

Erratum: A reference bacterial genome dataset generated on the MinION™ portable single-molecule nanopore sequencer

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Recently we noticed that we could not reproduce Figure three (Figure 1 here) while analysing this data as part of a new experiment [1]. This was due to a modification to the script used for extracting sequence alignment profiles from the dataset [2]. On further investigation we found that an error in this script had been reported and a fix supplied by an anonymous online contributor on October 27th 2014 via Github [3]. The error prevented mismatches from being properly counted in the calculation of read accuracy (insertions and deletions were). We therefore present updated versions of Figures three (Figure 1 here) and four (Figure 2 here) generated by the corrected script. We are grateful to the anonymous contributor who noticed this error. The manuscript text and tables are unaffected.

We would also like to correct the spelling of Minh Duc Cao in the Acknowledgements section.

We apologise for any inconvenience caused by this error.

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Received: 31 December 2014 Accepted: 5 January 2015

Published online: 13 February 2015

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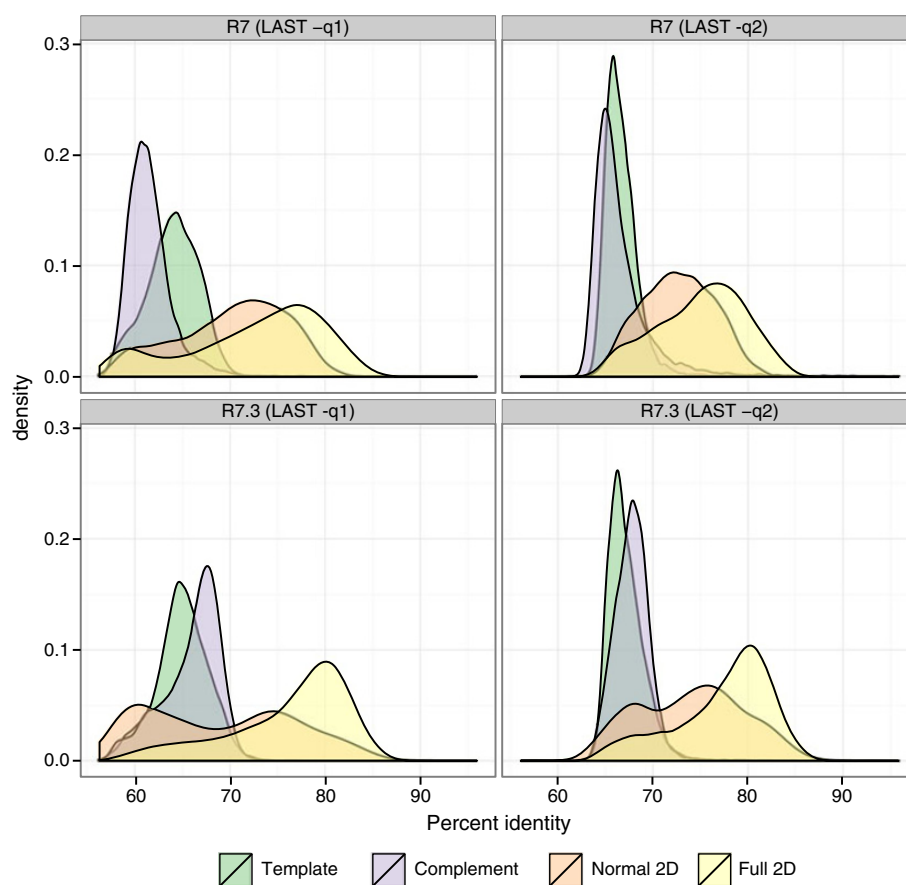


Figure 1 Kernel density plots showing accuracy for R7 and R7.3 chemistries with two different values for the LAST substitution penalty score.

