

Department of Mathematical Sciences
Colloquium

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*Neural Networks for the Prediction of Replication
Origins in Herpesviruses*

Biological studies have indicated that the locations of replication origins of herpesviruses are associated with DNA regions rich in repetitive sequences. Based on this observation, computational methods have been created to classify regions of DNA as being close or not close to a replication origin. Unfortunately, these methods provide low positive predictive values for acceptable levels of sensitivity. Two new ideas related to this subject will be presented in this talk. First, the potential of new DNA sequence features not related to repetitive structures, such as AT content, dinucleotide scores, and standardized window positions, to help with the classification process will be explored. Second, the capacity of artificial neural networks to perform this classification will be shown. This presentation will demonstrate that neural networks produce better predictive performance than the existing methods.

**Friday, December 2, 2005 at 3 pm. in Bell Hall 143
The University of Texas at El Paso**

Refreshments will be served in front of the colloquium room,
15 minutes before the start of the colloquium.

For further information, please contact Dr. Pavel Šolín, Bell Hall 220. Phone:
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