

# Introduction

Over the years, a variety of models have been proposed to describe the effects of natural selection on protein-coding sequences. Traditionally, the focus has been on estimating the evolutionary rate ratio,  $\omega = dN/dS$ , the rate of nonsynonymous to synonymous substitutions, which indicates how quickly a protein’s constituent amino acids change. Following early counting methods for estimating  $dN/dS$  (e.g. refs [1] and [2]), mechanistic codon substitution models (see ref. [3] for a comprehensive review) have taken a leading role as the inference method of choice since their introduction in the 1990s [4, 5]. These so-called  $\omega$  models have seen great success in the field of molecular evolution and are widely used to examine the strength of selection pressure in protein-coding sequences.

More recently, a second class of models, known as mutation-selection-balance (MutSel) models, has emerged as a popular alternative to  $\omega$  models. MutSel models explicitly model the dynamic balance between mutation and selection, lending a potentially more precise and realistic description of the evolutionary process than do  $\omega$  models, which merely model the final outcome (e.g. substitution) of the underlying mutation-selection interplay [6–9]. Unlike  $\omega$  models, MutSel models yield estimates of amino acid selection coefficients, which indicate the extent to which natural selection favors, or disfavors, particular amino acids at protein positions. These selection coefficients, which can in turn be scaled relative to a focal amino acid, the primary parameters of interest that MutSel models produce. Although MutSel models were first introduced over 15 years ago [6], they have seen virtually no use due to their high computational expense. However, recently, several computationally tractable model implementations have emerged [10, 11], allowing for the first time the potential for widespread use.

Although both  $\omega$  and MutSel models describe the same fundamental process of protein-coding sequence evolution along a phylogeny, it is largely unknown how these two classes of models relate to one another. In particular, as these inference methods have been developed independently, it remains an open question whether or not parameter estimates from one model are comparable to those of the other model. Therefore, while certain rhetorical arguments may be made in favor of using one method over another, there is currently no formalized, concrete rationale to guide researchers in their methodological choices.

Here, we aim to formalize the relationship between  $\omega$  and MutSel models by examining the extent to which their focal parameters,  $\omega$  and scaled amino acid selection coefficients, yield overlapping information about the evolutionary process. To this end, we derive a mathematical relationship

these models' primary parameters from which one can infer  $\omega$  values from selection coefficients alone. Using a simulation approach, we verify that  $\omega$  values estimated using selection coefficients alone correspond precisely to those inferred using the standard maximum likelihood  $\omega$  inference approach. Further, we prove that, under conditions of symmetric mutation rates, this relationship holds only under regimes of purifying selection or neutral evolution ( $dN/dS \leq 1$ ). This proof reveals that MutSel models are inherently unable to describe accurately protein evolution under a regime of positive diversifying selection, or when  $dN/dS > 1$ . This result has important implications for circumstances under which MutSel model use is justified.

Moreover, using this relationship as a benchmark, we have uncovered some potential biases inherent in  $\omega$  inference methods. Typically, inference framework performance is assessed through simulating datasets which adhere to the underlying model's assumptions. However, this strategy can only confirm that inference methods are behaving as expected; it cannot confirm that the underlying model accurately represents the evolutionary process. Instead, we suggest an alternate approach to benchmark inference methods, and indeed evolutionary models: assessing the extent to which distinct models agree may serve as a novel, robust strategy to determine the accuracy of different modeling frameworks.

## Methods

### Sequence simulation and omega inference

We simulated protein-coding sequences as a continuous-time Markov process [12] according to the MutSel model proposed by [6]. This model's instantaneous rate matrix  $Q = q_{ij}$ , which describes the probability of substitution from codon  $i$  to codon  $j$ , is given by

$$Q_{ij} = \begin{cases} 0 & \text{multiple nucleotide changes} \\ f_{ij}\mu_{ij} & \text{single nucleotide transversion} \\ f_{ij}\mu_{ij}\kappa & \text{single nucleotide transition} \end{cases}, \quad (1)$$

where  $\mu_{ij}$  is the symmetric nucleotide mutation rate and  $f_{ij}$  is the fixation probability from codon  $i$  to  $j$ . The fixation probability is defined as

$$f_{ij} = \ln\left(\frac{\pi_j\mu_{ij}}{\pi_i\mu_{ji}}\right) / \left(1 - \frac{\pi_i\mu_{ji}}{\pi_j\mu_{ij}}\right), \quad (2)$$

where  $\pi_i$  is the equilibrium frequency of codon  $i$ .

