Connecting Taxonomic Backbones using Global Names Tools

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Abstract

Biodiversity taxonomy provides a means to organize information about living organisms into maintainable tree- or graph-like structures (taxonomic backbones). Taxonomy is tightly bound to biodiversity nomenclature—a collection of recommendations, rules and conventions for naming living organisms. Species are often considered to be the most important unit of taxonomy structures. Keeping scientific names of species and other taxa accurate and up to date are major challenges during creation and maintenance of large taxonomic backbones.

Global Names Architecture (Global Names) is an initiative that developed tools and databases for detecting, parsing, and verifying scientific names. Verification tools also provide information about which taxonomic and nomenclatural resources contain information for a given scientific name. Taxonomic intelligence provided by resources aggregated by Global Names allows resolving of taxon names from different backbones, even if their "current" scientific names vary.

Parsing of scientific names with GNparser allows for normalization of names, making them comparable. Fast name matching (reconciliation) and discovery of a taxonomic meaning (resolution) by GNverifier connects information from various resources. The most recently developed tools by Global Names provide name verification and taxon matching on an unprecedented scale.

During this presentation we are going to describe Global Names tools and show how they can be used for reconciliation of lexical variants of scientific names, for extracting the authorship metadata, how names can be verified and resolved, and how data can be connected to a variety of biodiversity resources.

Keywords

biodiversity, scientific name, nomenclature, taxonomy

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Presented at

TDWG 2021

Hosting institution

University of Illinois at Urbana-Champaign

Conflicts of interest