A meta-analysis of bioinformatics software benchmarks reveals that publication-bias unduly influences software accuracy

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Abstract

Computational biology has provided widely used and powerful software tools for testing and making inferences about biological data. In the face of rapidly increasing volumes of data, heuristic methods that trade software speed for accuracy must be employed. We are interested in testing for trade-offs between speed and accuracy and for other factors that are indicative of accurate software.

We have extracted accuracy and speed ranks from independent benchmarks of computational biology software of different software tools, and evaluated the factors that are likely to influence accuracy e.g. speed, author reputation, journal impact, recency or developer efforts.

We found that software speed, author reputation, journal impact, the number of citations and age are all unreliable predictors of software accuracy. This is unfortunate because citations, author and journal reputation are frequently used reasons for selecting software tools. Our results do show that accurate bioinformatic software tools are generally the product of many gradual improvements, often from multiple developers, based upon matching GitHub records with benchmark results. In addition, we find that the field of bioinformatics has an excess of slow and inaccurate software tools, this is consistent across many sub-disciplines. Meanwhile, there are few tools that are middle-of-road in terms of accuracy and speed trade-offs. We hypothesise that a form of publication-bias unduly influences the publication and development of bioinformatic software. In other words, software that is intermediate in terms of both speed and accuracy may be difficult to publish due to author, editor and reviewer practices. This leaves an unfortunate gap in the literature as the ideal tools may fall in the gap e.g. high accuracy is generally not useful if years of CPU time is required, while high speed is not useful if the results are very inaccurate.

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Background

Computational biology software is widely used and has produced some of the most cited publications in the entire scientific corpus [1, 2, 3]. This highly-cited software includes implementations of methods for sequence alignment and homology inference [4, 5, 6, 7], phylogenetic analysis [8, 9, 10, 11, 12], statistical analysis of survival patterns in biomedicine [13, 14], biomolecular structure analysis [15, 16, 17, 18, 19], visualization and data collection [20, 21]. However, the popularity of a software tool does not necessarily mean that it is accurate or computationally efficient, instead usability, ease of installation, operating system and other factors may play a greater role in a software tool's popularity. Indeed, there have been several notable incidences where inaccurate software has caused considerable harm [?, 22, 23].

Progress in the biological sciences is increasingly limited by the ability to analyse large volumes of data, therefore the dependence of biologists on software is also increasing [24]. There is an increasing reliance on technological solutions for automating biological data generation (e.g. next-generation sequencing, mass-spectroscopy, cell-tracking and species tracking), therefore the biological sciences have become increasingly dependent upon computational software for processing large quantities of data [24]. As a consequence, the computational efficiency of data processing and analysis software is of great importance to decrease the energy, climate impact, and time costs of research [25]. Furthermore, even small error

rates can have major impacts on the number of false inferences as datasets become larger [26].

The gold-standard for determining accuracy is for independent researchers to conduct benchmarks, which can serve a useful role in reducing the over-optimistic reporting of software accuracy [27, 28, 29] and the self-assessment trap [30, 31]. Benchmark studies typically use a number of positive and negative control datasets, predictions from different software tools can then be partitioned into true or false groups and a variety of metrics can be used to evaluate the performance differences [32, 33, 29]. The aim of these benchmarks is to independently identify tools that make acceptable compromises in terms of balancing speed with discriminating true and false predictions, and are therefore suited for wide adoption by the community.

For common computational biology tasks, a proliferation of software-based solutions often exists [34, 35, 36, 37, 38]. While this is a good problem to have, and points to a diversity of options from which practical solutions can be selected, having many possible options creates a dilemma for users. In the absence of any recent gold-standard benchmarks, how should scientific software be selected? In the following we presume that "biological accuracy" is the most desirable feature for a software tool. Biological accuracy is the degree to which predictions or measurements reflect the biological truths based on expert-derived curated datasets (see Methods for the mathematical definition used here). In some fields biological accuracy is very difficult to ascertain, for example, in phylogenetics it is nearly impossible in most cases to know the true ancestral relationships between organisms. In situations like this, researchers may use simulated or high-confidence datasets.

