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Sensitive and fast mapping of di-base encoded reads

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The authors find it worth mentioning that the parameters used to run the PerM mapper were not optimal to achieve full sensitivity. Based on the new recommendations of the developers of PerM, we used the latest version of PerM (v. 0.3.6), and updated two parameters as follows:

- –seed F2 (full sensitivity for 1 SNPs); -v 2 (number of mismatches); -k 1 000 000 (maximum number of alignment for a read); -A (report all possible mapping for a reads).

Previously, we have used '–seed S20 -k 10000 -v 4'. With this update, PerM now achieves full sensitivity in our simulation experiment. With real datasets (Table 6), PerM tends to map more reads compared with Bowtie, but maps slightly less than Mapreads and SOCS.

We would like to apologize for the previous parameter sets we used for PerM, due to our misinterpretation of its documentation. We now update the relevant rows in Tables 3 and 6 as follows.

Table 3. Performance of PerM with simulated datasets considering the new parameters

Dataset	Mapper	Time (min)	Map locations	Reads mapped (%)
Set 1	PerM	9	46 854 056	**100**
Set 2	PerM	6	17 290 574	**100**
Set 3	PerM	6	24 525 864	**100**

Reads are simulated from human reference genome build 35 (chromosome 1). Set 1: no errors; Set 2: color errors; Set 3: substitutions.

Table 6. Performance of PerM with real datasets using the new parameters

Dataset	Mapper	Time (min)	Map locations	Reads mapped (%)
NA18507	PerM	35	51 012 126	35.2
NA10847	PerM	130	132 417 348	44.6
NA12156	PerM	116	64 821 620	31.1