For each simulation, we generated scaled amino acid selection coefficients,  $s_a$ , by fixing one coefficient to 0 and drawing the remaining 19 values from a normal distribution  $\mathcal{N} \sim (0, \lambda)$ . The standard deviation parameter  $\lambda$  effectively represents the strength of selection; smaller  $\lambda$  values will produce similar amino acid fitness values, whereas larger values will naturally lead to a stronger preference for certain amino acids. For each simulation, we selected a value for  $\lambda$  from  $\mathcal{U} \sim (0.5, 3.5)$ . We converted these selection coefficients to steady-state amino acid frequencies  $\pi_a$  according to

$$\pi_a = \frac{e^{s_a}}{\sum_b e^{s_b}}, \quad (3)$$

where the denominator sums over all 20 amino acids [13]. These frequencies were then assigned to amino acids, and subsequently converted to codon frequencies (assuming no codon bias).

We simulated protein-coding sequences along a 10-taxon phylogeny, with all branch lengths equal to 0.01, beginning with a root sequence selected using steady-state codon frequencies. Unless otherwise stated, we simulated alignments of 500,000 codon positions with a global, symmetric mutation rate  $\mu_{xy} = 10^{-5}$ , and a value for  $\kappa$  was drawn from  $\mathcal{U} \sim (1, 5)$ . A single evolutionary model was applied to all positions in the simulated sequences, meaning that we did not incorporate any site-wise variation into the evolutionary process. While this lack of site-wise heterogeneity is unrealistic for real sequence evolution, it allows us to verify our derived relationship between selection coefficients and  $\omega$  with a sufficiently sized data set.

For each simulated alignment, we inferred  $\omega$  in two main ways; first, we calculated  $\omega$  using the mathematical framework described in (??)–(9), and second, we inferred  $\omega$  used the standard maximum likelihood M0 model [14], which uses the GY94 rate matrix [4], as implemented in HyPhy [15]. The GY94 matrix includes the primary parameters  $\omega$ ,  $\kappa$ , and equilibrium codon frequencies. As it is well-known that the manner of specification for the latter two parameters strongly influences  $\omega$  estimates [12, 16], we inferred  $\omega$  under a variety of model parameterizations, including three  $\kappa$  parameterizations ( $\kappa$  fixed to 1,  $\kappa$  fixed to its true value, and  $\kappa$  as a free parameter), and four codon frequency specifications (equal codon frequencies, F3x4 codon frequencies [5], CF3x4 codon frequencies [17] and empirical, or F61, codon frequencies [4]). These different specifications yielded twelve maximum likelihood  $\omega$  inferences per simulated alignment. All code used is freely available at **github**.

## Results

### Mathematical relationship between selection coefficients and omega

We describe here how to calculate  $dN/dS$  from the parameters of a MutSel model. We assume the following: (i) the mutational process is symmetric, such that  $\mu_{xy} = \mu_{yx}$  for all nucleotide pairs  $xy$ ; (ii) all synonymous codons for a given amino acid have the same fitness; there is no synonymous rate variation or codon bias.

In the framework of a MutSel model, we can write the steady-state frequency of amino acid  $a$  as

$$\pi_a = \frac{e^{s_a}}{\sum_b e^{s_b}}, \quad (4)$$

where the sum in the denominator runs over all 20 amino acids [18]. Here,  $s_a$  is the scaled selection coefficient for amino acid  $a$ ; larger  $s_a$  values correspond to higher frequencies of amino acid  $a$ , and corresponds precisely to MutSel model parameters [6]. Amino acid frequencies can be subsequently converted to codon frequencies, assuming no codon bias, as

$$\pi_i = \pi_a / n_a, \quad (5)$$

where  $i$  is any codon coding for amino acid  $a$  and  $n_a$  is the total number of codons which code for  $a$ .

The fixation probability for a mutation from codon  $i$  to codon  $j$  is [6, 18]

$$f_{ij} = \frac{1 - (\pi_i/\pi_j)^{1/N_e}}{1 - \pi_i/\pi_j} \approx \frac{1}{N_e} \frac{\ln \pi_j - \ln \pi_i}{1 - \pi_i/\pi_j}, \quad (6)$$

where  $N_e$  is the effective population size. We can calculate an evolutionary rate Using this framework, we can calculate an evolutionary rate by summing over all fixation probabilities weighted by the frequency of the originating codon. Further, we can establish expressions specifically for nonsynonymous and synonymous evolutionary rate, and then divide them in order to obtain a value for the evolutionary rate ratio  $dN/dS$ .

