Jabba: Hybrid Error Correction of Long Sequencing Reads

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Background. Third generation sequencing techniques produce longer reads with higher error rates than second generation methods. While the improved read lengths can provide useful information for downstream analysis, the higher error rates can complicate the required mapping or alignment. Hybrid strategies have been proposed to correct the long reads using accurate short reads. Mapping short reads on long reads may eliminate up to 99% of all errors in bacterial datasets, however this requires significant amounts of computing resources. Mapping the long reads on a k-mer frequencies based de Bruijn graph is significantly more efficient, but loses some accuracy on larger genomes.

Description. We present Jabba, a hybrid method to correct long reads by mapping them on a corrected de Bruijn graph. First, accurate second generation reads are used to build a de Bruijn graph, which is then corrected based on standard topological graph correction methods. Finally a path in the graph is then found by using maximal exact matches between a long erroneous read and the nodes of the de Bruijn graph. This path then dictates the corrected sequence.

Conclusions. Jabba achieves comparable gain to other available tools for bacteria and other small genomes. For larger genomes Jabba keeps performing well, while others either can not practically handle these at all, or only at significantly reduced gain.

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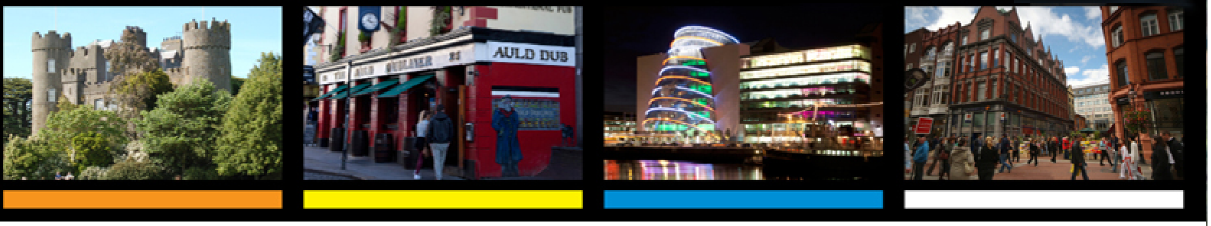

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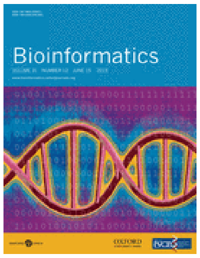

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