H3ABioNet
Pan African Bioinformatics Network for H3Africa

Issue 18: September 2016

H3ABioNet

In This Issue

Continue the conversation:

#bioinformatics #Africa
#H3ABioNet @H3ABionet

Foreword

We are currently, as I am sure many others are, preoccupied with developing proposals for the new H3Africa RFAs. Nevertheless, H3ABioNet activities have continued to progress mostly due to capable staff and students in the network.

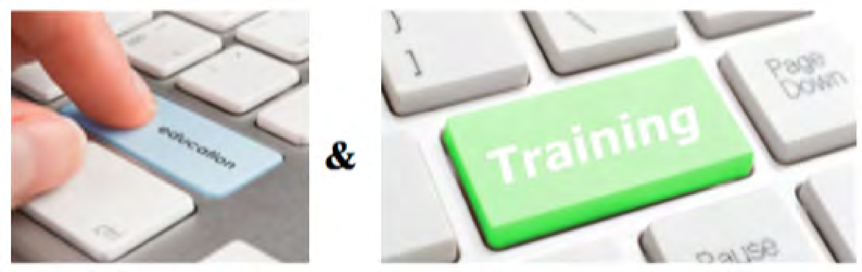
The Cloud and DREAM Challenge for Malaria hackathons were successful and I was fortunate to attend at least a day of both events and experience the wonderful enthusiasm of the participants. It is inspiring to see new ideas flow in these collaborative environments as scientists from different disciplines interact. In this newsletter we also report the first results from our training follow up survey, which generally demonstrate positive impact. Our youth have been educating us on the wonders of social media, and this newsletter sees the first implementation of some of the ideas in the User Support Working Group coordinated social media strategy.

Finally, I invite you to read on to see what we have been up to this last month.

H3ABioNet

Education and Training Working Group

Education and Training Working Group



The final workshop for the year was presented in collaboration with the International Network for Data Analysis (INDA) at the Institut Pasteur in Senegal from 3rd - 14th October 2016. The two-week workshop focused on statistical approaches for NGS data analysis and consisted of theoretical lectures during the first week followed by hands on practical sessions during the second week. H3ABioNet was involved in assisting with the organisation and planning of the workshop and funded two trainers and five participants to attend the workshop.

The *Introduction to Bioinformatics Course* has been going well and draws to an end in the middle of October. Like the participants, we have learnt a great deal from the experience of running a course like this for the first time and we will be doing an in depth analysis of the course once it is completed. We would like to carefully evaluate what worked and what didn't in order to improve the course for future iterations.

H3ABioNet has hosted a number of courses to date and has collected the associated training material for these courses. This is a valuable resource that can be utilised by others; however, currently the course material is only accessible via the H3ABioNet webpage and has not been well catalogued or curated. Therefore, a taskforce has been established to curate all H3ABioNet training material. This process will include ensuring that all course material is collected for each course, tagging the course with the relevant EDAM ontology search terms, adding the courses to the *eGenomics* catalogue for searching, and creating a dedicated page on the H3ABioNet website with a categorical listing of the courses. Upon completion we hope to create a well-curated and organised training material resource that may be easily found and used by others.

As mentioned in the last newsletter, we have received the results from our 6-month training, follow-up survey. The results from the survey, focusing on the impact of training to date and the identification of topics and types of activities for future trainings, are outlined in an article in the current newsletter.

#H3ABioNetEducationAndTraining

Nicky Mulder and Shaun Aron

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Infrastructure Working Group

Infrastructure Working Group

After a busy August, in September the Infrastructure Working Group (ISWG) was involved with behind-the-scenes work.

Roll out of the Globus Online and Netmap end points has slowed, and we encourage nodes who haven't participated to contact their ISWG rep to get started as soon as possible. Updates to the eBiokits have been made thanks to the hard work of our collaborators at the Swedish University of Agricultural Sciences (SLU) - we are currently running a pilot study to test the update procedures and SOPs and we should be able to complete the upgrade of other sites soon.

