

REVIEW OF GenChek V2.

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Methodology:

To evaluate GenChek V2. I imported 6 sequences that I have previously developed and am very familiar with. These 6 sequences were chosen based on their relative level of relatedness to one another. I ran all imported DNA sequences through all DNA analysis functions except for the electropherogram viewer (did not have a chromatogram to analyze), as well as various supplied protein sequences through all protein analysis functions.

Initial impressions:

Although Java programs can be "buggy" and lack-luster in appearance, this program does an excellent job departing from the norm. It looks very attractive and has many useful features.

Intuitiveness/ ease of use:

Easy to browse, with a clean and somewhat intuitive interface. The program certainly needs to come with a user manual and a tutorial, as many features (and user settings within a feature) need to be explained. The help menu is a great resource, which does an excellent job explaining the various features, and their applications. However, like many Java-based programs, this program lacks a "PC intuitive" scheme. It does not allow for simple drag-and-drop functions, and some right-click features are available in some screens, but not in others.

Interface:

The interface is clean and mostly straightforward. There are times when the window containing data does not resize properly and leaves information cut-off by the edge of the window - this may or may not be a bug. The program has great map and graph features that generate high quality color renditions of data and gene maps.

Functionality and Features:

The program packages a very impressive battery of analysis tools.

The tools that performed best for nucleotide analysis include: The contig assembly module, restriction enzyme analysis, the ORF finding module, the BLAST suite, multiple sequence alignment (for DNA), and the primer design module. Especially surprising was the above average performing primer design module. Primer analysis was quick and efficient, with an easy read-out and informative "expert" data options. In contrast to the listed modules that performed well, some modules did not function as anticipated. The trim vector function was not capable of "trimming" vector sequences from an imported gene-containing vector. Likewise, the gene finder tool could not positively identify a known gene in a vector sequence. Furthermore, the necessity to search genes *only* from human, fly and rice limits the overall usefulness of this feature, since many researchers are interested in other organisms such as, mouse, yeast, worm, and bacteria.

Furthermore, hybrid sequences, such as those from vectors, contain DNA from many sources (such as bacteria, human, mouse, etc), and as such, limiting gene searches to only one organism at a time further limits the usefulness of this tool. It should be noted that an unexpected result came from a negative-control experiment carried out with the alignment tool, where 2 non-related sequences that should have no alignment similarities, yielded a positive alignment.

Some nucleotide analysis tools could not be used at all, simply because the tool did not function when clicked on. These tools include the web interface tools (for both DNA and protein). Although the promise that these tools hold is both exciting and useful for the researcher, an evaluation of its usability could not be made at this time.

Tools that performed best for protein analysis include: The amino acid frequency and composition analysis tool, the amino acid molecular weight tool, the protease digest module, the statistical analysis tool, the hydrophathy plot tool, and the charge vs. pH curve. Especially impressive was the protease digest tool, which gives a clear and simple digest analysis for many common proteases.

Quality/ Stability:

The overall quality and stability of this program is well above average as compared to other java-based programs. The program never crashed during operation and even when conducting long complex analysis, the program remained stable. Most given tasks were accomplished quickly by the cognate tool. Only in the cases of the web interface tools and trim module, did a tool not accomplish a given task. There were only a small number of potential bugs encountered (see below for full discussion on Bugs), but nothing serious enough to distract from the work done by the program. A surprising number of complex tools are included in this package, yet the program behaved predictably and did not seem to consume too much RAM in the process.

Value and Overall Impressions:

This program has many valuable sequence analysis tools that enable the cataloging and maintenance of sequence data derived primarily from sequencing reactions. The usefulness of this program is further enhanced by the clean out-put format that most data is presented in – facilitating the integration of generated data into other programs. The overall stability and usefulness of the tools included make GenChek V2 a very comprehensive analysis tool. However, I feel that the applicability of this program is mainly limited to facilities that generate a lot of sequence data (eg. facilities that do large-scale mutational analysis screens). Molecular biology labs that mainly concentrate on targeted gene disruption/ and or manipulation may be more interested in better vector analysis/ vector design tools. It is therefore my opinion that this program is best suited for researches involved in screening protocols, but perhaps not for those involved in complex vector design and/or gene manipulation (cloning) work.

Potential Bugs:

- 1) When conducting a sequence alignment, the bar graph generated represents “quality” values that are not reported in the lower left corner of the Align Viewer window. The text gives a value of zero (0) for all qualities of sequence.
- 2) Many imported sequences showed length discrepancies of exactly 2 nucleotides when compared to the original sequence (the imported sequence is 2 nucleotides shorter). It is unclear what is causing the discrepancy since not all imported sequences show a difference in length when compared to the original sequence. Furthermore, when comparing the original and imported sequences, the beginning and end of the sequence seem to remain unchanged.
- 3) When using the hydropathy plot, after adding annotation, one cannot move, resize or change the text on the plot. This is problematic as one usually needs to change or move the added text during annotation.