A number of possible predictors of software quality are used by the community of computational biology software users [39, 40, 41]. Some accessible, quantifiable and frequently used proxies for identifying high quality software include: **1. Recency:** recently published software tools may have built upon the results of past work, or be an update to an existing software. Therefore these may be more accurate and faster. **2. Wide adoption:** a software tool may be widely used because it is fast and accurate, or because it is well-supported and user-friendly. In fact, "large user base", "word-of-mouth", "wide-adoption", "personal recommendation," and "recommendation from a close colleague," are frequent responses to surveys of "how do scientists select software?" [39, 40, 41]. **3. Journal impact:** high profile journals are run by editors and reviewers who carefully select and curate the best manuscripts. Therefore, high impact journals may be more likely to select manuscripts describing good software [42]. **4. Author/Group reputation:** the key to any project is the skills of the people involved, including maintaining a high collective intelligence [40, 43, 44]. As a consequence, an argument could be made that well respected and high-profile authors will produce better software [45, 46]. **5. Speed:** software tools frequently trade accuracy for speed. For example, heuristic software such as the popular homology search tool, BLAST, compromises the mathematical guarantee of optimal solutions for more speed

[4, 7]. Some researchers may naively interpret this fact as slower software is likely to be more accurate. But speed may also be influenced by the programming language [47], and the level of hardware optimisation [48, 49]; however, the implementation generally has more of an impact (e.g. brute-force approaches versus rapid and sensitive pre-filtering [50, 51]).

Other factors that are less quantifiable that influence whether a software tool is selected include: whether the documentation is good, user-friendly, word-of-mouth and "used in a similar analysis" [41]. However, citation metrics may be a useful proxy for the above.

With the wide adoption of GitHub ($\approx 47\%$ of the **499** tools included in this study could be linked to a GitHub repository), quantifiable data on software development such as the number of contributors to code, number of code changes and versions is also available [52, 53, 54].

In the following study, we explore factors that may be indicative of software accuracy. This, in our opinion, should be one of the prime reasons for selecting a software tool. We have mined the large and freely accessible PubMed database [55] for benchmarks of computational biology software, and manually extracted accuracy and speed rankings for **499** unique software tools. For each tool, we have collected measures that may be predictive of accuracy, and may be subjectively employed by the research community as a proxy for software quality. These include relative speed, relative age, the productivity and impact of the corresponding authors, journal impact and the number of citations.

Results

We have collected relative accuracy and speed ranks for **499** distinct software tools. This software has been developed for solving broad cross-section computational biology tasks. Each software tool was benchmarked in at least one of **69** publications that satisfy the Boulesteix criteria [56]. In brief, the Boulesteix criteria are: 1. the main focus of the article is a benchmark. 2. the authors are reasonably neutral. 3. the test data and evaluation criteria are sensible.

For each of the publications describing these tools, we have (where possible) collected the journal's H5-index (Google Scholar Metrics), the maximum H-index and corresponding M-indices [45] for the corresponding authors for each tool, and the number of times the publication(s) associated with a tool has been cited using Google Scholar (data collected over a 6 month period in late 2020). Note that citation metrics are not static and will change over time. In addition, where possible we also extract the version number, the number of commits and number of contributors from GitHub repositories.

We have computed the Spearman's correlation coefficient for each pairwise combination of the mean normalised accuracy and speed ranks, with the year published, mean relative age (compared to software in the same benchmarks), journal H5 metrics, the total number of citations, the relative number of citations (compared to software in the same benchmarks) and the maximum H- and corresponding M-indices for the cor-

responding authors, version number, and numbers of commits and contributors. The results are presented in Figure 1A. We find significant associations between most of the citation-based metrics (journal H5, citations, relative citations, H-index and M-index). There is also a negative correlation between the year of publication, the relative age and many of the citation-based metrics.