We continue work on completing the H3ABioNet pipelines after the successful Cloud Hackathon, which we reported on last month. Four project teams are working on completing the pipelines on genome-wide association studies, next generation sequence data, metagenomics, and imputation. Further, work on a paper has started. You can read more about the Cloud Hackathon in this month's issue of the newsletter.

The H3A Participants Recruitment Database is now in use, and about a dozen people at NIH have access to the dashboard. Some modifications are being made in response to requests. Work on the H3A Archive has resumed now that our new developer, Ziyaad Parker, is on board. We hope to submit the first H3A data to EGA shortly.

#H3ABioNetInfrastructure

Scott Hazelhurst and Suresh Maslamoney

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Research Working Group

Research Working Group

During the month of September, the H3ABioNet webinar series took place on September 22nd under the theme of "Metabolic and Structural Modelling". The first speaker was Dr. Rowan Hatherley, postdoctoral fellow from Rhodes University, South Africa, who presented PRIMO: An easy to use, interactive protein-modeling platform for users from different backgrounds. The second speaker was Itunuoluwa Isewon, a PhD student from Covenant University, Nigeria, who presented computational methods for the identification of transcriptional regulators from the genome of *Plasmodium falciparum*. Both speakers gave great talks that are relevant to the H3Africa projects.

As mentioned in last month's issue, we organized a joint H3ABioNet, University of Notre Dame and IBM Research Africa Hackathon on Malaria Drug Resistance for a DREAM challenge during the period 6th-10th September 2016 in Johannesburg, South Africa - look out for the feature article on the hackathon in next month's issue of the newsletter.

The Research Working Group (RSWG) is working on launching the H3ABioNet Bioinformatics Research Digest (BioRD). BioRD will compile of a list of the recent bioinformatics articles pertinent to the H3ABioNet/ H3Africa projects. A summary of selected articles will be published as BioRD newsletter on a quarterly basis. We are aiming to get the first issue published by the end of October. BioRD aims to be accessible, providing accurate and up-to-date research briefings on computational genomics and bioinformatics.

The Research working group is also seeking volunteers for and nominations from H3ABioNet graduate students who are keen and active to work as H3ABioNet representatives at the Communities of Special Interests / Special Interest Groups (COSIs / SIGs) within the ISMB and ISCB. The representatives will report back to the RSWG every 3 months, or whenever seems necessary if there is a deadline for an event or urgent issue that needs RSWG immediate decision or approval. The main aim of this programme is to allow our graduate students to build an international network as well as to promote the H3ABioNet activities to the global research community.

#H3ABioNetResearch

Faisal Fadlemola and Amel Ghouila

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User Support Working Group

User Support Working Group

The User Support Working Group (USWG) is excited to announce the launch of a coordinated media strategy aimed at encouraging H3ABioNet members to have a look at the newsletter each month and at allowing greater engagement of H3ABioNet members on social media platforms, namely; *Facebook* and *Twitter*. Engaging via social media will create an online presence for H3ABioNet and may encourage others to join the conversation too, thereby growing our audience. Have a look at *PLOS Biol. 11(4)* (doi:10.1371/journal.pbio.1001535), *PLOS Biol. 14(2)* (doi:10.1371/journal.pbio.1002373), and *Nature 536* (Nature. 2016 Aug 1;536(7614):113-4) articles, which detail the importance of social media for scientists.

You may have noticed the introduction of general, and article specific, #hashtags in this month's edition of the newsletter - use these to continue the conversations highlighted in the newsletter, or to start a conversation of your own, on Facebook or Twitter, that you think is relevant to the bioinformatics community. See links to H3ABioNet social media sites, as well as the general hashtags to be used in all posts, in the side bar of this newsletter. Article specific hashtags appear at the end of each article.

Amel Ghouila @AmelGhouila · 6 sept.

