Informatics in Drug Discovery

Workshop on a "Drug Discovery" Approach to Breakthroughs in Batteries September 8-9, Cambridge Ernst R. Dow, Ph.D. dow@lilly.com Group Leader / Senior Information Consultant, Eli Lilly and Company

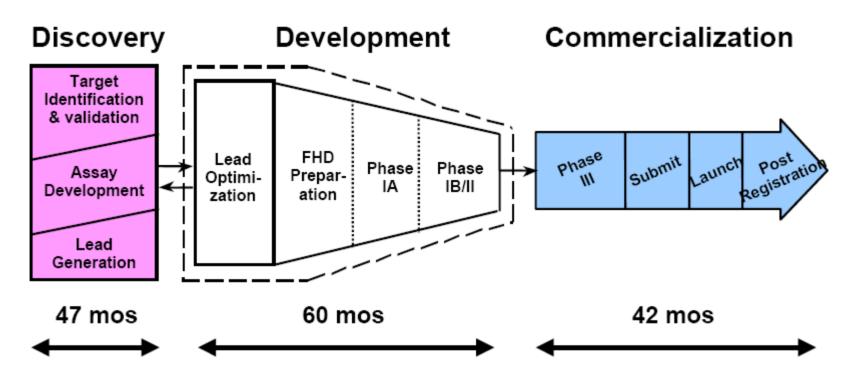
Answers That Matter.

Overview

- Brief overview of drug development
- QSAR quantitative structure activity relationships
- Combinatorial synthesis
- Microarrays
- Data integration
- Phenotypic screening
- Managing research

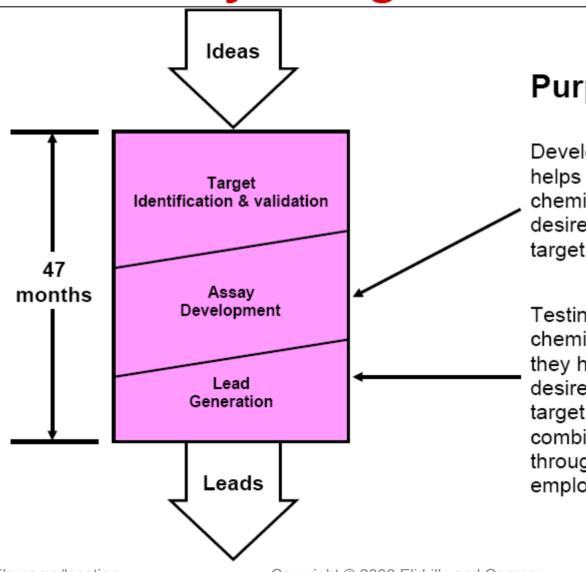
Our Development Process – The "Rocketship"

From Targets to Products



Our development process takes on average about 12 years to go from targets to products with an overall probability of success of about 2%

Discovery - Targets to Leads



Purpose:

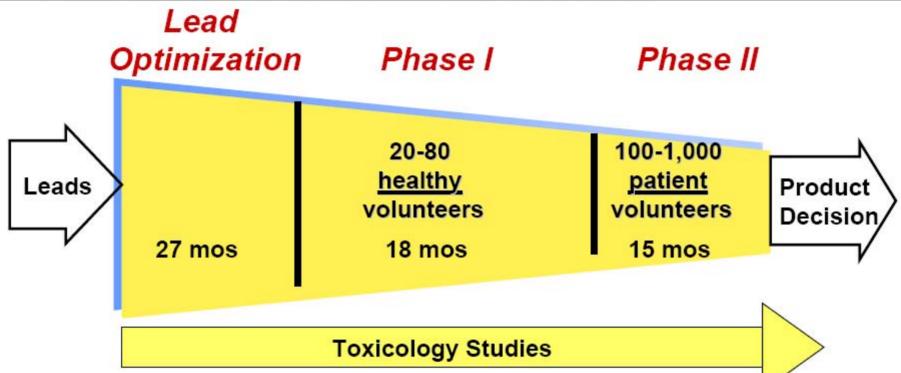
Develop a "screen" or test that helps us to determine if a chemical compound has the desired biological effect on a target

Testing or screening various chemical agents to determine if they have some level of the desired biological effect on a given target. Chemical libraries, combinatorial chemistry, and high throughput screening are employed here.

