Computational Models to Decipher Biological Problems and Boost Biotech Productivity

Nov. 4, 2013 — Researchers from the Centre for Genomic Regulation (CRG) and Consejo Superior de Investigaciones Científicas (CSIC) have designed mathematical models that will allow us to understand basic concepts of metabolic and genetic regulatory systems as well as to optimize the production of drugs and other biotechnological products. The work, published in the scientific journal *PLoS Computational Biology*, is part of the EU project BioPreDyn, which aims to develop computational models to analyze multi-scale biological networks.

Systems biology is a relatively new field that attempts to understand complex biological problems. For instance, both temporal and spatial inputs are important in regulating genes, and minute differences in these inputs can be amplified to cause drastic changes in the output a regulatory network can produce. Predicting these systems through computational models based on data is a powerful tool useful for basic research as well as for commercial biotechnology (such as producing nutraceuticals and biopharmaceuticals). Based on such approaches,, the EC-funded project BioPreDyn aims to develop models to predict cellular systems.

In the paper published today in *PLOS Computational Biology*, groups led by the BioPreDyn project coordinator Johannes Jaeger (at the CRG) and Julio R. Banga (at IIM-CSIC) demonstrate a model that can closely predict post-transcriptional gene regulation. In this case, they studied the development of body segments in the fruit fly. The researchers developed algorithms to use in a "systems biology modeling cycle," in which they repeatedly fit a model to gene expression data obtained from laboratory experiments until a good fit was obtained between the predicted and the measured outcomes. "What is important in our study is that we proved that there was a unique and consistent solution to the fitting problem, something that has never before been achieved for a realistic complex model of gene regulation," stated Dr. Jaeger. "This is a big step towards applying the systems biology cycle routinely, in all kinds of biological contexts. Fly development is basic research, but our methods can also be applied for optimizing biotechnological processes, such as the production of food additives or drugs using microorganisms," added Dr. Jaeger.

The collaborative project BioPreDyn aims to develop and then incorporate a vast range of algorithmic tools, such as the one developed in the Jaeger and Banga labs, into an overarching software suite. Working towards this end, BioPreDyn has eleven partners from eight countries, including three industrial partners (Evolva, InSilico Biotechnology, and the CoSMo Company). The software suite will permit end-users (irrespective of their computational skills) to easily access and use the algorithms for their own specific purposes, such as for improving metabolic conditions in organisms used to produce nutraceutical ingredients.

Story Source:

The above story is based on materials provided by **Centre for Genomic Regulation**.

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Journal Reference:

1. Kolja Becker, Eva Balsa-Canto, Damjan Cicin-Sain, Astrid Hoermann, Hilde Janssens, Julio R. Banga, Johannes

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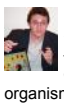

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Jaeger. **Reverse-Engineering Post-Transcriptional Regulation of Gap Genes in Drosophila melanogaster**. *PLoS Computational Biology*, 2013; 9 (10): e1003281 DOI: 10.1371/journal.pcbi.1003281

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