Four interesting examples ...

... of how technology developments support new business models.

Richard Padley, Managing Director, Semantico.
Example #1 is about Researchers. Specifically its about focus on researcher needs. It starts with a piece of researcher focussed technology that creates some interesting opportunities.
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Who’s heard about ORCID? You may not know its being developed by Semantico. Socially validated platform for Discovery, Attribution, & Disambiguation in the scholarly record. Stakeholders are Researchers, libraries, funding agencies, & Publishers. Many important consequences will follow; facilitates calculation of more sophisticated measures of impact – author metrics – e.g. h-index
Will feed into Altmetrics phenomenon. Triangulation rather than single measure of impact. Tech: Big data, firehose, hadoop, NoSQL datastores, API level integration. SAAS business model. Returning to h-index is ...
Who’s seen this? Google scholar metrics, launched 1 April. This is no joke. H-index. Another elephant in the room is the biggest business model shift ...
Researcher focussed business model. Publishing sold is a service, not a physical good, or a licence to access IP. Paraphrase Ahmed Hindawi: increased competition, differentiation around the service. OA raises the bar. Service is for authors; differentiation in adding value for authors.
Example #2 User Generated Content. RMM in print until 7e; but often supplemented with local notes and modifications. Tech: Flexible XML content database for R/W content. Allows seamless presentation of published & UGC. Like a Wiki BUT private to each subscribing institution. Audit trail. Innovation is delivering Content in Context for clinical practitioners, rather than bus model.
Example #3
Business Goals 1: Drive subscriber usage, 2: Reach a new market with new model – day pass SEO project for CABI. 1.5M abstracts
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Swine as models in biomedical research.

Title: Swine as models in biomedical research.

Authors: Pennington, L. R.; Weiskopf, R. B.; Hannon, J. F.

Editor: Swindle, M. M.


Record Number: 19942200241

Abstract:
The Seventh Charles River International Symposium was held at Danvers, Massachusetts in September 1989. 18 symposium contributions deal with the use of Yucatan and Hanford minipigs and ordinary pigs in cardiovascular research and in a variety of other topics, such as renal transplantation (L. R. Pennington, pp. 35-43), use of swine in the study of anaesthetics, by R. B. Weiskopf and others (96-117), congenital cardiovascular disease in pigs, by M. M. Swindle and others (176-184), and haemorrhagic shock, by J. P. Hannon (197-245). A previous book on swine in biomedical research appeared in 1986 (edited by M. E. Tumbleson, published by Plenum Press, New York).
Visitors increased 1200 to 36,000 (+3000%); Subscriber visits to 5000 (+400%)
Not SEO – Politics & Google making up the rules as they go along.
Example #4. Data mining. Sydney Brenner: "Data mining means my data are mine, and your data are mine, too."

Improve UX, Increase discoverability, stickiness – lower cost/download. Slice/dice to create new products. Lower production costs, improve consistency, time to market. Parsing whole sentences, sentiment, citation typing. >equiv terms >search >medical. Large scale meta-analyses (Pharma). Highly targeted advertising:
The Mycobacterium tuberculosis Drugome and its Polypharmacological Implications

Sarah L. Kinings1, Li Xie1, Kingston H. Fung1, Richard M. Jackson1, Lei Xie2, Philip E. Bourne3,4

1Institute of Molecular and Cellular Biology and Auditory Centre for Structural Molecular Biology, University of Leeds, Leeds, United Kingdom. 2San Diego Supercomputer Center, University of California, San Diego, La Jolla, California, United States of America. 3Biology, School of Pharmacy and Pharmaceutical Sciences, University of California, San Diego, La Jolla, California, United States of America. 4Biomatics Program, University of California, San Diego, La Jolla, California, United States of America.

Abstract
We report a computational approach that integrates structural bioinformatics, molecular modelling and systems biology to construct a drug-target network on a structural proteome-wide scale. The approach has been applied to the genome of Mycobacterium tuberculosis (M.tuberculosis), the causative agent of one of today's most widely spread infectious diseases. The resulting drug-target interaction network for all structurally characterized approved drugs bound to putative M.tuberculosis receptors, we refer to as the 'TB-drugome'. The TB-drugome reveals that approximately one-third of the drugs examined have the potential to be repositioned to treat tuberculosis and that many currently unexplored M.tuberculosis receptors may be chemically druggable and could serve as novel anti-tuberculosis targets. Furthermore, a detailed analysis of the TB-drugome has shed new light on the controversial issues surrounding drug-target networks [1-3]. Indeed, our results support the idea that drug-target networks are inherently modular, and further that any observed randomness is mainly caused by biased target coverage. The TB-drugome (http://myco.ut.ee/drugome/TB) has the potential to be a valuable resource in the development of safe and efficient anti-tuberculosis drugs. More generally, the methodology may be applied to other pathogens of interest with results improving as more of their structural proteomes are determined through the continued efforts of structural biologists.

