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Genome Informatics Series Vol. 22 Proceedings of the 9th Annual International Workshop on Bioinformatics and Systems Biology (IBSB 2009) , Boston University, Boston, USA

Genome Informatics 2009

This volume contains papers presented at the 20th International Conference on Genome Informatics (GIW 2009) held at the Pacifico Yokohama, Japan from December 14 to 16, 2009. The GIW Series provides an international forum for the presentation and discussion of original research papers on all aspects of bioinformatics, computational biology and systems biology.

Genome Informatics 2009 - World Scientific

Genome informatics 2009 : proceedings of the 20th international conference : Pacifico Yokohama, Japan, 14-16 December 2009. [Shinichi Morishita; Sang Yup Lee; Yasubumi Sakakibara;] -- "This volume contains papers presented at the 20th International Conference on Genome Informatics (GIW 2009) held at the Pacifico Yokohama, Japan from December 14 to 16, 2009.

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CO-EVOLUTION OF METABOLISM AND PROTEIN SEQUENCES

Results. We present GWAMAR, a tool we have developed for detecting of drug resistance-associated mutations in bacteria through comparative analysis of whole-genome sequences. The pipeline of GWAMAR comprises several steps. First, for a set of closely related bacterial genomes, it employs eCAMBer to identify homologous gene families.

GWAMAR: Genome-wide assessment of mutations associated ...

10/2012 - present: Post-doctoral researcher, Genome Informatics, Essen University Hospital. 12/2012: PhD degree at Free University Amsterdam, the Netherlands. 12/2010 - 05/2011 and 01/2010 - 02/2010: Scientific visitor in the Bioinformatics group at INRIA Rennes, France.

Inken Wohlers - Genome Informatics

Sequencing informatics: These projects develop new and improved methods for processing, aligning, and formatting sequence reads, performing genome assembly, and extracting sequence features. Function analyses: Gene regulation, gene expression, epigenetic modifications, and methylation all shape the relationships between genes and phenotypes.

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Dr. Phillippy is head of the Genome Informatics Section and a tenure-track investigator in the Computational and Statistical Genomics Branch at the National Human Genome Research Institute. In 2000, Dr. Phillippy began working as a bioinformatics research assistant for Dr. Arthur Delcher at Loyola University Maryland, and received his B.S. in ...

Adam M. Phillippy, Ph.D. - Genome.gov

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Genome informatics is a field of computational molecular biology and branch of informatics that uses computers, software, and computational solution techniques to make observations, resolve problems, and manage data related to the genomic function of DNA sequences, comparison of gene structures, determination of the tertiary structure of all proteins, and other molecular biological activities.

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Bult CJ, Richardson JE, Blake JA, Kadin JA, Ringwald M, Eppig JT, and the Mouse Genome Database Group. 2000. Mouse genome informatics in a new age of biological inquiry. Proceedings of the IEEE International Symposium on Bio-Informatics and Biomedical Engineering: 29-32. Eppig JT. 2000. Electronic Tools for Accessing the Mouse Genome.

MGI-Mouse Genome Informatics Publications

Mikania cordata, the only native congener of the invasive weed Mikania micrantha in China, is an ideal species for comparative study to reveal the invasion mechanism. However, its genome resources are lagging far behind its congener, which limits the comparative genomic analysis. Our goal is to characterize the genome of M. cordata by next-generation sequencing and propose a scheme for long ...

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