



H3ABioNet *Newsletter*

Pan African Bioinformatics Network for H3Africa

Issue 25: May 2018



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Foreword

Welcome to the first official newsletter for phase 2.0 of H3ABioNet. We are already more than 6 months into the renewal, but have had delays in preparing the newsletter as our training coordinator and newsletter editor, Kim Gurwitz, left to take up a new position in Cambridge.

This has been a busy period of setting up the many new and existing projects in Active Collab, a project management system. This will help us to more easily track tasks and deliverables. The existing projects from phase I have continued and many of the new projects have already made good progress.

During this period we held a kick-off meeting for the renewal, which welcomed old friends and introduced new nodes into the consortium. A report on the meeting can be found later in this issue. Many H3ABioNet members also attended the 11th H3Africa consortium meeting in Uganda where we met some of the new H3Africa grant awardees. We look forward to working with them to provide informatics support for their projects.

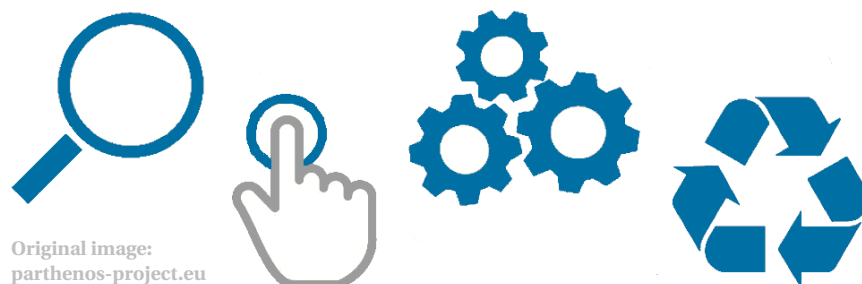


In this issue of the newsletter you will notice a new look, which has been assembled by Kirsty Lee Garson from CBIO at UCT. We felt it was important to refresh the look and feel of the newsletter for phase 2.0. The pages all have links between them, and to our social media platforms. In this first issue we introduce the 8 work packages which are responsible for driving all the projects in H3ABioNet, together with their chairs and co-chairs. This should provide an overview of the focus areas and projects of the network for the next 5 years. We also feature report backs from the kick-off meeting and a software/data carpentry training workshop attended by some of the H3ABioNet staff.

I invite you now to read on to find out more about our plans for H3ABioNet phase 2.0.

Nicky Mulder
H3ABioNet PI

Data & Standards Work Package



CHAIR:

Judit Kumuthini

Dr Judit Kumuthini received her BSc in Biomedical Science, and MSc in Bioinformatics in the UK. She completed her PhD in Bioinformatics at the University of Cranfield, UK, investigating genetic network extraction using a Bayesian belief framework. After completing a post-doctoral research fellowship at the University of Cape Town, she became the Bioinformatics Manager at the CPGR and is currently the PI and node manager of the **CPGR node** in South Africa.

Judit is actively involved as a member or node manager in various other networks and societies, including EMBnet, GOBLET, SASBi, ITFoM, PGEnI, ASBCB, ISCB and the Genomic Standards Consortium. She has also trained and supervised many postgraduate students in Europe and in Africa. Her research interests include African genetic rare diseases, personalized medicine, pharmacogenomics, standardization and good practice, information management and visualization, and e-learning.

Contact: judit.kumuthini@cpgr.org.za

CO-CHAIR:

Raphael Sangeda

Dr Raphael Sangeda is a lecturer in the De-

partment of Pharmaceutical Microbiology at the **MUHAS node** in Tanzania. He graduated with a B. Pharm from Dr MGR Medical University, Chennai, India in 1998. In 2005, he obtained his MSc in Medical Microbiology at the Jomo Kenyatta University of Agriculture and Technology. In 2005, he joined Katholieke Universiteit Leuven, now KU Leuven, in Belgium, where he graduated with an M. Pharm (2006), an MSc. in Bioinformatics (2008) and a PhD on the use of bioinformatics approaches to predict HIV drug resistance (2013).

Raphael's research interests include the use of Genome Wide Association Studies (GWAS) in investigating the genetic epidemiology of Human Immunodeficiency Virus, Hepatitis B virus and Hepatitis C virus infections in individuals with Sickle Cell Disease.

OBJECTIVE:

The objective of the Data & Standards Work Package is to design and implement guidelines and tools to allow for effective standardisation and harmonisation of H3Africa data (including genomic, experimental, clinical and disease-specific data).

This will involve the use of appropriate standards (e.g. **GA4GH**, **FAIR**) and ontologies, in order to add value to all data produced by the H3Africa consortium.

