H3ABioNet
Pan African Bioinformatics Network for H3Africa

Issue 21: April 2017

H3ABioNet

In This Issue

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Foreword

Just three months to go until the official end of the H3ABioNet grant. We eagerly await the final outcome of our renewal application. In the mean time, the working groups and task forces are busy wrapping up projects, and documenting and disseminating results. At Central, we are working on a revamp of the H3ABioNet website to improve its ease of use and to raise the visibility of some of our outputs.

The last few months has been productive for the working groups. Training has continued with a microbiome workshop run by the Wits node under the AWI-Gen project. H3ABioNet helped with some of the teaching, and provided travel fellowships to attend. We are excited to be running the second round of the Introduction to Bioinformatics course, which now has even more classrooms and more participants! We hope lessons learnt from the first iteration will help to make it even more successful. The research working group is continuing to provide access to research through the webinar series and more recently the research digest. Please do volunteer for paper reviews and seminars.

As the current grant period draws to an end we are increasing our outreach activities with the ambassador program introduced by the user support working group. We hope these ambassadors, together with the node PIs, will disseminate news and outputs of H3ABioNet regionally and increase awareness of bioinformatics in their institutions and local governments. We need to focus more heavily on long term sustainability of what we have built. In this newsletter you will also read about public outreach activities to the youth through mGenAfrica. Please enjoy reading about this and our other highlights for the month.
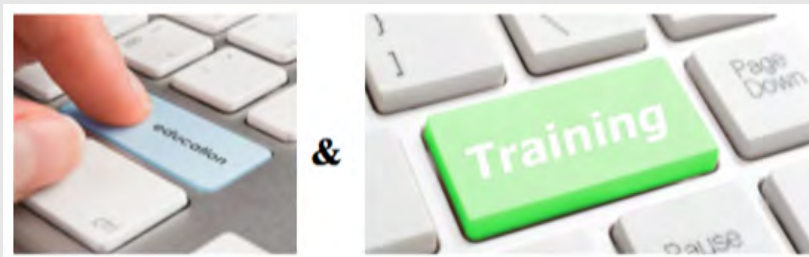
Nicola Mulder

H3ABioNet

Education and Training Working Group

Education and Training Working Group

The working group has been busy with various on-going projects, with a major focus on final plans and preparations for the upcoming Online Introduction to Bioinformatics *IBT_2017* course.

Based on a survey sent out to identify potential classrooms, IBT_2017 will run from the 9th May 2017 to 4th August 2017 with 2 contact sessions a week, from 10:30 to 14:30 CAT every Tuesday and Thursday. The call for participants was sent out at the end of March and we have had an overwhelming response to the course again this year. There are currently 27 registered classrooms across the African continent with roughly 600 participants registered to attend the course! Due to the tremendous interest in the course, several additional classrooms have been set up to allow students from different regions of the participating countries to access the classrooms. In addition, we have some new classrooms in countries like Burkina Faso and Ethiopia. Although the core content and design of the course has remained the same as IBT_2016, based on the feedback received, a number of changes have been introduced to improve the course. One of these changes includes the introduction of a set of training sessions prior to the start of the course, aimed at equipping the on the ground teaching assistants and staff with the necessary skills to coordinate and assist participants efficiently. We are looking forward to a successful and exciting course!

On the workshop front, H3ABioNet together with the H3Africa *AWI-Gen project*, based at the University of the Witwatersrand, hosted a workshop focused on the analysis of microbiome data from the 29th to 31st March 2017. You may read more about this workshop in this issue of the H3ABioNet newsletter.

An on going project of the working group has been the updating of the MSc curriculum website resource. In collaboration with the various individuals involved in the development of the original modules, each module is being updated and standardised. In addition, a guidelines document is being created for those interested in using the resource to implement an MSc in bioinformatics at their institution.

Finally, as mentioned in last month's newsletter, planning is underway on developing the framework and content for a career development workshop proposed to be run alongside the H3ABioNet SAB meeting and ASBCB conference in October this year. We would like to tailor this workshop as best we can to provide a valuable opportunity for postgraduate students and early career scientists to develop the skills necessary to enter and excel in an academic career. The current proposed format would have two streams, one tailored to postgraduate students and the other focused on early career scientists. As we are still in the early stages of developing the workshop curriculum, we welcome any insights and suggestions of topics to be included in the workshop. Please send any suggestions to Kim Gurwitz (kim.gurwitz@uct.ac.za) with the subject line Career Development Workshop.

