

- dN/dS analyses on coding sequence MSAs are ubiquitous (1000s of papers each year): very useful biological insights.
- A very large fraction of analyzed MSAs contain “local” alignment errors.
- Sensitive statistical methods often interpret these errors as evolutionary signal.
- The problem is only exacerbated in larger MSAs with more divergent species
- Can we turn the sensitivity of these methods to our advantage to find and “filter” the errors.
- Based on very simple intuition and extensions of “tried-and-true” methods.

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