

New Insights on Modern Evolutionary Analyses

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Journal of Phylogenetics and Evolutionary Biology is one of the most popular open access journals among the phylogeneticists and publishes peer-reviewed scholarly articles on contemporary topics in evolutionary biology including developmental genetics, developmental biology, epigenetic and inheritable modifications among biological organisms, evolutionary genetics systems biology and phylogenetics. The Journal lays special emphasis on bioinformatics and computational phylogenetics as well as molecular phylogeny.

The Journal was established in the year 2013 and has been consistently publishing peer-reviewed articles at a frequency of four issues per year. In the preceding year, the Journal has published nine articles that included editorials, short note communications and systematic reviews. These articles were contributed by nice authors from different countries. All the issues were released in strict adherence to publication timeliness. The topics that were covered in volume six included organ donation, transplantation and phylogenetic trees. Recent publications of the Journal include a review article on gene and species tree congruence as well as another review article on usage of specific codon in phylogenomic model construction.

Latest research activities have been focusing on evolutionary analysis, biodiversity and homology analysis utilizing modern algorithms and software's particularly in the context of ever increasing biological structural and functional data sets and constant efforts are being made to bring in flexibility and greater reliability in analytical interpretations. Miller et al. [1] have observed that with the availability of datasets derived from whole genome sequencing, the phylogenetic algorithms for classification of limited number of species have become obstinate. DNA sequencing based novel approaches including codon usage bias for establishing phylogenetic relationship among species was evident. However, the codon choice has immense significance in establishing phylogenetic relation because the transcription, translation, protein expression and the phenotype varies with

respect to the type of codon. In addition, the number of codons, the position of codons, and whole genome nucleotide composition lead to induction of functional variation. Therefore, the phylogenies produced by the organisms tend to vary. In this context, Miller et al. [1] proposed gene specific analysis to incorporate specific codon usage bias among phylogenetic models.

Abijo et al. [2] have observed that there is lack of congruence between the gene trees and species trees even between even closely related species, while it is a common phenomenon that traits exhibited by the organisms is the direct result of their genetic composition. Some of the factors that contribute to this disparity include hybridization of gene, gene duplication, horizontal transfer and incomplete lineage that increase gene diversity however, building models by accounting these factors also could not account for the discord due to lack of computational and statistical power. In an attempt to address this problem, Abijo et al. [2] described factors affecting gene and species tree disparity and proposed some of the different models to correctly reconcile species tree and the gene tree.

I take this opportunity to convey my heartiest congratulations to all the contributing authors, expert subject reviewers and editors for timely compilation of the sixth volume and we are very enthusiastic for the release of the first issue in the current year.

References

1. Justin B Miller, Michael F Whiting, John SK Kauwe and Perry G Ridge. "How Codon Usage Biases Affect Our Ability to Recover the Tree of Life." *J Phylogenetics Evol Biol* 8(2021).
2. Abijo T, Ossai C, Bello O and Oluwasanmi OL. "Finding a Final Common Path for the Gene Trees and Species Trees Congruence." *J Phylogenetics Evol Biol* 7(2019): 210.

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