Data on the number of updates to software tools from GitHub such as the number of versions, commits and contributors **was significantly correlated with accuracy (respective Spearman's rhos = 0.13, 0.22, 0.21, respective uncorrected P-values = 0.0027, 0.00079, 0.0013). These features were not correlated with speed however (see Figure 1A).** We also found that author reputation metrics, journal impacts and the age of tools were generally **not** correlated with either tool accuracy or speed (see Figure 1). The strongest association was between accuracy and **the relative number of citations** (Spearman's rho = **0.092, P-value = 0.047**). But the effect size is only just over the significance threshold and may be explained by multiple-testing.

In order to gain a deeper understanding of the distribution of available bioinformatic software tools on a speed versus accuracy landscape, we ran a permutation test. The ranks extracted from each benchmark were randomly permuted, generating 1,000 randomized speed and accuracy ranks. In the cells of a 10×10 grid spanning the normalised speed and accuracy ranks we computed a Z-score for the observed number of tools in a cell, compared to the expected distributions generated by 1,000 randomized ranks. The results of this are shown in Figure 2. We identified **18** bins where there was a significant excess or dearth of tools. For example, there was an excess of "slow and inaccurate" software (**Z=2.50, P-value=0.0063**). We find that the amount of software classed as "fast and accurate", "fast and inaccurate" and "slow and accurate" are at approximately the expected proportions based upon the permutation test. While there are very few tools placed in the middle of the ranks on accuracy and speed. The number of significant results is in excess, and is not due to multiple testing, as the probability of finding **18** of 100 tests significant by chance is low (P-value = 2.2×10^{-6}, exact binomial test).

There is a major reduction in the number of software tools that are classed as intermediate in terms of both speed and accuracy based on permutation tests (see Methods for details, Figure 2). The cells corresponding to the four central deciles are highlighted (**Z = -1.9, -2.5, -2.9 and -1.1, P-values = 0.03, 0.006, 0.002 and 0.14**, respectively, reading from top to bottom, left to right). We also tested the relative age of the software tools in the indicated corners and central regions of the speed vs accuracy plot. We found that the "slow and inaccurate" tools ($N = 27$) were generally published earlier than "fast and accurate" tools ($N = 23$) (**W = 341, P=0.005, one-tailed Wilcoxon test**) (Figure S7).

Conclusion

We have gathered data on the relative speeds and accuracies of **499** bioinformatic tools from **69** benchmarks published between 2005 and 2020. **Our results suggest there are major benefits for long term support for software [57].** The finding of a strong relationship between the number of commits to GitHub (i.e. software updates) and accuracy, highlights the benefits of long-term development.

Our study finds little evidence to support that impact-based metrics have any relationship with software quality, this is unfortunate as these are frequently cited reasons for selecting software tools [41]. This implies that the high citation rates for bioinformatic software [1, 2, 3] is more a reflection of other factors such as user-friendliness or the Matthew Effect [58, 59] other than accuracy.

We found the lack of a correlation between software speed and accuracy surprising. The slower software tools are over-represented at both high and low levels of accuracy (Figure 2). In addition, we find an under-representation of software that has intermediate levels of both accuracy and speed. A possible explanation for this is that bioinformatic software tools are bound by a form of publication-bias [60, **?**]. That is, the probability that a study being published is influenced by the results it contains [**?**]. The community of developers, reviewers and editors may be unwilling to publish software that is not highly ranked on speed or accuracy. If correct, this may have unfortunate consequences. We also found that slow and inaccurate software is generally published earlier than fast and accurate tools **(P=0.007, one-tailed Wilcoxon test)**, therefore comparisons were not required to publish the slow and inaccurate tools.

DESCRIBE STUDY LIMITATIONS...

