

## Advanced Workshop in Whole Genome Sequence Analysis for Microbial Diagnostics

TIME	Monday 5th of November 2018	Tuesday 6th of November 2018
8:30-9:00	Registration and light breakfast	Light breakfast
9:00-9:15	Workshop and participants introduction	Welcome back and intro
9:15-9:30		Presentation: Read mapping to identify contaminating reads, and SNPs
9:30-9:45	Presentation: Intro to working command line	
9:45-10:00	Ex. 1: Commandline on Mac/Windows	Ex. 5: Read mapping with BWA Id. of depth, contaminating reads, SNPs
10:00-10:15		
10:15-10:30	Ex. 1. recap	
10:30-10:45	Coffee	Coffee
10:45-11:00	Presentation: Amazon Web Service (AWS) - Cloud Computing	Ex. 5, continued
11:00-11:15	Presentation: Linux software installation and repositories	
11:15-11:30	Ex. 2: Initialising and accessing your first AWS instance	
11:30-11:45		Ex. 5. recap
11:45-12:00		Presentation: Intro to PATRIC. Examining identified SNPs
12:00-12:15	Lunch	Lunch
12:15-12:30		
12:30-12:45		
12:45-13:00		
13:00-13:15	Presentation: Short read quality assessment and trimming	Presentation: CGE databases and -methods run commandline
13:15-13:30		Presentation: Docker - software in containers
13:30-13:45	Ex. 3: Short read quality assessment with FASTQC Trimming with Cutadapt	Ex. 6: Running CGE methods command line Simple bash script to run many isolates/methods
13:45-14:00		
14:00-14:15		
14:15-14:30		
14:30-14:45	Ex. 3 recap	Ex. 6. recap
14:45-15:00		
15:00-15:15	Coffee	Coffee
15:15-15:30	Presentation: Assembly and draft genome quality assessment	Presentation: NDtree
15:30-15:45	Ex. 4: Short read assembly with SPAdes Quality evaluation with QUAST  (Long read assembly with minimap2/miniasm/racon)	Ex. 7: Generating phylogenetic trees commandline Tree visualisations
15:45-16:00		
16:00-16:15		Ex. 7. recap
16:15-16:30		
16:30-16:45	Ex. 4 recap	Evaluation and workshop end
16:45-17:00		