

# Analysis

## Work in Progress

This feature is currently under active development. This will be release in the next **Open CGA 2.0**

One of the main goals of OpenCGA is to provide a secure analytical platform for executing the most demanding and complex genomic analysis today. OpenCGA supports *big data* variant and clinical interpretation analysis. OpenCGA implements some of the most common analysis today, for doing so

Customositation

## Table of Contents:

- Analysis Framework
- Analysis Catalogue
  - Native Analysis
    - Variant analysis
    - Clinical Interpretation Analysis
  - Custom Analysis (plugins)
- Wrapped Analysis

## Analysis Framework

OpenCGA implements an **Analysis Framework** that allows the quick development of **Native Analysis** and **Wrapped Analysis**. **Native Analysis** make use of the internal OpenCGA APIs and therefore are implemented in Java, this allow an easy implementation and the best scalability and performance. Some native analysis have implemented inside OpenCGA and are provided as part of OpenCGA. Users can also implement native analysis outside the OpenCGA source code as a **plugin**, this can easily installed in your OpenCGA installation.

**Wrapped Analysis** act as connectors to external binaries that can be implemented in any programming language, for instance *PlinkWrappedAnalysis* can query OpenCGA Variant Storage and export a PED/MAP or VCF file and execute Plink.

## Analysis Catalogue

### Native Analysis

There are several **native variant analysis** implemented in OpenCGA, these use internal the different internal APIs developed to provide a scalable and high-performance implementation. Occasionally, these analysis can store results in the variant storage to allow users to filter by them, for instance GWAS analysis can be stored and/or indexed for filtering.

### Variant analysis

Variant Analysis aim to implement the most common genetic analysis, at the moment are implemented:

- Basic statistics
- Genome wide association studies

### Clinical Interpretation Analysis

Clinical Interpretation Analysis allow to to discover variants or genes involved in

- Cancer Interpretation Analysis
- Secondary Findings

### Custom Analysis (*plugins*)

User can easily install Native Analysis implemented externally to OpenCGA source code. We are considering creating a repository for the users, a tutorial is coming soon.

### Wrapped Analysis

You can use external tools using the wrapper analysis. Some tools are being implemented naively

and available to all users.

- Plink