Short Reads

Thermo Electron and Fisher Scientific announced a \$10.6 billion all-stock merger. The combined company will be called Thermo Fisher Scientific. Fisher's CEO Paul Montrone will step down, and Thermo CEO Marijn Dekkers will become president and CEO of the new entity.

## The UK's Biotechnology and Biological Sciences Research

Council has awarded £27 million to create three naw centers for integrative systems biology at the Universities of Edinburgh, Nottingham, and Oxford. These will join the three other centers created last year at Imperial College, Manchester, and

In an attempt to settle
their patent dispute, ABI parent
Applera and Beckman Coulter
have agreed to pay each other
royalty-bearing licenses for their
respective technologies. The
settlement resolves "all outstanding
legal disputes" regarding Beckman's
CE and PCR technologies, as
well as Applera's breach-ofcontract allegations.

The Virginia Bioinformatics Institute and Brazil's Oswaldo Cruz Foundation have teamed up to develop drugs, vaccines, diagnostics, and other technologies for infectious diseases, which include dengue faver, HIV/ AIDS, hepatitis C, influenza, pneumonia, and malaria. METAGENOMICS

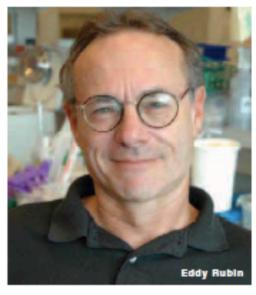
## FROM JGI, COMMUNITY ARCHIVES FOR THE MICROBIAL SET

More than 250 microbial genomes have been sequenced to date and, with 700 more projects in the works, making sense of that flood of data has never looked more daunting. This is no surprise to scientists at the Joint Genome Institute, which has spearheaded nearly a quarter of the world's bacterial genome projects. To help researchers make sense of it all, the institute recently launched IMG/M, an experimental metagenome data management and analysis system.

"IMG/M arose from our interest in making it easier for users to access and analyze their data," says JGI Director Eddy Rubin. Advances in sequencing technology have made it possible to sequence a microbial genome in a day, he says, which presents the risk that some genomes will be neglected due to the sheer volume of data available.

Hence the creation of IMG/M, which builds on JGI's integrated microbial genomes (IMG) system and extends its comparative tools to metagenome data. The IMG system, built through a collaboration with Lawrence Berkeley National Lab, is updated quarterly and contains both draft and complete JGI genomes, in addition to other publicly available microbial genomes. Researchers interested in analysis, as opposed to just browsing the bank, can navigate the samples by phenotypes, ecotype, disease, and relevance.

According to Victor Markowitz, head of Lawrence Berkeley National Laboratory's Biological Data Management and Technology Center and the system's chief architect, the idea was always to broaden IMG's remit. "Once we had IMG, we asked what it would take to extend [the system] to metagenomes," Markowitz says. It took a lot, especially in terms of conceptual organization of the raw data. Whereas IMG charts isolate genomes for which assembly and gene prediction is done, IMG/M must contend with data from entire microbial com-



munities for which assembly scaffolds come from different organisms.

Given those complexities, the LBNL team forged ahead to create a repository capable of evolving with its diverse data sets. Working on the system mostly on weekends, the group built IMG/M over a period of five months, and a preliminary version was distributed for expert testing at the end of last year. One of the early users, JGI's Phil Hugenholtz, test drove the system to analyze enhanced biological phosphorus removing (EBPR) sewage sludge metagenomes, which yielded results slated to appear in an upcoming paper.

Hugenholtz also helped train the system on other microbial communities recently sequenced by JGI, including microbes colonizing the termite hindgut. "Termites are world-class biomass converters," says Rubin, and understanding those metabolic pathways may help meet "one of our greatest needs to convert cellulose into starch for alternative fuel development."

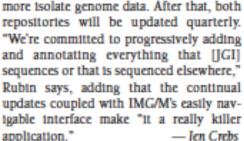
In addition to isolate genomes found in IMG 1.3, the current version of IMG/M contains metagenomic sequences generated from several environmental samples. At press time, there were data from two EBPR

News Roundup

sludge samples, three deep sea "whale fall" carcasses courtesy of Rubin's team, an agricultural sotl sample, and an acid mine drainage biofilm. These samples are representative of a range of species diversity, dominant organism abundance, and sequencing depth.

The next version of IMG/M is slated for July 1, when IMG will also be loaded with

more isolate genome data. After that, both sequences or that is sequenced elsewhere," application."



## Seymour Benzer, Caltech's

Drosophila genomics pioneer, received the \$500,000 Albany Medical Center Prize, which is the US's largest monetary award for medicine and biomedical research.

Danish drug developer Santaris Pharma has created a MicroRNA Research Consortium in partnership with the Department for Medical Biochemistry and Genetics at the University of Copenhagen. The new consortium is partially supported by a grant from the the Danish Advanced Technology Foundation worth €1.3 million. which will be matched by the University of Copenhagen and Santaris Pharma.

Mittipore has plans to acquire Serologicals for \$1.4 billion in cash - which is about how much revenue the combined company will make this year. The acquisition will close on June 30.

Petican Life Sciences, one of the newer reagent shops on the block, has raised \$100 million in private equity for acquisitions and development. The company also completed its first acquisition, that of PML Microbiologicals, originally announced last December.

Third Wave Technologies has made two new appointments to its senior management team: Jorge Garces has been appointed vice president of product and platform development, and Cindy Ahn has been appointed vice president and general counsel.



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