File name/location

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Development – Leads to Product Decision

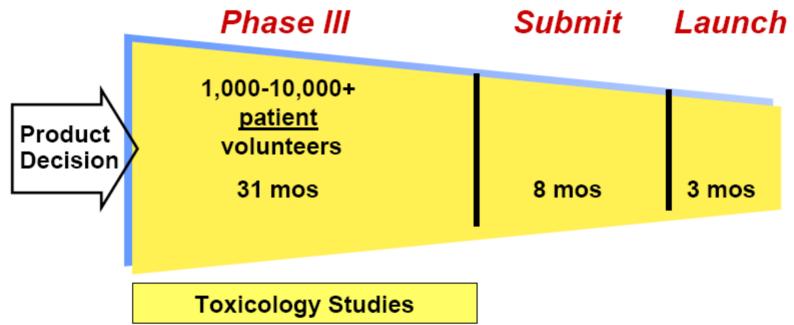


Purpose:

Lead compounds refined and optimized to give a **drug candidate** prior to going into humans. Tox, ADME, and PK studies begin.

First human dose is administered. Small doses given to healthy volunteers to test tolerance,safety, and dosing. First efficacy dose given. Looking for therapeutic response and possible side effects. Most perilous time approx. 75% will fail in Phase II.

Commercialization – Product Decision to Launch



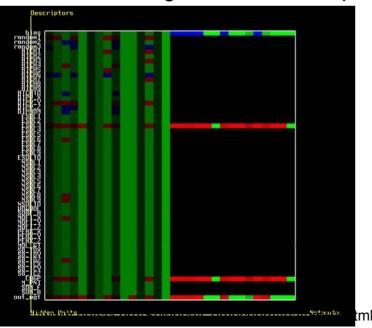
Purpose:

Biggest dollar spend as we study efficacy in thousands of patients worldwide to support a launch. Performance is often evaluated versus competitive drugs. Registration documents are prepared and submitted.

Dialogue with FDA during regulatory review process. First approval and launch. Followed quickly by approval and launch in many other countries.

QSAR: Quantitative Structure Activity Relationship

- ~1990 Have a set (10s) of molecules with an activity measure against an assay. Chemically intuitive descriptors are used to describe the molecules. Linear models used to find relationship between descriptors and activity.
- Could not realistically predict activity in new chemical spaces, but chemists could learn which descriptors would drive changes in activity and synthesize new
- Chemists would focus on synthesizing molecules that would vary those descriptors the most since they would presumably have the most effect on activity and the understanding of the chemical space.



This figure shows using an artificial neural network for variable selection in QSAR. The weights of a different neural network are shown in each column, with the descriptors that were included in the reduced set on the right hand side. Green colors indicate weights near 0 and red or blue indicate positive or negative values. Note that several random inputs were used and these were then used to filter (prune) other inputs to build the smaller set of descriptors.

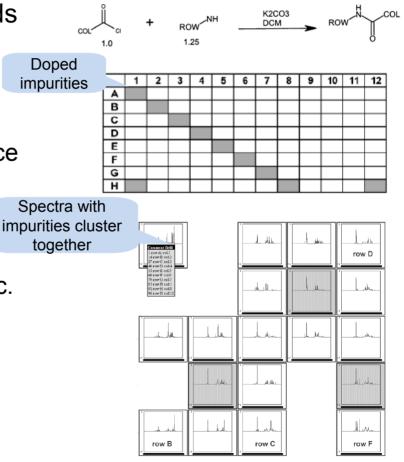
There are now companies that specialize in the model building, e.g. http://www.leadscope.com

High Throughput Screening

- Mid 90's large pharma gets involved in HTS
- Assumptions:
 - If we screen enough compounds, we will find new drugs.
 - In vitro assay is a good measure for affecting the target.
 - We understand biology enough to know that modifying the target will have the desired effect on human disease.
- Reality:
 - Too many "hits".
 - Hits were often not drug-like molecules.
 - Too many of the "hits" were false positives.
 - Impurities could cause the activity.
- Currently:
 - Don't screen blindly.
 - Save screening until once there is a starting point.
 - Informatics used to select a diverse library of compounds.

