

Cheminformatics and Toxicogenomics for Toxicity Prediction and Mechanistic Insight

George Daston

Overview

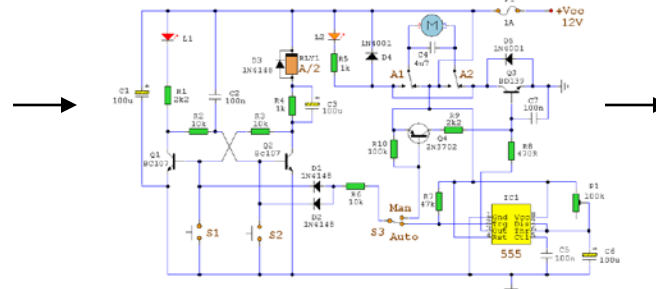
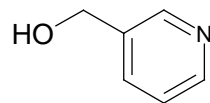
- Tiered approach to predicting toxicity of new chemicals
 - Cheminformatics- supported SAR
 - High-content methods to assess SAR solutions
- Identifying MOA using cheminformatics and toxicogenomics
 - MOA ontology
 - Connectivity mapping

Toxicology: From an Empirical to a Predictive Science



Traditional Approach (Black box):
Use a model that we have (some)
confidence in, but incomplete
understanding of how it works

Desired Approach:
Predictions based on
deep, fundamental
understanding

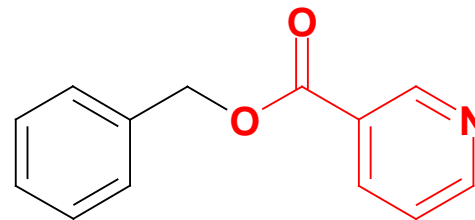


Taking Advantage of the Existing Literature

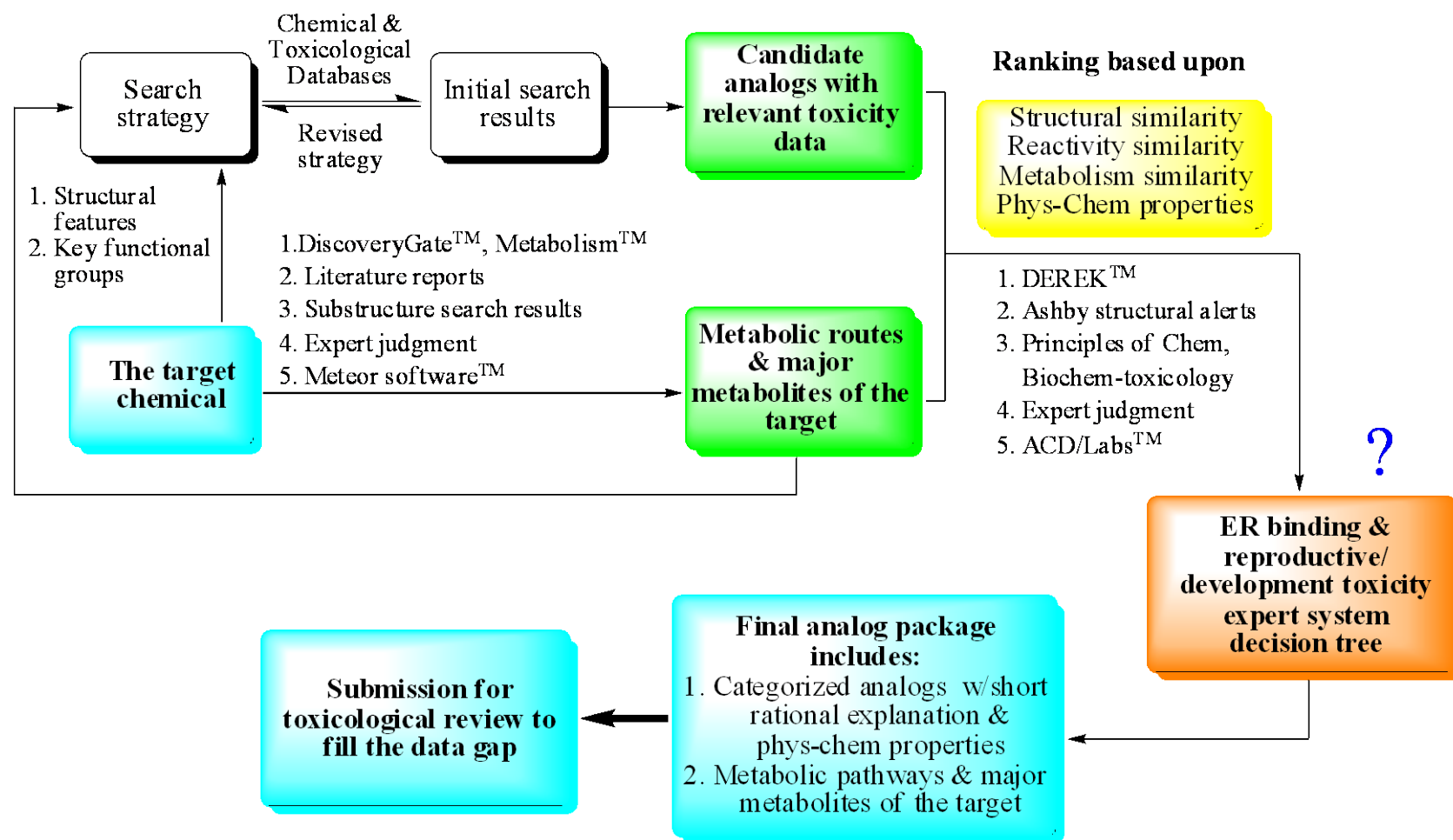
- Considerable outcome data in DART (almost 12,000 entries in publicly available databases)
- Pressing need is to identify initial molecular events
- Effort needed to connect initial events with tissue/organ level effects

