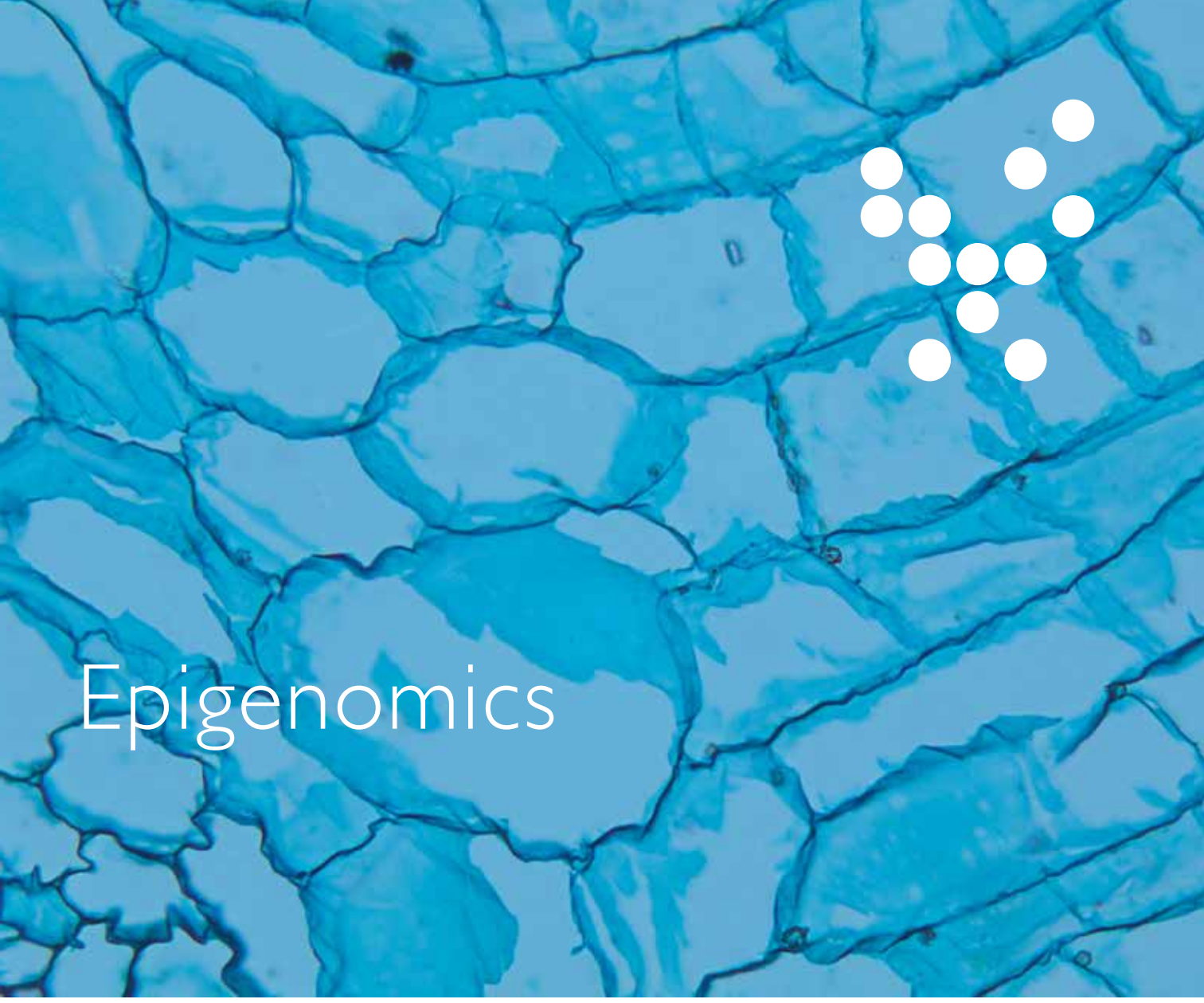
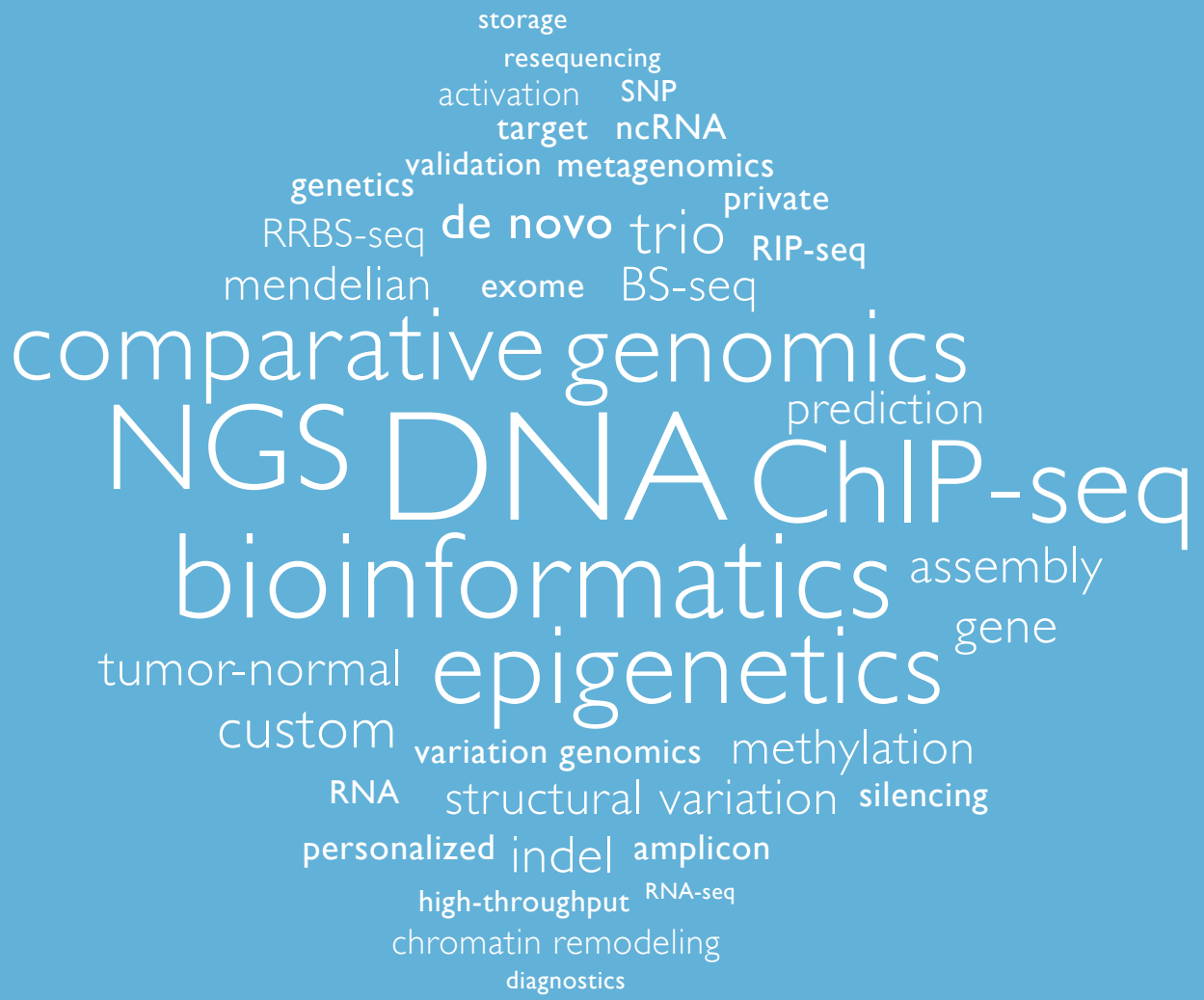