#H3ABioNetEducationAndTraining   **Nicky Mulder and Shaun Aron**

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Infrastructure Working Group

Infrastructure Working Group
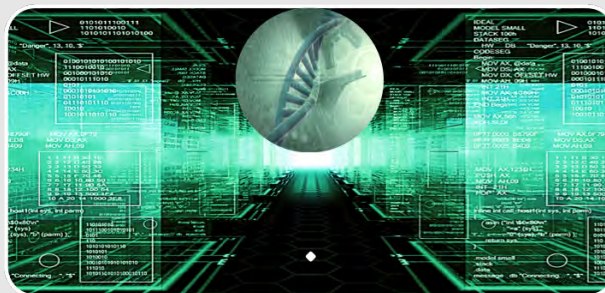
April has been a relatively quiet month for the Infrastructure Working Group (ISWG), but a lot of work continues behind the scenes.

- The Data Management Taskforce continues to prepare for the deluge of data that will shortly be submitted by research projects for onward transmission to the EGA. We are also working on a catalogue/database that will be used by researchers for searching H3Africa data.
- Our rollout of Globus Online endpoints and the Netmap project continues. As we end our first 5 years, we urge all nodes to check the status of their endpoints or if they have not yet installed, to please do so.
- The Cloud/Pipelines project is wrapping up. Some of the work was delayed by other projects but it is now a priority to finish this work.
- The System Administration Task Force is continuing to work on documentation.

Scott Hazelhurst and Suresh Maslamoney

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Research Working Group

The first issue of the Bioinformatics Research Digest (BioRes Digest) was published last month within the H3ABioNet Newsletter as a special issue. The editorial team of the BioRes Digest would like to receive perspective feedback, suggestions, and comments from the members of the H3ABioNet consortium on any ideas and additions to improve the subsequent issues of the digest. The second issue of BioRes Digest will be launched in June 2017 within a special issue of the H3ABioNet Newsletter. The editorial team will be more than happy to receive your feedback and inputs before the end of May to address some for the 2nd issue or for subsequent issues of the digest. Dr. Juanid Gamieldien from SANBI has volunteered to give a brief summary of his recent publication entitled *A practical guide to filtering and prioritizing genetic variants* as the main article summary for the 2nd issue of the digest. We hope that others, and especially graduate students, will volunteer for the September and December issues.

The theme for the H3ABioNet seminar series for March 2017 was "Variants calling from NGS datasets". Three graduate students presented at this month's seminar, including: 1. Mattew Kendzior, a graduate student at the University of Illinois at Urbana-Champaign (UIUC) working towards his Masters of Science in bioinformatics; 2. Junyu Li, an undergraduate student in her senior year at University of Illinois at Urbana Champain, studying molecular biology and minor in computer science; and 3. Azza Ahmed, a PhD candidate at the H3ABioNet Sudan node, University of Khartoum, targeting the areas of statistical and mathematical methods and pipelines of data analysis in Genome Wide Association Studies (GWAS) and Next-Generation Sequencing (NGS). Mattew, Junyu and Azza happened to work closely with each other during Azza's H3ABioNet internship at the University of Illinois during the summer of 2016. Both Mattew and Junyus' talk was on "Variant calling by assembly: complex variants and repeats in populations of complex genomes", whereas Azza's talk was on "Variant calling optimization".

The theme for the H3ABioNet seminar series for April 2017 was on "Biomedical Informatics". The chair of the Research Working Group invited Professor William Hersh, a well-known leader and innovator in biomedical informatics both in education and research, to present. He is Director of OHSU's Biomedical Informatics Graduate Program, which is one of the largest of its kind in the world and offers Masters and PhD degrees. Dr. Hersh also spearheaded OHSU's efforts in distance learning for biomedical informatics, which are available up to the masters degree level. Prof. Hersh's talk on Thursday April 20th was a phenomenal H3ABioNet seminar event among all the presentations in the H3ABioNet seminar series. His talk attracted more than 20 participants from H3ABioNet and one member of the SAB. Prof. Hersh stressed the issue of using Electronic Health Records (EHR) to predict patients at risk for readmission and identifying patients who might demonstrate improved outcomes. The full talk could be accessed on *his website*.

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Research Working Group

The Research working group chairs will prepare a Google document for assigning members of the Research working group to their node's projects. The assigned individuals will report back on the status of each project every 6 months.

