

The Improper Scientist

Official Magazine of the African Society for
Bioinformatics and Computational Biology
Issue 10 April 2019

From the Editor's desk

Dear Reader

Since our last newsletter we are delighted to welcome Verena Ras as part of the editorial team, an additional role that she now carries with her current responsibility as the training coordinator at H3Abionet. Her experience will undoubtedly be of value to our newsletter.



A wide range of Bioinformatics capacity building activities continue to roll out across the continent. In this issue of the Improper Scientist we feature the new African Center of Excellence in Bioinformatics that was launched in Uganda, and the recently held NGS workshop in Johannesburg that was taught and hosted jointly by the Wellcome Genome Campus Advanced Courses and Scientific Conferences, University of the Witwatersrand and the H3Abionet.

This quarter we meet Ms Azza Ahmed in our Women in Data Science interview. She is a lecturer in the Department of Electrical and Electronic Engineering (Faculty of Engineering) at the University of Khartoum, Sudan.

Among the events highlighted in the 2019 calendar, please update your calendars with the dates of the next ASBCB conference that will be held 10-13 November 2019 in Kumasi, Ghana followed by two days of workshops. We are planning a full line up of speakers that covers human, animal and plant bioinformatics.

It is with sadness that we note the passing of one of the pioneers of Science, the late Professor Sydney Brenner. We include a tribute to him in this newsletter.

While we are celebrating the momentum and success stories of many bioinformatics initiatives across Africa, it is worth noting the injustice suffered by our colleagues and in particular those in Sudan. Professor Muntaser Ibrahim, a leading Sudanese geneticist has been detained repeatedly for speaking out against the country's repressive regime. Professor Mutaser Ibrahim should be released to continue his invaluable contribution to building scientific excellence in Sudan that includes the next generation of scientists.

A handwritten signature in black ink, appearing to read 'Alan Christoffels'.

Alan
Alan Christoffels (Editor)
@alangchris

Save The Date!!

1. 07 - 12 April 2019, Practical Aspects of Drug Discovery: At the Interface of Biology, Chemistry and Pharmacology, Cape Town, South Africa, . Application and bursary deadline 18 Dec 2018 (at 23:59 UTC), Wellcome Centre for Anti-Infectives Research (WCAIR), Drug Discovery and Development Centre (H3D), UCT.
2. 8 - 12 April 2019, 13th Meeting of the H3Africa Consortium, , Tunisia
3. 24 - 26 June 2019, The Nigerian bioinformatics and genomics network and first Nigerian bioinformatics conference. .
<http://www.ngbioinformaticsconference.com>. Application Deadline 10 May 2019.
Registration link: goo.gl/W7MikH
4. 23 - 28 June 2019, Viral Bioinformatics and Genomics, . Makerere University, Kampala, Uganda.
<https://coursesandconferences.wellcomegenomecampus.org/our-events/viral-bioinformatics-genomics-uganda-2019/>
5. 21 - 25 July 2019, 27th Conference on Intelligent Systems for Molecular Biology (ISMB) and 18th European Conference on Computational Biology (ECCB). Basel Switzerland
6. August 2019 MSc in Bioinformatics and PhD in Bioinformatics. Makerere University, Kampala, Uganda
<https://www.mak.ac.ug/slide/call-masters-phd-applications-college-health-sciences>
7. 7 - 9 August 2019, 5th African conference on emerging infectious diseases and biosecurity. Sheraton Hotel, Abuja, Nigeria.
8. 01st July – 09th August 2019, (With a one week break in-between). Eastern Africa Network of Bioinformatics Training (EANBiT) Project Activity: 5-weeks Residential Bioinformatics Training Course. Venue: Pwani University and Kemri Wellcome Trust Program (KWTRP), Kilifi and Icipe, Nairobi
9. 29th July – 02nd August, 2019, Eastern Africa Network of Bioinformatics Training (EANBiT) Project in conjunction with University of Pennsylvania, EuPathDB Community Activity: EuPathDB genomics databases workshop. Venue: Icipe, Nairobi
10. 11 - 13 November 2019, ASBCB conference. Kumasi Ghana.
11. 14 - 15 November 2019, ASBCB Conference Workshops Kumasi Ghana, .
12. 08 - 13 September 2019, Helminth Bioinformatics (Accra, Ghana), . Application and bursary deadline 09 May Deadlines (at 23:59 UTC)
<https://coursesandconferences.wellcomegenomecampus.org/our-events/helminth-bioinformatics-ghana-2019/>
13. April 5, 9:30 EDT Twitter chat (#CRAM is an efficient method for storing compressed genomic sequence data -@Nicky_Mulder of @H3Africa) to learn more: #CRAM4GH on twitter. <http://ga4gh.org/cram>
14. Funding call: <https://www.aasciences.ac.ke/news/grand-challenges-africa-funding-opportunity-using-data-improve-maternal-neonatal-and-child>

