SAGESA Research and Training Network Activities

1. SAGESA Launch and Needs Assessment Workshop

Objectives
- Official launch of SAGESA Network – the first Africa AMR genomics research and training network.
- Discuss needs and gaps within the region with regards to application of genomics for AMR surveillance – a focus on training needs and network development
- Provide an overview of the planned/proposed SAGESA activities and discuss the future of the network

2. SAGESA Network Curriculum

Needs assessment analysis guided the development of the SAGESA Curriculum consisting of 5 webinars and a 3 Day bioinformatics workshop. Feedback was collected after each event. Click on links below for:

[Webinar schedule](#)
[AMR Bioinformatics Course](#)

Media and Networking Platforms
[Join Slack Workspace](#)
[Visit SAGESA website](#)
[Follow us on Twitter](#) and keep growing the network
Consent [SAGESA consent form](#)

SAGESA Core Team

Alice Matimba – WCS
Stanford Kwenda – NICD
Monica Abrudan – CGPS
Isabela Malta – WCS
Dusanka Nikolic – WCS
Joconiah Chirenda – UZ

SAGESA Webinar Schedule

February – July 2022

Webinar Title	Title and objective	Session outline (All sessions were held virtually and CAT timezone)
Data analysis pipelines and Galaxy, Nextrain *Organised by:* *Stanford Kwenda* *Isabela Malta* *Monica Abrudan* *Dusanka Nikolic*	To provide an overview of workflows and tools used for WGS analysis and AMR genomic surveillance	Date: 4 february 2022 11:00 Welcome – *Stanford Kwenda* 11:05 Data analysis pipelines and Galaxy – ***Peter Van Heusdsen*** 12:05 Coffee break 12:10 Data analysis pipelines, Nextrain, Q&A – *Moderation by Stanford Kwenda* 12:40 SAGESA announcements – *Alice Matimba* 12:50 Wrap-up & evaluation poll – *Dusanka Nikolic*
Samples to Sequencing *Organised by:* *Joconiah Chirenda* *Isabela Malta* *Dusanka Nikolic*	Discuss issues around sample and data collection, sample processing, sequencing technologies and procurement issues	Date: 25 February 2022 11:00 Welcome and meeting opening – *Joconiah Chirenda* 11:05 Sample preparation: Lessons from the field – ***Tapfumanei Mashe/David Amin****i* 11:35 Experiences from the SAGESA community – *ALL* 11:45 Sequencing tools – ***Taya Forde*** 12:15 Q&A plus experiences from the community – *Moderation by Taya Forde* 12:25 Break 12:30 Short case studies on Samples to Sequencing – ***Sabelle Jallow*** 12:50 Announcements – *Joconiah Chirenda* 12:55 Wrap-up & evaluation poll – *Dusanka Nikolic* 13:00 End

AMR genomics tools and databases *Organised by:* *Stanford Kwenda* *Isabela Malta* *Monica Abrudan* *Dusanka Nikolic*	Discuss genomics tools and resources available for AMR prediction and global pathogen surveillance	Date: 18 March 2022 11:00 Welcome 11:05 AMR prediction tools & databases overview – **Narender Kumar** 11:40 rMAP + Q&As – **Ivan Sserwadda** 12:05 Question and answer and experiences from the community – *Moderation by S Kwenda* 12:10 Coffee break 12:15 Pathogenwatch + Q&As – **Silvia Argimon** 12:50 SAGESA Announcements – *Alice Matimba* 12:55 Wrap-up & evaluation poll – *Dusanka Nikolic* 13:00 End
Skills lab 1: Study design and grant writing *Organised by* *Isabela Malta* *Alice Matimba* *Joconiah Chirenda* *Dusanka Nikolic* *Stanford Kwenda*	To provide tools and resources on how to get started with grant writing, project design and management, and collaborating on a grant project team	Date: 8 April 2022 11.00 Welcome – *Isabela Malta* 11.05 Key elements for grant writing – presentation and Q&A – *Helena Kuivaniemi* 11.45 Logistics and Project Management, How to design a project – *Vicky Nembaware* 12.10 Break 12.15 Successes and failures Part 1 – *Boua Palwendé Romuald* 12.25 Successes and failures Part 2 – *John Ndemi Kiiru* 12.35 Success and failures – Open discussion – *Joconiah Chirenda* 12.50 Activity for Session 2 – *Samantha Sampson* 12.55 Feedback and wrap-up – *Stanford Kwenda*
Skills lab 2: Grant writing Project *Organised by* *Isabela Malta* *Alice Matimba* *Joconiah Chirenda* *Dusanka Nikolic* *Stanford Kwenda*	To discuss grant project assignments and provide feedback	Date: 8 July 2022 10:00 Welcome – *Isabela* 10:05 Aims Page Presentation Group 1: *John, Sheila, Geoffrey, Lesley, Richmond* 10:10 Aims Page Presentation Group 2: *Mulemba, Musa, George, Oscar* 10:15 Aims Page Presentation Group 3: *Azra, Emmanuel, James, Shamsudin, Rhama* 10:20 General feedback and remarks – *Helena and Sam* 10:30 NIH Biosketches – *Gerard* 10:50 New assignment plan – *Helena and Sam* 11:00 Break 11:05 Network discussions – *Dusanka* 11:50 Wrap-up – *Isabela*

AMR Bioinformatics Course – (Virtual)

25–27 May 2022

CONTENTS

Course overview

[Course website](#)

In collaboration with the [National Institute of Communicable Diseases (NICD)](#), South Africa , we are pleased to announce the AMR Bioinformatics course as part of the [SAGESA network](#) aimed at training and building capacity for genomic surveillance of AMR in Africa.

