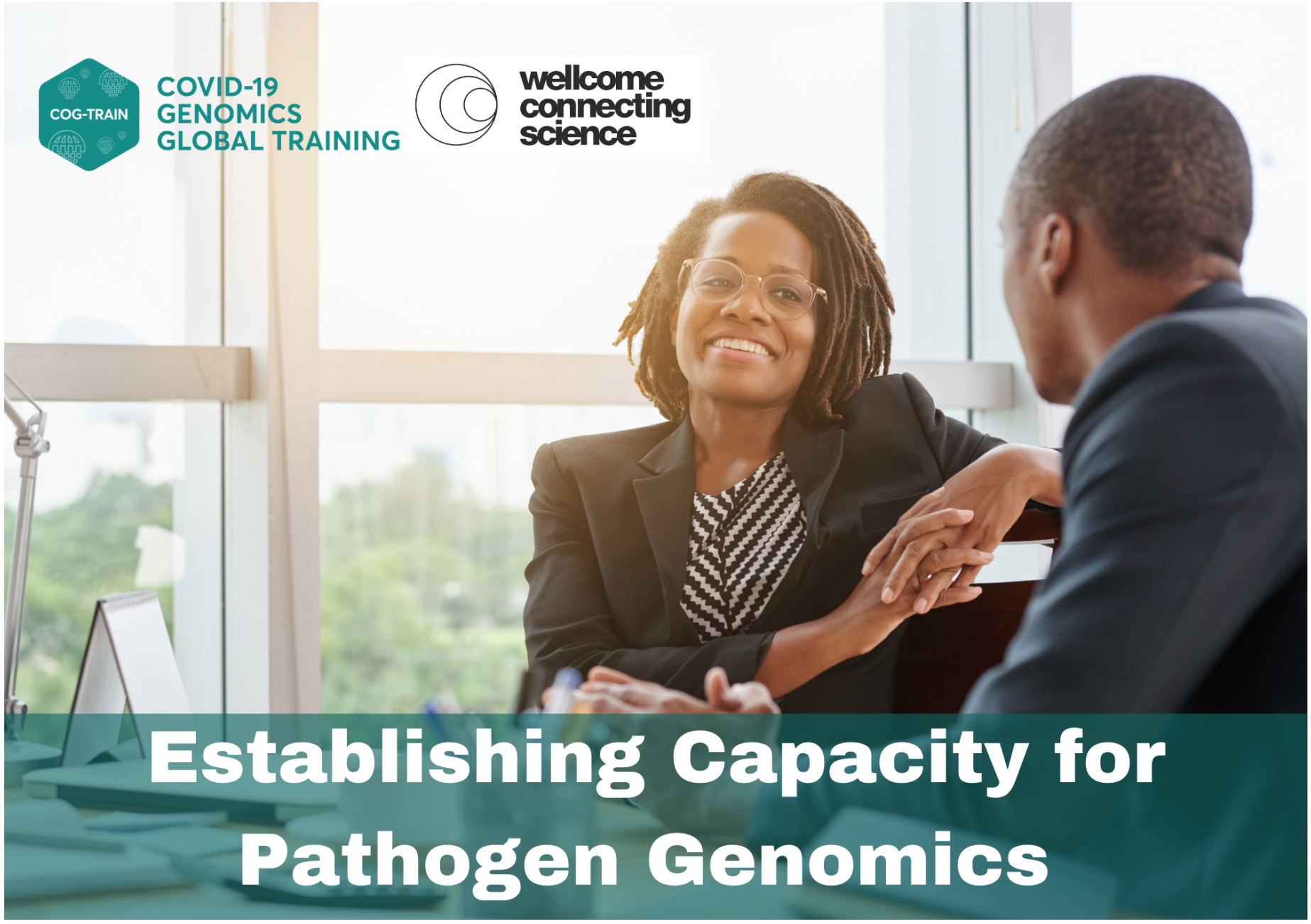
COG-TRAIN
COVID-19
GENOMICS
GLOBAL TRAINING
wellcome
connecting
science
Establishing Capacity for
Pathogen Genomics

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Organisers and developers

Name	Institution
Abebe Asefa	Ethiopian Public Health Institute, Ethiopia
Alice Matimba	Wellcome Connecting Science, United Kingdom
Amadou Diallo	Institut Pasteur de Dakar, Senegal
Aquilla Kanzi	African Society of Laboratory Medicine, Ethiopia
Brenda Kwambana	Malawi Liverpool Wellcome Trust, Malawi
Dawit Wolday	Ethiopian Public Health Institute
Fatma Guerfali	Institut Pasteur de Tunis, Tunisia
Fatuma Guleid	KEMRI-Wellcome Trust Research Programme, Kenya
Francis Chikuse	Africa Centre for Disease Control, Namibia
George Githinji	KEMRI-Wellcome Trust Research Programme, Kenya
Gerald Mboowa	Africa Pathogen Genomics Initiative, Ethiopia
Harris Onywera	Africa Pathogen Genomics Initiative, Ethiopia
John Tembo	HerpeZ, Zambia
Jonathan Emmanuel Chukwuemeka	Institute of Human Virology, Nigeria
Jorge Batista Da Rocha	Wellcome Connecting Science, United Kingdom
Kareemah Suleiman	Institute of Human Virology, Nigeria
Kirsty Lee Garson	University of Cape Town, South Africa
Leigh Jackson	University of Exeter, United Kingdom
Liã Bárbara Arruda	Wellcome Connecting Science, United Kingdom
Linzy Elton	University College London, United Kingdom
Luria Leslie Founou	Centre of Expertise and Biological Diagnostic of Cameroon, Cameroon
Melanie Sharpe	Wellcome Connecting Science, United Kingdom
Sam Oyola	International Livestock Research Institute, Kenya
Shavanthi Rajatileka	Wellcome Sanger Institute, United Kingdom
Stanford Kwenda	National Institute for Communicable Diseases, South Africa
Tapfumanei Mashe	National Microbiology Reference Laboratory, Zimbabwe
Treasa Creavin	Wellcome Connecting Science, United Kingdom

Programme

Establishing Capacity for Pathogen Genomics
7 - 12 May 2023
Ethiopian Public Health Institute, Addis Ababa

	Sunday 7 May	Monday 8 May	Tuesday 9 May	Wednesday 10 May	Thursday 11 May	Friday 12 May	
	Introduction	Capacity Development Overview	Specimen and Sequencing	Data tools and pipelines	Frameworks, guidelines, comm & decision-making	Projects, networks & action planning	
07:00	Pre-workshop access via LMS	Breakfast (hotel residents only)	Breakfast (hotel residents only)	Breakfast (hotel residents only)	Breakfast (hotel residents only)	Breakfast (hotel residents only)	07:00
07:30		*Transport to EPHI*	*Transport to EPHI*	*Transport to EPHI*	*Transport to EPHI*	*Transport to EPHI*	07:30
08:00		Welcome to EPHI, Housekeeping	Arrival and day recap	Arrival and day recap	Arrival and day recap	Arrival and day recap	08:00
08:30		Developing capacity for pathogen genomics	Specimen and data collection and processing	Setting up data infrastructure, processes	Frameworks and guidelines	Outline - Plan a genomics capacity project	08:30
09:00					Ethics of Specimen and Data sharing		09:00
09:30		Practical approaches - specimen, genomics and data infrastructure		Genomic data workflows, analysis, linkage, integration, interpretation			09:30
10:00							10:00
10:30		Coffee break	Coffee break	Coffee break	Coffee break	Coffee break	10:30
11:00		Practical approaches - Genomics for public health interventions	Molecular microbiology	Genomic data workflows, analysis, linkage, integration, interpretation cond.	Building sustainability - Funding, Resources, Stakeholders, Skills	Present - Plan a genomics capacity project	11:00
11:30							11:30
12:00	REGISTRATION & LUNCH	Challenges and opportunities - Group action planning					12:00
12:30			Setting up genomic sequencing				12:30
13:00	Welcome and Introductions	LUNCH	LUNCH	LUNCH	LUNCH	LUNCH	13:00
13:30							13:30
14:00		Design genomics training I - Training design elements	Setting up genomic sequencing infrastructure, processes cond.	Data science tools for public health	Communication of data & public health decision-making	Action planning - networks and mentorship	14:00
14:30	Learning & Traning Skills						14:30
15:00			Translating to own contexts I- sample to sequencing	Translating to own contexts II- data analysis workflows			15:00
15:30						Workshop wrap-up	15:30
16:00	Coffee break	Coffee break	Coffee break	Coffee break	Coffee break	Coffee & end of workshop	16:00
16:30	Intro seminars - Pathogen Genomics in Africa	Establishing needs for pathogen genomics skills development	Design genomics training II - Specimen to sequencing	Designing training III - Data analysis, tools and resources	Communication of data & public health decision-making cond.	*Transport to hotel*	16:30
17:00							17:00
17:30	Networking session	End of day wrap-up	End of day wrap-up	End of day wrap-up	Introduction to Project		17:30
18:00		*Transport to hotel*	*Transport to hotel*	*Transport to hotel*	*Transport to hotel*		18:00
18:30	Welcome dinner (ALL)						18:30
19:00		Dinner (hotel residents only)	Dinner (hotel residents only)	Dinner (hotel residents only)	Dinner (hotel residents only)	Dinner (hotel residents only)	19:00
19:30							19:30
20:00							20:00
	Sunday 7 May	Monday 8 May	Tuesday 9 May	Wednesday 10 May	Thursday 11 May	Friday 12 May	