Bioinformatics Capacity

African Center of Excellence in Bioinformatics and Data Intensive Sciences launched at Makerere University

On Thursday, 21st March 2019, the Infectious Diseases Institute (IDI) and the Colleges of Health Sciences (CHS) and Computing and Information Sciences (CoCIS) in partnership with the US Government's National Institute of Allergy and Infectious Diseases and the Office of Cyber Infrastructure and Computational Biology (NIH/NIAID/OCICB) launched the African Centre of Excellence (ACE) in Bioinformatics and Data Intensive Sciences at the IDI-McKinnell Knowledge Centre, Makerere University.

The first of its kind outside the US and on the Makerere Campus, the ACE will be a centre for computational biology and big data analysis. Guests at the launch were treated to a tour of the state-of-the-art facilities consisting of a Virtual Reality (VR) room complete with the most advanced equipment and software, a Tele Learning Centre featuring world-class projection and acoustic equipment and the high-performance computing cluster. The ACE also features a collaborative room with collaborative spaces and amenities

<https://news.mak.ac.ug/2019/03/mak-launches-ace-bioinformatics-and-data-intensive-sciences>



African Centre of Excellence in Bioinformatics and Data Intensive Science launched at Makerere University, Uganda

Next Generation Sequencing (NGS) Bioinformatics, University of Witwatersrand, Johannesburg, South Africa from the 27 January - 01 February 2019

The Next Generation Sequencing (NGS) Bioinformatics was held at the University of Witwatersrand, Johannesburg, South Africa from the 27 January - 01 February 2019 which was also the first overseas NGS Bioinformatics course organized by the Wellcome Genome Campus Advanced Courses and Scientific Conferences (ACSC) in Africa. This was organized by the Wellcome Genome Campus Advanced Courses and Scientific Conferences (ACSC) in collaboration with the University of Witwatersrand, Johannesburg, H3ABioNet (The Pan African Bioinformatics Network for H3Africa). A total of 30 students (postgraduate to postdoctoral fellows) all over Africa were trained to harness the power of next generation sequencing technologies to address a wide range of biological questions in their respective institutions.

Public lectures/presentations were given by Prof. Scott Hazelhurst and Jacqui Keane, on High Performance Computing on public repositories. The program covered the following topics; Introduction to NGS technologies; Introduction to the unix command line; Advanced unix for bioinformatics; NGS data formats and tools; Sequence alignment and QC; SNP/indel theory and practical; Structural variation theory and practical; RNA-seq analysis; ChIP-seq analysis; Sequencing data visualisation with the Integrated Genomics Viewer (IGV); Accessing public sequencing repositories.

Instructors were both from the Wellcome Genome Campus (Thomas Keane, Jacqui Keane, Petr Danecek, and Victoria Offord) and the H3ABioNet network including Shaun Aron, Gerrit Botha, Amel Ghouila, Fatma Guerfali, Phelelani Mpangase, & Sumir Panji). Students also had the opportunity to work on various projects which they presented on the final day.



