

Module 3

SARS-CoV-2 whole genome sequencing

Day 3



21 May 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

Friday 21st May 09.00 – 13.00 CET



Lectures



Exercises



SurveyMonkey

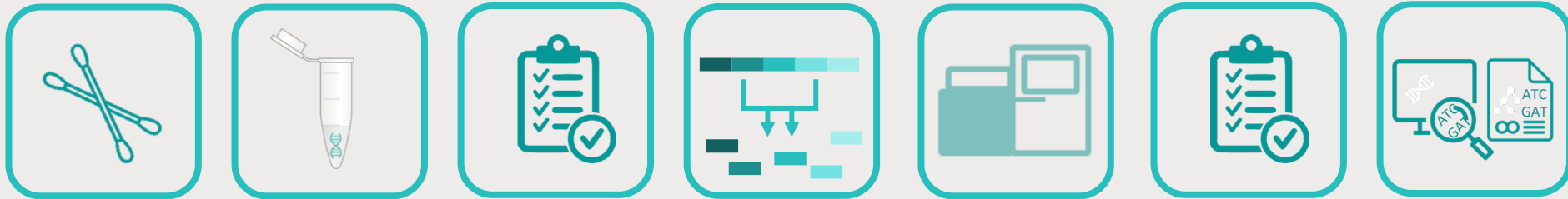
Day 3: Friday – 21 May 2021 – SARS-CoV-2 WGS bioinformatics workflows and online tools

Join Zoom call and Slack channel to attend

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)	Pernille Nilsson (DTU, Denmark)
09.15 – 09.45	[8] Recap on the vet lab workflow. (Live)	Jinal Bhiman (NICD, South Africa)
09.45 – 10.15	[9] Galaxy pipeline: Bioinformatics pipeline used for SARS-CoV-2 genome assemble using a reference. QC of sequence outputs from Galaxy (Live)	Cathrine Scheepers, (NICD, South Africa)
10.15 – 10.30	BREAK	
10.30 - 11.00	[10] Exatype pipeline: Bioinformatic pipelines used for SARS-CoV-2 genome assemble using a reference. QC of sequence outputs from Exatype (Pre-recorded)	Simon Travers (Hyrax Biosciences)
11.00 – 11.30	[11a] Introduction to Nextstrain online tool: Demonstration of data analysis at Nextstrain. (Pre-recorded)	Bright Adu, Frank Oteng/Noguchi team (NMIMR, Ghana)
11.30 – 12.00	BREAK	
12.00 – 12.30	[11b] Introduction to PANGOLin and COVDB online tools: Demonstration of data analysis at PANGOLin and Stanford University – implication of mutations reported in literature (vaccine escape etc.) (Live)	Daniel Amoako (NICD, South Africa)
12.30 – 12.45	[9_10E] Introduction to Exercise: Going from raw reads to analyzed genome assemblies. Assemble WGS, generate FASTA, look at QC, assign lineage and clade, compare Galaxy and Exatype outputs. Low, medium and high quality test set for generating the QC report will be provided.	
12.45 -13.00	Q&A and Wrap-up (Live)	Pernille Nilsson (DTU, Denmark)

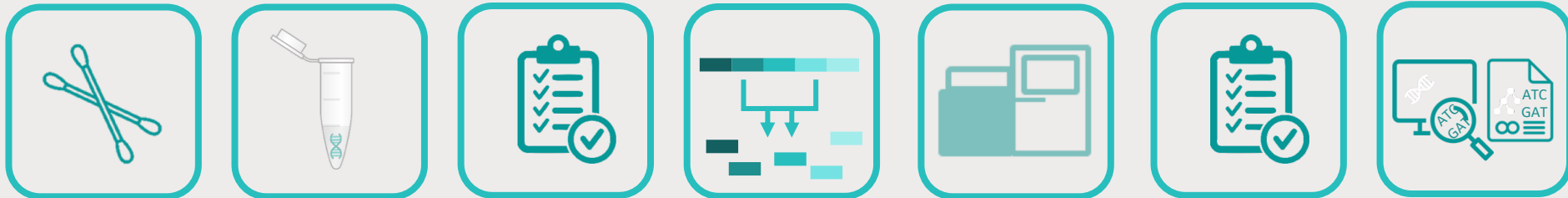
[8] Recap on the vet lab workflow

Jinal Bhiman (NICD, South Africa)



[9] Galaxy pipeline

Cathrine Scheepers (NICD, South Africa)





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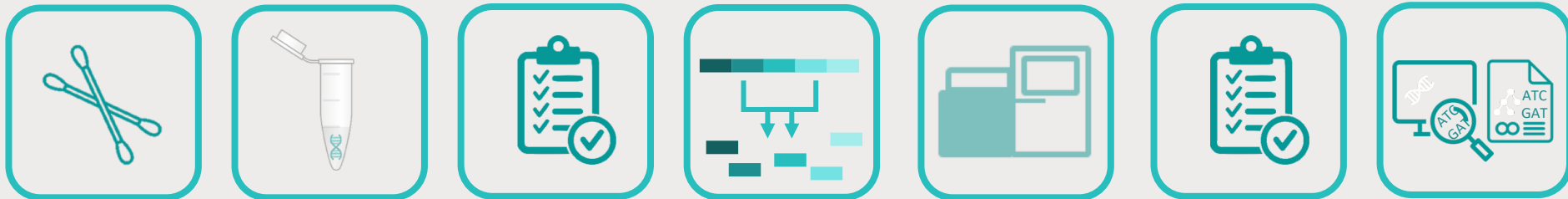
BREAK

