

CORRECTION Open Access

Correction: Detection and classification of peaks in 5' cap RNA sequencing data

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Correction

After the publication of this work [1], we became aware of several errors.

- 1. The headings of Table 1 and Table 2 have been swapped. Table 1 heading should read: "Summary of features and how they are calculated" while Table 2 heading should read: "Number of peaks found by Poisson thresholding of sliding window method."
- 2. In Methods section, the last sentence of 'Peak finding' should read: "Finally, any peak windows separated by less than **50** (not 30) base pairs are merged into a single peak."
- 3. In Results section, 'Classification evaluation', description of Figure 4B should read: "Recall is essentially the same as for the internal feature set, while a moderate improvement of **precision** is observed". Description of Figure 4C should read: "Precision is better, relative to the internal feature set."
- 4. One of the software packages we used, Genomic Ranges has been published recently, and can now be referenced [2].

The changes do not affect the correctness of the method described. We regret any inconvenience that these errors might have caused.

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References

- Strbenac D, Armstrong NJ, Yang JYH: Detection and classification of peaks in 5' cap RNA sequencing data. BMC Genomics 2013, 14(Suppl 5):S9.
- Lawrence M, Huber W, Pagès H, Aboyoun P, Carlson M, Gentleman R, Morgan MT, Carey VJ: Software for computing and annotating genomic ranges. PLoS Comput Biol 2013, 9:e1003118.

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