Kicking off the #DREAMofMalaria hackathon @H3ABionet #IBMResearchWITS #bioinformatics #Africa

Great example of a tweet with effective use of event specific hashtags (e.g. #DREAMofMalaria) and general hashtags (e.g. #Africa). Notice the double arrow sign at the bottom of the image which indicates 'retweets' - the number of times the tweet has been shared by others

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User Support Working Group

Continue the conversation:

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Hashtags ’101’

What are hashtags?

Hashtags (indicated by the hash sign **#***) categorize a tweet, thereby adding it to Twitter’s ever-evolving, curated database of tweets (a ’tweet’ is the 140- or less character message that one posts on Twitter).*

Why are hashtags important?

Using hashtags increases the visibility of your ideas. By using hashtags, other people are able to find your tweet when searching for tweets on a particular topic. For example, someone interested in bioinformatics might search ***#bioinformatics****. If your tweet contains this hashtag, it would be included in the search results.*

What does ’trending’ mean?

A topic is said to be ’trending’ if lots of people are tweeting about it.
Let’s get ***#bioinformatics*** *in* ***#Africa*** *trending!*

Pro tips

- When tweeting, include ’@H3ABionet’ to ensure that your post appears on the H3ABioNet Twitter account page.
- Twitter is case sensitive.
- Add images to your tweets (as in the example above) to catch people’s attention.

#H3ABioNetUserSupport

Jonathan Kayondo and Pandam Salifu

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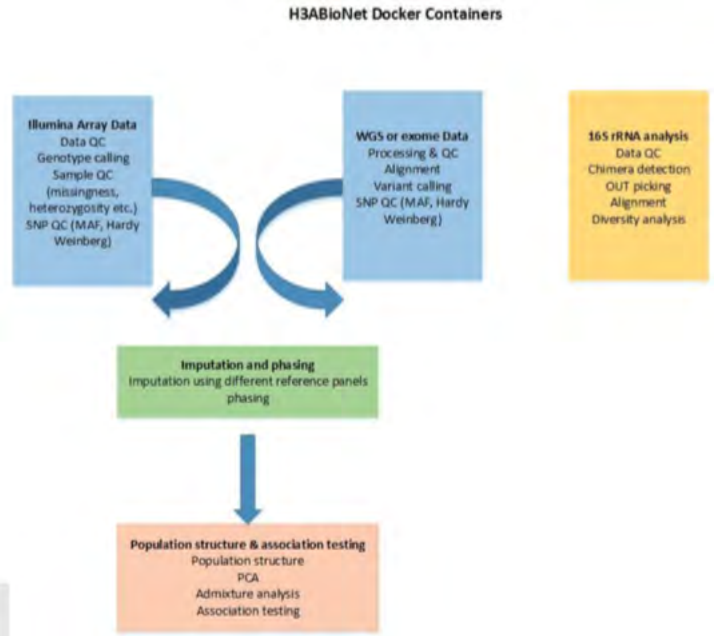
H3ABioNet Cloud Computing Hackathon

H3ABioNet Cloud Computing Hackathon

H3ABioNet held its first ever hackathon between August 22nd and August 26th 2016, at the University of Pretoria. The H3ABioNet Cloud Computing Hackathon was aimed at producing portable, cloud deployable Docker containers for a variety of bioinformatics workflows that include variant calling, 16S rRNA metagenomics, quality control, genotype calling, and imputation and phasing for Genome wide association studies (see figure below) based on the *H3ABioNet SOPs*.



H3ABioNet Docker Containers

Dockerization provides a method to package and manage software, tools and workflows within a portable environment / container, similar to virtualization but with a smaller computing overhead on a server compared to virtualization. Docker containers can easily be developed and deployed on compute (mainly cloud based) environments, and can be used by a variety of groups to ensure consistent analysis in terms of tools, software versions, and workflows used.

