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# GA4GH-Driver Project: Driver Project-Global Alliance for Genomics and Health

## Description

This project aims at supporting and enhancing modern oncology, by implementing a cultural, technological and legal integrated framework (EUCANCan) across Europe and Canada, for the efficient analysis, management and sharing of cancer genomic data. This cooperative framework is not only expected to immediately contribute to improve biomedical research in cancer, but to also serve as a model for globalizing and enriching Personalized Medicine initiatives, allowing the exchange of data, clinical experience and information across different NHS.

To answer specific questions regarding the biology of tumors, and to find better diagnosis and treatment protocols, thousands of genomic studies around the world are constantly generating large amounts of genomic and phenotypic data from thousands of cancer patients. For the analysis and interpretation of all these large and complex datasets, the research community has been building over the past years large and complex bioinformatic (methodologic) and computing infrastructures that have proven to be able to efficiently identify and interpret promising diagnosis and treatment biomarkers for oncology, and other diseases. These infrastructures need to integrate analytical methods, which are able to identify genomic changes and interpret them in the context of disease, with robust data management protocols for the optimal flow and storage of these valuable datasets. At the same time, to take full advantage of all this data and to further increase the chances of discovering new and valuable disease biomarkers, beyond original clinical studies, these infrastructures also need to implement protocols and frameworks that allow the sharing of this data within the research community. The revision and reanalysis of existing biomedical data using new and improved methodologies and the possibility of combining existing datasets into wider and larger meta-analysis, are very effective strategies to increase the chances of achieving new and relevant discoveries from the data, as they can reach and interpret higher and more complex molecular patterns of the disease that were hidden from the firsts analyses.

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