

SASBi

Newsletter

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UNIVERSITY of the
WESTERN CAPE



SANBI
South African National
Bioinformatics Institute

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PRESIDENT'S LETTER

Greetings!

I have now served as your president for 3 years and Ruben Cloete, Oleg Reva, Alisa Postma, Phelelani Mpangase, Cedric Werely, Mahtaab Hayat, Tulio de Oliveira, Yuman Moosa and Werner Smidt have served as the other Council Members. Due to COVID-19 pandemic the Council's term has been extended till April 2022, when we hope to have our SASG/SASBi BIO2022 Conference and elect a new president and new council members.

We have continued to work hard to revitalize SASBi. For example, we established SASBi as a group on the "Google Groups" platform to facilitate communication. To post on the group you can send

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Prof Gerard Tromp

Photograph: Stefan Els

an e-mail to sasobioinformatics@googlegroups.com. Aside from announcements, the group can be used for discussions of bioinformatic topics. Note that the group is moderated to avoid abuse and reduce spam.

In October 2020, we launched our virtual seminar series. We have now organized four virtual seminars. Recordings of them are available in recently established SASBi YouTube channel, which can be accessed here: [SASBi YouTube](#). Our next virtual seminar will take place on 16 November at 11:00. The speaker is Prof. **Nicola Mulder** from the University of Cape Town. She will give a presentation entitled “**Genomics applications in the biomedical sciences: African perspectives**”

We are also proud to inform you that SASBi became a member of the **South African Council for Natural Scientific Professions** (SACNASP), which will allow our conferences and workshops to be used towards continuing professional education.

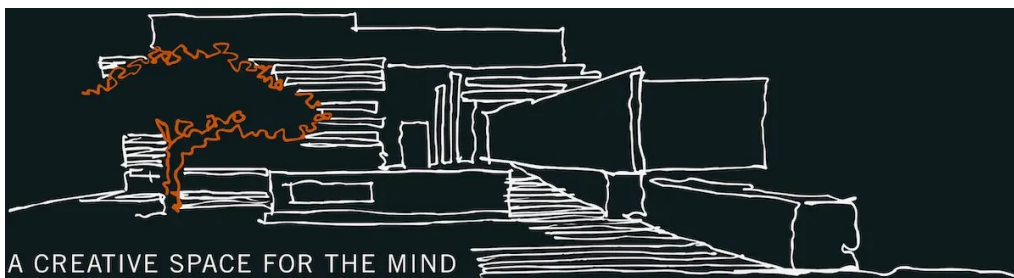
To improve our visibility as a Society, we have established SASBi Silver and Gold Awards. The Silver Award is meant for a more junior bioinformatician with 5-20 years of experience after a PhD degree and who has made

major contributions to a minimum of two peer-reviewed publications and advanced the discipline of bioinformatics by teaching, advising or public advocacy. The Gold Award is meant for a more senior bioinformatician with over 20 years of experience after a PhD degree and who has made major contributions to several recent publications and advanced the discipline of bioinformatics by teaching, mentoring, advising or public advocacy. Both Silver and Gold award winners are also expected to have been active in our Society. Call for nominations is now open and the first award winners to these awards will be announced during the BIO2022 Conference.

In 2019, SASBi and SAGS committed to working more closely together and have had reciprocal representation on each other's councils to promote collaboration and communication. One of the most important collaborations is planning for the next conference, which was scheduled for September 2020, but had to be postponed twice due to the COVID-19 pandemic and [BIO2022](#) is now scheduled for 24-27 April 2022 as a [hybrid event](#). It is important to note that the registration fee for virtual attendees will be R2,500 for faculty and staff, and R1,000 for students. The venue selected is the Stellenbosch Institute for Advanced Study ([stias](#)). More detail can be obtained [below](#) or at the [BIO2022 conference website](#).

Organization for the conference has been extremely challenging and most recently the venue decided to reorganize its offerings, deciding to no longer host large conferences. Both SASBi and SAGS have therefore decided that the conference will no longer be postponed and that the conference will be presented in hybrid format. We appeal to members and interested parties to register for the meeting as soon as possible, and to participate fully. Our society is only as vital as its membership and the participation of that membership.

