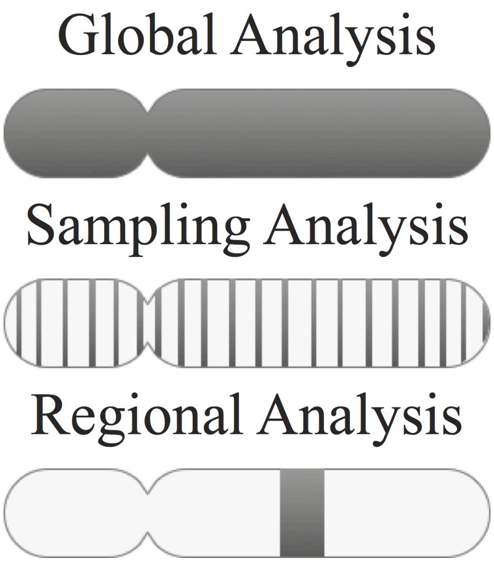
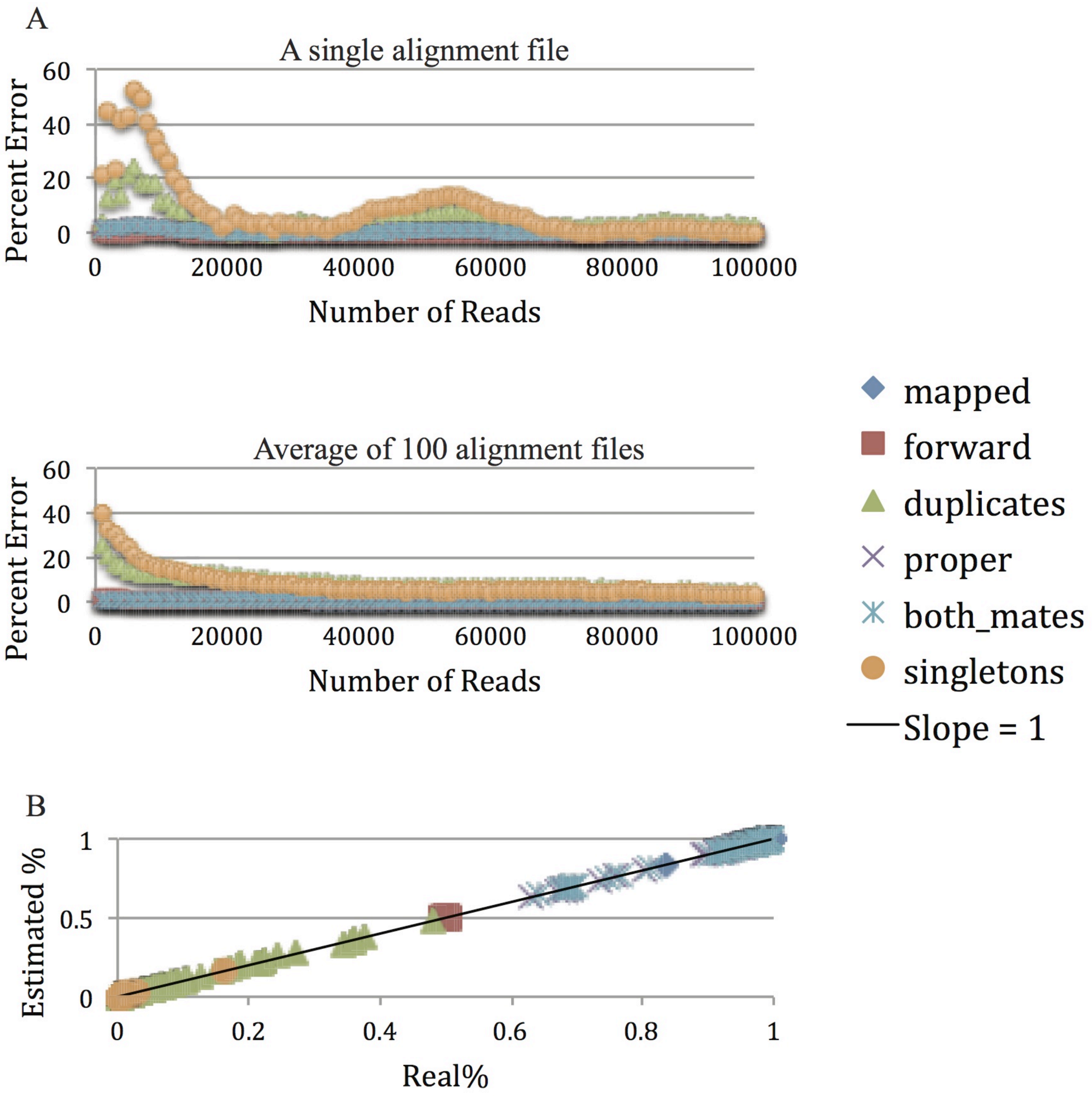


