Correction

LineageSpecificSeqgen: generating sequence data with lineage-specific variation in the proportion of variable sites
Liat Shavit Grievink*, David Penny, Mike D Hendy and Barbara R Holland

Address: The Allan Wilson Centre for Molecular Ecology and Evolution, Massey University, Private Bag 11 222, Palmerston North, New Zealand

Email: Liat Shavit Grievink* - l.shavit@massey.ac.nz; David Penny - d.penny@massey.ac.nz; Mike D Hendy - m.hendy@massey.ac.nz; Barbara R Holland - b.r.holland@massey.ac.nz

* Corresponding author

Abstract


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