Introduction to WGS in AMR surveillance – Day 4

Course offered by SEQAFRICA

The Fleming Fund
Regional Grants

22 February 2021

Pernille Nilsson

Virtual Housekeeping

Please **turn off your cameras and microphones** – this will help with bandwidth and maximise audibility.

Do frequently **use Slack** to share comments and ask questions. Keep the chat constructive, respectful and on topic!

For Q&A's **use Slack to submit your questions!** Please upvote (give a thumbs-up) to the questions that you like.

The session is being **recorded for distribution to participants** as a post course resource as well as for future iterations of the course.

Agenda

Monday 22nd February 09:00 – 12:00

Day 4: Monday – 22 Feb 2021 – Focus Join Zoom for Day 4		
08.45 – 09.00	**Joining the call** – Assistance will be provided at this time to help participants join	
09.00 – 09.15	**Welcome and Introduction (Live)**	
09.15 – 10.15	[10] **Phylogeny: construction, visualization and interpretation.** Tools: Microreact (Pre-recorded Lecture)	Erkison Odih (UI, Nigeria)
10.15 – 10.30	**BREAK**	
10.30 – 11.00	[10E] **Exercise on phylogeny**: Participants will be given an exercise on phylogeny (Live introduction). To be handed in through SurveyMonkey link prior to attending Day 5.	Erkison Odih (UI), Sonda Tolbert (KCRI) and Ayorinde Afolayan (UI)
11.00 – 11.30	[11] **Genotype to Phenotype: Prediction of AMR by WGS** (Pre-recorded Lecture)	Jette Sejer Kjeldgaard (DTU, Denmark)
11.30 – 11.45	[11E] **Exercise Phenotype based on genotype:** Determining phenotype based on genotype. (Live introduction). To be handed in through SurveyMonkey link prior to attending Day 5.	Jette Sejer Kjeldgaard (DTU, Denmark)
11.45 – 12.00	**Q&A and Wrap-up (Live)**	

[10] Phylogeny: construction, visualization and interpretation

Erkison Odih (UI, Nigeria)

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BREAK

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[10E] Exercise in phylogeny

In this session you will learn how to view phylogenetic trees using FigTree, as well as import tree and metadata into Microreact (it is advisable to create a new Microreact account).

You have been provided with a phylogenetic tree and metadata via *Jottacloud*.

- Download the phylogenetic tree (file format .nwk) and metadata file (.csv) to your computer via the *Jottacloud* link provided to you via email
- Follow the instructions in the word file on *Jottacloud* describing how to view the phylogenetic tree and metadata in the programs
- Study the output results and answer the questions in the following survey:
  https://www.surveymonkey.com/r/10Ephylogeny

[11] Genotype to Phenotype: Prediction of AMR by WGS

Jette Sejer Kjeldgaard (DTU, Denmark)

[11E] Exercise in Phenotype based on genotype

Jette Sejer Kjeldgaard (DTU, Denmark)

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Q&A

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Agenda

Wednesday 24nd February 09:00 – 12:00

Day 5: Wednesday – 24 Feb 2021 – Results and Nagoya protocol Join Zoom for Day 5		
08.45 – 09.00	**Joining the call** – Assistance will be provided at this time to help participants join	
09.00 – 09.15	**Welcome and Introduction (Live)**	
09.15 – 10.15	Going through results from exercises **5E and 9E** (Live)	
10.15 – 10.30	**BREAK**	
10.30 – 11.00	Going through results from exercises **10E and 11E** (Live)	
11.00 – 11.30	**BREAK**	
11.30 – 12.15	[12] **The Nagoya protocol: An introduction**	Carolina Dos Santos Ribeiro (RIVM)
12.15 – 12.30	Q&A and Wrap-up (Live)	

Contact us for more information

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Thank you

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