



What is ARPHA Writing Tool 2.0 (AWT)?

ARPHA Writing Tool (AWT) is an **XML-based authoring tool**, which **allows researchers**: co-authors, but also linguistic editors, proofreaders and colleagues, **to conveniently and collaboratively work on their manuscripts** and **prepare them for submission**. It is used as a primary manuscript submission interface in several scientific journals hosted on the ARPHA publishing platform, amongst them are the [Biodiversity Data Journal](#), [Research Ideas and Outcomes \(RIO Journal\)](#), [One Ecosystem](#) and others.

With the AWT, users take advantage of **a variety of data import and semantic tagging features** in order to save time and efforts, but also to ensure **machine-readability** and **ontology-linked interoperability of publications**.

What's new and unique in AWT 2.0?

On top of an **improved user interface**, the AWT 2.0 version presents its collaborative platform and functionalities as a **standalone authoring tool**. By enabling users to **import and export their (XML-JATS) manuscripts** at any time, the AWT 2.0 prompts wider use of XML-born and FAIR scientific publications.

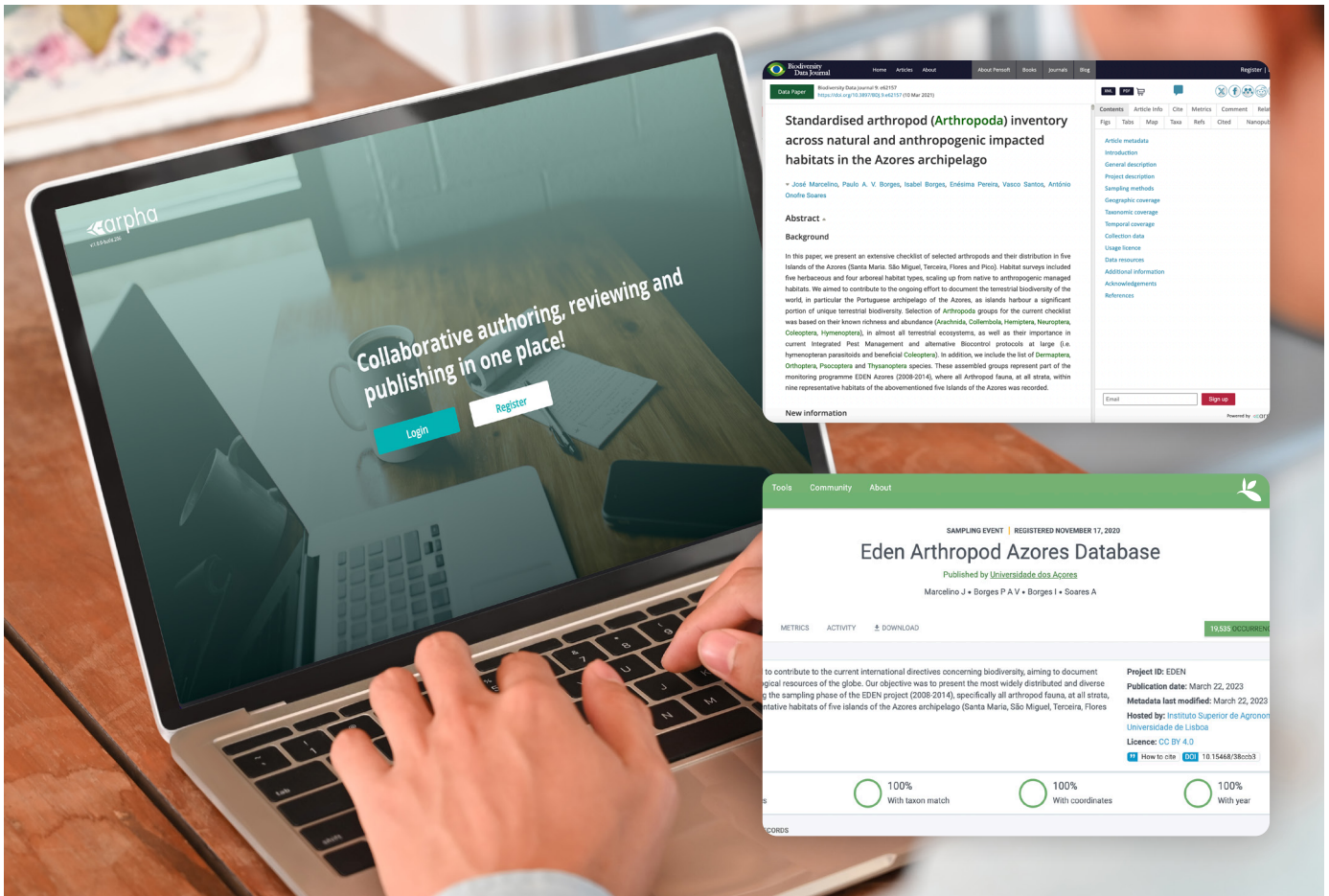
AWT 2.0 is the first authoring tool to provide **ontology-linked tagging**. It also supports **import of structured data** from external resources and **semantic enhancements** for **literature citations** (e.g. citation intent based on the Citation Typing Ontology (CiTO)). Thus, users can personally check the semantic meaning and accuracy of the terms and taxon names in their manuscripts.

What biodiversity researchers particularly enjoy in AWT 2.0?

Originally designed for the Biodiversity Data Journal, AWT offers **features and workflows designed for the biodiversity science community**. Amongst the most notable benefits specially designed for the domain of biodiversity science are various **biodiversity-specific data import and export features**; and **bi-directional links** with leading **biodiversity data aggregators** (e.g. GBIF, BOLD, INSDC, Catalogue of Life, ChecklistBank, TreatmentBank, BHL, Biodiversity Literature Repository (BLR), BiodiversityPMC (SiBILS)).

As a result, biodiversity scientists will be happy to find AWT 2.0 a well-rounded collaborative authoring environment, where they can discuss and edit manuscripts before submitting them to a journal.





What challenges does AWT 2.0 address?

The deluge of **scattered biodiversity data**, in addition to its natural evolution (e.g. synonymisations, re-descriptions), make it particularly challenging for biodiversity databases to **identify** and **interlink data** within scientific publications, while also **disambiguating different terms** and entities.

As a result, authors, as well as publication sources and databases are currently struggling to ensure that **biodiversity data remains FAIR, linked and efficient** for the next generation of scientists. **Post-publication text** and **data mining**, as well as **literature exploration** in general are costly services in a pressing need for optimisation.

AWT 2.0 in practice

Biodiversity researchers may easily import Darwin Core-compliant species occurrence data through web services or publish their biodiversity dataset (e.g. species occurrence dataset uploaded to GBIF) as a formal scientific publication.

To do this, they will simply create a Data paper manuscript in the AWT 2.0, upload their data directly from GBIF and then add their narrative, in order to provide further context. Apart from the direct import, authors will also benefit from a list of predefined sections available in the data paper template and semantic enrichments, which will allow for each mentioned taxon to be mapped and linked to relevant databases.

