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Integrating biodiversity data by name matching to shared reference lists

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Abstract

The process of combining biodiversity data from multiple sources currently starts with matching of the Latin name strings for the organisms used in each dataset. Datasets often contain names that cannot be unambiguously matched. The reasons for this are complex. They arise from the nomenclatural codes that have evolved over many decades as well as human and computer error. In smaller studies these issues can be resolved manually but in the larger studies, such as plot monitoring networks, or when combining data from very different domains, such as ecological and molecular phylogenetic data, they become a major hurdle.

The solution is to match each dataset to a reference name list. Through a process of name matching the Latin name used in the data is augmented with an unambiguous identifier supplied by the list. The name matching process only has to be done once and then the data can be combined with any other data set that has been matched to the same reference list. Unfortunately each reference list has its own implementation of how to do the name matching.

The Flanders Marine Institute (VLIZ) and Royal Botanic Garden Edinburgh manage large reference lists including the World Register of Marine Species (WoRMS), PESI and the World Flora Online. We have been working on a shared name matching standard that could be implemented by other reference lists. This should make it easier for researchers to align data with any reference list without having to learn a new system and it would facilitate tooling in the future.

We will present the results of our work on the Taxonomic Name Linking Services (TNLS) which was funded as part the Horizon Europe Research and Innovation programme within the framework of the TETTRIs (Grant Nr. 101081903).