

---

<b>Title</b>	Your incredible work to present at the Bioinformatics Open Source Conference
<b>Author</b>	<i>Presenting Author</i> , Author Two, Author Three ...
<b>Affiliation</b>	<a href="http://www.open-bio.org/wiki/Main_Page">http://www.open-bio.org/wiki/Main_Page</a>
<b>Contact</b>	your@email.com
<b>URL</b>	<a href="http://www.open-bio.org/wiki/BOSC_2015">http://www.open-bio.org/wiki/BOSC_2015</a> (links to source code and project website)
<b>License</b>	Name of your <a href="#">open source license</a> (and link if non-standard)

---

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. In particular, COPO uses a Web front-end and a set of APIs (Application Programming Interfaces) to facilitate the aggregation of disparate sources of information into logical profiles representing a body of research. A profile can contain, for example, sequence of data, source codes, and pdf files, all of which are described with associated meta data. In the first instance, the system is positioned as a brokering system, providing a useable interface to different repositories in order to offload the burden of data deposition from scientists.