

Welcome to the BDAthlon at IWBD 2017! Before your team gets started hacking, please take 10-15 minutes to read through the BDAthlon rules and descriptions of the challenges.

Submission Instructions

All teams' solutions must be submitted to the appropriate BDAthlon repository on GitHub by 7:30 AM on Aug. 9th. For example, if team "Penguin Style" is submitting a solution to challenge 1, they must upload their solution's code and associated materials to the repository with the URL https://github.com/BDAthlon/2017-Penguin_Style-1. In addition to code, each solution must include a README file that contains a description of the project and instructions on how to build and run it. Finally, each solution must include an Open Source Initiative approved license (see Intellectual Property).

Software Development

Teams are permitted to use any software development tool, game engine, IDE, or programming language that they prefer. All code submitted as part of a solution must be written during the BDAthlon (8:00 AM on Aug. 8th to 7:30 AM on Aug. 9th). The only exception is that teams are permitted to use any publicly available library, API, or framework, provided that it is subject to an Open Source Initiative approved license (see Intellectual Property). Teams must document in their project's README file all external libraries, APIs, and frameworks used in their project.

Judging

All solutions will be judged by a subset of the IWBD 2017 organizing committee and scored according to the general criteria below, in addition to the more specific functional criteria listed for each challenge.

1. Originality - Does the software have unique features?
2. User Experience - Is the software intuitive to use?
3. Technical Proficiency - Does the software reflect good engineering practices (e.g. modularity)?

Intellectual Property¹

By submitting a Solution in this Contest, entrants warrant and represent that their Solution, including the programming and related material, is open source and is released subject to the Open Source Initiative approved licenses (<https://opensource.org/licenses>) and not subject to the proprietary rights of any person or entity.

Warranty¹

Participants warrant that their Solutions are their own original work and, as such, they are the sole and exclusive owner and rights holder of the submitted Solution and that they have the right to submit the Solution in the Contest and grant all required licenses. Each entrant agrees not to submit any Solution that (1) infringes any third party proprietary rights, intellectual property rights, industrial property rights, personal or moral rights or any other rights, including without limitation, copyright, trademark, patent, trade secret, privacy, publicity or confidentiality obligations; or (2) otherwise violates the applicable state, federal, local or provincial law.

¹Adapted from the rules of the Google I/O Hackathon Challenge

1. A Registry of Synthetic Biology Glyphs

Over the past 20 years, the visual representation of genetic sequence features, parts, and constructs has evolved considerably, from simple colored blocks to a variety of glyphs capturing different sequence functions (Figure 1). During this time, organizations such as the Synthetic Biology Open Language (SBOL) Developers Group have made considerable progress in cataloguing commonly used synthetic biology glyphs and establishing standard procedures for curating new ones. What the greater synthetic biology community still lacks, however, is a common online resource for aggregating and distributing data for genetic design visualization.

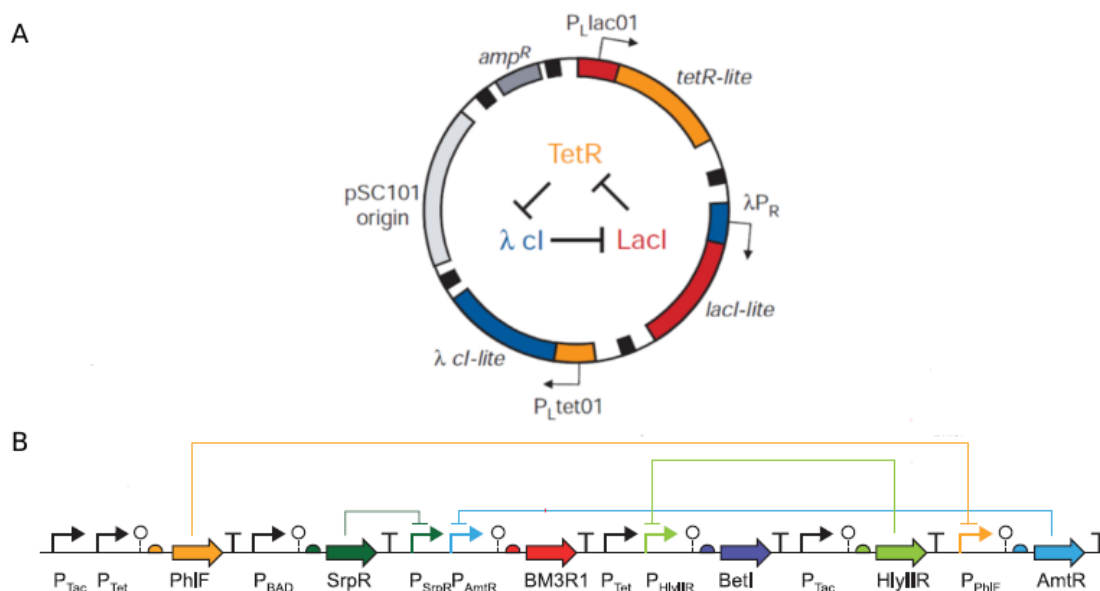


Figure 1: **Genetic circuit diagrams containing examples of synthetic biology glyphs.** Shown here are the repressilator [1] (A) and a priority detector [2] (B).

