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Gene identification software

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Abstract

The GRAIL server is one of the many internet resources for predicting genes in uncharacterized genomic DNA.

Content

The GRAIL server is one of the many internet resources for predicting genes in uncharacterized genomic DNA. GRAIL has gene models for five different organisms: human, mouse, *Arabidopsis*, *Drosophila* and *Escherichia coli*. A list of possible exons, their positions, reading frames, and scores is returned after submitting a sequence analysis.

Navigation

The interface to GRAIL is somewhat confusing. Rather than start with a simple sequence-submission form, the user is presented with a mostly blank page with three buttons at the top: 'New Grail Analysis', 'Upload Grail Dataset', and 'New GenQuest Search'. As new users are unlikely to know what the last two buttons are for, there seems no need to have them here. In fact, if you click on 'New GenQuest Search', nothing happens. Clicking on 'New Grail Analysis' generates a page that allows you to choose an organism. As mentioned above, you only have a choice of five. It is not clear whether the server can be reliably used to analyze a sequence from another organism. After choosing the organism, a request form is generated. This form gives a variety of choices, depending on the organism, of what types of exons to find, and whether to identify polyadenylation sites, CpG islands, repetitive DNA or simple repeats. After submitting the request, a list of exons with positions, frames, and scores is presented. Currently this is all that you can do. Clicking on some of the optional buttons at the bottom of the page, such as 'Draw Results Image' or 'GenQuest Search', result in a message that says '!!! It's Coming Soon !!!'. Given that it has been four years since the last update, I suspect that these features will not be coming any time soon.

Reporter's comments

Timeliness

Last updated 12 February 1996.

Best feature

The usefulness of GRAIL information is usually realized when integrated into a gene annotation program. So, there is an option to download the GRAIL results so that they can be utilized by another program. Unfortunately, most of these programs are UNIX-based and most casual users do not have access to them.

Worst feature

Navigating the site is difficult and the output is useless without an external helper program of some kind.

Wish list

Too numerous to list. It appears, however, that the initial GRAIL server has been or will be supplanted by GrailEXP, a more sophisticated gene modeling program that builds on the exon-predicting power of GRAIL by adding homology-based prediction. Homology-based prediction is a very powerful method of identifying genes, especially when expressed sequence tags and protein sequences can be incorporated into the prediction algorithms. At the time of writing, however, it appears that this system is working only for human or mouse sequences. While using a mouse sequence worked quite well; choosing the *Arabidopsis* option and submitting several trial sequences gave no results at all.

Related websites

There are a number of gene prediction websites, including PROCRUSTES, GeneMark, Genie and GENSCAN.

Table of links

GRAIL: gene recognition and assembly internet link

GrailEXP

PROCRUSTES

GeneMark

Genie

GENSCAN

References

1. GRAIL: gene recognition and assembly internet link.