

	CPU Time	Wall clock time	Bowtie Speedup	Peak virtual memory usage	Reads mapped
Bowtie -n 1	8m:29s	10m:26s	-	1,169 MB	71.6%
Maq -n 1	6h:36m:57s	6h:38m:53s	38.2x	804 MB	70.3%
Bowtie	21m:32s	23m:27s	-	1,169 MB	76.5%
Maq	17h:46m:35s	17h:53m:07s	45.8x	804 MB	73.8%

Table 1: Performance measurements for mapping 8.96M 35bp Illumina/Solexa reads against the whole human genome on a single CPU of a workstation with a 2.40GHz Intel Core 2 Q6600 processor and 2 GB of RAM. Bowtie speedup is calculated with respect to wall clock time. Both CPU time and wall clock times are included to demonstrate that no one tool suffers disproportionately from I/O pauses or contention with other processes on the system. Note that Maq indexes the reads as it maps them, whereas Bowtie requires that an index of the genome be pre-built. The cost of building the Bowtie index is not included in these timings since we expect that in practice that cost will be rapidly amortized across multiple mapping jobs, or that the researcher will simply download a pre-built index from a shared repository in much less time than is required to build from scratch. Reads are taken from the 1000-Genomes project pilot via the NCBI Short Read archive, accession #SRR001115 and trimmed to 35bps. Reference sequences were the contigs of Genbank human genome build 36.3. Soap was not run because its memory footprint would have exceeded the physical RAM of the workstation. For the Maq runs, the reads were first divided into chunks of 2M reads each, as per the Maq Manual. Maq v0.6.6 was used.