The organizing committee for the H3ABioNet Malaria DREAM Hackathon finished writing up the concept paper for the Hackathon that will be distributed soon to all participants of the hackathon. We invite their comments, suggestions and approval for submission as co-authors. The co-chair, with representatives from the IBM Africa Research and the Notre Dam University, presented two posters on the Malaria DREAM Hackathon during the Sage Bionetworks Assembly in Seattle, Washington, USA on April 20-22nd 2017. The poster of the co-chair was mainly on the Hackathon as means of knowledge transfer whereas the poster of the representative of the Notre Dam University was focused mainly on the data analysis and findings.
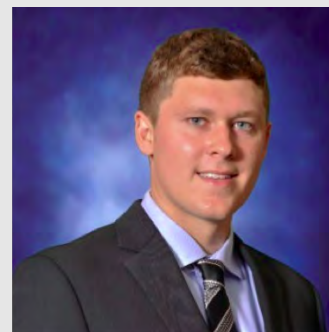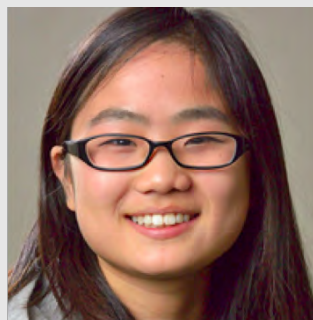
H3ABioNet Webinar for March 2017 with 3 presenters on the theme of "Variants calling from NGS datasets". Left to Right: Azza Ahmed is a PhD candidate at the H3ABioNet Sudan Node, University of Khartoum. Junyu Li is an undergraduate student in her senior year at University of Illinois at Urbana Champain. Mattew Kendzior is a graduate student at the University of Illinois at Urbana-Champaign (UIUC).

H3ABioNet Webinar for April 2017 presented by Prof. William Hersh, from Oregon Health & Science University on the theme of "Biomedical Informatics".

#H3ABioNetResearch

Faisal Fadlelmola and Amel Ghouila

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User Support Working Group

User Support Working Group

The User Support Working Group (USWG) launched a successful Journal Club in March, which was premiered with an exciting talk from Dr. Nicholas Harding on graph-based theory. In April Dr. Alia Benkhala presented an article on prediction of disease progression outcome in recent undifferentiated arthritis cases to aid decisions on appropriate treatment regimens. The H3ABioNet journal club sessions have been well attended and the series continues.

The USWG has revisited the plan to publish a helpdesk article to introduce the network-developed resources available to the wider scientific community and to share our development/operational experiences. The helpdesk is a platform that brings together existing expertise within the network to provide bioinformatics technical support.

This year has been productive; the USWG revisited the earlier much-talked about establishment of ambassadors to undertake the Network continent-wide outreach activities. The framework and policy document on the ambassadors (liaisons) has been drafted, which clarifies the roles and responsibilities. Briefly, their roles and responsibilities include:

- Liaise with social media team
- Amplify our social media campaigns within their nodes
- Raise visibility of H3ABioNet within the nodes (and further circulating network profile and planned activities through bulletins, flyers among others)
- Provide feedback to USWG on emerging bioinformatics needs/issues from the nodes

The required profiles, and skill sets for the ambassadors include:

- Ideally, students (MSc, PhD) or Postdocs
- Good communication skills
- The ability coordinate events
- Social media savvy
- Networking skills

The social media taskforce has been meeting biweekly to liaise regarding the implementation of the coordinated media strategy. Further, the taskforce has developed a set of guidelines for publicizing content on social media, which has been shared with the wider USWG for comment.

#H3ABioNetUserSupport

Jonathan Kayondo and Pandam Salifu

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**Node Assessment
Taskforce Report**

Node Assessment Taskforce Report

Activities for the Node Assessment Task Force (NATF) had been dormant for most of 2016, after both the CBIO group (Prof. Nicky Mulder) and the CUBRE group (Prof. Ezekiel Adebiyi) submitted successful accreditation exercises in late 2015. This has suddenly changed, and we are happy to report several significant developments over the last few months.

Firstly, the Sudan Node (Prof. Faisal Fadlelmola) took the genomic variant calling accreditation exercise in December 2016 - January 2017. The report they submitted was examined by our panel of external experts, who unanimously agreed that is was of excellent quality. As a result, the Sudan node is now the second H3ABioNet node outside of South Africa to have successfully submitted itself to the accreditation process, and it deserves heartfelt congratulations for its effort. Female graduate students Azza Ahmed, Rehab Ahmed, and Somia Mohammed made up the core team for the exercise.

Secondly, we submitted to PLoS Computational Biology a paper describing our experiences with preparing and running the Node Accreditation Exercises. The manuscript, entitled "Assessing Computational Genomics Skills: Our Experience in the H3ABioNet African Bioinformatics Network", was accepted for publication in February, and should appear online soon. Authors include the active members of the NATF, the people who prepared the materials for the exercises, and the members of the teams who submitted to them. We will share the manuscript with all H3ABioNet members as soon as it is ready for publication. We are confident that it will show the scientific community what can be achieved in the African context.

