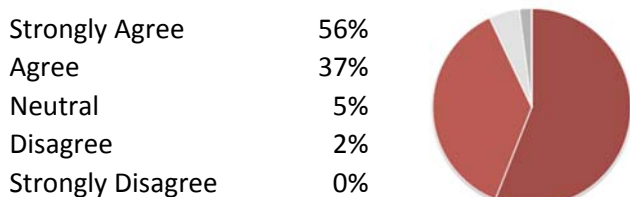
FEEDBACK ANALYSIS

Thirty-five per cent of attendees at AMSI BioInfoSummer 2016 completed the online survey to provide their feedback and comments on the event. There was particular satisfaction with the quality of the event and speakers, with 96 per cent of responses agreeing or strongly agreeing that the speaker knowledge of the subject content was high. In rating their overall experience at the event on a scale of 1 to 10, where 1 is Poor and 10 is Excellent, the respondents' average rating was 8.1.
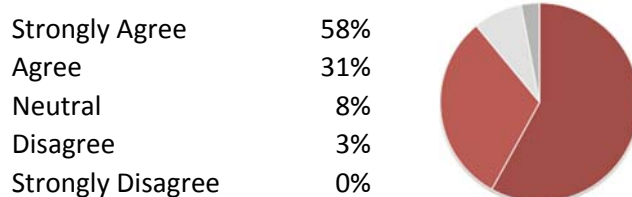
The responses received to the variety of questions were all very positive, with over 80 per cent of the attendees indicating that they "Strongly Agreed" or "Agreed" that the event was well-organised and of a high standard, and that they would recommend the event to others. Program extras were also well-received, particularly the Poster Talks and Poster Session with 96 per cent of attendees agreeing that these were good opportunities to learn about other research areas.

In explaining their primary motivation or reason for attending AMSI BioInfoSummer, 39 per cent of respondents indicated that they had wanted to broaden their knowledge, while 44 per cent indicated that the program related to their research interest.
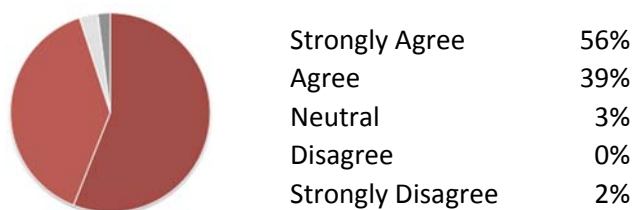
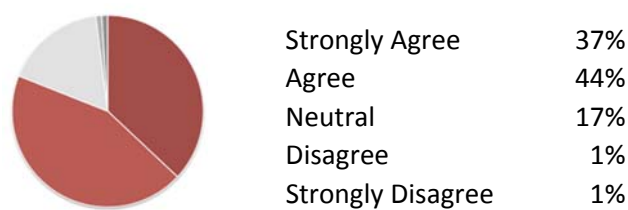## OVERALL, BIOINFOSUMMER WAS OF A HIGH STANDARD

Strongly Agree	56%
Agree	37%
Neutral	5%
Disagree	2%
Strongly Disagree	0%

OVERALL, THE SCHOOL WAS WELL-ORGANISED

Strongly Agree	58%
Agree	31%
Neutral	8%
Disagree	3%
Strongly Disagree	0%

THE PRESENTATIONS WERE PROFESSIONAL AND ENGAGING

Strongly Agree	56%
Agree	39%
Neutral	3%
Disagree	0%
Strongly Disagree	2%

THE CONTENT PRESENTED WAS RELEVANT TO MY STUDY/PROFESSION

Strongly Agree	37%
Agree	44%
Neutral	17%
Disagree	1%
Strongly Disagree	1%

I FOUND THE SOCIAL EVENTS A GOOD OPPORTUNITY TO NETWORK

Strongly Agree	28%
Agree	55%
Neutral	11%
Disagree	4%
Strongly Disagree	2%
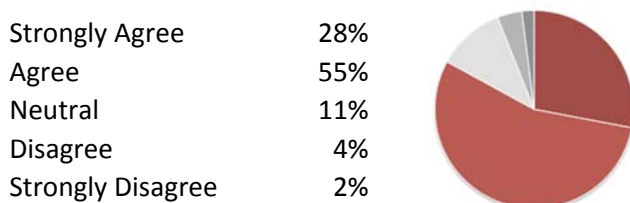
I WOULD RECOMMEND BIOINFOSUMMER TO OTHERS

Strongly Agree	50%
Agree	32%
Neutral	16%
Disagree	2%
Strongly Disagree	0%
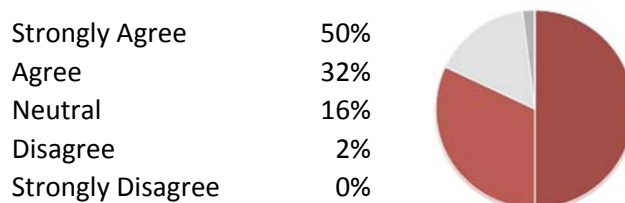
STUDENT PROFILE

YOUTUBE TO BIOINFOSUMMER:
THE GUTS OF DATA ANALYSIS

Daniela Gaio, University of Technology Sydney

Having taught herself coding using instructional videos on YouTube, PhD student Daniela Gaio arrived at AMSI BioInfoSummer 2016 (BIS) with some gaps to fill.

