SASBi | UNIVERSITEIT VAN PRETORIA / UNIVERSITY OF PRETORIA / YUNIBESITHI YA PRETORIA | **South African Society for Bioinformatics**
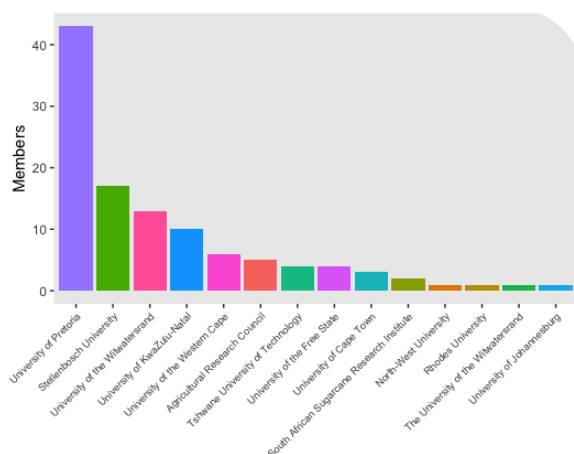
Council Corner

SASBi member affiliations 2019

Alisa Postma, Werner Smidt and Oleg Reva

The South African Society for Bioinformatics was established in September 2012. This national association seeks to promote the discipline of bioinformatics both locally and internationally. Membership of this society is closely linked to the bi-annual conference hosted jointly by SASBi and the South African Genetics Society (SAGS). The figure above illustrates the current distribution of affiliations of all local SASBi members. In future, the society hopes to attract more members, especially from institutions which are currently under-represented. This will enable SASBi to optimise the application and accessibility of bioinformatics and computational biology to address the needs of South Africa.

Volume 2, April 2019

Inside:

Bioinformatics at the University of Pretoria

Fourie Joubert

Bioinformatics went public for the first time at the University of Pretoria in 1999, when Fourie Joubert presented a bioinformatics short course together with Winston Hide and Janet Kelso from SANBI. This was followed by a long series of short courses presented at UP over the years.

The Bioinformatics and Computational Biology Unit was established in 2003, with a grant from the University of Pretoria for R 3,7 million, together with floor space on top of the new FABI Square building. At the same time, BSc Hons, MSc and PhD programmes in bioinformatics were approved by SAQA, and the Unit was ready to start functioning. The Unit has since then been involved in undergraduate training, post-graduate training, research, support and services. In the years 2003 – 2008 the Unit was funded by the National Bioinformatics Network, which allowed for the appointment of additional contract staff members during the period. Professor Oleg Reva was appointed by UP as academic staff member in 2006, and Oliver Bezuidt was appointed as academic staff member from 2009-2012. Mr. Johann Swart was appointed as system administrator in 2011. The Unit was converted to the Centre for Bioinformatics and Computational Biology in 2014. The longest-remaining student who is still involved is Werner Smidt, who did his Hons in 2006 and is still situated in the Centre as a visiting researcher.

The BSc Hons degree consists of course work (around 50 lectures/ practical sessions) and a research project, while the MSc and PhD degrees are research-based. The unit runs short courses on a regular basis, with our last course in February having focused on RNASeq analysis, presented by Mark Robinson who is the author of edgeR (https://bioconductor.org/packages/release/bioc/html/edgeR.html).

Computational infrastructure and storage is made available to all students and staff at the University of Pretoria across several campuses.

Short courses such as these are mostly arranged and funded by the African Centre for Genome Technologies (ACGT), which is a collaboration between UP, Wits, UJ, the CSIR and the ARC.

The current user account database contains 277 users (not all necessarily currently active) and the software module definitions contain 252 packages. We were fortunate enough to have recently obtained R7 million from the University of Pretoria to upgrade our computational infrastructure, which was primarily invested in SuperMicro high-performance computing equipment.