Thirdly, the number of Nodes taking the exercises has recently exploded. The CBIO Node has taken the 16S rDNA metagenomics exercise in February-March 2017, and their report is currently being reviewed. The Wits Node is taking the same exercise starting in April. The Malawi and Egypt Nodes have announced their intention to submit to the genomic variant calling exercise in the near future, and are preparing for it by analyzing the training datasets and fine-tuning their workflows. The NABDA Node (Nigeria) is similarly preparing for the 16S rDNA metagenomics exercise.

We are very pleased to see that a little over four years after the discussions at the first AGM in Cape Town in 2012, the H3ABioNet community is seeing the value of being formally assessed for its technical skills in computational genomics, which are essential to support the research activities of the H3Africa consortium. We are even more gratified that all of the reports submitted so far have been judged to be of excellent quality by our external experts, proving that African research groups can hold their own in international comparisons. It is our sincere hope that by the end of the second H3ABioNet funding period, every Node will have proven their technical ability to fully participate in the genomic revolution.

Victor Jongeneel

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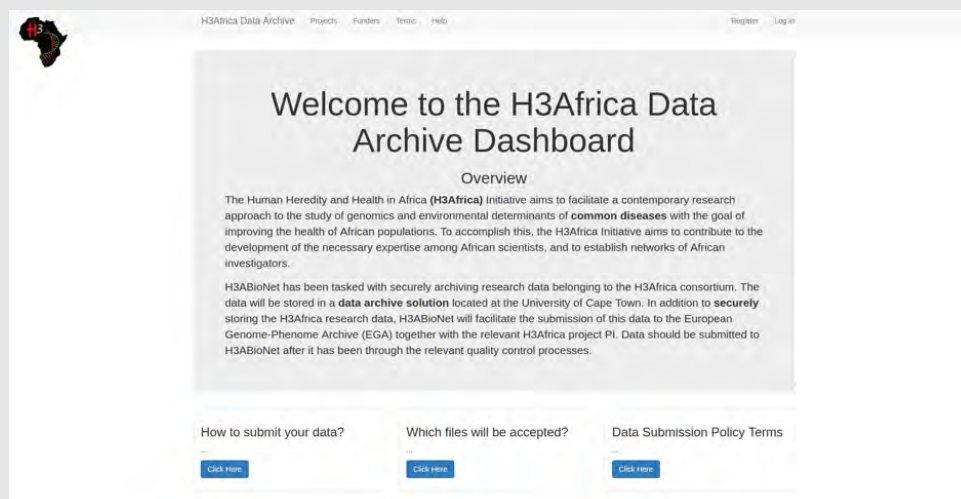#bioinformatics #Africa
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H3Africa Data Archive Dashboard

H3Africa Data Archive Dashboard

The NIH and Wellcome Trust have funded multiple projects on genomic research where data is required to be deposited into a public repository. One such repository is The European Genome-phenome Archive (EGA), which stores sequence and genotype data. Access is determined by a formal application procedure for the purpose of secure storage and distribution. Informed consents are required for specifying controlled release requirements. H3Africa acknowledges that researchers from the H3Africa data generating projects based in Africa can benefit tremendously from the data sharing capabilities of the Internet by using the appropriate technologies. As such, H3Africa has developed a repository to meet this end: the H3Africa Data Archive is the effort between the H3Africa data generating projects, H3ABioNet and the EGA.

To facilitate the project, H3ABioNet has developed an interactive Archive Web Dashboard. The dashboard intends to track the progress of data submissions. This requires the development of a front-end user interface as well as a back-end. The technologies that are used for the front-end are: HTML, CSS, JavaScript, and Bootstrap. The Django Web Framework, Python with a range of libraries, PostgreSQL, and Ubuntu are used for the back-end. H3ABioNet will maintain the security of the system, support users with data submission and facilitate the data transfer. This will enable users the opportunity to submit their data and keep track of their submission status. The goal is to ensure efficient data flow between researchers, the archive and the EGA. Nine months after the data is in secure storage, H3ABioNet will convert the data into an XML format ready for submission to EGA.

Currently, testing of the platform is underway making use of various user case scenarios such as: submitter, PI, funder. We hope to go live with the platform soon.