- **Difficult to test publication biases**

- **Heterogeneous measures of accuracy between benchmarks**

- **possible lack of independence between different benchmarks**

- **Non-uniform inclusion of tools in different benchmarks – some tools ranked many times (e.g. velvet and soap assemblers ranked 26 different times)**

- **How to deal with inconsistently reported versioning of software?**

- **Metrics and tools performance are all moving targets, only a snap shot is used here**

We propose that the full spectrum of software tool accuracies and speeds serve a useful purpose to the research community. Like negative results, if honestly reported, illustrate to the research community that certain approaches are not practical research avenues [61, 62, 63]. The current practices of publishers, editors, reviewers and authors of software tools
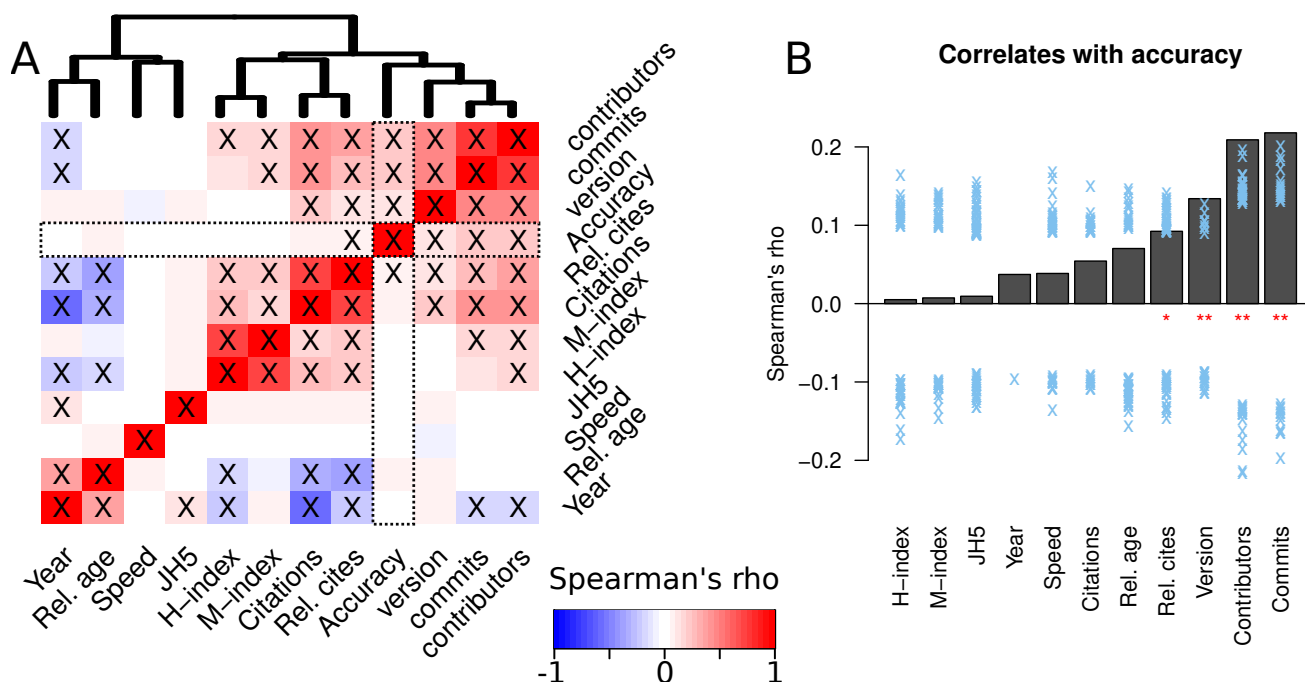
Figure 1. A. A heatmap indicating the relationships between proposed predictors of software quality. Spearman's rho is used to infer correlations between metrics such as the H- and M-indices of corresponding authors, number of citations, journal impact factors and H5 indices, the year and relative age of software and the mean relative rankings of software speed and accuracy. Red colours indicate a positive correlation, blue colours indicate a negative correlation. Correlations with an uncorrected P-value less than 0.05 are indicated with a 'X'. The dashed rectangular area is illustrated in more detail in **B**, the relationship between speed and accuracy is shown in more detail in **Figure 2**. **B.** A barplot illustrating the correlation, as measured by Spearman's rho, between normalised accuracy ranks and software tool features that may be predictive of accuracy. In order to give an appreciation of the difference between the observed effect-sizes and significant effect sizes, we generated 1000 permuted accuracy ranks for each benchmark and recorded Spearman's rho for the significant correlations with an uncorrected P-value less than 0.05. These values are marked with blues 'X's in the barplot. Significant correlations are marked with red asterisks.

therefore deprive our community of tools for building effective and productive workflows.