Initial Screening for Human Hazards

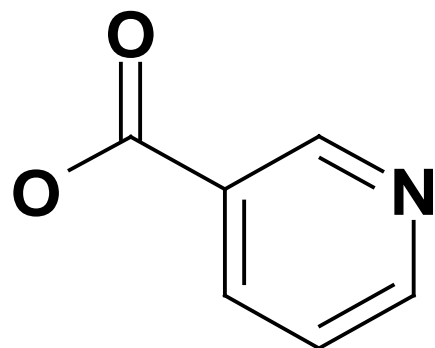
- Substructure searching
 - Genotoxicity (19,300)
 - Carcinogenicity (15,800)
 - Skin Sensitization (9,400)
 - Skin Irritation (10,400)
 - Reproductive/Developmental Toxicity (11,300)
 - Subchronic/Chronic Toxicity (15,100)
 - Acute Toxicity (68,500)
- All assessment captured in CHS
- External Data Sources: BIBRA*, Cal Prop 65*, CTFA*, HERA*, HPV*, OECD*, IPCS*, NICNAS*, RIFM/FEMA*, SCCP*, WHO/JECFA*,
SciFinder, ToxNet, ATSDR, CPDB, ECETOC, ECB, IARC ,
Thompson/MicroMedix, NTP, RTECS/NIOSH, Scopus, TSCATS, others



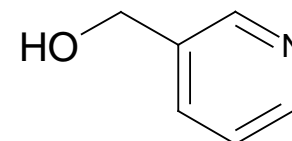
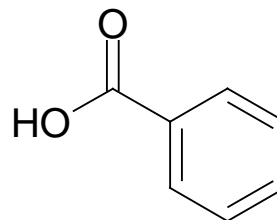
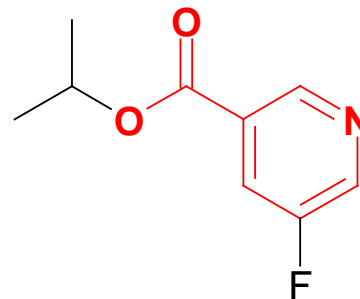
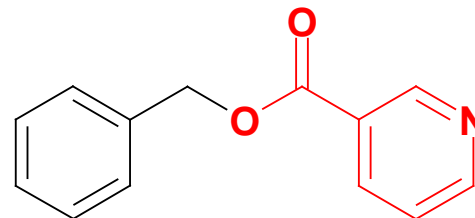
Flow chart of new analog identification & evaluation process



