Essential guidelines for computational method benchmarking

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Abstract

In computational biology and other sciences, researchers are frequently faced with a choice between several computational methods for performing data analyses. Benchmarking studies aim to rigorously compare the performance of different methods using well-characterized benchmark datasets, to determine the strengths of each method or to provide recommendations regarding the best choice of method for an analysis. However, benchmarking studies must be carefully designed and implemented to provide accurate and unbiased results. Here, we summarize key practical guidelines and recommendations for performing high-quality benchmarking analyses, based on our own experiences in computational biology.
Introduction

Many fields of computational research are characterized by a growing number of available methods for data analysis. For example, at the time of writing, more than 320 methods are available for analyzing data from single-cell RNA-sequencing experiments [1]. For experimental researchers and method users, this represents both an opportunity and a challenge, since method choice can significantly affect conclusions.

Benchmarking studies are carried out by computational researchers to compare the performance of different methods, using reference datasets and a range of evaluation criteria. Benchmarks may be performed by authors of new methods to demonstrate performance improvements or other advantages; by independent groups interested in systematically comparing existing methods; or organized as community challenges. ‘Neutral’ benchmarking studies, i.e., those performed independently from new method development by authors without a perceived conflict of interest, and with a focus on the comparison itself, are especially valuable for the research community since there is no perception of bias [2,3].

From our experience conducting benchmarking studies in computational biology, we have learned several key lessons that we aim to synthesize in this review. A number of previous reviews have addressed this topic from a range of perspectives, including: overall commentaries and recommendations on benchmarking design [2,4–9]; surveys of design practices followed by existing benchmarks [7]; the importance of neutral benchmarking studies [3]; principles for the design of real-data benchmarking studies [10,11] and simulation studies [12]; the incorporation of meta-analysis techniques into benchmarking [13–15]; the organization and role of community challenges [16,17]; and discussions on benchmarking design for specific types of methods [18,19].

Our aim is to complement these previous reviews by providing a summary of essential practical guidelines and recommendations for designing, performing, and interpreting benchmarking analyses. Our target audience consists of computational researchers who are interested in performing a benchmarking study, or who have already begun one. Our review spans the full ‘pipeline’ of benchmarking, from defining the purpose and scope to best practices for reproducibility of published results. The review is structured as a series of guidelines, which are summarized in Box 1, and each explained in detail in the corresponding section. We use examples from computational biology; however, we expect that most arguments apply equally to other fields. We hope that these guidelines will continue the discussion on benchmarking design, as well as assisting computational researchers to design and implement rigorous, informative, and unbiased benchmarking analyses.
Box 1: Summary of guidelines

The guidelines in this review can be summarized in the following set of recommendations. Each recommendation is discussed in more detail in the corresponding section in the text.

1. Define the purpose and scope of the benchmark.
2. Include all relevant methods.
3. Select (or design) representative datasets.
4. Choose appropriate parameter values and software versions.
5. Evaluate and rank methods according to key quantitative performance metrics.
6. Evaluate secondary measures including runtimes and computational requirements, user-friendliness, code quality, and documentation quality.
7. Interpret results and provide guidelines or recommendations from both user and method developer perspectives.
8. Publish and distribute results in an accessible format.
9. Design the benchmark to enable future extensions.
10. Follow reproducible research best practices, in particular by making all code and data publicly available.

Defining the purpose and scope

The purpose and scope of a benchmark should be clearly defined at the beginning of the study, and will fundamentally guide the design and implementation. In general, we can define three broad types of benchmarking studies: (i) those by method developers, to demonstrate the merits of their approach (e.g., [20–24]); (ii) neutral studies performed to systematically compare methods for a certain analysis, either conducted directly by an independent group (e.g., [25–34]) or in collaboration with method authors (e.g., [35]); or, (iii) those organized in the form of a community challenge, such as those from the DREAM [36–40], FlowCAP [41,42], CASP [43], Assemblathon [44,45], and MAQC/SEQC [46–48] consortia.

A crucial question to consider is how detailed the benchmark should be. For a neutral benchmark, all methods should be assessed comprehensively, including evaluations according to key performance metrics for several datasets, as well as secondary measures such as user-friendliness and documentation quality. Ideally, the evaluations should test a range of values for major parameters of each method. To minimize perceived bias, the research group conducting the benchmark should be approximately equally familiar with all included methods, reflecting typical usage of the methods by independent researchers [3]. Alternatively, the group could include the original method authors, so that each method is evaluated under optimal usage conditions; methods whose authors decline to take part should be reported. In either
case, care should be taken to avoid bias due to focusing attention on certain methods when tuning parameters or fixing bugs. Strategies to avoid these types of biases, such as the use of blinding, have been previously proposed [10].