The H3Africa Data Archive interface

#H3AfricaDashboard

Ziyaad Parker

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mGenAfrica

What is MGenAfrica?

mGenAfrica is an online and mobile app which allows high school learners to access information about biomedical research in Africa. They can:

- Learn about career options (Career Spotlight) and opportunities (Training Opportunities)
- Interact with research staff (Live Chat) in these fields
- Share knowledge/thoughts (Have Your Say) and help translate terms (Translation Corner)
- Test their knowledge (Quiz)
- Listen and get some information through cool videos, audios etc.

mGenAfrica aims to increase awareness and uptake of tertiary education and careers in genomics and the biomedical field. In addition, it aims to increase literacy and awareness around research and the contribution of genetics and genomics to human health. mGenAfrica is funded through the Pan African Bioinformatics Network (H3ABioNet) and supported by two Working Groups from the Human, Heredity and Health in Africa (H3Africa) Consortium: the H3Africa Education and Coordinated Training (ECTWG) and Community Engagement Working Group (CE).

If you are keen to inspire the next generation of research staff via online platforms, then mGenAfrica is an ideal platform for you! Click *here* to register as a volunteer.

As a volunteer:

- You will be required to load your profile and some fun pictures of yourself
- Set aside at least one hour per year to text-chat to some high school learners (we will share a schedule of classes and the slots they booked with you)
- If you can, write a short story to highlight a research concept on your work!

When funding permits we will look into some incentives for research staff. Let us know if you have any ideas, comments or feedback about the incentives or any other ideas we can use to improve this platform. For further information, questions or suggestions please contact Dr Victoria Nembaware (victoria.nembaware@uct.ac.za) or submit via our *online feedback form*.

Please read the piece below written by the South African Society for Bioinformatics Student council, in which they describe an exhibition featuring a demonstration of the mGenAfrica app to primary and high school students.

Victoria Nembaware

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South African Society for Bioinformatics Student Council Activities

The South African Society for Bioinformatics Student Council attended the South African National Science Festival (Scifest) this year in Grahamstown, thanks to the generous sponsorship of Inqaba Biotec, H3ABioNet, Sydney Brenner Institute for Molecular Bioscience (SBIMB), and the Swiss-South Africa Joint Research Programme (FNSNF). We hosted an exhibition and a workshop over the entire duration of the festival, 8 to 14 March 2017.

The Exhibition

At our exhibition we showed videos explaining bioinformatics in three different languages, as well as a video from mGenAfrica (a web app developed by H3ABioNet) explaining genetics simply to primary and high school learners. We found that the bioinformatics videos appealed to the older learners in high school (Grades 10 to 12). Learners of all ages, as well as educators, were intrigued by the video from mGenAfrica and it drew many people to our table. Learners who were interested in either genetics or IT were interested in bioinformatics and were willing to have a look at the web app.

We also had a DNA 'model' that represented how long DNA would be if it was stretched out from one cell. This was enjoyed by learners of all ages (Grades 2 to 12) as well as students in university, parents and educators. Most visitors were very shocked to discover that DNA is so long and can fit into a tiny cell. This brought about discussion on how DNA can fit into a cell, and what its function is.

The DNA model then led onto a very short 'sequence alignment', where visitors were welcome to attempt to align a sequence to a reference sequence and find 'mutations'. Again, this was enjoyed by all ages. Children as young as 8 years old asked intriguing questions such as "Why are there only 4 letters?", "Is this why we all look different?" and "Can these mutations cause other diseases?"

Matric students assumed that the sequence alignment was a base pairing exercise and immediately went on to match the base pairs to the reference sequence. After a bit of explaining, however, they caught the gist of it and understood what a sequence alignment actually is and what its function is in bioinformatics. We also put out a laptop with a game one of our team members designed using Python. Some visitors were very intrigued by it, especially those who had an interest in coding.

The Workshop

The aim of the workshop was to introduce high school learners to bioinformatics, both as a field of study and a career choice. This was done through a case study of the evolution of taste receptors adapted from *DNA to Darwin*. The case study introduces the learners to the basics of bioinformatics, i.e., databases, sequences, sequence alignment and phylogenetic analysis.