Pre-course

Pre-course - Self-paced		
Self- paced on Padlet	Introduce yourself	Jorge Batista Da Rocha; Liã Bárbara Arruda
Self-paced on LMS	Sign-up to LMS	Jorge Batista Da Rocha; Liã Bárbara Arruda
Self-paced on LMS	Overview of adult learning principles and training design techniques	Alice Matimba; Leigh Jackson; Liã Bárbara Arruda
Self-paced on LMS	Overview of genomics and pathogen data science	Liã Bárbara Arruda, Leigh Jackson; Jorge Batista Da Rocha

Pre-course - Sunday 7 May - Introduction		
12:00 - 13:00	Registration and lunch	Melanie Sharpe; Abebe Assefa
13:00 - 13.20	Welcome to Ethiopia	Harris Onywera; Abebe Assefa; Invited guest - EPHI Director
13:20 - 13:40	Workshop Introduction	Alice Matimba; Treasa Creavin
13:40 - 14:10	Facilitator introductions	Harris Onywera; Liã Bárbara Arruda
14:10 - 15:00	Participant introductions	Leigh Jackson; Harris Onywera
15:00 - 15:30	Coffee break	
15:30 - 16:30	Workshop L&T skills	Alice Matimba; Liã Bárbara Arruda; Treasa Creavin; Leigh Jackson
16:30 - 16:45	Intro seminar 1 - Status of pathogen genomics in Africa	Harris Onywera
16:45 - 17:00	Intro seminar 2 - Pathogen genomics in Ethiopia	Invited guest - Helen Saro
17:00 - 18:00	Networking event	ALL

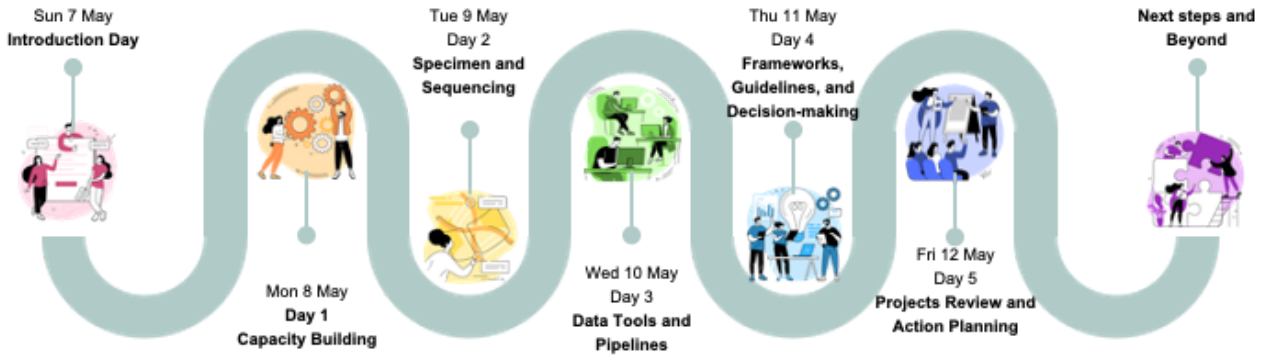
Day 1 - Capacity Development Overview

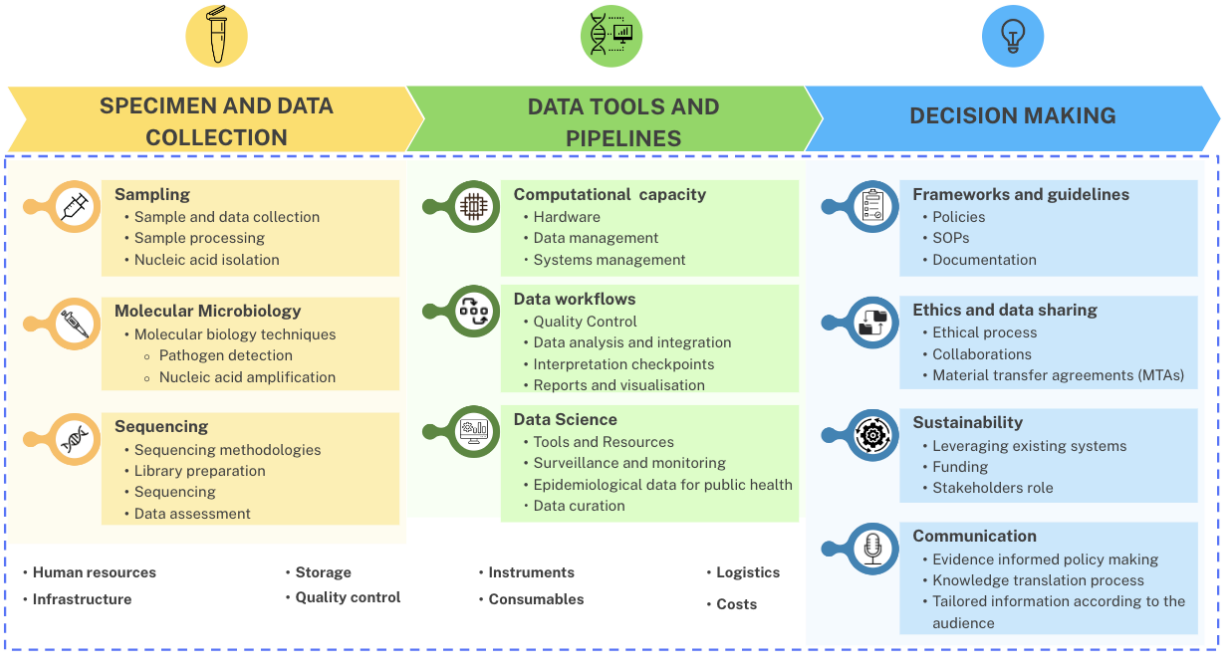
Day 1 - Monday 8 May - Capacity Development Overview		
08:00 - 08:30	Welcome to EPHI and Housekeeping	Abebe Aseffa; EPHI Training Centre Head
08:30 - 09:30	Developing capacity for pathogen genomics	Alice Matimba; Liã Bárbara Arruda; Linzy Elton; Harris Onywera; Treasa Creavin
09:30 - 10:30	Practical approaches - specimen, genomics and data infrastructure	Kareemah Suleiman; Aquilla Kanzi, Shavanthi Rajatileka, Gerald Mboowa, Dawwol Wol; Linzy Elton
10:30 - 11:00	Coffee break	
11:00 - 12:00	Practical approaches - Genomics for public health interventions	Tapfumanei Mashe; Francis Chikuse; Luria Leslie Founou
12:00 - 13:00	Challenges and opportunities - Group action planning	Kirsty Lee Garson; Treasa Creavin; Harris Onywera; John Tembo; Emmanuel Chukwuemeka; Tapfumanei Mashe
13:00 - 14:00	Lunch	
14:00 - 16:00	Design genomics training I - Training design elements	Alice Matimba; Stanford Kwenda; Luria Leslie Founou; Leigh Jackson; Treasa Creavin; Linzy Elton; Shavanthi Rajatileka
16:00 - 16:30	Coffee break	
16:30 - 17:30	Establishing needs for pathogen genomics skills development	Liã Bárbara Arruda; Dawwol Wol; Treasa Creavin; Samuel Oyola; George Githinji; Francis Chikuse; Linzy Elton
17:45 - 18:00	End of day reflection	All

Day 1 Session 1

Developing capacity for pathogen genomics

Course roadmap





Day 1 Session 1 - Analysis of current status

Day 1 Session 2 activity

What are the key focus capacity development areas needed in your country?

Consider the following components, what the current situation is and what you think might need to be put in place:

Institute and Country	

Lab facilities, infrastructure and Equipment	
What is currently in place?	What is needed?
Computing facilities, infrastructure and Equipment	
What is currently in place?	What is needed?
Quality Management	
What is currently in place?	What is needed?
Policy/governance	
What is currently in place?	What is needed?

