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### **Pseudo DNA sequence generation of noncoding distributions using stream cipher mechanism**

**Jeffrey Zheng**

Yunnan University, China

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 noncoding 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, a Pseudo DNA Variant Map PDVM is discussed to represent multiple maps that uses four Meta symbols as same as DNA or RNA representations. System architecture of key components and core mechanism on the PDVM are presented. Key modules, equations and their I/O parameters are discussed. Applying the PDVM, different sets of real DNA sequences from both sample animals (noncoding DNA) and plants (coding DNA) genomes are collected in comparison with pseudo DNA sequences generated by stream ciphers RC4/HC-256 to show their intrinsic properties in higher levels of similar relationships among relevant DNA sequences on 2D maps. Sample 2D maps are listed and their characteristics are illustrated under controllable environment. Visual results are analyzed to explore their intrinsic properties on selected genome sequences.

#### **Biography**

Jeffrey Zheng has completed his PhD in 1994 from Monash University. He is the Professor and Head at 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 noncoding DNA/RNA mechanism to use variant logic construction.

[conjugatesys@gmail.com](mailto:conjugatesys@gmail.com)