Participants of the NGS Bioinformatics course held at the University of the Witwatersrand, Johannesburg, South Africa

Biobanking and Biosecurity

**Biobanks improve the integrity of scientific research
by Dominique Anderson, Alan Christoffels
and Carmen Swanepoel**



Biobanks are repositories which receive, store, process and disseminate specimens. These include DNA derived from humans and animals; bacterial strains; and environmental samples like plants and soil. Biobanks also provide the vital infrastructure for research to support scientific advancement and innovation. In the developed world, biobanks are well established and generally well funded and supported. There are also biobanks in the developing world like regions in Africa, most notably in South Africa and Nigeria – but the technology is really still in its infancy. Simple issues like internet connectivity, access to reliable water and electricity supply, which are all necessary to run biobanks, are common.

Yet it's in the developing world that biobanks could be especially powerful tools. For example, having access to the rich genetic diversity across Africa would allow researchers to understand disease, develop better diagnostics and treatments, medicines and vaccines, geared toward the continent's population.

Crucially, they can also improve scientists' ability to replicate results and experiments, a process known as reproducibility. This is very important because being able to reproduce research verifies results and means it can be trusted. Biobanks have high quality assurance and control measures in place, making them safe, reliable spaces to store material for repeated testing that could lead to trustworthy science that saves lives. This is why low and middle income countries, like those in Africa, should prioritise setting up biobanks despite the high cost and other challenges.

A reproducibility crisis

A recent study has shown that, across the world, scientists' ability to reproduce research is staggeringly low. More than 70% of the 1500 scientific participants in the study could not replicate other scientists' experiments. And half were unable to replicate their own experiments. This costs a huge amount of money. In the US alone, the estimated financial burden of not being able to replicate research translates to approximately \$28 billion per year that's being spent on life science research which cannot be replicated.

Why don't researchers rigorously investigate the reproducibility of experimental works before releasing the findings? There are a few reasons. Firstly, research costs money; costs for any lab are already high and staff may not want to spend more than they believe is necessary. Secondly, reproducing experiments takes time – and when scientists are developing novel therapies for diseases, for instance, time can cost lives. The study also identified study design, biological samples, laboratory protocols, and data analysis and reporting as issues. So it stands to reason that implementing standard best practices and adhering to them could partially ease the crisis. That's where biobanks come in.



Quality assurance

Most biobanks, whether small or large, have high quality assurance and control measures in place. Without this, they won't generate the trust needed to function well. They ensure that sample transportation, processing, storage and analysis are done according to standard methods. They manage risk to ensure the biospecimens they store for different researchers or teams are viable and retain their quality.

Biobanks which follow best practice guidelines can be mediators for reproducible scientific research as they ensure that protocols are applied in a standardised, harmonised way.

This means that researchers who use a biobank can have some level of comfort that, at a bare minimum, any biological sample used in an experiment is consistent and controlled. For example, biobanks that use Laboratory Information Management System software can track and log a sample's life cycle to ensure its quality hasn't been compromised. For example, Baobab LIMS was developed at the University of the Western Cape as a management system for human biobanks.

Sample quality is critical in research, as it will influence later analysis. Biobanks are also an important tool for smaller laboratories that don't have the finances to get international accreditation, or don't have the right equipment for analysing specific samples.

Benefits outweigh costs

It may seem like a no-brainer to establish biobanks everywhere, given all the benefits they offer.

But there are some barriers to this happening in the developing world. Cost is one. Biobanks are generally non-profit. Non-commercial medical biobanks cannot sell specimens, as this would equate to trade in human tissue and is unethical. So biobanks' fee structure is aimed entirely at cost-recovery.

There's also a lack of highly skilled and trained personnel. There are some international certificates and courses specifically for biobanking, offered in North America and Europe but for the most part, skilled scientists could be trained to become proficient and staff biobanks.

These issues should be dealt with by policy makers, governments and science stakeholders. The benefits of establishing more biobanks clearly outweigh the costs – especially in the face of the ever increasing direct and indirect cost of research that cannot be reproduced and the growing need to preserve Africa's rich genomic resources.

