

Highlights from the 1st Student Symposium on Computational Biology and Life Sciences, organised by ISCB Regional Student Group, UK

Farzana Rahman¹, Rohit Farmer², Sayoni Das³, Fatima Vayani⁴, Mehedi Hassan^{1*}

Abstract

This short report summarises the scientific content and activities of a student-led event, the 1st student symposium by the UK Regional Student Group of the International Society for Computational Biology. The event took place on October 2014.

Keywords

meeting report — ISCB — Student Council — Regional Student Group

¹Genomics and Computational Biology Research Group, University of South Wales, CF371DL, UK

²School of Biosciences, University of Birmingham, Birmingham, B152TT, UK

³Research Department of Structural and Molecular Biology, UCL, WC1E6BT, UK

⁴Algorithms and Bioinformatics Group, King's College London, UK

*Corresponding author: imehedi@iscb.org

Contents

Introduction	1
1 1st Student Symposium on Computational Biology and Life Sciences	1
1.1 Scope and format of the meeting	1
1.2 List of keynote speakers	2
1.3 Keynotes Summary	2
1.4 Student and Early Career Researchers Presentations	2
1.5 Award Winners	3
2 Conclusion	3
3 Future Editions	3
Future Editions	3
Acknowledgments	3
References	3

Background

The UK Regional Student Group (RSG UK) of the International Society for Computational Biology is part of the global network of students and early stage post-doctoral researchers. The group was formed in December 2013, with a vision to strengthen and enhance the existing young computational biologists' network through dynamic activities. We felt the urge to initiate a platform for tomorrow's computational biologists in the United Kingdom and took the inspirations from similar initiatives to form our group[1, 2]. We aim to build a wider

network to promote next generation of computational biologists in the UK.

Our current leadership and members include research students and postdoctoral researchers from computational biology and life sciences backgrounds. The community offers networking, soft skill enhancement opportunities for both undergraduate and post-graduate students, and to develop the relationship between young computational biologists and academic/industry partners within UK.

1. 1st Student Symposium on Computational Biology and Life Sciences

The inaugural event of scientific networking activity of the group was the 1st Student Symposium on Computational Biology and Life Science on 8th October 2014. The event took place at the University of South Wales, UK. The symposium took inspirations from the workshops and conferences arranged by the ISCB Student Council and its regional student groups across the globe [3, 4, 5]. Fujitsu Ltd, a global provider of information technology services and HPCWales, a pan-wales supercomputing infrastructure, supported the event.

1.1 Scope and format of the meeting

The main scope of this meeting was to create opportunities for students and young researchers to interact with senior academics and investigators from all over the UK where they can discuss ideas, exchange knowledge and build networks. In addition, four distinguished scientists were invited to deliver keynote speeches.

The traditional scientific component of the meeting consisted of three sessions of oral presentations by Students and postdoctoral researchers. The sessions also included four keynote presentations from senior scientists and one inaugural presentation on RSGs and their roles.

Dr Rhobert Lewis from the University of South Wales gave a welcome note. Dr Manuel Corpas, the founder of the ISCB Student Council, delivered a keynote to provide an overview of developing next generation of Computational Biologists through the Regional Student Groups across the globe.

Dedicated poster sessions and industrial partner talks took place during coffee breaks between oral sessions. As part of the industrial partner talk, Dr Jonathan Mullins, from Moleculomics Ltd., gave a short presentation on generating high-value genome-scale molecular information to increase and improve knowledge of interactions between organisms and chemical compounds using the tools and services developed by Moleculomics Ltd.

The RSG UK team received more than 20 abstracts from students who wished to present their work at the symposium. The submitted abstracts were peer-reviewed by ten independent reviewers of which five reviewers were senior academic and principal investigators and other five reviewers were mid-career researchers. The reviews selected a total of six abstracts for oral presentations, and twelve abstracts for poster presentations. Overall, 65 delegates from 24 UK institutions and industries attended the symposium and the programme.

All abstracts accepted for oral and poster presentations are available online from <http://rsg-uk.iscbsc.org/sym2014/>.

1.2 List of keynote speakers

Following scientists generously agreed and delivered keynotes speeches on the day.

- Dr Alex Bateman (EMBL-EBI, Cambridge University)
- Dr Natasha De Vere (National Botanic Garden of Wales)
- Dr Chris Creevey (IEBRS, Aberystwyth University),
- Dr Tatiana Tatarinova (University of Southern California)

1.3 Keynotes Summary

Dr Natasha de Vere's keynote speech gave an overview of her work on DNA Barcoding of Welsh and UK flora to create an open access resource for people, wildlife and the environment [6]. In 2012, Dr. de Vere led a team to complete the barcoding of all of the Welsh flora and now working on barcoding all of

the British flora.