Continued: Bioinformatics at the University of Pretoria

The current primary infrastructure consists of a 96-core SMP server with 3TB RAM, a blade chassis with 10 x 28-core blades and 128GB RAM per blade, a 40Gbps Infiniband interconnect, a virtual machine host server running 22 VM's, 80 TB of NFS4 storage for home directories, 1.2 PB Lustre on ZFS storage for data, and 1.5 PB ZFS storage for Bacula-based disk backups (see http://wiki.bi.up.ac.za). Jobs are submitted via Torque and scheduled by Maui. Additionally, there are > 10 other servers for specialized tasks together with around 5 servers hosted for other groups across campus. Web-based services include Galaxy, WebApollo, Redmine, Redcap, a Globus endpoint and a wide range of in-house developed resources. The Centre has a dedicated DMZ via UP's Palo Alto NG Firewall and a 28 PC training laboratory.

Current research projects and collaborations include cancer genomes, stem cell transcriptomes, cystic fibrosis, HLA genes, CYP genes, bacterial genomes, tools for detecting horizontally-transferred elements, nematode genomes, insect genomes, mammal genomes, plant genomes and many others. For more information, please visit http://www.bi.up.ac.za or contact fourie.joubert@up.ac.za.
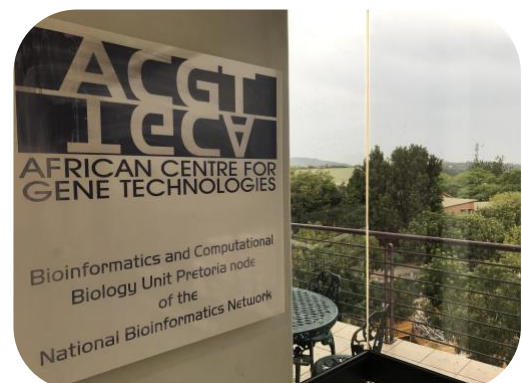
SASBi student council: Scifest Africa 2019

Scifest Africa is an annual event and it is the largest science festival in Africa.

Mahtaab Hayat

The SASBi-SC attended Scifest Africa 2019 in Grahamstown from 6 to 12 March. The theme this year was "Discover Your Element". The student council team was joined by the H3A Bionet Outreach team.

The SASBi-SC hosted an exhibition stand as well as a workshop to teach learners and teachers from across the country more about genetics and bioinformatics. The exhibition stand had games and quizzes for visitors to play and answer. A small sequence alignment simulation, an example of how long DNA is and a protein building model were a few of the games that could be played at the exhibition. The workshops, held throughout the week, explained basic genomics and the evolution of taste genes.

The team had an immense opportunity to introduce genetics and bioinformatics to school learners, as they saw hundreds of children at the exhibition table, and a total of 156 learners at the workshop over the duration of the week.
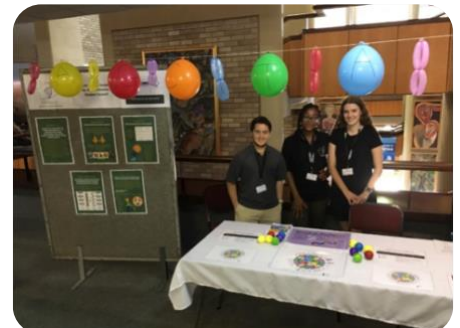

Above: Laura Cottino explaining the genetic code to learners.

Below: SASBi Student Council members Jorge da Rocha, Bertha Baye and Laura Cottino.

Below left: Paballo Chauke (H3A Bionet affiliated) demonstrating to learners at Scifest Africa 2019.

Our next project is hosting the **Young Researchers' Symposium** (YRS) with the **Southern African Society of Human Genetics** (SASHG) Young Researcher's Forum. The YRS will be taking place on **3 August 2019** at **Intaka Island Eco-Centre in Cape Town.** This is one day prior to the biannual SASHG Congress. Be sure to submit your abstracts for both the conference and symposium! Abstracts can be submitted here: https://sashg2019.co.za/call-abstracts/. The deadline is on **12 April 2019.**

Bioinformatics Workshop Report: visit to MMUST in Kenya

Dillon Muzondiwa

A workshop themed harnessing *"Whole Genome Sequencing (WGS) to strengthen sub-typing and antibiotic resistance monitoring of E. coli and other pathogens in developing countries"* was hosted by the Department of Biological Sciences at Masinde Muliro University of Science and Technology (MMUST) in Kenya from the 28 January to the 1 February 2019. The workshop attracted researchers and students from a broad range of disciplines which include biotechnology, genetics, wildlife conservation, comparative genomics, antimicrobial resistances, infectious diseases and veterinary sciences. The aim of the workshop was to attract both seasoned and upcoming researchers to the exciting world of WGS and also to showcase some of the ground breaking WGS based research being undertaken by some of the participants.

