



INSTITUTE FOR GENOMICS AND EVOLUTIONARY MEDICINE

## Closed codon models: just a hopeless dream?



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The “Lie closure” of a set of matrices is the smallest matrix Lie algebra (a linear space of matrices closed under the operation  $[A, B] = AB - BA$ ) which contains the set. In the context of Markov chain theory, if a set of rate matrices form a Lie algebra, their corresponding Markov matrices are closed under matrix multiplication, which has been found to be a useful property in phylogenetics. Inspired by previous research involving Lie closures of DNA models, it was hypothesised that finding the Lie closure of a codon model could help to solve the problem of mis-estimation of the synonymous/non-synonymous rate ratio,  $\omega$ . There is a second method of finding a Lie algebra associated to a model: instead of beginning the Lie closure process with the smallest linear space that contains the model (the linear closure), we change any non-linear constraints of the model to additive ones, which results in an alternative linear space for which the Lie closure is found. Under both processes, it was found that closed codon models would require thousands of parameters and any partial solution to this problem that was of a reasonable size violated stochasticity. Investigation of toy models indicated that finding the Lie closure of matrix linear spaces which deviated only slightly from a simple model resulted in a Lie closure that was close to having the maximum number of parameters possible. Given that Lie closures are not practical, we propose further consideration of the variants of linearly closed models.

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