Continued

Data & Standards Work Package

PROJECTS:

1. Ontology Mapping

This project is carried over from the previous round of H3ABioNet. The purpose of the project is to:

- select the ontologies that will be used for the mapping of H3Africa data
- identify and address gaps in these ontologies
- develop guidelines for the mapping of H3Africa data
- implement ontology mapping and validation

2. Minimum Data & Data Dictionaries

This project aims to identify and develop domain-specific minimum information collections and reporting guidelines, as well as identify and/or develop data dictionaries relevant to H3Africa research projects. The project is associated with the Standard CRF Project (led by Dr Alia Benkahla), which aims to expand on standard patient information in a domain-specific manner.

The project will involve H3Africa community engagement. It is currently driven by two standardisation projects relevant to H3Africa - stroke and kidney disease research, and clinical data reporting.

3. Data Management Plans

This project consists of several activities, including:

- the review of existing data management and governance plans
- the development of new or updated guidelines
- the development of common repositories for data management plans
- recommending and providing assistance with tools for managing data and metadata.

The project will also investigate the use of the integrated Rule-Oriented Data System (**iRODS**) for data transfer and provenance.

4. FAIR Data

This project aims to develop capacity within H3ABioNet and H3Africa for producing data that is **findable, accessible, interoperable** and **reproducible** (FAIR). Activities include the identification of relevant literature and SOPs. In addition, the project will involve developing new SOPs where necessary, as well as developing a process for making data FAIR. The SOPs will be implemented once sufficient H3Africa data has been generated and adequate metadata captured.

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Health Informatics Work Package



CHAIR:

Nicki Tiffin

Nicki started her research career in paediatric molecular genetics and molecular endocrinology research. She then shifted her focus to health genomics and bioinformatics approaches to investigating disease in African populations, as well as related ethical issues.

Nicki completed a Master's in Public Health in epidemiology, and worked on secondment to the Western Cape Government Health Department to assist with developing the infrastructure and governance for the Provincial Health Data Centre.

Nicki is currently part of the data integration platform with CIDRI-Africa and the **CBIO node** at the University of Cape Town.

CO-CHAIR:

Katherine Johnston

With a long-standing desire to play a role

in advances in genetic research, Katherine moved from a position as Head Clinical Data Manager at AHRI, Durban to join the **CBIO node** as an H3ABioNet Software Developer.

She completed an honours degree in Computer Science and Economics, and started her career working in EHR systems development. Having developed a passion for helping medical professionals in the field of patient care, by building useful electronic tools for them, she joined CAPRISA as a Clinical Data Manager in 2004 and worked with enjoyment in this field for the next 13 years.

During this time, she got married and had three precious babies, the first of whom has Down Syndrome. As a result, she finds herself unexpectedly combining her interest in genetics, health informatics and patient care with her love for her children, advocating for inclusivity and research advancements in medical care and software development to benefit all genetically diverse people in Africa.

Continued

Health Informatics Work Package

OBJECTIVE:

The Health Informatics Work Package consists of three projects, which are focused on clinical databasing as well as data management best practices and their implementation.

PROJECTS:

1. Phenotype harmonisation and establishing standardised case report forms (CRFs)

This project, lead by Alia Benkahla, will build upon the phenotype harmonisation which was undertaken during the first five years of H3ABioNet.

It will involve defining core CRF fields for use across the H3A Consortium using [PhenX standardisation](#). In addition, Africa-centric ethnic and linguistic ontologies will be developed.

2. Guidelines for RedCAP clinical databasing

The second project, led by Katherine Johnston and Sumir Panji, will include the development of guidelines for principles and best practice, minimum data standards, functionality for data export and logging of data use, template CRFs, clinical data governance, data presentation and interoperability (e.g. [HL7](#) and [FHIR](#) specifications).

3. Meta-analysis databasing

Thirdly, Katherine Johnston will lead a project that will involve developing and prototyping metadata analysis principles, guidelines and implementation, in collaboration with the H3Africa Cardiovascular Disease (CVD) Working Group. The project will combine data from several H3Africa projects for meta-analysis of CVD across those studies.

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Pipelines & Computing Work Package



CHAIR:

Christopher Fields

Chris Fields is the Associate Director of the High Performance Computing in Biology (HPCBio) group at the University of Illinois at Urbana-Champaign (UIUC), and is the PI of the **UIUC node**. We are collaborating with Victor Jongeneel, the former PI of the UIUC node, in this round of H3ABioNet.

In the first round of H3ABioNet, Chris, along with HPCBio/**NCSA** members Liudmila Mainzer, Jenny Drnevich, Jessica Holmes and Radhika Khetani participated in the Node Assessment Task Force. This included writing SOPs, choosing initial data sets for testing and evaluation, and assisting with assessment reviews.

Liudmila and HPCBio group member Gloria Rendon also played a key role, in collaboration with Gerrit Botha and H3Africa members, in processing the initial H3Africa sequence data on NCSA's Blue Waters supercomputer; this data would later prove instrumental in the design of the H3A genotyping array.

