

Week 1: Foundational Skills					
	Monday	Tuesday	Wednesday	Thursday	Friday
Column 1	08/06/2026	17/08/2026	18/08/2026	19/08/2026	20/08/2026
	Infrastructure and Linux	Linux	R	R	R
Time					
8:30 - 9:00	Admin	Admin	Admin	Admin	Admin
09:00 - 10:30	Introductions and Student F	Advanced Linux	R Basics recap	R statistics	R scripting
10:30 - 11:00	Tea	Tea	Tea	Tea	Tea
11:00 - 12:00	Flash talks continued and H	Advanced Linux	Data in R	R statistics	R scripting
12:00 - 13:00	High performance computir				
13:00- 14:00	Lunch	Lunch	Lunch	Lunch	Lunch
14:00 - 15:30	High performance computir	Advanced Linux	Data wrangling in R	R visualisation	R markdown/github
15:30 - 16:00	Tea	Tea	Tea	Tea	Tea
16:00 - 17:30	Linux basics recap	Advanced Linux	Data wrangling in R	R visualisation	R markdown/github

Week 2: Human Genomics (Parallel Stream)					
	Monday	Tuesday	Wednesday	Thursday	Friday
Column 1	24/07/2026	25/07/2026	26/07/2026	27/07/2026	28/07/2026
Time					
8:30 - 9:00	Admin	Admin	Admin	Admin	Admin
09:00 - 10:30	Introduction to Human Genomics: Overview of data QC and analysis workflow. Human NGS read alignment strategies, alignment algorithms, and alignment file formats (SAM/BAM)	Variant filtering and exploration – Single-sample and multisample VCF files Introduction to workflow automation using Nextflow	Phasing concepts and practical example using 1000 Genomes Project data	Introduction to structural variation, including structural variants (SVs) and copy number variants (CNVs), followed by analytical approaches.	Final questions, troubleshooting, and course wrap-up.
10:30 - 11:00	Tea	Tea	Tea	Tea	Tea
11:00 - 13:00	Practical: Read alignment using BWA-MEM, followed by assessment of alignment quality and coverage metrics.	Practical: human variant calling workflow automation using Nextflow	Overview of long-read sequencing technologies and data analysis tools	Practical: Structural variant calling and annotation	Course assessment
13:00- 14:00	Lunch	Lunch	Lunch	Lunch	Lunch
14:00 - 15:30	Principles of human variant calling, variant types, variant quality metrics, and introduction to VCF files. Practical: Variant calling practical using GATK HaplotypeCaller, followed by exploration and interpretation of variant call outputs.	Principles of variant annotation, annotation resources, population databases, and functional prediction tools. Introduction to variant interpretation, the ACMG/AMP guidelines, and evidence used for variant classification.	Practical: Oxford Nanopore read alignment and variant calling	Practical: Structural variant calling and annotation (continued)	General discussion, participant feedback, and recommended resources for further learning.
15:30 - 16:00	Tea	Tea	Tea	Tea	Tea

16:00 - 17:30	Variant calling practical (continued). Troubleshooting, discussion, and recap.	Practical: Variant annotation, filtering strategies, and prioritisation of candidate variants. Case study on variant interpretation and candidate variant prioritisation.	Practical: Long read variant phasing. Discussion and recap	Discussion and recap	Closing remarks.
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Week 2: Pathogen Genomics (Parallel Stream)					
	Monday	Tuesday	Wednesday	Thursday	Friday
08:30 - 09:00	24/07/2026	25/07/2026	26/07/2026	27/07/2026	28/07/2026
09:00 - 10:30	Intro to Pathogen Genomics (Epidemiology frameworks and sequencing data types)	SARS-CoV-2 Variant Calling (Amplicon sequencing, primer schemes, and variant types)	Klebsiella Genomics & Assembly (Plasmid biology, de novo assembly vs. mapping strategies)	Phylogenetic Reconstruction (Multiple sequence alignment and Maximum Likelihood inference)	Capstone Briefing (Introduction to Viral vs. Bacterial assessment tracks)
10:30 - 11:00	Tea	Tea	Tea	Tea	Tea
11:00 - 12:00	Read Quality & Alignment Theory (Quality control metrics and filtering)	Viral Lineage & Automated Pipelines (The ARTIC protocol design)	Antimicrobial Resistance (Mechanisms of resistance and virulence)	Epidemiological Visualisation (Linking metadata to trees)	Dataset Allocation & Planning (Accessing evaluation data on HPC)
12:00 - 13:00	Read Quality & Alignment Theory (Reference mapping mechanics on HPC)	Viral Lineage & Automated Pipelines (Phylodynamic nomenclature via Nextstrain)	Antimicrobial Resistance (Database structures including NCBI and ResFinder)	Epidemiological Visualisation (Spatial-temporal tracking principles)	Dataset Allocation & Planning (Analytical pipeline design validation)
13:00 - 14:00	Lunch	Lunch	Lunch	Lunch	Lunch
14:00 - 15:30	Quality Control (Run FastQC, FastP, and aggregate with MultiQC)	Viral Variant Extraction (Variant calling and consensus generation with iVar and BCFTools)	Bacterial Assembly Workflows (Deploying the automated Bactopia pipeline for Klebsiella)	Tree Building on HPC (Align sequences using MAFFT and infer trees using IQ-TREE)	Capstone Execution (Independent processing of raw SARS-CoV-2 or Klebsiella data)
15:30 - 16:00	Tea	Tea	Tea	Tea	Tea
16:00 - 17:30	Reference Mapping (Read alignment against SARS-CoV-2 reference using BWA-MEM or Bowtie2)	Viral Surveillance Pipelines (Run ARTIC pipeline and visualize via Nextstrain)	AMR & Virulence Profiling (Screen assemblies with AMRFinderPlus and ResFinder)	Genomic Epidemiology Integration (Combine phylogenetic trees with metadata in Microreact)	Project Presentations (Deliver epidemiological insights and course closure)

