Primary Findings

In OpenCGA, users can retrieve primary findings by defining a variant query according to the their needs. Multiple query filters can be used in the query: a list of panels, sample names, consequence types, population frequencies, biotypes, family segregation... For each retrieved variant, a reported variant will be created with its reported events and tier values.

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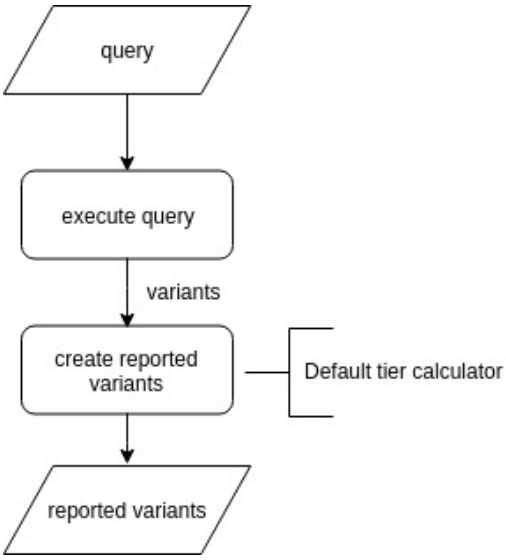
Implementation

OpenCGA implements the primary finding analysis by executing a variant query defined by the user and then, creating the reported events for those variants and using the default tier calculator to assign the corresponding tier value.



Input parameters

- A variant query

Output results

- List of reported variants