CO-CHAIR:

Shakuntala Baichoo

Shakuntala Baichoo is a Senior Lecturer at the University of Mauritius. She is also the PI of the University of Mauritius **SANBio node**. In the first round of H3ABioNet, she was a member of the Education & Training Working Group and the Cloud Computing & Pipelines Taskforce. Shakuntala has been involved in the development of the **H3ABioNet 16S rDNA analysis package** using the Common Workflow Language (CWL).

SECRETARIAT:

Azza Ahmed

Azza Ahmed is a PhD student and member of the **University of Khartoum node** in Sudan, and a lecturer in the Department of Electrical and Electronic Engineering at the same institution. During the first phase of H3ABioNet, she contributed to its activities through involvement in the Research and Infrastructure Working Groups. She is continuing her involvement in these areas during the current phase.

Continued

Pipelines & Computing Work Package

PROJECTS:

1. Provision of computing infrastructure

Project Lead: Suresh Maslamoney
Status: The development of the single sign-on and infrastructure draft project plan is in progress. Activities have begun with work from the previous round being carried over.

2. Node accreditation

Project Lead: Victor Jongeneel
Status: Activity is underway.

3. Development and deployment of workflows

Project Lead: Sumir Panji
Status: In progress. Work from the previous round is being carried over.

4. Single sign-on system for H3ABioNet systems/portals

Project Lead: Suresh Maslamoney
Status: In progress.

5. Data QC

Project Lead: Gerrit Botha
Status: To be merged with project 3 as an integrated part of workflows.

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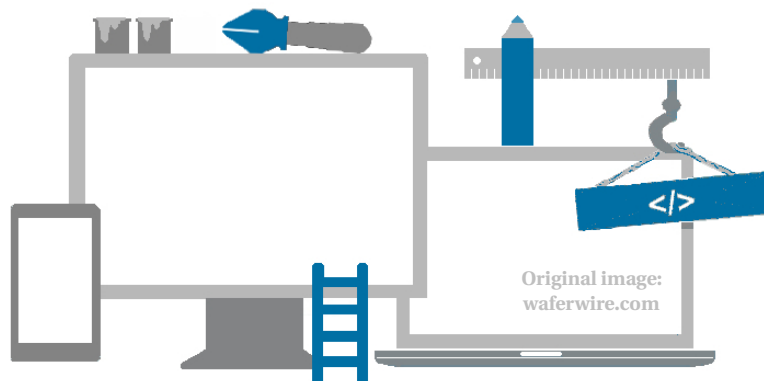
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Tools & Web Services Work Package



CHAIR:

Scott Hazelhurst

Scott Hazelhurst is based at the School of Electrical & Information Engineering at the University of the Witwatersrand, with a cross-appointment at the Sydney Brenner Institute for Molecular Bioscience. He is a computer scientist by training, having received his BScHons and MSc degrees from Wits and his PhD from the University of British Columbia.

Scott has been involved in bioinformatics research since 2002. His bioinformatics interests include population structure, GWAS and the microbiome; his computing interests include high performance computing and pipelines. He has been involved with H3ABioNet since its inception and was previous chair of the Infrastructure Working Group. He is also a collaborator on the H3A AWI-Gen project exploring cardio-metabolic disorders in African populations.

CO-CHAIR:

Itunu Isewon

Itunu Isewon is based at the [Covenant University node](#) in Nigeria.

PROJECTS:

1. Human Mutation Analysis (HUMA) database and web server

The [HUMA database and web server](#) ([Brown *et al.*](#)) was developed at Rhodes University as a platform for the analysis of genetic variation in humans.

This project, led by Ozlem Tastan Bishop, will extend the work.

2. Big data analytics and machine learning tools for application to biomedical data

The main aim of this project, led by Amel Ghouila, is to promote the use of Machine Learning techniques to analyse different kinds of biological data, in order to solve various biological problems. It will provide resources, guidelines and developmental support to facilitate the use and integration of existing packages and also develop new tools where needed.

In addition, big data analytics methods will be incorporated into bioinformatics analyses which are related to H3Africa projects, in order to improve the efficiency and accuracy of these analyses.

3. Genesis visualisation tool

[Genesis](#) is a tool that was developed at Wits for the visualisation of population structure and admixture. This project, led by Scott Hazelhurst, will further develop the tool.

Continued

Tools & Web Services Work Package

3. Integrative multi-omics-based simulation framework

This project, led by Emile Chimusa, will develop tools to enable sequencing data simulations, with the aim of furthering our understanding of the effect of evolutionary and demographic characteristics on omics variation. This will give researchers the capacity to assess and design novel analytical approaches which leverage the characteristics of genomes of populations with African ancestry. Similarly, a synthetic metagenomic dataset with diverse taxonomic composition will assist in improving metagenomic tool development and metagenomic data analysis design.