We would welcome your input! If you have suggestions, please contact any of the Council or Student Council members, as appropriate.



stias



Stellenbosch Institute for Advanced Study – STIAS

SASBi Student Council: Virtual Symposium

Over the course of three days 185 attendees joined the SASBi Student Council (SASBi-SC) and SAGS Student Representatives online for oral and rapid fire presentations presented by the young researchers from all over Africa. The event was held over 3 days; from the 14th to the 16th of September. Big congratulations to the prize winners:

Best Oral Presentation:	Diego Castillo
Second Best Oral Presentation:	Darisia Moonsamy
Best Rapid Fire Presentation:	Anandi Bierman
Second Best Rapid Fire Presentation:	Lauren Martin

A big thank you to our sponsors for their contribution to the SASBi-SC/SAGS 2021 Virtual Student Symposium!

Platinum sponsors:	Inqaba Biotech and Separations
Silver sponsors:	Anatech, Apex Scientific, Ascendis Medical/The Scientific Group, Diagnostech, and Esco Technologies

The Conference was recorded so that individuals who could not attend can benefit from the proceedings. Recordings of all sessions are available at the [SASBi-SC YouTube](#) page.

Thank you to each and every attendee for contributing to making the SASBi-SC/SAGS 2021 Virtual Student Symposium a great success! We hope to see everyone in person for the SASBi-SC/SAGS 2022 Student Symposium on Sunday the 24th of April 2022.

SASBi Virtual Seminar Series

On October 20, 2020, SASBi launched its Virtual Seminar Series. The first speaker of the series was Prof. David Tabb of Stellenbosch University. He presented *"PCA-Powered Quality Control for Large-Scale Proteomics Experiments."*

The second virtual seminar took place on April 20, 2021 and was presented by SASBi President Prof. Gerard Tromp: *"The South African Society for Bioinformatics and the Great Covid-19 Pandemic: Where are we in 2021?"*.

The third virtual seminar presented by Prof. Özlem Tastan Bishop from Rhodes University, was on July 20, 2021: *"Analysis of SARS-CoV-2 Mpro Protein in the Presence of Evolutionary Mutations: Potential Drug Development for COVID-19 via Structural Bioinformatics Approaches"*.

The fourth virtual seminar was presented on August 17, 2021 by Prof. Tulio de Oliveira, Past President of SASBi, who recently moved to Stellenbosch University: *"COVID-19 Genomics Surveillance in Africa"*.

We have established a YouTube channel for the recordings of these virtual seminars which you can access via the [SASBi website's seminar page](#).

Stay tuned for the next SASBi virtual seminar planned for November 16, 2021 at 11:00 via MS Teams:

Speaker: Prof. Nicola Mulder, UCT

Topic: *"Genomics applications in the biomedical sciences: African perspectives"*

Microsoft Teams meeting

Join on your computer or mobile app

[Click here to join the meeting](#)

529319312@t.plcm.vc

Video Conference ID: 126 564 575 6

[Alternative VTC instructions](#)

SARS-CoV-2 analysis training with Galaxy: a perspective from Africa

Peter van Heusden

The switch to online bioinformatics training forced by the COVID-19 pandemic has opened spaces for collaboration in ways that were previously limited by geography. One of these collaborative opportunities has been the series of Galaxy training events run from the start of 2021. February saw the [Galaxy Smörgåsbord](#), organised by members of the Galaxy Training Network, June training component of the [Galaxy Community Conference](#) and August [SARS-CoV-2 Data Analysis and Monitoring with Galaxy](#) (due to be repeated in [October](#)).



