



Systems Biology for

Drug Discovery

as applied to NSAID safety problem

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Health, disease and therapeutic intervention in terms of network modelling

- Input output behaviour of biological networks
- Health: balance of input and output, adequate response to perturbation
- Disease: balance is disturbed, due to suppression or activation of certain stages, resulting in inadequate output
- Goal of therapy: to restore the normal balance by targeting key components/checkpoints of networks by drugs
- Therapeutic resistance loss of the sensitivity of the output to the drug

Key To Future Medical Breakthroughs Is Systems Biology, Say Leading European Scientists

- High Complexity of biochemical networks underlying cell functioning
- If disturbed can result in a disease (diabetes, cancer..- network diseases)
- Conventional approaches of biology are not suitable for the analysis of these elaborate webs of interactions, which is why drug design often fails
- Knocking out one target in a pathway is not productive disease will by-pass the drug (network robustness)
- Systems Biology approaches (computational modelling and analysis) should be engaged to develop smarter therapeutic strategies and predict drug safety and efficacy.

Systems medicine

- aimed at exploitation of systems biology approaches to develop prognostic and predictive models for diagnostics and therapeutic applications
- there is not yet an established arsenal of computational approaches, methods, and techniques applicable for model-based diagnostics and design of therapeutic strategies
- specific techniques of model analysis need to be developed to allow for application of general models in the context of therapeutic research.

Kinetic Modeling (KM) Approach

•Takes into account all properties of the biosystem (protein structure, mechanism, stoichiometry, dynamics and regulation)

•Clearly describes the key properties of the biosystem in terms of easily understandable and measurable parameters (Vmax, Km, Kd, Ki, IC50..)

•Reproduces all known responses of the biosystem to external and internal perturbations and therapeutic interventions

> Kinetic Modeling in Systems Biology, Demin, Goryanin Chapman & Hall/CRC, 2008

Kinetic modelling approach

- 1. Pathway reconstruction and static model development: elucidation of stoichiometry of the network, identifying key cross-talks and regulations
- 2. Generation of the system of ODEs describing dynamics of the metabolic/signalling network:

 $dx/dt=N\cdot v(x;e,K)$ Here, $x=[x_1,...x_m]$ is vector of compound concentrations and $v=[v_1,...v_n]$ is vector of rate laws

3. Modelling metabolic, signalling and transport processes:

Detailed description of the catalytic cycles of key proteins, derivation of rate equations

- 4. Prameterisation of the model (literature, experiments, fitting)
- 5. Validation of submodels on the base of *in vitro* and cell extract data
- 6. Validation of the whole model using *in vivo* dynamic data (genomics, proteomics, metabolomics)

Application of the validated model to practical problems: e.g. in pharmaceutical industry - drug resistance, safety

Practical applications

- Various analyses of the validated model, e.g.:
 - In silico experiments to test various hypothesis on the mechanisms of disease and drug action
 - E.g. test how modifications within the network can affect its inputoutput behaviour
 - Local and global sensitivity analysis to generate ideas on
 - Drug targets
 - Biomarkers
 - Combination therapies

Challenges in translating theory into clinical practice:

- Extrapolation to a multi-layered context, from molecular to cellular, tissue,... and organism level
- High level of individual variability of the networks, e.g. in cancer – to be addressed by personalised medicine
- Complex dynamical aspects
 - pharmaco-kinetics and pharmaco-dynamics effects,
 - drug scheduling,
 - circadian rhythms...
- Incomplete knowledge on the biological networks underlying disease onset and progression
- limitations imposed by the number of elements which a tractable model can include

Context layers to consider...