The H3ABioNet Cloud Computing Hackathon was physically attended by 18 individuals and virtually by 5 individuals from Mauritius, Morocco, Nigeria, South Africa, Sudan, Tunisia, and USA, and was hosted at the Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria by Professor Fourie Joubert, head of the *UP Bioinformatics and Computational Biology Unit*. The participants were divided into teams and each team worked on one of the bioinformatics analysis pipelines. Each team comprised bioinformaticians familiar with that workflow, software developers, and systems administrators.

Day one of the H3ABioNet Cloud Computing Hackathon was devoted to an introduction and to training in the technologies that would be used during subsequent days. This included hands-on tutorials by Prof. Scott Hazelhurst on *Nextflow*, Dr. Michael Crusoe on *Common Workflow Language (CWL)* and Dr. Brain O'Connor on Dockerization and *Dockstore.org*. The workflow languages are used to chain the various bioinformatics pipeline components together in order to facilitate reproducible science and assist with their portability. Experts Prof. Scott Hazelhurst and Dr. Michael Crusoe provided support in these areas.

H3ABioNet

H3ABioNet Cloud Computing Hackathon

The teams organized themselves and set their work schedules, according to the tasks that they had set themselves for the remaining four days, to meet the hackathon goals. In order to facilitate and ensure a productive hackathon, management tools - such as *Trello* and *Scrum Methodology* - was used. The teams / participants set up their daily *Trello* cards in the morning and reported back daily to each other and to virtual attendees in the evening on what they had accomplished, what they struggled with, and their subsequent plans for the following day. All the while, teams continuously committed code to GitHub in order to keep the repository up to date. The actual room used for the hackthon was for the most part silent, with team members communicating via *Slack* (except for the odd outburst of "Success!!!"). The communication and management tools used for this hackathon were, and will continue to be, important as these tools facilitate interaction between and across team members, and will enable the participants to continue to work in a structured manner once back at their respective Institutions and across different time zones.

Part of novelty of the H3ABioNet Cloud Computing Hackathon was all the participants selected were involved in the latter stages of the planning and setting of some of the outcomes for the hackathon. Key recommendations during the hackathon planning meetings were that the Docker containers and pipelines developed should be able to be used within heterogeneous African research compute environments with portability and good documentation being key. This is especially important considering that access to Cloud computing environments within Africa is still in its infancy, compared to more developed regions such as the USA and Europe. Hence, it was decided that development and testing of the pipelines should occur on a single machine, ported to a cluster or High Performance Computing environment, and then finally tested and deployed on cloud based platforms (*Amazon*, *Microsoft Azzure*, *IBM Bluemix*, and the new *African Research Cloud initiative*).

The participants on the H3ABioNet Cloud Computing Hackathon were extremely driven with each day ending later then the previous day. Towards the end of the week, the participants just decided to go for dinner straight from the hackathon venue to be more time efficient and to enable more work to get done. The last day of the hackathon wrapped with a 20 minute talk by each team on their progress by the end of the hackathon and what needs to be completed by the team members after the hackathon. Many individuals mentioned their wish for an extra day or two to continue working! Currently, the H3ABioNet Cloud Computing Hackathon participants and organizers are meeting fortnightly to work on completing the pipelines, getting them tested by different groups, and planning a publication. The H3ABioNet Cloud Computing Hackathon has been an extremely important milestone for H3ABioNet as it brought together people within the Network with various skills to work on focused projects. It signalled the shift from capacity building to utilizing the capacity developed in order to tackle problems specific to the heterogeneous African computing environments, as defined and implemented by the African based participants.

