

*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.

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### Contact Us

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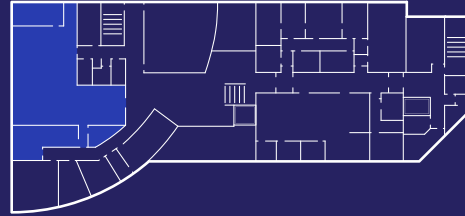
## Core Facility for Bioinformatics



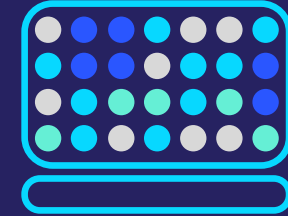
## ABOUT THE FACILITY

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

- + Data Processing and Analysis
- + High-Performance Computing
- + Trainings (available upon request)

*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

NAME	PROCESSOR BRAND	NO. OF CORES	CLOCK SPEED (GHz)	MEMORY (GB)
SMP1	AMD	64	2.4	768
SMP2	AMD	64	2.4	512
Phi1	Intel	32	2.5	64

## WORKFLOW

Sample Preparation

Library Preparation

Sequencing

Initial Data Processing

Data Analysis