

Sequenceserver: a modern graphical user interface for custom BLAST databases

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Project Website: <http://sequenceserver.com>

Source Code: <https://github.com/wurmlab/sequenceserver>

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Main Text of Abstract

The dramatic drop in DNA sequencing costs has created many opportunities for novel research that require comparing newly obtained and previously known sequences. This is commonly done with BLAST, yet using BLAST directly on new datasets requires substantial technical skills or helpful colleagues. Furthermore, graphical interfaces for BLAST are challenging to install and largely mimic underlying computational processes rather than work patterns of researchers.

We combined a user-centric design philosophy with sustainable software development approaches to create Sequenceserver. The innovations in Sequenceserver over other BLAST servers are at three levels. First, our software can be rapidly installed and used on custom datasets for individual use or sharing with a community. Second, by analysing user input and using simple algorithms, Sequenceserver reduces the amount of decisions the user must make, provides interactive visual feedback, and prevents common potential errors that would otherwise cause erroneous results. Finally, Sequenceserver provides multiple highly visual and text-based output options that mirror the requirements and work patterns of researchers.

The result of our approach has been quite successful as demonstrated by >27 mentions of the software in peer-reviewed publications. We believe the software, our user-centric design philosophy, community building and sustainable development approach, and the customisable codebase will be of significant interest to the OBF community.