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# Registry of BioBricks Models using CellML

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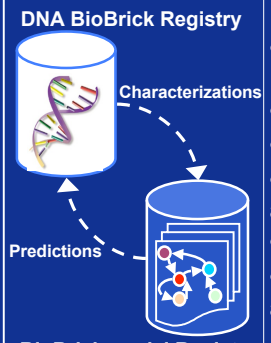
## ABSTRACT

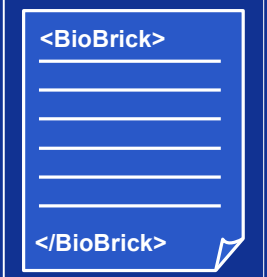
One of the main goals in Synthetic Biology is to assess the feasibility of building novel biological systems from interchangeable and standardized parts. In order to collect and share parts, a Registry of standardized DNA BioBricks[1] has been established at the MIT. BioBricks can be assembled to form 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**.

## Motivations behind a Registry of BioBrick Models



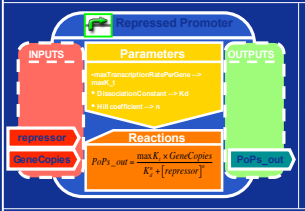

- to **store**, **search** and **curate** models related to standardized DNA Biobricks.
- to gain a **deeper understanding** of the function of BioBricks.
- to promote the **re-usability** of BioBrick models.
- to **explore through simulations** the properties of de-novo assemblies of parts.
- to progress 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**.

## Properties needed for a biobrick description language



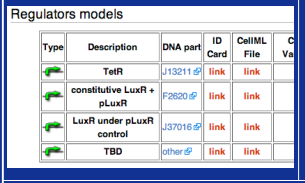

- **Human** and **machine readable**
- Enable the description of **qualitative and quantitative models** of biochemical networks.
- Enable the definition of modules (as biobricks have inputs/outputs)
- Enable the defintion of **hierarchies between modules** (as a system is composed of sub-systems or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

## Generic CellML architecture for BioBricks



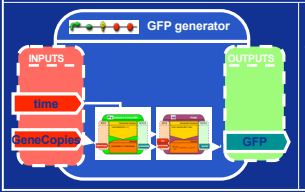

First, we explore the definition of modular and re-usable models to represent the available DNA BioBricks. A series of generic model architectures[2] in CellML (www.cellml.org) is defined for most of the types of parts encountered in the DNA registry (plasmid, promoter, RBS, proteins, riboswitch etc.).Interfaces and import mechanisms in CellML enable a modular and re-usable design.

## Catalog of quantitative BioBrick models




Second, a catalog of quantitative models based on already characterized parts is presented[3]. 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 BioBricks models




To conclude, the versatility of the approach is demonstrated by simulating different systems from a set of pre-defined models.

## 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.

## REFERENCES

[1] BioBricks Registry at MIT, http://parts.mit.edu

[2] BioBrick model architecture: http://openwetware.org/wiki/Registry_of_Standard_Biological_Models/Basic_Component_Models

[3] BioBrick model catalog: http://openwetware.org/wiki/Registry_of_Standard_Biological_Models/Model_Catalog