Searching GRASP- Substructure Searching



Search Structure



Output – Substructure Searching

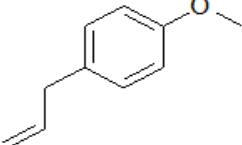
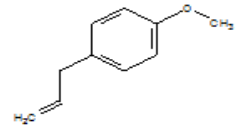
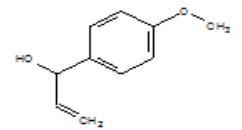
RS3 Excel [rpd v2.3.0 :: TL5734] - Carcinogenicity Example 2.xls

Type a question for help

File Edit View Insert Format Tools Data Window Help RS3 Discovery

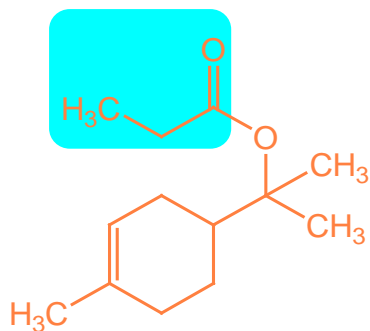
Σ %

H1

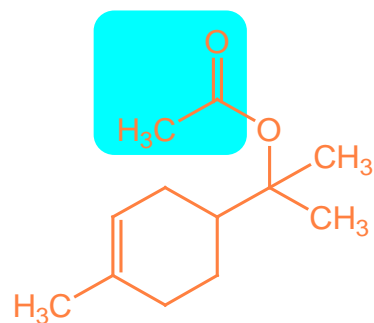
	A	B	C	D	E	F	G	H
1		SEARCH STRUCTURE						
2	Substances							
3		A. Alias	B. CAS No.	C. Study Type	D. Species	E. Route of Admin.	F. Result	N. Ref. Journal
4								
5	103652	ANISOLE, p-ALLYL-	140-67-0	BIOASSAY	MOUSE	DIET		RIFM
6	103652	ANISOLE, p-ALLYL-	140-67-0	BIOASSAY	MOUSE	GAVAGE		RIFM
7	103652	ANISOLE, p-ALLYL-	140-67-0	BIOASSAY	MOUSE		+	RTECS
8	103652	ANISOLE, p-ALLYL-	140-67-0	CA PROP 65			F +	http://potency.berkeley.edu
9	103652	ANISOLE, p-ALLYL-	140-67-0	OTHER	MOUSE	INTRAGASTRIC	M +	http://www.cephha.org/pj
10	103652	ANISOLE, p-ALLYL-	140-67-0	VSD	MOUSE	DIET		PHS149
11								
12	104455	BENZYL ALCOHOL, p-METHOXY-alpha-VINYL-	51410-44-7	BIOASSAY	MOUSE		+	RTECS
12	104455	BENZYL ALCOHOL, p-METHOXY-alpha-VINYL-	51410-44-7	BIOASSAY	MOUSE		F +	http://potency.berkeley.edu

