WEEK 1: Morning (9-12)	Monday	Tuesday	Wednesday	Thursday	Friday
	Course intro *Short talk (9-9.45)*: ”Welcome and introduction to course” *“Speed-networking”(10-11)*: “Get to know your fellow course participants” *Lecture (11-12)*: “Intro to bash and the unix universe”	**Getting started with Python** *Short talk (9-9.30)*: “Python introduction” *Practical (9.30-10.30):* “Python introduction” *Lecture (10.30-10.50):* “Python as a bioinformatical tool” *Practical (10.50-12)*: “Getting started with python*”*	**Sequencing and raw-data QC** *Lecture (9.00 - 9.30):* “Introduction to sequencing” *Lecture (9.40 – 10.45):* “Overview of sequencing technologies” *Interactive Lecture/Practical (11.00 – 12.00):* “Sequencing Quality”	**Genome assembly** *Lecture (9-9.30):* “Genome assembly strategies” *Practical (9.30 -11):* “Bacterial genome assembly with short reads” *Practical (11-12):* “Basic assembly QC stats”	**Genome assembly** *Lecture (9-9.30):* “Intro to long-read and hybrid genome assembly” *Practical (9.30-11):* “Long-read and hybrid assembly” *Practical (11-12):* “Genome assembly comparison”

WEEK 1: Afternoon (13-16.30)	Monday	Tuesday	Wednesday	Thursday	Friday
	Getting started with the command-line and Bash *Short talk (13-13.20):* Command-line introduction *Practical (13.20-14.20):* Getting started with the command-line *Short talk (14.30-14.45):* Bash introduction *Practical (14.45-16.30)*: Getting started with bash	**Advancing in programming** *Lecture (13-13.20):* "Programming recap and Biopython deep-dive" *Coding session (13.20-16.20):* "Multiple exercises command-line, bash and python" (participants choice) *Lecture (16.20-16.30):* "Programming wrap-up"	**Sequencing and raw-data QC** *Lecture/Practical (13.00-15.00):* "Quality control of sequencing data" *Lecture/Practical (15:00-16.30):* "Contamination control, sample aggregation, and wrap-up"	**Genome assembly** *Lecture/practical (13-14.00):* "Contamination" *Coding session (14.00-16.30): Biopython for assembly analysis*	**Genome analysis intro** *Lecture/Practical (13-15):* "Blast, in-silico MLST and gene annotation" *Coding session (15-16.30):* Biopython continued, or practical catch-up (Participants choice)

WEEK 2: Morning	Monday	Tuesday	Wednesday	Thursday	Friday
	AMR *Lecture (9-10):* "WGS-based detection of antimicrobial resistance (AMR) in bacteria" *Practical (10.20-12)*: "Use of bioinformatics tools and databases for WGS-based detection of AMR in bacteria"	**Getting started with phylogenies** *Lecture (9-10):* "Evolution and phylogenies" *Practical (10.20-12)*: "Sequence handling and alignment"	**Pipeline development** *Lecture (9-9.45):* "Basic principles of automation" *Practical (10.00-11.45):* "Pipeline development – scaling number of tools and samples"	**Data sharing** *Lecture (9-9.45):* "Introduction to sequence databases and data sharing" *Practical (10.00-11.15):* "Uploading raw sequence data to ENA" *Practical (11.15-12):* "Data exploration and retrieval using ENA resources"	**Whats next?** *Lecture (9-9.45):* "Outlook on genome sequencing for disease surveillance" *Site-visits (10-11):* Tour of the sequencing labs at SSI, meet the staff *Mentor-chats (11-12):* Individual chats with participants to discuss continued learning. Free code session for remaining particpants.

WEEK 2: Afternoon	Monday	Tuesday	Wednesday	Thursday	Friday
	Tuberculosis profiling *Lecture (13-14):* "Tuberculosis - the world's deadliest curable disease" *Practical (14-16.30): "M.tuberculosis* outbreak investigation and antibiotic resistance determination with TB-profiler"	**Getting started with phylogenies** *Lecture (13-14):* "Phylogenetic methods" *Practical (14.30-16.30)*: "Inferring phylogenies"	**Pipeline development** *Practical (12.45-15.30):* "Pipeline development – from raw reads to data sharing" *Coding session (15.30-16.30*): Further exercises on writing pipelines (participants choice)	**Data sharing** *Lecture (13-13.45):* "Intro to online tools for genome analysis, data sharing and visualization, developed by ECDC) *Practical (14-16.30):* "Exploring Microreact, EpiPulse and Tessy"	**Whats next?** *Mentor-chats (13-14):* Individual chats with participants to discuss continued learning. Free code session for remaining particpants. *Evaluation survey* (14-14.30): "Course evaluation" *Mingle and wrap-up*