For example, we can write the synonymous rate  $K_S$  as

$$K_S = N_e \sum_i \sum_{j \in \mathcal{S}_i} \pi_i f_{ij} \mu_{ij}, \quad (7)$$

where  $\mathcal{S}_i$  is the set of codons that are synonymous to codon  $i$  and differ from it by one nucleotide substitution. To normalize  $K_S$ , we divide it by the number of synonymous sites, which we calculate

according to the mutational opportunity definition of a site [4, 12] as

$$L_S = \sum_i \sum_{j \in \mathcal{S}_i} \pi_i \mu_{ij}. \quad (8)$$

Under the assumption that all synonymous codons have equal fitness, and hence all synonymous mutations are selectively neutral, we have  $f_{ij} = 1/N_e$  [19], and thus we find that  $dS$ , the synonymous rate per synonymous site, is equal to 1.

Similarly, we can derive an expression for  $dN$ , the non-synonymous rate per non-synonymous site, and we find

$$dN = \frac{K_N}{L_N} = \frac{N_e \sum_i \sum_{j \in \mathcal{N}_i} \pi_i f_{ij} \mu_{ij}}{\sum_i \sum_{j \in \mathcal{N}_i} \pi_i \mu_{ij}}, \quad (9)$$

where  $\mathcal{N}_i$  is the set of codons that are nonsynonymous to codon  $i$  and differ from it by one nucleotide substitution. The quantities  $K_N$  and  $L_N$  are defined as in Eqs. (7) and (8) but summing over  $j \in \mathcal{N}_i$  instead of  $j \in \mathcal{S}_i$ . Equations (4)–(9) establish a connection between the scaled amino acid selection coefficients  $s_a$  (i.e., the primary parameters of a MutSel model) and the evolutionary rate ratio  $dN/dS$ .

### Scaled selection coefficients fully encapsulate $\omega$

To validate our derived relationship between scaled selection coefficients and  $\omega$ , we simulated protein-coding sequences along a 10-taxon phylogeny according to the Halpern-Bruno mutation-selection model [6], assuming no codon bias and symmetric nucleotide mutation rates. We calculated an  $\omega$  for each simulated alignment using the derivations given in equations (4)–(9) as well as standard (ML) methods, according to the GY94 [4] rate matrix, as implemented in the HyPhy batch language [15].

As shown in Figure 1A,  $\omega$  values derived using selection coefficients agree nearly perfectly with those inferred using standard maximum likelihood methods. We additionally demonstrate convergence of these values with increasing amounts of data, represented by simulated alignment length (Figure 1B). Taken together, these results clearly show that MutSel model parameters fully encapsulate information regarding the evolutionary rate ratio,  $\omega$ , and that the results from MutSel and  $\omega$  models are largely in agreement.

Moreover, as seen in Figure 1A, estimates for  $\omega$  never exceed 1, but rather all reflect a regime of purifying selection. In fact, in SuppMat, we prove that, when calculated using amino acid selection coefficients,  $\omega$  is always less than or equal to 1. This important insight reveals that, while MutSel models fully agree with  $\omega$  models, they only do so under conditions of purifying selection or neutral

evolution. MutSel models, therefore, are inherently unable to describe protein evolution under positive, diversifying selection ( $\omega > 1$ ).

## Influence of ML model parameterizations

ML  $\omega$  values reported in the previous subsection were obtained by fixing  $\kappa$  parameter in the GY94 rate matrix to its true simulated value, and specifying equal codon frequencies. However, it is well-known that different ML parameterizations can influence its  $\omega$  estimation [12, 16, 20]. Therefore, we additionally inferred ML  $\omega$  values according to 11 other model parameterizations. Specifically, we inferred  $\omega$  when  $\kappa$  was either a free parameter of the model, fixed to its true value, or fixed to 1, and we examined different equilibrium codon frequency specifications, including equal codon frequencies, frequencies calculated using either the F3x4 [5] or the CF3x4 [17] estimators, or empirical codon frequencies as taken from the simulated alignment. Table 1 shows how the  $\omega$  values estimated according to these different ML parameterizations relate to the  $\omega$  values as calculated using equations (4)–(9).