Day 1 Session 4 - Challenges and Opportunities - Group Action Planning

Small Group Activity Discussion

- Challenges and opportunities in implementing pathogen genomics in home countries (Include economic, scientific, technical, cultural issues) - **15 minutes**
- Identify individual and group strengths in addressing these challenges - **10 minutes**
- How will this workshop help towards addressing the challenges or strengthening current work? - **10 minutes**
- Group report back - **15 minutes**

Day 1 Session 5 - Training design elements

Activity 1: Writing goals and objectives

Based on the statement below and outline the following.

- Summary of the problem
- What is your proposed intervention?
- How do you set out to address this problem?
- What is your goal?
- What is/are the objective(s) - how will your goal be achieved?

Viral genomics and bioinformatics training intervention case study

Viral diseases including zoonotic infections, are a major public health burden, causing millions of deaths worldwide. Challenges faced include limited access to resources and infrastructure for timely diagnosis and surveillance. SARS-Cov-2 and ebola have been devastating to health systems, economies and many communities in Africa. Rapid and accurate detection using genomics technologies enables early warning of circulating variants of concern and for appropriate interventions to be implemented and minimise death risk.

Advances in research technologies are enabling access to improved detection, surveillance and management of diseases. In recent years, next-generation sequencing (NGS) technologies have played an important role in the viral identification, classification, drug resistance and treatment and surveillance. Early identification of a virus and quick analysis of its genome will aid in better treatment and help in controlling the disease's spread. However, expert knowledge of viral genome sequence analysis is required. However, there is limited knowledge and expertise in the analysis and interpretation of genomics data generated from large-scale sequencing. Bioinformatics skills are in high demand among researchers and clinical staff, and yet training opportunities are few and often held as once-off workshops.

Activity 2: Needs assessment

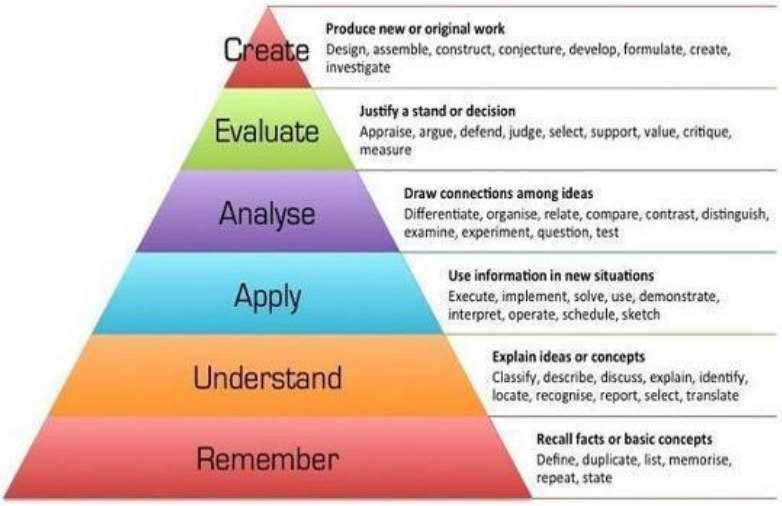
Read the statement below and outline the following

- What other information do you need?
- How will you collect it?
- Now refine your goal, objectives, target audience given the additional information from the needs assessment

Needs assessment survey results for genomics training

To demonstrate the need for training in viral genomics and bioinformatics, we conducted a survey targeted at microbiologists. Of the 170 respondents, approximately 85% stated that their work includes the use of genomics or bioinformatics. The vast majority of respondents perform basic bioinformatic tasks with 57% using NGS data in their work. However, a substantial fraction stated that at least part of their NGS analyses are performed outside of their own institution in other locations within and outside their country (Figure 1). For the small proportion of researchers that do not perform any genomics/bioinformatics studies, the majority (~65%) say they would like to include these topics in their research, but they do not have the expertise in-house. We will use this data as a first step to address the bioinformatics skills gap targeted at viral genomics research.

Activity 3: Learning outcomes activity



Formula for writing LOs:

Active verb (what participants will be able to do); Object (what is the item referred to); Qualifying phrase (for context). Below are learning outcomes from a viral genomics course. Complete the table below by indicating 1. Bloom's level. Highlight or make a note of verb, object and contextual phrase

Learning outcome	Bloom's level
Apply Unix/Linux command-line and write basic shell scripts for automating bioinformatics tasks	
Evaluate genome assemblies using statistics and visualisations	
Select and apply appropriate software tools to call variants from a genome assembly.	
Compute multiple sequence alignments and construct phylogenetic trees to understand viral evolution and transmission dynamics	
Build a pipeline for analysis, interpretation and identification of viral pathogens.	
Identify effective methods for disseminating knowledge and skills in viral bioinformatics	

Activity 4: Assessment

Assessment Part 1: How to use assessment for learning

- Choose a letter - A, B, C
- Read the statements corresponding to your letter below
- Reflect on what this implies to you and your learning and training practice

Assessment for learning statements

A. How do trainers determine what type of formative assessment strategy to use?

- Trainers need to determine what aspect of participant learning they want to assess. They then need to consider the learning preferences of their participants.
- Formative assessment strategies can be given to participants individually, as pairs, in small groups, or as a group.
- Trainers should not rely on one type of assessment strategy. A variety of individual and group formative assessment strategies should be used.
- Individual strategies allow trainers to get a clear picture of each participant and their understanding of the concept or skill being measured.
- Group strategies provide trainers with general information about participant learning that can be used to plan the training.

B. How can trainers use the formative assessment information?

- Trainers use the assessment information to assess how their current training strategies are working with their participants.
- If there are participants who are struggling, trainers may need to work individually with a participant, present information in other ways, or adapt their current training strategy.
- Participants, who have appeared to master the outcome or goal being formally assessed, may need to be further assessed or have learning opportunities planned that challenge them and are designed at their level of understanding.
- Trainers are also able to identify misunderstandings that participants may have and adapt their training accordingly.

C. How can participants use the formative assessment information?

- Participants need to determine what aspect of their learning they want to assess and how best to do it considering their own learning preferences.
- Participants can use assessment information to determine what they need to do to achieve the goals or outcomes of the session.
- Participants may need to adapt or change their learning to master learning outcomes.
- If participants are not achieving at an expected rate, they can look at the strategies they are using for learning and decide whether they need to change their current learning strategies or adopt new ways of learning.
- The information provided by formative assessment strategies can also be used to help participants reflect on current learning goals or set new goals.

Add your reflections/responses here:

Assessment Part 2: Techniques to meaningfully assess learning
For each of the LO's listed below determine what techniques can learners and trainers use to assess learning (Remember Bloom's levels from remembering to creating)

Learning outcome	Techniques/methods of assessment
Identify appropriate training resources for use in training pathogen genomics and surveillance tools.	
Deliver pathogen genomic data science training to professionals working in genomic epidemiology, surveillance and outbreak investigation.	
Evaluate the self-developed training and knowledge sharing of pathogen genomic data science.	
Create sequencing libraries and analyse samples derived from patients with viral infections.	
Evaluate how to improve the efficiency of NGS by carrying out variations in library preparation technique e.g. target enrichment	
Demonstrate how viral WGS can be used to inform transmission patterns and evaluate the effectiveness of interventions	

Example assessment techniques include
Simple techniques like question banks, quizzes, peer assessment (get them to frame and ask each other questions), bingo grids to debates, reflective journals, self-assessing work against checklists, one-minute essays, learners explaining concepts in their own words, learners teaching each other a concept or skill to designing leaflets about an aspect of research writing, real-world scenarios, designing posters as a guide, reflective writing tasks etc.

- **Discuss as a group**
  - Which levels of thinking do you think are the easiest/hardest to identify assessment techniques for?
  - Which of the techniques (that are new to you) would you like to try straight away in your training and/or teaching?

Activity 5 - Outline your training

Guidelines	Notes (short bullet points)
Title. Working Title for the Session, Training, Module, Event, Presentation	
Goal and Objectives Background and justification - Why is the training needed? What is the big gap or questions that this training fulfils, why is it important, relevant? What is the goal?	
Target audience. Who is this event or training aimed at? What are the prerequisites.	
Learning outcomes What learners should be able to demonstrate in terms of knowledge, skills and attitudes after the course. At the end of this workshop, participants will be able to…	
Logistic information Venue? Format? Length of training/sessions	
Content. What topics will be covered?	
Activities. What activities, exercises and instructional strategies will be used? What training resources, software, datasets, online tools, datasets, servers?	
Assessment. How can the Learning Outcomes be assessed? Describe the assessment plan and provide details on what will be assessed, when and how.	
Delivery. Who will deliver the training/session/presentation? Why are you or they, the best to deliver the training?	
Facilities, infrastructure, equipment. Spaces, platforms needed by (1) you and the training team and (2) by the participants	
Potential challenges. Constraints and limitations and possible ways to address/overcome these.	
Feedback and Evaluation. What feedback will you collect, when and how? How will you evaluate success?	