Combinatorial Synthesis: chemical reactions in plates

- Rapidly generate novel compounds with defined chemistry for screening
- Each row and each column has 1 compound
 - 8 + 12 starting compounds produce
 96 new compounds
- Use flow NMR to verify structure each well
 - Identifies outlier spectra to show undesired products, impurities, etc.
 - Many of these can be generated and it takes a trained NMR spectroscopist to interpret the spectra.
 - Tedious
- Informatics used to speed up and simplify the interpretation of NMR spectra by grouping similar spectra – outliers to go corners



J. Comb. Chem., 4 (6), 622 -629, 2002

Microarrays / Gene Chips

What are Microarrays?

- Measure the expression level of essentially all the genes in a single sample
- Each chip has 30,000-50,000 probes: each can be a separate experiment
- Compare normal sample to treated sample
- Cannot simply use a pvalue for filtering: 10,000 experiments with a pvalue of 0.01 → 100 false positives

How to interpret so many results?

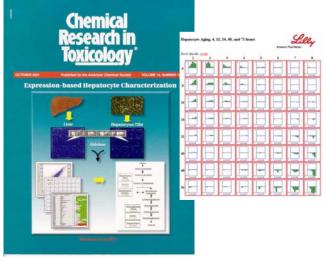
- Biologists are the experts in their therapeutic area not informatics
- Often very familiar with a handful of genes and pathways
- 1000s of probesets changing
 - Easy to generate 1000s of hypotheses!
- Hypotheses can change based on arbitrary filtering criteria much subjectivity
- Subjectivity makes it hard to know when one is done analyzing the data



Gene Analysis

1999 "List of Genes"

- 6,800 probesets on Affymetrix chip
- Clustering HC, SOM, others
- Annotations ~ 30%
- Each chip tremendously expensive (few chips / study)
- Filter by fold change
- Pvalues
- "guilt by association"



2008 "Biological Context"

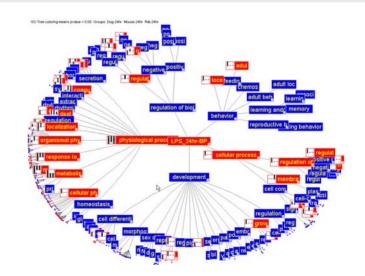
56,000 probesets on Affymetrix chip

Clustering – HC, SOM, others

Annotations ~85%

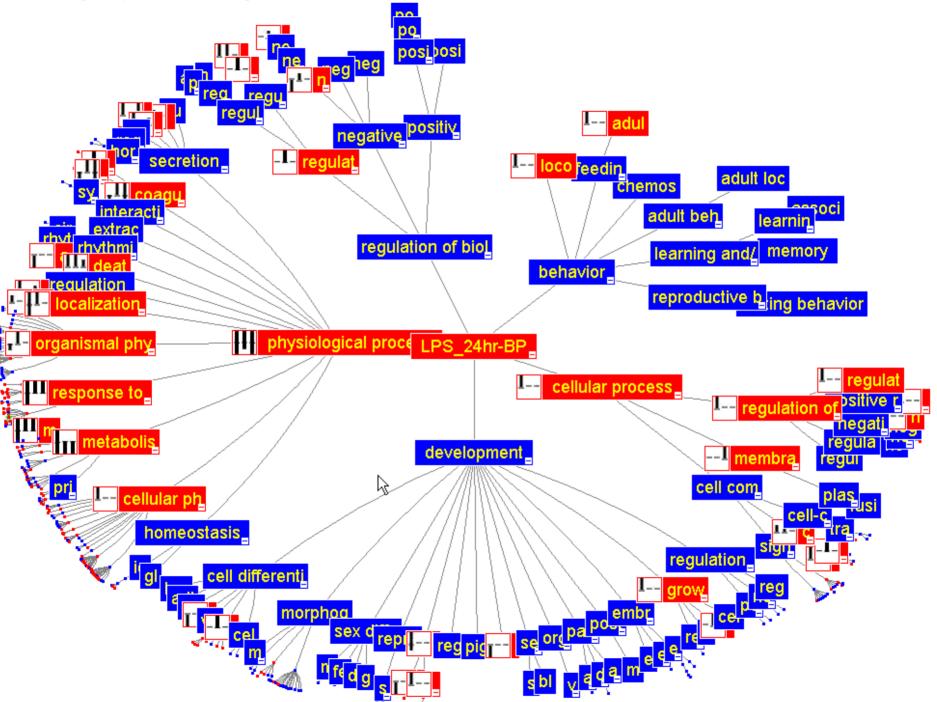
Each chip less expensive (many chips / study)

