

Abstract

In the last couple of decades, high-throughput sequencing has steadily become more effective and orders of magnitude cheaper. With the potential for millions of genomes being sequenced in the coming years, tools for analysing the large amounts of sequenced data will become increasingly important. Recent work in alignment-free genotyping methods have shown that alignment-free methods where we use statistical methods on analysis of *k*mers from sequenced reads can give competitive accuracies while being significantly faster compared to more established alignment-based methods. A recently published genotyper, KAGE, showed that an alignment-free genotyper implemented in Python could yield competitive accuracies while being more than 10 times faster than any other known method. This thesis explores how parts of KAGE that deals with large matrix- and array-operations can be GPU accelerated, and finally presents GKAGE, a GPU accelerated version of KAGE. GKAGE achieves up to 10 times speed up compared to KAGE and is able to genotype a human individual in only a few minutes on consumer grade hardware.