The second keynote speech by Dr Alex Bateman underlined the impacts of biological databases in modern day computational biology research and highlighted the importance of the role of bio-curators in biological studies. Dr. Bateman emphasised the role of biocurators by addressing them as the "unsung heroes of biology" who orders and make sense of the immense primary literature for us. He encouraged the audience in participating contributing to public encyclopaedia the Wikipedia and shared his recent experiences with some initiatives to inspire the scientific community in enriching Wikipedia. [7, 8, 9] In the second part of his talk he gave our delegates an overview of his career path, which included some invaluable advice for young researchers hoping to make their way into a successful research career.

The third keynote speech by Dr Christopher Creevey, highlighted development of system-level approaches in understanding microbial community interactions by identifying genomic factors influencing phenotypic changes in organisms from Bacteria to Eukaryotes. Dr. Creevey's talk included the [10] which aims to generate a reference set of rumen microbial genome sequences. The project surveyed the rumen bacterial diversity to examine the culturable fraction of the rumen bacterial microbiome and reported that there are few novel but many uncultured taxa within the rumen bacterial microbiome. In addition, they have identified taxa where further cultivation efforts are clearly required.

Finally, Dr Tatiana Tatarinova's keynote speech presented two novel algorithms, GPS [11] and reAdmix [12] to determine biogeographic origins of individuals. Both methods are species-independent and were successfully applied to analysis of humans, plants and animals. Tatiana also told about exciting aspects of bioinformatician's life, such as field trips to remote parts of the Earth to find nearly extinct species, studies of ancient DNA and efforts to analyze and preserve DNA of disappearing Native Siberians.

1.4 Student and Early Career Researchers Presentations

There were two presentations from Post Doctoral research fellows and four presentations from current Ph.D. students. In the first post-doctoral talk, Dr Romain Studer from EMBL-EBI, Cambridge, UK discussed his current research on finding evolutionary pattern of the phosphoproteome in 18 yeast species. Dr Studer highlighted that till date the investigate of Phosphoproteome mostly covers model species (e.g. human, baker's yeast), and there is a lack of comprehensive phylogenetic analysis of phosphorylation. He and his colleagues are currently working on estimating the evolutionary analysis of phosphosites in yeast species.

Dr Ranjit Das from Sheffield University gave the second

post-doctoral talk, where he discussed the evolution of miRNAs and their targets among hominoid primates. Dr Das is working on identifying and understanding the uniquely gained and lost miRNAs within hominoids and its potential implications.

In the student presentation section, Sam Nicholls from Aberystwyth University presented Goldilocks, a Python package that provides users with functionality for locating suitable regions with a genome for analysis. Goldilocks package is available at <https://github.com/SamStudio8/goldilocks>.

Francesco Rubino from Aberystwyth University gave an insight into metagenomics analysis of the rumen microbiome that reveals functional isoforms driven from niche differentiation for nutrient acquisition.

Silvia Bartolucci from Kings College London, presented a statistical approach to investigate basic, systematic features exhibited by adaptive immune systems. Silvia's work focuses on Dynamical analysis of diluted associative networks: a minimal model for the adaptive immune system.

Russel Sutherland from Kings College London presented their work on tumor grade prediction across multiple adenocarcinomas using exome sequencing data.

1.5 Award Winners

The High Performance Computing Wales (HPCW) consortium, and Fujitsu Services UK limited sponsored two travel fellowships that were awarded to Silvia Bartolucci and Vasileios Panagiotis Lenis to attend and present at the Symposium.

A judging committee formed of senior researchers present at the event, selected three speakers for three awards; one for the oral presentation and two for poster presentations. Sam Nicholls from the Aberystwyth University received the best oral presentation award for his work titled "Goldilocks: Locating genomic regions that are 'just right'".

Danielle Avancini received best poster award for his poster titled "A Molecular Dynamic Web Server for Analysis of DNA Structure" and the runner up poster award went to Stefani Dritsa for his poster titled "Towards the increase of the thermostability of a psychrophilic enzyme".

The oral and poster presentation award were generously sponsored by the graduate research center of the University of South Wales, UK. Sam Nicholls, Danielle Avancini and Stefani Dritsa received F1000 awards for their presentations at the RSG UK symposium.

In addition to the aforementioned awards, High Performance Computing Wales chose Karen Sinu Ting's work on "Concatominations: identifying unstable taxa in morpho-

logical and phylogenomic supertrees using Safe Taxonomic Reduction" that gives Karen to get exclusive supercomputing access and support from HPC Wales facility.

2. Conclusion

The initiative of forming the RSG UK and hosting the symposium was highly appreciated among peers, delegates and sponsors. The quality of the student presentations and high profile keynotes were greatly admired. The participants agreed that the nature of the symposium and the scope of networking best suited their interest. Symposium organisers received positive feedback and comments from senior and junior researchers alike. Despite being organised by a newly formed group with very small initial membership, the attendance was excellent, which reflects that the symposium news was well disseminated. Overall, the symposium was a great success.