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SASBi Student Council Activities

The workshop included both a lecture presentation and hands-on activities using an eBioKit server from the University of the Witwatersrand and 5 laptops hired from *Telnet*. The lecture presentation introduced the learners to the cell, genes, transcripts and proteins. After this, the learners were introduced to the 5 basic tastes that humans can sense, i.e., sweet, sour, savoury (umami), bitter and salty. The proteins and genes that are responsible for the recognition of the basic tastes were explained, with the focus being on the sweet and umami taste receptors. These two tastes have the T1R3 trans-membrane protein in common. Learners were given a manual with instructions on how to go about the analysis of the receptors from the sweet and umami tastes. There were basically 3 analysis steps for the workshop:

- Retrieval of the protein sequences from the Ensembl database on the eBioKit server
- Alignment of the sequences using the wEMBOSS tool on the eBioKit server
- Viewing the sequence alignments and producing a phylogenetic tree using Jalview

For each of these steps, a walk-through example was carried out and explained so that the learners knew what they were doing and why. As we only had 5 laptops, about 2 - 4 learners were assigned to each laptop. After the learners had retrieved the sequences, carried out the multiple sequence alignment and produced the phylogenetic tree, the learners were engaged in a discussion of what the results meant. They were also given a real life example of taste in animals using the panda bear, which has lost its ability to taste meaty flavours, and thus its diet consist only of plants. The workshop attracted mostly learners interested in biology. There was no attendance on the first and last day as shown in the table below. On the first day most high school educators came to see what workshops and exhibitions they could send their learners to before bringing the learners to the Scifest. On the last day, there were few students. Most attendance was over the weekend.

Number of Learners in Attendance for Each Day of the Workshop

Day (8-14 March 2017)	Number of Learners Attended
Wednesday	0
Thursday	8
Friday	21
Saturday	18
Sunday	20
Monday	12
Tuesday	0

The learners and educators at the festival were very inquisitive and showed interested in bioinformatics and its application to real life problems. A workshop like this is clearly beneficial to young minds who have interest in both biology and computers.

South African Society for Bioinformatics Student Council

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**Meet the H3ABioNet PI**
Prof. Oyekanmi Nash

Meet the H3ABioNet PI

Interview of Prof. Oyekanmi Nash
PI of National Biotechnology Development Agency - NABDA,
Nigeria, H3ABioNet node
by Rehab Ahmed

Prof Oyekanmi Nash

Interviewer: My name is Ms. Rehab Ahmed; a PhD student at the University of Khartoum. I am affiliated to the H3ABioNet Sudan Node, at the *Center for Bioinformatics and Systems Biology* (CBSB) at the Faculty of Science. I am honoured to start the 'Meet the PI' interview series and to have this great opportunity to talk to Professor Nash and report on our meeting. Generally he talked about himself, his institution, bioinformatics and the H3ABioNet.
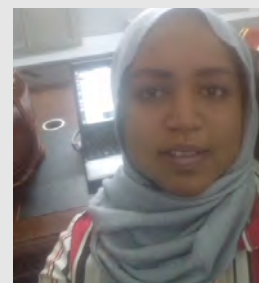
Here are the details of the meeting:

Rehab: Tell us a bit about yourself

Prof. Nash: My name is Oyekanmi Nash, a Molecular Geneticist and the PI of H3ABioNet Node at the National Biotechnology Development Agency (NABDA), Abuja, Nigeria. I am the Director of the Center for Genomics Research and Innovation in the Agency. I started my academic life at the University of Ibadan in Nigeria, where I obtained my first and second degree in biochemistry. I worked briefly after that at the Federal Institute of Industrial Research, Oshodi (FIIRO), Lagos before traversing the globe for deeper understanding of the DNA. After I got my PhD in Korea University, Seoul, I joined the Canadian Protein Engineering Network Center of Excellence (PENCE) at the University of British Colombia, Vancouver as a Postdoctoral Fellow. Subsequently, I was at the Albert Einstein College of Medicine, New York as a Research Associate.

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Meet the H3ABioNet PI
Prof. Oyekanmi Nash

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Rehab: May you elaborate on NABDA a bit?

Prof. Nash: NABDA is the Nigerian government agency set up to promote, coordinate, and set research agenda in biotechnology for the country. It was established in 2001 in Abuja and has six zonal biotechnology centers in six, first generation universities across the six geo-ecological zones of the country including Ibadan, Port-Harcourt, Nsukka, Zaria, Jos and Maiduguri Universities. I am also in charge of the NABDA-Southwest Center of Excellence at the University of Ibadan.

Rehab: How did you get into bioinformatics?

Prof Nash: That's a good one and I am happy to answer this question. As said earlier, after my PhD studies in Seoul, I was privileged to get a post doc position at The University of British Colombia in Canada. My project then was on the molecular evolution of the glycosyl hydrolases to what we had christened "glycosynthases". As a biologist, bioinformatics was just coming up and it became very useful in the studies. My mentor was Francis Ouellette who had just returned to Canada then, from the United States to initiate what was called the Canadian Bioinformatics Network (CBN). I had my training in the summer of 2001. It was actually after the training that I promised him that we are going to fashion something along the line of CBN in Africa. In 2003, the West African Bioinformatics Workshop Series commenced in Ibadan - with the full backing of Winston Hide?s South African Bioinformatics Institute and seed fund from the WHO-TDR and Wellcome Trust. We have not looked back since then, culminating in the founding of the African Bioinformatics Network (ABioNet) in Abuja (in 2008). The rest is history. So I started as a bioinformatics tools user and became a promoter for bioinformatics education, training, research, and development.

