# **Computational Genomics Core**

The Computational Genomics Core (CGC) supports the Einstein community by providing essential informatics resources and infrastructure for the analysis and interpretation of large genomic and epigenomic datasets, providing for timely and standardized delivery of data to investigators, and to organize and present tutorials for data retrieval and analysis using the provided tools and methodologies. The CGC develop primary analysis pipelines, analysis and visualization tools for application-specific handling of data using open-source and commercial analysis tools. All tools are maintained and deployed in a manner that optimally supports the research activities of individual investigators. The CGC provides support pipelines for massively parallel sequencing based assays performed through the Epigenomics Shared Facility (ESF) and the Genomics core.

The facility consists of two full time bioinformaticians with expertise in the different levels of data analysis from primary stages when transforming raw sequence into biological information to more integrative analysis comparing different groups of assays and integrating with other sources of data.

The CGC pipeline catalogue includes quality control assessment and primary analysis for:

- Transcriptome Analysis (RNA-seq)

- Sequence Variant detection (Whole Genome Sequencing/Exome Sequencing)

- Chromatin Analysis (ATAC-seq/ChIP-seq)

- Methylome Analysis (Bisulfite Sequencing/HELP-Tagging/HELP-GT)

- Single cell Transcriptome Analysis (Chromium 10X)

Consultation on study design and customized analysis are also available and encouraged.

The delivery will vary depending on the analysis but always includes quality control report, raw and process data as well as code and settings used during the analysis to assure reproducibility of the findings.

The core is also involved in training by providing tutorials covering software and analysis methodologies.

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