10.30 – 10.45 CET



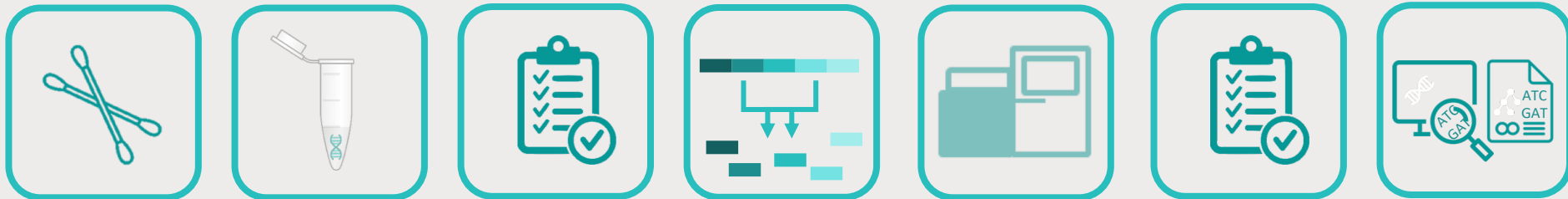
[10] Exatype pipeline

Simon Travers (Hyrax Biosciences)



[11a] Introduction to Nextstrain online tool

Bright Adu, Frank Oteng/Noguchi team (NMIMR, Ghana)





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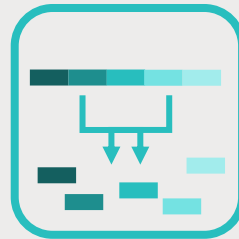
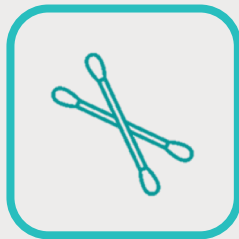
BREAK

12.00 – 12.20 CET



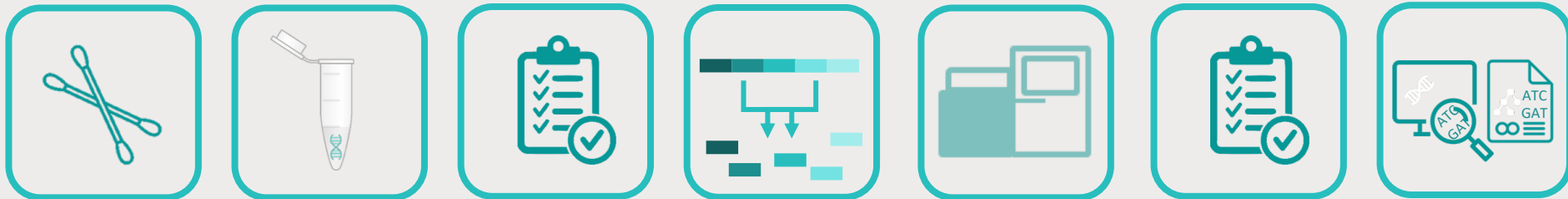
[11b] Introduction to PANGOLin and COVDB online tools

Daniel Amoako (NICD, South Africa)



[9_10E] Introduction to Exercise: Going from raw reads to analyzed genome assemblies.

Cathrine Scheepers, Daniel Amoako (NICD, South Africa)



Case study

There are 7 reported positive cases of SARS-CoV-2 in location **X** which needed urgent sequencing to ascertain the potential threat. You have been provided with the raw sequencing data for all 7 samples, generated via Illumina NextSeq using the ARTIC protocol (FastQ Format).

For all 7 samples you need to:

1. Assemble the full genome using Galaxy and Exatype
2. Assess the quality of each sample and flag those that might be poor quality
3. Assign lineage (pangolin) and clades (nextclade) for each sample and also assess quality based on pangolin and nextclade outputs
4. Compare the quality assignments between Galaxy and Exatype
5. Compare the lineage and clade assignments between Galaxy and Exatype
6. Identify any mutations or variants of concern/interest
7. Create a report that outlines this information and your recommendations to your Department of Health.



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Q&A






Agenda

Friday 28st May 09.00 – 13.00 CET

Preparations: Download PyMoL

Day 4: Friday– 28 May 2021 – Mutant impact assessment, data sharing and review of exercises/quizzes

Join Zoom call and Slack channel to attend

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)	Pernille Nilsson (DTU, Denmark)
 09.15 – 09.45	[12] Introduction to PyMoL: Predictive assessment of impact of mutations based on spike structure (For novel mutations). (Pre-recorded)	Constantinos Kurt Wibmer (NICD, South Africa)
 09.45 – 10.00	[12E] Exercise: Plot given set of mutations on structure and suggest functional role for these. (Live)	Constantinos Kurt Wibmer (NICD, South Africa)
10.00 – 10.45	BREAK (work on PyMoL exercise)	
 10.45 - 11.15	[13] Data sharing and uploading to GISAID: Overview of the GISAID database, polices and uploading (including compulsory metadata). (Pre-recorded)	Anne von Gottberg (NICD, South Africa)
11.15 – 11.30	Going through results from Quiz 7Q (Live)	
11.30 – 12.00	BREAK	
12.00 – 13.00	Going through results from 11E (Live)	
13.00 – 13.15	Q&A and Close (Live)	Pernille Nilsson (DTU, Denmark)

Thank you



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