Day 1 Session 6 - Establishing needs for pathogen genomics skills development

In your facility/team, do you have human resources/personnel with the following skills/competencies?

SPECIMEN AND DATA COLLECTION

Sampling	**Molecular microbiology**	**Sequencing**
☐ Sampling strategy	☐ Conventional PCR	☐ Library preparation
☐ Sample collection	☐ Real-time PCR	☐ Loading sequencer
☐ Sample processing	☐ Agarose electrophoresis	☐ Sequencing assessment
☐ Sample storage	☐ Sample storage	☐ Sample storage
☐ Nucleic acid isolation	☐ Record keeping	☐ Record keeping
☐ Data collection	☐ Documentation	☐ Documentation
☐ Record keeping	☐ Quality control	☐ Quality control
☐ Documentation	☐ Logistics	☐ Logistics
☐ Quality control	☐ Inventory	☐ Inventory
☐ Logistics	☐	☐
☐ Inventory	☐	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐

In your facility/team, do you have human resources/personnel with the following skills/competencies?

DATA TOOLS AND PIPELINES

Processing capacity	Data workflows	Data science
☐ Hardware maintenance	☐ Documentation	☐ Tools
☐ Data curation and storage	☐ Metadata	☐ Surveillance and monitoring
☐ Record keeping	☐ Quality control	☐ Interpretation
☐ Documentation	☐ Analyses	☐ Reporting
☐ Quality control	☐ Interpretation	☐ Visualisation
☐ Logistics	☐ Data integration	☐ Record keeping
☐ Inventory	☐ Visualisation	☐ Documentation
☐	☐ Reporting	☐ Quality control
☐	☐ Record keeping	☐ Logistics
☐	☐ Inventory	☐ Inventory
☐	☐ Logistics	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐
☐	☐	☐

In your facility/team, do you have human resources/personnel with the following skills/competencies?

DECISION MAKING

Frameworks and guidelines	Ethics and data sharing	Sustainability	Communication
☐ Policies	☐ Consent	☐ Funding	☐ Evidence-informed policymakers
☐ SOPs	☐ Memoranda of understanding (MoU)	☐ Clear role of stakeholders	☐ Knowledge translation processes
☐ Record keeping	☐ Material transfer agreements (MTAs)	☐ Improvement of existing systems	☐ Communication of tailored information to each audience
☐ Documentation	☐ Record keeping	☐	☐
☐ Quality control	☐ Documentation	☐	☐
☐ Logistics	☐ Quality control	☐	☐
☐ Inventory	☐ Logistics	☐	☐
☐	☐ Inventory	☐	☐
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☐	☐	☐	☐

Day 2 - Specimen and Sequencing

Tuesday 9 May - Specimen and Sequencing		
08:00 - 08:30	Day recap	All
08:30 - 10:30	Specimen and data collection and processing	Emmanuel Chukwuemeka; Kareemah Suleiman; Liã Bárbara Arruda
10:30 - 11:00	Coffee break	
11:00 - 12:30	Molecular microbiology	Luria Leslie Founou; (Brenda Kwambana); Liã Bárbara Arruda
12:30 - 13:00	Setting up genomic sequencing infrastructure	Linzy Elton; John Tembo; Shavanthi Rajatileka; Liã Bárbara Arruda
13:00 - 14:00	Lunch	
14:00 - 15:00	Setting up genomic sequencing infrastructure cond.	Linzy Elton; John Tembo; Shavanthi Rajatileka; Liã Bárbara Arruda
15:00 - 16:00	Workshop Translating to own contexts - sample to sequencing	Liã Bárbara Arruda; John Tembo; Emmanuel Chukwuemeka; Kareemah Suleiman; Linzy Elton; Luria Leslie Founou; Shavanthi Rajatileka
16:00 - 16:30	Coffee break	
16:30 - 17:45	Design genomics training - from specimen to sequencing	Liã Bárbara Arruda; Luria Leslie Founou; John Tembo; Emmanuel Chukwuemeka; Kareemah Suleiman; Shavanthi Rajatileka; Linzy Elton
17:45 - 18:00	End of day reflection	ALL

Day 2 Session 1 - Specimen and data collection and processing

Activity on Sample Storage

Introduction of activity
Groups will be split into 2

Group 1: Case study (Sample receipt)
A facility sends a sample to your lab for processing and storage. You notice a discrepancy between the sample manifest and the actual sample. What steps do you take to resolve the problem?

Group 2: Case study (Acceptance criteria)
A sample that doesn't meet the acceptance criteria was delivered to your lab. What actions do you take to deal with the circumstance?

-Discussion and presentation by groups

Day 2 Session 2 - Molecular Microbiology

Africa CDC have given you a grant of USD 500,000 to set up a molecular microbiology laboratory training facility at your institution. You have been given a building of 200 m2 (10m by 20m). Can you outline the key priorities and design of your facilities? Think about the building itself, equipment, consumables/materials/reagents, personnel, security, etc. you will need to have in your facility.

1. You will be randomly split into six groups
2. Use the tickets on the shopping list to build your lab.
3. Choose all that apply, and take into consideration the price and the funds provided
4. Use the provided blank sheets, pencils, rulers, etc., to draw your molecular microbiology lab
5. Use PowerPoint or flipchart to:
    a. Summarize the infrastructure, activities, assays and team in your lab – one slide
    b. Justify the items you bought – one slide/sheet

List of tickets:

Physical separation in wood (Price of one Room)
USD $1850

Low fuel consuming and silent generator 1000 KVA (with installation)
USD $1500

Physical separation in aluminium and pyrex glasses (price of one room)
USD $3500

Whole-Lab generator 10,000KVA (with installation)
USD $30000

Physical separation in concrete blocks (price of one room)
USD $2500

Air conditionner (each)
USD $750

Electric supply (installation)
USD $5700

Air pressure system installation
USD $5250

Electric supply (installation and upgrade to standard)
USD $9500

Cold room installation (-20°C)
USD $19800

Water supply (installation)
USD $3400

Cold room installation (2-8°C)
USD $16200

Water supply (installation and upgrade to standard)
USD $7800

Incubation room (32 - 40°C)
USD $22100

Power pac supply
USD $850

Ultra-Low temperature freezer ThermoFIsher 650L (-80°C)
USD $13500

Eppendorf CryoCube F570 Freezer -80°c, 230V/ 50Hz, 570L
USD $10100

Horizontal electrophoretic apparatus + 1 casting gel, 1 tray and 1 combs
USD $1850

Horizontal electrophoretic apparatus + 1 casting gel, 1 tray and 2 combs
USD $1850

Liebherr Biofreezer -60°C, 215L, USD $2035

Vertical electrophoretic apparatus + 1 casting gel, 1 tray and 2 combs
USD $2250

Liebherr Biofreezer -20°C, 265L, USD $1100

UV transilluminator
USD $450

Liebherr Fridge 2-8°C#, 258L
USD $850

Biological Safety cabinet - class II
USD $15200

Gel documentation system Syngene, USD $5490

Laminar airflow cabinet
USD $7500

Gel documentation system Cleaver diagnostics
USD $3910

Biological Safety cabinet - class I
USD $7500

Gel documentation system Biorad XR+
USD $6250

Biological Safety cabinet - class III
USD $28900

Microcentrifuge with rotor 1.5 ml
USD $2300

Additionnal microcentrifuge rotor
USD $ 570

pH-meter
USD 650

Micropipette Gilson (each)
USD $450

Thermal cycler Biorad T100
USD $3500

Incubator O2 80L
USD $4500

Real time PCR Machine QuantStudio 5 ThermoFisher
USD $30800

Incubator O2 50L
USD $3500

Conventional autoclave 50L
USD $1340

Fully automated dry sterilizer 150L
USD $8500

Fully automated autoclave 150L
USD $7500

Digital dry bath
USD $790

Conventional autoclave 100L
USD $2100

Real-time PCR machine BioRad CFX+XR for research and diagnostic use
USD $65000

Conventional autoclave 50L
USD $1340

Real-time PCR machine BioRad CFX+XR for research use only
USD $22000

Fully automated extraction machine
USD $34760

Project manager (annual salary)
USD $24900

Water bath 50L
USD $430

Accountant (annual salary)
USD $18500

BSc molecular scientist (annual salary)
USD $10500

Intern MSc (annual salary)
USD $9500

MSc Research fellow (annual salary)
USD $15500

Spin-down
USD $630

Senior Research Fellow (annual salary)
USD $22000

Cleaning service (annual fees)
USD $15000

Institutional Overheads (annual fees)
USD $37000

Finance manager (annual salary)
USD $28600

Voltage Regulator 1000W
USD $90

Voltage Regulator 5000W
USD $195

UPS 1000 W
USD $120

UPS 560W
USD $90

UPS 2500W
USD $175

Day 2 Session 3 - Sequencing

Participants will be put into 6 groups:

Activity 1: Each group will be be tasked with setting up a sequencing laboratory scenario. You will be given a worksheet with different parts of the set-up, you must decide in your group what would fit best for your scenario

Activity 2: You will be given a scenario and information about different sequencing platforms. You must decide within your group which is the most appropriate and why.

