***Kubernetes is a versatile tool to provide WebApps for data exploration on individual omics projects***

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**Background**

High-throughput (HT) screens of complex biological systems such as the proteome, transcriptome or genome generate extensive amounts of data. These services are typically supplied by technical facilities of research institutions in order to bundle the technical expertise and to provide access and assistance to end users. Primary results are often produced by pipelines, providing relevant features in extensive spreadsheet tables. Since interactive exploration and visualization of HT data is a key aspect for the analysis and understanding of the biological systems under investigation, we recently developed WIlsON, an interactive workbench for analysis and visualization of multi-omics data. It is primarily intended to empower screening platforms to offer access to pre-calculated HT screen results to the non-computational scientist. Facilitated by an open file format, WIlsON supports all types of omics screens, serves results via a web-based dashboard, and enables end users to perform analyses and generate publication-ready plots. However, for most bioinformatics service facilities, infrastructure aspects such as the provision of web services, or storage and computational capacities represent a major strain, binding valuable personnel. Utilization of cloud resources such as de.NBI is a versatile alternative solution for on premise IT infrastructures, allowing to reduce costs and to focus on bioinformatics aspects.

**Methods and results**

Here we utilize the Kubernetes open-source software provided at the de.NBI hub at the JLU Gießen. It hosts containerized services such as WIlsON in a horizontally scaling infrastructure. A tool named KASSIo (Kubernetes Assistant) was developed in-house to deploy and manage WebApp containers for individual projects automatically, triggered by analysis pipelines after completion An advanced workflow includes I) reduction of all configuration data for a whole omics project to a single JSON formatted file allowing deployment and updating of individual projects, II) utilization of an on premise S3 storage for sensitive data as permanent storage system, and III) a centralized and secure handling of user authentication and data access via randomized URLs.

**Discussion**

Utilizing cloud computing resources for temporary computational loads demanded by data analysis pipelines or more permanent services such as WebApps is a worthwhile alternative to on premise IT infrastructures. However, making use of the resources provided by the de.NBI generate an urgent need to acquire the respective knowhow as most university training courses for bioinformaticians do not address this field yet.