



CLOUD WORKFLOWS DEVELOPED IN BBMRI COMPETENCE CENTER OF EGI-ENGAGE

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Introduction

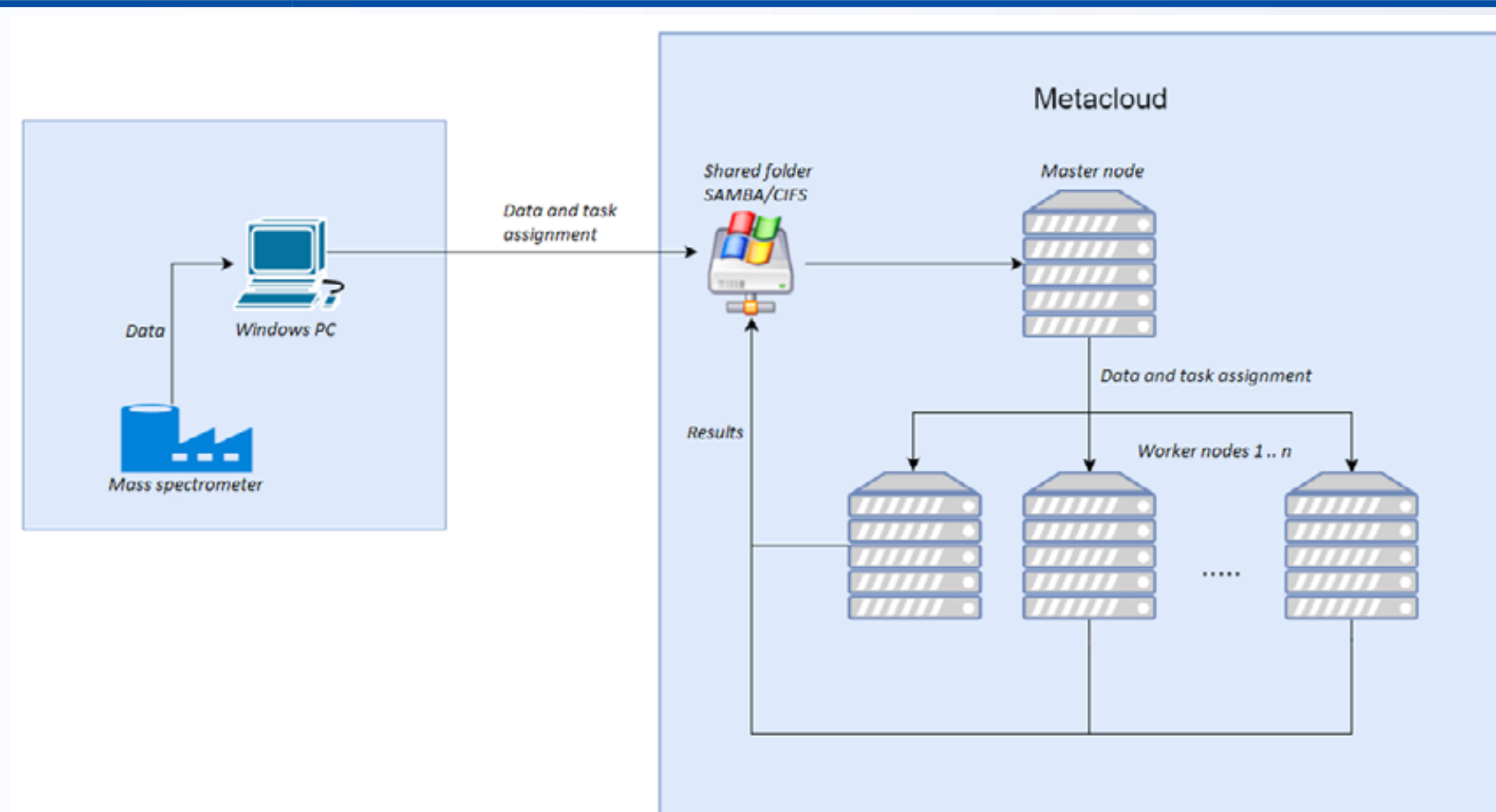
Three technology demonstrators developed withing BBMRI Competence Centre in EGI-Engage:

- proteomic workflows deployed by BBMRI.cz,
- complex genomic workflows deployed by BBMRI-NL,
- BiobankCloud-based workflows deployed by BBMRI.se/KTH.