Activity 3: Each group will be given a sequencing set-up 'problem' and must come up with a solution.

Task 1, scenario 1
You are tasked with setting up Next Generation Sequencing platform in your laboratory for surveillance of AMR within the hospital setting to track outbreaks of AMR or other nosocomial pathogens within the wards.

- What kind of sample preparation methods do you plan to use, and what lab infrastructure do you need to have in place to process those samples safely?

- What types of infectious pathogens do you anticipate you will have to handle and how will this this impact the design of your lab and the sequencing infrastructure you will need?

- What kind of sequencing platform(s) do you plan to use, and how will you decide which one(s) are best for your particular research needs?

- What computational resources will you need to process and analyze your sequencing data, and how will you acquire and manage these resources?

- Given what you currently know about requirements for sequencing what additional infrastructure or equipment would be required in your setting to successfully carry out Next Generation Sequencing and why?

Task 1, scenario 2
You are tasked with setting up a Next-Generation Sequencing platform in your laboratory for surveillance multi drug resistant tuberculosis or MDR TB within the National Program. Your Ministry of Health would like to understand origin and spread of multi-drug resistant tuberculosis within your healthcare system and the community.

- What kind of sample preparation methods do you plan to use, and what lab infrastructure do you need to have in place to process those samples safely?

- What types of infectious pathogens do you anticipate you will have to handle and how will this this impact the design of your lab and sequencing infrastructure you will need?

- What kind of sequencing platform(s) do you plan to use, and how will you decide which one(s) are best for your particular research needs?

- What computational resources will you need to process and analyze your sequencing data, and how will you acquire and manage these resources?

- Given what you currently know about requirements for sequencing what additional infrastructure or equipment would be required in your setting to successfully carry out Next Generation Sequencing and why?

Task 1, scenario 3
You are tasked with setting up Next Generation Sequencing platform in your laboratory for surveillance multi drug-resistant tuberculosis or MDR TB within the National Program. Your Ministry of Health would like to understand origin and spread of multi-drug resistant tuberculosis within your healthcare system and the community.

- What kind of sample preparation methods do you plan to use, and what lab infrastructure do you need to have in place to process those samples safely?

- What types of infectious pathogens do you anticipate you will have to handle and how will this this impact the design of your lab and sequencing infrastructure you will need?

- What kind of sequencing platform(s) do you plan to use, and how will you decide which one(s) are best for your particular research needs?

- What computational resources will you need to process and analyze your sequencing data, and how will you acquire and manage these resources?

- Given what you currently know about requirements for sequencing what additional infrastructure or equipment would be required in your setting to successfully carry out Next Generation Sequencing and why?

Task 2 Scenario

You are tasked with setting up a Next-Generation Sequencing platform in your laboratory for surveillance multi drug-resistant tuberculosis (MDR-TB) within the National Program. You have a choice between various platforms including Illumina MiSeq and the Oxford Nanopore Technologies MinION platform. Discuss the differences between the two and factors you would consider in your choice.

The platforms

Illumina MiSeq

The **Illumina MiSeq** is a popular next-generation sequencing (NGS) platform that allows for high-throughput DNA sequencing. The setup of an Illumina MiSeq platform typically involves several requirements, including:

MiSeq Instrument: The primary requirement is the Illumina MiSeq instrument itself, which is a benchtop sequencer that performs the sequencing run. The instrument requires proper installation, calibration, and maintenance as per the manufacturer's instructions.

MiSeq Reagent Kit: The appropriate Illumina MiSeq reagent kit is required for the sequencing run, which includes sequencing reagents, primers, and flow cells. The specific reagent kit depends on the type of sequencing to be performed, such as DNA sequencing, RNA sequencing, or targeted sequencing.

MiSeq Flow Cell: The MiSeq flow cell is a consumable component of the instrument that contains the surface where sequencing occurs. It should be properly installed according to the manufacturer's instructions.

Library Preparation: DNA or RNA samples to be sequenced on the MiSeq need to be prepared as libraries, which involves several steps such as DNA or RNA extraction, library construction, and library amplification. The library preparation protocols may vary depending on the type of sequencing and the specific library preparation kit used.
Quality Control: Proper quality control measures should be implemented to ensure the integrity of the DNA or RNA samples, as well as the library preparation process. This may include assessing the quantity and quality of the DNA or RNA samples, as well as library size distribution and concentration measurement.

Sequencing Run Setup: The sequencing run on the MiSeq requires the setup of a sequencing recipe, including the selection of the appropriate reagent kit, sequencing parameters, and sample indexing. This is typically done using the MiSeq control software provided by Illumina.

Bioinformatics Analysis: After the sequencing run is completed, the raw sequencing data generated by the MiSeq needs to be analyzed using bioinformatics software for data processing, alignment, and variant calling, depending on the specific research or clinical application.

Proper Laboratory Conditions: The Illumina MiSeq instrument requires a controlled laboratory environment with stable temperature and humidity levels. The instrument should be installed on a level bench or table with proper power supply and ventilation.

MinION from Oxford Nanopore Technologies

The **MinION** from **ONT** is a portable next-generation sequencing (NGS) platform developed by Oxford Nanopore Technologies. The setup of a MinION platform involves several requirements, including:

MinION Device: The MinION device itself is the primary requirement, which is a portable, handheld sequencer that performs the sequencing run. The MinION device requires proper setup, including charging the device, installing the appropriate flow cell, and connecting it to a compatible computer or mobile device.

Flow Cells: The MinION platform uses disposable flow cells that contain nanopores where the sequencing occurs. The appropriate type of flow cell should be selected depending on the specific application, such as DNA sequencing, RNA sequencing, or direct RNA sequencing. Flow cells should be properly handled and used in accordance with the manufacturer's instructions.

Reagents: Oxford Nanopore Technologies provides a variety of reagents for library preparation and sequencing on the MinION platform, including library preparation kits,

sequencing kits, and other consumables. The specific reagents required will depend on the type of sequencing being performed and the specific library preparation method used.
Library Preparation: DNA or RNA samples to be sequenced on the MinION need to be prepared as libraries, which involves several steps such as DNA or RNA extraction, library construction, and library amplification. The library preparation protocols may vary depending on the type of sequencing and the specific library preparation kit used.

Quality Control: Proper quality control measures should be implemented to ensure the integrity of the DNA or RNA samples, as well as the library preparation process. This may include assessing the quantity and quality of the DNA or RNA samples, as well as library size distribution and concentration measurement.

Sequencing Run Setup: The sequencing run on the MinION requires the setup of a sequencing recipe, including the selection of the appropriate sequencing kit, sequencing parameters, and sample indexing. This is typically done using the Oxford Nanopore Technologies' MinKNOW software, which runs on a connected computer or mobile device.
Bioinformatics Analysis: After the sequencing run is completed, the raw sequencing data generated by the MinION needs to be analyzed using bioinformatics software for data processing, alignment, and variant calling, depending on the specific research or clinical application. Oxford Nanopore Technologies provides several software options, such as Albacore, Guppy, and others, for data analysis.

Proper Laboratory Conditions: While the MinION is a portable device, it still requires a controlled laboratory environment with stable temperature and humidity levels. The device should be used on a clean, level bench or table with proper power supply and ventilation.

It's important to note that the requirements for setting up a MinION platform may vary depending on the specific version of the device and the application being performed. It's always recommended to consult the manufacturer's instructions, protocols, and guidelines for the proper setup and operation of the MinION platform.

The ONT MinION Vs Illumina MiSeq

Platform Size and Portability: The MinION is a portable handheld sequencer that can be used in various locations, including in the field, due to its small size and portability. On the other hand, the MiSeq is a benchtop sequencer that requires a dedicated laboratory space with appropriate infrastructure, such as a stable power supply, temperature control, and ventilation.

Flow Cells vs. Reagent Cartridges: The MinION uses disposable flow cells that contain nanopores where the sequencing occurs, while the MiSeq uses reagent cartridges that contain all the necessary reagents for library preparation and sequencing. Flow cells in the MinION need to be properly handled and installed, while reagent cartridges in the MiSeq are replaced before each sequencing run. Flow cells can be reused this is not the case with MinION Cartridges. Both cartridges and flowcells are required to be stored at specific temperatures so refrigeration and the ability to maintain cold chain is required.

Library Preparation: The library preparation protocols for the MinION and the MiSeq differ. However, what is required in terms of laboratory equipment and reagents for initial library preparation steps are very similar outside of reagent kit-specific enzymes or reagents.

