Cell Illustrator/JS: Social Systems Biology

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ABSTRACT

Cell Illustrator/JS is a browser-based application for modeling, simulating and visualization cells and biological pathways. It is aimed at the biological scientists working at the bench.

Cell Illustrator/JS allows for the viewing and editing of CSML 3.0 models directly in the browser, therefore creating a fast and uncomplicated access to the models and to model making from every internet-connected device. Cell Illustrator/JS builds on the experience gained by developing the Java-based Cell Illustrator application, but crucially improves on availability and usability. Being web-based also enables the real-time sharing of CSML models by embedding fully functional model in personal websites, which can increase the exposure and the communication of the research.

Human Genome Center, Institute of Medical Science University of Tokyo, 4-6-1 Shirokanedai, Minatoku Tokyo 108-8639, Japan *e-mail: tremmel@hgc.jp **Keywords:** Biological Pathways, Simulation, Modeling, CSML, Collaborative, Social, Javascript.

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1 INTRODUCTION

Simulation of cells and biological pathways has been called one of the grand challenges of Cell Biology and Bioinformatics. Our group has been developing the Cell Illustrator platform since 1999 and together with the Cell System Markup Language (CSML), we are providing a stable and proven framework for simulating cells and biological pathways. However, recent advancements in webbrowser technology allow us to deliver the Cell Illustrator application not as a Java-downloadable application, but as a browser based web-service.

Here we introduce Cell Illustrator/JS, a Javascript-implementation of Cell Illustrator. Cell Illustrator/JS retains the proven concepts of Cell Illustrator, while at the same time offering new possibilities in sharing, collaborating and embedding biological pathways and models. Like cells, Systems Biologists don't exist on their own, but through interaction with others. Cell Illustrator/JS facilitates collaboration and sharing and enables the biological researcher to concentrate on his research.

In the next chapter, we will briefly outline the background of the Cell Illustrator project. Chapter 3 will deal with the technicalities of the implementation and the possibilities opening up with a Browser-based approach. In Chapter 4 we mention an example deployment of Cell Illustrator/JS and in Chapter 5 we will investigate possible future directions.

2 BACKGROUND

Cell Illustrator is a Systems Biology application for modeling, simulating and visualizing biological pathways. It features a rich Graphical User Interface (GUI), which make the processes of modeling and simulating accessible to the target audience, biological scientists working at the bench. Cell Illustrator uses version 3.0 of the Cell System Markup Language (CSML) to display and distribute models in an open format [1].

Cell Illustrator uses an extension of hybrid functional Petri nets is used, so that models can include various information such as DNA sequences, molecular density, 3D localization, frame-shift, translation and biochemical reactions.

Development for Cell Illustrator started in 1999 under the name of Genomic Object Net [2], the first public release was in 2002, the current version of the software is 5.0. [3,4]

Cell Illustrator is implemented in Java, which allows the running of the same application on a variety of operating systems. While Java is well suited in providing a single runtime for various systems, it lacks most the speed and ease of operation that are expected and demanded of modern web services.

New standards, such as HTML5, CSS3 and Javascript 1.8 (ECMAScript 5) are challenging the claim of Java as being the only choice for cross-operating system application development. We came to the conclusion, that most operations relevant for Cell Illustrator and technically possible with Java should also be possible within modern web browsers using Javascript.

Therefore we introduce an implementation of Cell Illustrator in Javascript, aptly called Cell Illustrator/JS. With this new development we aim combine the depth of Cell Illustrator with the agility of browser-based applications to provide bench scientists with a richer, more convenient and more accessible way of modeling, simulating and visualizing their pathways and cells.

3 TECHNICAL OVERVIEW

Cell Illustrator/JS relies on HTML5 and JavaScript to deliver a Desktop Application-like experience with the Web Browser. The HTML5 Canvas-element is used for the drawing operations. Web Workers, a way of multi-threading within the browser enable us to deliver a smooth, non-blocking user experience.

Cell Illustrator/JS can import and export CSML 3.0 encoded models. A native, JSON-based representation of CSML is used for client-server communication and database storage. CI/JS can also work in offline mode, where CSML models can be imported directly from the local hard disk and saved in the local memory.

Having established the technical grounding of Cell Illustrator/JS, we can explore the features, which distinguish Cell Illustrator/JS from it's Java-based relative.

When Cell Illustrator/JS is coupled with a backend database, it becomes possible to save the models and the complete incremental modeling history in the online database. This also enables the biological researcher to access his models from every connected computer, without having to install a dedicated application. Having the data online also allows for sharing by embedding the models in personal websites and blogs. Compared to the Java-implementation, Cell Illustrator/JS has the advantage of a lower barrier-of-entry. Whereas with the Java-implementation, it is necessary to download the software – even with Java Web Start – this experience can be time-consuming and less than rewarding. With Cell Illustrator/JS we enable our end-users to focus on research task.

4 DISCUSSION

MACPAK, the Macrophage Curated Pathway Knowledgebase [3], is currently serving over 200 manually curated CSML models of Macrophages. These models can currently be viewed in the browser only as images; they can be downloaded as CSML files and opened with the Java version of Cell Illustrator. While this situation is workable, it is far from ideal.

Cell Illustrator/JS allows the model to be interactively viewed and simulated directly within the Browser, thus eliminating the need for downloading the Java-Application and therefore lowering the barrier of interaction.

Registered users of the MACPAK site can also use the *Cloning* Feature, which makes a copy of the current model and allows for editing and changing the selected model directly in the browser.

5 CONCLUSION AND OUTLOOK

With Cell Illustrator/JS we show, that it is feasible to create a browser-based application that encompasses most of the features usually found only in Desktop Application. The nature of online applications allows us also to enhance the social and collaborative aspects of the software and of the activity of working with the application.

Also, by having created a JavaScript version of Cell Illustrator, it is possible to port Cell Illustrator/JS to a variety of touch-based tablet devices with minimal effort, therefore bringing the application even closer to the hands of the bench biologists.

REFERENCES

- [1] [1] http://www.csml.org/
- [2] [2] Nagasaki M, Doi A, Matsuno H, Miyano S. Genomic Object Net: a platform for modeling and simulating biopathways. *Applied Bioinformatics*. 2: 181-4 (2003)
- [3] [3] http://cionline.hgc.jp/
- [4] [4] Nagasaki M, Saito A, Jeong E, Li C, Kojima K, Ikeda E, Miyano S, Cell Illustrator 4.0: A computational platform for systems biology, *In Silico Biol.*, 10, 0002, 2010.
- [5] [5] Nagasaki M, Saito A, Fujita A, Tremmel G, Ueno K, Ikeda E, Jeong E and Miyano S, "Systems biology model repository for macrophage pathway simulation.," *Bioinformatics* (Oxford, England), Apr. 2011.