OpenEBench Scientific Communities in 2022: More Communities, Better Support, Deeper Interactions

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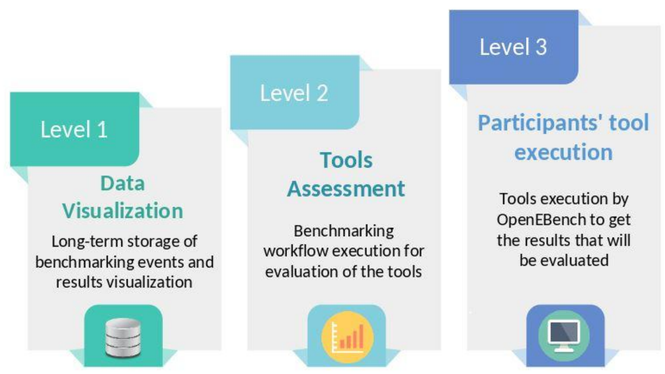
OpenEBench is the ELIXIR benchmarking and technical monitoring open-data platform for bioinformatics software and it has been part of the ELIXIR Tools Platform since its inception. OpenEBench provides scientific communities with an online infrastructure to perform unbiased and objective benchmarking evaluations and to make the results freely available on a public website (https://openebench.bsc.es/). Between 2019 and 2022, the number of communities actively collaborating with OpenEBench has doubled, from four to eight, and many more (up to 11) to come.

Community-driven benchmarking

- Mix of skills and knowledge from the different members that guarantees a complete and unbiased benchmarking
- People with a similar background that want to collaborate in the understanding of specific scientific problems
- Follows the principles of Open Science to foster reproducibility and data sharing
- Useful for a wider group of people: software developers and users
- Improvement and co-development of OpenEBench with the communities

Levels of engagement

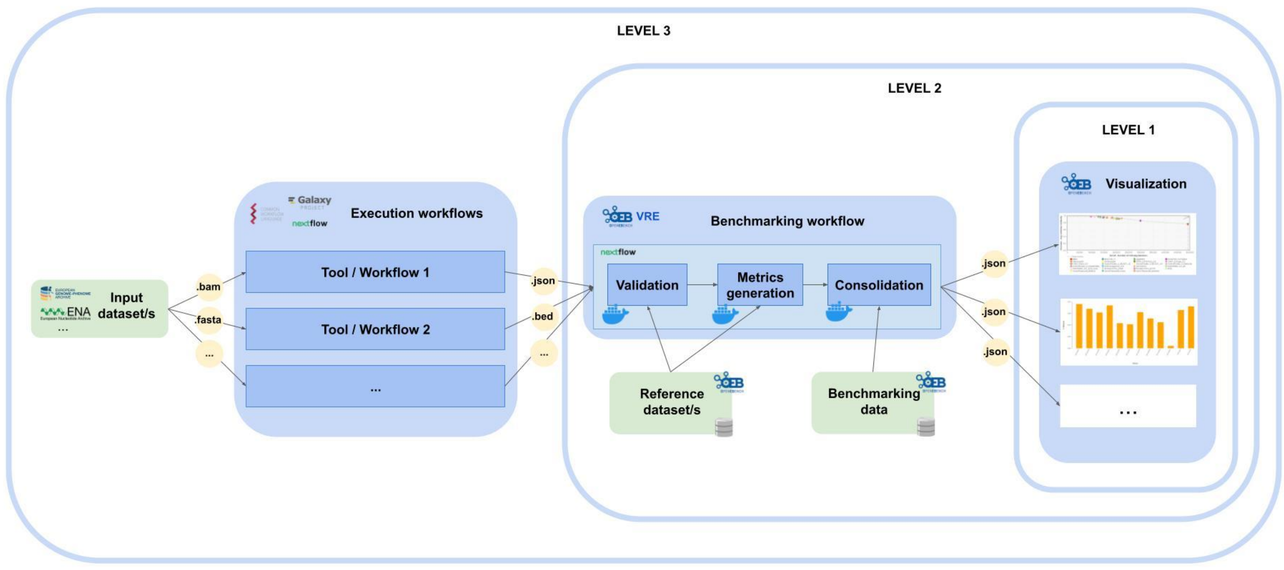


- **Level 1** is used for the long-term storage of benchmarking results aiming at reproducibility and provenance.
- **Level 2** allows the community to use benchmarking workflows to assess participants' performance. Those workflows compute one or more evaluation metrics given one or more reference datasets. **See example**: https://github.com/iRNA-COSI/APAeval
- **Level 3** goes further and the whole benchmarking process is performed at OpenEBench. Therefore, in this level, the participants' tools that are going to be evaluated are also run by OpenEBench.

How to start?

- **Scope of the benchmark:** the relevant scientific questions that the benchmarking event has to answer.
- **Evaluation metrics:** what metrics are going to be used to evaluate the performance of the different tools/pipelines.
- **Reference datasets**: which datasets can be useful as gold standards for the benchmarking evaluation.
- **Tools to evaluate**: what pipelines are going to be part of the comparative evaluation.
- **Level of engagement**: what level of engagement would be useful for the community to adopt.
- **Benchmarking workflow**: once all the above is organized, the benchmarking workflow that will run in OpenEBench is developed.

Benchmarking process



1. Execution of the tools or workflows with some input datasets in order to get the predictions that are going to be used for the benchmarking. This can be done, for example, using Galaxy, Nextflow or Common Workflow Language.
2. Run the benchmarking workflow which includes three steps: **validation**, **metrics computation** and **results consolidation**. During the validation, the input file format is checked and the content of the file is validated. Then, during the metrics computation, the predictions are compared with the reference datasets. Finally, during the consolidation, the results of a particular tool are merged into the community's data.
3. Long-term storage of benchmarking events and challenges to make the results of the performance of the tools available in the OpenEBench webpage.

For more information
openebench.readthedocs.io

Communities involved

ELIXIR communities

hCNV · Rare Diseases · Proteomics · 3D Bioinfo · IDP · Single cell omics

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