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Variant maps to identify coding and non-coding DNA sequences of genomes selected from multiple species

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In recent years, many DNA sequencing projects are developed on cells, plants and animals over the world into huge DNA databases. Researchers notice that mammalian genomes encode thousands of large non-coding RNAs (lncRNAs), interact with chromatin regulatory complexes, and are thought to play a role in localizing these complexes to target loci across the genome. It is a challenge target using higher dimensional tools to organize various complex interactive properties as visual maps. In this talk, Variant maps are used to provide models and experiment results using visual representation techniques to distinguish multiple species – *Salmonella*, *Caenorhabditis elegans*, *Arabidopsis*, *Pan troglodytes* and human genomes between coding and non-coding sequences selected. Our model uses probability measurements on the DNA sequences to separate coding and non-coding regions respectively to generate visual patterns to identify different sequences. Sample 2D maps are listed and their characteristics are illustrated under controllable environment. Visual results are analyzed to explore their intrinsic properties on selected multiple species of genome sequences.

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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