**AUTOMATED COMPARISON OF ALIGMENT TOOLS: BBMAP, BOWTIE 2 AND NEXTGENMAP**

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High-throughput sequencing has increased the amount of genomic data available by many orders of magnitude since the emergence of sequencing technologies. To make sense of this data, research pipelines rely on the alignment of the obtained millions of reads against a known reference genome. Since the amounts of data make manual comparisons impractical, this process (known as mapping) is entirely performed by computational tools. Mapping tools differ in the selection of input parameters offered, rely on a variety of algorithms, and are commonly called through the command line, which could seem confusing or intimidating for some users. Moreover, the output format of some statistical tools used to assess this programs can be too verbose and cumbersome, obstructing the evaluation and comparison of the alignments. As a result, the mapper and settings chosen are often just assumed, without prior testing nor optimization. In this study, a pipeline to compare and evaluate alignments was developed, which generates mappings with all combination of parameters possible, given the specifications of a single configuration file. Then, it gathers statistics of all the mappings produced in a single R tibble, and provides an interactive web-browser application to visualize and save custom-made plots of the results. The alignment tools BBMap, Bowtie2, and NextGenMap were evaluated for 48 parameter settings against 35 sets of filtered transcriptomic reads of the lichen-forming fungus *Peltigera membranacea*. The mapping quality, general error rate, percentage of mapped reads, and the number of mismatches, were contrasted against each other to develop a ranking of the mapper settings, revealing candidate settings with improved mappings.