

Institute for Computational Medicine

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Simulcast to Talbot Library, 709 Traylor Bldg



Computational Approaches to RNA Genomics and Design

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Abstract:

RNAs are wonderfully versatile molecules. Recent discoveries reveal that RNA molecules play vital roles in cellular function and disease, and have applications in functional genomics and the design of molecular sensors. We will describe graph theory-based and other computational methods to uncover natural non-coding RNAs in genomes, isolate synthetic functional RNAs from large sequence pools, and predict novel antibiotic targets on ribosomal RNAs. These efforts are conducted in conjunction with multidisciplinary experimental collaborators. Our graph theory description of RNA molecules predicts the diversity, abundance, and organization of the RNA structure universe. The predicted RNA-like structures provide a unifying framework for identifying functional RNAs. Specifically, we exploit such RNA-like structures to identify several novel non-coding RNAs in the human chromosome region associated with Prader-Willi and Angelman syndromes. As a complementary strategy, we use synthetic functional RNA motifs to identify their genomic counterparts which may have cellular roles similar to riboswitches. In parallel to genome searches, we have developed computational approaches for enhancing in vitro selection technology – an experimental technique for isolating functional RNAs from large sequence pools – by engineering structurally diverse RNA pools. This work combines pool synthesis concepts, graph theory, and analysis of RNA sequence/structure space to design sequence pools. In addition, we employ thermodynamic methods for siRNA design to predict known and novel antibiotic targets on ribosomal RNAs. Thus, our computational approaches offer tools for advancing RNA genomics, identifying RNAs implicated in diseases, improving in vitro selection technology, and predicting antibiotic-binding targets.