Several important insights into the behavior of ML  $\omega$  models can be gained from these results. First, it is clear that equal codon frequencies dramatically outperform all other specifications. Under this frequency specification, ML also estimates  $\kappa$  fairly accurately while maintaining an extremely high  $\omega$  correlation of 0.993. Second, the F3x4 and CF3x4 frequency estimators perform nearly identically to one another, and neither frequency specification estimates  $\omega$  values which correlate with our derived  $\omega$ . Finally, when empirical codon frequencies are used,  $\omega$  estimates have a moderately strong, negative correlation. In fact, under this frequency specification, ML  $\omega$  values are dramatically inflated, as illustrated in Figure 2. As we have proven that, when calculated from scaled selection coefficients,  $\omega$  is necessarily less than or equal to 1, we interpret the use of F3x4 or empirical codon frequencies effectively as ML model misspecifications, leading to grossly elevated  $dN/dS$  values. However, it is interesting to note that, while ML yields the most accurate  $\kappa$  estimates when codon frequencies are set to 1/61 each, all frequency specifications yield  $\kappa$  estimates which correlate relatively strongly with the true  $\kappa$  values. Thus, the ML model’s ability to accurately estimate  $\kappa$  appears much more robust to codon frequency specifications than its ability to estimate  $\omega$ .

Thus, the question emerges of why specifying equal codon frequencies leads to precisely accurate  $dN/dS$  estimates, whereas the other, more commonly used specifications produce incorrect and biased estimates. The basis for including codon frequencies in mechanistic codon substitution

models is to capture biases in the underlying nucleotide base frequencies [12, 16]. Indeed, our simulations produced alignments with a wide array of GC-content values (ranging from 0.23 - 0.72), yet the GC-content had no effect on  $\omega$  correlations ( $p = 0.55$ , when  $\text{lm}(\text{derived ml} + \text{gc})$ ). Importantly, as we adopted symmetric mutation rates in our simulations, these varying degrees of GC-content were not caused by any bias towards unequal base frequencies, but rather by codon fitness differences alone, as dictated by amino acid propensities. Thus, the correct frequencies to specify in ML inference should reflect those frequencies which would be present *in the absence* of selection, which in this case corresponds to equal codon frequencies.

To further demonstrate this point, we conducted additional simulations which used asymmetric mutation rates. We adopted the asymmetric mutation scheme proposed in [18] that promotes compositional bias either towards an AT-rich or GC-rich sequence. We simulated sequences according to two broad simulation frameworks: one in which equilibrium codon frequencies were determined as before (e.g. from Boltzmann-distributed amino acid frequencies), and the other in which all codons had an equal equilibrium frequency of  $1/61$ . In other words, the former scenario produced GC-content biases from two sources (mutation and selection), whereas the latter scenario produced GC-content bias from only mutation.

Results here were pretty straightforward - when only mutation produced the unequal base frequencies, ML performed roughly the same across frequency specifications (albeit a slight error increase when  $f3 \times 4$ ) and when kappa was true or a free parameter. Interesting, when kappa was fixed to 1 here, ML systematically underestimated omega. However in cases when kappa was a free parameter, ML basically got omega and kappa correct.

However, when we simulated with selection and asymmetric mutation, ML was largely unable to capture the derived omega value. Oddly enough, ML performed the best when kappa was fixed to 1, and equal frequencies dramatically outperformed other freq specs, although again even this specification did not perform excellently - strongly correlated omegas at  $r=0.94$  (when kappa 1 and freq equal), but hardly the robust 1-1 relationship recovered under a symmetric scheme.

Thus, it seems as though codon frequencies are, in the simulations we have conducted here, a confounding parameter, considering that everything worked best when they were set to equal (and thus might as well not be there at all). Indeed, even when mutation alone drove the emergence of unequal base frequencies, equal was still best. **HOWEVER** - It is very very important to note that selection was still apparently much stronger than mutation, since gc content barely changed at all. When  $\text{kappa} = 1$  for the selection runs, gc content did increase by about 3% give or take, but when

no selection and just mutation driving the gc stuff, the gc content of the data was still basically the same as that of the input codons.