These workshops are building on an established training platform, the [usegalaxy.* servers](#), and network of content creators (the aforementioned [GTN](#)) and volunteers (including myself, from [SANBI](#) in South Africa) and a training model based on pre-recorded videos (with captions to increase accessibility) and real-time support using chat on Slack. I noticed last year that this format was increasing participation from Africa. Over 50 people participated in the Smörgåsbord from South Africa, Nigeria, Kenya and six other African countries. The turnout for the SARS-CoV-2 data analysis workshop was even more dramatic, with 352 out of the 766 participants registered for the workshop coming from the African continent. Arabic-speaking countries were especially well represented with Egypt (83), Sudan (43), Algeria (11) and Morocco (9) among the top ten African countries participating. The Arabic speaking contingent was welcomed with a [video](#) by Engy Nasr and Abdulrahman Yahia Azab introducing the Galaxy Arabic community. Other countries well represented in the participants were Nigeria (68), Kenya (23), Ghana (22) and South Africa (13).

I reached out to a few of the participants to learn from them about their experiences. Dr Yohannes Gedamu Gebre is an Assistant Professor at Wollo University in Ethiopia. His research focus is in Plant Sciences but he teaches a general course in genomics and bioinformatics to undergraduates and postgraduates at the university. During his PhD he used the [RepeatExplorer](#) server (itself running a suite of Galaxy tools) to analyse the genome of *Eragrostis tef*, a grain native to the Horn of Africa, so he had some familiarity with the platform, but was new to understanding SARS-CoV-2 bioinformatics. While funding challenges limit his access to Next Generation Sequencing and thus the ability to generate data for his own research, he plans to continue to use Galaxy for teaching and data analysis.

Dr Benson Kidenya is a medical doctor and molecular biologist from the Catholic University of Health and Allied Sciences in Tanzania. He also teaches bioinformatics to both undergraduates and postgraduate students and intends to use Galaxy and the Galaxy Training Network materials to

expand his own biological knowledge. As a molecular biologist, his teaching focuses on basic techniques in bioinformatics ranging from sequence matching through primer design, restriction enzyme and peptide digest mapping and more.

While both participants appreciated the clarity and breadth of the GTN materials, they also both encountered technical difficulties with, on the one hand, finding the correct tool for an analysis and on the other hand, interpreting error messages when things went wrong. While these problems could be addressed during the course (and similar issues get addressed daily on the Galaxy community [help forum](#) and the GTN Gitter chat), they do illustrate some of the problems beginners face when trying to work their own way through teaching material.

Language proved another challenge during the course, with some Francophone participants saying that the lecturers spoke too fast. While the pre-recorded videos with captions (first auto generated and then edited for clarity and correctness) can help overcome problems of accent and to some extent can be automatically translated, live engagement (in Zoom calls) still poses a challenge in a multilingual environment. There's no simple solution for this problem but it does show the importance of presentation and creating opportunities for asking questions.

Talking to course participants, it's clear that the field of bioinformatics has expanded greatly both in terms of people engaging with the discipline and in the range of problems being addressed. Whereas bioinformatics has in the past been a strongly research focused field, where practitioners could be expected to spend years learning about sequence analysis and making sense of tools and data, the field has now attracted large numbers of people for whom the main focus is rapidly computing and interpreting results. These might come from many fields, from agronomy and biotechnology to microbiology and zoology. The degree to which they are interested in bioinformatics research and engineering (that is the construction and validation of new workflows, tools and algorithms) varies, with some aiming to be simply "bioinformatics users" and others extending their skills towards building new tools and interfaces.



Galaxy

As is noted in the recent [Ten Simple Rules publication](#) on organizing a bioinformatics course in Low and Middle Income Countries (LMICs), one should always keep the "big picture" in mind. Teaching courses accessible to African participants is a start, but how do we involve African researchers in both building bioinformatics solutions in

line with their needs and creating content and leading teaching engagement? The NIH / ASBCB [codeathons](#) assist in addressing one part of this problem, as does SASBi's online events, but we still have far to go to build an inclusive and active community of practice for bioinformaticians and allied disciplines on the African continent.

