Computational systems biology: The integration of data across multiple levels of biological organization to understand how perturbations of normal biology become adverse heath effects

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NRC Committee on Models in the Regulatory Process, Workshop on Emerging Issues for Regulatory Environmental Modeling, National Academy of Sciences, Washington, DC, December 2, 2005



• This presentation may not reflect official policy of the US. EPA.

Outline

- Biological mechanisms of dose-response and risk assessment
- Computational systems biology
- Example and technical challenges
- Regulatory acceptance

Biological mechanisms of dose-response and risk assessment

Typical high dose rodent data – what do they tell us?







Partition the problem into manageable parts



Motivations

- Widespread recognition that chemical-specific highto-low dose extrapolation may differ from default approaches.
- Concern that some high dose mechanisms may not be relevant.
- Need to protect the public health.
- Need to avoid unnecessary loss of access to useful materials.
- Need to do *good science* in support of human health risk assessment.

Computational systems biology

Enabling ("Omic") Technologies











Computational modeling as an adjunct to laboratory research



(Formal + intuitive modeling)

The state-of-the-art



International e. coli Alliance

 Goal is to develop a molecular-level computational model of *e*. *coli*.



Computational tools

ATM curated Pathway from Pathway Assist®



Computational tools



Systems biology workbench

Example and technical challenges

• Skin irritation

- MAPK, IL-1a, and NF-kB computational "modules"
- High throughput overexpression data to characterize
 IL-1a MAPK interaction with respect to NF-kB



Modular Composition of IL-1 Signaling





Constitutive NF-KB Signaling Module



NF-KB Module Simulation

 Parameters from existing NF-κB model (Hoffmann et al., 2002) and refined to fit experimental data in literature



The IB–NF-B Signaling Module: Temporal Control and Selective Gene Activation Alexander Hoffmann, Andre Levchenko, Martin L. Scott, David Baltimore Science 298:1241 – 1245, 2002



6 hr

MAPK intracellular signaling cascades





MAPK time-course and bifurcation after a short pulse of PDGF



IL-1 MAPK crosstalk and NFkB activation



High throughput



Arrayed, full-length genes set in 384-well plates



Gain-of-function screen





Homeostasis, health, and disease Normal health Environmental stressor Adaptive changes in biochemical and physiological networks

Normal variation \rightarrow frank toxicity



Attractors and biology



The critical feature of a regulatory network is that eventually it will reenter a state that it previously encountered and cycle repeatedly. 34

Health and disease



Practical and technical challenges

- Identification of network topology
- Parameter values
- Level of detail
 - Practical constraints
- Lumping
- "Functional modules"
 - MAPK amplifier
 - Cell cycle
 - Toolbox
- Coordination!!!!

Modular description of a cell



http://www.gnsbiotech.com/biology.php

Regulatory acceptance



How compatible are research and risk assessment?

- Structurally complex models tend to illuminate sources of uncertainty
 - Models with hidden uncertainties may be preferred
- Large databases and associated models tend to identify questions for further research
 - Lose focus on what the existing data are telling us
- Sophisticated models require sophisticated evaluation
 - Ad hoc review groups
 - Balance interests rather than avoid real or perceived conflicts of interest

Acknowledgements

• EPA NCCT

- Bob Kavlock, Jerry Blancato, Hugh Barton, Woody Setzer
- *CIIT Centers for Health Research* Rusty Thomas, Mel Andersen
- Purdue
 - Yanan Zheng
- Wright State University
 - Jim McDougal



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