



BGen

Bioinformatics and Applied Genomics Unit

A Versatile High-Throughput Sequencing and
Single-Cell Genomics Platform

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Senior Researcher

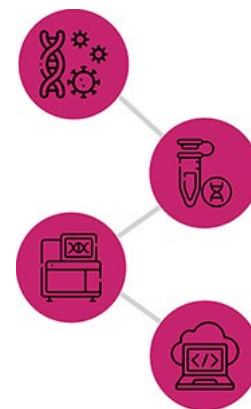
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Bioinformatics and Applied Genomics Unit

BiGen comprises both Wet-lab and Dry-lab Infrastructures

Mission

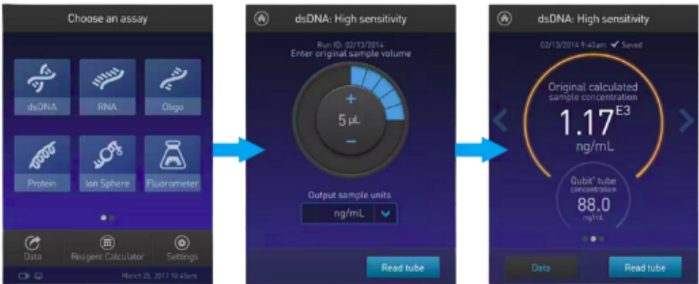
- Development of applications relevant to HT sequencing technologies and single cell genomics
- Development of bioinformatics pipelines for the analysis of large-scale datasets (big-data)
- Provision of services both in the academia and the industry



