

Correction

LineageSpecificSeqgen: generating sequence data with lineage-specific variation in the proportion of variable sites

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Published: 13 August 2009

Received: 12 August 2009

BMC Evolutionary Biology 2009, 9:200 doi:10.1186/1471-2148-9-200

Accepted: 13 August 2009

This article is available from: <http://www.biomedcentral.com/1471-2148/9/200>

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Abstract

Correction to Shavit Grievink L, Penny D, Hendy MD, Holland BR: **LineageSpecificSeqgen: generating sequence data with lineage-specific variation in the proportion of variable sites**. *BMC Evol Biol* 2008, **8**(1):317.

Correction

Since publication of our article [1], we discovered an error in the second example. For this example, we state in the paper, we used the program MrBayes [2] with the JC+I+Cov model. However, we now found that, albeit appearances, this model is not implemented in MrBayes [2]. In fact, no combination of I+Cov (e.g. HKY+I+Cov, GTR+G+I+Cov) is currently implemented in MrBayes [2]. Instead, the program ignores the I parameter, so tree reconstruction in this example was therefore effectively done using the JC+Cov model. This does not affect the conclusion of our paper that phylogenetic estimation can be misleading for sequence data simulated with lineage-specific properties.

References

1. Shavit Grievink L, Penny D, Hendy MD, Holland BR: **LineageSpecificSeqgen: generating sequence data with lineage-specific variation in the proportion of variable sites**. *BMC Evol Biol* 2008, **8**(1):317.
2. Ronquist F, Huelsenbeck JP: **MrBayes 3: Bayesian phylogenetic inference under mixed models**. *Bioinformatics* 2003, **19**(12):1572-1574.

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2008-11-21

<http://hdl.handle.net/10179/9703>

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