Rehab: What are your research interests?

Prof. Nash: As I've told you, my background is in biochemistry and genetics. So my research interests have been in genome evolution, biologics and bio-pharmaceuticals. With regard to our focus within the H3ABioNet, these are on genome wide analysis studies and microbiome analysis.

Rehab: What do you enjoy most about your job?

Prof. Nash: The area of molecular biology and bioinformatics is interdisciplinary. So I enjoyed using these subjects to think deeply and to answer research questions in genome and evolution R and D.

Rehab: What do you enjoy least about your job?

Prof. Nash: Huh! The horizon of bioinformatics is so wide and you have to do many things.

Rehab: How has being a part of the H3ABioNet community impacted your research group?

Prof. Nash: To be honest, the H3ABioNet is our dream that has come true. Like I said we started as small team in 2003 when we set out to lay the framework for Bioinformatics education, training and research in West Africa. The Malaria Research and Training Center (MRTC), Mali was there from the beginning. When H3ABioNet came in 2012, it has changed the landscape of Bioinformatics education and research in Africa. Recently, the *Introduction to Bioinformatics course (IBT)* has provided another opportunity to reach out to other institutions in Nigeria and Africa.

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Meet the H3ABioNet PI
Prof. Oyekanmi Nash

Prof. Nash *cont.*: Specifically, for H3ABioNet NABDA Node, H3ABioNet had lifted us up, including funding of my Post doc fellow (Segun Fatumo) at Sanger Center (in GWAS), and a pre-doc intern (Deborah Fasesan) trained in microbiome analysis at the University of Illinois at Urbana Champaign Node (Supervisor: Victor Jongeneel).

Rehab: What advice would you give a young person that is interested in pursuing a career in bioinformatics?

Prof. Nash: I tell my students and young staff that if bioinformatics was there before I started my PhD, I would have joined Bioinformatics right away after my first degree. So just get started as soon as possible - and flourish.

Rehab: Tell us something about yourself that not many of your colleagues know e.g. hidden talent, hobby.

Prof. Nash: So, many people might not know my passion for music. I was actually a member of a choir before. I also love to play lawn tennis, and I am an avid movie goer (top on the list: musical movies). Finally, I love traveling.

Final words…

Prof Nash: When it comes to bioinformatics in Africa, I don't feel like it has reached what I was anticipating it to be, years ago. I am really looking into more development in bioinformatics R and D across the continent. In the past 5 years, H3ABioNet has set the foundations for continental and regional collaborations and we are looking for more from these regions. I feel it is my duty to continue to promote bioinformatics. With regard to my node, we are working to get accredited very soon in GWAS and microbiome analysis. We plan to establish regional and international collaboration in those two areas.

Finally, I would like to thank everyone involved in developing bioinformatics capacity in Africa. My thanks go to Professors Ayoade Oduola, Winston Hide, Seydou Doumbia, Raphael Isokpehi, Jessica Kissinger, Nicola Mulder, Raphael Isokpehi, Daniel Masiga, Alia Benkahla, Faisal Fadlelmola, and many other people that we may not be able to mention here.

#MeetthePI

Rehab Ahmed and Oyekanmi Nash

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Microbiome Course

Wits/AWI-Gen/H3ABioNet Microbiome Course

The Wits H3ABioNet node, with support from H3ABioNet and the H3A AWI-Gen project, organised a successful microbiome course from 29-31 March, preceded by one day *Introduction to Linux* course on 28 March. H3ABioNet and SANBio supported 7 travel fellowships from across Africa.

The course was very well supported – over 85 people applied for the course, and we were only able to accept 23 participants for this hands-on course which covered experimental design as well as bioinformatics analyses using both 16S and shot-gun sequencing.

The lecturers for the course were Professor Ami Bhatt from Stanford University and Fiona Tamburini, one a PhD student in Dr Bhatt's lab, and Gerrit Botha, from the CBIO Node at UCT. The lectures and practical work were very well received. There is increasing interest in microbiome work across Africa and this is reflected by the enthusiasm by which the course participants reacted to the course and the exciting work that was planned.