In conclusion, when diffs in gc-content are driven by mutational processes alone, we are mostly ok. when, however, selective forces contribute to compositional, for instance by favoring gc-rich codons, inference is wacky, but best when equal frequencies are specified. Thus, we see no reason to continue including this parameter, at least in cases of purifying selection. Although we are able to test only ML performance when evolving under steady-state, we also suspect that eq freqs shouldnt be there for positive selection either, because if positive selection is happening then clearly the system is not at equilibrium and thus using steady-state codon frequencies is a logical flaw.

Important result from our study was the methodological approach of benchmarking ML methods. This is not typically how benchmarking is done, but probably represents something very robust. The specific approach here is somewhat limited;

We have two possible explanations for this trend. The first is that these results reflect a broad misinterpretation of how the equilibrium codon frequencies parameters should be specified in mechanistic codon models. Typically, these values are taken directly from the given data and fixed in the model to reduce the number of parameters inferred. However, the codon frequencies observed in the data set represent those which exist *after* natural selection has acted on the sequence. Instead, the model should use the codon frequencies which would exist *in the absence of natural selection*. Selection, alternatively, acts to tune this frequencies to increase protein fitness. If one specifies equilibrium frequencies which exist after natural selection has acted on the protein sequence (i.e., frequencies measured directly from the data), then the influence of selection pressure is incorporated into these values. The desirable outcome, however, is that the  $dN/dS$  parameter measures the selective strength. If other parameters in this model contain selection information, estimates for  $dN/dS$  will not accurately capture selective effects.

The second explanation is that a single parameter  $dN/dS$  is in effect representing two distinct values; on one hand,  $dN/dS$  indicates the strength of selective constraint. On the other hand,

## Discussion

Here, we have derived a formal mathematical relationship between the parameter estimates of MutSel and mechanistic codon models. Through a simulation approach, we validated this relationship and demonstrated that these models yield nearly identical results. However, we additionally found that MutSel models necessarily cannot describe scenarios in which positive or diversifying selection



occurs, or when  $dN/dS > 1$ . Although it is generally acknowledged that MutSel models carry the assumption of purifying selection, we formalize and prove this result. These findings have important implications for how and when these models should be applied. In cases of purifying selection or neutral evolution, these two competing models are virtually no different from one another, and thus use of either model is fully justified. Alternatively, if positive selection is occurring, MutSel models cannot be used as they mathematically cannot capture the actual evolutionary process.

This study highlights the importance of examining the similarities and differences among different evolutionary model classes. While some may prefer one model over another, it is important to have a full understanding of why one model might be applied over another. Our results demonstrate that, for circumstances of purifying selection or neutral, the models are robust and in agreement. However, be careful, because sometimes they don't agree, and this is equally important.

Now, for the frequency specification: does this really matter? Typically, when one measures codon frequencies from the data set, codon frequencies are treated as global parameters rather than site-specific. Thus, equilibrium codon frequency parameters effectively represent an average across the entire data set, naturally lead to a flatter distribution of codon frequencies. Our simulated data sets, on the other hand, were evolved according to a single parameter site, leading to more constrained global codon frequencies. Therefore, the extent to which bias introduced by incorrect frequency specifications was driven by how far from equal we're talking.

Caveat about how our math relies on symmetric mutation rates and/or equal mutation rates, depending on which one ends up happening.

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Table 1: Effect of ML parameterizations on inference.

Codon frequencies	$\kappa$ parameterization	$\omega$ correlation	$\omega$ error	$\kappa$ correlation	$\kappa$ error
Equal	True	<b>0.999</b>	0.012		
Equal	1	<b>0.951</b>	0.22		
Equal	Free	<b>0.993</b>	0.045	<b>0.869</b>	0.148
F3x4	True	0.077	5.284		
F3x4	1	0.032	3.553		
F3x4	Free	0.147	2.152	<b>0.772</b>	0.215
CF3x4	True	0.076	5.265		
CF3x4	1	0.022	3.519		
CF3x4	Free	0.149	2.141	<b>0.764</b>	0.22
Empirical	True	<b>-0.62</b>	51.851		
Empirical	1	<b>-0.61</b>	28.06		
Empirical	Free	<b>-0.608</b>	59.792	<b>0.76</b>	0.244

Codon frequency specifications were either set as equal (1/61 per codon), calculated from the F3x4 estimator [5], calculated from the CF3x4 estimator [17], or set equal to the simulated alignment's empirical frequencies.  $\kappa$  was specified as either a fixed value, its true simulated value or 1, or as a free parameter of the model. Correlations given are between the ML  $\omega$  estimate and our derived  $\omega$  values. Error refers to the mean absolute error between these two  $\omega$  estimates. Similar values for  $\kappa$  are shown for those inferences where  $\kappa$  was a free parameter of the model. bold corresponds to  $p < 1^{-10}$ . Nothing else was significant.