Quality control

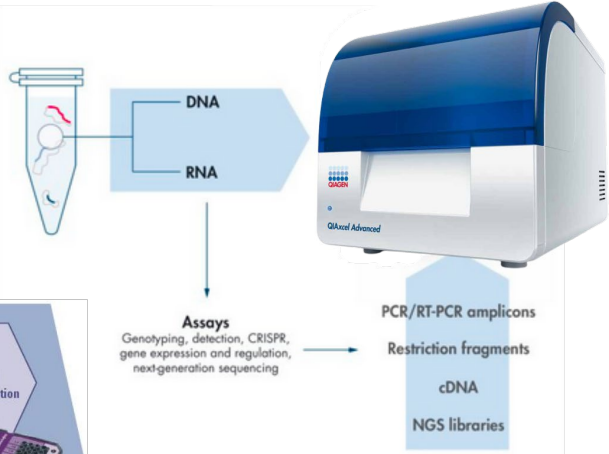
Qubit 4.0 Fluorometer

Thermo Fisher Scientific



QIAxcel Advanced System

QIAGEN



3 minutes

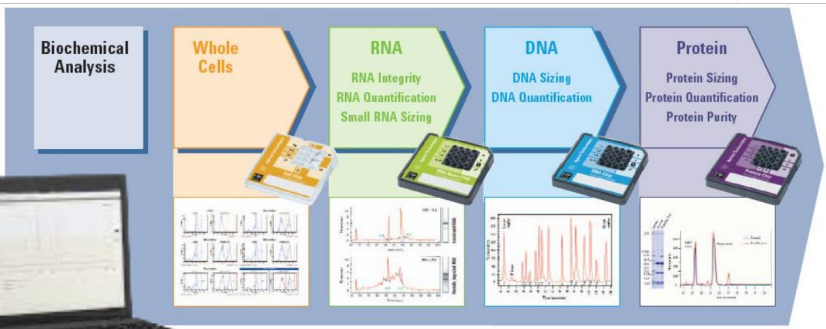
96 samples

3–5_{bp}

0.1_{ng/µl}

BioAnalyzer 2100

Agilent



High Throughput Sequencing Core Facility

A fully equipped, versatile NGS laboratory

MinION
Oxford Nanopore



iSeq 100
Illumina



Ion GeneStudio S5
Ion Torrent



NextSeq 2000
Illumina



Flow Cell	Flonge
50 Gb	2.8 Gb

1.2 Gb

520	530	540
1-2 Gb	4-8 Gb	10-15 Gb

P1	P2	P3
10-60 Gb	40-180 Gb	60-360 Gb

1.5-10 M single end

4 M single or paired end

6 M	20 M	80 M
single end		

200 M	800 M	2.4 B
single or paired end		

500 bp - 2.3 Mb

150 bp

200 - 600 bp

50 - 300 bp

up to 48 h

9 - 19 h

12 - 20 h

10 - 44 h

Throughput

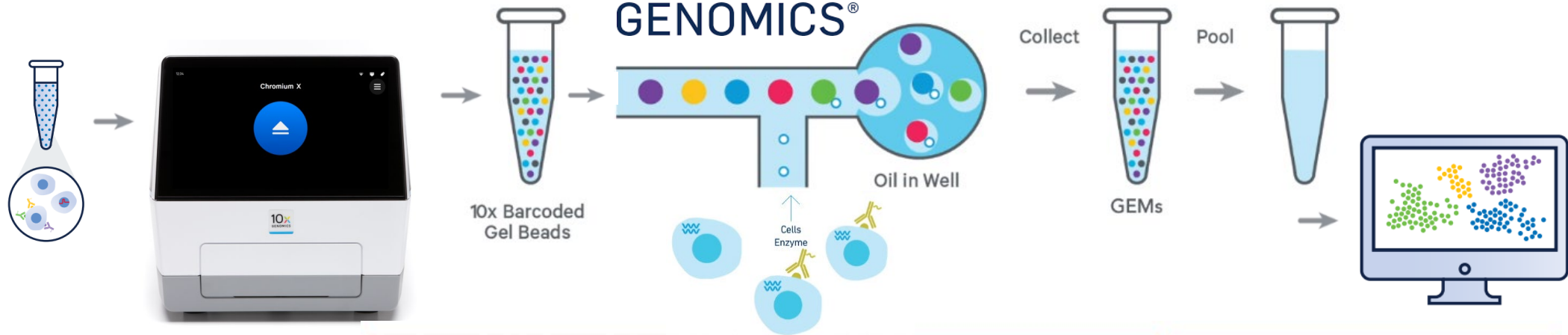
Reads (N)

Read length

Run Time



Single Cell Facility



Single Cell 3' LT Reagent Kits

Single Cell 3' Reagent Kits

Single Cell 3' HT Reagent Kits

Cell number per channel	100-1000	500-10,000	2,000-20,000
Applications	Pilot studies Common cell type identification	Highly heterogenous sample identification Rare population identification	Large scale experiments Highly heterogenous samples Ultra rare populations

BiGen runs both custom and ready-to-use NGS assays:

Pre-processing

- Total DNA and RNA extraction and purification from any tissue
- Ribodepletion / poly-A enrichment / globin removal / DNase treatment

Library preparation

- Whole Genome Sequencing (WGS) for viruses, bacteria, fungi, parasites, animals
- Whole Exome Sequencing (WES) library preparation, both target-enrichment- and amplicon-based
- Whole transcriptome, 3'quantseq and single cell RNAseq
- Custom Target Enrichment by hybridisation for regions of interest, from any WGS library preparation
- Targeted gene panels (Comprehensive Cancer, Pharmacogenomics, Inherited disease etc)
- Whole genome bisulfite sequencing (WGBS)
- Assay for Transposase-Accessible Chromatin (ATAC-seq) and single cell ATAC-seq
- Chromatin immunoprecipitation sequencing (ChIP-seq)
- (...)

Big Data analytics

Development of Bioinformatics tools and pipelines

WGS: Full genome reconstruction, denovo assembly, SNPs and structural variations calling, functional annotation / Genome Wide Association Studies (GWAS)

RNAseq: Differential gene expression analysis, Gene Ontologies enrichment analysis and clustering, network analysis

Metagenomics and Metaviromics, microbiome enrichment analysis, Phylogenetics, phylogenomics, phylogenomics, phylogenomics, phylogenomics

methy-Seq: patterns recognition and profiles comparison

ATAC-seq peak calling, differential analysis and annotation, motif enrichment, footprinting, and nucleosome position analysis

Development of an open-access, interactive, NGS Bioinformatics platform with NGS – oriented, “ready to use” toolsets and pipelines

BXGen Bioinformatics and Applied Genomics Unit



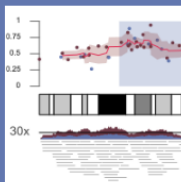
[homepage](#) [workflows](#) [tools](#) [contact](#)



Genomic Analyses made easy

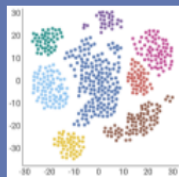
ready to use, end-to-end workflows

run one or connect multiple tools into a workflow



Genomics

[genomics tools](#)



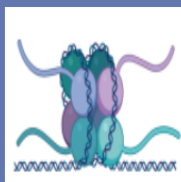
Transcriptomics

[transcriptomics tools](#)



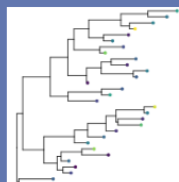
Metagenomics

[mothur pipeline, kraken pipeline, graphs](#)



Epigenomics

[methylation, atac-seq](#)



Epidemiology

[phylogenetics, phylogenomics](#)



Single Tools

[every tool we use](#)