Group picture of the H3ABioNet Cloud Computing Hackathon physically attending participants on day one: looking fresh and ready for "hacking"

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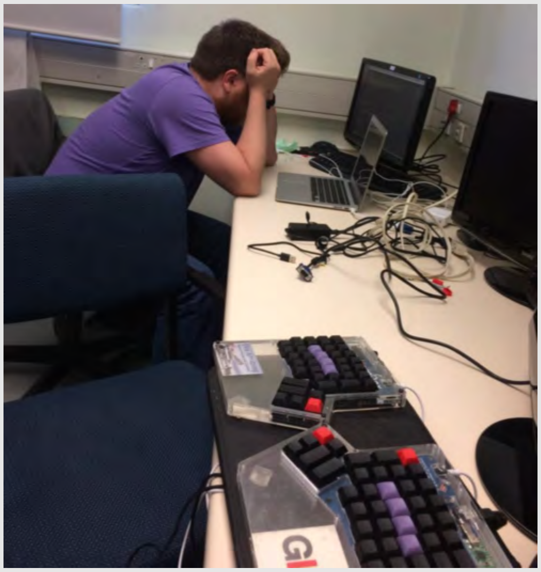
H3ABioNet Cloud Computing Hackathon

Mustafa Alghali and Phelelani Mpangase going over some code for the exome variant calling from NGS data team before the daily report back sessions



One of the highlights of the H3ABioNet Cloud Computing Hackathon - Don Armstrong's keyboard (although Ayton Meintjes doesn't seem too impressed!)

#cloudcomputing #hackathon

Sumir Panji

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IBT corner

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IBT corner

In September, participants of the online Introduction to Bioinformatics (IBT) course learnt about *Protein Structure Bioinformatics* and *Phylogenetics*. In addition, participants had an opportunity to reflect on and consolidate what had been learnt in previous course modules during the 'consolidation week'. This was also an opportunity for participants to reflect on how they might incorporate the bioinformatics skills learnt into their own research projects. For example, ICIPE classroom ran a 'data clinic' during which participants were able to get advice from teaching assistants, and their peers, on how to analyze their data.

Meet some of the 'faces' of the IBT course, below.

Left top: ICIPE, Kenya; Left bottom: NMIMR, Ghana; Right top: INRA, Morocco; Right bottom: CBSB, Sudan

Read more about the IBT participants and volunteer IBT staff at *ICIPE*, *INRA*, *NMIMR*, and *CBSB* classrooms on the *IBT course website*.

Upload your own IBT photos so we can see what your classroom has been up to!

#IBT_2016

Kim Gurwitz

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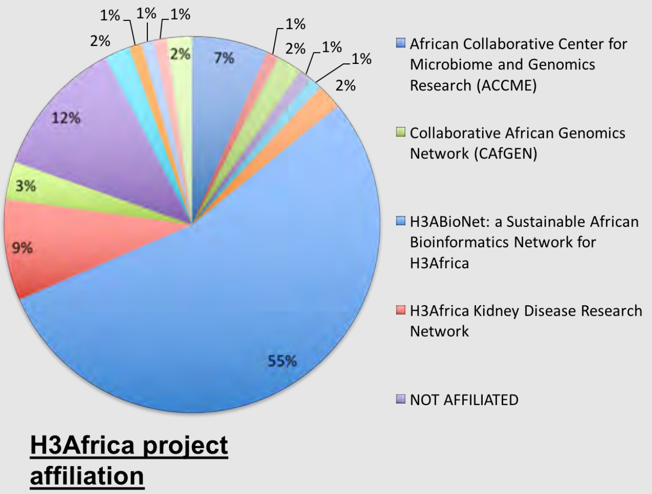
Education and Training Follow-up Survey

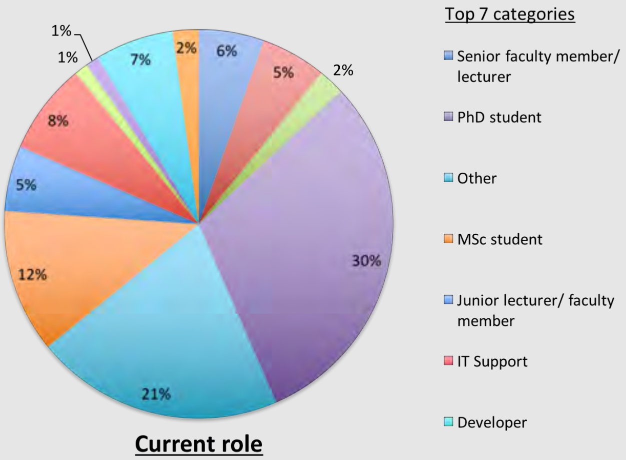
Education and Training Follow-up Survey: first set of results

