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BioAnalyzer: A tool for RNA local secondary structure prediction and visualization

RNA local secondary structures can act as RNA structural motifs, which are involved in various biological functions including gene regulation, genetic control, and gene replication. Thus, prediction of these RNA local secondary structures may be helpful in understanding their biological functions. Our group recently (Wan et al. 2005) developed a novel algorithm and associated software package called Rnall for RNA local secondary structure prediction; however, Rnall was not designed for visualization and was developed on Linux/Unix platforms. This may inconvenience many in the biological community who are more comfortable working with other operating systems. Thus, BioAnalyzer was developed as a platform-independent Graphical User Interface (GUI) for RNA local secondary structure prediction and visualization. Last year we implemented BioAnalyzer in Java to achieve the desired level of platform-independence. BioAnalyzer predicts and visualizes all Rnall local secondary structures by scanning the genomes, sending user-selected chunks to Rnall for structure prediction, sending Rnall's output to Naview, and then displaying Naview's output. Intermediary steps are shown, such as displaying the scanned genes and various data, their associated structures from Rnall, links to the textual output from Rnall, and the picture generated by Naview. All this functionality is combined in one GUI for easy access to any parts of the data flows and quick retesting. This year we added more functionality, including full display of Rnall structure predictions and their associated energy, dynamic 3D graphs, zooming and selection capabilities, and advanced annotation searching. In the process we've squashed many bugs and hope to release a public version soon.