The goal of this challenge is to develop a website, web app, or other online resource that enables users to view, rate, submit, and download synthetic biology glyphs. Applications will be judged primarily on the basis of the following features and criteria:

Feature	Criteria
View	Users should be able to browse collections of synthetic biology glyphs and access meta-data associated with these glyphs. The best registries will provide search capability for finding glyphs and link to relevant glyph meta-data, such as sequence feature definitions from the Sequence Ontology (http://www.sequenceontology.org).
Rate	Users that want to rate glyphs should be required to make an account. The best registries will implement a thoughtful system for rating glyphs and incorporating these ratings into the user experience of discovering new glyphs.

Submit	Users with accounts should be able submit new glyphs. The best registries will be capable of accepting a wide variety of image formats and have a system for categorizing submitted glyphs into appropriate collections.
Download	Users should be able to download collections of glyphs. The best registries will offer multiple image formats when downloading glyphs and will come prepopulated with an existing set of glyphs, such as those catalogued by the SBOL Visual standard.

2. Green Globes

Have you ever heard of a game called Green Globes? It’s a great way to teach kids about graphing functions. The goal of the game is to write a function that intersects the most green circles when graphed on the xy-plane (Figure 2).

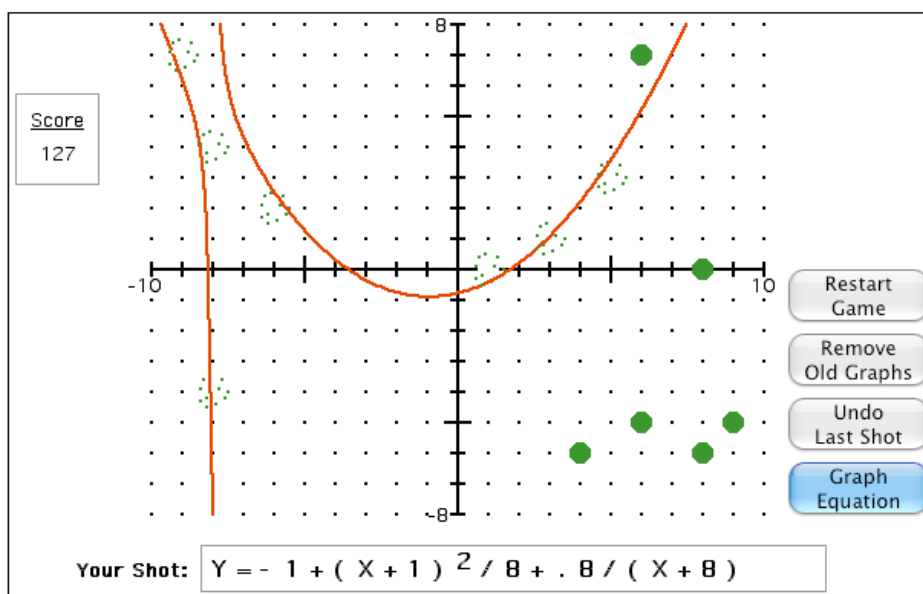


Figure 2: **Screenshot of Green Globes.** Obtained from www.greenglobs.net.

The goal of this challenge is to develop a biochemical version of the green globes game. In this version of the game, instead of writing a function, players will build a biochemical model consisting of reactions and species. The players’ goal is to build a model that, when simulated, produces data on the amounts of its biochemical species over time that intersect the most green circles. The games resulting from this challenge will be judged primarily on the basis of the following features and criteria:

Feature	Criteria
Modeling	Players should be able to build a biochemical model in the language and/or mathematical framework of your choosing. The best games will provide some degree of automation so that players do not have to manually write out every portion of their models.

Simulation	Players should be able to simulate their models and receive a score based on the number of green circles intersected. The green circles should be randomly distributed at the beginning of the game. The best games will provide clear visualizations of the simulation results and the green circles before and after simulation.
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References

- [1] Michael B. Elowitz and Stanislas Leibler, *A synthetic oscillatory network of transcriptional regulators*, Nature, vol. 403, pp. 335-338, 2000.
- [2] Alec A. K. Nielsen et al., *Genetic circuit design automation*, Science, vol. 352, 2016.
- [3] Jacqueline Y. Quinn et al., *SBOL Visual: A graphical language for genetic designs*, PLOS Biology, vol. 13, pp. 1-9, 2015.