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RIKEN

GenoCon: An international science and technology competition supporting future specialists in rational genome design for Synthetic Biology

First-ever contest in rational genome design based on semantic-web technology

Summary:

- A challenge for green innovation: rational genome design of a plant with an environmental detoxification function.
- Collection and sharing of genome-design theories and programs from researchers around the world.
- Web-based contest aimed at supporting a future generation of scientists – including a category for high-school students.

The Bioinformatics And Systems Engineering (BASE), a division of RIKEN, Japan's flagship research institute, is holding its first ever International Rational Genome Design^{*1} Contest (GenoCon) on the semantic web. The contest makes use of an information infrastructure for life science research known as the RIKEN Scientists' Networking System (SciNeS^{*2}) and will take place between May 25 and September 30.

Built upon semantic web technology, GenoCon is the first contest of its kind, offering contestants the chance to compete in technologies for rational genome design. To succeed, contestants must make effective use of genomic and protein data contained in SciNeS database clusters to design DNA sequences that improve plant physiology. In the first GenoCon, contestants are asked to design a DNA sequence conferring to the model organism *Arabidopsis thaliana* the functionality to effectively eliminate and detoxify airborne Formaldehyde.

For their part, contestants are constrained to so-called bioinformatics activities, designing DNA sequences from genomic-related information in a browser-based programming environment provided by SciNeS (Fig.1). RIKEN and other research institutes are then responsible for inserting these DNA sequences into genomes and evaluating experimentally the functions of the resulting *Arabidopsis thaliana* plants.

A new web-based framework for collaboration in synthetic biology, referred to as "open-optimization research^{*3}", is provided to GenoCon contestants to help make effective use of DNA information resources in creating improved bio-resources. Genome design theories and programs submitted by contestants from all over the world will be compiled within RIKEN SciNeS and shared under a Creative Commons Public License, contributing to advancements in biomass engineering and other fields of Green Biotechnology.

GenoCon also offers, in addition to categories for Japanese and international researchers and university students, a category specifically for high-school students. Just as ROBOCON (Robot Contest), GenoCon thus provides opportunities for young people to

learn about the most cutting-edge science with a sense of pleasure, bringing intellectual excitement to the field of Life Science and supporting a future generation of scientists.

GenoCon will be accepting entries to the contest starting May 25, 2010 at the official GenoCon website: <http://genocon.org/sw/wiki/en/cria196s1i/>.

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*1 Rational Genome Design

“Rational Design” is a methodology for finding the optimal structure of substances introduced into target organisms for the purpose of conferring new functions to them. The methodology uses an algorithm that determines the optimal structure logically based on data obtained from the organism.

“Rational Genome Design” is a methodology for finding optimal DNA sequences that confer new functions to a target organism. “Rational Drug Design” is a methodology for finding optimal compound chemical structure which confers a desired function to an organism.

*2 RIKEN SciNeS

RIKEN SciNeS (Scientists’ Networking System) is a web system built upon the “Semantic Web”. Making use of the latest cloud computing technology, the system is capable of simultaneously hosting upwards of thousands of virtual laboratories, providing every individual user with access control to each data item. The system is being developed and operated by the Bioinformatics And Systems Engineering (BASE) division of RIKEN (<http://scines.org>).

Virtual labs on the RIKEN SciNeS system enable each lab owner (researcher) to easily create and publish databases without the need to maintain individual web servers. This information infrastructure can be beneficial for researchers in implementing international collaborative research. In addition, each virtual lab can also organize competitions or initiate open participatory research.

GenoCon is to be organized using one of the virtual labs on RIKEN SciNeS. Each contestant in GenoCon establishes a workspace (named “My Page”) in the virtual lab (named “GenoCon”). Virtual labs on RIKEN SciNeS are used as an integrated life science information infrastructure incorporating functions including a programming environment, a digital lab notes system, and information resources for biomass engineering research activities. By releasing some of these functions, GenoCon offers an environment for open-optimization research in which contestants can submit more optimal DNA sequence designs, potentially conferring to the plant *Arabidopsis* the target function assigned by the GenoCon organizers.

*3 Open Optimization Research

RIKEN SciNeS provides a new framework for collaboration called “Open Optimization Research” in which the process for optimizing an invention is carried out by numerous contestants/participants in an open manner, rather than by members of the closed group of inventors.

It is often the case that a DNA sequence is initially synthesized by researchers in order to verify a given idea in the easiest way possible. However, this initially-tested DNA sequence may not be optimal among the patented DNA sequences that are claimed to confer a desired function to a living organism.