False discovery rates (multiple testing correction) Gene Ontology

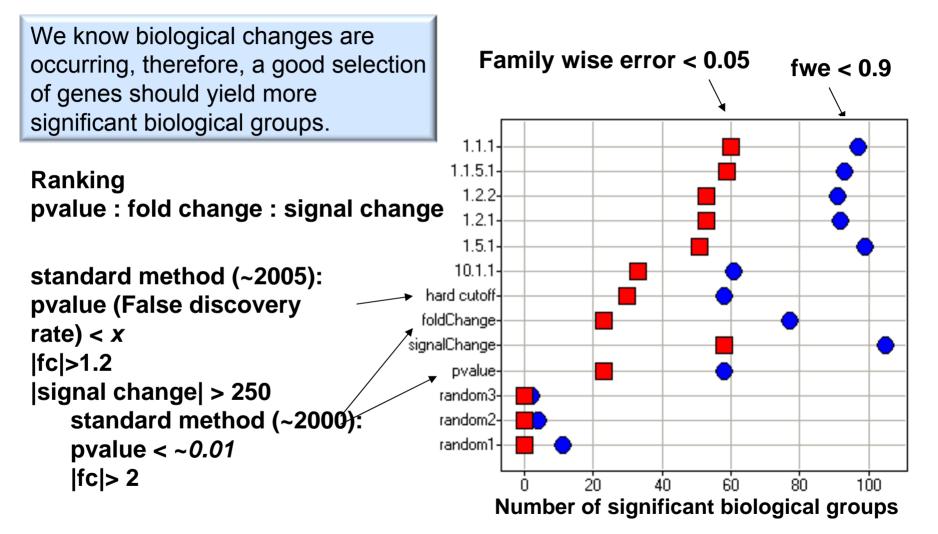


Chem. Res. Toxicol., 14 (9), 1218 -1231, 2001.

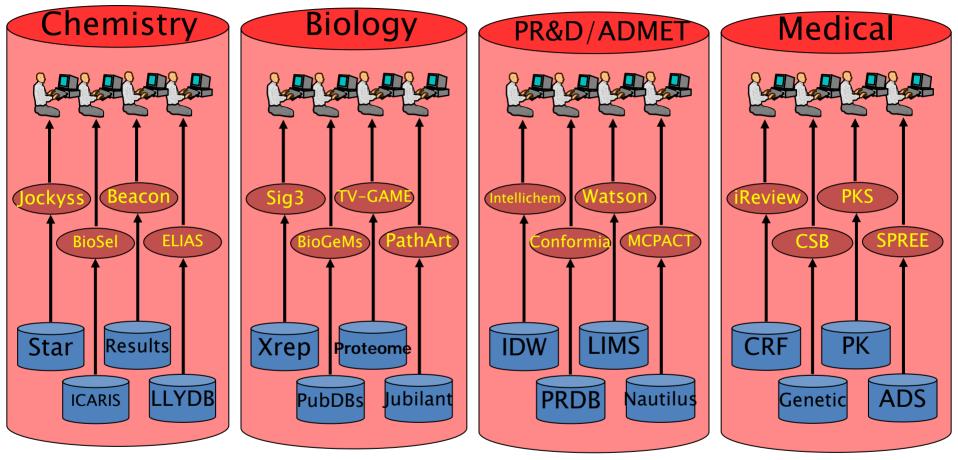
GO Tree coloring means pvalue < 0.05 Groups: Dog-24hr Mouse-24hr Rat-24hr



