

Eurofins-Viracor Center of Excellence for **Bioinformatics & Al**

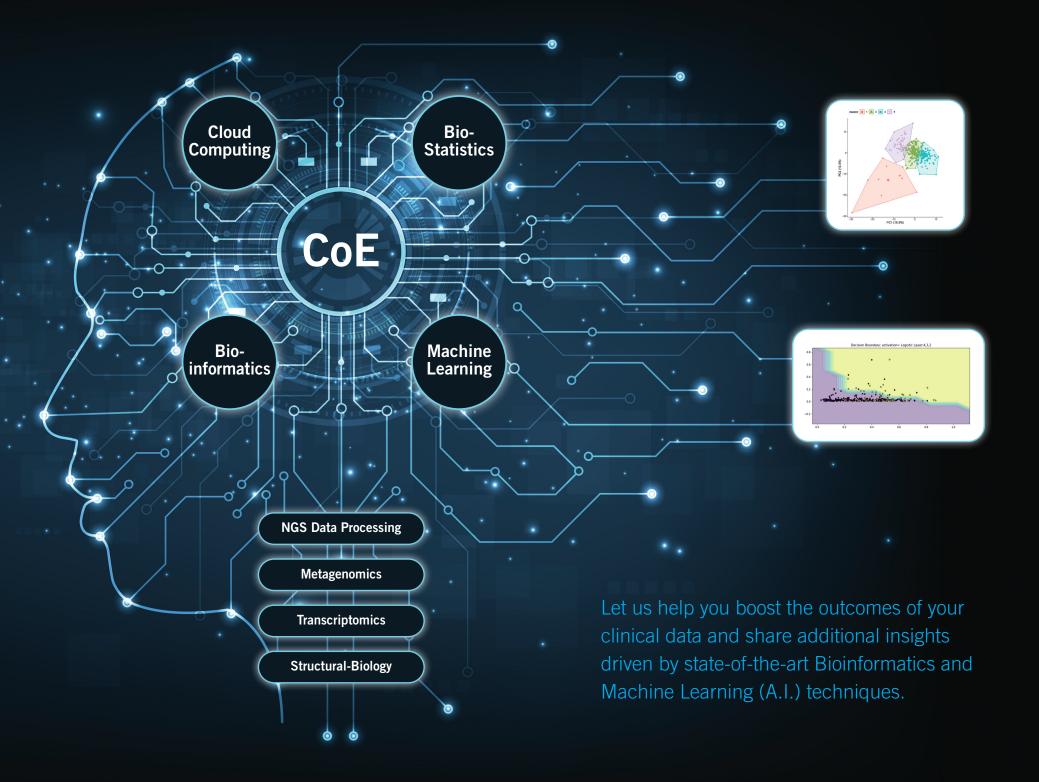
Eurofins-Viracor Center of Excellence for **Bioinformatics & AI**

Bioinformatics and computational biology along with machine learning skills has emerged to make a significant impact on the outcomes of clinical research. Analysis of the ever-increasing size and dimensions of biological data such as DNA/RNA sequencing, gene-expression, whole genome methylation etc., requires professional bioinformatics expertise and high-performance computing resources. The Eurofins-Viracor Center of Excellence for Bioinformatics & AI, with it's six-member core team (3 PhD and 3 MS), brings together strong interdisciplinary expertise in Bioinformatics, artificial intelligence (Classical & Deep learning), Biostatistics and Cloud computing.

We are committed to conducting outstanding clinical and translational research that increases the overall understanding of disease-associated biological processes, drug development, and therapeutic responses. The center stimulates and facilitates collaboration among computational scientists, laboratory and clinical investigators. Our current computing-power is distributed over the clouds and multiple high-throughput local Linux servers, ensuring rapid turnaround time.

In this era of Big Data biomedicine, the V-E CoE for Bioinformatics and AI develops analytic methods to help clients and collaborators to study the increasingly diverse and complex data that are collected from human cells, tissues, and patients. We focus on analyzing, visualizing, and mining data from experiments that profile the molecular state of human cells and tissues by transcriptomics, epigenomics, proteomics, and metabolomics to integrate these datasets to advance precision medicine and therapy development.

Our aim is to translate genomic, epigenomic, and RNA expression data into scientific knowledge and insights for advancing precision medicine.



Our bioinformaticians, data scientists, and IT specialists provide a range of services including:

- NGS data processing with cloud computing capabilities-- (RNASeq, Whole Exome Sequencing, ctDNA, cfDNA, WGBS etc.)
- Viral gene-variant reporting in the format recommended by the Division of Antiviral Products (DAVP).
- Pattern recognition in high-dimensional omics data (genomics, metagenomics, proteomics, metabolomics etc.)
- Use clinical data to develop predictive models diagnosing diseases or different clinical outcomes.
- Medical image analysis (e.g. tumor biopsy images)
- Finding complex patterns in the time-series or temporal data (e.g. clinical trial data)
- Unsupervised analysis of high-dimensional data such as gene-expression (RNASeq data) or Flow cytometry.

Perfroming analysis of molecular and phenotypic data from:

- NGS data processing
- Metagenomics
- Transcriptomics
- Structural-Biology
- Flow Cytometry





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