

Potential impact of recombination on sitewise approaches for detecting positive natural selection.

[Shriner D](#), [Nickle DC](#), [Jensen MA](#), [Mullins JI](#).

Department of Microbiology, University of Washington School of Medicine, Seattle, WA 98195-8070, USA. dshriner@u.washington.edu

Current sitewise methods for detecting positive selection on gene sequences (the de facto standard being the CODEML method (Yang et al., 2000)) assume no recombination. This paper presents simulation results indicating that violation of this assumption can lead to false positive detection of sites undergoing positive selection. Through the use of population-scaled mutation and recombination rates, simulations can be performed that permit the generation of appropriate null distributions corresponding to neutral expectations in the presence of recombination, thereby allowing for a more accurate estimation of positive selection.