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Introduction:

Bioinformatics is a new scientific discipline that combines biology, computer science, mathematics, and statistics into a broad-based field that will have profound impacts on all fields of biology. Bioinformatics is expected to substantially impact on scientific, engineering and economic development of the world.

Objectives:

The objectives of *IJBRA* are to develop, promote and coordinate the development and practice of bioinformatics and computational biology. *IJBRA* aims to help professionals working in the field, academic educators and policy-makers to contribute, to disseminate knowledge, and to learn from each other's work. The international dimension is emphasized in order to overcome cultural and national barriers and to meet the needs of accelerating technological changes and exchanges in the global economy. *IJBRA* is an outstanding outlet that can shape a significant body of research in the field of bioinformatics and computational biology and in which results can be shared across institutions, governments, researchers and students, and also industry.

Contents:

IJBRA publishes original and review papers, technical reports, case studies, conference reports, management reports, book reviews, and notes, commentaries, and news. Contribution may be by submission or invitation, and suggestions for special issues and publications are welcome.

Subject Coverage:

Although the possible set of paper topics is large and we encourage submission on any area within the scope of bioinformatics and computational biology, the following areas are particularly suitable (but not exhaustive):

- Bioinformatic Databases,
- Bio-Grid,
- Bio-Ontology and Data Mining,
- Computational Genomics ,
- Computational Proteomics,
- Data Visualization,
- DNA Assembly, Clustering, and Mapping,
- Gene Expression and Microarrays,
- Gene Identification and Annotation,
- High Performance Computing,
- Parallel Algorithms for Biological Analysis,
- Parallel Architectures for Biological Applications,
- Biomedical Image Processing (Segmentation, Registration, Fusion),
- Molecular Modeling and Simulation,
- Molecular Evolution and Phylogeny,
- Molecular Sequence Analysis,
- Phylogeny Reconstruction Algorithms,
- Protein Structure Prediction,
- Sequence Search and Alignment,
- System Biology,
- Signaling and Computation Biomedical Data Engineering,
- Telemedicine.