Epigenomics

IGATech


storage
resequencing
activation
SNP
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private
RRBS-seq
de novo
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exome
BS-seq
comparative genomics
prediction
NGS
DNA
ChIP-seq
bioinformatics
assembly
gene
tumor-normal
epigenetics
custom
variation genomics
methylation
RNA
structural variation
silencing
personalized
indel
amplicon
high-throughput
RNA-seq
chromatin remodeling
diagnostics

NGS
Next Generation Services

IGATech

IGATech is the leading Italian provider of genomic research services using Illumina Next Generation Sequencing (NGS) technology.
We are the largest lab in Italy offering these services on a wide range of organisms: we have experience with humans, other animals, plants and microorganisms.
The company has direct access to the scientific and technological resources of its founder, the Institute of Applied Genomics (IGA), which has gained an outstanding reputation in genomic research through participation in genome sequencing projects both at a national and international level.
Among the genomic research services provided, the company also offers a wide variety of bioinformatic services such as conventional and custom analyses and customer-oriented software development.

Epigenomics

ILLUMINA SEQUENCING TECHNOLOGY

The Illumina massively parallel sequencing technology makes multiple gigabases of data from several million templates economically available, enabling new approaches to genomic characterization. The Illumina technology allows tipically genome center-like studies to be accomplished at the individual laboratory level. A single technology workflow is capable of supporting genome-wide analyses as different as DNA sequencing (de novo and resequencing), gene expression, transcriptome characterization and expression control including small RNA discovery, protein-DNA interactions and CpG methlyation status. Our company is a certified service provider (CSPro) of Illumina genomic sequencing.

