

# Standardisation for Synthetic Biology

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## **Introduction**

Synthetic biology pursues the deliberate design or redesign and construction of novel biological and biologically based parts, devices, and systems to perform new functions for useful purposes. As an engineering discipline, synthetic biology uses engineering principles and methodologies for the design, construction, and characterization of biological systems to be applied in industrial, environmental, and other applications.

These engineering principles form a bottom-up iterative design–build–test– learn (DBTL) approach, in which the engineer builds from the bottom by combining basic biological parts into devices and then into systems. Essential for the success of this inherently modular approach of bottom-up synthetic biology, there are some issues that need to be addressed, namely:

- The need to have a standardized process of information in cells. Inputs, outputs and the algorithmic fundamentals that relate them are not yet unmistakably characterised.
- The need to start from well-characterized parts. Currently, there is still a gap between the possibility of designing a system and its real implementation in the lab. This gap can be partially attributed to both the lack of repeatable and standardized measurements, and the absence of well-characterised biological parts.

This workshop present an overview of what is being done in the area of standardisation for synthetic biology.

The workshop is organized into three modules:

### **1. Cellular computations: standardising the process of information.**

**Presenter: Angel Goñi-Moreno**

The design and implementation of genetic circuits using metaphors and abstractions from engineering is an extremely active field of research. A number of devices, such as logic gates, multiplexers, adders and sequential circuits, have been implemented successfully in cells – mainly using synthetic gene regulatory networks as toolkit.

This module aims at opening a discussion on what we can learn from theoretical computer science in terms of the process of information. Combinatorial logic, for instance, establishes a very basic set of

rules, and the resulting combinatorial circuits are devices with limited capabilities of information processing. Other computing models, such as finite automata or the Turing Machine, are way more powerful yet less explored in-vivo.

In contrast to computing (and engineering), the process of information in cells is not standardised. Inputs, outputs and the algorithmic fundamentals that relate them are not unmistakably characterised. Therefore, it is difficult to transit from basic combinatorial logic to more complex models of computation.

*This module will last around 60 min.*

2. **Standards in plant synthetic biology.**

**Presenter: Diego Orzáez**

Plant Synthetic Biology aims to address the challenges of sustainability and productivity in agriculture through advanced genetic engineering, using standardization and modularity as driving concepts.

In this module, new standards for the assembly and the description of modular plant genetic elements (phytobricks) will be presented. With these standards, collections of increasingly complex phytobricks, ranging from basic regulatory elements to programmable transcription factors or small circuits, are being constructed. The long-term goal is to enable circuit engineering in crop plants, so that we can take control of relevant endogenous processes such as flowering time, senescence, or newly engineered programs such as synthetic defense mechanisms or added-value metabolic pathways.

*This module will last around 40 min.*

3. **Fluorescence calibration, parts characterization and IGEM measurement committee.**

**Presenter: Alejandro Vignoni**

In this module, an easy-to-use methodology that embodies both a calibration procedure and a multiobjective optimization approach to characterize biological parts will be presented. The calibration procedure generates values for specific fluorescence per cell expressed as standard units of molecules of equivalent fluorescein per particle.

The use of absolute standard units enhances the characterization of model parameters for biological parts by bringing measurements and estimations results from different sources into a common domain, so they can be integrated and compared faithfully. The multiobjective optimization procedure exploits these concepts by estimating the values of the model parameters, which represent biological parts of interest, while considering a varied range of experimental and circuit contexts.

What we will learn in this module can be used as a guide for good practices in dry and wet laboratories; thus allowing not only portability between models, but is also useful for generating libraries of tested and well characterized biological parts.

**As an extra:** We will explain what the ***IGEM measurement committee*** is and what are the efforts being undertaken towards standardisation in synthetic biology by teaching good measurements practices in initial levels of a synthetic biologist education.

*This module will last around 60 min.*