GGARG: AN R PACKAGE FOR VISUALISATION OF (ANCESTRAL) RECOMBINATION AND HORIZONTAL GENE TRANSFER IN PHYLOGENETIC TREES

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Phylogenetic analysis is essential for the understanding of the evolutionary history and relationships of organisms. Recombination and related evolutionary events additionally increase the complexity of these relationships as can be observed in SARS-CoV2, HBV, HIV and various other viruses. Recent advances in evolutionary analysis tools make it possible to account for recombination or horizontal gene transfer in phylogenies. Specialised tools for visualisation of these events, however, are limited and visualisations of tree-based phylogenetic networks often require additional manual manipulation in graphics software.

ggARG is an R package that allows users to visualise and annotate publication-grade tree-based phylogenetic networks such as Ancestral Recombination Graphs (ARGs) or phylogenies describing horizontal gene transfer. We present an R package that is built as an extension of the popular "ggtree" library, allowing users to take advantage of the flexibility and customizability of "ggtree" while also providing specific functionality for tree-based phylogenetic networks. *ggARG* utilises the *Grammar of Graphics*-syntax for seamless and intuitive integration of both packages and also improves legibility of the tree-based phylogenetic networks by minimising the number of edge crossings describing reticulate events.

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