The Protection of Personal Information Act (POPIA)

Dominique Anderson

The Protection of Personal Information Act (POPIA) promotes the constitutional right to privacy and came into full effect in July 2021, following a year grace period by the Information regulator, to allow for organizations to become compliant. POPIA was derived from the EU-GDPR and mandates that anyone processing (ANY operation or activity concerning personal information) personal information of any individual, regardless of nationality, within the borders of South Africa, abide by the conditions set out within the Act. Personal information is defined in the Act as “information relating to an identifiable, living, natural person, and where it is applicable, an identifiable, existing juristic person” (<https://popia.co.za/section-1-definitions/>). Personal information is further classified into special personal information and is considered sensitive information, needing greater safeguards in place to protect the data subject from identification and, importantly, re-identification. The POPI Act will undoubtedly have an impact on bioinformatics which process large amounts of personal information, especially special and sensitive personal information. Researchers in the field will need to understand how to comply with the eight lawful conditions for processing of personal information, which are accountability, process limitation, purpose specification, further process limitation, information quality, openness, security safeguards and data subject participation. These conditions provide a ‘template’ which can be used for privacy by design in research projects. For researchers working with ‘-omics’, which is considered special personal information in the biometrics category, careful project design with privacy as the fundamental basis will need to be implemented. Researchers and responsible parties will do well to know which policies and procedures are in place for all aspects of information management. Genomic data creates compliance complications due to the fact that hereditary information cannot be fully de-identified and may also result in the identification of closely related individuals. As such metadata minimization may be required to decrease re-identification risk via linkage with secondary identifiers. Those working with human pathogen genomes will need to consider and document the processes in place to discard inevitable human genome contamination in samples. Furthermore, POPIA has



defined criteria for the flow of information outside the borders of South Africa, and as such, data transfer agreements will be critical, especially when data is transferred to a country which does not have a similar data protection law in place. In addition, risk assessments will become commonplace and data access committees should be considered by institutions. It will be important to ensure governance frameworks are in-line with the POPIA and inter-institution communication will have to be strengthened to ensure that the appropriate organisational and technical safeguards are in place to protect personal information. Being compliant with POPIA means logically thinking about what is reasonably practical now – in terms of technology and skill, but also in the future.

Under section 7 of the act, a code of conduct can be developed and submitted to the information regulator for approval, and if approved, the code is legally binding to the bodies, it represents. Earlier this year, ASSAf led a consultative process amongst the research sector of South Africa to develop a Code of Conduct for Research. The main purpose of which is to ensure POPIA compliance in the research community, to provide guidance to the research community, to promote uniformity in the interpretation and application of the act and meet international standards of data protection which is required for trans-border information flow between trusted partners and create alignment with other legislation and regulatory frameworks that govern research in South Africa. The take home message is that POPIA compliance will be an absolute requirement but should not be perceived as a hinderance to research and open-science.



HOME ABOUT MEMBERS MANAGEMENT MEDIA DOCUMENTS CONTACT PORTAL VACANCIES

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THE INFORMATION REGULATOR IS, AMONG OTHERS, EMPOWERED TO MONITOR AND ENFORCE COMPLIANCE BY PUBLIC AND PRIVATE BODIES WITH THE PROVISIONS OF THE PROMOTION OF ACCESS TO INFORMATION ACT, 2000 (ACT 2 OF 2000), AND THE PROTECTION OF PERSONAL INFORMATION ACT, 2013 (ACT 4 OF 2013).



Webinar Video: International Day of Universal Access to Information (IDUAI) 2021 webinar video available [04 Oct 2021]



Webinar Invite: Unpacking the POPI Act Webinar on 30 Sep 2021 at 13h00 [24 Sep 2021]



Notification of a security compromise in terms of Section 22 of Protection of Personal Information Act, 4 of 2013 (POPIA) [24 Sep]



CEO's Pledge relating to enterprise-wide risk management and compliance [21 Sep]



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registration of Information Officers.