The workshop was a great platform for networking as it brought together researchers and scientists from partnering institutions such as the University of Malawi, University of Pretoria (SA), University of Cambridge (UK) and Kenya Medical Research Institute (KEMRI). The various speakers had a chance to highlight some of their efforts in tackling regional as well as global challenges. Dr. Anthony Sifuna from the host institution kicked off the workshop by sharing some of the work they are doing on *E. coli* genomics. He went on to explain their vision of establishing MMUST as a regional bioinformatics hub and some of the challenges they are facing as a young institution. Samuel Kidman (University of Cambridge) left no stone unturned in explaining what WGS involves and how it can be applied in various scientific disciplines. Dr. Martin Welch (University of

Cambridge) who was one of the international keynote speakers shared his work *Pseudomonas aeruginosa* and cystic fibrosis. He went on to highlight some of his experiences and challenges in working with NGS in its early days and how they are exploiting NGS data to generate new antibacterial therapies.

Dr. John Kiiru (KEMRI) gave an eye-opening talk on the rise in anti-microbial drug resistance in Africa due to misuse of antibiotics in both humans and animals. Prof. Oleg Reva (University of Pretoria), one of the keynote speakers, shared their cutting age research on how they are using comparative genomics and epigenetics in monitoring and combating drug resistant infections. Dr. Benjamin Kumwenda (University of Malawi) used his work on salmonella to demonstrate how WGS is being applied in the southern African region. Two of the students were awarded the chance to speak at the workshop. Michael John Ambutsi, who is the first bioinformatics master's student at MMUST presented his project proposal on *P. aeruginosa* comparative genomics. The students were inspired by one of their fellow young researchers, Dillon Muzondiwa (University of Pretoria) whose master's research project involved developing an online tool for the rapid diagnosis of drug resistance in *M. tuberculosis*.

The visiting team of researchers from KEMRI, University of Pretoria, University of Malawi, and University of Cambridge when they paid a courtesy call to the vice chancellor of MMUST.

The workshop programme ended with interactive sessions where attendees were required to work in teams in order to familiarize themselves with some of the bioinformatics tools that are available for researchers. One such session was led by Prof. Oleg Reva who gave an interactive lecture using the UGENE bioinformatics software as well as some novel algorithms developed by his team to teach on topics that ranged from genome mapping to constructing phylogenetic trees. The minor technical challenges did not deter Dr. Kumwenda from delivering his practical lecture on working with bacterial genomes. Through the use of virtual machines, he led a demonstration on how to work with the Artemis and Act software on *E. coli* genomes. The interactive sessions were followed by a "Q and A" session where the attendees were given a chance to ask some of the distinguished researchers questions pertaining to their research challenges as well as their personal experiences.

In conclusion, the workshop went a long way in equipping the delegates with relevant information on the current trends in WGS technologies. The inclusive and interdisciplinary format of this workshop allowed for the flow of ideas as well as partnership building among the various attendees. Since this was the first workshop of this kind in that region, the workshop was also a great way of inspiring current students to broaden their horizons in terms of their future prospects. This was evidenced by the high student turnout despite the fact that exams were in full swing at the host institution. The workshop was also a great boost for the host institution because one of the resolutions passed was to establish a regional bioinformatics hub at MMUST with the help of the supporting partners. This regional hub will facilitate infrastructural development as well as student exchange programs with established research groups.

Student Profiles:
BSc Honours in Bioinformatics at University of Pretoria

Setshaba Taukobong

Q: What advice would you give students considering pursuing bioinformatics for postgraduate studies?