An existing tool which we have developed will serve as the basis for the project. **Fractal-SIM** (Mugo *et al.*), is an integrative whole multi-omics-based simulation framework, emulating various properties of human NGS datasets. Using similar principles, we will develop metagenomics mock scenario-based sample simulations, mimicking the interactions between human genotypes, environments and microbial communities, which could impact human disease susceptibility.

4. Reference graphs and methods for large-scale structural variant calling

The primary aim of this project is to develop methods of representing genomes as

graphs, in particular, a reference graph suitable for African populations. This will form the basis for developing techniques for detecting large-scale variants.

5. African reference panel and imputation service

This project will involve building a service with a curated reference panel and providing the necessary HPC facilities to enable H3Africa projects genotyping large cohorts to accurately impute from this data.

6. Development of a statistic for genetic association testing on multifactorial phenotypes in family-based design

The goal of this project is to develop an open source program which computes a family-based statistic testing for association between a phenotype (regardless of the distribution) and a set of independent multi-allelic markers.

In doing so, we will address challenges such as non-specified distribution of traits, related individuals, population admixture and linkage disequilibrium among markers.

The purpose of the tool is to contribute to detecting single effect as well as joint effects of genetic mutations on infectious disease traits, either qualitative or quantitative, in family-based design.

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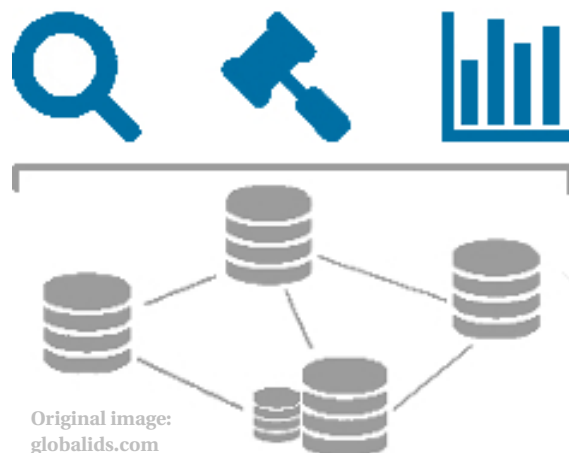
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Databases & Resources Work Package



CHAIR:

Faisal M. Fadlelmola

Professor Faisal M. Fadlelmola is the PI of the **University of Khartoum node** in Sudan.

biome data, including the wide variety of data produced by H3Africa projects

- creating a web portal integrating tools and resources for microbiome data analysis
- maintaining and updating this web portal

CO-CHAIR:

Kais Ghedira

Dr Kais Ghedira is an Assistant Professor in Bioinformatics and co-investigator of the **Institute Pasteur de Tunis node** in Tunisia.

2. African Precision Medicine Portal

This project will develop a web portal that gathers information on clinical and pharmacogenomic data relevant to Africa, with the aim of facilitating the study and development of precision medicine for African populations.

SECRETARIAT:

Deborah Fasesan

Ms Deborah Fasesan is a member of the **NABDA node** in Abuja, Nigeria and a PhD candidate at the University of Ibadan.

3. African Variation Database

This project will involve creating a database of the African genetic variation detected and identified by research projects in African populations.

PROJECTS:

1. African Microbiome Portal

This project involves:

- collecting information about African micro-

4. Data & Biospecimen Access Committee (DBAC) Support Resources

This project will develop the tools needed by the DBAC to carry out their duties.

Continued

Databases & Resources Work Package

5. H3Africa Archive

This project will be centred around hosting H3Africa data and facilitating submission to the **EGA** and other public repositories for long-term archival storage. The project will involve assisting users to submit data to the H3Africa Archive and to format data as required for submission to the EGA.

6. Patient Recruitment Database

This is an ongoing project, aimed at creating a database to monitor the progress of patient recruitment for the different H3Africa projects.

7. Pharmacogenomics Portal For African Populations

This project will:

- report pharmacovigilance
- consolidate and provide documentation for available data
- extend the Pharmacogenetic Database of African Populations - this will form part of the African Precision Medicine Portal

These projects are led by 12 project co-leads and involve more than 60 H3ABioNet members. While some projects have already started having meetings and exchanging ideas using the Slack platform, most of the project leads are still

working on their project plans offline.

One project has been submitted to the MC for review and approval thus far (Data Archive Management System). It was agreed that project plans would be finalized by the end of March.

Title		Status
African Microbiome Portal		Ongoing, project plan being developed
African Precision Medicine Portal		Ongoing, project plan being developed
African Variation Database		Not started yet
Data & Biospecimen Access Committee Support Resources		Continued from first phase of H3ABioNet
H3Africa Archive		Ongoing, project plan submitted
Patient Recruitment Database		Ongoing, project plan being developed
Pharmacogenomics Portal For African Populations		Ongoing, project plan being developed

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Data Integration Work Package



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CHAIR:

Cheikh Loucoubar

Mathematician, PhD in Statistical Genetics and specialized in statistical methods for complex diseases traits. Head of the Biostatistics, Bioinformatics and Modeling Group at the Institut Pasteur de Dakar - a group whose research focus is the development of statistical methods and tools for genetic association analysis of infectious diseases. Teacher in Statistical Genetics, Biostatistics and R Statistical Software at the Gaston Berger and Cheikh Anta Diop universities in Senegal.