Incorporating biology can change assumptions about filtering



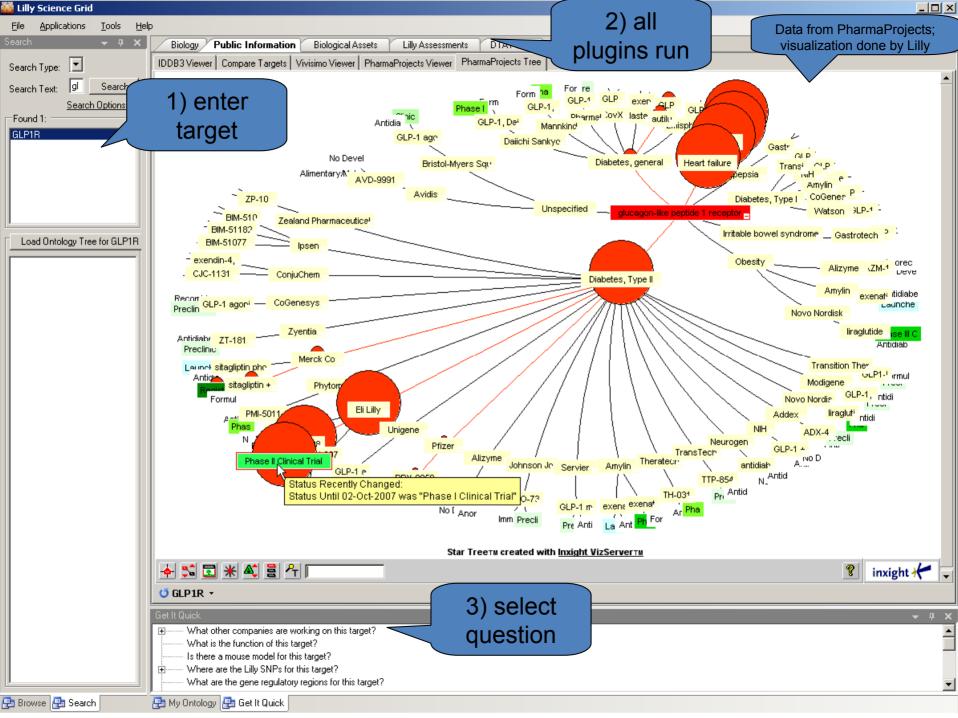
Where are Internal Data? Silos of Silos



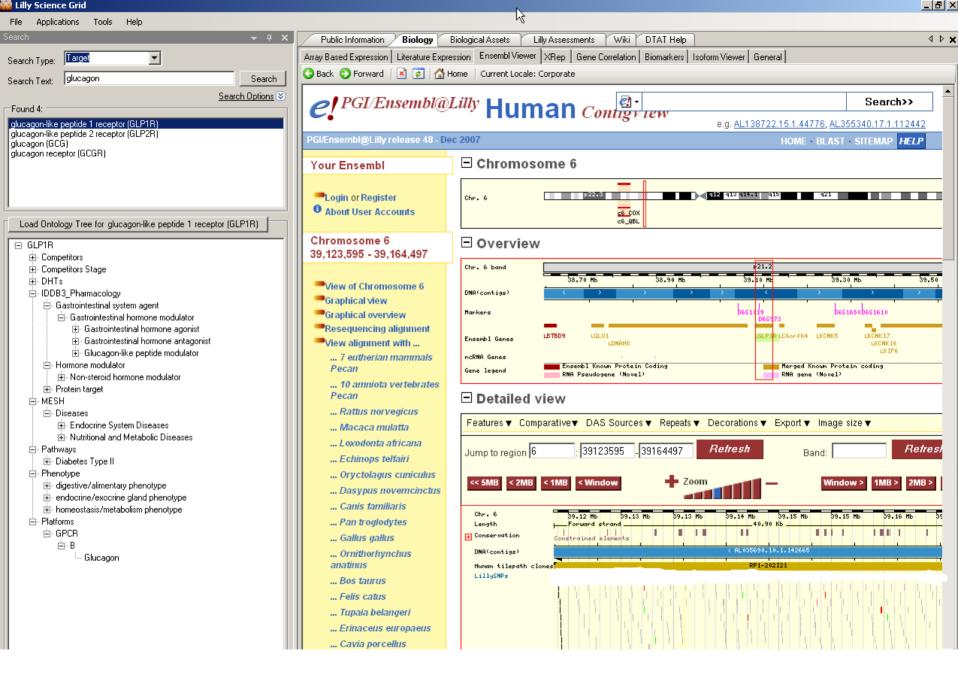
- $\boldsymbol{\cdot}$ Tools, application, and data are standalone with limited interaction
- ·Scientists have great difficulty finding their data and associated tools
- Asking cross-domain questions (e.g. Discovery + Medical) very difficult
- •Support becoming very impractical estimated 400+ individual tools across silos
- I argor problem in older companies and regulated industries

How do we address?