"BIS helped me put the pieces together from my own learning. I came away with a better understanding of the data-analysis steps in genomic, transcriptional and proteomic analysis," she says.

Currently studying the microbial community of the gut in health and disease, the University of Technology Sydney student also gained valuable contacts within the field.

"I was excited to meet and network with highly-skilled people also working on projects within the bioinformatics space," she explains.

With a background in genetics, microbiology and neurobiology, Daniela is new to bioinformatics, having entered the field only last year.

"As I strive to understand the health impacts of the microbiome on the gut, bioinformatics allows me to explore different aspects of biology. I can zoom in on cellular processes, use tools to investigate interactions of molecules and make sense out of large datasets," she explains.

Undertaking your own data analysis and learning how to write your own scripts, she believes, is the only way you can fully appreciate your data's meaning.

"Without bioinformatics skills, if the output differs from your expectations you are not equipped to understand the results and seek other explanations for the outcome," she says.

This powerful BIS experience may have been out-of-reach for Daniela, if not for funding assistance through a Choose Maths grant. Funded by the BHP Billiton Foundation as part of the Choose Maths project, it is this support that she believes is vital to empower women in mathematics and remove barriers to attending events.

"We need to kill the stereotype that women are less talented than men at subjects such as mathematics and bioinformatics. In fact often we are more precise and disciplined, powerful features for these fields," she says.

Keen to also take advantage of AMSI's internship opportunities and develop her computational data analysis expertise, Daniela already has a clear vision for an industry future.

"I want to work in a probiotics industry. I would love to discover how to develop cocktails of probiotics, the decision-making process and trials in order to determine their clinical effectiveness in relieving gastrointestinal symptoms," she says.

Learning more of diseases & behaviours using amazing dog genetic models

PUBLIC LECTURE

PART OF **AMSI BIOINFOSUMMER 2016**

6PM TUESDAY 29 NOV 2016
FLENTJE LECTURE THEATRE
THE UNIVERSITY OF ADELAIDE

PROFESSOR CLAIRE WADE

FACULTY OF VETERINARY SCIENCE, THE UNIVERSITY OF SYDNEY

What makes a pointing dog point or a hunting dog retrieve? What genetic differences underpin these large behavioural differences between them?

Professor Claire Wade from the University of Sydney explores the differences in dog breeds and their highly and reproducibly diverse nature in both external body characteristics and their intrinsic behaviours.

Through extensive DNA sequencing assisting the mapping of disease and behaviour phenotypes, we learn more of what makes dogs (and us) tick!

IMAGE: OVERLAPS BETWEEN KNOWN BIOLOGICAL PROCESSES BY VILLE-PETTERI MÄKINEN, SAHMRI

AMSI RESEARCH

MEDIA RELEASE

DISCOVERING THE WHY OF DOGS

Adelaide, South Australia — 24 November 2016

Have you ever wondered why greyhounds can outrun Usain Bolt, beagles can sniff out the faintest scent or kelpies are such good workers?

The Australian Mathematical Sciences Institute's BioInfoSummer Public Lecturer Professor Claire Wade is using genetics to answer these questions. A geneticist with The University of Sydney's Faculty of Veterinary Science, she believes these insights may not only help us improve pet health and welfare, but advance our understanding of human biology and treatment targets.

"Studying the genetics behind behaviours in dogs such as athleticism or separation anxiety has potential to open new treatment avenues not only for our pets but for us as well," Professor Wade explains.

There are two broad types of dog breeds, ancient breeds and then all the others. As well as genetics and DNA, the breed groups share a long history of being manipulated by humans.

"We have been making use of the inherent abilities of dogs for a long time. We've used artificial selection to concentrate specific abilities to fit breeds for purpose, from hunting and racing to working on farms," says Professor Wade.

Professor Wade's work has focused on identifying variations within breeds, beneficial mutations prevalent across a breed as a result of natural selection, a process referred to selective sweeping.

"Selective sweeps have provided insights into behaviour variations within a breed. For example, we've found that kelpies are good working dogs partly due to their insensitivity to prickles, greyhound athleticism is a case of good cardiovascular genes and Nova Scotia duck trolling retrievers have genes that affect their ability to taste bitter things, like citrus," she explains.