CO-CHAIR:

Segun Fatumo

Research Fellow in Statistical Genetics, working in two distinct research areas. The first involves implementing approaches in genetics research to associate specific genetic variations with cardio-metabolic traits in Ugandan participants. The second area of research involves characterizing the trans-generational genomic impact of genocide exposure and post-traumatic stress disorder (PTSD) in female survivors of the Rwandan genocide and their offspring.

OBJECTIVE:

To identify existing data integration tools and to make these available via a portal. This may include tools for protein-protein interaction networks, pathway analysis, regulatory networks and integration of different types of omics data.

PROJECTS:

The work package is made up of three projects:

Title	Project lead
Systems biology analysis tools/portal	Ezekiel Adebiyi
Statistical modeling of complex genomic and environmental data	Nicki Tiffin
Meta-analysis tools	Gaston Mazandu

Continued

Data Integration Work Package

CONTRIBUTORS:

Alia Benkahla	Gerrit Botha	Nicki Tiffin
Anisah Ghoorah	Ghaith Ben Abdessalem	Postdoctoral fellow (Nicki Tiffin)
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Cheikh Loucoubar	Kais Ghedira	Parker Lamptey
Graduate student (Cheikh Loucoubar)	Lilia Romdhane	PhD candidate (Gaston Mazandu)
Cherif Ben Hamda	Maia Lesosky	Postdoc TBH
Dare Falola	Mamadou Diop	Rahma Mkaouar
Ebo Turkson	Marion Adebisi	Samah Sami
Ezekiel Adebisi	Maroua Boujemaa	Segun Fatumo
Faisal Fadlilmola	Maryam Diarra	Somia Mohamed
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Training Work Package



CHAIR:

Nicky Mulder

Prof Mulder is PI of H3ABioNet and has been involved in bioinformatics training and education for more than 10 years. She is involved in the Global Organisation for Bioinformatics Learning, Education and Training (**GOBLET**), and is co-chair of the **ISCB Education Committee**. Nicky also initiated the development of the **African Bioinformatics Education Committee**, to provide guidelines for the development of bioinformatics degrees in Africa.

CO-CHAIR:

Shaun Aron

Shaun Aron is based at the **University of the Witwatersrand node** and has been involved in the education and training activities of the network since its inception. He has developed and taught a number of courses, ranging from the online Introduction to Bioinformatics (IBT) course to GWAS courses. He is involved in research aimed at exploring the historical movements and interactions of African populations.

OBJECTIVE:

The Training Work Package will be continuing and expanding on the initial work carried out by the Education and Training Working Group dur-

ing phase I of H3ABioNet. A major focus of the first phase of H3ABioNet was the development and implementation of a number of training programs and products to improve bioinformatics capacity within the network and other H3Africa projects. A selection of these projects have been carried over into the new round of the project for completion, together with the identification of new projects aimed at continuing to build a sustainable environment for providing high-quality bioinformatics training on the continent.

PROJECTS:

1. Specialized short-courses

The work package will still be responsible for assessing the need for short, topic-specific workshops within both the network and the greater H3Africa community.

Currently, we are gauging interest in a workshop to develop skills in analysing data generated by the new H3Africa Genotyping Array.

We have also identified a number of potential workshops/jamborees/hackathons for the upcoming year and will continue to assess where and when would be best to host these.

Continued

Training Work Package

2. Online Courses

Although there has been some delay in starting the online Introduction to Bioinformatics (IBT) Course this year, this is another major project for the work package.

In addition, we would like to trial the platform for running a more advanced short course, with an already-developed 16S rDNA course earmarked for this.

As a separate project, we are also planning on running the Genomic Medicine Course again, which utilises the same platform as the IBT course.

3. Managing Training Initiatives & Assessing Their Impact

Some additional ongoing projects include updating and further developing HTrainDB, a system used for tracking the careers and development of trainees, and for managing training workshop calls and applications.

4. Projects Related To H3ABioNet Training Material

Another ongoing project is the curation and transcribing of existing H3ABioNet training material, with a separate group looking into defining and mapping competencies to

H3ABioNet training material.

5. Partnering With Fogarty Training Grants Recipients

One of the major new projects for the work package is aimed at establishing a close collaboration with the Fogarty Training Grants in order to assess possible synergies and areas where the capacity developed within H3ABioNet could be leveraged to assist the training programs.

6. Projects To Ensure Sustainability

The final two new projects are both aimed at continuing to develop sustainable training programs within the network.

The Train-the-Trainer Project aims to develop a platform to train and create a network of experienced trainers in a variety of bioinformatics areas.