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Contact Us
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Save the Date

BIO2022 CONFERENCE

24-27 April 2022 for main conference

28 April 2022 for SASBi Workshop: "Structural Bioinformatics and Drug Discovery for Cancer and Mycobacterial Infections"

Venue: STIAS and Virtual (hybrid conference)

Details: [Conference website](#)

Key dates:

- ♦ Early Bird Registration: until 15 December 2021
- ♦ Late Registration: until 14 February 2022
- ♦ Abstract Submission: until 15 December 2021
- ♦ Notification of acceptance: 31 January 2022
- ♦ SASBi Award Nominations: until 15 February 2022

Co-chairs: Clint Rhode (SAGS) & Gerard Tromp (SASBi)



Structural Bioinformatics and Drug Discovery for Cancer and Mycobacterial Infections

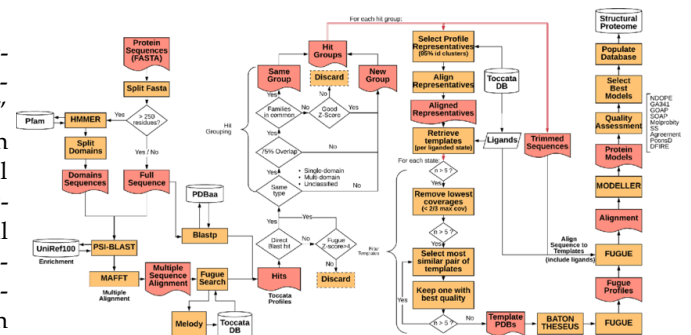
Tom L Blundell, Keynote Speaker for BIO2022

Department of Biochemistry, Cambridge University

tlb20@cam.ac.uk

Knowledge derived from genome sequences of humans and pathogens has the potential to accelerate diagnosis, prognosis and cure of disease. We are moving quickly into an era of precision medicine, not only in familial diseases where a mutation in a human gene is important, but also for understanding somatic mutations in cancer. Equally important, the genome sequences of pathogens, for example in tuberculosis or leprosy, can give clues about the choice of existing drugs, repurposing of others, and the design of new ones to combat the increasing occurrence of drug resistance.

I will discuss computational aspects of structure-guided fragment-based screening techniques that have proved effective in lead discovery not only for classical enzyme targets but also for less "druggable" targets such as protein-protein interfaces. I will discuss progress in using these approaches for targets in cancer, and also in mycobacterial infections including tuberculosis ([Chopin](#)), cystic fibrosis infections ([Mabellini](#)) and leprosy. I will also review our computational approaches using both statistical potentials (SDM) and machine learning methods (mCSM) for understanding mechanisms of drug resistance and for understanding mutations in cancer as developed in our COSMIC database.



Flowchart for MabelliniDB

Student Profiles @ UWC

Lunathi Mhlali Ndondlo

MSc Candidate: Bioinformatics, South African National Bioinformatics Institute, University of the Western Cape

What is your current project?

My current project is about exploiting *Mycobacterium tuberculosis* using structural bioinformatics. The end goal is to identify potential drugs that display activity against a specific enzyme that can be used to decrease TB prevalence.

Please fill us in on your career up to this point?

I started with a degree in Biotechnology with the notion of becoming a molecular biologist, then 'changed' fields during my Honours due to the project I chose. Now, I am pursuing a MSc in Bioinformatics because I was inquisitive about the link between computers and biological issues, especially health care related biological issues.

If you could give advice to students who are new in the field, what would you say?

Always be prepared to learn something new. If you come from wet-bench work, there is no need to fear computers and soak up as much as you can from those with more experience.

If you could preach about something to other scientists, what would it be? (For example, "Please add your data to a repository once it's published" or "Please stop using the word 'uhm' in presentations".)

A link between computational work and wet-bench work will always exist, so start learning about computational work as early as you can. The sooner the better. Also BACK UP YOUR WORK.

What are your hobbies/activities you do in your free time?

Listening to music, watching series and being with friends..

If you were an animal - what would you be and why?

I would probably be a Bichon Frise (dog) because they have an easygoing temperament and are fluffy.

If you could change one thing about yourself, what would it be?

Nothing at all as that would offset where I am right now.