The Education and Training Working Group (E&T WG) is keenly interested in taking stock of its training activities to determine their impact, as well as to identify topics and suggestions for future training activities. To this end, a follow-up survey is sent to H3ABioNet workshop participants through an automated service set up in REDCap. We intend to collect feedback every 6 months. Overall the feedback from the most recent set of responses has been very positive, encouraging and informative. Below are some figures and responses from participants summarising some of the main survey results.

Who filled in the survey?



Pie chart showing the H3Africa affiliations of respondents to the survey



Pie chart showing the current roles of respondents to the survey

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Education and Training Follow-up survey

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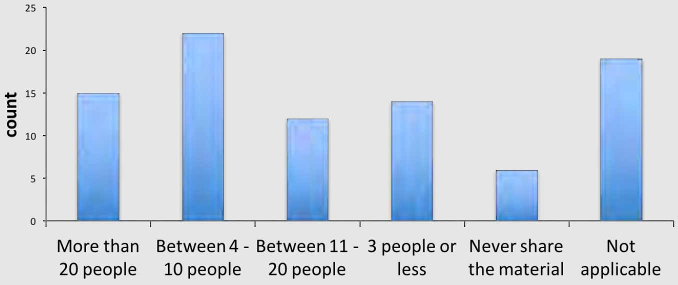
How many people, on average, did you share the H3ABioNet training material/information with?



Pie chart showing the H3Africa affiliations of respondents to the survey

Participant responses: How did you share knowledge gained from H3ABioNet funded training activities?

- *Held a seminar*
- *Shared pipelines and scripts*
- *Trained staff and students in metagenomics analysis in preparation for node accreditation*
- *Held an Introductory Bioinformatics and Linux Course with members of staff*
- *Provided MSc project consulting*

Summary of responses to survey questions

Question	Yes	No
Did H3ABioNet training activities enhance your skills/career?	95.1%	4.9%
Would you be comfortable teaching the subject you received training in?	77.2%	22.8%
Did H3ABioNet training lead to or facilitate publication of your work or submission of your thesis for degree purposes?	35.8%	64.2%
Do you currently have any datasets that require analysis or that can be used in a training workshop?	33.6%	66.3%
Did H3ABioNet training lead to or facilitate a new collaboration for you?	45.6%	54.4%

Participants Responses: Did H3ABioNet training activities enhance your skills/career?

As a professor and a developer of undergraduate as well as post graduate curricula for Bioinformatics in my country, I really benefited from this valuable GOBLET workshop

Data management training in 2014 has equipped me to be a better research coordinator in terms of genomics data collection and quality control monitoring

Education and Training Follow-up survey

...different members from my lab have participated in H3ABioNet trainings which helped them a lot, and by consequence helped me to develop some skills in my lab.

The workshops of which I took part helped me advance in my analysis and PhD thesis. Learn more about bioinformatics analysis and organise workshops in my home country.

Participants Responses: Do you have any suggestions/comments on how H3ABioNet can help you improve your skills/career?

Suggestions for types of training:

- *Tailored for specific career goals to enable people focus on a specific area and keep to that track*
- *Online, MOOCs vs. face to face (proponents for both)*
- *Hackathons*

Suggestions to make training more useful:

- *Provide information at least a couple of weeks before workshops so that students can understand, digest and be more familiar with the subject before starting the workshop.*
- *Mentorship program (capacity building at all levels)*
- *Make data available so that people can practice analyses*
- *Involve the participants in a research project so they can apply what was learnt- 'collaboration with implementation'.*
- *Website to share analyses and code*
- *More long term training for persons who don't have a background in computer and data management.*
- *Encouraging research networks*
- *Advertising experts in different fields on the ASBCB website that we can contact for directions on specific areas.*

In terms of future training, there were requests for training in biostatistics, metagenomics/microbiome analysis, whole genome, exome and RNA-seq analysis, GWAS and population genetics and cloud computing. Most participants felt that the most efficient form of training is through face-to-face intensive courses. The survey provided some useful insights and guidance for the E&T WG consider in planning future H3ABioNet training activities.

