WikiDust: a TinkerCell Plugin to Annotate and Share Network Models

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ABSTRACT

Summary: We present WikiDust, a software tool that (a) facilitates searches for DNA components, and (b) produces annotated web-ready images for improved sharing of designs. WikiDust is a plugin for TinkerCell, a CAD design tool for genetic regulatory networks. WikiDust leverages the SBOL standard to connect TinkerCell to the Registry of Standard Biological Parts. Using standard languages and components facilitates efficient communication and reuse of models.
Availability: WikiDust is available through TinkerCell's automatic plugin installation feature. TinkerCell can be downloaded from http://www.tinkercell.com, and source code for WikiDust can be found at http://www.tinkercell.com/plugins/wikidust .
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1 INTRODUCTION

Synthetic biology has succeeded in designing genetic networks using relatively few components and small, highly motivated teams. In order to reach the eventual goal of robust, useful synthetic organisms, current research must be scaled up dramatically. Advances in quantitative modeling will be needed (Purnick and Weiss, 2009), as will extensive automation (Carrera *et al.*, 2009). But advances in collaboration are also essential. Researchers will have to build on each others' work to design, construct, and test systems that are too complex for any small group to investigate fully. To do that, they must overcome a technical hurdle: data about genetic networks is currently stored and published in a wide variety of lab-specific formats. This may be convenient in the short term context of an individual project, but it makes communication on a large scale difficult and inaccurate.

As their focus shifts to larger projects, synthetic biologists will benefit from adopting standards that make data available for reuse in new situations. One such proposed standard is the Synthetic Biology Open language, or SBOL (http://sbolstandard.org). It defines two complementary formats for managing information about DNA constructs: a graphical notation (SBOLv) (Rodriguez *et al.*, 2009) for presenting sequence level designs visually, and a data model (SBOL semantic) (Galdzicki *et al.*, 2009) for representing them in software. SBOLv is a set of unambiguous, easily drawn glyphs representing DNA features like "promoter," "CDS," or "primer binding site." Similar schematics have been highly successful in other engineering disciplines—blueprints and circuit diagrams are two familiar examples. A standard visual language for synthetic biology would enable people from different labs, companies, or parts of the world to communicate their designs quickly and accurately. SBOL semantic plays an analogous role for computer programs: it is an information-sharing framework that allows different software tools to communicate efficiently. It is built atop standard web technologies like RDF and SPARQL, and makes it easy to compile information from different databases.

Here we present WikiDust, a new software tool that uses SBOL to streamline the description of genetic regulatory networks. WikiDust is a plugin for TinkerCell, a synthetic biology computer-aided design (CAD) tool (Chandran *et al.*, 2009). TinkerCell provides a palette of generic "items": DNA components represented by SBOLv symbols, as well as small molecules, proteins and cellular compartments. Items can be dragged onto the canvas and arranged graphically (Fig1a) into network models. Stoichiometric and kinetic parameters can also be added, and the resulting network dynamics can be simulated deterministically or stochastically.

WikiDust enhances TinkerCell in two ways. First, it uses SBOL to retrieve components from the Registry of Standard Biological Parts (http://partsregistry.org) for use in new designs. The Registry is both a physical collection of publicly available DNA components ("parts" or "BioBricks") and a collaborative website describing their use. Unfortunately, although data about parts can be downloaded as XML documents, there is no effective way to search for them. Recently, we developed the SBPkb, a mirror of the Registry data, but encoded using the SBOL-semantic standard (Galdzicki *et al.*, 2011). The SBPkb provides search capabilities via standard semantic web querying technology, and WikiDust leverages them to help users find and retrieve appropriate parts. Second, WikiDust allows TinkerCell users to generate imagemaps of their designs. When these imagemaps are published, they include direct links back to the matching Registry component pages.

2 CAPABILITIES

WikiDust was originally created as part of the University of Washington project submitted to the 2010 International Genetically Engineered Machine (iGEM), competition (http://igem.org). It provides two major capabilities: users can quickly annotate DNA components in TinkerCell, and they can share annotated diagrams of their designs on the web. The output is an image containing SBOLv glyphs hyperlinked to reference information on the Parts Registry.

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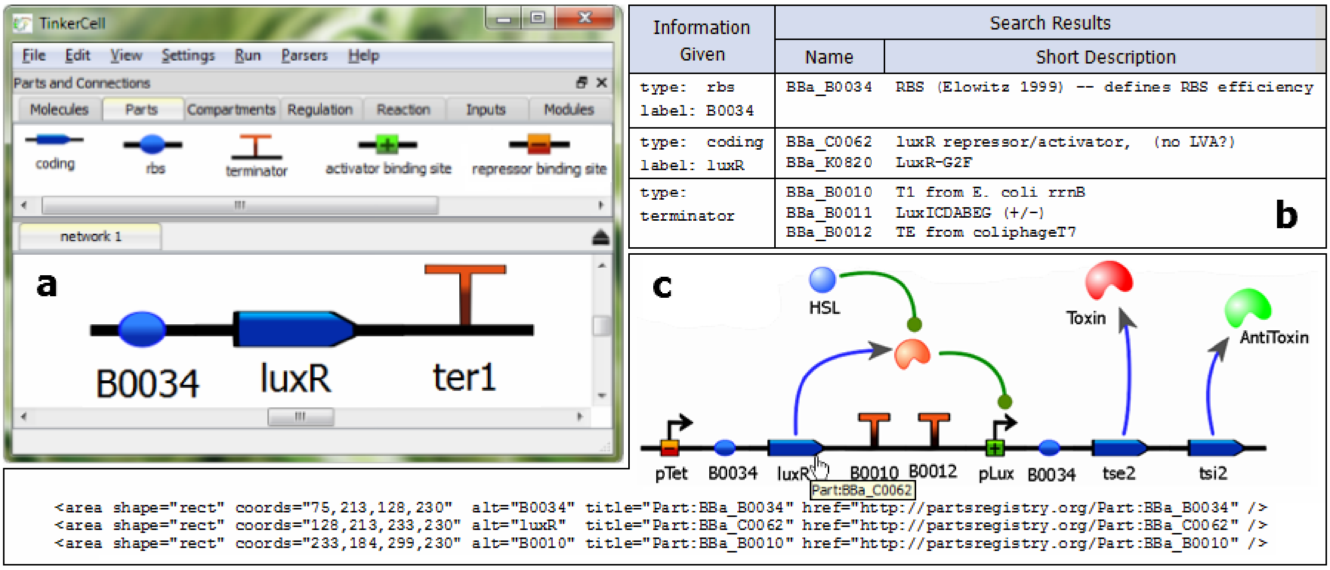

