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## 6 Faster than neutral evolution of constrained sequences: the complex interplay of mutational biases and weak selection.

Lawrie DS, Petrov DA, Messer PW  
Genome Biol Evol. 2011; 3:383-95

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**Julien Dutheil** and **Nicolas Galtier**, Université Montpellier II, France. **F1000**  
**Genomics & Genetics**

**6** RECOMMENDED21 Sep 2011 | **New Finding**

Functional inference from comparative genome analyses has been based on a simple but strong principle: functional sequences evolve more slowly than neutral ones. This important paper by Lawrie et al. questions this basic assumption.

The authors demonstrate that mutational biases cause constrained sequences to evolve faster than the neutral expectation if selection is weak and if the mutational bias favors states that are counterselected. The effect is stronger as the mutational bias increases. These results recapitulate earlier results from McVean and Charlesworth {1}. The authors also demonstrate how this phenomenon, in practice, affects comparative methods used for the detection of constraints. This work is important because it demonstrates that accounting for mutational biases is required to accurately and precisely infer regions of the genome under purifying selection. As it has been shown that neutral biases also interfere with the detection of positive selection (see ref {2}, on which Nicolas Galtier is an author), this article largely contributes to the rising message that the proper accounting for molecular mechanisms of genome evolution is the next challenge for increasing the predictive power of genome scans.

## References:

- {1} McVean and Charlesworth, Genet Res 1999, 74:145-58 Please [click here for the full text](#) of this article.  
{2} Ratnakumar et al. Philos Trans R Soc Lond B Biol Sci 2010, 365:2571-80 [[PMID:20643747](#)].

**Competing interests:** None declared

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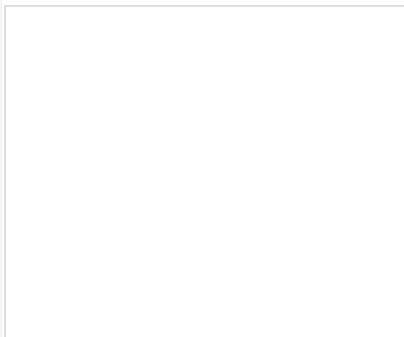
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