Publication of BioCompute Objects (IEEE-2791-2020) created from Galaxy workflow invocations

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BioCompute is the colloquial term for the standard (IEEE-2791-2020) designed to communicate High-throughput Sequencing (HTS) analysis results, data set creation, data curation, and bioinformatics verification protocols. A BioCompute Object (BCO) is a JSON file that adheres to the IEEE-2791-2020 schema.

The BioCompute concept was conceived by researchers at The George Washington University and the US Food and Drug Administration (FDA). The goal was to ease the burden associated with regulatory review of large high-throughput sequencing projects by offering a standardized reporting template. This standard is supported by Google Cloud for workflow sharing and by the FDA Centers, CDER, CBER, and CFSAN, for regulatory submissions on a voluntary submitter basis. Contributions to the BioCompute community have been made by individuals from NIH, Harvard, several biotech and pharma companies, EMBL-EBI, and the Galaxy community.

Last year at GCC 2020 we presented "Implementation of the IEEE-2791-2020 standard (BioCompute Objects) in Galaxy workflow invocations" (https://vimeo.com/437704225). to demonstrate the Galaxy update that allowed the export of an IEEE compliant BCOs via the workflow invocation. This year we will present how that output can be deposited into the BioCompute Database (currently in BETA)[https://beta.portal.aws.biochemistry.gwu.edu]. There are two methods available for depositing a BCO via direct entry or via API submission. Both of these methods allow a user to deposit an object that may or may not be complete, and then continue to edit it before publication. We chose this protocol so that all external platforms would have the same system to complete and publish BCOs.