Information Given	Search Results	
	Name	Short Description
type: rbs label: B0034	BBa_B0034	RBS (Elowitz 1999) -- defines RBS efficiency
type: coding label: luxR	BBa_C0062 BBa_K0820	luxR repressor/activator, (no LVA?) LuxR-G2F
type: terminator	BBa_B0010 BBa_B0011 BBa_B0012	T1 from E. coli rrnB LuxICDABEG (+/-) TE from coliphageT7

```
<area shape="rect" coords="75,213,128,230"  alt="B0034" title="Part:BBa_B0034" href="http://partsregistry.org/Part:BBa_B0034" />
<area shape="rect" coords="128,213,233,230" alt="luxR"  title="Part:BBa_C0062" href="http://partsregistry.org/Part:BBa_C0062" />
<area shape="rect" coords="233,184,299,230" alt="B0010" title="Part:BBa_B0010" href="http://partsregistry.org/Part:BBa_B0010" />
```

Fig. 1. (a) Creating a network model in TinkerCell. Three DNA components, represented by SBOLv glyphs, are connected to form a contiguous strand. The ribosome binding site and coding sequence have been given a BioBrick name and a nickname, respectively; the terminator retains its default label.
(b) Searching the SBPkb. Results were obtained by right-clicking on components in Fig1a and selecting *Annotate from parts database (SBPkb)*. Given a BioBrick name (B0034), WikiDust immediately finds the right match. Two candidates are returned for a coding sequence called luxR: the sequence itself, and a composite part that includes it. There are many more results for the terminator, because only its type is known. (Note that the first 3 are shown out of 25)
(c) An HTML imagemap. A diagram of the finished model appears on the iGEM wiki at http://2010.igem.org/Team:Washington/Gram_Negative_Design . Also shown is an excerpt from the code used to make it interactive. Hovering the mouse over each component reveals its BioBrick name, and clicking it links to the Parts Registry.

2.1 Annotating DNA Components

The SBPkb accepts detailed searches using the SPARQL query language (http://www.w3.org/TR/rdf-sparql-query). However, WikiDust hides their complex syntax from end users; it uses information already entered in TinkerCell (Fig 1b) to find annotated components. Users can then refine their search by entering a keyword or phrase, and can easily open the corresponding Registry web pages for detailed information. WikiDust uses the search results to fill in missing information in TinkerCell.

2.2 Exporting an Imagemap

Once a network model is completed, WikiDust can publish it as an interactive diagram. Selecting *Export Imagemap* from TinkerCell's *Run* menu (Fig 1a) brings up a series of options: the name and size of the image can be adjusted, as well as whether HTML or Wiki Markup (http://en.wikipedia.org/wiki/Help:Wiki_markup) code will be used. Imagemaps can be automatically uploaded to MediaWiki sites that support them. Alternatively, an image is generated with matching code (Fig 1c) that can be pasted into any website.

3 CONCLUSION

WikiDust uses information from the SBPkb to simplify the creation of network models in TinkerCell, and exports diagrams of these models for use on the web. It integrates research, modeling, and publishing into a comprehensive workflow, and demonstrates the feasibility of using SBOL to reuse information in new contexts. We hope that by mediating among many popular formats and knowledge resources, WikiDust and SBOL will help lower the technical barriers to information exchange.

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REFERENCES

Carrera, J., Rodrigo, G., and Jaramillo, A. (2009). Towards the automated engineering of a synthetic genome. *Mol. BioSyst.*, **5**, 733–743.

Chandran, D., Bergmann, F. T., and Sauro, H. M. (2009). TinkerCell: modular CAD tool for synthetic biology. *Journal of biological engineering*, **3**, 19.

Galdzicki, M., Chandran, D., Nielsen, A., Morrison, J., Cowell, M., Grnberg, R., Sleight, S., and Sauro, H. (2009). BBF RFC 31: Provisional BioBrick Language (PoBoL).

Galdzicki, M., Rodriguez, C., Chandran, D., Sauro, H. M., and Gennari, J. H. (2011). Standard Biological Parts Knowledgebase. *PLoS ONE*, **6**(2), e17005.

Purnick, P. E. M. and Weiss, R. (2009). The second wave of synthetic biology: from modules to systems. *Nature reviews. Molecular cell biology*, **10**(6), 410–22.

Rodriguez, C., Bartram, S., Ramasubramanian, A., and Endy, D. (2009). BBF RFC 16: Synthetic Biology Open Language Visual (SBOLv) Specification.