This article was originally published in The Conversation.
Read the original article at:

<https://theconversation.com/how-biobanks-can-help-improve-the-integrity-of-scientific-research-100035>

Women in Data Science



Azza Ahmed

1. Describe your current job.

I'm a PhD student at the Center for Bioinformatics and Systems Biology (Faculty of Science) of the University of Khartoum; and also a Faculty lecturer at the Department of Electrical and Electronic Engineering (Faculty of Engineering) of the same University.

2. What are your research interests.

I'm interested in mathematical modeling and computations. Currently, I apply such approaches to the analysis of Next Generation Sequencing (NGS) and Genome Wide Association Studies (GWAS) data.

3. What was your career path?

Academic and somewhat linear: I joined as a teaching assistant upon graduating with flying colors from my Department of Electrical and Electronic Engineering at the University of Khartoum. Later, this led to my PECK-funded MSc studies in Cybernetics at the University of Reading (UK); and also paved the way for my H3ABioNet-funded PhD in Bioinformatics.

4. How big is the gender bias in your institution/country and what opportunities are there to promote women.

The history of Modern-day women movement in Sudan dates back to the early 1940s with many achievements and tangible effects on the political and societal movements in the country even from those early days. Yet, there is enormous cultural, ethnical and religious heterogeneity within Sudan as a whole that makes generalizations quite inaccurate and unfair. I can more confidently talk about numbers from my own institution and Faculty of Engineering as it is probably universally male dominated.

In my home Department of Electrical and Electronic Engineering, and merely a decade ago, there were only 2 tenure-track female staff members. Today, this number has more than doubled. More interestingly though, our last 3 department heads have been females. In fact, 2015 marked the appointment of the first female Deputy Dean of the Faculty of Engineering.

5. Can you get names of a few women computational scientists/Bioinformatics people at your institutions?

I have been privileged to work first-hand with very powerful and successful female Computational scientist/Electrical Engineers, who have been leaders within the country and Africa. From my home Department of Electrical and Electronic Engineering: Dr Tahani Abd Allah Attia, who also served as Sudan's Minister of Communications and Information Technology, and Dr Iman Abul Mali Abdel Rahman who; besides her pioneering local and Arab activities in research and education, also served as the Vice Chairperson of UbuntuNet Alliance.

Hot Off The Press!!

Tackling rare genetic diseases within Africa using Whole Genome Sequencing

Myasthenia gravis (MG) is a long-term neuromuscular disease characterised by muscle weakness. Although generally rare in the population, its variant ophthalmoplegic sub-phenotype of MG (OP-MG) has early onset and has been recently linked with African ancestry coupled with chemoresistance among some patients. Researchers at the University of Cape Town, Cape Town, South Africa, with Dr. Melissa Nel as first author, have successfully applied Whole Genome Sequencing technologies among African myasthenic individuals to identify candidate genes and pathways that may contribute to OP-MG susceptibility among African populations.

Read full paper here: <https://www.frontiersin.org/articles/10.3389/fgene.2019.00136/full>

The African Genome Resource is the best genotype imputation method for samples from South African Cohorts (SAC)

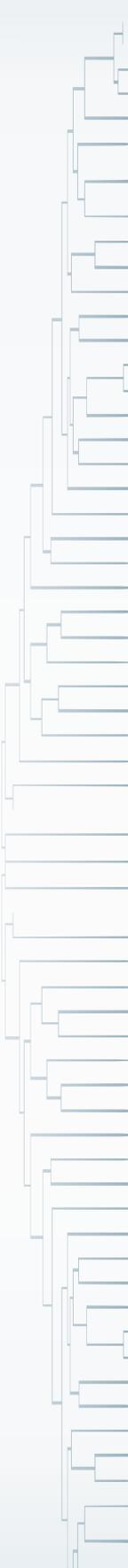
Genotype imputation remains an indispensable process of genome-wide association studies (GWAS) and meta-analysis of population genomics data from different platforms. However, despite the sheer number of tools available (both commercial and free-access) selecting the best performing tools for genotype imputation may be challenging, particularly for bioinformaticians or computational biologists who are just starting out. In a seminal paper published in frontiers in genetics journal, researchers at the Stellenbosch University with Haiko Schurz and Stephanie J. Müller as co-first authors evaluated the accuracy of imputation methods in a five way-imputation methods. It turns out that the African Genome Resource is the best reference panel for imputation of missing genotypes in samples from the South African Cohorts (SAC) population which is implemented via the freely accessible Sanger Imputation Server.

