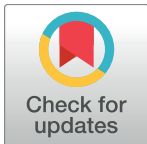


CORRECTION

Correction: Can quartet analyses combining maximum likelihood estimation and Hennigian logic overcome long branch attraction in phylogenomic sequence data?

The *PLOS ONE* Staff

There are multiple errors in [Fig 1](#). The authors have provided a corrected version here. The publisher apologizes for the error.



 OPEN ACCESS

Citation: The *PLOS ONE* Staff (2017) Correction: Can quartet analyses combining maximum likelihood estimation and Hennigian logic overcome long branch attraction in phylogenomic sequence data? *PLoS ONE* 12(10): e0186617. <https://doi.org/10.1371/journal.pone.0186617>

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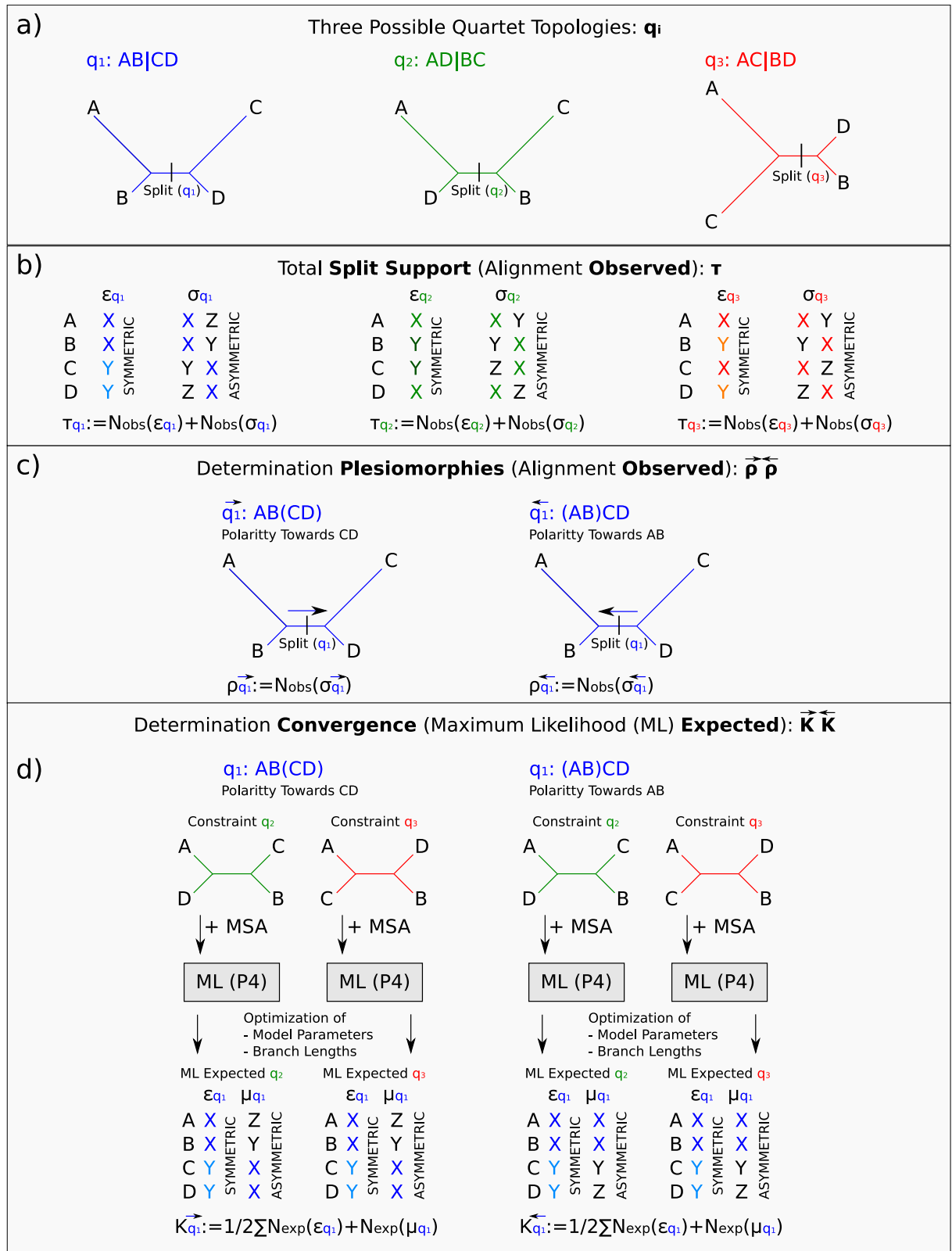


Fig 1. Flowchart of the *PhyQuart* algorithm. Simplified flowchart showing a) each of the three possible quartet relationships for a set of 4 sequences (q_1, q_2, q_3), b) the site-pattern classification of observed (N_{obs}) symmetric (ϵ_{q_i}) and asymmetric (σ_{q_i}) support (τ_{q_i}), c) the determination of plesiomorphic (old) split-supporting site-patterns given two different polarities of character transformation

along the internal branch of each possible quartet tree, $\rho_{\bar{q}_1}$ and ρ_{q_1} , and d) estimation of expected convergent split-supporting site-patterns ($\kappa_{\bar{q}_1}, \kappa_{q_1}$) supporting quartet q_1 in ML split pattern estimations using branch length and model optimization on constraint topologies of the other two possible quartet relationships (q_2, q_3).

<https://doi.org/10.1371/journal.pone.0186617.g001>

Reference

1. Kück P, Wilkinson M, Groß C, Foster PG, Wägele JW (2017) Can quartet analyses combining maximum likelihood estimation and Hennigian logic overcome long branch attraction in phylogenomic sequence data? PLoS ONE 12(8): e0183393. <https://doi.org/10.1371/journal.pone.0183393> PMID: 28841676