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**Ming-Ying Leung\*** (mleung@utsa.edu), Division of Mathematics and Statistics, University of Texas at San Antonio, San Antonio, TX 78249. *Poisson Approximations in DNA Sequence Analysis*. Preliminary report.

The international efforts put into various large-scale genome sequencing initiatives have brought about an enormous amount of DNA sequence data. Mathematical methods have been playing an increasingly important role in the analysis and interpretation of these rapidly accumulating data. Some probabilistic results related to the distribution of palindromes on DNA sequences will be presented in this talk. This study is motivated by the observation of a high concentration of palindromes around the replication origins of several viral DNA genomes. The results are obtained by modeling the DNA sequence as an infinite chain of nucleotide bases independently sampled from the alphabet A, C, G, T and applying the Chen-Stein Poisson approximation techniques to a sequence of dependent Bernoulli random variables. (Received October 02, 2000)