#H3ABioNetEducationAndTraining
#TrainingGoals

Shaun Aron and Kim Gurwitz

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Announcements

- Congratulations to Judith Kumuthini from CPGR, South Africa for her recent publication in PLoS One titled *A European Spectrum of Pharmacogenomic Biomarkers: Implications for Clinical Pharmacogenomics* (*PMID: 27636550*)

- The CPGR node welcomed two new recruits, Dr. Gordon Wells and Mr. Abraham van der Berg, to the H3ABioNet consortium.

- Welcome to Tinashe Chikowore from the Northwest University who is a new SANBio / H3ABioNet intern at Wits' bioinformatics Node.

- Congratulation to Rosaline Macharia from ICIPE, Kenya for her publication in PLoS Neglected Tropical Diseases titled *Genome-Wide Comparative Analysis of Chemosensory Gene Families in Five Tsetse Fly Species* (*doi: 10.1371/journal.pntd.0004421*)

- H3ABioNet is reassigning all consortium Node members to specific working groups and task forces based on their expertise and the focus of these working groups and task forces. Expect unsubscribe and subscribe notices from h3abionet.list.org in the next couple of days and also periodically check your spam folder to ensure that you are not missing important consortium and working group / task force emails.

Any announcements for the next edition of the H3ABioNet newsletter may be sent to:

kim.gurwitz@uct.ac.za AND sumir.panji@uct.ac.za

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H3ABioNet

Upcoming Events

Upcoming Events

- **19th to 22nd October 2016**: *International Conference on Rare Diseases and Orphan Drugs* (ICORD) for 2016, RareX has an extended program, to incorporate patients, their families and caregivers as well as support groups and minority groups within the rare disease community, Stellenbosch, South Africa

- **October 27th to October 31st 2016**: *Ninth H3Africa consortium meeting*, Mauritius.

- **November 1st to November 4th 2016**: H3ABioNet Scientific Advisory Board and Annual General Meeting, Cape Town, South Africa.

- **November 6th to November 10th 2016**: *Ninth Annual RECOMB/ISCB Conference* on Regulatory and Systems Genomics, with DREAM Challenges and Cytoscape Workshop, Phoenix, Arizona, USA.

- **November 15th 2016**: H3Africa Informatics Network and other related H3Africa grant submission deadline.

- **November 21st to November 23rd 2016**: *The Fourth International Society for Computational Biology Latin America Bioinformatics Conference* (ISCB-LA), jointly organized with A2B2C, will take place in Buenos Aires, Argentina.

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

Any upcoming events for the next edition of the H3ABioNet newsletter may be sent to:

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Upcoming H3ABioNet working group meeting schedule

Upcoming H3ABioNet working group meeting schedule*

*Schedule until end October 2016

Summary of H3ABioNet upcoming working group meetings

Month	Date	Day	Working Group (WG)	Time (UTC)
October	14th	Friday	User Support WG meeting	9:00
October	14th	Friday	Research WG meeting	11:00
October	20th	Thursday	H3ABioNet Seminar Series	13:00
October	20th	Thursday	Cloud computing meeting	14:00
October	21st	Friday	Infrastructure WG meeting	13:00
October	25th	Tuesday	Education and Training WG meeting	11:00
October	28th	Friday	User Support WG meeting	9:00

Timezone conversions to UTC for all H3ABioNet working group meetings

UTC Time Offset	Time Zone Name	Region/ Country in the Time Zone offset
-5 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, Sudan, Zambia
+3 hours	WAT	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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