



UNIVERSITEIT VAN PRETORIA
UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA

SASBi

South African Society for
Bioinformatics

Bioinformatics at the University of Pretoria



Fourie Joubert

We have been active in Bioinformatics at the University of Pretoria since the late 90's, when we started presenting training workshops. The Bioinformatics and Computational Biology Unit was established in 2003, and we also moved into our current facilities in that year. The Centre for Bioinformatics and Computational Biology became an official Centre of the University in 2014. Prof Oleg Reva joined us in 2006, and Mr Johann Swart (System Administrator) in 2011.

April 2021

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Bioinformatics at the University of Pretoria

When we started the Centre in 2003, we operated exclusively with Silicon Graphics equipment, and many Indy's, O2's, Octane2's and an Origin 2400 16x processor server. Shortly thereafter, we received a Sun V880, a Sun 1TB Storage Array and a Sun L180 tape robot. Our next hardware upgrade was in 2010, with an IBM Blade Centre (112x cores) and 20TB of storage. This was followed by a series of Dell upgrades. Our latest upgrade was in 2017 with a 10-blade SuperMicro chassis (280x cores), around 2.8PB of storage and a 96-core server with 3TB of RAM. The University of Pretoria is currently working on a design for central HPC for the University, and I am the current Chair of the HPC committee.

We have been presenting short courses for national participants since 1998, and have continued doing so on a regular basis particularly in cooperation with H3ABioNet, although this has recently been hampered by COVID.



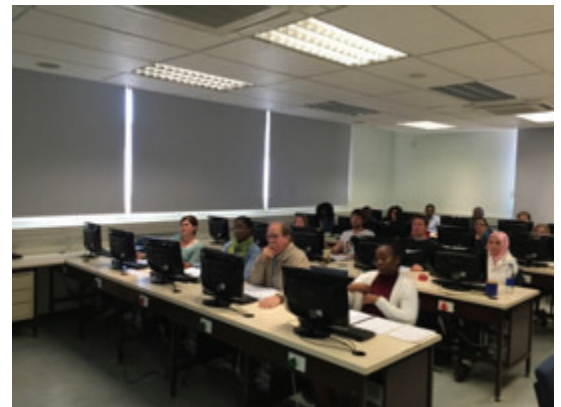
Computational infrastructure and storage is made available to all students and staff at the University of Pretoria across several campuses.

Continued: Bioinformatics at the University of Pretoria

We currently have 28 students in the Centre (9 Hons, 14 MSc and 5 PhD), and the research being performed ranges from viruses, bacteria, fungi, nematodes, insects, plants, animals and humans. We collaborate very widely nationally and internationally. We are of course also involved in a COVID project, where we are collaborating with Prof Michael Pepper at UP's Department of Medical Immunology on COVID patient genomics (one of seven collaborative projects with his group).

We provide a wide range of services to students and staff on campus. We currently have > 150 persons with active logins on our systems, and have around 170 packages listed in our software module configuration system. We provide scientific help and advice with NGS and bioinformatics design, planning and analysis to all needy persons as far as is possible.

Due to COVID, we are mostly working from home, except for Werner Smidt, who is a permanent fixture in the lab. Our face-to-face BSc Hons classes until were rudely interrupted last week by a COVID outbreak in the University of Pretoria female residences leading to a lockdown of contact teaching on campus. These classes are now also temporarily conducted online. We have discovered that for many of us, productivity can remain high without access to campus, but certainly miss the social aspects and cannot wait for a return to normality. We wish you all a healthy and safe 2021, and hopefully rapid access to effective vaccinations!



The Carpentries

Angelique van Rensburg

[Software Carpentry](#), [Data Carpentry](#) and [Library Carpentry](#) aim to teach researchers and related stakeholders foundational computing and data skills. The Carpentries is a fiscally sponsored project of Community Initiative that works with member universities and research organisations to introduce high-quality digital skills workshops to their organisations.

Software Carpentry, Data Carpentry, and Library Carpentry are projects of The Carpentries. We teach essential computing and data skills to research communities. We exist because the skills needed to do computational, data-intensive research are not offered as basic research training at most universities.

The Carpentries partners with institutions to build research capacity within the institution. We facilitate [two-day](#) in-person and [5 half-days](#) online workshops that introduce best practices around programming and data analysis to staff and students (i.e researchers and/or library and information-related communities). With an annual membership, we will help you to deliver impactful workshops, on a growing range of topics, quickly and easily. Also, membership includes training of instructors at host institutions so organisations can be self-sufficient.

The Carpentries workshops are taught by trained, peer, volunteer instructors who all completed an Instructor Training program. Such programs teach instructional pedagogy and the practicalities of teaching a Carpentries workshop. These instructors join our global community, sharing lessons, teaching tips and practices with each other. We continue mentoring these instructors, who, with their learners, become the core of new communities at your institution.