By contrast, when introducing a new method, the focus of the benchmark will be on evaluating the relative merits of the new method, which may be sufficiently achieved by comparing against a smaller set of state-of-the-art methods, using only a single set of optimal parameters for the competing methods. Some advantages of a new method may fall outside the scope of a benchmark, e.g., a new method may enable more flexible analyses than previous methods (e.g., beyond two-group comparisons in differential analyses [20]).

Finally, results should be summarized in the context of the original purpose and scope of the benchmark. For example, for a neutral benchmark, it will be useful to provide clear guidelines for method users, and to highlight weaknesses in current methods so that these can be addressed by method developers. On the other hand, benchmarks performed to introduce a new method should discuss what the new method offers compared to the current state-of-the-art.

Selection of methods

The selection of methods to include in the benchmark will be guided by the purpose and scope of the study. For example, for a neutral benchmark, the aim should be to include all available methods for a certain type of analysis, to provide readers with a comprehensive overview. In this case, the publication describing the benchmark will also function as a review of the literature, so it will be useful to include detailed information describing each method; e.g., in the form of a summary table (see Table 1 in [29] or Table 1 in [27]). Alternatively, it may make sense to include only a subset of methods, by defining inclusion criteria: e.g., all methods that: (i) provide freely available software implementations; (ii) are available for commonly used operating systems; and, (iii) can successfully be installed without errors. Such criteria should be chosen without favoring any preferred methods, and exclusion of any widely used methods should be explained. A useful strategy can be to involve method authors within the process, since method authors may provide additional details on the optimal usage of their methods. In addition, community involvement can lead to new collaborations and inspire future method development. However, the overall neutrality of the resulting research team should be considered. Finally, if the benchmark is formally organized as a community challenge, the selection of methods will be determined by the participants. In this case, it is important to communicate the initiative widely, to ensure that all method authors are aware of it; this can be facilitated by organizing the initiative through an established network, such as DREAM challenges.
When developing a new method, it is generally sufficient to select a representative subset of existing methods to compare against. For example, this could consist of the current best-performing methods (if known), a simple ‘baseline’ method, and any methods that are widely used. The selection of competing methods should ensure an accurate and, as far as possible, unbiased assessment of the relative merits of the new approach. In fast-moving fields, method developers should be prepared to update their benchmarks or design them to easily allow extensions as new methods emerge.

Selection (or design) of datasets

The selection of reference datasets is a critical design choice. If suitable publicly accessible datasets cannot be found in the literature, they will need to be generated or constructed, either experimentally or by simulation. Including a variety of datasets ensures that methods can be evaluated under a wide range of conditions. In general, reference datasets can be grouped into two main categories: simulated (or synthetic) and real (or experimental).

Simulated data have the advantage that a known true signal (or ‘ground truth’) can easily be introduced; e.g., whether a gene is truly differentially expressed. Quantitative performance metrics measuring the ability to recover the known truth can then be used to rank methods. However, it is important to carefully design a simulation that accurately reflects relevant properties of real data; this can be achieved by inspecting empirical summaries of both simulated and real datasets (e.g., using automated tools [49]). The set of empirical summaries to use is context-specific; e.g., for single-cell RNA-sequencing, dropout profiles and dispersion-mean relationships should be compared [28]; for DNA methylation, correlation patterns among neighboring CpG sites should be investigated [50]; for comparing mapping algorithms, error profiles of the sequencing platforms should be considered [51]. Simplified simulations can also be useful; e.g., to evaluate a new method under a basic scenario, or to systematically test aspects such as scalability and stability. An additional advantage of simulated data is that it is possible to generate as much data as required; e.g., to average out random fluctuations and draw statistically valid conclusions. In all cases, the design strategy used to construct the simulations should be clearly explained.

