**Experiences introducing a Confluence based ELN at BiRC**

The Confluence based ELN system labbook.au.dk was introduced at the Bioinformatics Research Centre in August 2016. The system was offered as a general platform for *research documentation* that could make it easier for the individual researcher to follow the rules for responsible conduct of research at AU. Researchers were not forced to use the system but encouraged to investigate and compare it against their existing workflows for research documentation.

The Bioinformatics Research Centre consists of research groups that focus on developing and applying methods for large amounts of biomolecular data, typically genome data. The research activities can roughly be divided into: (1) developing mathematical models and algorithms, (2) developing software tools based on developed models and algorithms, and (3) large scale data analysis that typically involves running computationally intensive pipelines on a High-Performance Computer (at BiRC typically the GenomeDK cluster, http://genome.au.dk) followed by interpretation of the obtained results.

The different research activities at BiRC have different needs for research document and data management. The large amounts of genomic data are securely stored and accessed via GenomeDK. Source code for software tools in development is managed and documented in version control systems. At BiRC, the use of Git and GitHub is widespread. Computational Pipelines for large scale data analysis are developed as workflows. At BiRC, typically using the locally developed gwf tool (https://gwf.readthedocs.io/en/latest/), where developed workflows are also typically managed and documented using Git. Also, systems like Jupyter Notebook for tying source code, documentation, and results together in a single executable document is heavily used for reproducible data analysis.

The current installation of labbook.au.dk does easily integrated the above functionality and focuses mainly on being a platform for shared research documentation. The researchers at BiRC could easily appreciate the value of labbook.au.dk as a platform for shared research documentation, but the functionality it offered (shared Wiki-style documents) did not appear substantial enough to replace existing "home-grown" workflows for sharing documentation and data, e.g. in shared folders on GenomeDK. The learning curve for adopting labbook.au.dk combined with the expected outcome compare to existing workflows therefore did not convince many researchers to adopt labbook.au.dk.

Our experience is that computational research like bioinformatics, and data science in general, certainly can benefit from ELN systems like labbook.au.dk, and that the researchers in such disciplines appreciate the functionality in systems like Confluence. However, in these disciplines many researchers, properly due to their natural interest in computational solutions and tools, already have established well-functioning workflows for documenting and sharing research documentation. These locally established workflows might not offer the larger-scale collaborative functionalities of e.g. Confluence, but they work very well in the groups where they have been developed. Replacing such systems in a bottom-fashion can be difficult as they in many cases are the results of a lot of customization making them extremely applicable for their intended use locally. We strongly believe that it is not beneficiary to force a common documentation system upon such researchers unless absolutely required, but believe that the institution should nudge the development of established workflows in order to make sure that they obey the requirements of secure storage and data management.

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