Read full paper here: <https://www.frontiersin.org/articles/10.3389/fgene.2019.00034/full>

Macrophage migrating inhibitory factor expression is associated with Trypanosoma brucei gambiense infection and is controlled by trans-acting expression quantitative trait loci in the Guinean population.

Infection by Trypanosoma brucei gambiense is characterized by a wide array of clinical outcomes, ranging from asymptomatic to acute disease and even spontaneous cure. In this study, Kabore and colleagues investigated the association between macrophage migrating inhibitory factor (MIF), an important pro-inflammatory cytokine that plays a central role in both innate and acquired immunity, and disease outcome during T. b. gambiense infection. A genome wide eQTL analysis was conducted on 29 controls, 128 cases and 15 latently infected individuals for whom expression and genotype data were both available.

Read the full paper here: <https://doi: 10.1016/j.meegid.2019.03.021>



Association between IL1 gene polymorphism and human African trypanosomiasis in populations of sleeping sickness foci of southern Cameroon

Besides the well-established environmental and behavioural risks of becoming infected, there is evidence for a genetic component to the response to trypanosome infection. Ofon and colleagues undertook a candidate gene case-control study to investigate genetic associations. This study revealed that one SNP rs1800794 of IL1A and one VNTR rs2234663 of IL1RN were associated with the increased risk to be infected by *Trypanosoma brucei gambiense* and develop sleeping sickness in southern Cameroon.

Read the full paper here: <https://doi: 10.1371/journal.pntd.0007283>

Designing novel possible kinase inhibitor derivatives as therapeutics against *Mycobacterium tuberculosis*: An in silico study.

Rv2984 is one of the polyphosphate kinases present in *Mycobacterium tuberculosis* involved in the catalytic synthesis of inorganic polyphosphate, which plays an essential role in bacterial virulence and drug resistance. Consequently, the structure of Rv2984 was investigated and an 18 membered compound library was designed by altering the scaffolds of computationally identified inhibitors. The top scoring inhibitors showed relatively higher binding affinities against Rv2984 compared to the first line drugs Isoniazid and Rifampici.

Read the full paper here: <https://doi: 10.1038/s41598-019-40621-7>

FTO haplotyping underlines high obesity risk for European populations

Rv2984 is one of the polyphosphate kinases present in *Mycobacterium tuberculosis* involved in the catalytic synthesis of inorganic polyphosphate, which plays an essential role in bacterial virulence and drug resistance. Consequently, the structure of Rv2984 was investigated and an 18 membered compound library was designed by altering the scaffolds of computationally identified inhibitors. The top scoring inhibitors showed relatively higher binding affinities against Rv2984 compared to the first line drugs Isoniazid and Rifampici.

Read the full paper here: <https://doi: 10.1038/s41598-019-40621-7>

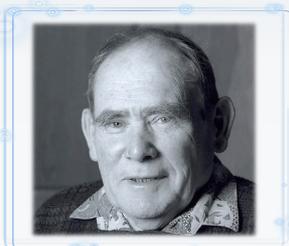
Ten simple rules for organizing a webinar series

In this paper Fadlelmola et al describe ten simple rules for hosting a regular webinar series with particular emphasis on resource-constrained communities in Africa. These rules are derived from experiences gained and lessons learnt while organizing and running the H3ABioNet bioinformatics webinar series.