Bioinformatics Analysis: The bioinformatics analysis for data processing, alignment, and variant calling may also differ between the MinION and the MiSeq, as they generate different types of sequencing data. The MinION generates long-read data with base-called sequences, while the MiSeq generates short-read data in paired-end or single-end formats. Therefore, the bioinformatics analysis pipelines and software used for data analysis may vary accordingly.

Laboratory Infrastructure: The laboratory infrastructure requirements for the MinION and the MiSeq may also differ. The MinION, being a portable device, can be used in a variety of laboratory settings with basic requirements for power supply and ventilation. The MiSeq, being a benchtop sequencer, requires a dedicated laboratory space with appropriate infrastructure, including a stable power supply, temperature control, and ventilation, both require specific sequencing consumables.

Something to note on throughput: *Whilst traditionally, Oxford Nanopore have concentrated on small-throughput sequencers such as the MinION, they also produce larger scale platforms, such as the GridION and PromethION. The costs for these are on a par with the same-sized Illumina machines. Conversely, Illumina is now manufacturing smaller models, such as the iSeq, which cost less than the traditional MiSeq models. The flexibility of these platforms may influence your decision about 'futureproofing' your sequencing plan.*

Chemistries

MinION Flow Cells: The MinION flow cells use a nanopore-based sequencing technology, where a single-stranded DNA molecule is threaded through a nanopore, and the DNA bases passing through the nanopore are detected in real-time as electrical signals. The MinION flow cells contain arrays of nanopores, and each nanopore can be used for multiple sequencing events, allowing for long read lengths.

MiSeq Cartridges: The MiSeq cartridges use a sequencing-by-synthesis (SBS) chemistry, which is based on reversible terminator chemistry. In this approach, DNA molecules are sequenced using fluorescently labelled reversible terminators that are incorporated into the growing DNA strand during DNA synthesis. After each cycle, the fluorescent label is detected, and the reversible terminator is chemically cleaved to allow for the next round of DNA synthesis. The MiSeq cartridges contain reagents for library preparation, cluster generation, and sequencing, and they are replaced before each sequencing run.
It's important to note that the chemistries used in MinION flow cells and MiSeq cartridges are fundamentally different, and they have their own advantages and limitations. MinION nanopore sequencing is known for its ability to generate long reads, which is useful for applications such as de novo genome assembly, structural variant detection, and characterization of complex regions of the genome. MiSeq SBS sequencing, on the other hand, generates shorter reads but typically has higher accuracy and is well-suited for applications such as targeted sequencing, amplicon sequencing, and small genome sequencing.

Analytical Considerations

Advantages of MinION (Oxford Nanopore Technologies):

Long Read Lengths: MinION generates long reads, often spanning several kilobases or even longer, which can be advantageous for applications such as de novo genome assembly, structural variant detection, and characterization of complex regions of the genome.

Real-time Sequencing: MinION provides real-time sequencing, allowing for rapid data generation and on-the-fly data analysis, which can be useful for certain applications, such as real-time pathogen identification or field-based sequencing.

Portability and Flexibility: MinION is a portable handheld sequencer that can be used in various locations, including in the field, due to its small size and portability. It offers flexibility in library preparation protocols and can be used with a variety of sample types, including DNA, RNA, and direct RNA sequencing.

Rapid Turnaround Time: MinION can provide relatively rapid turnaround times for sequencing, as library preparation and sequencing can be completed in a matter of hours, depending on the application and library preparation method.

Lower Instrument Cost: MinION has a relatively lower upfront instrument cost compared to Illumina sequencers, making it more accessible for smaller research labs or projects with budget constraints. A MinION starter pack usually costs around $1000, but you will need to consider computing costs too. Because it is relatively cheap, a MinION device could be installed in multiple regional laboratories, rather than just in a single central one.

Disadvantages of MinION:

Lower Sequencing Accuracy: MinION has lower sequencing accuracy compared to Illumina sequencers, with higher error rates in base calling, insertion, and deletion errors. This can impact applications that require high accuracy, such as variant calling and precise genome annotation.

Higher Sequencing Error Rates in Homopolymer Regions: whilst the long reads can span repeated regions better than short read sequencing, the MinION device can have higher error rates in homopolymer regions, which are stretches of repeated nucleotides, when basecalling, resulting in challenges in alignment in these regions.

Limited Throughput: The MinION device has lower throughput compared to Illumina sequencers, as it can generate fewer reads and lower data output per run, which may not be suitable for projects requiring high coverage or large-scale sequencing. This is very dependent on the library preparation kits used, or what you plan to sequence, but generally, you can sequence ~12-24 whole genomes on a MinION.

Advantages of MiSeq (Illumina):

High Sequencing Accuracy: MiSeq generates highly accurate sequencing data with low error rates, making it suitable for applications that require high accuracy, such as variant calling and precise genome annotation.

High Throughput: The MiSeq has higher throughput (up to 96 whole genome samples) compared to the MinION device, as it can generate a large number of reads and higher data output per run, making it suitable for projects requiring high coverage or large-scale sequencing.

Disadvantages of MiSeq (Illumina):

High start-up costs: The MiSeq can cost around $60,000 to set up, but does not require the additional purchase of a powerful computer to run the sequencing.

Not real-time: Once you start a sequencing run (which can be hours to days long), you will have to wait until the run has finished to access and analyse the data.

Not portable: The MiSeq is a large, heavy machine and would not be suitable for field use! Due to its cost, it is likely that a single MiSeq machine at a central laboratory would service multiple regional centres.

It's important to note that both the MinION and the MiSeq have their own advantages and limitations, and the choice of platform depends on the specific research or clinical application, budget, and other factors. It's always recommended to consult the manufacturer's instructions, protocols, and guidelines for the proper setup and operation of the respective NGS platforms.

Task 3, scenario 1

Biosafety: e.g. You are requested to sequence Tuberculosis samples but only have a Biosafety Level 3 (BSL3) laboratory. How do you work around that?

Task 3, scenario 2

Limited Physical Space e.g. You have challenges with space or lay out of the lab that creates problems with having a unidirectional workflow.

How do you work around that?

Task 3, scenario 3

Limited Internet Connectivity: You have challenges with Internet connection at your site. How would you account for this in your setup e.g. what platform would you order?

Scenario 4

Budgetary Constraints: You have challenges procuring SPRI beads or other consumables due to budgetary constraints. How do you work around it?

Day 2 Session 4 - Translating to own contexts - sample to sequencing

1. On LMS, assess the provided checklists found on the toolkit
2. Identify challenges to implementing the checklist and write them down
3. Individually, elaborate/adapt your own checklist

4. Indicate one of the challenges you would have to implement any methods, infrastructure or competencies and propose a solution.
5. Deadline for the assignment 12 Jun 2023

Day 2 Session 5 - Design genomics training - from specimen to sequencing

Example 1
What activities you could apply to evaluate if the participants can determine sample types for each test/analysis? (10 min discussion)

Example 2
What other learning outcomes (LO) this session could have?
How would you design activities and evaluations for each LO?
In a group, propose **one** new learning outcome, activity and assessment (10 min discussion)

Example:

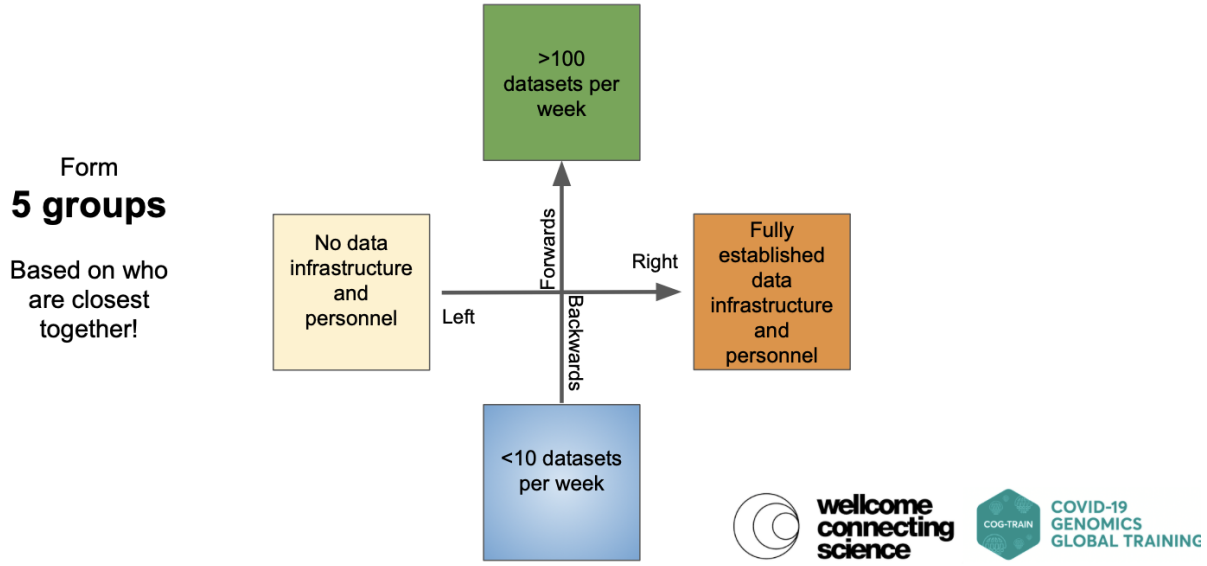
Expected (Learning) Outcome	**Activities and assessment**
Reproduce good practices of pipetting when loading a flow cell	Show the trainee(s) good practices when pipetting the how it affects the loading of flowcells, including potential pitfalls and troubleshooting. Ask the trainee to load a dummy flowcell and observe their technique. Ask what they could do to improve their technique or to avoid mistakes. Ask them to repeat the loading 3 times and to identify if they are improving and becoming more confident on the technique.