A: If you love biology and anything computer-based, you should go for it.

Q: Dream destination?

A: Tokyo, Japan

Sade Magabotha

Q: Why did you decide to further your education in bioinformatics?

A: I decided to study bioinformatics because I find information systems interesting and combining biology with it is a bonus.

Q: Favourite animal, and why?

A: An Elephant because they are majestic, social animals with great memory.

The Centre for Bioinformatics and Computational Biology has 2 academic staff members and one system administrator. There *are 8 BSc Honours students*, 5 MSc students, 4 PhD students and one post-doctoral fellow. *We've interviewed our Honours 2019 class and got to know them a little better. (Compiled by Tiego Mohlaba)*

Graeme Ford

Q: Why did you decide to further your education in Bioinformatics?

A: A multi-disciplinary, multi-departmental qualification at the forefront of modern science. To say I thought the notion was 'cool' is an understatement.

Q: Favourite animal and why?

A: The peacock! It is my "spirit personality" but what stuck is that apparently, they eat just about anything they come across which I can relate to. Also, they are just pretty, noble birds who look awesome and have instinctual sass and make the most random sound ever!

Tiego Mohlaba

Q: What is your current project on?

A: Dothistroma fungi

Q: Who is the best sports person in your opinion, and why?

A: Serena Williams … need I say more, 23 Grand Slams and she's still dominating the game

Kgopotso Phakwago

Q: What advice would you give to students considering pursuing bioinformatics for postgraduate studies?

A: Go for it. You only need discipline, time management, and also having a lot of fun because everything you do/learn is a learning experience

Q: Who is the best sport star in your opinion and why?

A: Lionel Andres Messi, because he is joyful to watch, plus he doesn't just kick the ball, he massages it to the back of the net.

Hamish Craze

Q: What is your current project on?

A: Automated Disease Detection in Maize Crops using Machine Learning.
Q: Words to live by?
A: Treat people as though they've got something to teach you.

Mondli Xaba

Q: Why did you decide to further your education in bioinformatics?

A: I chose Bioinformatics because I was tired of wearing a lab coat and working in the lab. The world is also moving towards a digital age so why not move with it?

Q: Three things or people you would take if stranded on a deserted island?

A: An axe, large buckets and a fishing rod (other people will waste food and water).

Ingrid Roloff

Q: What is your current project on?

A: Computational detection of cooperative binding and cis-regulatory modules involving Eucalyptus transcription factors associated with wood development.

Q: Words to live by?

A: "We're all stories in the end, just make it a good one." (The Doctor, Doctor Who)

Upcoming events

3 August: Young Researchers' Symposium (YRS) with the Southern African Society of Human Genetics (SASHG) Young Researcher's Forum, Intaka Island Eco-Centre in Cape Town. https://sashg2019.co.za/call-abstracts/.

3-6 August, 2019: 18th Biennial Congress of SASHG, Century City Conference Centre, Cape Town. www.sashg2019.co.za

9-11 September, 2019: RNA informatics, Wellcome Genome Campus, UK.

15-20 September, 2019: Emerging Statistical Challenges and Methods for Analysis of Human Microbiome Data Banff, Alberta, Canada. https://www.birs.ca/events/2019/5-day-workshops/19w5221

16-19 September, 2019: German Conference on Bioinformatics, Heidelberg, Germany. https://gcb2019.de/

16-18 October, 2019: Plant Genomes in a Changing Environment, Wellcome Genome Campus, UK. https://coursesandconferences.wellcomegenome campus.org/our-events/plant-genomes-2019/

25 October, 2019: Exploring Human Host-Microbiome Interactions in Health and Disease, Wellcome Genome Campus, UK.

6-8 November, 2019: Epigenetics of Common Diseases, Wellcome Genome Campus, UK. https://coursesandconferences.wellcomegenome campus.org/our-events/epigenomics-common-diseases-2019/

2020: SASBi/SAGS Conference, Cape Town
1-13 March, 2021: International Congress on Human Genetics (ICHG), Cape Town. http://www.ifhgs.org/pages/meeting_ichg.shtml