Susceptibilities to DNA Structural Transitions within Eukaryotic Genomes DINA ZHABINSKAYA, CRAIG BENHAM, SALLY MADDEN, University of California at Davis — We analyze the competitive transitions to alternate secondary DNA structures in a negatively supercoiled DNA molecule of kilobase length and specified base sequence. We use statistical mechanics to calculate the competition among all regions within the sequence that are susceptible to transitions to alternate structures. We use an approximate numerical method since the calculation of an exact partition function is numerically cumbersome for DNA molecules of lengths longer than hundreds of base pairs. This method yields accurate results in reasonable computational times. We implement algorithms that calculate the competition between transitions to denatured states and to Z-form DNA. We analyze these transitions near the transcription start sites (TSS) of a set of eukaryotic genes. We find an enhancement of Z-forming regions upstream of the TSS and a depletion of denatured regions around the start sites. We confirm that these finding are statistically significant by comparing our results to a set of randomized genes with preserved base composition at each position relative to the gene start sites. When we study the correlation of these transitions in orthologous mouse and human genes we find a clear evolutionary conservation of both types of transitions around the TSS.

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