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Poster Title: **"TinkerCell, a flexible application for analysis of biological systems"**

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Abstract:

TinkerCell is a visual modeling application with a C and Python interface that allows third-party algorithms or libraries to interact with TinkerCell's visual interface. At present, the functionalities include deterministic and stochastic simulation, steady state analysis, flux balance analysis using LPsolve C library, graph analysis through the NetworkX python module, and all the functionalities of PySCeS python module, including sensitivity and structural analysis. A few other unique features, such as automatic generation of all combinations of a protein with multiple binding sites, are also included. The hope is for TinkerCell to serve as a host for various C and Python algorithms that the community has to offer. In addition to the C and Python interface, TinkerCell models contain meta-data pertaining to each item, which will allow direct communication with databases. The intent for such a structure is to support a biological ``parts database'' in the future. A parts database is one from which synthetic biologists can retrieve components for building synthetic networks, much like electrical engineers purchase electronic components. TinkerCell models can store information such as DNA sequence and data tables, which can then be used by the C and Python programs. TinkerCell also supports modularity. Modules are constructed visually by placing a model inside a box and specifying the "interface" items for the module. Such modules can be connected using the interface items, allowing complex models to be built using existing modules, thus allowing synthetic biologists to build new synthetic networks using existing ones. This feature will also serve as a platform for quickly exploring different types of modules and their characteristic features when they are connected to other modules.

TinkerCell is a free and open-source project. Downloads, tutorials, and documentations are available at www.tinkercell.com