In addition, the Software and Data Carpentry Project will assess the need for providing these specialized training courses within the larger H3Africa community, will establish a framework for presenting the training events and will train local trainers for presenting future workshops.

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Sustainability & Outreach Work Package

CHAIR:

Jonathan Kayondo

Dr. Jonathan Kayondo is a Senior Research Officer (SRO) at the Uganda Virus Research Institute (UVRI), with a training background in Biochemistry, Chemistry and Molecular Genetics. His research involves investigating disease vectors and pathogens, with a focus on the genetics of malaria-transmitting mosquitoes and HIV drug resistance. He is currently involved in research which explores the control of malaria vectors using engineered endonucleases, profiling potential arboviral vectors in Uganda, and the design of more sensitive molecular



assays for detection of HIV-drug resistance minority variants.

Jonathan also contributes to bioinformatics capacity development and training through a number of partnerships at the institute. Various analysis pipelines for metagenomics and variant calling are being developed to enhance pathogen detection for research

purposes or disease outbreak investigations.

Jonathan served H3ABioNet I in various capacities, including the roles of **UVRI node** PI, chair of the User Support Working Group (USWG), member of the Education and Training Working Group (ETWG) and facilitator in the Introduction to Bioinformatics course series (IBT-2016 and IBT-2017).

Contact: jkayondo@uvri.go.ug
jkayondo@gmail.com

CO-CHAIR:

Amel Ghouila [@AmelGhouila](#)

A computer scientist by background, Amel Ghouila earned her PhD in Bioinformatics from the LIRMM Laboratory, Montpellier, France. She is currently a bioinformatician at the **Institut Pasteur de Tunis node** in Tunisia, where she works on the frame of the H3ABioNet consortium.



Amel served as the co-chair of the Research Working Group for the past three years and contributed to various activities within the consortium such as education and training. She is an open science advocate who is passionate about knowledge transfer. Her main research interests are in Data Science and Bioinformatics of Pathogens using NGS data.

In her spare time, Amel runs the Technovation program in Tunisia, which teaches girls how to address challenges in their communities using coding.

Contact: amel.ghouila@gmail.com

OBJECTIVE:

The Sustainability & Outreach Work Package is designed to disseminate H3ABioNet outputs and activities across and beyond the consortium, and develop plans for long-term sustainability.

Continued

Sustainability & Outreach Work Package

PROJECTS:

This year we will reach out through a combination of new projects and selected activities carried over from the previous round of H3ABioNet, as follows:

Description	Status
Managing an integrated social media platform for promoting consortium events and products	Ongoing, continued from previous round
Designing marketing materials as communication tools for consortium outreach and publicity	Ongoing, continued from previous round
Coordinating Open Science groups	Starting in April, building on activities from previous round
Management and development of the Help Desk	Ongoing, continued from previous round
Preparing and publishing the H3ABioNet newsletter	Ongoing, continued from previous round
Additional activities including: <ul style="list-style-type: none"> • improving the website • connecting H3ABioNet with other international consortia and initiatives • public engagement • Women in Data Science activities 	Ongoing, continued from previous round

CONTRIBUTING TO THE WORK PACKAGE:

The Sustainability and Outreach Work Package monthly meetings will take place on the **third Thursday of every month at 12PM CAT**. There is still opportunity for volunteers to sign up for any of these projects/activities. If you are interested in becoming involved, please contact the chair and co-chair.

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Report: H3ABioNet 2.0 Kick-off Meeting



The H3ABioNet 2.0 kick-off meeting took place at the Victoria and Alfred Waterfront in Cape Town, during the third week of November 2017. It was attended by 48 H3ABioNet personnel from 26 of the 28 H3ABioNet nodes. Many of the attendees were PIs and personnel continuing from H3ABioNet 1.0, while others were from new H3ABioNet nodes joining for the first time as part of H3ABioNet 2.0. The new nodes had met in October 2017 to propose and brainstorm projects in anticipation of the kick-off meeting.

The first day of the meeting commenced with welcomes and introductions by Prof. Nicky Mulder. This was followed by 10-minute presentations from each of the research groups which make up the H3ABioNet nodes, as a way of introducing themselves. Each H3ABioNet node presentation provided descriptions of (i) the background of the node, (ii) their research focus area, (iii) their computational- and training-related resources, (iv) current staff and their expertise, (v) the node's expected contributions to the various work packages

and projects within H3ABioNet and (vi) their expectations from H3ABioNet. The final node presentation was completed up by late afternoon, leaving time for Scientific Advisory Board (SAB) nominations.

In the close-out meeting of H3ABioNet 1.0 in October 2017, the existing H3ABioNet SAB was dissolved and node PIs were asked to think of suitable nominees for the new SAB, based on the expertise required. The categories of expertise deemed to be necessary for H3ABioNet 2.0 were Bioinformatics, African Population Genetics, Bioinformatics Education, Health Informatics, Big Data and Ethics. To end off day one of the meeting, brief oral motivations about the suitability of the proposed candidates were provided by the nominating PIs. Thereafter, an online poll was opened in which each node could provide a single vote for their preferred candidate before the close of the kick-off meeting.