Read full paper here: <https://doi: 10.1371/journal.pcbi.1006671>

by Samuel Terkper Ahuno and Alan Christoffels

Sydney Brenner (1927-2019) A baobab has fallen



On the 5th April 2019, A*STAR, the Agency for Science, Technology and Research, Singapore's leading research agency announced the death of Sydney Brenner. For those of us who knew (or knew of) him, we immediately understood the impact of the loss of one of the pioneers of 20th century science. On a personal note, I was transported back to my postdoctoral days in his laboratory. I recalled the times he would visit the lab every two months and engage individually with each member of the laboratory. I had a lot to reminisce about while sitting at the University of Western Cape Science Faculty graduation and seeing our students graduate and about to embark on a scientific journey that will definitely transform their lives. The conversations with Brenner showed evidence of a man who read widely and could engage on any topic and bring it back to the science at hand. It helps to remind ourselves of his immense contribution to science.

Sydney Brenner was born a South African of Lithuanian descent who at the age of 15 obtained a scholarship to study medicine at the University of Witwatersrand (WITS) in Johannesburg, South Africa. Subsequently, he read for his DPhil at Oxford University in the UK and returned to South Africa for a few years before taking up a position at the MRC Laboratory of Molecular Biology at Cambridge where he shared an office for 20 years with Francis Crick (the co-discoverer of DNA).

Brenner is known for his pioneering work in the field of molecular and development biology. Together with John Sulston and Robert Horvitz, they shared the Nobel Prize in Medicine in 2002 for their work on *Caenorhabditis elegans*. They studied *C.elegans* to determine how cells divide and create new functions. Brenner used an Ethyl methanesulphonate to induce mutations in the worm and, in turn, these mutations had an effect on organ development. His findings lay the foundation for others such as John Sulston and Robert Horvitz to expand on programmed cell death. These three individuals ushered in a new field of human disease research with *C.elegans* as a model organism for subsequent genetics research.

Brenner's best-known contribution to scientific research was in 1961 when he, through cleverly designed experiments, discovered that sets of three bases in the DNA sequence signify the correct string of amino acids that must be used by the ribosomes to assemble proteins. He called these three bases "codons". He was also responsible for identifying two of the 3 stop codons. His contribution to other discoveries included messenger RNA (mRNA) – the molecule that produces amino acids in the cell.

Sydney Brenner was also renowned for his wit. On one occasion, reflecting on his time as the director of the Laboratory of Molecular Biology in Cambridge and bemoaning administration he is known to have said: 'You become a mediator between two impossible groups, the monsters above and the idiots below.'

Following on from his directorships of the UK MRC's Laboratory of Molecular Biology (1979–86) and Molecular Genetics Unit (1986–91), he established the Molecular Science Institute in California in 1996. In 2000 he became the Distinguished Professor at the Salk Institute for Biological Studies. He continued to divide his time between California and Cambridge until 2004 when he settled in Singapore for health reasons.

He contributed significantly to developing scientific capacity in Singapore, and it was during these years, specifically 2001-2007, that I had the privilege of working and publishing with him as a postdoctoral fellow. He established two laboratories specifically for Singapore graduates who returned from completing their PhDs' abroad.



This environment allowed young scientists to develop their own research projects and follow through with their ideas. This was in contrast to the more common practice of spending a few years doing a postdoc in someone else's team and at times not having the space or the scope for personal scientific growth.

Much of the interactions that I had with Brenner during these years strengthened my resolve to persevere with projects even though others might attempt to derail it. The one characteristic I did not imbibe from Brenner was his refusal to use slides during a presentation. He was adamant that slides are used to reflect on the past, and he felt that he was very much investigating new areas of scientific enquiry.

Sydney held strong views on the way we conduct scientific research today. He was opposed to the insane drive to publish volumes of papers as a metric for good science. This was eloquently described by him in his tribute to Professor Fred Sanger (<http://science.sciencemag.org/content/343/6168/262.full>): "A Fred Sanger would not survive today's world of science. With continuous reporting and appraisals, some committee would note that he published little of import between insulin in 1952 and his first paper on RNA sequencing in 1967 with another long gap until DNA sequencing in 1977. He would be labelled as unproductive, and his modest personal support would be denied. We no longer have a culture that allows individuals to embark on long-term—and what would be considered today extremely risky—projects."