At the beginning of 2021, The Carpentries has taught more than 74 600 learners in 46 countries around the world. With more than 90 member organisations, The Carpentries will help you develop a skilled community of researchers who can adapt to the rapidly changing digital skills landscape.



instructors



learners



workshops

* Learners count is estimated based on average workshop attendance of 25

Student Profiles:

MSc in Bioinformatics at University of Pretoria

Mondli Xaba

Q: What is your current project on?

A: Long read sequencing and genome assembly

Q: Do you have an analogy to use when describing your project to the general public?

A: Putting together a DNA puzzle to see what makes an organism what it is.

Q: What legislation would you change to improve how science in your field is done?

A: Stop the market based approach to science and research. Science is about satisfying human curiosity and bettering lives and the environment, not a "get me the best product" scheme.

Q: Which is your favourite amino acid?

A: Whichever one spends most of its time slacking instead of working is my "amigo acid."



Mia Truter

Q: Do you have an analogy to use when describing your project to the general public?

A: I tell people that I am a data analyst, but for biological data. People tend to know what data analytics is in a business context, so I just extend their idea of that to the biological field.

Q: What excites you about your current project? What makes you get up in the morning?

A: I love figuring things out. I think that's my main motivation, to be honest. The process of having a problem and spending time struggling to fix it, and then coming up with a workable solution. That sense of accomplishment when your code works is what I live for.

Q: What is your favourite programming language or analysis tool?

A: I really like Python. It's user friendly and fun to work with.



Hannes Strydom

Q: How did you end up here? Why did you become a scientist?

A: I wanted to create human-animal hybrids. Studied biotechnology, realised I hate wet-lab work. Moved over to Bioinformatics because I've always loved programming (My father is a java developer) and then was offered an opportunity to do a Bioinformatics project with applied mathematics mixed in.

Q: What advice would you give to someone who is interested in studying Bioinformatics?

A: Don't get stuck on the manuals, most of bioinformatics is learnt through doing and not reading. Stay curious - even things unrelated to your field might help you down the line.

Q: Which is your favourite amino acid?

A: Tryptophan - because it's the precursor to serotonin, and that makes me happy.



Hleliwe Hlanze

Q: What is your current project on? Why is it important?

A: The project is about modelling the evolutionary trajectories of drug resistance in the human adapted lineages of the Mycobacterium tuberculosis complex (MTBC). The project is important because it will shed light on how the genetic background of a strain plays a role in the development of drug resistance and the successful transmission of resistant strains.

Q: What excites you about your current project? What makes you get up in the morning?

A: Tuberculosis (TB) is a well-studied disease, however a lot still needs to be known about drug resistance and how it is maintained in bacterial populations, this knowledge gap is exciting to me. The possibility of discovering new/unknown processes that may exist in the acquisition of drug resistance in TB.



Graeme Ford

Q: What is your current project on? Why is it important?

A: I study Pharmacogenetics which is the study of the underlying genetics that influences drug response. My research focuses on the idea of being able to pre-emptively identify how someone will respond to medication before they even take it.

Q: Are there ways you might profit from your ideas, research or results?

A: The ultimate goal of my research is to partner with industry to help develop products doctors will use when dealing with patients. In that regard, I could very well profit from helping equip the medical industry with the tools it needs to render better care.



Maano Malima

Q: Do you have an analogy to use when describing your project to the general public?

A: A cattle genome is like a Christmas gift present, you never know what is inside until you employ bioinformatics tools to open it.

Q: What legislation would you change to improve how science in your field is done?

A: One of the limitations in research is funding and structuring the funding legislature in a way that favours all parties involved e.g., students, principal investigator, etc. will improve how research is conducted in my field. Another point is that experts from different fields should be part of panels of any board that discusses models of funding research.

Q: What is your favourite programming language or analysis tool?

A: The Genome Analysis Toolkit (GATK)



Albertien van Heerden

Q: What is your current project on? Why is it important?

A: Investigating the genetics of migration in the Asian Houbara bustard. This partial migrant bird species is of cultural and economical importance to countries in and around the Arabian peninsula. Conservation of this species is very important because it is threatened by over-hunting. Captive breeding and release programmes can benefit from increased knowledge of the genetic background of the species, because releasing captive-bred birds into wild populations with similar migratory behaviours increase their chances of survival.

Q: What legislation would you change to improve how science in your field is done?

A: I would like it if conservation experts had a greater influence on the decisions made regarding conservation legislation and implementation.

Q: What advice would you give to someone who is interested in studying Bioinformatics?

A: Don't be intimidated by programming and start learning as soon as possible.



Upcoming events

26 September 2021: SASBi-SC/SAGS 2021 Student Symposium, Protea Hotel, Stellenbosch.

Registration:

https://docs.google.com/forms/d/e/1FAIpQLSfmFnJfhXtA2C5uFclKwnPUxb319ERX7felGZUs_zWS7fR8g/viewform

April – August 2021 SASBi/SAGS Virtual Symposium

20 April: Gerard Tromp

22 June: Ozlem Tastan Bishop

17 August: Nicky Mulder

March/April 2022: SASBi/SAGS Hybrid Conference

Details to be announced
