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Poster presentation

Registry of BioBricks models using CellML

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Introduction

One of the main goals in Synthetic Biology is to assess the feasibility of building novel biological systems from interchangeable and standardized parts. In order to collect and share parts, a Registry of standardized DNA BioBricks http://parts.mit.edu/registry has been established at the MIT. BioBricks can be assembled to form devices and systems to operate in living cells. Design of reliable devices and systems would benefit from accurate models of system function. To predict the function of systems built from many parts, we need to have accurate models for the parts and mechanisms to easily compose those part models into a system model. Therefore, in parallel to increasing the number of parts available and characterising them experimentally, a logical extension to the Registry would be to build a Registry of BioBrick models to complement the physical parts.

A key aspect in this effort is the use of a description language able to describe and support the BioBrick concepts of modularity and abstraction.

Results

In this article, we demonstrate that such a Registry of BioBrick Models is achievable. A mock-up is provided based on the great flexibility and modularity offered by CellML http://www.cellml.org.

Following the steps of already successful model registries such as the CellML registry or BioModel registry http://www.ebi.ac.uk/biomodels/, a BioBrick Model Registry will enable the curation of models. Using CellML and a MIRIAM annotation scheme will guarantee compliance with the previously cited registries. However, a strong emphasis is made on coupling the DNA BioBrick characterisation with their corresponding models. An iterative process between qualitative modelling and experimental characterization will insure consistency. The proposed framework could be the foundation of a future CAD environment for Synthetic Biology.

Conclusion

The concept of a Registry of BioBrick models based on CellML has been demonstrated. It takes advantage of CellML flexibility and modularity to provide a catalog of quantitative models which are standardized, modular and re-usable. With the increase of available physical DNA parts in the MIT Registry, as well as the characterisation of these parts, such a repository will help to provide a deeper understanding of the BioBrick properties and speed up the process of building new devices and systems. But more importantly, it will help to federate the growing number of contributions from the modeling community and build on the experimental characterization of BioBricks.

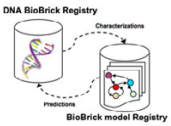
Motivations behind a Registry of BioBrick Models	
	• to **store**, **search** and **curate** models related to standardized DNA Biobricks. • to gain a **deeper understanding** of the function of BioBricks. • to promote the **re-usability** of BioBrick models. • to **explore through simulations** the properties of de-novo assemblies of parts. • to **store**, **search** and **curate** models related to standardized DNA Biobricks to progress towards a **faster/cheaper development process**. • to complement the **open-source spirit** of Synthetic Biology and open-up a new form of ***in Silico*** **contributions**.

Figure 1
Motivations behind a Registry of BioBrick Models

Properties needed for BioBrick description language	
	• **Human** and **machine** readable. • Enable the description of **qualitative and quantitative models** of biochemical networks. • Enable the definition of **modules** (as biobricks have inputs/outputs). • Enable the definition of **hierarchies between modules** (as a system will be composed of sub-systems or devices). • Enable a minimum **annotation scheme** to comply with the Minimum information requested in the annotation of biochemical models (MIRIAM).

Figure 2
Properties needed for BioBrick description language

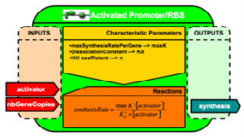
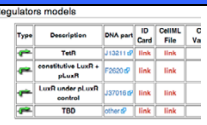
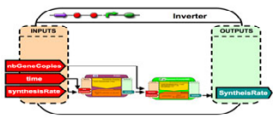
Generic CellML architecture for BioBricks	
	First, we explore the definition of modular and re-usable models to represent the available DNA BioBricks. A series of generic model architectures [http://openwetware.org/wiki/Registry_of_Standard_Biological_Models/Basic_Component_Models] in CellML is defined for most of the types of parts encountered in the DNA registry (plasmid, promoter, RBS, proteins, riboswitch etc.).Interfaces and import mechanisms in CellML enable a modular and re-usable design.
Catalog of quantitative BioBrick models	
	Second, a catalog of quantitative models [http://openwetware.org/wiki/Registry_of_Standard_Biological_Models/Model_Catalog] based on already characterized parts is presented. An ongoing effort to characterize BioBricks experimentally is providing us data to move from a qualitative description to a more quantitative one.
Building simulations from modular BioBrick models	
	To conclude, the versatility of the approach is demonstrated by simulating different systems from a set of pre-defined models.

Figure 3
The framework of BioBrick Model Registry