SEQUENCING AND BIOINFORMATICS SERVICE OF FISABIO-PUBLIC HEALTH

DESCRIPTION OF THE TECHNOLOGY

During the last 10 years, we have observed an exponential growth and improvement of DNA sequencing methods with the development of Next Generation Sequencing (NGS). Currently, this acronym involves second and third generation methods, better known as high throughput sequencing or massive sequencing. NGS opens nowadays a wide landscape of possibilities in several fields related with biological science and public health.

In order to promote these advances is crucial to have appropriate sequencing platforms as well as trained and experienced staff in these techniques.

In this regard, and with the aim of promoting biomedical research, the Sequencing and Bioinformatics Service of FISABIO-Public Health was launched.

Sequencing facilities

The Sequencing and Bioinformatics Service of FISABIO is equipped with two Illumina MiSeq sequencers. Moreover, it is part of the Oxford Nanopore MinION access program acting as a beta tester of one of the last third generation sequencers. Shortly a NextSeq500 Illumina sequencer will be acquired.

The Service also has independent laboratories equipped with all the needs for biological sample processing, nucleic acids extraction and sequencing libraries preparation.

Computing Infrastructure

The Sequencing and Bioinformatics Service is equipped with the appropriate IT facilities to manage the data produced by high-throughput sequencers. It is provided with its own 32 Core with 128Gb Ram server, backup units, several desktop computers for computing and analysis equipment for quality control.

MARKET APPLICATION SECTORS

- Clinical microbiology and epidemiology.
- Studies of human microbiome communities and their relationship with health and disease.
- Microbiological safety in Public Health and in agro-food industry.
- Plague control.
- Human genetics.

TECHNICAL ADVANTAGES AND BUSINESS BENEFITS

Massive sequencing analysis offers numerous solutions applicable to a variety of current issues in research, such as:

- Whole-genome sequencing of organisms not sequenced previously (*de novo* sequencing) to study its features and functions, focusing, within the health sector, on sequencing genomes of pathogenic microorganisms and mutualistic microorganisms interacting with the human body;
- Re-sequencing of organisms whose genomes are already known, including human, for the study of mutations, alterations or genetic reassortment;
- Sequencing focused on the set of coding regions of the genome or exomes;
- Sequencing of specific genes sets such as those related to diseases, known as clinical exomes;
- Sequencing of Total DNA in complex samples composed of multiple organisms, known as metagenome;
- Sequencing of 16S ribosomal RNA gene amplicons for the taxonomic characterization of microbial communities;
- Sequencing of RNA transcript as representative of gene expression of an organism, also known as transcriptome or RNA-seq;
- Sequencing of small RNAs;
- Sequencing of RNA transcript of complex samples composed of multiple organisms, known as metatranscriptome;

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- Sequencing of DNA regions with epigenetic modifications, such as methylome;
- Sequencing of genome-wide DNA binding sites searching for transcription factors for studying specific interactions on gene expression, known as ChIP-Seq (Chromatin Inmuno-Precipitation Sequencing).

CURRENT STATE OF DEVELOPMENT

The next-generation DNA sequencers are especially aimed at generating really high number of sequences thereby producing Giga bases (Gb) of DNA sequences in a single run. Due to an improvement in instruments and sequencing chemistry, the production cost per Gb has dropped down and nowadays, this decrease continues.

This trend allows genomic sequencing to be a tool of direct application in multiple research areas and projects. Its powerful data generation, high quality of the sequences, ability to multiplex a large number of samples with little effort and speed of execution of sequencing protocols, make this technology a highly powerful tool capable of both performing *de novo* sequencing, genomics and transcriptomics, as well as being routinely applied in diagnostics and clinical analysis.

Applications currently available in the Service:

- Transcriptome sequencing and analysis
- Sequencing and analysis of eukaryotic and prokaryotic genomes and whole-genome sequencing of viruses.
- Amplicon sequencing and analysis
- Metagenomic / Metatranscriptomic analysis

INTELLECTUAL PROPERTY RIGHTS

The Service has the equipment and know-how needed for the comprehensive approach to projects that require the application of massive sequencing, both from its conception through consulting and technical/scientific support, as during its performance, completion and publication.

COLABORATION SOUGHT

FISABIO offers to the scientific and technological community a specialized service of Sequencing and Bioinformatics, and collaboration on research projects, service contract and consulting.

RELATED IMAGES

CONTACT

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