Antimicrobial resistance (AMR) is a global public health emergency and threatens the safe delivery of modern medical care. Global projections of the negative impact of AMR predict the loss of nearly 10 million lives and a cumulative loss of global production up to 100 trillion US dollars by 2050. AMR requires immediate, concerted, international, collaborative action to monitor its prevalence and spread throughout the world. The importance of this has been recognised both by the United Nations and by the World Health Organisation; the latter has published a list of priority pathogens and a global strategy for AMR surveillance.

The challenges of controlling AMR in low- and middle-income countries (LMICs) may be considerable for several reasons. Firstly, antibiotics may be available for human and animal use without a prescription, resulting in unregulated use. Secondly, accurate data on antimicrobial prescription or consumption may not be readily available. Thirdly, there may be limited knowledge about the appropriate use of antibiotics and a lack of antimicrobial policies or stewardship programmes. Finally, there may be limitations in healthcare facilities and laboratory capacity for the detection and management of AMR.

This 3-day workshop aims to address some of these challenges by improving the knowledge and skills of individuals interested in antimicrobial resistance in bacterial pathogens in Africa. It will contain hands-on WGS-based bacterial typing methods such as AMR detection, cgMLST, MLST, core genome SNP based phylogenetic analysis.

Target audience

This workshop is free to attend and open to <u>SAGESA</u> network members based in Africa who are actively engaged in, or soon to commence, research, clinical practice, provision of clinical services, or policy development related to AMR in bacteria. To join the network <u>please click on this link</u>.

Learning outcomes

At the end of the course participants should be able to
- Implement data workflows and bioinformatic analysis of genomic sequence data, including risk and resistance prediction for bacterial epi and pandemic response
- Explain Genomic surveillance and linking epidemiological data, outbreak analyses and global contexts, geographical contexts
- Demonstrate interpretation and application in public health and epidemic/pandemic response

Content and activities overview
- Genomic data analysis
- Interpretation for various applications
- Training support mentorship and networking

Organising and training team

Organisers and developers
Wellcome Connecting Science – Isabela Malta, Alice Matimba, Dusanka Nikolic, Melanie Sharpe
National Institutes of Communicable Diseases – Stanford Kwenda
University of Zimbabwe – Joconiah Chirenda

Module leads
- <u>Annie Chan</u>, National Institute for Communicable Diseases, South Africa
- <u>Arun Decano</u>, St. Andrews University, UK
- <u>Erikson Odih</u>, University of Ibadan, Nigeria
- <u>Narendar Kumar</u>, Wellcome Sanger Institute, UK
- <u>Pimlapas Leekitcharoenphon (Shinny)</u>, National Food Institute, Denmark
- <u>Stan Kwenda</u>, National Institute for Communicable Diseases, South Africa

Guest Speakers
- Plenary Lecture: <u>Rene Hendriksen</u>, National Food Institute, Denmark
- Lecture 1: <u>Zamantungwa Khumalo</u>, ClinVet, South Africa
- Lecture 2: <u>Joconiah Chirenda</u>, University of Zimbabwe, Zimbabwe
- Lecture 3: <u>Sabelle Jallow</u>, National Institute for Communicable Diseases, South Africa
- Lecture 4: <u>Lavania Joseph</u>, National Institute for Communicable Diseases, South Africa
- Lecture 5: <u>Michelle Lowe</u>, National Institute for Communicable Diseases, South Africa

