# OMICS International
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# 3rd International Conference on
# Integrative Biology

**August 04-06, 2015   Valencia, Spain**

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## Creative approaches for computational genomics

Associated with advanced next generation of sequencing technologies to capture various variations on cancers & diseases, huge amount of genomic sequences are ensembled & collected in worldwide databases. There are urgent requirements for modern genomic analysts to apply advanced tools & technologies to index, retrieve, visualize & search genomic sequential information more conveniently.

This workshop organizes a group of creative researchers & students together to discuss the state of the arts technologies in addition to exploring new schemes for computational genomics. All levels of approaches are encouraged on the concepts, ideas, models, tools, packages and practices of computational methods for the identification and characterization of functional elements & components from DNA sequence data. The primary target of this workshop is the theory and practice of algorithms in computational genomics, with the goals of using current methods for biological discovery and developing creative algorithms & approaches.

This workshop focuses on approaches for extracting and organizing information from similarity aspects on indexing & clustering of protein and DNA sequences through sequence database searches, feature measurements & visualizations.

Additional topics include:

*Disease sequences: cancer, infectious diseases, cardiovascular disease and psychiatric dysfunctions
*Coding & non-coding RNA/DNA sequencing data
*Novel ideas & models to identify functional components of genomic variations
*Randomness measurements & visualizations
*Generation & simulation mechanism on pseudo RNA/DNA sequences
*Geometric & topological invariant measurements
*Mathematical modelling on variations
*Probability & statistical analysis
*Combinatorial & permutation models
*Efficient computational schemes on clustering genomic sequences
*Content-based genomic sequence indexes & retrievals
*Integration of genetic and sequence information in genomic databases
*Genome browsers and feature visualizations

### Biography

Jeffrey Zheng has completed his PhD in 1994 from Monash University. He is the Professor and Head at the Department of Information Security, School of Software, Yunnan University from 2004. He has published more than 200 papers in national and international conferences, reputed journals and serving as an Editorial Board Member of Information Acquisition. He is active working on exploring mysteries of coding and non-coding DNA/RNA mechanism to use variant logic construction.

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