The most reliable way to select software tools is through neutral software benchmarks [56]. We are hopeful that this, along with steps to reduce the publication-bias we have described, will reduce the over-optimistic and misleading reporting of tool accuracy [27, 28, 30].

Methods

In order to evaluate predictors of computational biology software accuracy, we mined the published literature, extracted data from articles, connected these with bibliometric databases, and tested for correlates with accuracy. We outline these steps in further detail below.

Criteria for inclusion: We are interested in using computational biology benchmarks that satisfy Anne-Laure Boulesteix's (ALB) three criteria for a "neutral comparison study" [56]. Firstly, the main focus of the article is the comparison and **not** the introduction of a new tool. Secondly, the authors should be reasonably neutral, which means that the authors should

not generally have been involved in the development of the tools included in the benchmark. Thirdly, the test data and evaluation criteria should be sensible. This means that the test data should be independent of data that tools have been trained upon, and that the evaluation measures appropriately quantify correct and incorrect predictions.

Literature mining: We identified an initial list of 10 benchmark articles that satisfy the ALB-criteria. These were identified based upon previous knowledge of published articles and were supplemented with several literature searches (e.g. '"benchmark" AND "cputime"' was used to query both GoogleScholar and Pubmed [55, 64]). We used these articles to seed a machine-learning approach for identifying further candidate articles and to identify new search terms to include.

For our machine-learning-based literature screening, we computed a score $(s(a))$ for each article that tells us the likelihood that it is a benchmark. In brief, our approaches uses 3 stages:

1. Remove high frequency words from the title and abstract of candidate articles (e.g. 'the', 'and', 'of', 'to', 'a', ...)
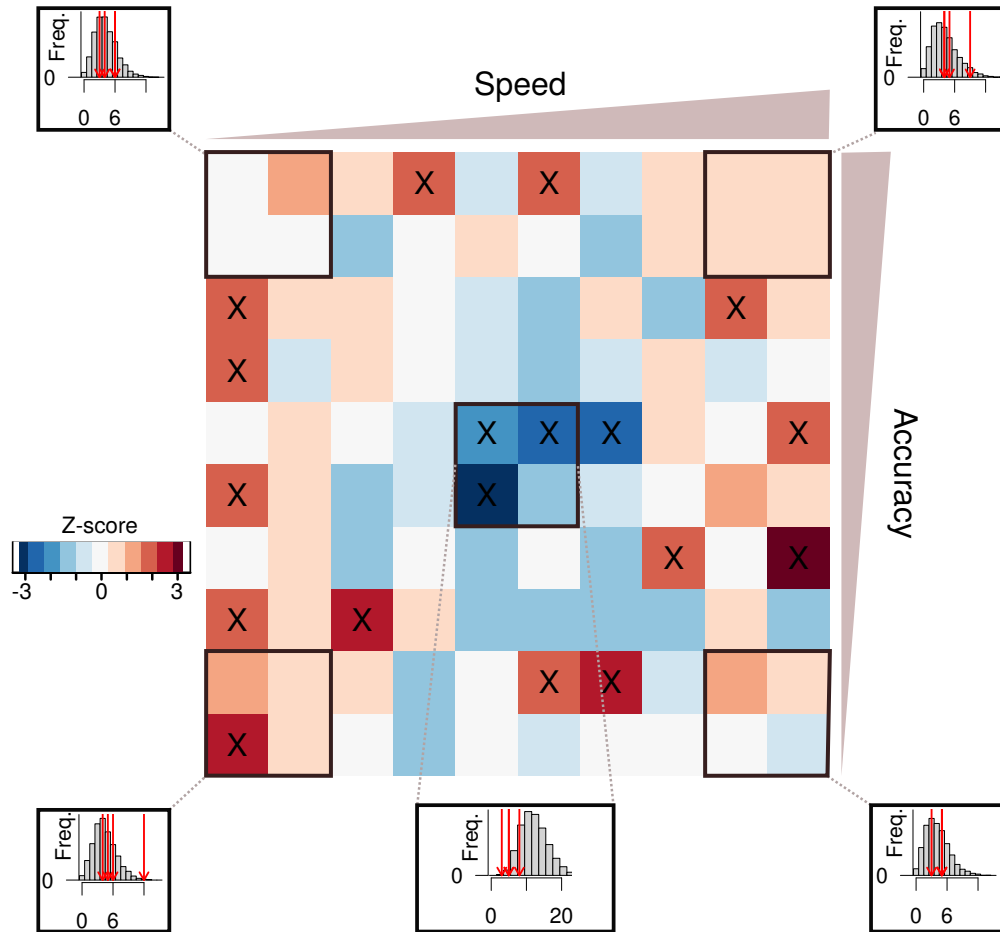
Figure 2. A heatmap indicating the relative paucity or abundance of software in the range of possible accuracy and speed rankings. Red colours indicate an abundance of software tools in an accuracy and speed category, while blue colours indicate scarcity of software in an accuracy and speed category. The abundance is quantified using a Z-score computation for each bin, this is derived from 10,000 random permutations of the speed and accuracy ranks from each benchmark. Mean normalised ranks of accuracy and speed have been binned into 100 classes (a 10×10 grid) that range from comparatively slow/inaccurate to comparatively fast/accurate. Z-scores with a P-value less than 0.05 are indicated with a 'X'.