Timetable

Pre Course	AMR Bioinformatics Workshop - Africa. 25th to 27th of April				
Pre-course intro	Time	**Wednesday**	**Thursday**	**Friday**	Time
Participants Intro		25/5/2022	26/5/2022	27/5/2022	
	08:30	Genomic surveillance Over			08:30
Overview of lab workflow, Zamantungwa Khumalo, ClinVet	09:00	Intro to sequence data; QC of raw sequence data Contamination & species ID (lecture & practical 1) *Annie Chan*	AMR detection & surveillance (seminar) *Rene Hendriksen*	Phylogenetic analysis (SNP-based and cgMLST) (lecture & practical 5) *Pimlapas Leekitcharoenphon*	09:00
	09:30				09:30
	10:00		Intro to bacterial subtyping approaches (lecture) *Erikson Odih*		10:00
	10:30				10:30
		Break	Break	Break	
	11:00	Lab based AMR typing using ASTs (Lecture) *Sabelle Jallow*	Bacterial subtyping approaches (practical 4) *Erikson Odih*	Phylogenetic analysis (SNP-based tree construction) (group project 2) *Pimlapas*	11:00
	11:30				11:30
	12:00	Lunch Break			12:00
	12:30	De novo assembly vs. ref based mapping (lecture & practical 2) *Arun Decano*	Case studies: genomic surveillance in public health (TB) *Lavania Joseph*	Case studies: genomic surveillance in public health *Michelle Lowe* (pre-	12:30
	13:00				13:00
	13:30		AMR typing - WGS data (lecture) *Arun Decano*	Transmission analysis (lecture & practical 6) *Narender Kumar*	13:30
	14:00				14:00
	14:30				14:30
	15:00	Break	Break	Break	15:00
	15:30	Genome annotation (lecture & practical 3) *Stan Kwenda*	AMR typing using WGS data (group project 1) *Arun Decano, Stan Kwenda, Narender Kumar*		15:30
	16:00			Wrap up and network discussion	16:00
	16:30				16:30

Course materials

accessible via Github repository –
https://github.com/WCSCourses/AMR-Bio-Africa-2022

Introductory session
- Welcome and overview
- Reading material

Session 1: Intro to sequence data & QC
- Introductory presentation
- Hands-on exercises manual
- Hands-on exercises example commands

Session 2: Genome assembly
- Introductory presentation
- Hands-on exercises manual

Session 3: Genome annotation
- Introductory presentation
- Hands-on exercises manual
- Hands-on exercises online version

Session 4: Bacteria subtyping
- Introductory presentation
- Hands-on exercises manual

Session 5: AMR detection
- Introductory presentation
- Hands-on exercises manual

Session 6: Phylogenetic analysis
- Introductory presentation
- Visualization presentation
- Hands-on exercises manual

Session 7: Transmission analysis
- Introductory presentation
- Hands-on exercises manual
- Use this link to navigate to the microreact instance for this tutorial

Session 8: SAGESA Network discussion
- Course feedback

*Some content was adapted from the WCS AMR for Bacterial Pathogens Course

Software and datasets

Software Name	Version*	Link	Session
Anaconda3			Raw sequence data QC
FastQC	0.11.9		De novo assembly
MultiQC	1.6		AMR prediction
Trim-galore	0.6.2		Genome annotation
BactInspector	0.1.3		Reference based mapping
Shovill	1.1.0		General tools
QUAST	5.0.2		
abricate + (preloaded resfinder DB & NCBI DB)	1.0.1		
prokka			
snippy			
bwa			
bowtie2			
samtools	1.11		
R + TidyVerse			

Planning and development

Technical resources and platforms

All participants and training team members will use own laptops, and should have access internet.

- Minimum requirements for the computer should be 8GB RAM, i5 processor and 80GB hard disk space
- All have to install Virtual Box to use a Virtual Machine containing all software and datasets
- Zoom as the meeting platform, participants pre-register
- Slack Workspace for interactions, Q&A and networking
- All courses materials compiled on Github repository

Advertising and marketing

- Directly to SAGESA members via emails and Slack
- WCS Newletters, Twitter and LinkedIn Platforms
- SAGESA Twitter
- Personal networks in Africa region

Application and selection

- Application set up in V1 platform
- Based on justification and relevance of work or research; Benefit to current work and to colleagues
- Application received – over 300
- No. of applications accepted – 43

Application form questions:

1. First name
2. Last name
3. Current role
4. Department, institute
5. Country
6. Nationality
7. Highest level of qualification
8. Subject area of work
9. Previous jobs (please list up to a maximum of 3)
10. Justification for attending this course. Please note that our courses are frequently oversubscribed and the selection committee relies heavily on this section to make its decision. Please provide an outline of your work (research project(s) and/or clinical/healthcare activities)
11. How will you use the training to benefit your work?
12. Are you currently generating or analysing genome sequence data?
13. How would you rate your skills in command line/Linux?
14. What is your computer processor (e.g i3, i5, i7...)
15. Do you have a stable internet connection?

Post-course feedback questions

Refer to attachments separately

Timelines Overview

Item	Activity	Dates	Respons.
Finalise course description	Programme outline; target audience, pre-requisites	Done	AM/IM
Development and delivery teams	Finalise module leads, instructors, facilitators, assistants	Get confirmation by 28/02	IM/SK
Curriculum	Course plan – Develop module outlines, objectives, activities	18/03	AM/IM/SK
Call for participant applications, review and selection	Application forms	Open: 16/03 Close: 15/04 Selection: 25/04	IM/MS
Develop training materials	Lecture videos, resources and contact session guides	15/04	Training team
Reviewing and testing	All materials including VM and software and datasets to be tested and approved	29/04	MA/SK
Course delivery	Virtual delivery	25 – 27 May	All
Feedback	Participant and training team feedback	10/06	All

Acknowledgements