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Computational phylogenetics is the application of computational algorithms, methods, and programs to phylogenetic analyses. The goal is to assemble a phylogenetic tree representing a hypothesis about the evolutionary ancestry of a set of genes, species, or other taxa. For example, these techniques have been used to explore the family tree of hominid species and the relationships between ...

Computational phylogenetics - Wikipedia

Title: vFoam: a new set of volume of fluid solvers for turbulent isothermal multiphase flows

Computational Physics authors/titles recent submissions

Title Authors Published Abstract Publication Details; Easy Email Encryption with Easy Key Management John S. Koh, Steven M. Bellovin, Jason Nieh

Technical Reports | Department of Computer Science

The Jorgensen Research Group has developed several programs for research in computational chemistry and drug discovery. They are freely available to academic users.

William L. Jorgensen Research Group - Software - BOSS

Drug design, often referred to as rational drug design or simply rational design, is the inventive process of finding new medications based on the knowledge of a biological target. The drug is most commonly an organic small molecule that activates or inhibits the function of a biomolecule such as a protein, which in turn results in a therapeutic benefit to the patient.

Drug design - Wikipedia

http://arep.med.harvard.edu/labgc/. A key approach in genomic research is to divide the cellular contents into distinct sub-populations, each given an -omic term ...

Biopharmaceutical -Omics & -omics glossary taxonomy

Title Image based in situ sequencing as a basis for learning tissue morphology Biography Carolina Wählby, Professor at the Department of Information Technology, Uppsala University is head of the Centre for Image Analysis at Uppsala University and focusing on digital image processing and analysis in the interface between biomedicine, microscopy, and computer science.

ECDP 2019

Although genomewide RNA expression analysis has become a routine tool in biomedical research, extracting biological insight from such information remains a major challenge. Here, we describe a powerful analytical method called Gene Set Enrichment Analysis (GSEA) for interpreting gene expression data. The method derives its power by focusing on gene sets, that is, groups of genes that share ...

Gene set enrichment analysis: A knowledge-based approach

1 Syllabus for DBT-JRF BET examination General Comments: Question paper will have two parts, Part-A

(General aptitude & General Biotechnology) and Part-B (General plus specialized branches

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Topical Software. This page indexes add-on software and other resources relevant to SciPy, categorized by scientific discipline or computational topic.

Topical Software - SciPy.org

Advanced options. Topic Area

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18 NOEER 2016 Figure 1. pH evolution during the conventional gastrointestinal environment simulation (left axis) and drug release from a commercial diclofenac extended-release tablet (right axis).

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