

Genome-Scale Kinetic Models

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BACKGROUND

Historically, genome-scale analysis has used bottom-up reconstruction of available, biochemical information (from high-throughput datasets and public archives) to provide a snapshot of biochemical relationships in a network. While this approach has been extremely useful, it is an obvious simplification of real, dynamic systems, which continually change in response to perturbations.

TECHNOLOGY DESCRIPTION

UC San Diego inventors have developed an approach for the construction of dynamic genome-scale mathematical models and their governing equations, which can be used to build and analyze dynamic models of biological networks and to predict responses to environmental and genetic perturbations.

ADVANTAGES

The invention identifies over-riding principles and concepts, which are readily translated to models constructed upon different assumptions. Also, while validated for one metabolic pathway, this has direct applicability to other biological processes, including but not limited to signaling networks, small metabolite regulation, transcription, and translation. The approach described for constructing models is scaleable and practical for large networks, given the increasing availability of various high-throughput data, such as metabolomic data.

RELATED MATERIALS

- ▶ Jamshidi N, Palsson BO “Formulating genome-scale kinetic models in the post-genome era” Mol Syst Biol 2008, 4:171
- ▶ http://gcrg.ucsd.edu/Personnel/Palsson_Publications

PATENT STATUS

Country	Type	Number	Dated	Case
United States Of America	Issued Patent	8,301,393	10/30/2012	2008-180

Additional Patent Pending

CONTACT

University of California, San Diego
Office of Innovation and Commercialization
innovation@ucsd.edu
tel: 858.534.5815.



OTHER INFORMATION

KEYWORDS

dynamic, model, genomic, fluxomic,
pathway, process, signaling, network,
gradient, thermodynamic, Jacobian,
dual, hierarchical, time-scale
decomposition, regulation

CATEGORIZED AS

- ▶ **Medical**
 - ▶ Other
 - ▶ Research Tools
- ▶ **Research Tools**
 - ▶ Bioinformatics

RELATED CASES

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