

# Smarti - A fast short read alignment algorithm

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## Abstract

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*Background: Short read alignment is the problem of aligning a set of short subsequences of a genome produced by a sequencer, called reads, to a known reference sequence. Publicly available tools such as Bowtie solve this problem, but runtime must be reduced to handle current and future alignment projects in an acceptable amount of time since sequencing technologies improve and produce huge amounts of reads and get faster rapidly.*

*Results: We present an algorithm to solve the problem efficiently on currently available desktop computer architectures, with the requirement of only 4GB RAM for even the human genome. Our implementation reaches a speedup of up to a factor of 23 compared to the current best available aligner Bowtie, with a marginal decrease in the amount of aligned reads. The implementation supports multi core CPUs while reaching a speedup of 1.9 on an architecture with two cores.*

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