

Correction

Open Access

Uncovering rate variation of lateral gene transfer during bacterial genome evolution

Weilong Hao and G Brian Golding*

Address: Department of Biology, McMaster University, Hamilton, Ontario, Canada, L8S 4K1

Email: Weilong Hao - haow@indiana.edu; G Brian Golding* - golding@mcmaster.ca

* Corresponding author

Published: 25 November 2008

Received: 20 October 2008

BMC Genomics 2008, 9:556 doi:10.1186/1471-2164-9-556

Accepted: 25 November 2008

This article is available from: <http://www.biomedcentral.com/1471-2164/9/556>

© 2008 Hao and Golding; licensee BioMed Central Ltd.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

On page 11 of our publication [1], the correction for missing data in a discrete Γ distribution was conducted as

$$Q_+ = \prod_{i=1}^N L_+^i = \prod_{i=1}^N \sum_{j=1}^M p_j \frac{L^i(\mu_j)}{1 - L^i(\mu_j)}. \quad (1)$$

This correction, equation (1), is only correct when the category probabilities p_j have no effect on observability. Because the category probabilities have an effect on observability, the appropriate correction is

$$Q_+ = \prod_{i=1}^N L_+^i = \prod_{i=1}^N \frac{\sum_{j=1}^M p_j L^i(\mu_j)}{1 - \sum_{j=1}^M p_j L^i(\mu_j)}. \quad (2)$$

Here N is the total number of gene families and M is the number of rate categories. Analyses based on equation (2) as opposed to equation (1) revealed remarkably similar results and all conclusions made based on the old method remain qualitatively unchanged. The additional analyses and the altered tables are provided in Additional File 1 and also available at <http://evol.mcmaster.ca/~weilong/research.html>. We thank Dr. Matt Spencer for pointing out the difference in averaging methods and thank Drs. David Bryant, Ofir Cohen, Miklós Csűrös, Tal Pupko, and Ed Susko for communication of ideas.

Additional material

Additional file 1

Click here for file

[<http://www.biomedcentral.com/content/supplementary/1471-2164-9-556-S1.pdf>]

References

1. Hao W, Golding GB: **Uncovering rate variation of lateral gene transfer during bacterial genome evolution.** *BMC Genomics* 2008, **9**:235.