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Title: "The Geography of Gene Function: Spatial constraints in gene expression and regulation in eukaryotic genomes"

(https://computational-genomics.weebly.com/)

Abstract

Advances in genomic technologies have revealed that chromosomal architecture is a dynamic entity that shapes genomic function, rather than just a structural framework. Synthetic biology research has shown that fundamental biological processes, such as chromatin structure organization and RNA transcription, can occur in random DNA sequences with low specificity. This suggests that function emerges from context-specific constraints imposed on pervasive genomic activity. We will present spatial constraints in eukaryotic genomes in both one and three-dimensional contexts. Starting with the simple genome of S. cerevisiae, we will demonstrate a strong functional segregation related to the genome's structure, function, and evolutionary history. Examining more complex genomes, we will discuss examples of underlying spatial constraints, including the co-expression of nearby genes, the formation of regulatory hubs in three dimensions, and the role of genome architectural proteins in mediating gene regulation in disease and development. The goal is to show how the organization of the cell nucleus influences the translation of initial biochemical signals into widespread changes in gene expression.

biosketch:

Christoforos Nikolaou is the group leader of the Computational Genomics Group at the Biomedical Sciences Research Center "Alexander Fleming" in Athens, Greece (https://computational-genomics.weebly.com/). Born in Athens in 1978, he trained in biochemistry before earning a PhD in Molecular Biology from the University of Athens in 2005. As a post-doctoral fellow he worked at Barcelona's Centre de Regulacio Genomica (CRG) from 2006 to 2009. From 2010 to 2020, he served as Assistant Professor of Bioinformatics at the University of Crete's Biology Department, also contributing to its MSc program in Bioinformatics. His work centers on genome architecture, evolution, computational epigenomics, chromatin structure and the links between DNA composition, chromatin structure and gene expression regulation. He has co-authored a (modest) number of original papers on genome structure, chromatin and gene regulation. He is also the author of two textbooks on "Computational Biology" and "Data Analysis" (that some students have to read) and a collection of short stories of fiction (that some students pretend to have read).