

Exploring Microbial Diversity Through a Comprehensive Metagenomic Analysis Pipeline

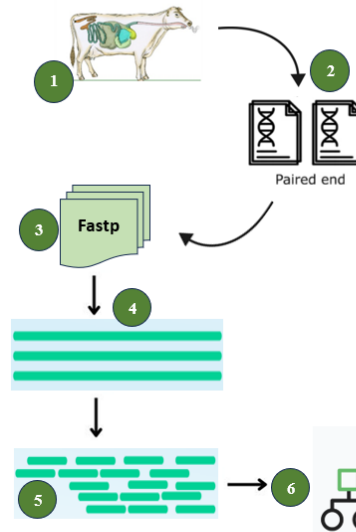


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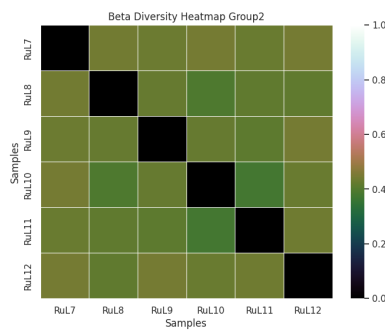
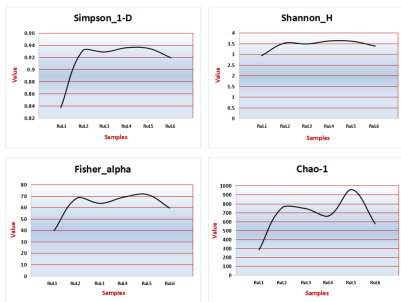
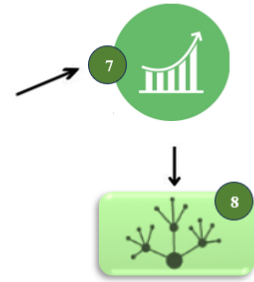
Standard Workflow

Overview
 In this metagenomics analysis, quality checks of the raw reads were conducted, followed by the generation of clean reads. These clean reads were then subjected to metagenome assembly. Taxonomic classification was achieved, revealing the abundance and diversity of bacteria and archaea. This approach provided a comprehensive view of the microbial landscape within our metagenomic dataset.

Motivation
 Discover how metagenomics is revolutionizing animal health, offering personalized care, early disease detection, and enhanced agricultural practices. Join us in shaping a brighter future for animal well-being and environmental conservation through cutting-edge metagenomic insights.



- 1 Cattle Rumen
- 2 Raw Data
- 3 Quality Control (Fastp)
- 4 Clean Data
- 5 Metagenomic Assembly (Megahit)
- 6 Taxonomical classification (Kraken2)
- 7 Comparative and Statistical Metagenomics (Alpha Beta Diversity, PCA, PCoA)
- 8 Functional Metagenomics (Identification of Metabolites, Protein Coding Predictions and Microbial pathway analysis)



- The metagenomic analysis employed Nextflow, a scalable framework, for efficient processing.
- Comparative, statistical, and functional metagenomics analyses are driving advancements in understanding complex ecosystems, aiding in the development of tailored solutions for agriculture, ecological conservation, and human health.
- This analysis signifies the future potential of scalable metagenomics in diverse fields, including agriculture, environment, and health research.