Experimental data, by definition, reflect the properties of real data, but often do not contain a known ground truth, making it difficult to calculate performance metrics. Instead, methods may be evaluated by comparing them against each other, or against a current widely accepted method or ‘gold standard’ (e.g., manual gating to define cell populations in high-dimensional cytometry data [29,41], or fluorescence in situ hybridization (FISH) to validate absolute copy number predictions [6]). In the context of supervised learning, the response variable to be predicted is known in the manually labeled training and test data. However, individual datasets should not be over-used, and using the same dataset for both method development and
evaluation should be avoided, due to the risk of overfitting and overly optimistic results [52,53]. In some cases, it is also possible to design experimental datasets containing an approximate ground truth. Examples include: (i) ‘spiking in’ synthetic RNA molecules at known relative concentrations [54] in RNA-sequencing experiments (e.g., [48,55]); (ii) large-scale validation of gene expression measurements by quantitative polymerase chain reaction (qPCR) (e.g., [48]); (iii) using genes located on sex chromosomes as a proxy for silencing of DNA methylation status (e.g., [24,56]); (iv) using fluorescence-activated cell sorting (FACS) to sort cells into known subpopulations prior to single-cell RNA-sequencing (e.g., [28,57,58]); or, (v) mixing different cell lines to create ‘pseudo-cells’ [59]. Alternatively, experimental datasets may be evaluated qualitatively, for example by judging whether each method can recover previous discoveries. However, this strategy relies on the validity of previous results, and may not enable a simple ranking of methods.

A further technique is to design ‘semi-simulated’ datasets that combine real experimental data with an ‘in silico’ (i.e., computational) spike-in signal, e.g., by combining cells or genes from ‘null’ (e.g., healthy) samples with a subset of cells or genes from samples expected to contain a true differential signal [20,60,61]. This strategy can create datasets with more realistic levels of variability, together with a known ground truth, thus allowing quantitative performance metrics to be calculated.

Overall, there is no perfect reference dataset. Simulated data may not capture all properties of real data, and even when experimental data include an approximate ground truth, the correct level of variability may not be easily represented. For example, it can be difficult to ensure that the variability of spiked-in material is appropriate, or that independent measurements on cell line data represent a relevant scenario for experiments on outbred populations. Experimental data may also have different structure depending on the technological platform used, which should be represented in the benchmark. In some cases in the literature, individual datasets have also been found to be unrepresentative, leading to biased assessment of methods (e.g., [62]). The use of experimental design principles can mitigate some of these issues. In our view, the key to benchmarking is diversity of evaluations, i.e., using a range of metrics and datasets that span the range of those that might be encountered in practice, so that performance estimates can be credibly extrapolated to datasets that the method will be applied to in future.

Parameters and software versions

Parameter settings can have a crucial impact on performance. For many methods, tuning parameters to optimal values requires significant effort and expertise. Some methods have a large number of tunable parameters; documentation and examples can provide guidance on the most important ones. For a neutral benchmark, a range of parameter values should be considered for each method. Importantly, the selection of parameter values should comply with
the neutrality principle, i.e., certain methods should not be favored over others through more extensive parameter tuning.

There are three major strategies for choosing parameters. The first (and simplest) is to use default values for all parameters. Default parameters may be adequate for some methods, although this is difficult to judge in advance. While this may reflect typical usage by untrained users, it is usually too simplistic for a neutral benchmark. The second strategy is to choose parameters based on previous experience, or values published in the literature for certain datasets. This relies on familiarity with the methods and literature, reflecting usage by expert users. The third strategy is to use a systematic or automated parameter tuning procedure; e.g., a ‘grid search’ to optimize across ranges of values for multiple parameters, or techniques such as cross-validation (e.g., [26]). The strategies may also be combined; e.g., setting non-critical parameters to default values (strategy 1), using values shown to give good performance in previous work or the literature for other parameters (strategy 2), and performing a grid search for one or more key parameters (strategy 3). Regardless of the strategy, neutrality should be considered: comparing methods with the same strategy makes sense, while comparing one method with default parameters against another with extensive tuning is likely to give biased results.

For smaller benchmarks performed to introduce a new method, comparing against a single set of optimal parameter values for competing methods is often sufficient; these values may be selected during initial exploratory work, or by consulting documentation. However, as outlined above, bias may be introduced by tuning the parameters of the new method more extensively. Results should be cautiously interpreted, to avoid over-optimistic reporting due to expending more ‘researcher degrees of freedom’ on tuning the new method [5,63].

Software versions can also influence results, especially if updates include major changes to methodology (e.g., [64]). Final results should generally be based on the latest available versions, which may require re-running some methods if updates become available during the course of a benchmark.

