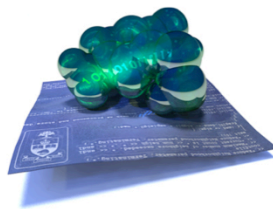


A
BIOINFORMATICS
COURSE

QUANTIFYING SELECTIVE PRESSURE



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Uses of explicit phylogenetic analysis include distinguishing *neutral* and adaptive evolution, and distinguishing genes that are under *recent purifying selection*.

Almost all evolutionary change is in fact assumed to be neutral.

Adaptive change, or *positive selection* or *purifying selection* can be found by comparing the ratio of synonymous to non-synonymous mutations in coding sequences.

$$\omega = dN / dS$$

non-synonymous rate

synonymous rate

Interpreting a gene as being under “recent purifying selection” is based on evidence regarding phenotypic differences between closely related species. For example: genes associated with the human language ability are expected to be under recent purifying selection relative to their orthologues in the higher primates.

In order to detect purifying selection we evaluate the ratio of synonymous to non-synonymous mutations.

Note that the non-synonymous rate ω may be time-dependently different in different lineages.

For a recent discussion see: Bárbara D Bitarello, Rodrigo dos Santos Francisco and Diogo Meyer. 2014. Variation of nonsynonymous/synonymous rate ratios at HLA. bioRxiv: <http://dx.doi.org/10.1101/008342>

(<http://biorxiv.org/content/biorxiv/early/2014/08/22/008342.1.full.pdf>)

Recent positive selection reduces genetic variability.

Detecting recent positive selection requires considering population size. Bottlenecks can cause false positives.

Directional selection, balancing selection and purifying selection leave distinct signatures.

For a recent novel method to address the statistics of detecting recent positive selection, see: Lee, H. 2011. A new test for detecting recent positive selection that is free from the confounding impacts of demography. *Mol Biol Evol.* 2011 28(1):365-75.

<http://steipe.biochemistry.utoronto.ca/abc>

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