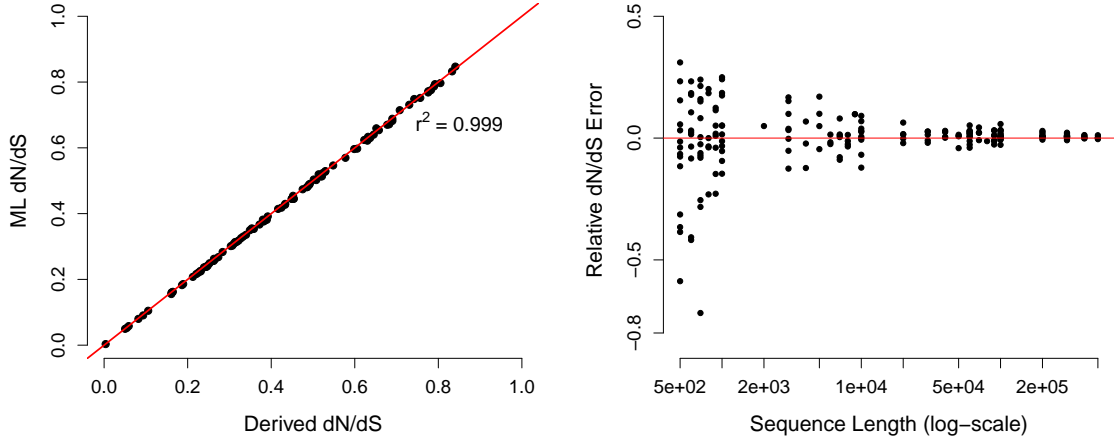


Figure 1: Relationship works exceedingly well. Left panel shows 100 points, each of which corresponds to single simulation. Note that here the ml inference is shown for equal codon frequency specs and kappa fixed to true value (a similar plot for free kappa is shown in suppfigs, but results are qualitatively identical.) Right panels shows convergence of omega values as data set size (represented as simulated alignment length) increases. The y-axis indicates relative error of the ML  $dN/dS$  estimates, and the x-axis indicates sequence length on a log-scale. As the sequence length, or the data set size, increases, the two  $dN/dS$  estimates converge to the same value.

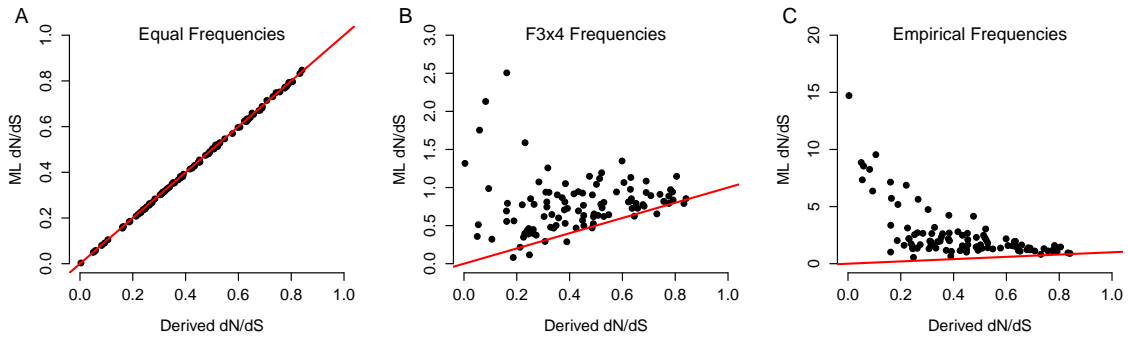


Figure 2: Issues with frequency specifications abound. In each plot, red line indicates 1:1 agreement, so note the y-axis differences. Relationship between omega values only really exists when equal codon frequencies are specified. When f3x4 or true freqs used, there is the potential to end up with dramatically inflated values. cf3x4 not shown because its results are statistically the same as f3x4.