Evaluation criteria: key quantitative performance metrics

Ranking of methods will usually rely on one or more quantitative performance metrics (Figure 1a provides a schematic overview of frequently used metrics). The choice of metric depends primarily on the type of method. For example, for classification methods (e.g., using reference datasets with a ground truth), metrics include the true positive rate (TPR; sensitivity or recall), false positive rate (FPR; 1 - specificity), and false discovery rate (FDR). For clustering methods, common metrics include the F1 score, adjusted Rand index, normalized mutual information, precision, and recall (e.g., [25,29,41]); some of these can be calculated at the cluster level as
well as averaged (and optionally weighted) across clusters. Several of these metrics can also be compared visually to capture the tradeoff between sensitivity and specificity, e.g., using receiver operating characteristic (ROC) curves (TPR vs. FPR), TPR vs. FDR curves, or precision-recall (PR) curves (Figure 1b). For some imbalanced datasets, PR curves have been shown to be more informative than ROC curves [65]. These visual metrics can also be summarized as a single number, such as area under the ROC curve (AUROC) or area under the PR curve (AUPR).

For methods with continuous-valued output (e.g., effect sizes), metrics include the root mean square error (RMSE), distance measures, Pearson correlation, sum of absolute log-ratios, log-modulus, and cross-entropy. Further classes of methods include those generating graphs, phylogenetic trees, overlapping clusters, or distributions; these require more complex metrics. In some cases, custom metrics may need to be developed (e.g., [27]). When designing custom metrics, it is important to assess their reliability across a range of prediction values (e.g., [66,67]). For some metrics, it may also be useful to assess uncertainty, e.g., via confidence intervals. If multiple metrics are considered, the final rankings may be combined or weighted to produce an overall ranking. In the context of supervised learning, classification or prediction accuracy can be evaluated by cross-validation or on a separate, labeled test dataset.

Additional metrics that do not rely on a ground truth include measures of stability, stochasticity, and robustness. These measures may be quantified by running methods multiple times using different inputs or subsampled data. ‘Missing values’ may occur if a method does not return any values for a certain metric, e.g., due to a failure to converge or other computational issues such as excessive runtime or memory requirements. Fallback solutions such as imputation may be considered in this case [68], which should be transparently reported. For non-deterministic methods (e.g., with random starts or stochastic optimization), variability in results when using different random seeds or subsampled data should be characterized. In addition, in the absence of ground truth, null comparisons can be constructed by randomizing group labels such that datasets do not contain any true signal, which can provide information on expected error rates (e.g., [20,24]). However, null comparisons must be designed carefully to avoid confounding by batch or population structure.
Figure 1. Summary and examples of performance metrics. (a) Schematic overview of classes of frequently used performance metrics, including examples (gray boxes). (b) Examples of popular visualizations of quantitative performance metrics for classification methods, using reference datasets with a ground truth: (i) ROC curves, (ii) TPR vs. FDR curves (circles represent observed TPR and FDR at typical FDR cutoffs of 1%, 5%, and 10%; filled circles indicate observed FDR lower than or equal to the imposed cutoff), and (iii) PR curves. Visualizations in (b) generated using iCOBRA R/Bioconductor package [69].
Evaluation criteria: secondary measures

In addition to the key quantitative performance metrics, methods should also be evaluated according to secondary measures including runtime, scalability, and other computational requirements, as well as qualitative aspects such as user-friendliness, code quality, and documentation quality (Figure 1a).

In our experience, runtimes and scalability can vary enormously between methods; e.g., runtimes for clustering algorithms ranged from minutes to days for the same datasets [29]. Similarly, memory and other computational requirements can vary widely. Depending on the scope of the benchmark, runtimes and scalability may be investigated systematically, e.g., by varying the number of cells or genes in a single-cell RNA-sequencing dataset [25,28]. In many cases, there is a tradeoff between performance and computational requirements. In practice, if computational requirements for a top-performing method are prohibitive (e.g., requiring a high-performance server instead of a standard laptop), then a lower-ranked method may be preferred by some users.