This article and others sparked rebuttal and responses by other scientists who attempted to demonstrate that the NIH grant system would support someone of the caliber of the late Professor Fred Sanger. It was evident that Sydney yet again was able to initiate a broader conversation and cause people to reflect on how we do science and he did so with insight and carefully chosen words.

In 2014 during an interview with Elizabeth Dzung on "how academia and publishing are destroying scientific innovation", Brenner used his wit and humor to draw an analogy with the creation of the world (<http://bit.ly/BrennerOnPublishing>): "He wouldn't have survived. Even God wouldn't get a grant today because somebody on the committee would say, oh those were very interesting experiments (creating the universe), but they've never been repeated. And then someone else would say, yes and he did it a long time ago, what's he done recently? And a third would say, to top it all, he published it all in an un-refereed journal (The Bible)."

Sydney Brenner pushed interdisciplinary or maybe even non-disciplinary research. He held to the view that the progress made in biology was due to significant contributions of physicists who knew little about biology. He maintained that ignorance of a topic drives innovation. I appreciated his unconventional approach to building research teams when I joined his and Professor Byrappa Venkatesh's Marine Molecular genetics team in Singapore. Brenner was not concerned that I had no background in marine science. He would meet with me as he did other lab members every 2-3 months and would be keenly interested in the details of how I used bioinformatics approaches to study the puffer fish (*Fugu rubripes*) genome. I would get a glimpse of how little I knew when he would open his laptop and take out some computer code that he wrote in a language that I had never seen in my life. What did this encourage you to do? Yet, he always encouraged me, and each team member, and often had us laughing at his funny one-liners. The one I always remember is 'Alan you seem to like this idea of systems biology. When I was your age we called it physiology!'

As a community of data scientists in the African Society of Bioinformatics and Computational Biology who straddle a number of disciplines, may the life of Sydney Brenner encourage us to strive for interdisciplinary research that catalyzes innovation and creativity. While acknowledging the importance of publishing our scientific findings, we need to hold our respective academic institutions and funding agencies accountable when they use publications as the over-riding metric for innovation and scientific performance.

Hamba Kahle Sydney

by Alan Christoffels

COSI Corner

Community Of Special Interest Groups

We launched the community of special interest groups at the ASBCB conference in Entebbe in October 2017. It is hard work for individuals to rally support and sustain the momentum felt at the Entebbe conference. I would urge all those who are looking for a smaller community of disciplinespecific scientists to get involved in the COSIs. Here is a reminder of the groups that were initiated and the contact details.

Structural Biology and Drug design (structuralbio@asbcb.org)

Metagenomics group (metagenomics@asbcb.org)

Pathogens group (pathogen@asbcb.org)

Population genomics (popgen@asbcb.org)

System administration (sysadmin@asbcb.org)

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ThankGod Ebenezer, Earlham Institute (formerly The Genome Analysis Centre - TGAC)

Norwich Research Park Innovation Centre

Ahuno Samuel Terkper, Kwame Nkrumah University of Science and Technology (KNUST)

Ryman Shoko, School of Natural Sciences and Mathematics, Chinhoyi University of Technology,

Verena Ras, Computational Biology Division, University Of Cape Town

We welcome volunteers who wish to contribute in the following areas fo the magazine:

* Editorial Team

* Individuals to aid in translating the newetter to French and Portugeuse

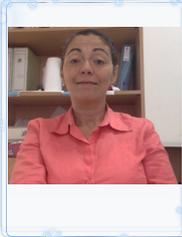
* Layout and Design - we are looking for individuals who wish to exercise their creativity in improving the look and design of the magazine

Please submit all contributions to:
contact @asbcb.org

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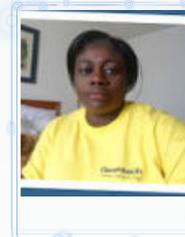
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Vision

To facilitate the development of African scientists as leaders in bioinformatics and computational biology

Mission

To be a scholarly society dedicated to advancing, developing and promoting bioinformatics and computational biology in Africa.

Serve a global membership through distribution of valuable information about training, education, employment and relevant news from related fields.

Encourage the application of bioinformatics in Africa to improve the livelihood of people.