Integrative Biology-2013
OMICS Group Conferences
Accelerating Scientific Discovery
International Conference on
Integrative Biology Summit
August 5-7, 2013 Embassy Suites Las Vegas, USA

Detecting symmetric properties of genomes based on 2d maps of variant phase space

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Abstract

Visualization Methods have played a key role in the Human Genome Project. After further development more than a decade, larger numbers of Genome Databases are established and mass Genome-wide gene expression measurements are developed. In current situation, it is necessary to shift targets in computational cell biology from collecting sequencial data to making higher-level interpretation and exploring efficient content-based retrieval mechanism for genomes.Mammalian genomes encode thousands of large noncoding RNAs (lncRNAs), many of which regulate gene expression, interact with chromatin regulatory complexes, and are thought to play a role in localizing these complexes to target loci across the genome. Using higher dimensional visualization tools, their complex interactive properties could be organized as different visual maps. Variant technique as an emerging scheme applies multiple maps that uses four meta symbols as same as DNA or RNA representations. Different genome sequences are used for analysis to show their intrinsic symmetric properties and characteristics of those genome sequences under 2D maps of variant phase space. A set of sample maps are included and their characteristics are illustrated.