All of the tools have been made available open source and the workflows have been validated not only on **EGI.eu infrastructure**, but also inside the **private clouds of the biobanks** to allow for processing of very sensitive personal data.

Proteomic Processing Workflow (BBMRI.cz)

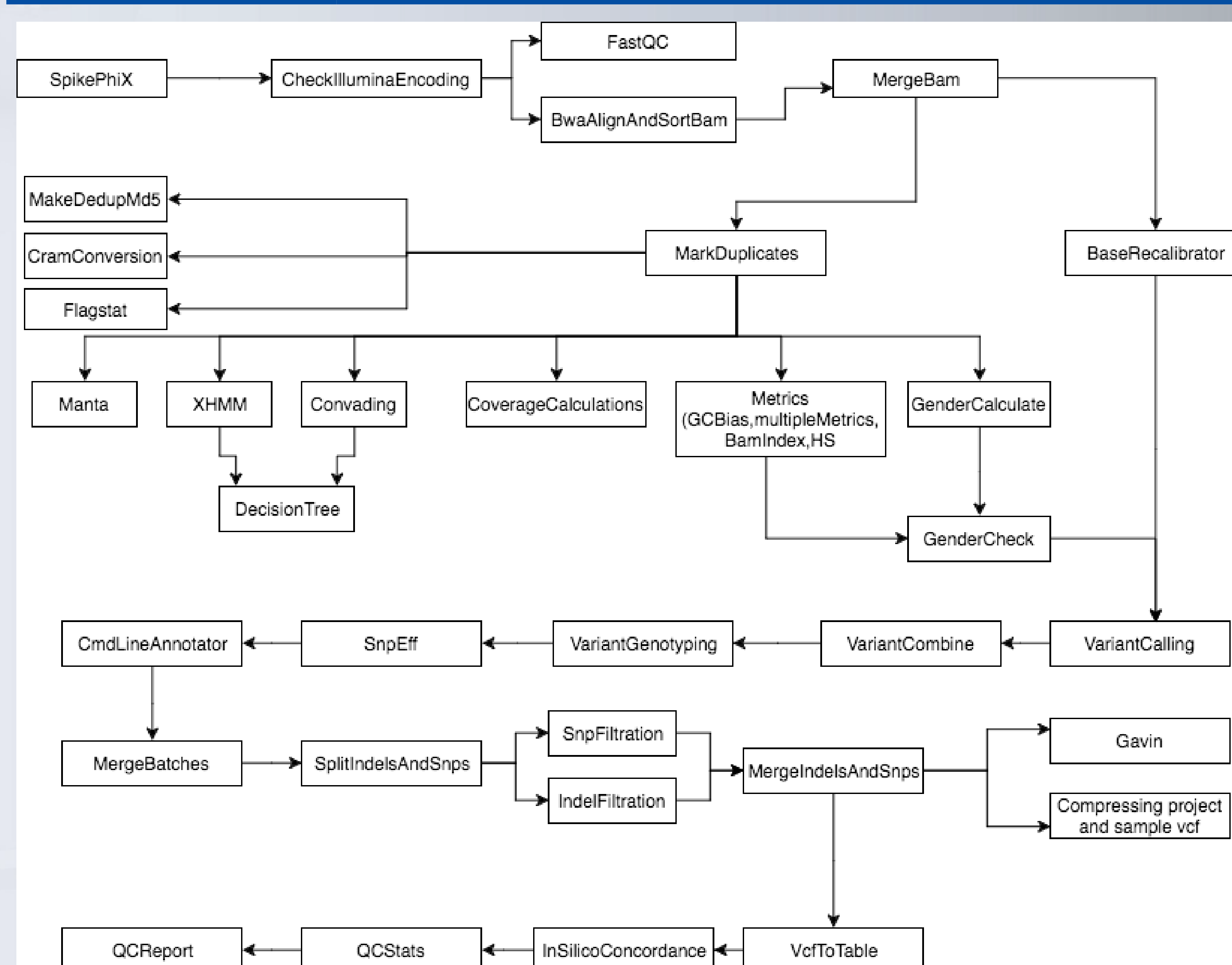
Description	The SW tools used to analyse proteins are often Windows-based with GUI frontends for interactive visualization of the processing, which makes them uneasy deployable to cloud environment. Our pilot presents a way how to deploy Skyline, which is widely used in proteomics. Communication with it is maintained using queue, messages and CLI without direct access of user to the workstation.
License	MIT
Source code, documentation	https://github.com/cduongt/skyline-rabbitmq



