1010-92-62 **Namhee Kim*** (nk401@cims.nyu.edu), 31 Washington Place, New York, NY 10003, and **Hin Hark Gan** and **Tamar Schlick**. *Discovering Novel Functional RNAs using Graph Theory.*

In vitro selection technology is a versatile experimental tool for discovering novel synthetic functional RNA molecules from large random sequence pools. However, most functional RNAs identified from random sequence pools are small molecules with simple folding motifs or topologies. Even if the size limitation can be alleviated technically, discovering complex functional RNA molecules this way may be limited because our computational analysis suggests that most random sequences fold into simple tree topologies. To significantly increase the probability of discovering functional RNAs, we develop an approach for engineering sequence pools possessing both simple and complex tree topologies.

We will present an approach using graph theory to represent RNA secondary structures and analyze RNA's structure space. This approach can identify many novel RNA motifs for applications in RNA genomics and RNA sequence pool design. Specifically, the talk will describe an RNA pool design algorithm combining graph theory and biased mutations and some preliminary applications to design of novel functional RNAs. (Received August 19, 2005)