

Essential command line bioinformatics and genome analysis

Session	Time	Type	Topic
1	9:30 – 10:30	Onboarding	The Linux / Ubuntu environment
	10:30 – 12:30	Onboarding	Installing an Ubuntu virtual machine
	13:30 – 14:30	Lecture	Command line coding
	14:30 – 16:30	Tutorial	Navigating, copying, cat, grep, paste, awk, etc.
2	9:30 – 10:30	Lecture	Local alignment and BLAST
	10:30 – 12:30	Tutorial	Build and search a BLAST database
	13:30 – 14:30	Lecture	Sequencing and alignment
	14:30 – 16:30	Tutorial	FastQC, Bowtie, SAM tools, IGV
3	9:30 – 10:30	Lecture	Writing pipelines
	10:30 – 12:30	Tutorial	Loops, sample sheets, input options
	13:30 – 14:30	Lecture	Polymorphism
	14:30 – 16:30	Tutorial	VCF tools, Freebayes, snpEFF
4	9:30 – 10:30	Lecture	Population polymorphism, and Visualising
	10:30 – 12:30	Tutorial	Circos and Oncoplot
	13:30 – 14:30	Lecture	Multiple sequence alignment and trees
	14:30 – 16:30	Tutorial	Clustal and Mafft
5	9:30 – 10:30	Lecture	Annotations
	10:30 – 12:30	Tutorial	Annotations
	13:30 – 14:30	Lecture	ChIP-seq, ATAC-seq, Cut and Tag
	14:30 – 16:30	Tutorial	Peak calling, differential peaks
6	9:30 – 10:30	Lecture	RNA-seq alignment
	10:30 – 12:30	Tutorial	Gapped aligners and read counting
	13:30 – 14:30	Lecture	Differential expression
	14:30 – 16:30	Tutorial	DESeq2 and Searchlight2

Please note, after day 3, attendees can skip any of days 4-6 if the topic is not relevant to them. For example, not everyone will be interested in epigenomics on day 5.

More information at: www.immunology.org/training/bioinformatics-training.