Day 3 - Data tools and pipelines

Day 3 - Wednesday 10 May - Data tools and pipelines		
08:00 - 08:30	Day recap	ALL
08:30 - 09:30	Setting up data infrastructure, processes	George Githinji; Aquilla Kanzi; Gerald Mboowa; Leigh Jackson; (Jorge Batista Da Rocha);
09:30 - 10:30	Genomic data workflows, analysis, linkage, integration, analysis, interpretation	Stanford Kwenda; Kirsty Lee Garson; (Fatma Guerfali); George Githinji; Leigh Jackson; Amadou Diallo
10:30 - 11:00	Coffee break	
11:00 - 13:00	Genomic data workflows, analysis, linkage, integration, analysis, interpretation cond.	Stanford Kwenda; Kirsty Lee Garson; (Fatma Guerfali); George Githinji; Samuel Oyola; Amadou Diallo; Leigh Jackson; (Jorge Batista Da Rocha)
13:00 - 14:00	Lunch	
14:00 - 15:00	Data science for public health tools	Kirsty Lee Garson; Aquilla Kanzi (Fatma Guerfali); Leigh Jackson
15:00 - 16:00	Workshop Translating to own contexts - data	Stanford Kwenda; Kirsty Lee Garson; George Githinji; Aquilla Kanzi; Samuel Oyola;Amadou Diallo; Leigh Jackson; (Jorge Batista Da Rocha)
16:00 - 16:30	Coffee break	
16:30 - 17:45	Designing training for data analysis - tools and resources	Leigh Jackson; Stanford Kwenda; Kirsty Lee Garson; George Githinji; Aquilla Kanzi; Samuel Oyola; Alice Matimba; (Jorge Batista Da Rocha)
17:45 - 18:00	End of day reflection	ALL

Day 3 Session 1 - Setting up data infrastructure and processes

Needs Assessment Activity: Sort into groups by moving across the room according to the needs or characteristics of your research teams



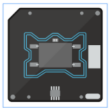
Activity: Manage computer infrastructure for analysis

You are the Lead Data Manager for your analysis team:

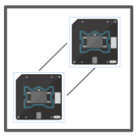
1. You have been given a defined dataset of sequencing data to analyse
2. Purchasing equipment and setup is instant in this scenario!
3. Process as many samples in a 24-hour day as possible
4. Create a system to process the data so your team can begin analysis!

Based on the cost and performance sheet and the group breakdowns:

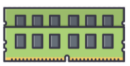
Costs and Performance Sheet:



Single CPU:
1 Sample per hour
Costs $200



Dual core CPU:
2 samples per hour
Costs $300



RAM:
Each sample running through the workflow requires 4GB of RAM
Cost: $50 for 8GB RAM

Storage:
Each sample is 10GB in sizes
The output of each analysis is 5GB in size
Cost: $50 for 500GB storage

Rent Cloud Computing:
The cloud can process 3 samples per hour
Costs: $50 per hour for running
Costs: $20 per 1000GB of data stored
The cloud is hosted in USA

wellcome connecting science
COG-TRAIN COVID-19 GENOMICS GLOBAL TRAINING

Group Tasks

Group 1: Budget = $500	Group 2: Budget = $750	Group 3: Budget = $1200	Group 4: Budget = $2000	Group 5: Budget = $400
Number of Samples: 24	Number of Samples: 48	Number of Samples: 72	Number of Samples: 100	Number of Samples: 10
Condition: All data must be backed up once	Condition: Input files must be deleted	Condition: Power cuts 12hrs per day	Condition: The data is sovereign	Condition: Outputs must be backed up once

wellcome connecting science
COG-TRAIN COVID-19 GENOMICS GLOBAL TRAINING

Day 3 Session 2 - Data workflows for analysis and interpretation

Activity 1 + 2:
Follow the outlined instructions from the session leads for the activities of this session.
Participate in quizzes and engage in discussions with your groups.

General activity:
You are the data management group for a response to an outbreak of Marburg virus

- Work with your groups to design an analysis workflow
- You have to process 10 samples per day and diagnosis is critical
- You have access to human resources and budget for equipment
- But not infinite budgets! You will be audited after
- Simplicity and speed are priorities

Day 3 Session 3: Data science for public health tools

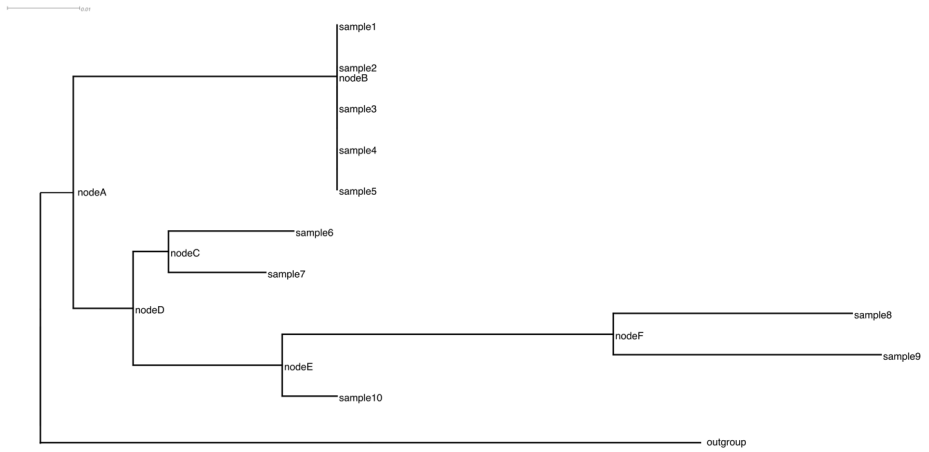
You will review case examples, use the post-it notes and show your view on these based on the instructions from the session leads.

Day 3 Session 4: Translate to your own contexts

1. On LMS, assess the provided checklists for Day 3 found on the toolkit
2. Identify challenges to implementing the checklist and write them down
3. Individually, elaborate/adapt your own checklist
4. Indicate one of the challenges you would have to implement any methods, infrastructure or competencies and propose a solution.
5. Deadline for the assignment 12 Jun 2023

Day 3 Session 5: Design training for data analysis

Activities:
Phylogenetics Multiple choice - work in groups and answer the following:



Question 1. based on the tree above, what internal node corresponds to the most recent common ancestor of samples 8 and 10:

- Node F
- Node D
- Sample 7
- Node E

Question 2. Based on the tree above, which group of samples are most closely related:

- Samples 1 to 5
- Samples 6 & 7
- Samples 6 to 10
- Samples 8 & 9

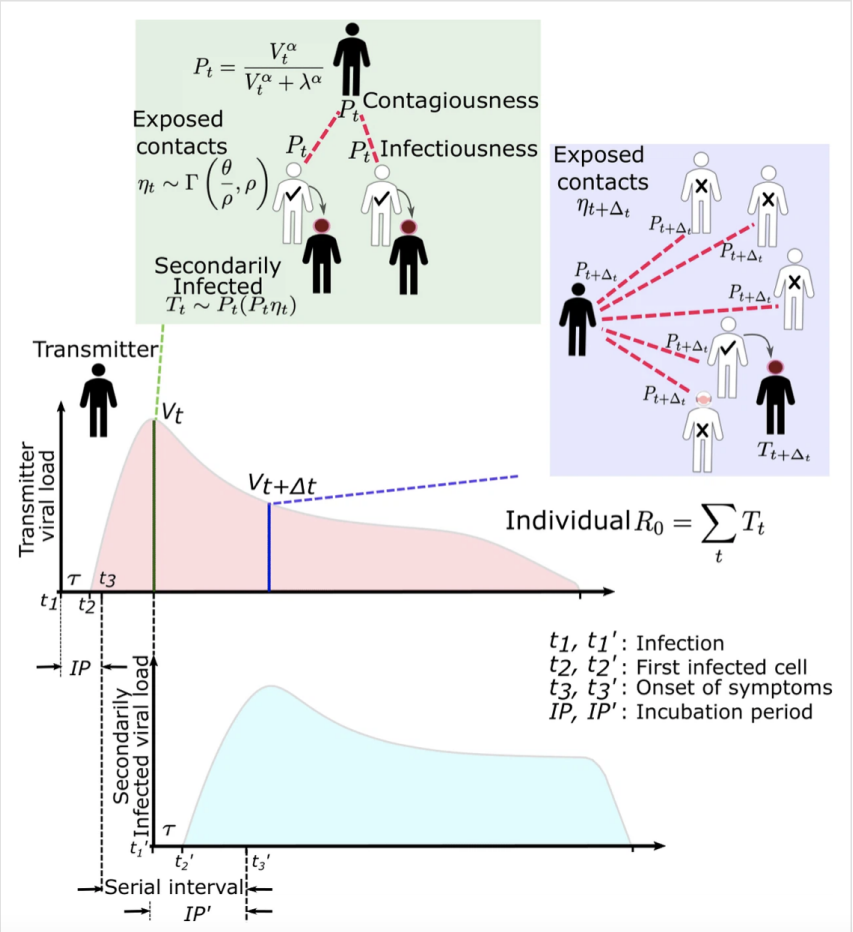
List in your groups (8mins)
A.) What are the benefits of using this activity to teach phylogenetics?
B.) What are the challenges in using such an activity?
C.) How would you improve on this activity?

