

Deciphering the genomic code to enable accurate disease diagnosis & cure malfunctions

Genomic disorders are diseases caused by the loss or gain of chromosomal/DNA material: copy number losses (deletion syndromes) and gains (duplication syndromes).

While the pace of advances in genomic science and technology has been rapid, more research is needed before we can fully realize the potential benefits from improved disease treatment and prevention.

One of the crucial challenges surrounding rare disease diagnosis is knowing exactly which of the many potentially functional variants found in a patient's genome is responsible for her/his disease. Integrating genome-wide genetic association data with genomic-scale annotation data has often led to a virtuous cycle of mutual advantage, such as defining the tissues, and sometimes also the specific cell types that are central to the pathogenesis of a specific disease.

New tools & results to better decipher genomic malfunctions

Over the last few years, three European projects, MRG GRAMMAR, BEYONDSEQ and PROSEQO, have working on tackling the challenges that are key to advancing the field.

The focus of the collaborative research marks a significant step towards deciphering the genomic code for a better understanding of genomic malfunctions. This is crucial for coming up with better cures for the malfunctions diagnosed, including genomic and personalised medicine.

The collective portfolio of the results from the three projects highlight novel technologies spanning DNA sequencing, biomarker discovery, genetic/genomic/ cytogenetic diagnostics. Other advances include generating new types of biological datasets for a much deeper understanding of the causes of many diseases.

Tools & Datasets

- » Cutting-edge tools for accurate and cost-effective Next Generation Sequencing, protein sequencing, advanced high-throughput DNA sequencing, biomarker discovery and genetic diagnostics.
- » Multifunctional platform and iterative improvements of the data analysis from the assessment of instrument performance in SMS, both of nucleic acids and amino acids.
- » Toolbox for integrated genetic and epigenetic profiling of single DNA molecules, for readout, extraction and quantification of medically relevant genomic information.
- » Reagents, prototype DNA barcoding devices and data analysis software for a range of applications.
- » Diagnosis/prognosis tools for hematological malignancies; spinal muscular atrophy and early diagnosis of colorectal and lung cancer.
- » Analysis of long individual DNA molecules without PCR-amplification by using emerging optical DNA mapping technologies.
- » New biological datasets that systematically explore all possible regulatory landscapes.
- » A comprehensive database containing the grammar rules of the regulatory code.

Technologies & Models

- » Sequencing technology to enhance optical detection and control the movement of molecules through optical trapping.
- » Optical technologies based on new plasmonic device, protein sequencing and single molecule DNA/RNA sequencing.
- » Analytical models to reconstruct the exact sequence from the signals recorded & predict enhancer activity in bacteria, yeast and mammalian cells.
- » Predictive nucleotide-level model of enhancer function to extract the underlying regulatory principles from data.
- » Algorithms to decipher extant natural regulatory code and interpret variations leading to a profoundly deeper understanding of the origins of many diseases.
- » Highly engineered systems for molecular translocation / movement control.
- » A novel approach for plasmonic enhanced FRET and SERS spectroscopy for the sequencing of proteins, along with new molecular designs for enhanced FRET spectroscopy rulers.



