Additional file 2

*γ***-MYN: a new algorithm for estimating Ka and Ks with consideration of variable substitution rates**

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1. Tamura-Nei Model

Table S1 Nucleotide Substitution Models

Note: α_1 , transitional rate between purines; α_2 , transitional rate between pyrimidines; β , transversional rate; g_N , frequencies of nucleotide N, where $N \in \{T, C, A, G\}$.

Under the assumption that the rate of nucleotide substitution λ is the same for all sites considered, Tamura and Nei used g_r , g_c , g_a and g_c to represent nucleotide

frequencies for T,C,A and G, respectively. They defined α_1 , α_2 and β as transitional rates between purines and between pyrimidines, and transversional rate, respectively. They derived the formulas (S1-S3) for the proportions of transitional differences between purines(P_1) and between pyrimidines(P_2) and of transversional differences(Q) over divergence time t [1, 2]:

$$
P_1 = \frac{2g_A g_G}{g_R} \{g_R + g_Y \exp(-2\beta t) - \exp[-2(g_R \alpha_1 + g_Y \beta)t] \}
$$
(S1)

$$
P_2 = \frac{2g_T g_C}{g_Y} \{g_Y + g_R \exp(-2\beta t) - \exp[-2(g_Y \alpha_2 + g_R \beta)t] \}
$$
(S2)

$$
Q = 2g_R g_Y[1 - \exp(-2\beta t)]
$$
 (S3)

where $g_R = g_A + g_G$ and $g_Y = g_T + g_C$.

2. Derivation of $\kappa_{\scriptscriptstyle R}$ and $\kappa_{\scriptscriptstyle Y}$

Under the assumption that the rate of nucleotide substitution λ approximately follows the gamma distribution, we derive the equations for estimating κ_R and κ_Y .

We consider Tamura-Nei Model, where the average substitution rate is given by $[1]\lambda = 2g_Ag_G\alpha_1 + 2g_Tg_C\alpha_2 + 2g_Rg_Y\beta$, where $g_R = g_A + g_G$ and $g_Y = g_T + g_C$. We assume that λ varies with nucleotide site according to the following gamma distribution [3, 4] :

$$
f(\lambda) = \frac{b^{\alpha}}{\tau(\alpha)} e^{-b\lambda} \lambda^{\alpha - 1}
$$
 (S4)

Where $\alpha = \overline{\lambda}^2 / V(\lambda)$ and $b = \alpha / \overline{\lambda}$, $\overline{\lambda}$ and $V(\lambda)$ being, respectively, the mean and variance of λ . $\tau(\alpha)$ is the gamma function. Here note that α is the square of the inverse of the coefficient of variation. To avoid using too many parameters, we set $b = \alpha$ so that the mean of the distribution is 1, with variance $1/\alpha$. The shape parameter α is then inversely related to the extent of rate variation at sites.

Therefore, if λ or α_1, α_2 and β follow the gamma distribution, the means of P_1, P_2 and Q are given by [1, 3, 4]

$$
\overline{P_1} = \int_0^{\infty} P_1 f(\lambda) d\lambda = \frac{2g_A g_G}{g_R} \left\{ g_R - \left[\frac{\alpha}{\alpha + 2(g_R \overline{\alpha_1} + g_Y \overline{\beta})t} \right]_0^{\infty} + g_Y \left(\frac{\alpha}{\alpha + 2 \overline{\beta}t} \right) \right\}, \text{(S5)}
$$
\n
$$
\overline{P_2} = \int_0^{\infty} P_2 f(\lambda) d\lambda = \frac{2g_T g_C}{g_Y} \left\{ g_Y - \left[\frac{\alpha}{\alpha + 2(g_Y \overline{\alpha_2} + g_R \overline{\beta})t} \right]_0^{\infty} + g_R \left(\frac{\alpha}{\alpha + 2 \overline{\beta}t} \right) \right\}, \text{(S6)}
$$

$$
\overline{Q} = \int_0^\infty Qf(\lambda)d\lambda = 2g_Rg_Y \left[1 - \left(\frac{\alpha}{\alpha + 2\overline{\beta}t}\right)^\alpha\right]
$$
(S7)

Where α_1 , α_2 and β are the means of α_1 , α_2 and β , respectively. From (S5), (S6) and (S7) we can get the transformation:

$$
2\overline{\alpha_1}t = \frac{\alpha}{g_R}[(1 - \frac{1}{2g_R}\overline{Q} - \frac{g_R}{2g_Ag_G}\overline{P_1})^{-1/\alpha} - g_Y(1 - \frac{1}{2g_Rg_Y}\overline{Q})^{-1/\alpha} - g_R],
$$
 (S8)

$$
2\overline{\alpha_2}t = \frac{\alpha}{g_Y}[(1 - \frac{1}{2g_Y}\overline{Q} - \frac{g_Y}{2g_Tg_C}\overline{P}_2)^{-1/\alpha} - g_R(1 - \frac{1}{2g_Rg_Y}\overline{Q})^{-1/\alpha} - g_Y],
$$
 (S9)

$$
2\overline{\beta}t = \alpha[(1 - \frac{1}{2g_Rg_Y}\overline{Q})^{-1/\alpha} - 1]
$$
 (S10)

In order to conveniently remember the meanings of P_1 , P_2 and Q , in our main manuscript we rename them as T_R , T_Y , V, respectively. Hence, the formulas for estimating κ_R , κ_Y and *d* are as follows.

$$
\kappa_R = \overline{\alpha_1} / \overline{\beta} = \frac{h - g_Y \times j - g_R}{g_R \times j - g_R},
$$
\n(S11)

$$
\kappa_{Y} = \overline{\alpha_{2}} / \overline{\beta} = \frac{i - g_{R} \times j - g_{Y}}{g_{Y} \times j - g_{Y}}
$$
\n(S12)

$$
d = 4g_A g_G \overline{\alpha_1 t} + 4g_T g_C \overline{\alpha_2 t} + 4g_R g_Y \overline{\beta t}
$$

=
$$
2\alpha \left[\frac{g_A g_G}{g_R} h + \frac{g_T g_C}{g_Y} i + \left(g_R g_Y - \frac{g_A g_G g_Y}{g_R} - \frac{g_T g_C g_R}{g_Y} \right) j - g_A g_G - g_T g_C - g_R g_Y \right]
$$

(s13)

Where

$$
h = \left(1 - \frac{1}{2g_R}V - \frac{g_R}{2g_Ag_G}T_R\right)^{-1/\alpha},
$$
\n(S14)

$$
i = \left(1 - \frac{1}{2g_Y}V - \frac{g_Y}{2g_Tg_C}T_Y\right)^{-1/\alpha},
$$
\n(S15)

$$
j = \left(1 - \frac{1}{2g_R g_Y}\right)^{-1/\alpha} \tag{S16}
$$

Reference

- 1. Tamura K, Nei M: **Estimation of the number of nucleotide substitutions in the control region of mitochondrial DNA in humans and chimpanzees.** *Mol Biol Evol* 1993, **10:**512-526.
- 2. Zhang Z, Li J, Yu J: **Computing Ka and Ks with a consideration of unequal transitional substitutions.** *BMC Evol Biol* 2006, **6:**44.
- 3. Jin L, Nei M: **Limitations of the evolutionary parsimony method of phylogenetic analysis.** *Mol Biol Evol* 1990, **7:**82-102.
- 4. Nei M, Gojobori T: **Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions.** *Mol Biol Evol* 1986, **3:**418-426.