

Biological Sequence Analysis Using The SeqAn C++ Library (Chapman & Hall/CRC Mathematical & Computational Biology) [Print Replica] [Kindle Edition] By Andreas Gogol-D

By Andreas Gogol-D

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Dynamic visual data mining: biological sequence -

Dynamic visual data mining 23 Nucleotide sequence analysis The nucleotide sequence analysis category consists of the following six modules (Figure 1):

<http://www.inderscienceonline.com/doi/pdf/10.1504/IJBRA.2005.006900>

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:: :: Biological -

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http://www.chare.ir/index.php?dispatch=products.view&product_id=92947

HMMER - Official Site -

HMMER is used for searching sequence databases for homologs of protein sequences, and for making protein sequence alignments. It implements methods using <http://hmmer.janelia.org/>

Where Traffic meets DNA: Mobility Mining using -

Where Traffic meets DNA: Mobility Mining using Biological Sequence Analysis Revisited <http://citeseerx.ist.psu.edu/viewdoc/summary?doi=10.1.1.231.2329>

bol.com | Biological Sequence Analysis Using the -

Biological Sequence Analysis Using Ebook. An Easy-to-Use Research Tool for Algorithm Testing and Development Before the SeqAn project, there was clearly a lack of <http://www.bol.com/nl/p/biological-sequence-analysis-using-the-seqan-c-library/1001004011473305/>

Sequence analysis - Wikipedia, the free -

In bioinformatics, sequence analysis is the process of subjecting a DNA, RNA or peptide sequence to any of a wide range of analytical methods to understand its http://en.wikipedia.org/wiki/Sequence_analysis

Biological Sequence Analysis: Probabilistic -

Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids, Richard Durbin, Sean R. Eddy, Anders Krogh, Graeme J. Mitchison <http://academic.research.microsoft.com/Publication/1394105/biological-sequence-analysis-probabilistic-models-of-proteins-and-nucleic-acids>

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Biological Sequence Analysis Using the SeqAn C++ Library (Chapman & Hall/CRC Mathematical and Computational Biology) [Andreas Gogol-D ring, Knut Reinert] on Amazon <http://www.amazon.com/Biological-Sequence-Analysis-Mathematical-Computational/dp/142007623X>

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Biological Sequence Analysis Using The SeqAn C++ Library (Chapman & Hall/CRC Mathematical & Computational Biology) <http://www.openisbn.com/isbn/9781420076233/>

Biological sequence analysis using regular -

1. Biotechniques. 1999 Jul;27(1):76-8. Biological sequence analysis using regular expressions. Horton RM. Attotron Biosensor Corporation, Carson City, NV, USA <http://www.ncbi.nlm.nih.gov/pubmed/10407669>

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<http://www.worldcat.org/title/biological-sequence-analysis-using-the-seqan-c-library/oclc/669518249>

Biological Sequence Analysis using the SeqAn C++ -

Before the SeqAn project, there was clearly a lack of available implementations in sequence analysis, even for standard tasks. Implementations of needed algorithmic

<http://publications.mi.fu-berlin.de/825/>

Experience using web services for biological -

Abstract. Programmatic access to data and tools through the web using so-called web services has an important role to play in bioinformatics. In this

<http://bib.oxfordjournals.org/lookup/doi/10.1093/bib/bbn029>

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<http://www.amazon.fr/Biological-Sequence-Analysis-Using-Library/dp/142007623X>

Programming Bioinformatics Chapman Computer -

Programming Bioinformatics Chapman Biological Sequence Analysis Using the SeqAn C++ Library (Chapman & Hall/CRC Mathematical and Computational Biology) by

<http://homeidea.rocks/post/programming-bioinformatics-chapman-computer-analysis/>

Bioinformatics - Wikipedia, the free encyclopedia -

In the context of genomics, annotation is the process of marking the genes and other biological features in a DNA sequence. This process needs to be automated because

<http://en.wikipedia.org/wiki/Bioinformatics>

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<http://www.openisbn.com/preview/142007623X/>

HMMER User s Guide. Biological Sequence Analysis -

HMMER User s Guide. Biological Sequence Analysis Using Profile Hidden Markov Models (2003)

<http://citeseerx.ist.psu.edu/viewdoc/summary?doi=10.1.1.314.4661>

Presentation "Center for Biological Sequence -

Center for Biological Sequence Analysis Database Searching Using alignment algorithms for finding similar sequences.

<http://slideplayer.com/slide/5134970/>

Hidden Markov Models and their Applications in -

Hidden Markov models (HMMs) have been extensively used in biological sequence analysis. In this paper, we give a tutorial review of HMMs and their applications in a

<http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2766791/>