When did you first realize you love science/computers?

Early primary because I asked my grandmother a lot of questions to the point where I resolved that I would just find them out myself. I then realized that Science was the only profession that allows me to have a closer look at the natural order of things. Computers are a recent addition to the path and curiosity about them got the best of me.

Describe what you were like at age 10?

I was a mix of a shy and very serious 10-year-old that loved working autonomously when it came to school work. I also loved painting and thought high school was going to be like High School Musical.

What do most people not know about you?

I am very opinionated.

What do you think you are best known for around the lab?

I haven't spent enough time with my lab members to be known for something, but I think it would be keeping to myself.



"Always be prepared to learn something new. If you come from wet-bench work, there is no need to fear computers and soak up as much as you can from those with more experience."

Keaghan Brown

MSc Candidate: Bioinformatics, South African National Bioinformatics Institute, University of the Western Cape

What is your current project?

Currently I am working on developing a set of computational tools to automatize the prioritization of potential resistance variants identified in HIV Integrase Subtype C and CRF02_AG.

Please fill us in on your career up to this point:

I did my undergraduate at UWC in Biotechnology, after which I did a 12-month internship at the South



(Continued on page 8)

African National Bioinformatics Institute (SANBI) under Prof. Alan Christoffels. During this time, I began familiarizing myself with the differing fields within the bioinformatic discipline. It was during the internship that I started taking an interest in the software development side of bioinformatics.

From there I went on to Honours at Stellenbosch University, where I worked under Prof. David Tabb, who developed a software related project for me to work on. I developed script to map the overall coverage of Mass Spectrometry (MS) data onto protein structures, map the depth of coverage of MS fragments and to visualize any PTMs from MS data on the structures within the context of HIV.

During this period, I started speaking to Drs. Ruben Cloete and Graeme Jacobs about the possibility of doing MSc under their supervision. From our discussions we developed the aforementioned project in which I developed script to automatically introduce mutations/variants and analyse the resultant structures to reduce the number of potential experimental confirmations that need to be conducted.

If you could give advice to students who are new in the field, what would you say?

Though it has been said numerous times, always ensure that anything project related be regularly backed up and that you learn to manage your time appropriately.

I personally have found it best to take breaks when I hit a big problem or after I have managed to solve one. This stops me from overworking, however that said when motivation strikes and the gears get turning start working ASAP as you might just find the solution to the problem you're stuck on.

When did you first realize you love science/computers?

I was in primary school when I first started taking a huge interest about the biological world and it wasn't until high school that I started taking interest in computers and the molecular biological side of things. Though I had excelled in biology, I had struggled to an extent with IT due to a number of factors and as such thought I would stick to biology only.

It was throughout undergrad I had been sent an article in which they had converted an image into a DNA sequence and then reversed back into an image, that my interest in the application of computers was reignited. Since then, I had decided that a field that incorporated both Molecular Biology and Computers was the way to go. I was fortunate enough that during the internship at SANBI, I the fortune of having several conversations with Dr. R. Cloete about programming in python, which eventually led me down the path I am currently taking.

What do you think you are best known for around the lab?

If there were anything I would consider being best known for is my incredibly loud voice and my tendencies to continuously go off on tangents resulting in me forgetting the original point of the conversation.

Do you have a science joke to share?

```
if coffee in mug == 100%:
    mood = "Content"
elif coffee in mug <= 50%:
    mood = "Critical"
elif coffee in mug == 0%:
    return error
```

Mohammed Hassan

MSc candidate: Bioinformatics, South African National Bioinformatics Institute, University of the Western Cape

What is your current project?

