

Bioboxes: Standardised bioinformatics tools using Docker containers.

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Project Website: <http://bioboxes.org/>

Source Code: <https://github.com/bioboxes>

License: MIT (<https://github.com/bioboxes/rfc/blob/master/LICENSE>)

We introduce the open-source community "bioboxes" which has the aim of simplifying bioinformatics tools through adopting common interfaces. The Docker project makes installing, running and reproducing the output of an application easier because all the dependencies can be provided by creating a "container" of the application. The bioboxes project furthers this concept by creating an interface standard so that containerised software of the same biobox type can be seamlessly interchanged.

Feedback and contributions of new biobox interfaces are managed using the Github issue system. Bioboxes provides documentation and software to help developers follow this standard. The bioboxes.org website provides instructions and guide on how to build a biobox. We also provide a validator tool that tests whether a container follows a biobox interface and thereby helps the developer create their own bioboxes. Furthermore we provide bioboxes in Github and our public Docker Hub repository for download and use.

Researchers with a whole selection of bioboxes at their fingertips can comprehensively evaluate many similar tools that have the same interface and improve the quality of their research. A system of well-defined bioboxes is an important step towards the making provenance easier and research more shareable and reproducible.