



Biological Sequence Analysis Using the SeqAn C++ Library (Chapman & Hall/CRC Mathematical and Computational Biology)

Andreas Gogol-Döring, Knut Reinert

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An Easy-to-Use Research Tool for Algorithm Testing and Development

Before the SeqAn project, there was clearly a lack of available implementations in sequence analysis, even for standard tasks. Implementations of needed algorithmic components were either unavailable or hard to access in third-party monolithic software products. Addressing these concerns, the developers of SeqAn created a comprehensive, easy-to-use, open source C++ library of efficient algorithms and data structures for the analysis of biological sequences. Written by the founders of this project, **Biological Sequence Analysis Using the SeqAn C++ Library** covers the SeqAn library, its documentation, and the supporting infrastructure.

The first part of the book describes the general library design. It introduces biological sequence analysis problems, discusses the benefit of using software libraries, summarizes the design principles and goals of SeqAn, details the main programming techniques used in SeqAn, and demonstrates the application of these techniques in various examples. Focusing on the components provided by SeqAn, the second part explores basic functionality, sequence data structures, alignments, pattern and motif searching, string indices, and graphs. The last part illustrates applications of SeqAn to genome alignment, consensus sequence in assembly projects, suffix array construction, and more.

This handy book describes a user-friendly library of efficient data types and algorithms for sequence analysis in computational biology. SeqAn enables not only the implementation of new algorithms, but also the sound analysis and comparison of existing algorithms.

Visit SeqAn for more information.

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