My research project is investigating the ABCC Drug transporters subfamily and their role in breast cancer treatment. Breast cancer cells develop resistance to many functionally and structurally unrelated anticancer drugs, due to a phenomenon known as Chemotherapy/Multidrug Resistance (MDR). MDR is a key obstacle that severely limits the efficacy of clinical chemotherapy in breast cancer treatment. MDR is frequently associated with increased efflux of anticancer drugs by increasing the expression of ABC drug transporters. Targeting ABCC Subfamily transporters is a promising approach for reducing or suppressing MDR in cancer treatment. I employ bioinformatics and computational methods to study chemotherapy treatment/resistance and ABCC genes reactivity, with particular focus on the breast cancer molecular pathology; effects on transport mechanisms; and the chemotherapy resistance effects. This includes mechanistic pathways and reactions in enzymes and solutions; sequences of ABCC genes and drug-metabolizing enzyme inhibitors,

(Continued on page 9)

"I personally have found it best to take breaks when I hit a big problem or after I have managed to solve one. This stops me from overworking, however that said when motivation strikes and the gears get turning start working ASAP as you might just find the solution to the problem you're stuck on."



exploring the binding sites, and transcription factors, promoter region to further understand ABCC gene structures and functions.

Please fill us in on your career up to this point:

My curiosity to understand the inner workings and complexities of living organisms formed a large part of my motivating to pursue a career within the discipline of Science and Technology. I obtained my B.Sc. degree in Biotechnology from Faculty of Science and Technology, Omdurman Islamic University (Sudan). After graduation in 2013, I enrolled for a year-contract internship and renewed for another year-contract in the ministry of sciences, technology and communications, Khartoum, Sudan. Then I decided to seek postgraduate studies somewhere outside my birth country. It has been my dream to travel for my graduate studies because I was selected in two international scholarships, the first one was for the American University in Cairo (AUC), the other one was China Government Scholarship for International Students. I couldn't go for the AUC Scholarship because of the Egyptian revaluation in 2012-2013, and the China Scholarship was delayed in the process of obtaining the visa, these delays and Chinese language requirements resulted in denied access. I had a conversation with one of my seniors at faculty and he gifted me a book for research, knowledge production and universities in Africa. After reading the book, I decided to make my way to South Africa. I completed an Honours degree (Class 2016-2017) in the Biotechnology Department at University of the Western Cape (UWC) under the supervision of Prof. Mongi Benjeddou in the Precision Medicine Unit, where my research focused on the inherited genetic differences in drug metabolic pathways. The abovementioned studies further ignited my interest within the arena of research and compelled me to enrol for my Master's degree, March 2020 in Computational Molecular Biology applied to disease diagnostics, which is the main research direction within the Bioinformatics Research Group (BRG) at UWC, under the leadership of Drs. Ashley Pretorius and Ashwil Klein. The overall aim of my research project was to study the ABC drug transporters involved with Tamoxifen multidrug resistance (MDR) in breast cancer treatment and management of African patients using several in-silico methodologies. The bioinformatics lab exposed me to a variety of databases including PharmGKB, TiGER, HPA, STRING, CTD, Kaplan Meier, SURVEXPRESS, and PROGENE. At the beginning of 2021, I registered for CODATA-RDA School of Research Data Science which was offered by University of Pretoria – Department of Information Science in Collaboration with DIRISA, SADiLaR, and NeDICC, South Africa, as from May to July over a period of ten weeks in ten different topics including: Open Science, Introduction to Unix Shell, Introduction to Git, Open and Collaborative Research, Research Data Management, Data Cleaning using Open Refine Software Application, Data Analysis and Visualization - using R, Data Intensive Social Science, Authorship Carpentry, Information Security, Machine Learning, Neural Networks, Research Computational Infrastructures. Currently, I am drafting two manuscripts from my Master's thesis to be published before the close of this year incorporate new training. I will start my PhD studies in 2022.

"As a researcher and scientist, I would like to advise new scholars to set high personal and academic standards for yourself, and live up to them. Listen to that little voice inside you that says, "I can do this." Affirm and believe in yourself. Realize that research is work; it's not play time. And last but not least, settle for nothing less than your very best. "

If you could give advice to students who are new in the field, what would you say?

Considering myself as a new student in the field of structural bioinformatics and data science as whole, the one and only advice I have to offer is to have patience while you are learning new skills especially in this field of science. As a researcher and scientist, I would like to advise new scholars to set high personal and academic standards for yourself, and live up to them. Listen to that little voice inside you that says, "I can do this." Affirm and believe in yourself. Realize that research is work; it's not play time. And last but not least, settle for nothing less than your very best.

