EOSCpilot
The European Open Science Cloud for Research Pilot Project

Science Demonstrator

Life Sciences & Health Research

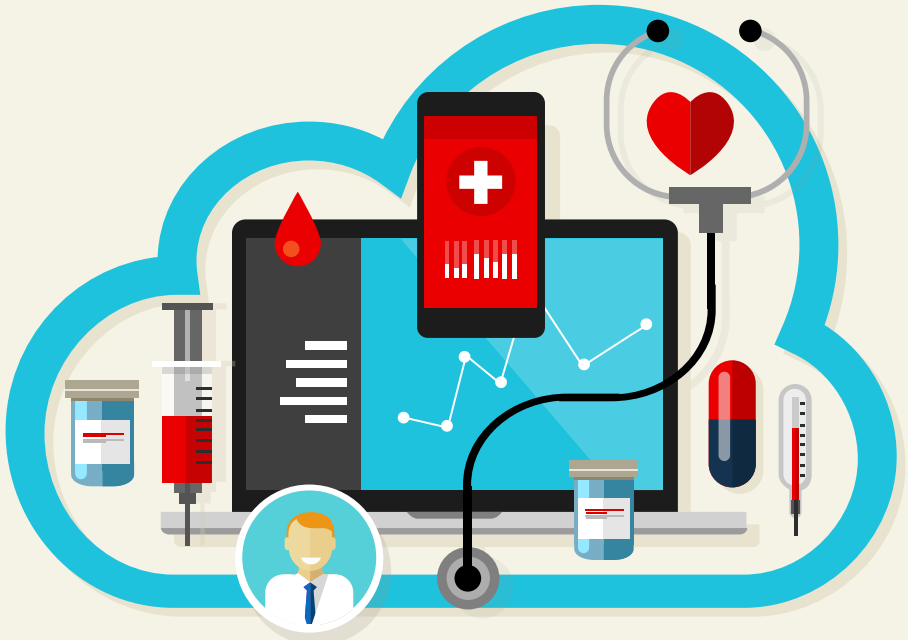
Pan-Cancer Analyses – Portable Federated Cloud-based Solution

Brief Overview

There are a multitude of challenges being faced in the life sciences, health, food, fishery and agriculture sectors. In cancer research, Europe has taken a technical lead within international consortia around cloud-based pan-cancer genomic analysis. This global competitive advantage can be maintained by leveraging open science analysis models around controlled access data sets developed in collaboration with researchers elsewhere in the world. These analysis frameworks could also be re-used to analyse cardiovascular and neuro-degenerative diseases as well as stimulating biotech/pharmaceutical industries to use public cancer genomic data in R&D.

Objectives

PanCancer aim is to develop interoperable IT frameworks to enable standardized sharing and large-scale processing of cancer genomes with other molecular and clinical data, to enable biological and translational breakthroughs. To do so, interoperable frameworks have been employed to process ~10,000 cancer Whole Genome Sequenced (WGS) tumour-normal pairs from 20most common cancer types. The main research objective is to uncover genome-wide patterns of different types of genetic variation, which requires availability of WGS data, and integrating these with molecular, demographic and clinical data. PanCancer will allow to proactively create suitable standards and interoperability



HORIZON 2020

EOSCPilot.eu has received funding from the European Commission's Horizon 2020 research and innovation programme under the Grant Agreement no 739563.

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Main achievements

The Butler scientific workflow framework has been set up and tested at three globally distributed cloud computing environments that are based on the OpenStack platform, these include: the EMBL-EBI Embassy Cloud in the UK, the Cyfronet cloud in Poland, and the ComputeCanada cloud in Canada.

- >400 high coverage whole genome samples (~60 TB of data) from the ICGC pediatric brain cancer cohort were downloaded to the ComputeCanada cloud and
- ~50 TB of public data from the 1000 Genomes project was loaded onto the Cyfronet environment from the EMBL/EBI data servers utilising Cyfronet's Oneprovider software.
- Butler was used to run a genomic alignment workflow (based on BWA and developed at The Sanger Institute) on >400 samples at ComputeCanada and >400 samples at EMBL/EBI Embassy cloud, with over 100 TB of data processed to date. Proper operation of the infrastructure was monitored by Butler's detailed monitoring and self-healing capabilities.

Recommendations for the implementation

- Improve the availability of computational resources
- Improve systems' stability and storage capabilities
- Introduce clear Service Level Agreements between service providers and service consumers to make clear the requirements asked by the consumers can be met

Partners of the SD

Genome Biology Unit, European Molecular Biology Laboratory (EMBL)

EMBL-EBI

Contacts
llevar@gmail.com

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