

projecet theses outline

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Read mapping is one of the key disciplines of sequence analysis today. A diverse selection of read-mapping tools has emerged over the last years, and while some of the differences are obvious, a comprehensive up-to-date comparison is not available.

Previous research on two unpublished datasets by the Lehrach department of Max-Planck-Institute has produced some contradicting results between two read mappers, BWA (Burrows-Wheeler-Alignment tool) and Bowtie. Both use the Burrows-Wheeler transformation, but BWA produces gapped alignments, while Bowtie is restricted to ungapped alignments. Curiously BWA's results on one dataset seem inferior, which is one reason to analyze these two programs further.

As part of this project, we will investigate the algorithmic differences and similarities of these two tools, and their influence on quality of results (sensitivity, specificity) and performance. To assess the quality, both programs will be compared with RazerS, a read-mapper that supports both gapped and ungapped alignments and uses a filter with explicit sensitivity control. The performance will be measured with an early version of the read mapper benchmark by Manuel Holtgrewe.