2. Compute a log-odds score for the remaining words

3. Use a sum of log-odds scores to give a total score for candidate articles

For stage 1, we identified a list of high frequency (e.g. $f(word) > 1/10,000$) words by pooling the content of two control texts [65, 66].

For stage 2, in order to compute a log-odds score for bioinformatic words, we computed the frequency of words that were not removed by our high frequency filter in two different groups of articles: bioinformatics-background and bioinformatics-benchmark articles. The text from bioinformatics-background articles were drawn from the bioinformatics literature, but these were not necessarily associated with benchmark studies. For background text we used Pubmed ([55, 64] to select 8,908 articles that contained the word "bioinformatics" in the title or abstract and were published between 2013 and

2015. We computed frequencies for each word by combining text from titles and abstracts for the background and training articles. A log-odds score is computed for each word using the following formula: $lo(word) = \log_2 \frac{f_{tr}(word)+\delta}{f_{bg}(word)+\delta}$, where δ is a prior probability ($\delta = 10^{-5}$, by default), $f_{bg}(word)$ and $f_{tr}(word)$ are the frequencies of a *word* in the background and training datasets respectively. Word frequencies are computed by counting the number of times a word appears in the pool of titles and abstracts, the counts are normalised by the total number of words in each set.

Thirdly, we also collected a group of candidate benchmark articles by mining Pubmed for articles that are likely to be benchmarks of bioinformatic software, these may match the terms: "((bioinformatics) AND (algorithms OR programs OR software)) AND (accuracy OR assessment OR benchmark OR comparison OR performance) AND (speed OR time)". Further terms used in this search were progressively added as relevant

enriched terms were identified in later iterations. The final query is given in **supplementary materials**.

A score is computed for each candidate article by summing the log-odds scores for the words in title and abstract, i.e. $s(a) = \sum_i^N lo(w_i)$. The high scoring candidate articles are then manually evaluated against the ALB-criteria. Accuracy and speed ranks are extracted from the articles that meet the criteria, and these are also added to the set of training articles. The evaluated candidate articles that do not meet the ALB-criteria are incorporated into the set of background articles. This process is iterated and has resulted in the identification of **69** benchmark articles, that contain **134** different benchmarks, together these rank **499** distinct software packages.

There is a potential for bias to have been introduced into this dataset. Some possible forms of bias include converging on a niche group of benchmark studies due to the literature mining technique that we have used. A further possibility is that benchmark studies themselves are biased, either including very high performing or very low performing software tools. To address each of these concerns we have attempted to be as comprehensive as possible in terms of benchmark inclusion, as well as include comprehensive benchmarks. By which we mean studies that include all available software tools that address a biological problem.