EPIGENOME SEQUENCING
Solving the genomic second code

Epigenetics is the study of changes in gene expression or cellular phenotype, some of which are heritable, caused by mechanisms other than changes in the underlying DNA sequence – hence the name epi-genetics (Greek: επί - over, above, outer).

CHROMATIN IMMUNOPRECIPITATION SEQUENCING (CHIP-SEQ)

ChIP-Seq is used to elucidate the complex circuitry of genetic regulatory networks, genetic pathways, and epigenetic mechanisms in living cells by determining how proteins interact with DNA. This approach enables discovery of novel transcription factor binding sites, identification of genes regulated by known transcription factors and co-regulators, direct comparison of regulatory events in different cell states (i.e. normal v. disease) and investigation of drug effects and other stimuli on regulatory pathways.

BISULFITE SEQUENCING (BS-SEQ)

DNA methylation has been shown to play an important role in a wide variety of biological processes, including silencing of transposable elements, stem cell differentiation, embryonic development, genomic imprinting and inflammation. Alteration of methylation patterns has been identified in many diseases, including cancer, diabetes, cardiovascular disease, inflammation and neurological disorders.

By combining bisulfite treatment of genomic DNA with NextGen Sequencing, it is possible to sensitively measure cytosine methylation on a genome-wide scale within specific sequence contexts.
By using restriction enzymes and bisulfite sequencing, it is possible to enrich for the areas of the genome that have a high CpG content. This approach, termed RRBS-seq (Reduced Representation Bisulfite Sequencing), reduces the amount of nucleotides needed to be sequenced to 1% of the genome size, allowing for a cost-effective single-base-pair resolution of methylated cytosines.
The third alternative is targeted bisulfite sequencing, which is able to specifically capture selected genomic regions of interest associated with a disease or phenotype.

Services list

LIBRARY PREPARATION AND SEQUENCING

- ChIP-seq
- Whole genome BS-seq (WGBS-seq)
- Reduced Representation BS-seq (RRBS-seq)
- Targeted Bisulfite Sequencing

BIOINFORMATICS SERVICES

CHIP-SEQ

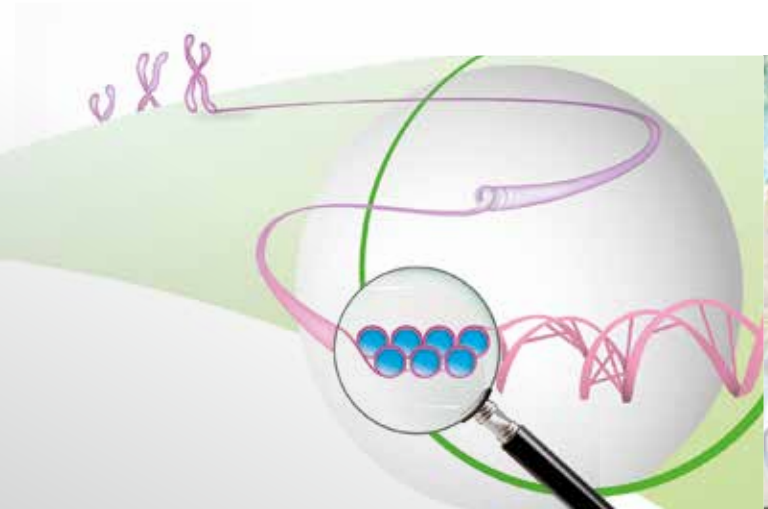
- Quality control
- Alignment to a reference
- Peak calling
- Annotation of ChIP-seq regions
- Visualization
- Sequence motif analysis
- Functional annotation of ChIP-seq target genes

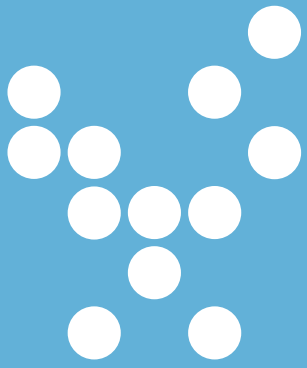
BS-SEQ

We have a proprietary software package for WGBS-seq, RRBS-seq and Targeted BS-seq data analysis.

- Quality control
- Post-sequencing estimation of conversion rate using Lambda spike-in
- Alignment to a reference
- Methylation calling at single cytosine level
- Whole genome methylation statistics (including distribution of methylation in the CG, CHG and CHH contexts in plants)
- Visualization of methylation distribution across the genome using CIRCOS images
- Identification of Differentially Methylated Regions (DMRs) between samples

Our team is always available to consult with you on study design to ensure correct sequencing and bioinformatics strategies are used to meet your goals.





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