Genomic Processing Workflow (BBMRI-NL)

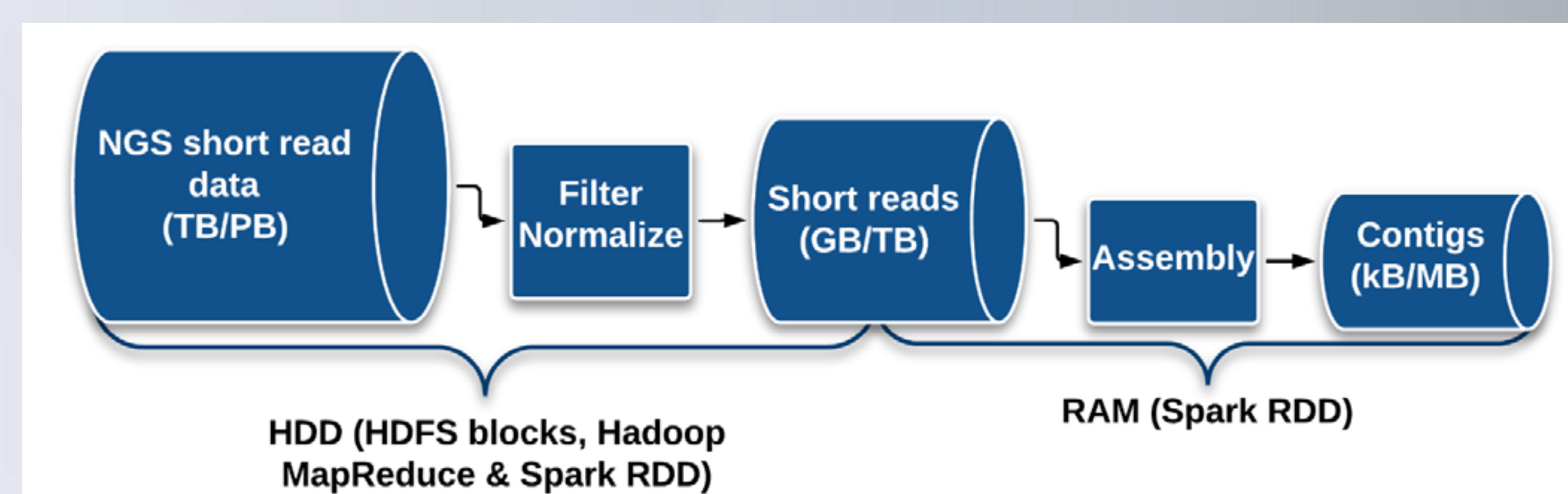
Description	Combination of Ansible playbooks to deploy a complete SLURM cluster on EGI cloud and DNA analysis pipeline including all dependencies and reference data.
License	MIT

Source code, documentation	pipeline: https://github.com/molgenis/NGS_DNA playbook : https://github.com/bbmri-nl/bbmri-nl-pipeline-deployment docs: https://molgenis.gitbooks.io/ngs_dna/
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BiobankCloud Workflows (BBMRI.se/KTH)

Description	This is a technology demonstrator of the pilot NGS analytical software developed for the BiobankCloud secure high-performance platform.
License	MIT
Source code, documentation	https://github.com/NGSeq/ViraPipe



Acknowledgements



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