Week 2: Metagenomics (Parallel Stream)					
	Monday	Tuesday	Wednesday	Thursday	Friday
Column 1	24/07/2026	25/07/2026	26/07/2026	27/07/2026	28/07/2026
Time					
8:30 - 9:00	Admin	Admin	Admin	Admin	Admin
09:00 - 10:30	Introduction to metagenomics approaches (shotgun vs amplicon); overview of sequencing platforms.	Diversity metrics: Alpha (richness, evenness, phylogenetic diversity); Beta diversity (Ordination techniques, PERMANOVA). Rarefaction.	Recap: shotgun vs amplicon metagenomics; Shotgun metagenomics workflow (from QC, taxonomy assignment, de novo assembly e.t.c)	Metagenome assembled genomes (MAGs) - definition, use cases, challenges. Metagenome Binning techniques.	Introduction to functional analysis of shotgun metagenomics (approaches and applications)
10:30 - 11:00	Tea	Tea	Tea	Tea	Tea
11:00 - 12:00	Experimental design principles; common pitfalls; Applications across fields with examples.	Community-level compositional analysis and Differential abundance analysis.	Read-based taxonomy assignment approaches	The MAG reconstruction pipeline.	Gene prediction (concepts, applications, tools and databases)
12:00 - 13:00	Reference databases; Overview of the analysis workflow for the week	R-based diversity analysis workflow.	Metagenome de novo assembly approaches	Map host-free reads back to assembly with Bowtie2. Convert to BAM with Samtools. Generate contig depth file.	Protein and pathway prediction (tools and databases)
13:00- 14:00	Lunch	Lunch	Lunch	Lunch	Lunch
14:00 - 15:30	Inspect raw FASTQ files: understand FASTQ format; Run FastQC & MultiQC on raw reads and interpret QC plots; Trim and filter reads using fastp; rerun FastQC on clean reads; compare before/after; Import clean reads using QIIME2.	Import features/taxonomy and sample metadata into R; Calculate and visualise alpha diversity metrics; Compare and visualize metrics across by sample groups.	Run FASTQC/MultiQC on shotgun reads. Trim adapters with fastp. Compare before/after QC stats; Remove human reads using Bowtie2 against GRCh38. Count reads before/after. Inspect % host contamination across samples.	Run MetaBAT2 on the assembly. Run MaxBin2 for comparison. Count bins produced by each binner and compare. Combine MetaBAT2 and MaxBin2 bins using DAS_Tool.	Mini project: Tasks and deliverables
15:30 - 16:00	Tea	Tea	Tea	Tea	Tea

16:00 - 17:30	Run DADA2 denoising, assign taxonomy with a pre-built SILVA classifier, generate feature and taxonomy tables.	Compute Bray-Curtis dissimilarity; perform ordination (PCoA/NMDS); run PERMANOVA; Run DESeq2/ANCOM-BC2 and compare results.	Run Kraken2 on cleaned reads. Apply Bracken for species-level abundance; Assemble host-free reads with metaSPAdes/MEGAHIT. Run QUAST for assembly statistics. Filter contigs $\geq$ 1,000 bp with SEQKIT. Compare assemblies.	Compare bin count and quality before and after refinement. Run CheckM2 on refined bins, classify by MIMAG quality tier. Run GTDB-Tk to assign taxonomy. Build summary table in R. Compare the taxonomy obtained here with that obtained using Kraken2/Bracken - Discussion.	Mini project: Presentation and discussion.
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Column 1	Monday	Tuesday	Wednesday	Thursday	Friday
Abridged Schedule	Week 1				
09:00 - 10:30	Introduction and participant flash talks	Linux	Linux	R	R
10:30 - 11:00	TEA Break				
11:00 - 13:00	Participant flash talks continued and HPC setup	Linux	Linux	R	R
13:00 - 14:00	LUNCH Break				
14:00 - 15:30	HPC/Linux?	Linux	R	R	IntroNGS General
15:30 - 16:00	TEA Break				
16:00 - 17:30	Linux	Linux	R	R	IntroNGS General
18:00	Participants depart to the hotel/ Session Ends	Participants depart to the hotel/ Session Ends	Participants depart to the hotel/ Session Ends	Participants depart to the hotel/ Session Ends	Participants depart to the hotel/ Session Ends
	Week 2				
09:00 - 10:30	R/Parallel Streams (1.5 hr)	R/Parallel Streams (1.5 hr)	R/Parallel Steams (1.5 hr)	R/Parallel Streams (1.5 hr)	Participant presentations
10:30 - 11:00	TEA Break				
11:00 - 13:00	Human Pathogen Metagenomics	Human Pathogen Metagenomics	Human Pathogen Metagenomics	Human Pathogen Metagenomics	Participants presentations
13:00 - 14:00	LUNCH Break				

Column 1	Monday	Tuesday	Wednesday	Thursday	Friday
14:00 - 15:30	Human Pathogen Metagenomics	Human Pathogen Metagenomics	Human Pathogen Metagenomics	Human Pathogen Metagenomics	Participant presentations
15:30 - 16:00	TEA Break				
16:00 - 17:30	Human	Human	Human Pathogen	Human	Participant presentations
18:00	Participants depart to the hotel/ Session Ends	Participants depart to the hotel/ Session Ends	Participants depart to the hotel/ Session Ends	Participants depart to the hotel/ Session Ends	Participants depart to the hotel/ Session Ends