Continued

Report: H3ABioNet 2.0 Kick-off Meeting

The morning session of day two involved talks about the administrative and reporting aspects of H3ABioNet. Prof. Mulder closed off the morning session by providing a recap on H3ABioNet 1.0. The remaining sessions had been set aside for brainstorming the various projects proposed since the close-out meeting. This discussion involved all personnel with input on possible contributions by each node, interspersed with 10-minute presentations on work carried over from H3ABioNet 1.0. Three of the eight H3ABioNet work packages (Data & Standards, Health Informatics, and Pipelines & Computing) were discussed in depth. The various projects and their progress will be periodically reported in subsequent issues of the H3ABioNet newsletter.

The remaining five H3ABioNet 2.0 work packages (Databases & Resources, Tools & Web services, Data Integration, Training and Sustainability & Outreach) were discussed on day 3. Various projects were proposed before being narrowed down, with shorter activities being separated from stand-alone projects. Attendees were asked to list the names

of members of their node who could contribute to each project along with an indication of how much time they could devote. They were also asked to disseminate information about the available projects and the related discussions, so that node members who were not in attendance could become involved.

The meeting ended with the announcement of the SAB nominees who had been selected. The top-ranked candidates were then approached to serve as members of the SAB for H3ABioNet 2.0 and accepted their positions. The selected members of the H3ABioNet 2.0 SAB are Prof. Michele Ramsay (African Population Genetics), Dr. Janet Kelso (Bioinformatics), Prof. William Hersh (Health Informatics), Prof. Terri Attwood (Bioinformatics Education), Dr. Odile Ouwe Missi Oukem-Boyer (Ethics) and Dr. Francis Ouellette (Big Data).

Sumir Panji
Node Manager

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Software & Data Carpentry Training



Four members of H3ABioNet attended a **recent Software and Data Carpentry Workshop**, which took place from 21 to 23 February. The workshop was aimed at individuals who wanted get involved in Software and Data Carpentry or similar training initiatives. The objective was for participants to develop the skills required to present these courses. The workshop covered the basics of educational psychology and lesson design, and demonstrated the use of these concepts in intensive workshops and regular classes. The workshop was sponsored by the DHET's Rural Campus Connectivity

Project II and was offered to participants at no cost.

The course included daily lectures presented by a variety of trainers, interspersed with practical activities and opportunities for feedback. Participants were able to interact with researchers from other disciplines. An especially interesting aspect was comparing how common tools are applied differently across these disciplines. The practical activities and short lessons presented were very effective, giving trainees room to practice what they had learnt.

Continued

Software & Data Carpentry Training



The workshop took place along South Africa's southern coastline, in the quiet town of Kleinmond. It provided trainees with a satisfying break from the bustling city. The training was both valuable and extremely enjoyable. Breakfasts and lunches were provided, as well as a group dinner at KabelJoe's seafood restaurant.

As part of the training, participants prepared lessons involving Data Carpentry (R programming) and Software Carpentry (Unix Shell) topics of their

choice. These short lessons were presented at the end of the workshop. As a result, the four members of H3ABioNet who attend the course are now certified Software and Data Carpentry instructors.

Lyndon Zass
CPGR node

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Announcements

Original images:
desotohs.desotoisd.org
northviewbandboosters.net



1. SELECTED RECENTLY-PUBLISHED ARTICLES

(a) Projects Initiated By Or Contributed To By H3ABioNet

- **Hackathons as a means of accelerating scientific discoveries and knowledge transfer**

Ghouila A *et al.*

- **HUMA: A platform for the analysis of genetic variation in humans**

Brown DK *et al.*

- **Organizing and running bioinformatics hackathons within Africa: The H3ABioNet cloud computing experience**

Ahmed A *et al.*

- **Whole-genome sequencing for an enhanced understanding of genetic variation among South Africans**

Choudhury A *et al.*

(b) ISCB Publications Involving H3ABioNet

- **Highlights of the second ISCB Student Council Symposium in Africa, 2017**

Rafael CN *et al.*

- **The development and application of bioinformatics core competencies to improve bioinformatics training and education**

mulder N *et al.*

Mulder N *et al.*

(c) Research Perspectives Related To H3Africa & H3ABioNet

- **Genomic Research Data Generation, Analysis and Sharing - Challenges in the African Setting**

Mulder N *et al.*

- **H3Africa: current perspectives**

Mulder N *et al.*

Thank you to the numerous contributors to the efforts and insights described in these publications.

Congratulations to all the authors.