Animal separation anxiety, something many dog owners live with and manage particularly over the silly season with holidays and long days away from home socialising, is also an area of interest for Professor Wade.

"As with most complex traits, anxiety is affected by a mix of genes and the environment. There is no evidence that any specific breed is more susceptible but it does seem to run in family lines (of any breed)," says Professor Wade.

Professor Wade believes breeding practices have played a role. She explains that "for hundreds of years we've selected affectionate dogs for breeding who appear to love us increasing the prevalence of anxiety in our companions."

Professor Wade will deliver the BioInfoSummer Public Lecture from 6pm Tuesday 29 November 2016 at the Flentje Lecture Theatre, Barr Smith Building (near Hub Central) at the University of Adelaide. Exploring the cutting edge of bioinformatics and mathematical and computational biology, BioInfoSummer runs from 28 November to 2 December at the University of Adelaide.

"Illustrating the cross-disciplinary application of mathematics and statistics, this event is a chance for advanced undergraduate and postgraduate students to experience this growing and important field," says AMSI Director Professor Geoff Prince.

DIRECTOR'S REPORT

ASSOCIATE PROFESSOR
GARY GLONEK

The University of Adelaide

BioInfoSummer 2016 was held at the University of Adelaide, hosted jointly by the School of Mathematical Sciences and the School of Biological Sciences, and attracted over 200 registrants.

As with the previous Adelaide BioInfoSummer meetings, BioInfoSummer 2016 was organised cooperatively by staff from the University of Adelaide, the University of South Australia, Flinders University and the South Australian Health and Medical Research Institute (SAHMRI).

The major themes were high-dimensional data and multivariate analysis, design and analysis of RNA-seq experiments, long-read sequencing data and eukaryotic whole-gene sequencing, as well as programming for bioinformatics. The program comprised a blend of research presentations by leading national and international researchers, and hands-on workshops on bioinformatics programming. It provided a unique exposure to the field of bioinformatics for PhD students and early-career researchers from a range of related areas.

The program featured 15 national and international speakers including Professor Orly Alter (University of Utah), Professor Simon Anders (Institute for Molecular Medicine Finland), Dr Jason Chin (Pacific Biosciences), Professor Mingyao Li (University of Pennsylvania) and Professor Xia Yang (University of California, Los Angeles).

The symposium commenced with a welcome to the University by Vice Chancellor Professor Warren Bebbington and was officially opened by acting Chief Executive Officer of the ARC Leanne Harvey. The opening address, entitled Codes, Genetics and the Genetic Code, was delivered by Professor Terry Speed. Parallel introductory sessions were provided after the welcome lunch.

A well-attended session on statistics for biologists was given in parallel to a wet lab session that introduced the basics of sequence-targeted DNA cleavage using restriction enzymes. The wet lab provided a valuable appreciation of the complexities of biological experimentation for participants with backgrounds in mathematics or computing.

In keeping with previous Adelaide BioInfoSummer meetings, the daily question competition ensured lively discussion at the end of each talk and a bioinformatics programming competition was run across the week. The poster competition attracted a number of outstanding entries and each presenter gave a one-minute presentation to the entire symposium before the main poster-viewing session. The judges had a difficult time deciding between so many high-quality posters and eventually awarded both the student prize and the unrestricted prize to student entries.

A vibrant social program, including the welcome reception and conference barbecue, provided valuable opportunities for networking. The well-attended COMBINE careers session held at the Austral Hotel provided further networking opportunities as the panel shared their experiences of bioinformatics career pathways. The

Public Lecture, presented by Professor Claire Wade from The University of Sydney, generated great interest among the BioInfoSummer participants and the broader community.

A Women in Science, Technology, Engineering and Mathematics (STEM) Lunch was organised in collaboration with the AUSTMS Women in Mathematics Special Interest Group (WIMSIG) and chaired by Alicia Oshlack, Head of Bioinformatics at the Murdoch Children's Research Institute. The lunch was very well-attended and also well-supported by the senior staff from the local universities.

The organising committee was keen to ensure gender balance in the program and was very pleased to have assembled a program of outstanding speakers with equal gender balance. It was also pleasing to note that the gender balance of the participants was similarly equal.

EVENT COMMITTEES

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

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- **Committee Chair:** Matt Ritchie, Walter and Eliza Hall Institute of Medical Research
- Nicola Armstrong, Murdoch University
- Gary Glonek, The University of Adelaide
- Barbara Holland, The University of Tasmania
- Jonathan Keith, Monash University
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- **Convenor:** David Adelson, The University of Adelaide
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- Thuc Le, The University of South Australia
- Ville-Petteri Mäkinen, SAHMRI
- Stephen Pederson, The University of Adelaide
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Organising Committee

- **Event Director:** Gary Glonek, The University of Adelaide
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