User-friendliness, installation procedures, and documentation quality can also be highly variable [70]. These aspects are crucial for users without extensive computational training, which includes many experimental researchers. Methods that have a simple installation procedure, with clear dependencies and automated testing using continuous integration, are generally more accessible and reliable. One way to achieve a streamlined installation procedure is by providing the method as a package, and distributing it via standard package repositories, such as CRAN and Bioconductor for R, or PyPI for Python. Package repositories enforce minimum standards for code quality, documentation, and automated testing, which provides users with guarantees regarding reliability and usability. Alternative options to distribute methods include GitHub and other code repositories or institutional websites, in the form of packages, source code, pre-built binaries, or custom scripts; however, these options do not provide users with the same guarantees. Availability across platforms (Windows, Mac, and Linux) and within popular programming languages for data analysis (e.g., R and Python) are also important. Availability of graphical user interfaces (GUIs) extends accessibility to users without command-line experience; however, methods that are only available via GUIs hinder reproducibility and are thus difficult to include in a systematic benchmark.

For many users, freely available and open source software will be preferred. Freely available software ensures broad accessibility, while open source software can be checked for bugs, adapted, or contributed to by experienced users. From the developer perspective, code quality and use of software development best practices, such as unit testing and continuous integration, are also important factors. Similarly, adherence to commonly used data formats (e.g., GFF/GTF files for genomic features, BAM/SAM files for sequence alignment data, or FCS files for flow or mass cytometry data) greatly improves accessibility and extendability. Evidence
of active package maintenance and recent bug fixes provide users with confidence that unexpected problems are likely to be addressed.

High-quality documentation is critical, including help pages for individual functions as well as extended tutorials demonstrating how to run complete analysis pipelines. Ideally, all code examples in the documentation should be continually tested; e.g., as done automatically by package repositories such as Bioconductor, or through continuous integration.

Interpretation, guidelines, and recommendations

To make the benchmark useful for readers, the results must be clearly interpreted and summarized from the perspective of the intended audience. For method users, results can be summarized in the form of guidelines or recommendations regarding the best choice of method; this will often include an overall ranking of methods (e.g., [27, 29, 41]). If different metrics produce conflicting rankings, the associated tradeoffs should be discussed (e.g., performance vs. runtime). Statistical inference techniques, such as statistical tests and confidence intervals, may be useful to determine whether an observed performance difference between methods is statistically significant. The interpretation may also involve biological or other domain knowledge to establish the scientific significance of the results; e.g., the practical significance of performance differences between the top methods. Where possible, neutrality principles should be preserved during the interpretation.

For method developers, the conclusions may include guidelines for the future development of methods; e.g., identifying limitations of current methods and highlighting possible areas for future work. By assisting method developers to focus their research efforts, high-quality benchmarks can have significant impact on the progress of computational fields of research.

Publication and distribution of results

Publishing results in a clear, accessible format ensures that readers will be able to understand them and apply them to their work. If the benchmark includes an overall ranking of methods, this can be presented using visualizations and summary tables (e.g., [27, 29, 41]). If several key performance metrics were used, more complex visualizations are also informative; e.g., flow charts to guide the optimal choice of method for different analyses [27]. For extensive benchmarks, it is also useful to create online resources to enable readers to interactively explore the results; and in particular, to distribute raw, pre-processed, and/or results data (e.g., [28, 69, 71–73]). In R, the Shiny framework provides a convenient system for building interactive
websites. Figure 2 displays an example of an interactive website to explore the results of a benchmark [27], created using Shiny.

In academic research, benchmark results will usually be summarized and published in a peer-reviewed article. For a neutral benchmark, the benchmark will be the main focus of the paper. For a benchmark performed to introduce a new method, the benchmark results will form one part of the exposition. We highly recommend publishing a preprint on a preprint server prior to peer review (e.g., bioRxiv or arXiv) to speed up distribution of results, broaden accessibility, and solicit additional feedback. Similarly, direct consultation with method authors once a draft is available can generate highly useful feedback. Finally, at publication time, considering open access options will further broaden accessibility.

Figure 2. Example of an interactive website allowing users to explore the results of a benchmarking study [27]. This website was created using the Shiny framework for R.

Enabling future extensions

Since new methods are continually emerging (e.g., [1]), published benchmarks can quickly become out of date. To avoid this, it is critical to design extensible benchmarks. For example, creating publicly accessible repositories containing reproducible code and data allows other researchers to extend the benchmark to include new methods or datasets, or to try different parameter settings or pre-processing procedures (e.g., [25–29]). New results can be published by the original authors as an online supplement or as updates to an interactive website.
In addition to raw data and code, it is also useful to provide pre-processed data and results (e.g., [25]), especially for computationally intensive benchmarks. This allows method developers to compare new methods more easily, since they can directly add a new method to the existing benchmark. This may be combined with an interactive website, where users can upload results from a new method, to be included in an updated comparison either automatically or by the original authors (e.g., [31,74,75]). ‘Continuous’ benchmarks, which are continually updated, are especially convenient (e.g., [76]).