Data extraction and processing: for each article that met the ALB-criteria and contained data on both the accuracy and speed from their tests we extracted ranks for each tool. Many articles contained multiple benchmarks, in these cases we selected a range of these, the provenance of which is stored with the accuracy metric and raw speed and accuracy rank data for each tool. In line with rank-based statistics, the cases where tools were tied are resolved by using a midpoint rank (e.g. if tool 3 and 4 are tied, the rank 3.5 is used) [67]. Each rank extraction was independently verified by at least one other co-author to ensure both the provenance of the data could be established and that the ranks were correct. The ranks for each benchmark were then normalised to lie between 0 and 1 using the formula $1 - \frac{r-1}{n-1}$ where 'r' is a tool's rank and 'n' is the number of tools in the benchmark. For tools that were benchmarked multiple times with multiple metrics (e.g. BWA is evaluated in 6 different articles [68, 69, 70, 71, 72, 73]) a mean normalised rank is used to summarise the accuracy and speed performance. Or, more formally:

$$accuracy = \sum_{i=1..N} 1 - \frac{r_i^{accuracy} - 1}{n_i - 1},$$

$$speed = \sum_{i=1..N} 1 - \frac{r_i^{speed} - 1}{n_i - 1}$$

For each tool we identified the corresponding publications in GoogleScholar, the total number of citations was recorded, the corresponding authors were also identified and if these had public GoogleScholar profiles we extracted their H-index and calculated a M-index ($\frac{H-index}{y}$) where 'y' is the number of years since their first publication. For the journals that each tool is published in we extracted the H5-index from GoogleScholar Metrics. The year of publication was also recorded for each tool. A "relative age" and "relative citations" was also computed for each tool. For each benchmark, software was ranked by year of first publication (or number of citations), ranks were assigned and then normalised as described above. Tools ranked in multiple evaluations were then assigned a mean value for "relative age" and "relative citations".

The papers describing tools were checked for information on version numbers and links to GitHub. Google was also employed to identify GitHub repositories. When a repository was matched with a tool, the number of "commits" and number of "contributors" was collected, when details of version numbers were provided, these were also harvested. Version numbers are inconsistently used between groups, and may begin at either 0 or 1. To counter this issue we have added '1' to all versions less than '1', e.g. version 0.31 become 1.31. In addition, multiple point releases may be used e.g. 'version 5.2.6', these have been mapped to the nearest decimal value '5.26'.

Statistical analysis: For each tool we have manually collected up to 12 different statistics from GoogleScholar, GitHub and directly from literature describing tools (1. corresponding author's H-index, 2. corresponding author's M-index, 3. journal H5 index, 4. normalised accuracy rank, 5. normalised speed rank, 6. number of citations, 7. relative age, 8. relative number of citations, 9. year first published, 10. version 11. number of commits to GitHub, 12. number of contributors to GitHub). These have been evaluated in a pairwise fashion to produce Figure 1 A&B, the R code for these is given in the GitHub repository (linked below).

For each benchmark of three or more tools, we extracted the published accuracy and speed ranks. In order to identify if there is an enrichment of certain accuracy and speed pairings we constructed a permutation test. The individual accuracy and speed ranks were reassigned to tools in a random fashion and each new accuracy and speed rank pairing was recorded. For each benchmark this procedure was repeated 10,000 times. These permuted rankings were normalised and compared to the real rankings to produce the 'X' points in Figure 1B and the heatmap and histograms in Figure 2. The heatmap in Figure 2 is based upon Z-scores ($Z = \frac{x - \bar{x}}{\sigma}$). For each cell in a 10×10 grid a Z-score is computed to illustrate the abundance or lack of tools in a cell relative to the permuted data.

Data availability

Raw datasets, software and documents are available under a CC-BY license:
`https://docs.google.com/spreadsheets/d/14xIY2PHNvxmV9MQLpbzSfFkuy1RlzDHbBOCZLJKcGu8/edit?usp=sharing`
and here:
`https://dx.doi.org/10.6084/m9.figshare.4299320.v1`

Additional documentation, code, figures and raw data is available here:

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https://github.com/Gardner-BinfLab/speed-
vs-accuracy-meta-analysis
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Acknowledgements

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