BIOE 147 - Project Proposal

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Much of what we have studied in class relies on repressor/activator protein and promoter pairs. We have seen that there is a limit to the size of circuit that you can construct, due to the lack of a library of orthogonal proteins. While great strides have been made in seeking out new orthogonal repressing/ activating proteins, it is worth noting that many of the papers that we review in lecture still use the same 3 promoter/repressor pairs. It is not a simple task to rationally design our way out of this predicament. Since proteins function is dependent upon structure, and the prediction of protein structure is a difficult task (to say the least), it would be beneficial to search elsewhere for a class of molecules that can act as a reliable parts family.

It is already well known that RNA plays a major role in transcriptional, and translational, regulation within the cell [1]. RNA, unlike protein, has well characterized canonical base pairing interactions. These interactions dominate the formation of secondary structure. Which makes RNA less recalcitrant to rational design than protein [2]. Many tools have appeared recently that not only quicly and accurately predict RNA secondary structure, but also predict tertiary structure (e.g. pseudoknots). Most of the published uses of these tools has been focused on thier application to a research topic, rather than the implementation of a broad range methodology and workflow for designing RNA-based circuits [4]. An article published last year by Keasling's lab states that, with their work, they sought to 'establish a foundation for developing computer-aided design platforms' [5]. With that in mind, we seek to implement a CAD platform for the compilation of biocircuits, that synthesizes the many tools, and techniques that have already been detailed, concerning the modeling of riboregulation. The tool itself will be similar to simple electrical circuit design tools, and will generate algorithmically optimized compositors that can be used to construct a given circuit. As an exmaple of the tool's viability, one of the circuits discussed in class, that was previously implemented with a repressor-protein/promoter methodology, will be be modeled with a riboregulatory methodology.

References

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