BioEdit: An important software for molecular biology

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License: Freeware Copyright 1991 - 2007 Tom Hall.
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Abstract

BioEdit is one of the most common program used in molecular biology studies. It was developed initially as a biological sequence alignment editor written for Windows only. It contains many features for sequence alignments modes of easy hand alignment, split window view, user defined color, information based shading and auto integration with other programs such as ClustalW and Blast. However, in the last few years it was developed dramatically to integrate many other features and functions and useful molecular tools for molecular biologist such as several modes of hand alignment, plasmid drawing and annotation, restriction mapping and much more. It became one of the widely used programs in molecular biology with its multipurpose tools in molecular biology. The freeware license and its efficient up to date modules beside its quick ability to produce results make it one of the most popular programs for molecular biologist nowadays.

History

In 1999, Tom Hall (Hall, 1999) has published his work on a user-friendly biological sequence alignment editor and analysis program while he was working in the department of microbiology, North Carolina State University. The program was used extensively ever since and quoted in many article in high ranking journals and used in many novel and diverse research application (Antonis et al., 2003; Ron et al., 2005; Chen et al., 2006; Aquifer Robert et al., 2003; Klaas et al., 2002).

Contribution to research

Many researchers in the field of Molecular biology have used BioEdit modules in during their original research. BioEdit was used for molecular studies of different organisms such as Virus genomes (Ron et al., 2005 Chen et al., 2006), Bacterial genome (Aquifer Robert et al., 2003) plant genome (Klaas et al., 2002) and animal genome (Hong et al., 2008). With many citations in peer reviewed journals, BioEdit became very important bioinformatics tool for molecular biologist, and more distinguished among other biological sequence alignment programs (Table 1). Most of sequence alignment programs do not have many other functions or useful tools for molecular biologist comparing to BioEdit.

Importable data formats


Advantages

- BioEdit is user friendly and can be downloaded free of charge online from many servers.
- BioEdit is a standalone program and has mutable functions for many applications
- It works under most windows version that exit today.
- The interface is user friendly.

Disadvantages

- BioEdit is no longer being maintained, and the documentation is out of date and no longer maintained since 2007.

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www.gerfbb.com
- Scoring in pair wise alignment functions does not agree with the example in the help document.
- The time BioEdit needs to analyze sequences increases very with their length.
- Some functions need some experience (eg. Plasmid design) and multiple steps to perform.

The limitation
- The last version was updated in 2007 and BioEdit is no longer being maintained.

BioEdit availability online
BioEdit can be downloaded from the following Servers for:
- http://www.mbio.ncsu.edu/bioedit/page2.html
- http://www.mybiosoftware.com/alignment/1013

Table 1: Some other online biological sequence alignment programme functions and availability

<table>
<thead>
<tr>
<th>Program</th>
<th>Function</th>
<th>Server</th>
</tr>
</thead>
<tbody>
<tr>
<td>LALIGN</td>
<td>Multiple, non-overlapping, local similarity modelling alignment; models the information content of the sequences Alignments for low identity membrane protein sequences based on various similarity criteria</td>
<td><a href="http://www.ch.embnet.org/software/LALIGN_form.html">http://www.ch.embnet.org/software/LALIGN_form.html</a></td>
</tr>
<tr>
<td>mAlign</td>
<td>Global:Global (GG), Global:Local (GL) alignment with statistics</td>
<td><a href="http://www.ch.embnet.org/software/ClustalW.html">http://www.ch.embnet.org/software/ClustalW.html</a></td>
</tr>
<tr>
<td>AlignMe</td>
<td>Dynamic programming/clustering</td>
<td><a href="http://multalin.toulouse.inra.fr/multalin/">http://multalin.toulouse.inra.fr/multalin/</a></td>
</tr>
<tr>
<td>GGSEARCH, GLSEARCH</td>
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References