What are your hobbies/activities you do in your free time?

I enjoy hiking and connecting with nature. Intellectual conversations interest me over a cup of coffee, or glass of a very good wine or a regal whiskey as much as reading intellectual and novel books also interest me. If you don't find me in the lab trying to figure out my research, I am either exercising and releasing those unwanted negative energies or busy making a lekker lamb oxtail potjiekos and ox trotters soup. Reggae Music is healing for my soul. My favourite color is [BLUE](#).

If you were an animal – what would you be and why?

I would consider my spirit animal is a phoenix because it symbolizes transformation, renewed energies and a passion zest for life. As a phoenix spirit animal one is reborn from ashes, signifying endurance and new beginnings. Phoenix is about overcoming darkness and rising to the challenge to become powerful and succeed and that is the exact me in nutshell.

Do you have a science joke to share?

Once upon time, an infectious disease walked into a bar. The bartender said, "We don't serve your kind here." It replied, "well, you are not a very good host, hahaha, good-bye."

Darius Riziki Martin

PhD candidate: Bioinformatics, South African National Bioinformatics Institute, University of the Western Cape

What is your current project?

The identification and characterisation of DNA/RNA aptamers for application in diagnosis of infectious dis-

Fill us in on your career up to this point:

I have been a molecular biologist for the past 10 years since I joined Kenyatta University back in 2009, then later in South Africa, at UWC from Honours in 2014 under the care of Professor Mervin Meyer at the Biotechnology department. My academic journey has since been an exciting one with lots of adventures in terms of acquiring laboratory skills as I enrolled for MSc and later for PhD. In my PhD, I decided to combine in silico in my research, guided by Dr Ruben Cloete, Prof Mervin Meyer, Prof Abram Madiehe and Prof Martin Onani. Presently, I am working on developing prototypes for the diagnosis of Ebola and TB biomarkers. I do this by the following: Firstly, I combine dry lab (bioinformatics) and wet lab to validate binding between potential ligands and the disease biomarkers (especially for Ebola and TB). Secondly, I employ in silico SELEX to identify and select aptamers (short DNA/RNA molecules) against the Ebola and TB biomarkers using our proprietary library aptamers. I then employ Molecular dynamics approach to identify the most stable aptamers for applications in diagnosis. At the moment, I would like to validate the in silico selected aptamers by wet lab (employing MicroScale Thermophoresis). Once I manage to prove this concept, then we can employ the same method for other diseases in future.

If you could give advice to students who are new in the field, what would you say?

The sky is the only limit, believe in yourself, develop self-discipline throughout your career, and go for what you believe in. Always remember, under the spur of necessity, we shall conquer!

What are your hobbies/activities you do in your free time?

Mentoring fellow students or juniors either in campus, outside campus or at home.

If you could change one thing about yourself, what would it be?

My kindness, people take it for granted and abuse it.

When did you first realize you love science/computers?

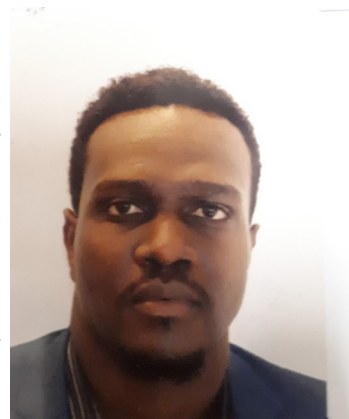
When I realized I could generate results computationally in a few months, without working years in the lab to get the same results.

What do most people not know about you?

They don't know that I like business and would probably turn my focus to business once I have proved the concept.

Do you have a science joke to share?

"What do you call an acid with an attitude? A-mean-oh acid."



"The sky is the only limit, believe in yourself, develop self-discipline throughout your career, and go for what you believe in. Always remember, under the spur of necessity, we shall conquer!"



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