

Title	Aiding the journey from data to publication in the plant sciences
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URL	https://github.com/collaborative-open-plant-omics/COPO.git
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The aim of open science is to make scientific research accessible to an inquiring public. This often involves mechanisms for preserving and publishing research artefacts such as data, methods, and software in an efficient and timely manner.

Existing mechanisms for enabling open science in plant research, particularly within the genomics field but also high-throughput transcriptomics, proteomics and metabolomics, are limited in a number of ways: (i) complicated and time-consuming procedures for repository deposition; (ii) digital gap or lack of interoperability between disparate information sources; (iii) sub-optimal search and retrieval facilities across data repositories.

We present COPO (Collaborative Open Plant Omics), an information aggregation and publishing platform, to help plant scientists publish and share research outputs, but also to ease access to important services across disparate sources of information. COPO is based on Django (<https://www.djangoproject.com>), a high-level Python Web framework that offers rapid development and pragmatic design. In particular, the system uses a Web front-end and a set of APIs (Application Programming Interfaces) to facilitate the aggregation of disparate research objects into logical profiles that represent a body of research. A profile can contain, for example, a sequence of data, source codes, and pdf files, all of which are well described with associated meta data. In the first instance, the system acts as a brokering service, providing a useable interface to different repositories in order to offload the burden of data deposition from scientists. Research objects (e.g., sequence data) can be submitted seamlessly to services such as EBI (<http://www.ebi.ac.uk>) data repositories and iRODS (<http://irods.org>), and accessions to these objects, which correspond to a profile, are persisted in COPO. Using these accessions (e.g., DOIs (Digital Object Identifiers)), a resolution component can then route user queries to the original objects.

By using high quality and stable APIs and virtualised resources, COPO has the potential of tying together other existing services such as: the ISATools metadata suite (<http://www.isa-tools.org>); Galaxy (<http://galaxyproject.org>), iPlant (<http://www.iplantcollaborative.org>) analytical platforms; figshare (<http://figshare.com>), Research Object, Scientific Data and Gigascience (<http://www.gigasciencejournal.com>) platforms. This provides much flexibility and ease of access to disparate and geographically distributed resources through a single point of access. For instance, by hooking into locally hosted instances of iPlant and Galaxy using profile workflows, experimental results may be easily reproduced and verified, or comparative studies may be conducted with alternative data.

We believe that the ongoing development of COPO will contribute to the state-of-the-art in enabling open science, particularly by offering the following utility:

- enforcing community-accepted standards for data representation
- facilitate submission to persistent archival resources, for data publication and citation
- enable seamless transition from data to analysis services
- facilitate discoverability through aggregated provenance (meta data) and suitable publication markup to link citable resources