Each group then reports back 1 point regarding the above questions (5 mins)

Group Activity: Data Visualisation (10 mins)

SARS-CoV-2 and influenza transmission model schematic.

https://elifesciences.org/articles/63537



Evaluate this figure and answer the following questions:
A.) Who is the intended audience for this figure?

B.) What would you require to train participants to make a figure such as this in terms of:

- Software?
- Computational resources?
- Input data?
- Trainer Expertise?

Day 4 - Frameworks, guidelines, communication and decision-making

Thursday 11 May - Frameworks, guidelines, communication & decision-making		
08:00 - 08:30	Day recap	ALL
08:30 - 09:00	Frameworks and guidelines for pathogen genomics	Aquilla Kanzi; Shavanthi Rajatileka
09:00 - 10:30	Ethics of Specimen and Data sharing	Leigh Jackson; Kareemah Suleiman; Emmanuel Chukwuemeka; Francis Chikuse; Gerald Mboowa
10:30 - 11:00	Coffee break	
11:00 - 13:00	Building sustainable models - Funding, Resources, Stakeholders, Skills	Stanford Kwenda; Kirsty Lee Garson; Samuel Oyola; Harris Onywera; Dawwol Wol; Luria Leslie Founou; Amadou Diallo
13:00 - 14:00	Lunch	
14:00 - 16:00	Communication of genomic data and public health decision-making	Tapfumanei Mashe; (Fatuma Guleid); Sam Oyola; Francis Chikuse; Alice Matimba; Treasa Creavin; Abebe Assefa; Invited guests -
16:00 - 16:30	Coffee break	
16:30 - 17:30	Communication of genomic data and public health decision-making cond.	Tapfumanei Mashe; (Fatuma Guleid); Sam Oyola; Francis Chikuse; Alice Matimba; Treasa Creavin; Abebe Assefa; Invited guests -
17:30 - 18:00	Introduction to Projects	ALL

Day 4 Session 1 - Framework, guidelines and policies

Activity 1
Briefly describe frameworks, guidelines and policies that have been implemented in your genomics laboratory.

Day 4 Session 2 Ethics of specimen and data sharing

Small Group Activity 1

- Requirements for ethical approval of research in your institute, country or subject area
- How requirements for ethical approval might change during an epidemic emergency
- Is there a way to have pre-approved protocols to reduce the time required for ethical approval?
- How could you design such a protocol to be flexible to different pathogens?

Small Group Activity 2

- What are the markers of equity and fairness in collaborations?
- To what extent are these markers fixed or flexible during outbreaks?
- How might a public health collaboration agreement look both within a country and internationally?

After discussing these issues, draft an agreement containing the key issues important to your group.

Small Group Activity 3

- Identify important ethical issues which you have encountered within your area of work, which are shared amongst your group and are any unique?
- Are there any additional issues that arise during outbreaks?
- How might you overcome or mitigate some of these issues?

Generate a checklist of things to consider to minimise ethical problems during the next outbreak or large-scale use of genomics in your field of interest

Day 4 Session 3 - Building sustainability - Resources, Stakeholders, Skills

Q1. Leveraging existing systems: What are the opportunities for leveraging existing public health and genomics initiatives to strengthen and implement pathogen genomics and surveillance? *(Notes: existing platforms for surveillance, research consortia, geopolitical environments e.g. Africa CDC)*

Q2. Funding: Where does funding come from? What strategies are effective in sourcing funding? What are some experiences (positive and negative in sourcing funding for genomics in public health?

Q3. Skills: How can training and professional skills development be improved towards developing a sustainable workforce?

Q4. Research: What are gaps and opportunities in research which could inform better practices (Quality management, Data sharing models which support sustainability, implementation research)

Q5. Role of stakeholders: What is the role of stakeholders in ensuring sustainability? *(Notes: Funders, companies, academic institutes, ministries, global collaborators)*

Day 4: Session 4 - Communication for public health decision-making

World Café setting and activities

Participants will be in groups of 5-6. Each group will have at least one of you as a key stakeholder. The stakeholder role is to coach and advise the group on how to present evidence with public health implications relevant to your backgrounds and departments. The stakeholders will also be invited to comment on the presentations made by the groups and participate generally throughout the session discussions.

Presenting Evidence Activity

Participants will work with the stakeholders at your table to draft a presentation for evidence based on findings from genomic analysis. There is a cholera outbreak in your country that may be transmitted across countries in your region. You lead the pathogen genomics surveillance team within the public health system. You have been requested to respond to this outbreak. You have coordinated the sample collection and referral. You have analysed the data and identified a strain. You are now required to present the evidence to the public health authorities and associated stakeholders. The evidence will inform public health response and may have implications for treatment. *(Notes: In preparing the statement reflect on what level of detail your stakeholder needs, are there things you need to know that they don't need to know).*

The evidence presentation should have brief statements of the following items

- What is the background?
- What did you do to generate the evidence?
- What were your findings?
- What does it mean?

Stakeholders

Dr. Getachew Tollera	EPHI Director
Dr. Mebratu Messebo	Ethiopia Ministry of Health
Saro Abdella	EPHI Head of Genomics Facility
Dr. Naod Wendrad	Ministry of Health
Dr Francis Chikuse	Africa CDC

Exercise 1 Worksheet: KT audience and goals

Please read the provided case study carefully. Imagine you are the researchers who conducted this study and you now want to share the findings as you believe they are important. You decide to design a KT strategy to help you with this. In this exercise, you will identify the target audience for this. Consider all audiences who need to know about this work and what you know about them (e.g are they open to change/listen to you? Is the research important to them? Would they be potential blockers of your work? etc). Note, you may identify different audience groups.

Audiences	
Who are they?	What do I know about them?

Identifying your goals:

Pick goals for each of the target audiences you have highlighted above. You might have different goals for the different audiences. When choosing a goal think of what level of action your goal is targeting i.e. increasing awareness, supporting decision-making, implementing something etc. Use those words where possible in your goals. Pick 2-3 goals for each target audience from the ones that you think are most important. List them below. Number 1 is the most important.

Example goals: awareness, learning, policy/practice change, behaviour change etc.

Exercise 2: Crafting messages

Using the case study provided, craft your findings, implications, and recommendation. Keep your messages short, concise, and clear. Use lay and easy to understand language. For this exercise, assume you are communicating with a policy audience only.

Finding/s

** stick to the findings that are most relevant and useful to your audience

Implications

** this section provides the “so what?” of your findings

Recommendations

** use action language e.g should, provide, implement etc. Also, mention *who* should take the action

Day 5 - Projects, networks and action planning

Day 5 - Friday 12 May - Projects, networks and action planning		
08:00 - 08:30	Day recap	ALL
08:30 - 10:30	Outline - Plan a genomics capacity project	Alice Matimba; Liã Bárbara Arruda; Leigh Jackson; Amadou Diallo; Shavanthi Rajatileka; Kirsty Lee Garson; Sam Oyola
10:30 - 11:00	Coffee break	
11:00 - 13:00	Present - Plan a genomics capacity project	ALL
13:00 - 14:00	Lunch	
14:00 - 15:30	Action planning - networks and mentorship	Stanford Kwenda; Luria Leslie Founou; John Tembo; Dawwol Wol; Shavanthi Rajatileka; Amadou Diallo; Treasa Crevin; Harris Onywera
15:30 - 16:00	Workshop wrap-up	ALL
16:00 - 16:30	Coffee & end of workshop	ALL
End of the workshop		