Introducing a new Centre of Excellence

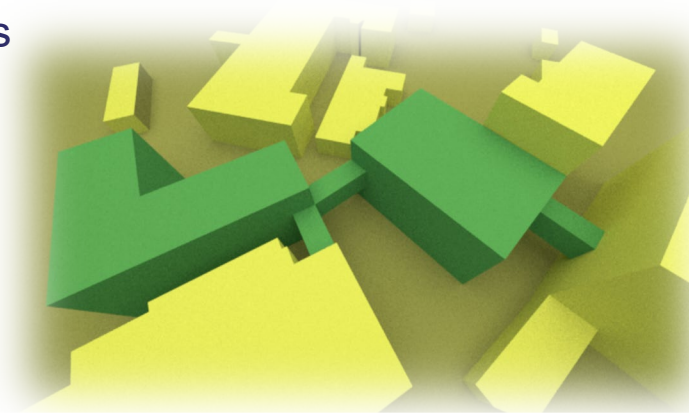
Hellenic Pasteur Institute - Pathogens Research Centre

The infrastructure based in **two buildings** in total **3,000 m²** will be located within the HPI grounds

Biosafety Level 3+ (BSL3+) and Animal (A-BSL3) laboratories (~300 m²)

State-of-the-art facilities equipped with robotic systems to enable culture isolation of BSL3 pathogens

Maintenance of *in vitro* and *in vivo* experimental models of infectious diseases.





Usability
User-friendly and
customizable GUIs



Time-saving
Fully automated, walk-away
solutions for NGS



Reproducibility
Workflow tested for consistency over
several run and sample size batches



Consistency:
In-house biological library prep
testing, sequencing and validation



Traceability
For a complete samples
and reagents tracking

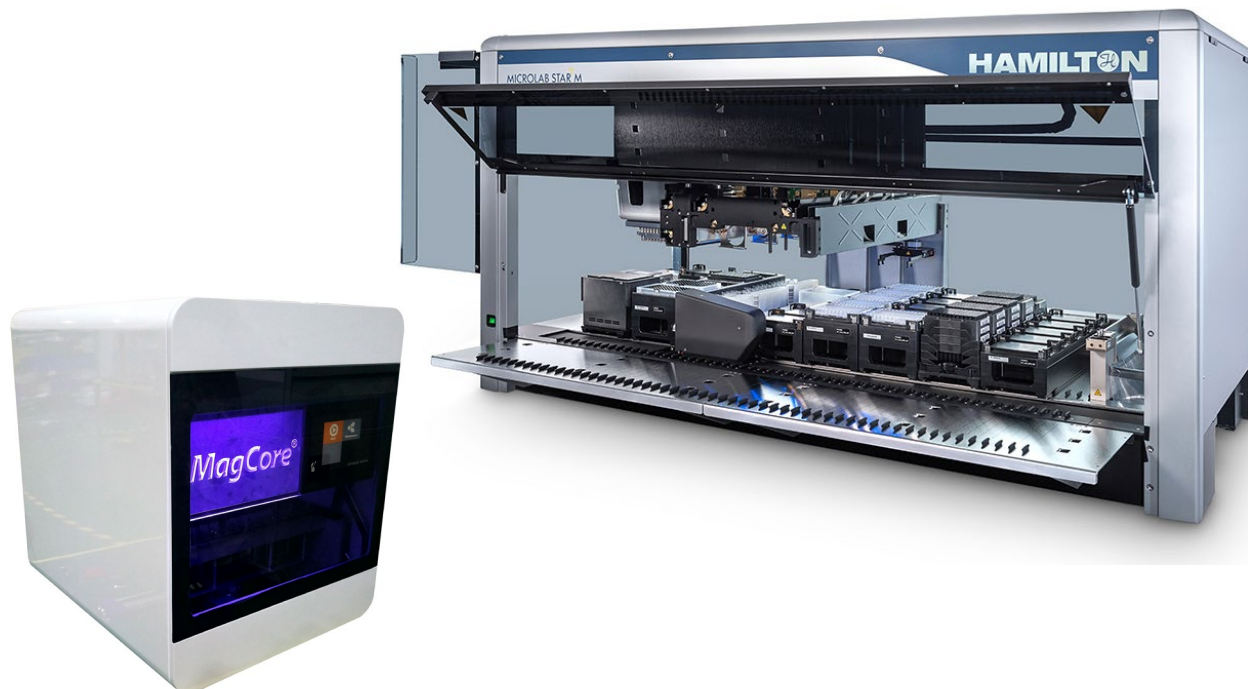


Safety
Automatic carrier and labware
loading with barcode reader

BGen

Taking NGS to the Next Level

Automation - Robotics



BiGen IT equipment

PC-linux and Mac workstations in a dedicated Bioinformatics lab

Access to the HPI High Performance Computing (HPC) infrastructure



~1M € Investment in high-end
GPU computing infrastructure

Thank you for your attention

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