- Intracellular microenvironment
 - regulation of protein activity by local concentration of substrates/ products and co-factors...
- Larger network context
 - Subsystem embedded in a larger network is subject to higher level regulation
- Cell-specific protein expression and gene regulation
 - Pathway structure and dynamics vary in different cell types...
- Organ/ organism level effects
 - Spatial aspects
- •

Example: Application of Systems Biology Approach to

Drug Safety Problem

"Too many pharmacological agents have entered into clinical practice for which considerable and potential life-threatening outcomes were recognized only AFTER a large number of patients had been treated"

Wall Street Journal – Thursday, January 26, 2006 quoting an editorial from same week's New England Journal of Medicine

Non-Steroidal Anti-Inflammatory Drugs

(NSAIDs) safety problem

Aspirin

•Ibuprofen

Naproxen

Indomethacin

•Celebrex ...

- NSAIDs popular drugs for pain relief and antipyretic, more recently started to be used in cancer and neurophysiology (depression).
- Main target COX1,2
- COX1 constitutive, COX2 induced at inflammation
- Aspirin (targeting both COX1 and COX2)

 risk of gastro-intestinal bleeding at medium/high dose
- Selective COX-2 inhibitors (Coxibs) developed to overcome GI side effects:
 - efficient in pain relief but with new dangerous side effects (heart attacks)
 - Vioxx withdrawal from the market cost Merck \$billions, with ongoing legal costs
 - FDA suggests Vioxx has contributed to >20 000 heart attacks & sudden cardiac deaths during its stay on market
- The exact mechanism of NSAID action, and the origin of many undesirable adverse effects still remain poorly understood.







- Static pathway reconstruction
- Intracellular level models:
 - Catalytic cycle of Drug Target (COX)
 - NSAID action on COX
 - Upstream and downstream metabolic and signalling pathways involved in response to NSAIDs
- Cell level models
 - NSAID action on platelets
 - NSAID action on endothelium cells
 - Combined platelet-endothelium-plasma
- Model of Blood circulation system
- Coupling with pharmacokinetic profiles



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The overall response to NSAIDs results from complex interplay of inductions/inhibitions in different branches of prostaglandin synthesis and further signalling

Pathway reconstruction for prostanoid signalling network







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The Cyclooxygenase Reaction

Cyclooxygenase (COX) is a membrane bound enzyme responsible for the oxidation of arachidonic acid to Prostaglandin G2 (PGG2) and the subsequent reduction of PGG2 to prostaglandin H2 (PGH2).





From Model to Simulation



step 1

Implement the ODE set in DBSlove or/and MATLAB (via SBML conversion)

Model Validation. Identification of kinetic parameters.



Parameters of the COX catalytic cycle identified on the base of experimental data available from literature





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Extended Cox-1/2 Model for Drug Action Modeling

Figure A: Extended Cox-1/2 model. Bottom panel – default Cox-1/2 model; Top panel – inhibition of Cox-1/2 by Aspirin and/or second Inhibitor.



Figure B: Cox cartoon of the simplified Cox1/2 inhibition mechanism.

Effects of inhibitors (NSAIDs) introduced to the COX model:

	Time dependence	Reversibility of binding	Selectivity to COX1,2
•Aspirin	+	-	1,2
 Indomethacin 	+	+	1,2
 Naproxen 	1-,2+	+	1,2
•Diclofenac	+	+	1
 Ibuprofen 	-	+	1,2
•Celecoxib	1-,2+	+	2
•Vioxx	1-,2+	+	2

1- COX1; 2 - COX2

Consistent description of experimental data on inhibitory effects of different NSAIDs



Prediction of NSAID action on target

-For both single drug and drug combinations:

-Aspirin, Ibuprofen, Naproxen, Celecoxib, Indomethacin, Diclofenac,...