3. Future Editions

The successful completion and turn-around of the 1st symposium encouraged to organise yearly symposium. The RSG UK is pleased to announce that the 2nd student symposium will be organised in 2015 in October at The Genome Analysis Centre (TGAC), Norwich. The aim is to arrange a symposium with a dedicated session for bioinformatics workshop. The further detail will be available on RSG UK website <http://rsg-uk.iscbsc.org/>.

Acknowledgments

The success of the student symposium organised by RSG UK hugely depended on the external and internal support from senior researchers, student lead activity enthusiasts and sponsors who helped to make the event a great success. Our special thanks to Prof. Denis Murphy, the faculty advisor of RSG UK, who encouraged the organisers to make the event a success since its inception. We are greatly thankful to the following people for their guidance and support in different aspect of the symposium arrangement Dr Timothy Ebbels (Imperial College London), Dr Erhan Elhaik (University of Sheffield), Dr Thomas Di Domenico (University of Cambridge), Dr Owain Kerton (University of South Wales), Umesh Nandal (University of Amsterdam), Chinmay Kumar Dwibedi (Ume University, Sweden), James Pack and Charlie Godfrey from HPC Wales, UK and Mehnaz Tabassum Khan from Khulna University, Bangladesh. Our special gratitude to Fujitsu Services UK Limited and HPC Wales Consortium for their financial and logistics support to the event. We would also like to extend our thanks to the Graduate Research Office of the University of South Wales, the International Society for Computational Biology's Student Council for their continuous support to make the symposium a great success.

References

- [1] Avinash Kumar Shanmugam, Geoff Macintyre, Magali Michaut, and Thomas Abeel. Ten simple rules for starting a regional student group. *PLoS Comput Biol*, 9(11):e1003340, 11 2013.
- [2] Aidan Budd, Manuel Corpas, Michelle D. Brazas, Jonathan C. Fuller, Jeremy Goecks, Nicola J. Mulder, Magali Michaut, B. F. Francis Ouellette, Aleksandra Pawlik, and Niklas Blomberg. A quick guide for building a successful bioinformatics community. *PLoS Comput Biol*, 11(2):e1003972, 02 2015.
- [3] Manuel Corpas. Graduate students band together to foster communication. *Nature*, 436:1204, 2005.
- [4] Geoff Macintyre, Magali Michaut, and Thomas Abeel. The regional student group program of the iscb student council: Stories from the road. *PLoS Comput Biol*, 9(9):e1003241, 09 2013.
- [5] Farzana Rahman, Katie Wilkins, Annika Jacobsen, Alexander Junge, Esmeralda Vicedo, Dan DeBlasio, Anupama Jigisha, and Tomas Di Domenico. Highlights from the tenth iscb student council symposium 2014. *BMC Bioinformatics*, 16(Suppl 2):A1, 2015.
- [6] Natasha de Vere, Tim CG Rich, Col R Ford, Sarah A Trinder, Charlotte Long, Chris W Moore, Danielle Satterthwaite, Helena Davies, Joel Allainguillaume, Sandra Ronca, et al. Dna barcoding the native flowering plants and conifers of wales. *PLoS One*, 7(6):e37945, 2012.
- [7] Robert D Finn, Paul P Gardner, and Alex Bateman. Making your database available through wikipedia: the pros and cons. *Nucleic acids research*, page gkr1195, 2011.
- [8] Darren W Logan, Massimo Sandal, Paul P Gardner, Magnus Manske, and Alex Bateman. Ten simple rules for editing wikipedia. *PLoS computational biology*, 6(9):e1000941, 2010.
- [9] Paul P Gardner, Jennifer Daub, John Tate, Benjamin L Moore, Isabelle H Osuch, Sam Griffiths-Jones, Robert D Finn, Eric P Nawrocki, Diana L Kolbe, Sean R Eddy, et al. Rfam: Wikipedia, clans and the “decimal” release. *Nucleic acids research*, 39(suppl 1):D141–D145, 2011.
- [10] Christopher J Creevey, William J Kelly, Gemma Henderson, and Sinead C Leahy. Determining the culturability of the rumen bacterial microbiome. *Microbial biotechnology*, 7(5):467–479, 2014.
- [11] Eran Elhaik, Tatiana Tatarinova, Dmitri Chebotarev, Ignazio S Piras, Carla Maria Calò, Antonella De Montis, Manuela Atzori, Monica Marini, Sergio Tofanelli, Paolo Francalacci, et al. Geographic population structure analysis of worldwide human populations infers their biogeographical origins. *Nature communications*, 5, 2014.
- [12] Konstantin Kozlov, Dmitry Chebotarov, Mehedi Hassan, Martin Triska, Petr Triska, Pavel Flegontov, and Tatiana

Tatarinova. Differential evolution approach to detect recent admixture. *arXiv preprint arXiv:1503.02117*, 2015.