2. NODE ACCREDITATION

Congratulations to the the following nodes for their recent accreditation:

- **NABDA:** 16S rRNA, GWAS
- **Institut Pasteur de Tunis:** 16S rRNA
- **Stellenbosch University:** variant calling from NGS data

Continued

Announcements

3. COURSE IN APPLIED BIOINFORMATICS

In March this year, the **ECBAG node** at Zagazig University started a training course in Applied Bioinformatics at the Training Unit for Biotechnology and Genomic Informatics.

The course is comprised of 12 modules, with each module made up of a series of lectures and practicals.

The course content is presented by Prof. Ahmed M. Alzohairy, with assistance from Medhat Radi and Mohammed A. Farahat.

The topics covered include:

- The potential of bioinformatics
- Manipulating biological sequences
- DNA sequence analysis

4. WORKING WITH PATHOGEN GENOMES COURSE

In June this year, the University of Cape Town will host the above-mentioned course.

It will be presented by members of the Infection Genomics teams at the Wellcome Trust Sanger Institute, as well as local trainers.

The course begins with training in the use

of genome analysis software (Artemis and ACT), developed at the Sanger Institute for genome exploration and comparative genomics.

It goes on to cover the mapping of Illumina sequence data, SNP calling, phylogenetics, genome assembly, genome annotation and RNA-seq.

5. YOUNG RESEARCHERS' SYMPOSIUM

This event, the second of its kind, took place at the Institut Pasteur de Tunis from 18 to 20 April 2018.

It showcased the work of young researchers and provided a platform for exchange with more established researchers.

The symposium involved four themes:

- Cancers, genetic diseases and predispositions
- Bioinformatics, biostatistics and biomathematics
- Infectious diseases
- Applied biotechnology

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Upcoming Events



1. RESEARCH SUPPORT & FUNDING OPPORTUNITIES

(a) **Addressing the Burden of Antimicrobial Resistance**

The African Academy of Sciences (AAS) and the South African Medical Research Council (SAMRC) are funding research to achieve this aim.

To apply: [AAS](#), [SAMRC](#).

View open calls from Grand Challenges partners [here](#).

Application deadline: 16 May 2018

Deadline for pitches: 5th of every month

(b) **Africa Science Desk**

This project provides funding to journalists in selected African countries to produce science stories aimed at local or global news markets.

[Learn more](#) or [apply](#).

(c) **Africa-India Mobility Fund**

This programme funds short-term visits for researchers from Africa and India to travel between the two.

To find out more: [English](#), [French](#).

(d) **African Career Accelerator Awards**

These awards, from the UK Global Challenges Research Fund, provide support for African post-doctoral researchers who are making the transition to being independent researchers.

Application deadline: 1 Jul 2018

(e) **African Postdoctoral Training Initiative**

This program is a partnership between the African Academy of Sciences ([AAS](#)), the U.S. National Institutes of Health ([NIH](#)) and the Bill & Melinda Gates Foundation ([BMGF](#)).

Find out more at the links above or apply [here](#).

Application deadline: 11 May 2018

(f) **Science and Language Mobility Scheme Africa**

This scheme offers travel grants for short-term visits for researchers in Franco and Anglophone Africa.

To find out more: [English](#), [French](#).

Application deadline: 25 May 2018

Continued

Upcoming Events

2. RESEARCH EVENTS & TRAINING OPPORTUNITIES

(a) **17th European Conference on Computational Biology**

Athens, Greece, 8-12 Sep 2018

This is the leading European event of its kind.

Deadline for abstracts: 15 May 2018

Early registration deadline: 29 Jul 2018

(b) **18th NETTAB Workshop: Building a FAIR Bioinformatics Environment**

Genova, Italy, 22-26 Oct 2018

Deadline for oral abstracts: 20 May 2018

Early registration deadline: 28 Sep 2018

(c) **2nd International Congress on Personalized Health Care**

Montreal, Canada, 23-26 Sep 2018

Deadline for abstracts: 27 May 2018

Early registration deadline: 22 June 2018

(d) **Bioinformatics and Genome Analysis Course**

Tunis, Tunisia, 10 Sep-14 Dec 2018

Application deadline: 23 Jun 2018

(e) **ISCB Conference**

Chicago, USA, 6-10 Jul 2018

This is the leading conference in the field.

Early registration deadline: 7 Jun 2018

(f) **Research Data Science Summer School & Workshops**

Trieste, Italy, Aug 2018

These events are co-organised by H3ABioNet.

Application deadline: 21 May 2018

i. **Summer School**, 6-17 Aug 2018

ii. **Advanced Workshops**, 20-24 Aug 2018

(g) **SASBi-SAGS Joint Congress**

Free State, South Africa, 16-18 Oct 2018

Deadline for abstracts: 29 Jun 2018

Registration deadline: 1 Jun 2018

(h) **SciDataCon-IDW Conference**

Gaborone, Botswana, 5-8 Nov 2018

Deadline for abstracts: 31 May 2018

Registration deadline: To be announced

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