The Wits node would like to thank: Ami, Fiona, and Gerrit for giving so freely of their time in coming to Wits; the H3ABioNet and AWI-Gen for the funding; and to Sumir Panj (CBIO node at UCT) and the staff of the Sydney Brenner Institute for Molecular Bioscience for their help in making this all happen. Please see below some pictures from the microbiome course.

Images from the Microbiome Course held at the University of the Witwatersrand, South Africa, 29-31 March

Scott Hazelhurst Back to Contents

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Issue 21: April 2017

H3ABioNet

Announcements

Announcements

- Breaking News: Congratulations to the CBIO Node at the University of Cape Town for successfully undertaking and becoming accredited for the H3ABioNet 16S rRNA data analysis Node accreditation.

- Congratulations to Dr Junaid Gamieldien from SANBI on his recent publication entitled *A practical guide to filtering and prioritizing genetic variants* (*doi 10.2144/000114492*)

- Congratulations to the MUHAS node on the issue of the Collaborative Consortium award for the establishment of the NIH Sickle Pan African Research Consortium (SPARCO), comprising three sites (Tanzania, Nigeria, Ghana) with MUHAS as a central hub.

- Congratulations to Prof. Ambroise Wonkam's group on their recent publication entitled *Clinical and genetic predictors of renal dysfunctions in sickle cell anaemia in Cameroon* (*doi 10.1111/bjh.14724*)

- Congratulations to Prof. Ambroise Wonkam who was awarded the NIH Sickle cell Data Coordinating Centre. Prof. Nicola Mulder is co-PI.

Do you have an ANNOUNCEMENT for upcoming editions of the H3ABioNet newsletter or for the H3ABioNet social media pages?

Tell us about your anouncements *here*

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Upcoming Events

Upcoming Events

- **June 4th to June 16th 2017**: *EMBO Practical Course in Bioinformatics and Genomics*, will take place in Thermi, Greece.

- **June 12th to June 16th**: Introduction to Genome-Wide Association Studies (GWAS) for complex diseases organised by The African Institute for Mathematical Sciences (AIMS) Ghana and the H3ABioNet Node of the Noguchi Memorial Institute for Medical Research (NMIMR) University of Ghana, hosted at NMIMR, Ghana. Read more *here*.

- **July 19th to July 21st 2017**: *NextComp 2017: Next Generation Computing Application Conference*, will take place in Republic of Mauritius.

- **July 21st to July 25th 2017**: *International Society for Computational Biology conference 2017 (ISCB ECCB 2017)*, will take place in Prague, Czech Republic.

- **August 13th to August 16th 2017**: *17th Biennial Congress of the Southern African Society for Human Genetics*, will take place in Durban, South Africa.
  Closing date for abstract submission has already passed (1 April 2017).

- **August 20th to August 23rd 2017**: *The 8th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB)*

  This year, the *Workshop on Algorithms in Bioinformatics (WABI)* will be co-located with ACM-BCB.

- **October 8th to October 9th 2017**: The H3ABioNet AGM/SAB meeting, Entebbe, Uganda.

- **Every third week of every month**: *CPGR Foundation in Genomics Course*, from standard molecular technologies to advanced 'omics' application in 3 days, aimed at scientists who are new to 'omics' as well as researchers interested in an overview of a dynamically evolving field.

- For a comprehensive list of bioinformatics and genomics conferences, please consult: *Conference service - Bioinformatics*

Do you have an EVENT for upcoming editions of the H3ABioNet newsletter or for the H3ABioNet social media pages?

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H3ABioNet

Upcoming H3ABioNet working group meeting schedule

Upcoming H3ABioNet working group meeting schedule*

*Schedule until end May 2017

Summary of H3ABioNet upcoming working group meetings

Month	Date	Day	Working Group (WG)	Time (UTC)
May	12th	Friday	Research WG	13:00
May	19th	Friday	User Support WG	9:00
May	23rd	Tuesday	Education and Training WG	11:00

Timezone conversions to UTC for all H3ABioNet working group meetings

UTC Time Offset	Time Zone Name	Region/ Country in the Time Zone offset
-6 hours	CDT	Chicago, USA
0 hours	GMT	Burkina Faso, Ghana, Mali, Morocco, Senegal
+1 hour	WAT	Cameroon, Chad, Gabon, Namibia, Nigeria, Niger, Tunisia
+2 hours	CAT	Botswana, Egypt, Malawi, South Africa, Zambia
+3 hours	EAT	Sudan, Ethiopia, Kenya,Tanzania, Uganda

This edition of the newsletter was compiled and edited by Kim Gurwitz. For any corrections, please contact Kim at kim.gurwitz@uct.ac.za

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