Supplementary Figure 1

Analysis Modalities

The region of the dataset being analyzed is depicted by the dark color. **Global Analysis.** The entire dataset is analyzed. This analysis typically takes hours to days to complete. **Sampling Analysis.** Global quantities of the entire dataset are estimated by random sampling. It is possible to complete this analysis in seconds. **Regional Analysis.** Users analyze a well-defined, small, continuous unit of data from a potentially large dataset, such as genomic sequence alignments in the region of a gene. This analysis can also be completed in seconds.



Supplementary Figure 2

Accuracy of sampling-based estimation of alignment file metrics

Sampling analysis of six metrics performed by BAM.IOBIO.IO is compared to accurate values obtained via end-to-end analysis. (A) Here the percent error of the sampling analysis is shown for each metric as a function of the number of alignment records analyzed. The evaluation of a single alignment file is shown (top) as well as an average of 100 alignment files (bottom) from the 1000 Genomes project. [REF] (B) Estimated values obtained via random sampling of 100,000 reads are plotted against the accurate values of 100 alignment files.

Supplemental Note 1, Scalability and Deployment, Licensing, and Implementation Details.

Scalability and Deployment

To ensure the necessary resources to provide real-time experience, BAM.IOBIO (and other IOBIO apps) has several deployment options that make this app viable for a very wide user base. First, users can access the web application from our own web servers, which are running on a powerful Amazon Cloud server, allowing many simultaneous analysis instances. If this app were to reach a larger user base, more servers and more powerful ones could be easily spun up to handle the increased demand. Second, because all source code is freely available, institutions with high usage will be able to offer this app running on their own systems for their users, distributing the computational load. Third, we are also working on solutions that will enable power users with the click of a button to “spin up” their own Amazon cloud servers to ensure high performance at their own (insubstantial) cost.

License

BAM.IOBIO uses the MIT License.

Implementation Details

BAM.IOBIO is a Javascript and HTML web application using HTML5 websockets for streaming data transfer and D3.js (http://d3js.org) for image creation. A web service (at http://bamstatsalive.iobio.io) running the UNIX program ***Bamstatsalive*** (https://github.com/yiq/bamstatsAlive), built with the Bamtools[6] API, is used to generate all alignment statistics. BAM.IOBIO requires that the browser in which the user runs the app supports websockets and the D3 JavaScript library: it currently works on the latest versions of the Chrome, Firefox, Safari and Internet Explorer browsers (see Supplementary Table 2). While some lower-performance WiFi networks and web proxy services do not support the advanced web features required by this application, we have found that BAM.IOBIO works well in most environments.

Supplemental Table 1, Time Evaluation

Duration of sampling analysis compared to whole file analysis is shown for a low coverage full genome dataset and an exome dataset from the 1000 Genome Project.

Sample Type (filesize)	**Sampled Analysis Time**	**While File Analysis Time**
Low Coverage (18gb)	6.4 seconds	~8 hours
Exome (14gb)	5.6 seconds	~6 hours

BAM.IOBIO Platform Compatibility

Test Case	MacOS			Linux (Ubuntu)		Windows			MacOSX - iPad		MacOSX iPhone5		Android Phone
	Chrome	Firefox	Safari	Firefox	Chrome	IE11	Chrome	Firefox	Chrome	Safari	Chrome	Safari	Chrome
	37.0	32.0	7.0	32	37	11	37.0	32.0	30	7.0	37.0	7.0	37.0
Load BAM file from URL	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass
Load local BAM file	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	n/a	n/a	n/a	n/a	n/a
Increase sample size 3X	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass
Subselect region on depth chart	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass
Subselect regions in quick succession	Pass	Pass	Pass	Pass	Pass	Limited	Pass	Pass	Pass	Pass	Pass	Limited	Pass
Use default BED file	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass
Use custom BED file	Pass	Pass	Pass	Pass	Pass	Pass	Pass	Pass	n/a	n/a	n/a	n/a	n/a

Supplemental Table 2, BAM.IOBIO Platform Compatibility

This table shows the outcome of testing major functionalities on a variety of platforms and browsers. Local file upload is not applicable (n/a) on mobile devices. With certain browser / platform combinations, selecting regions in quick succession may cause the app to become unresponsive (Limited).