

March 1, 2021

Microbial Resource Announcements Editorial Office

Dear Editorial Office:

Please accept this submission of our manuscript entitled “TinselR – An RShiny Application for Annotating Outbreak Trees”, for publication in Microbial Resource Announcements. This paper has been approved for submission by my co-authors, and all the original work in this paper is being submitted solely to your journal.

Across the United States, public health laboratories perform whole-genome sequencing for many pathogens, a milestone for protecting public health by understanding organismal relationships at a higher resolution than was previously possible. Yet, integrating phylogenetic data with epidemiological data to allow clear concise communication among clinicians, laboratorians, epidemiologists, and informaticians is still challenging. Once the data is integrated, empirically derived thresholds can be used to identify possible outbreaks, to inform the design of additional investigations, and identify potential transmission routes. Thus, creation and markup of phylogenetic trees with genetic and epidemiological data is an essential component for public health.

Our goal was to develop an open-source graphical user interface (GUI) for phylogenetic tree visualization and annotation usable by persons without specialized bioinformatics or data visualization skills. We use the R programming language with Shiny, its native library for creating web applications, to integrate three types of data: genetic distance matrix of single nucleotide polymorphisms, phylogenetic tree, and meta data for the task of annotating outbreak trees. Additionally, the R language contains many of the gold standard packages for phylogenetic analyses and visualization (e.g. ape, and ggtree) and thus conform to standard practices of phylogenetics. Once modified, these tree images are downloadable in various formats (pdf, png, or tiff) for presentations, publications, or other communications with collaborators. We make our application freely available via download from GitHub using functions available from the R devtools library and provide a vignette to provide greater detail for using the application located on GitHub as well.

Sincerely,

A handwritten signature in black ink, reading "Jennafer Hamlin". The script is cursive and fluid, with the first letter 'J' being particularly large and stylized.

Jennafer Hamlin