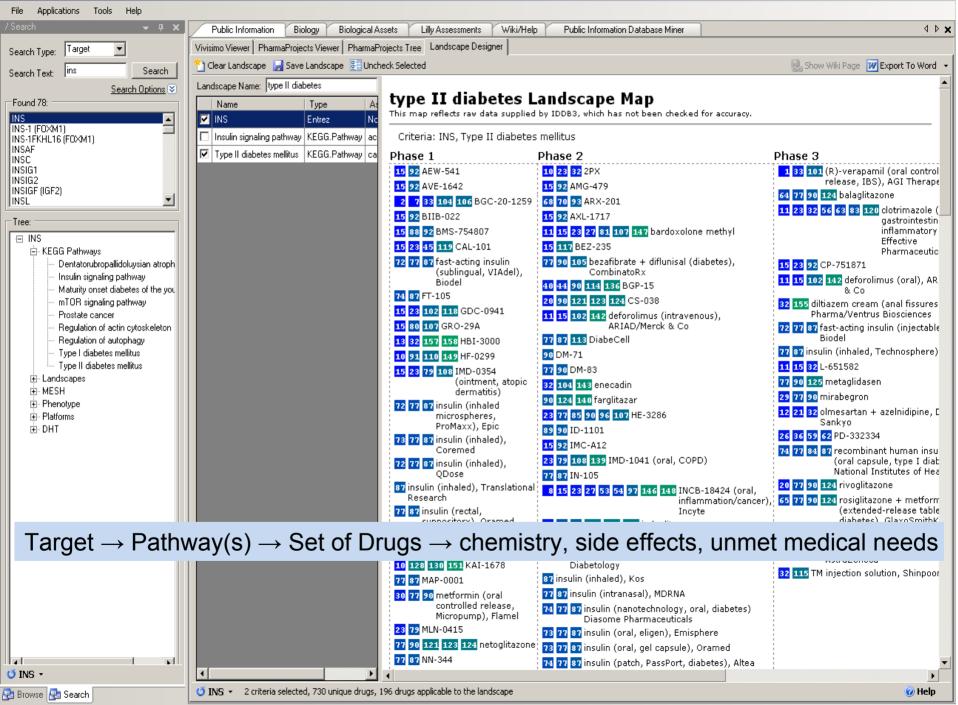
- Use Discovery Target Assessment Tool (DTAT)
 - DTAT allows scientists to evaluate drug targets. DTAT allows scientists to select the scientific question of interest and returns data that is in the appropriate context.
- Built upon Life Science Grid: LSG available on <u>http://www.sourceforge.net</u>
- Uses RDF (resource description format) to store information about targets, pharmacology, internal development, disease
- Plugins use "listeners" to respond to appropriate data type and serve information
- Question framework allows scientists to learn how each data source provides relevant data
 - Questions stay relatively constant, data and sources change.
 - If informatics is doing proper job, we are providing the best answers for the questions.



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	⊕ ► Receptor ligands(12)	Status: Completed	
	⊕ ► Inhibitors (20)	clinicaltrials.gov/show/NCT00393445 - ClinicalTrials.gov 1	
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		Category: C07H	
	Gene, Expression (7)	Date: -20-104 Patent: US7276593B2	
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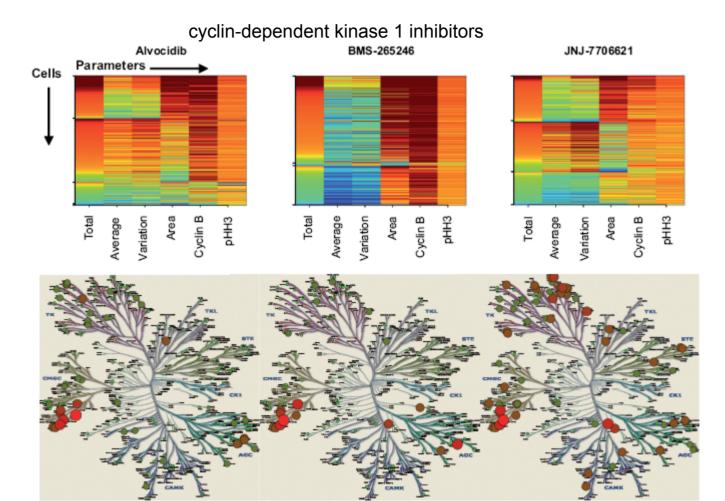


