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Practice Job Presentation

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Adaptive Evolution of Conserved Non-coding Elements

MONDAY, October 22, 2007 at 12:00 PM
110 Eckhart Hall, 5734 S. University Avenue

ABSTRACT

Conservation of DNA sequences across evolutionary history is a highly informative signal for identifying regions with important biological functions. In particular, conserved non-coding regions have been shown to be good candidates for containing regulatory elements that have roles in gene regulation. Recent studies have found that there are many thousands of conserved non-coding elements (CNCs) in vertebrate genomes and have suggested possible functions for some of these elements, but the function of most CNCs remains unknown. To study the evolution of CNCs, we developed a statistical method called the “shared rates test” to identify CNCs that show changes in evolutionary rates on particular branches of the mammalian phylogenetic tree. Those rate changes may indicate changes in the function of a CNC. We applied our method to CNCs of five mammalian genomes, and found that indeed many CNCs have experienced rate changes during their evolution. We also found a subset of CNCs showing accelerations in evolutionary rate that actually exceed the neutral rates, suggesting that adaptive evolution has shaped the evolution of those elements.