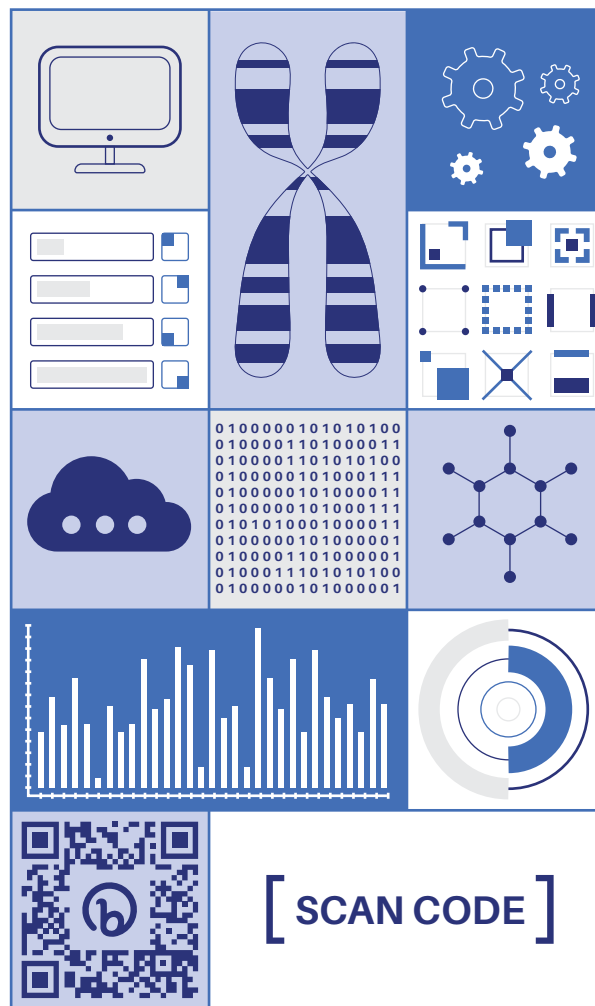




A suite of bioinformatics services from scripting to full project workflows

Core Facility for Bioinformatics (CFB) started as a capability-building project funded by the Department of Science and Technology (DOST) - Philippine Council for Industry, Energy and Emerging Technology Research and Development (PCIEERD). As the project ended in 2014, the core facility was integrated to the day-to-day operations of the Philippine Genome Center servicing researchers and students in Next Generation Sequence (NGS) data analysis, providing technical support, and giving training courses to further increase local competency in bioinformatics.



Contact Us

ADDRESS	Philippine Genome Center Building A. Ma. Regidor Street University of the Philippines Diliman Quezon City 1101, Philippines
LANDLINE	+63 • 2 • 8981 • 8500 local 4706
EMAIL	bioinformatics@pgc.up.edu.ph pgc@up.edu.ph
WEBSITE	https://pgc.up.edu.ph

UNIVERSITY OF THE PHILIPPINES
PHILIPPINE GENOME CENTER

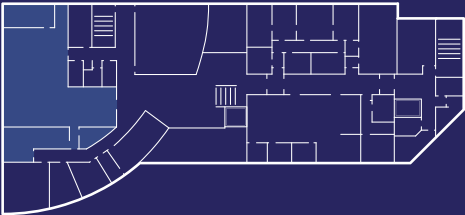
Core Facility for Bioinformatics



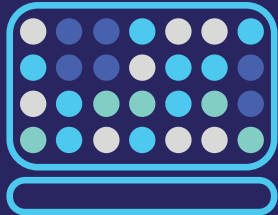
ABOUT THE FACILITY

A suite of Bioinformatics services from scripting to full project workflows. CFB pursues research programs that are relevant to PGC's thrusts, including the development of novel or improved computational techniques (i.e. algorithms) and tools (i.e., software), as well as collaborative research projects that aim to find solutions to complex and computing-intensive problems. The core facility also provides data processing and analytical services for clients wishing to outsource data analysis for their next-generation sequencing data, and make available high-performance computing servers for clients who wish to do their own data analysis.

LOCATION



L2



SERVICES OFFERED

- + Direct Access to High-Performance Computing Clusters
- + Bioinformatics Workshops and Training
- + Custom Bioinformatics Analysis Service

For other related services, send us an inquiry.

DATA PROCESSING AND ANALYSIS

- + Genome and Transcriptome Assembly
- + Variant / SNP Calling
- + Sequence Similarity Search
- + SSR / Microsatellite Search and Primer Design
- + Molecular Phylogenetics
- + Customized Workflows
- + Programming / Scripting

HIGH-PERFORMANCE COMPUTING

Access for analysis and storage of next-generation sequencing data. Software and databases for the following types of analysis are available:

- + NGS Data Quality Control
- + Genome, Transcriptome and Metagenome Assembly
- + Genome Alignment
- + Read Mapping and Variant Calling
- + Genome Annotation
- + Phylogenetic Analysis
- + Data Visualization
- + Statistical Analysis
- + Differential Gene Expression Analysis
- + Targeted (e.g. 16s) Metagenome Analysis
- + Sequence Similarity Search

Additional software can be installed upon request, free of charge.

COMPUTE RESOURCES

NODE NAME	PROCESSOR BRAND	NO. OF CORES	RAM (GB)	AVAILABILITY
cn36	Intel	64	256	All Users
cn37				
cn38				
cn39				
cn41	AMD	32	2048	Upon Request
cn43				

WORKFLOW

Sample
Preparation

Library
Preparation

Sequencing

Initial Data
Processing

Data Analysis