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Development of an interactive pipeline for Genome wide Association study

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The need for tailoring healthcare and treatment therapies to individual patients based on their genetic-makeup and other biological features is becoming more and more crucial in today's clinical practice. Genome Wide Association Study (GWAS) has been applied extensively to uncover several variations and genes in our DNA that are related to different diseases, traits and clinical symptoms. However, a typical GWAS analysis requires the use of numerous complex commands, codes and analysis from different languages. This makes research projects complex and time consuming for researchers. GWAS also requires the use of large computing and storage resources to perform state of art data analysis, which might not be available for most developing country researchers. We aim to develop an e-infrastructure web application that will provide state-of-the art GWAS analysis to local researchers. Back-end Web technologies to be used include JSP for business logic, JAX-RS for programmatic access to web application, nextflow, a workflow language, Liferay, FutureGateway, gLibrary etc. This solution will make GWAS analysis easier to perform, by requiring limited understanding of the computational needs and from researchers. This will also allow researchers focus mainly on research problem and give better and intuitive biological interpretation to the results.

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Session Classification: Presentation of use cases and their implementation stategies continued