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### Title

Correction to: Comprehensive benchmarking and ensemble approaches for metagenomic classifiers

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CORRECTION

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# Correction to: Comprehensive benchmarking and ensemble approaches for metagenomic classifiers

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**Correction to: *Genome Biol* (2017) 18:182**  
<https://doi.org/10.1186/s13059-017-1299-7>

Following publication of the original article [1], the authors would like to highlight the following two corrections:

- 1) The updated “Availability of data and materials” declaration to the article:  
The datasets and scripts supporting the conclusions of this article are freely and publicly available through the IMMSA server, <ftp://ftp-private.ncbi.nlm.nih.gov/nist-immsa/IMMSA/> Scripts used for analysis and generating figures are available at: [https://scu.med.cornell.edu/git/abm237/benchmarking\\_metagenomic\\_classifiers](https://scu.med.cornell.edu/git/abm237/benchmarking_metagenomic_classifiers)
- 2) The authors would like to clarify that the kraken db build command in the manuscript is for the bacterial database; the command for the standard db is available through the kraken manual: `kraken-build --standard --db $DBNAME`

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1. McIntyre ABR, et al. Comprehensive benchmarking and ensemble approaches for metagenomic classifiers. *Genome Biol.* 2017;18:182. <https://doi.org/10.1186/s13059-017-1299-7>.

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