Short description of the project

C++ library for biological sequence analysis
- Open Source “BSD 3-Clause License”
- Support for Linux, Windows and OS X

Key library functionalities
- Full-text indexing
- Sequence alignment
- Formatted Input / Output

Tools for high-throughput sequencing
- Flexbar – Read quality control
- Mason – Read simulation
- Yara – Read mapping
- Lambda – Protein BLAST
- And many more...

All tools are available as KNIME nodes

Progress report

Main achievements
- SeqAn 2.2.0 – Minor Release
- Established shorter release cycle
- Added intel compiler
- Continuous Integration ported to Jenkins
- Update notification for apps and library
- Improved manual and API doc
- Better KNIME Integration
- Parallelization of alignment module

Training
- SeqAn User Meeting

Outlook
- Planning SeqAn 3.0 – major release (2018)
- Continues Integration for Windows
- Continues Deployment
- User Meeting and Developer Meeting
- Automatic Docker builds

Publications

EPR-dictionaries: A practical and fast data structure for constant time searches in unidirectional and bidirectional FM-indices
C Parkarzetti, M Ehrhardt, K Reinert – RECOMB'16 (submitted)

de.NBI services

The de.NBI CIBI project partner at Free University of Berlin focuses on providing support and maintenance for the Open Source C++ library SeqAn as well as its associated tools. We offer to developers a high-quality software library together with continuous build and testing infrastructure, API documentation and a manual with guided tutorials. We provide support and consulting in using and extending current solutions through the GitHub issues platform or through our mailing list. In addition, we provide training and education events in the area of sequence analysis with focus on high-throughput sequencing.

de.NBI training and education
- 30th March 2016 – 1st April 2016
  o SeqAn User Meeting in Berlin