Pan-Genome Analysis: Exploring Core and Accessory Genomic Diversity

Program Overview

This capacity-building program provides an introduction to pan-genome analysis, focusing on core, accessory, and unique genomic components. Through a combination of theoretical principles and hands-on exercises, participants will explore genomic diversity, conduct pan-genome analyses, and confidently interpret results using real bacterial genome datasets and interactive discussions.

- **Duration:** 3 Weeks
- **Contact Sessions:** 2 contacts per week
- **Session Length:** 1.5 – 2 hours per session
- **Mode:** Virtual

Program Benefits

Participants will:

- Gain a strong conceptual foundation in pan-genomics
- Understand how genomic diversity is structured within species
- Understand the significance of pan-genome analysis in evolutionary and applied genomics
- Acquire practical experience with pan-genome analysis workflows
- Develop confidence in interpreting pan-genome results

Program Time Table

WEEK	SESSION	TOPICS COVERED
Week 1	Session 1	**Introduction to Pangenomics** • Definition of pangenomics • Scope and relevance in genomics research (focus on bacteria) • Brief theoretical overview of pangenomics in plants, humans, and animals • Why pangenomics matters
	Session 2	**Key Concepts in Pangenomics** • Core genome • Accessory (dispensable) genome • Unique / strain-specific genes • Highlight concept similarities across bacteria, plants, and animals
Week 2	Session 3	**Pangenomics Workflow** • Overview of pangenome analysis pipelines • Tools and software used (Geneious, BRIG, command-line tools) • Step-by-step workflow of pangenomic analysis • Understanding pangenome outputs

	Session 4	**Genome Data Preparation & Gene Classification (Hands-On I)** • Data collection and selection (bacterial genomes) • Genome assembly • Genome annotation • Identification of core, accessory, and unique genes using Geneious
Week 3	Session 5	**Pangenome Construction & Visualization (Hands-On II)** • Preparation of inputs for pangenome construction • Construction of pangenome using BRIG • Visualization of genomic diversity and gene distribution
	Session 6	**Interpretation & Visualization** • Pan-genome curves • Gene presence/absence matrices • Biological interpretation of results

Program Outcomes

By the end of the program, participants will be able to:

- Explain the concept of pan-genomics and its relevance in genomic research
- Conduct guided hands-on pan-genome analyses
- Identify core, accessory, and unique genes using Geneious software
- Generate pan-genomic visualisations using command prompt and BRIG software
- Interpret pan-genome curves and gene presence/absence matrices.