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# Minia on Raspberry Pi

## Assembling a 100 Mbp genome on a Credit Card Sized Computer

Guillaume Collet, Guillaume Rizk, Rayan Chikhi, Dominique Lavenier

### MINIA: contig de novo assembler

This work shows that the genome assembly program MINIA is able to assemble a 100 Mbp genome on a Raspberry Pi. The MINIA software was developed to drastically reduce the memory footprint needed for genome assembly, enabling human genomes to be assembled on a desktop computer. The efficiency of MINIA is based on the DSK k-mer counting [1] and a compact de Bruijn graph data structure [2]. Here we show that it is also able to successfully assemble a genome on a very low-end, low-power system with 512 MB RAM and a 32 GB flash drive.

### K-mer counting with DSK

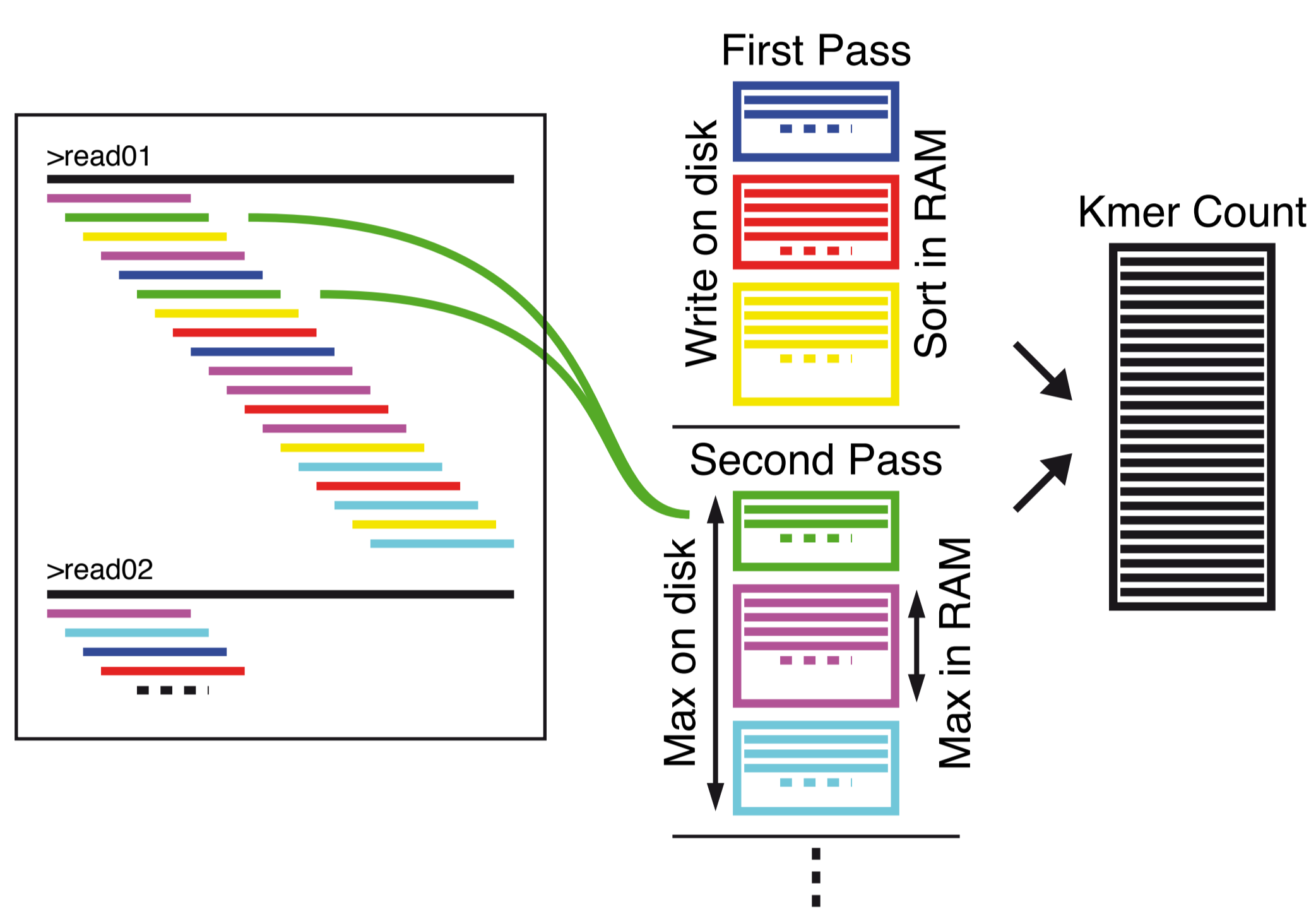


Figure 1: K-mer counting is performed by the fixed-memory and fixed-disk space algorithm DSK (Disk Streaming of K-mers). The set of k-mers is divided in partitions (colored boxes). Each k-mer is written only once on disk. Then, each partition is sorted and k-mers are counted. The trade-off between memory, disk-space, and computation allows to use DSK on a very small system.

