Algorithm Benchmarking Consortium (ABC)

Consortium model for systematic benchmarking of tools with flexible framework to incorporate emerging algorithms

Several dozen tools and algorithms are available for most computational biology research tasks with new algorithms and tools published weekly.

Systematic benchmarking of tools is a time- and resource-consuming endeavor, while lack of benchmarking carries with it several potential risks.

Published benchmarks are often performed by researchers with vested interest to show that their tool outperforms others' and do not allow for easy addition of new algorithms.

Phase	Use Case	Algorithms evaluated	Algorithms benchmarked	Timeline	Status
1	CyTOF data analysis	27	9	2021	Completed
2.1	scRNA-seq QC / ambient RNA	14	4	2021	Completed
2.2	scRNA-seq clustering	28	23	2022	Completed
3	Multi-omics target prioritization	39	10	2022	Completed
4	Cell type deconvolution	31	17	2022	Completed
5	scRNA-seq network reconstruction	31	13	2023	Completed
6	Spatial transcriptomics	21	9	2023	Completed
7	Cell-Cell communication	37	17	2024	Completed
8	Cell type annotation	37	15	2024	Completed
9	Spatial niche identification	88	31	2025	In progress
10	Causal regulators	40	27	2025	In progress

Time- and cost-efficient:
By pooling resources and distributing results, consortium model avoids the redundant benchmarking efforts across the member companies.

Independent:
Consortium has no vested interest in promoting its own algorithms, reducing the risk of assessment bias.

Need-driven:
Use cases are selected by applied computational biology teams at Pharma companies and are aligned to the current needs of the industry.

Comprehensive:
Dozens of algorithms are reviewed for each use case and a diverse selection of algorithms is shortlisted for benchmark.

Extendable:
Effort of curating ground-truth datasets is preserved through an extendable framework that allows for benchmarking of additional algorithms.

Transparent:
Benchmarking results, framework and ground-truth datasets are shared with consortium members.

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