



Evolution of the genome-wide distribution of genes and transposons

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Field: Mathematical and Computational Biology Degree: Ph.D.

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Abstract

Genomes exhibit a striking amount of complexity across a broad range of scales. This includes variation in the spatial distribution of features such as genes and transposable elements (TEs), which is observed both between species and among individuals in natural and artificial populations. Additionally, all eukaryotes studied to date have had gene duplications occur in their evolutionary history. In this dissertation, we develop a statistical method for analyzing relative changes in the expression of duplicated genes. We show that this method performs better than could otherwise be achieved using traditional methods of differential gene expression analysis. We apply this method to the analysis of subgenome expression dominance in two polyploid plant species. In both cases, it is shown that dominant subgenomes have a lower abundance of transposable elements. We then revisit the classical theory of the population genetics of transposable elements and show that the population variance in TE copy number predicted by this theory conflicts with empirical results from two naturally occurring and distinct populations. Finally, we develop both an analytic and simulation based approach to address this discrepancy, and discuss how these models can be connected with actual data as a step towards developing a more complete understanding of the evolution of the genome-wide distribution of genes and transposons.