Reproducible research best practices

Reproducibility of research findings has become an increasing concern in numerous areas of study [77]. In computational sciences, reproducibility of code scripts and data analyses has been recognized as a useful ‘minimum standard’ that enables other researchers to verify analyses [78]. This can be achieved by making all code and data (where permitted) available via public repositories. In a number of cases in the literature, access to code and data have enabled method developers to uncover potential errors in published benchmarks due to suboptimal usage of methods (e.g., [64,79,80]); this procedure is greatly simplified when code and data are made publicly available by default. Journal publication policies can play a crucial role in encouraging authors to follow these practices (e.g., [81]); experience shows that statements that code and data are ‘available on request’ are often insufficient [82]. In the context of benchmarking, code and data availability also provides further benefits for both method users and developers. For method users, public code repositories serve as a source of annotated code to run methods and build analysis pipelines, which is especially valuable for users without extensive computational experience. For developers, code repositories can act as a prototype for future method development work as well as extensions to the benchmark.

Parameter values and software versions used in the benchmark should also be clearly reported, to ensure complete reproducibility. For methods that are run using scripts, parameter values will be recorded within the scripts, which helps avoid errors. Where relevant, this should include random seeds. In R, the command ‘sessionInfo()’ gives a complete summary of package versions, as well as the version of R and the operating system. For methods only available via graphical interfaces, parameters and versions must be recorded manually, for example in a spreadsheet. Reproducible workflow frameworks, such as the Galaxy platform [83], can also be helpful when using graphical tools. A summary table of parameter values and software versions can be published as supplementary information along with the publication describing the benchmark (e.g., Supporting Information Table S1 in [29]).

Automated workflow management tools and specialized tools for organizing benchmarks provide sophisticated options for setting up benchmarks and creating a reproducible record of steps in a benchmarking pipeline, including software environments, package versions, and
parameter values. Examples include SummarizedBenchmark [84], DataPackageR [85], workflow [86], and Dynamic Statistical Comparisons [87]. Some tools (e.g., workflow) also provide streamlined options for publishing results. In machine learning, OpenML provides a sophisticated platform to organize and share benchmarks [88]. More general tools for managing computational workflows, including Snakemake [89], Make, Bioconda [90], and conda, can be customized to capture setup information (e.g., package versions). Containerization tools such as Docker and Singularity may be used to completely encapsulate a software environment for each method, preserving the package version as well as dependency packages and the operating system, and facilitating further distribution of methods to end users. For extensive benchmarks, additional best practices from software development are also useful, including unit testing and continuous integration.

Many free online tools and resources are available for sharing code and data. This includes GitHub and Bitbucket for code sharing; publicly funded data repositories for specific data types (including ArrayExpress [91], the Gene Expression Omnibus [92], and FlowRepository [93]); and more general data repositories including figshare, Dryad, Zenodo, Bioconductor ExperimentHub, and Mendeley Data. Custom data repositories (e.g., [28,69]) can be designed when additional flexibility is needed. Several repositories allow the creation of ‘digital object identifiers’ (DOIs) for code or data objects, which can be used for citation purposes. In general, preference should be given to publicly funded repositories, which provide greater guarantees for long-term archival stability [70].

An extensive literature exists on best practices for reproducible computational research (e.g., [94]). While the optimal level of computational reproducibility will depend on the scope of the benchmark and level of computational expertise, in our experience, almost all efforts in this area prove highly useful, especially by facilitating later adaptations or extensions to the study by ourselves or other researchers.

Summary

Benchmarking studies provide highly valuable information for users and developers of computational methods. However, designing informative benchmarks requires careful consideration of a number of key points. In this review, we have provided a series of practical guidelines and recommendations for rigorous benchmarking design and implementation (summarized in Box 1), based on our experiences in computational biology. We hope these guidelines will assist computational researchers to design high-quality benchmarks, which will contribute to scientific advances through informed selection of methods by users and targeting of research efforts by developers.
Author contributions

LMW proposed the project and drafted the manuscript. WS, RC, CS, AH, PG, ALB, YS, and MDR contributed ideas and references and contributed to drafting of the manuscript. YS and MDR supervised the project. All authors read and approved the final manuscript.

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Competing interests

The authors declare that they have no competing interests.
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