Conference Abstract

TaxonTableTools - A comprehensive, platform-independent graphical user interface software to explore and visualise DNA metabarcoding data

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Abstract

DNA-based identification methods, such as DNA metabarcoding, are increasingly used as biodiversity assessment tools in research and environmental management. Although powerful analysis software exists to process raw data, the translation of sequence read data into biological information and downstream analyses may be difficult for end users with limited expertise in bioinformatics. Thus, the need for easy-to-use, graphical user interface (GUI) software to analyze and visualize DNA metabarcoding data is growing. Here we present TaxonTableTools (TTT), a new platform-independent GUI that aims to fill this gap by providing simple, reproducible analysis and visualization workflows. The input format of TTT is a so-called "TaXon table". This data format can easily be generated within TTT from two common file formats that can be obtained using various published DNA metabarcoding pipelines: a read table and a taxonomy table. TTT offers a wide range of processing, filtering and analysis modules. The user can analyze and visualize basic statistics, such as read proportion per taxon, as well as more sophisticated visualizations such as interactive Krona charts for taxonomic data exploration, or complex parallel category diagrams to assess species distribution patterns. Venn diagrams can be calculated to compare taxon overlap among replicates, samples, or analysis methods. Various ecological analyses can be produced directly, including alpha or beta diversity estimates, rarefaction analyses, and principal coordinate or non-metric multidimensional

scaling plots. The taxonomy of a data set can be validated via the Global Biodiversity Information Facility (GBIF) API to check for synonyms and spelling mistakes. Furthermore, geographical distribution data can be automatically downloaded from GBIF. Additionally, TTT offers a conversion tool for DNA metabarcoding data into formats required for traditional, taxonomy-based analyses performed by regulatory bioassessment programs. Beyond that, TTT is able to produce fully interactive html-based graphics that can be analyzed in any web browser. The software comes with a manual and tutorial, is free and publicly available through GitHub (https://github.com/TillMacher/TaxonTableTools) or the Python package index (https://pypi.org/project/taxontabletools/).

Keywords

biodiversity, bioinformatics, biomonitoring, data analysis, eDNA, OTUs

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