

CORRECTION

# Correction: When Whole-Genome Alignments Just Won't Work: kSNP v2 Software for Alignment-Free SNP Discovery and Phylogenetics of Hundreds of Microbial Genomes

The PLOS ONE Staff

As the result of a bug in Kchooser, values of Fraction of Core kmers (FCK) were under-calculated by about a factor of two. As a result, the following sections of the paper were affected. The authors have uploaded a bug-fix version of Kchooser to SourceForge (<https://sourceforge.net/projects/ksnp>), along with an explanation of the issue.

In the Results and Discussion section, under the “Kchooser, a program to select an optimal k” subsection, there is an error in the third to final sentence and the second to final sentence. In the third to final sentence, “ $\geq 0.1$ ” should read “ $> 0.2$ .” In the second to final sentence, “ $-0.14029 - 0.19177 \log(\text{Branch length}), R = 0.99246$ ” should read “ $-0.24507 - 0.34278 \log(\text{Branch length}), R = 0.99265$ .” The correct sentences are as follow: “Based on these simulations it seems likely that when the fraction of core kmers is  $> 0.2$  over 90% of the SNPs will be identified by kSNP. At the optimum  $k = 13$ , the fraction of core kmers decreases very regularly as branch length (sequence variation) increases: Fraction of core kmers =  $-0.24507 - 0.34278 \log(\text{Branch length}), R = 0.99265$ .”



**Table 1. Optimum values of k for the examples in Table 2.**

Target Set	Optimum K	Fraction core kmersat optimum K
Example 1 <sup>1</sup>	13	0.124
Example 2 <sup>2</sup>	21	0.666
Filoviridae family	15	0.128
Rabies Lyssavirus	13	0.146
Rhabdoviridae family	13	0.030
<i>Acinetobacter</i>	19	0.021
<i>Escherichia coli O104:H4</i> clade	19	0.793
<i>Escherichia coli-Shigella</i> 68 finished genomes	19	0.525
<i>Escherichia coli-Shigella</i> including <i>O104:H4</i> strains from European outbreak	19	0.522

<sup>1</sup>Example 1 data set (provided with kSNP) consists of 11 equine encephalitis virus finished genomes.

<sup>2</sup>Example 2 data set provided with kSNP consists of 7 finished, 5 assembled and 2 raw read *E. coli* genomes.

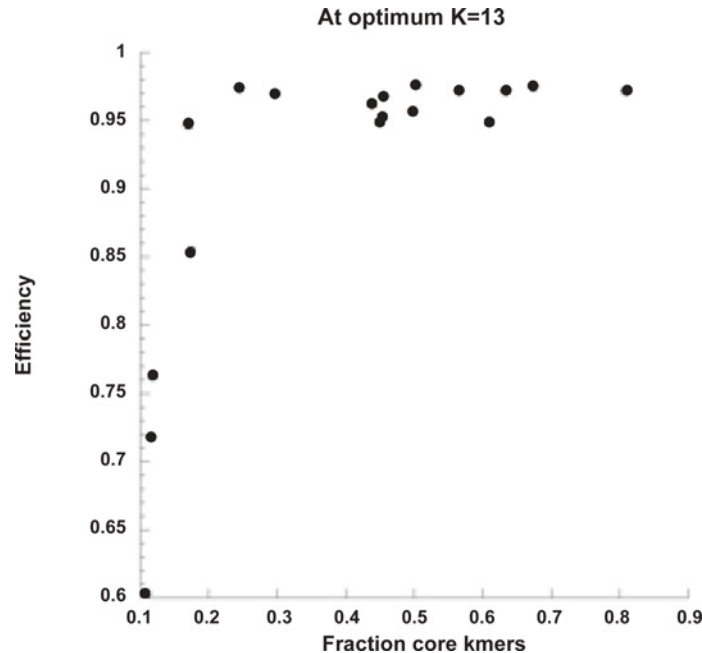
doi:10.1371/journal.pone.0118258.t001

**OPEN ACCESS**

**Citation:** The PLOS ONE Staff (2015) Correction: When Whole-Genome Alignments Just Won't Work: kSNP v2 Software for Alignment-Free SNP Discovery and Phylogenetics of Hundreds of Microbial Genomes. PLoS ONE 10(3): e0118258. doi:10.1371/journal.pone.0118258

**Published:** March 3, 2015

**Copyright:** © 2015 The PLOS ONE Staff. This is an open access article distributed under the terms of the [Creative Commons Attribution License](https://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.



**Fig. 3. kSNP efficiency vs the fraction of core kmers in simulated data sets.**

doi:10.1371/journal.pone.0118258.g001

Also in the Results and Discussion section, under the “Consequences of choosing a larger than optimal value of  $k$ ” subsection, there is an error in the first and third sentences. The number 0.1 should read 0.2. The correct first sentence is as follows: “Table 1 shows that for all of the viral genomes, and for the *Acinetobacter* genomes, at the optimum value of  $k$  the fraction of core kmers is well below 0.2, suggesting that a substantial fraction of the SNPs have not been detected.” The correct third sentence is as follows: “When the fraction of core kmers is below 0.2, there is a risk of missing a significant fraction of the SNPs.”

Additionally, there are errors in the “Fraction core kmers at optimum  $K$ ” column of Table 1. Please view the correct Table 1 below.

Further, Fig. 3 is incorrect. Please view the correct Fig. 3 here.

## Reference

- Gardner SN, Hall BG (2013) When Whole-Genome Alignments Just Won't Work: kSNP v2 Software for Alignment-Free SNP Discovery and Phylogenetics of Hundreds of Microbial Genomes. PLoS ONE 8 (12): e81760. doi: [10.1371/journal.pone.0081760](https://doi.org/10.1371/journal.pone.0081760) PMID: [24349125](https://pubmed.ncbi.nlm.nih.gov/24349125/)