C++ library for biological sequence analysis

• Open Source “BSD 3-Clause License”
• Support for Linux, Windows and OS X
• Support for GCC, CLANG, Visual Studio, ICPC (Intel)

Key library functionalities

• Full-text indexing
• Reference based alignment
• Formatted Input / Output
• Parallelized data structures and algorithms

Tools for high-throughput sequencing

• Flexbar – Read quality control
• Mason – Read simulation
• Yara – Read mapping
• Lambda – Protein BLAST
• And many more...

Infrastructure development

• Continuous integration and continuous deployment
• Benchmark tests with googlebench
• Code coverage tests

Training and education

• Added new training materials
• Developer, user meetings and conferences
• Online lectures and tutorials

Library & Application Development

• Continued development of SeqAn-3
• Vectorization and parallelization of alignments
• Search Schemes
• Fast and accurate identification of structural variation
• Exact read mapping for very large databases

Staff

• 1.0 full position (FTE)
• 1.0 student assistant (FTE)
• All positions are currently filled