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Lilly Science Grid

Phenotypic Drug Discovery



- In vivo (cell based assays), use imaging techniques to measure variety of biological parameters
- No need to choose a target and possibly be wrong!
- Current Opinion in Drug Discovery & Development 2008 11(3):338-345 Jonathan

Managing research

- Part of the challenge is how to manage the research, When development costs are high and failure is common, companies should structure research to seek truth first, success second.
- Project champions can often marshal resources to keep a project moving – may not be sufficiently motivated to do the experiment that could kill their idea
- Advocate early stages of research for "Truth Seekers". Evaluate many projects and rewarded for objectivity
- Since most molecules in the early stage fail, manage to assume failure of the asset instead of creating infrastructure to ramp up production early. This may delay a successful molecule, but otherwise there is a large opportunity cost as fewer early stage assets may be pursued.
- Clean up this page...
- "A More Rational Approach to New-Product Development", by Eric Bonabeau, Neil Bodick, and Robert W. Armstrong *Harv Bus Rev.* 2008 Mar;86(3):96-102

Summary

- Target focused research assumes we know enough biology to optimize the right things
 - Initially optimized one parameter: activity (optimize only the cathode)
 - Must also optimize side effects, safety margin, population effects, dosing, etc.
 - Adjust design parameters to gain the most information
 - Help interpret the results
 - Adding background information can improve quality of results (optimize entire battery)
 - Integrating many data sources can improve the decision quality
- Phenotypic screening (measure performance of the car which is made up of a set of batteries with powertrain etc.)
 - Advances in technology allows higher throughput cell based assays that measure biology
 - Can skip the target stage
- How to reward scientists to remove molecules from the pipeline?

Backups

Life Science Grid

- LSG an asynchronous web services (message oriented) "smart" client-side application deployed using Microsoft ClickOnce deployment strategy.
- Software Development: Microsoft Visual Studio 2005
- Client: Windows XP SP2, .NET Framework 2.0, WSE 3.0
- Server: Windows 2003 Enterprise Edition, SP1, .NET Framework 2.0 and IIS 6
- Databases Supported:
 - MySQL 5.0
 - Microsoft SQL Server 2005 Express Edition
 - Oracle Database 10g Express Edition



- Available on <u>http://www.sourceforge.net</u>
 Search for LSG
- Framework will include sample public domain plugins
- Documentation "how to" for software developers

Data is being generated at an increasing rate – how to get relevant data?

- Difficult or impossible for any scientist to know all the sources – scientists asked to work more outside their own areas
- Nucleic Acids Research, DB issue
 - 1078 databases, 110 more than last year
 - links to more than 80 databases have been updated
 - only 25 obsolete databases have been removed
- Multiple ways of describing the same or similar data (same or similar depends on point of view)
 - MESH, PathArt disease, PharmaProjects indications, gene ontology, IDDB3 Pharmacology
 - Intelligent people can disagree, e.g., gene x causes cancer or gene x does not cancer. Both could have the same numerical results and have a different arbitrary cutoff.
 - How does one query across overlapping data?

Data are generated faster than they can be understood

- Must find data that are relevant
 - Tremendous duplication
 - What is the current answer?
 - wheat from chaff
- Find connections in data
 - visualization
 - words
 - Statistics
- Difficulty measuring value of data, e.g. compare to compute speed
 - database quality
 - database 1 vs. database 2
 - agreement
 - quality measure of each element
- Data curation is expensive
- More than just having the data: ability to retrieve relevant decisionmaking information must be part of the value metric

Informatics in Drug Discovery

This talk will begin with a brief overview of the various stages of drug development. Model building and chemical methods will initially be described from the early 90s. These will serve as a basis for comparison for later methods such as high throughput screening, medium throughput screening, and phenotypic drug discovery. Microarrays, with their ability to measure gene changes across the entire genome, will be described as a means of interrogating biological systems with the associated challenges of understanding the results. Recent work using the Life Science Grid will be covered as a means of integrating relevant information from many sources. Finally, other organizational shifts will be discussed that may facilitate more efficient breakthroughs.