•Selective COX2 inhibitor can block aspirin effect – experimental phenomena observed, not previously explained

•Model based analysis allows for prediction of safer drug combinations

COX in the context of intracellular micro- conditions

COX catalysis and NSAID effects in real time and within real physiological substrate / product concentration range



Allows for properties of COX and NSAID inhibition to be translated into in vivo conditions

Intracellular microenvironment controls COX activity and dictates sensitivity to NSAIDs

model allowed to explain/predict many experimental phenomena:

- Discrepancies between in vitro / in vivo estimates of IC50 for Aspirin
- Origin of variability of *in vivo* experimental values of Aspirin IC50 intracellular micro- environmental concentrations of substrates
- Variability in COX-1/COX-2 selectivity results from intracellular conditions
- Attenuation of ASA effect by Celecoxib

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Kinetic modelling of NSAID action on COX-1: Focus on in vitro/in vivo aspects and drug combinations

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COX activity is controlled by intracellular microenvironmental conditions:

Arachidonic Acid and Reducing Co-substrate concentration



First valid explanation of discrepancies between in vitro / in vivo estimates of IC_{50} for Aspirin



Accumulation of acetylated COX gives rise to additional COX inhibition due to retained peroxidase activity

Modelling drug action on target under various regimes of drug administration

Low dose Aspirin, once daily









PGG2 PGH2







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Cell-type – specific

Intracellular

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Example: Adenylate Cyclase and Protein Kinase A Signalling

Identification of constants for AC activation model



* Chen-Goodspeed M, Lukan AN, Dessauer CW; Modeling of Galpha(s) and Galpha(i) regulation of human type V and VI adenylyl cyclase; J Biol Chem. 2005; 280(3):1808-16





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≻Organ level

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Platelet model **TXA**₂ biosynthesis ٠ transmembrane transport signalling pathways activated by prostanoids Ca²⁺ fluxes involved in platelet activation . NSAIDs action on cyclooxygenase • PGI₂ (ext), **R2** iloprost (IP); $PGD_{2}^{(ext)}$ (DP) Ph.Lip.-AA AMP Gs PLA₂ cAMP degradation AA (ext) PKA AA ATP COX-1 PIP₂ Ca²⁺ PKC inactivation PLC PGH₂ PGH₂ (ext) DAG IP3R TBXAS Gq PGE₂ (ext) PGD₂ (ext) ER degradation HHT TXA₂ Ca²⁺ TXA₂ (ext) **R1** Cathrombin. ATPase TXB₂ TXB₂ (ext) ADP, **ODE system:** TXA₂ (ext) 42 equations, 62 rate laws, **152 parameters**

Platelet model validated on perturbation experimental data with receptor agonists



Data from JBC(2002)277:29321

FIG. 1. Inhibition of thrombin-induced Ca²⁺ increases by iloprost in platelets. *A*, Fura-2-loaded platelets were stimulated with thrombin (1 unit/ml) and 30 s later with iloprost (1 μ M). *B*, conversely, platelets were first incubated with iloprost (1 μ M) and 1 min later stimulated with thrombin (1 unit/ml). Tracings show the increase in [Ca²⁺]_t measured in the presence of 1 mM extracellular Ca²⁺ and are representative of three observations with similar results.



High dose of iloprost effectively inhibits platelets activation by thrombin

Stimulation of platelets by iloprost leads to cAMPdependent PKA activation that phosphorilates IP3dependent calcium channels (IP3R) on endoplasmic reticulum (ER). This results in in the inhibition of IP3R sensitivity to IP3, and a decrease in Ca2+ outflux from ER





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Endothelium cell model







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- Intracellular

Cell-type – specific

-Organ level

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Platelet-Endothelium-Plasma model allows to assess potential cardiovascular risk after NSAID administration



Dose-response of the platelet-endotelium plasma system. Prediction of clotting risks for NSAIDS and combinations



Risk of clot formation increases with increase in COX2 selective inhibitor concentration under inflammatory conditions



Monitoring state of platelets in different parts of blood circulation



Activation

- (TXA2) Clotting risks monitored (proportional
- 1) Clotting risks monitored (proportional to intracellular Ca2+ concentration in platelets)
- 2) Maximal risk of clot formation is observed in leg veins
- 3) Capillaries of lungs and arms decrease risk of clot formation substantially

Systems Approach applied to drug safety

- *In silico* methods help to understand the efficacy, mode of action and potential dangerous side effects of drugs
- Model-based analysis and prediction of drug safety and efficacy
- Informed advice on drug dosing, scheduling and combinations

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