Introduction
The construction and analysis of molecular interaction networks provides a powerful means to understand the complexity of biological systems and to reveal hidden relationships between drugs, genes, proteins, and diseases. In particular, the study of drug-target networks may contribute to an improved understanding of the principles of polypharmacology and hence improved rational drug design [4]. In recent years, several computational methodologies have been developed to predict drug-target networks based on ligand chemistry [4-6], phenotypic changes resulting from drug perturbation [7,8], or on a combination of chemical features of drugs and sequence- or structural-based protein targets [10-12]. Extensive experimental and computational evaluation has proven that these methods are valuable for drug repurposing and side effect prediction. However, these methods are biased towards known drug-target pairs, which are mainly derived from well-established drug targets such as G-protein coupled receptors (GPCRs), which only cover a small portion of the human proteome. The lack of a broad spectrum of drug-target pairs is more severe in pathogens than in its homologues. For example, amongst the 3,999 protein encoded by the Mycobacterium leprae (M.leprae) genome, only nine (cmaA, cyp56B, embA, embB, emcA, fks, lamA, katG and rpoC) have been pharmacologically investigated [13]. Thus, drug-target networks that are constructed from only existing drug targets are retrospective, and less capable of discovering new druggable targets and predicting off-target profiles of new compounds on a proteome-wide scale. In addition, the incompleteness of drug-target data poses questions as to whether or not the topology of drug-target networks is inherently modular or random [1].

It is important to construct and analyze a proteome-wide drug-target network that includes not only the primary targets, but also all of the potential off-targets of the drugs in the network. Such a network, if available, would provide unparalleled opportunities for mapping a comprehensive drug-target space and understanding the molecular basis of drug efficacy, side effects and drug resistance, thereby providing the foundation for the rational design of polypharmacological (multi-target) drugs. For anti-infective drug discovery, where pharmacologically investigated targets only represent a small portion of the whole pathogen's proteome, it is more challenging to establish a proteome-wide drug-target network. The linkage of drugs to less explored proteins such as virulence factors, transport proteins and transduction factors will greatly expand the repository of anti-infective drug targets and provide new solutions for combating multi-drug and extensively drug resistant pathogens, and for repurposing existing drugs for new uses.

Structural bioinformatics provides an alternative and complementary way to extend drug-target networks to less characterized proteins on a proteome-wide scale. The structural coverage of a given pathogen proteome is usually much larger than the
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Sarah L. Kinnings, Li Xie, Kingston H. Fung, Richard M. Jackson, Lei Xie, Philip E. Bourne

Institute of Molecular and Cellular Biology and Astley Centre for Structural Molecular Biology, University of Leeds, Leeds, United Kingdom; 2 San Diego Supercomputer Center, University of California, San Diego, La Jolla, California, United States of America; 3 Sage Bionetworks, Seattle, Washington, United States of America; 4 Biocomputing Program, University of California, San Diego, La Jolla, California, United States of America

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Introduction

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It is important to construct and analyze a proteome-wide drug-target network that includes not only the primary targets, but also all of the potential off-targets of the drugs in the network. Such a network, if available, would provide unparalleled opportunities for mapping a comprehensive drug-target space and understanding the molecular basis of drug efficacy, side effects and drug resistance, thereby providing the foundation for the rational design of polypharmacological (multi-target) drugs. For anti-infection drug discovery, where pharmacologically investigated targets only represent a small portion of the whole pathogen’s proteome, it is more challenging to establish a proteome-wide drug-target network. The linkage of drugs to less explored proteins such as virulence factors, transport proteins and transcription factors will greatly expand the repository of anti-infectious drug targets and provide new solutions for combating multi-drug and extensively drug-resistant pathogens, and for repurposing existing drugs for new uses.

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