

Retraction and replacement of: FGeneBERT: function-driven pre-trained gene language model for metagenomics

This is a retraction and replacement of: Chenrui Duan, Zelin Zang, Yongjie Xu, Hang He, Siyuan Li, Zihan Liu, Zhen Lei, Ju-Sheng Zheng, Stan Z Li, FGeneBERT: function-driven pre-trained gene language model for metagenomics, *Briefings in Bioinformatics*, Volume 26, Issue 2, March 2025, bbaf149, <https://doi.org/10.1093/bib/bbaf149>.

In May 2025, a reader notified the Journal of several inaccuracies and inconsistencies in the original publication. The specific inaccuracies identified are outlined below:

- Incorrect reference to “MetaPhlAn5” instead of “MetaPhlAn4”
- Mischaracterization of ultrasonic fragmentation
- Ambiguity regarding ENA as a software vs. repository
- Inconsistent naming of the proposed model (“FGBERT” vs. “FGeneBERT”)
- Duplicate citation entries and typographical errors
- Misdefinition of degenerate DNA code “Y” and underestimation of FLOPs
- Inaccessibility of the model via the stated public link

The authors have subsequently corrected these inaccuracies and revised affected text, including tables. Given the nature and the number of the changes throughout the Introduction, Model Efficiency Analysis section under Results & Conclusions, Table 7, and Table 8, the Authors are retracting the original version of the article and replacing it with a new version, which has been reviewed and accepted by the editors. The new version has been republished as <https://doi.org/10.1093/bib/bbaf592>.