

AllGenetics' Training Week 2023

A primer on DNA metabarcoding analysis: from barcodes to biodiversity estimates

Room 1	Sunday	Monday	Tuesday	Wednesday	Thursday	Friday
09:00 - 10:00		Course introduction	Methods and tools to generate OTU/ASV abundance tables	Visualisation and interpretation of DNA metabarcoding results		
10:00 - 11:00		Experimental design, sample processing, library preparation, and sequencing strategies in DNA metabarcoding	Hands-on exercise: Methods and tools to generate OTU/ASV abundance tables	Introduction to diversity and functional analysis		
11:00 - 11:30		Coffee Break	Coffee Break	Coffee Break		
11:30 - 12:30		Choice of marker, primers and taxonomic reference database	Taxonomic assignment	Introduction to diversity and functional analysis		
12:30 - 13:30		Choice of marker, primers and taxonomic reference database	Hands-on exercise: Taxonomic assignment	Wrap up and take home messages; final questions and discussion.		
13:30 - 14:30		Lunch	Lunch	Lunch		
14:30 - 15:30		Data quality control and pre-processing	Post-processing of the taxonomic abundance tables			
15:30 - 16:00		Coffee Break	Coffee Break			
16:00 - 17:00		Hands-on exercise: Data quality control and pre-processing	Hands-on exercise: Post-processing of the taxonomic abundance tables			
17:00 - 18:00		Wrap up / working on your own data	Wrap up / working on your own data			

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Genome assembly: from reads to high-quality chromosome-level genomes

Room 2	Sunday	Monday	Tuesday	Wednesday	Thursday	Friday
09:00 - 10:00		Course introduction	Assembly QC and evaluation- tools and concepts	Hands-on exercise: manual genome curation		
10:00 - 11:00		Designing your whole genome sequencing experiment: from sample to sequences	Hands-on exercise: assembly QC and evaluation	Assembly discussions, questions or consultation on your own data analysis		
11:00 - 11:30		Coffee Break	Coffee Break	Coffee Break		
11:30 - 12:30		Data quality control, pre-processing and introduction to kmer analysis	Post-assembly processing: purging haplotype duplications, decontamination, organelle assembly	Intro to genome annotation: strategies, approaches and pipelines		
12:30 - 13:30		Use of kmers for genome characterisation	Hands-on exercise: purging haplotypes and genome decontamination	Wrap up and take home messages; final questions and discussion.		
13:30 - 14:30		Lunch	Lunch	Lunch		
14:30 - 15:30		Hands-on exercise: data quality control and genome characterisation using with kmer spectra	Using Hi-C data to assemble genomes to chromosome level			
15:30 - 16:00		Coffee Break	Coffee Break			
16:00 - 17:00		Introduction to genome assembly: strategies, approaches and pipelines	Hands-on exercise: scaffold assembly with Hi-C data			
17:00 - 18:00		Hands-on exercise: planning and running a primary assembly	Getting and interpreting our own Hi-C maps			

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Introduction to high-throughput sequencing: Illumina, PacBio, and Oxford Nanopore

	Sunday (Room 1)	Monday	Tuesday (Room 3)	Wednesday	Thursday	Friday
09:00 - 10:30	Introduction to high-throughput sequencing: from Sanger to Nanopore		Introduction to high-throughput sequencing: from Sanger to Nanopore			
10:30 - 11:00	Coffee Break		Coffee Break			
11:00 - 13:30	Sequencing technologies: Illumina, PacBio, and Nanopore		Sequencing technologies: Illumina, PacBio, and Nanopore			
13:30 - 14:30	Lunch		Lunch			
14:30 - 15:30	Applications of high-throughput sequencing, experimental design, and genomic library preparation		Applications of high-throughput sequencing, experimental design, and genomic library preparation			
15:30 - 16:00	Coffee Break		Coffee Break			
16:00 - 18:00	Data quality control		Data quality control			

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Metagenomic analysis: taxonomic and functional profiling from genomic data

Room 1	Sunday	Monday	Tuesday	Wednesday	Thursday	Friday
09:00 - 10:30					Hands-on exercise: data quality control, trimming and host decontamination.	Hands-on exercise: taxonomic and functional annotation.
10:30 - 11:30					Assembly, binning, and MAG generation.	Taxonomic and functional analysis using read-based (assembly-free) approaches.
11:30 - 12:00					Coffee Break	Coffee Break
12:00 - 13:30					Hands-on exercise: Assembly, binning, and MAG generation.	Eukaryotic and viral metagenomics.
13:30 - 14:30					Lunch	Lunch
14:30 - 15:30				Course introduction	Hands-on exercise: Assembly, binning, and MAG generation.	Hands-on exercise: Eukaryotic and viral metagenomics.
15:30 - 16:30				Experimental design, samples processing, genomic library construction, and sequencing strategies in metagenomics	Taxonomic and functional annotation.	
16:30 - 17:00				Coffee Break	Coffee Break	Coffee Break
17:00 - 18:00				Metagenomics bioinformatics	Hands-on exercise: taxonomic and functional annotation.	Wrap up and take home messages; final questions and discussion.
18:00 - 19:00				Data quality control, trimming and host decontamination.		

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RNA-seq data analysis: from raw reads to gene expression						
Room 3	Sunday	Monday	Tuesday	Wednesday	Thursday	Friday
09:00 - 10:00				Course introduction	Quantification of gene expression	Gene annotation and functional enrichment analysis
10:00 - 11:00				Experimental design, sample processing, library preparation, and sequencing strategies in RNA-seq		
11:00 - 11:30				Coffee Break	Coffee Break	Coffee Break
11:30 - 12:30				Data quality control and pre-processing	Hands-on exercise: Quantification of gene expression	Hands-on exercise: Gene annotation and functional enrichment analysis
12:30 - 13:30				Hands-on exercise: data quality control and pre-processing	Differential gene expression analysis	Wrap up and take home messages; final questions and discussion.
13:30 - 14:30				Lunch	Lunch	Lunch
14:30- 16:00				Mapping and assembling RNA-Seq reads	Hands-on exercise: Differential gene expression analysis I	
16:00 - 16:30				Coffee Break	Coffee Break	
16:30 - 18:00				Hands-on exercise: mapping and assembling RNA-Seq reads	Hands-on exercise: Differential gene expression analysis II	