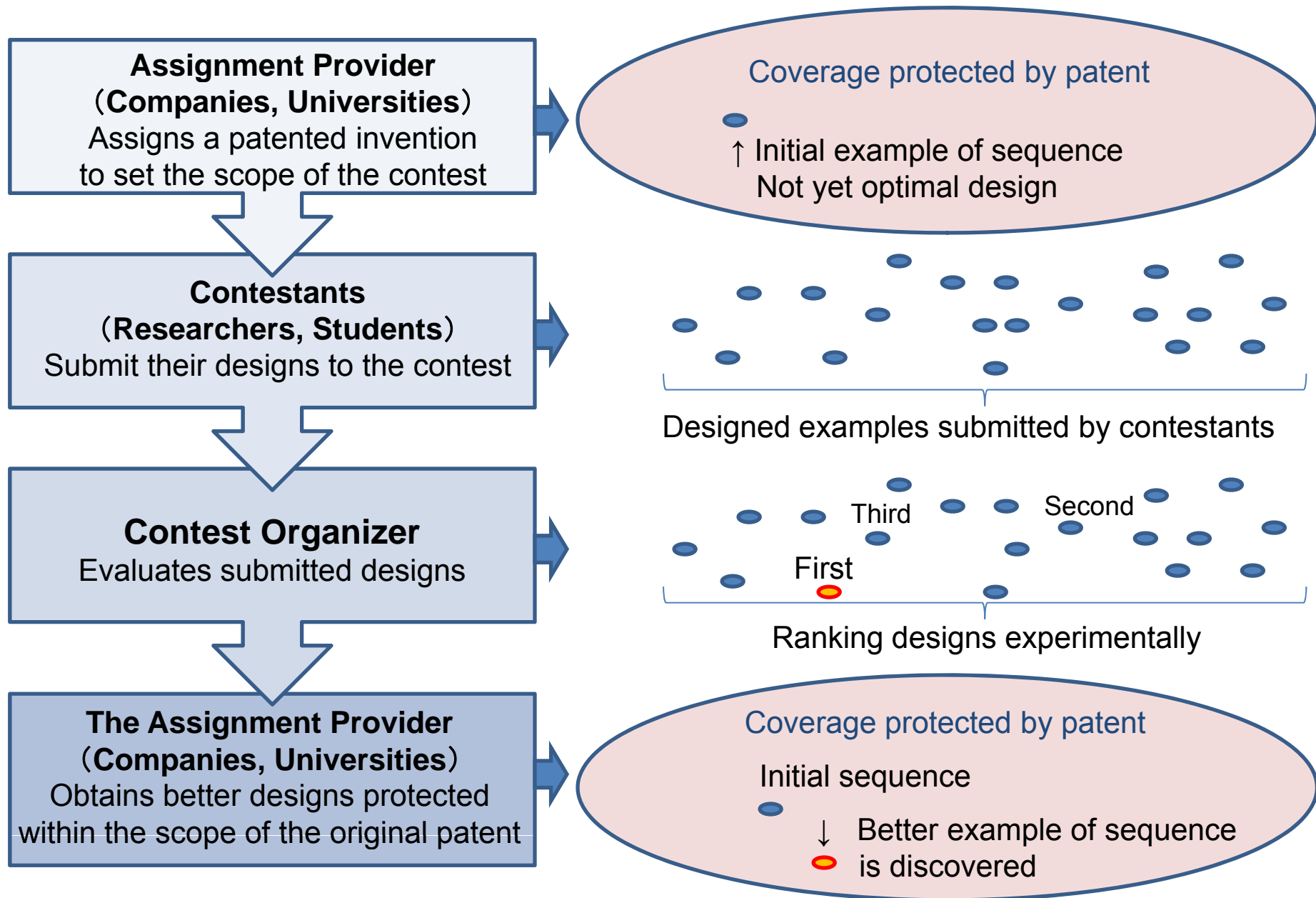
Optimal design of DNA sequences requires that researchers conduct enough tests to find

optimal examples among patented DNA sequences, which demands securing research financing. Designing optimal sequences also requires bioinformatics specialists with the skills to make use of existing knowledge and data while keeping in mind the genetic background of each organism. As a result of these requirements, many DNA sequences, while protected by patents, are never actually put into practical use by their inventors due to a lack of necessary resources (in a phenomenon referred to as the “Valley of Death”).

We propose Open Optimization Research as a way to overcome this problem by providing opportunities to optimize the design of DNA sequences with the help of external participants to the research process (Fig. 2). GenoCon offers incentives for researchers and sponsors that make it attractive for them to join the contest. (Fig.3)

Open Optimization Research is also a framework for “Open Innovation”, in which a company or a university with a desire to develop a practical use for its patented invention is matched with potential partners that have their own original technologies. A successful match can help propel an invention toward practical applications.

Figure 2: Flow of Open Optimization Research Processes



Contestants enjoy the contest and assignment providers obtain better examples of sequences.

Figure 3: Incentives for participants in “Open Optimization Research”