### Compact de Bruijn graph data structure

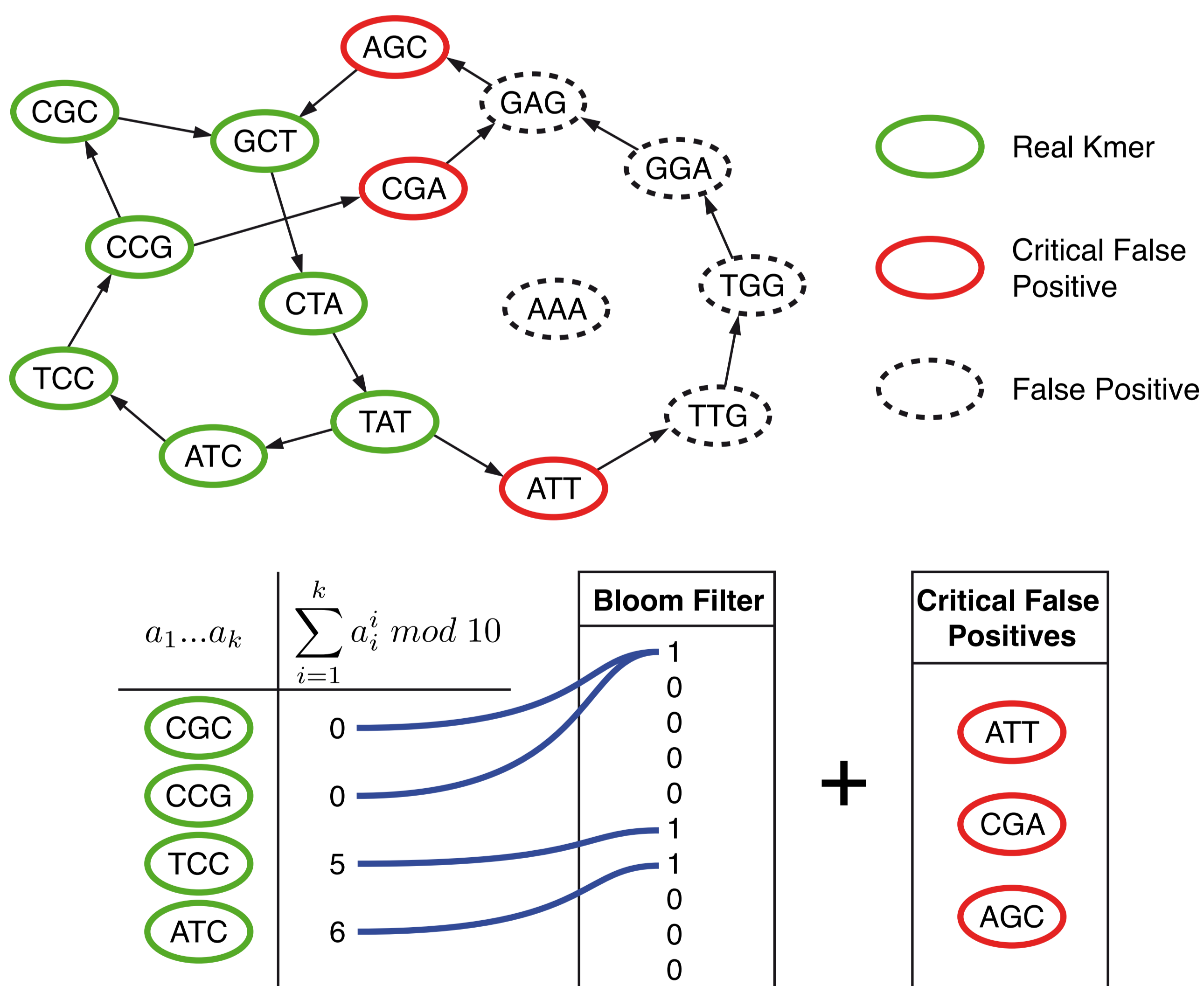


Figure 2: The probabilistic de Bruijn graph representation is obtained by inserting all the k-mers in a Bloom filter. Querying the Bloom filter for the membership of a k-mer may return a false positive answer. To avoid false positives, and consequently false branching, we propose to store the critical false positives only, in a separate structure. Thus false positives are not reachable.

### Picontigotron



### Raspberry Pi®

35€  
ARM11 700MHz  
512 MB RAM  
16 GB sdcard  
32 GB flash drive

Live demo  
during  
the poster sessions

### C. elegans assembly on Raspberry Pi

Our experiment consists in assembling the nematode *C. elegans*. We used 33 million unfiltered paired-end reads of length 100 bp (SRR065390), covering the genome at about 64x. Paired-end information was not used.

Method	Minia	SOAPdenovo	Velvet
System	Raspberry Pi	64GB/Xeon E5462	64GB/Xeon E5462
CPU Time (h)	18.9	6.25	13.5
Peak memory (GB)	<b>0.2</b>	29.6	30.6
Number of contigs (K)	29.5	29.5	28.2
Longest contig (Kbp)	75.2	90.9	62.6
Contig N50 (bp)	5741	5975	6031
Sum (Mbp)	86.4	88.3	90.4
Misassemblies	12	7	419
Genome fraction (%)	80.9	82.8	85.0
mismatches (per 100 kbp)	3.2	0.75	25.6

Table 1: De novo *C. elegans* contigs assembled by Minia [2], SOAPdenovo2 [4], and Velvet [3]. Assembly quality was computed using the QUAST software [5]. MINIA and Velvet were single-threaded. For SOAPdenovo2, the CPU time is the sum for each thread.

### MINIA applications

#### Human genome assembly with less than 6 GB RAM



<https://colibread.inria.fr/mapsembler2/>  
<https://colibread.inria.fr/read2snps/>

<http://minia.genouest.org/>



<http://kissplice.prabi.fr/>

#### References

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