Ready

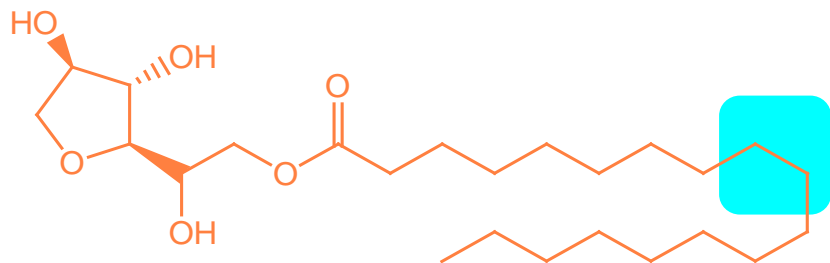
Suitable Analogs



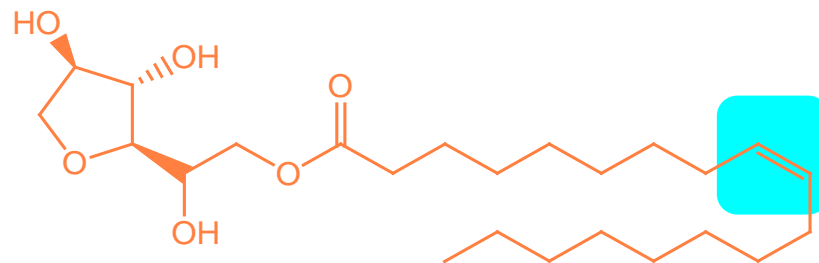
CAS# 80-27-3



CAS# 8007-35-0

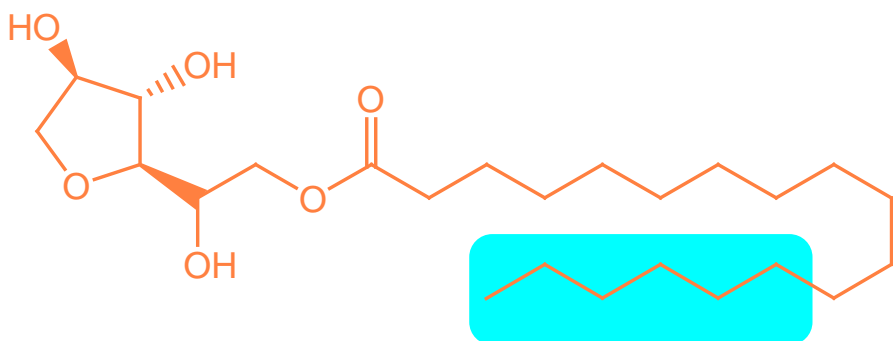


CAS# 1338-43-8

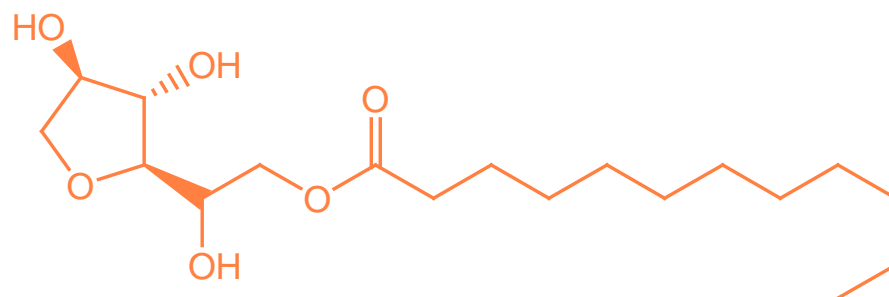


CAS# 8007-43-0

Possibly Suitable

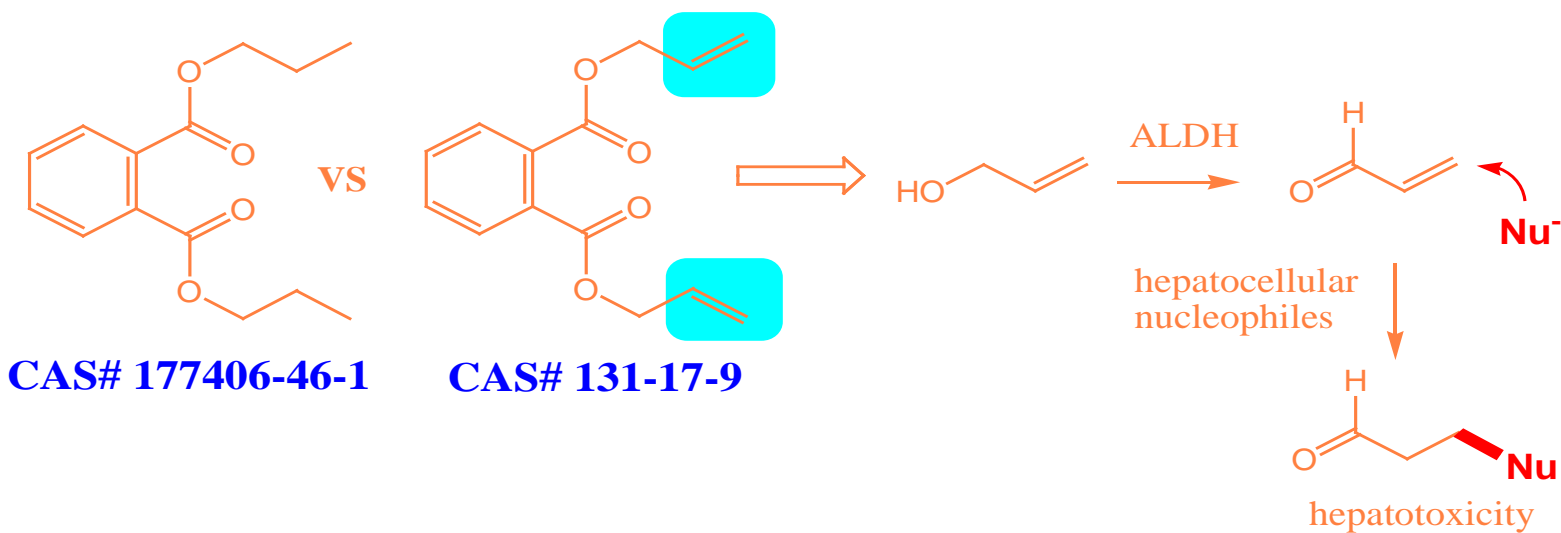


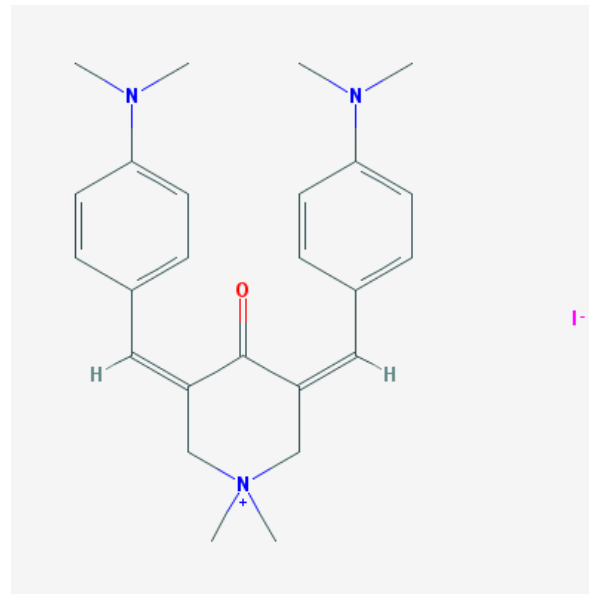
CAS# 1338-43-8



CAS# 1338-92-3

Unsuitable Analogs





- Nrf2 qHTS screen for inhibitors: counterscreen for cytotoxicity
- qHTS Assay for Inhibitors of RanGTP induced Rango (Ran-regulated importin-beta cargo) – Importin beta complex dissociation
- qHTS Assay for Inhibitors of JMJD2A-Tudor Domain

■ Chemical Probe
 ■ Active
 ■ Inactive
 ■ Inconclusive
 ■ Unspecified

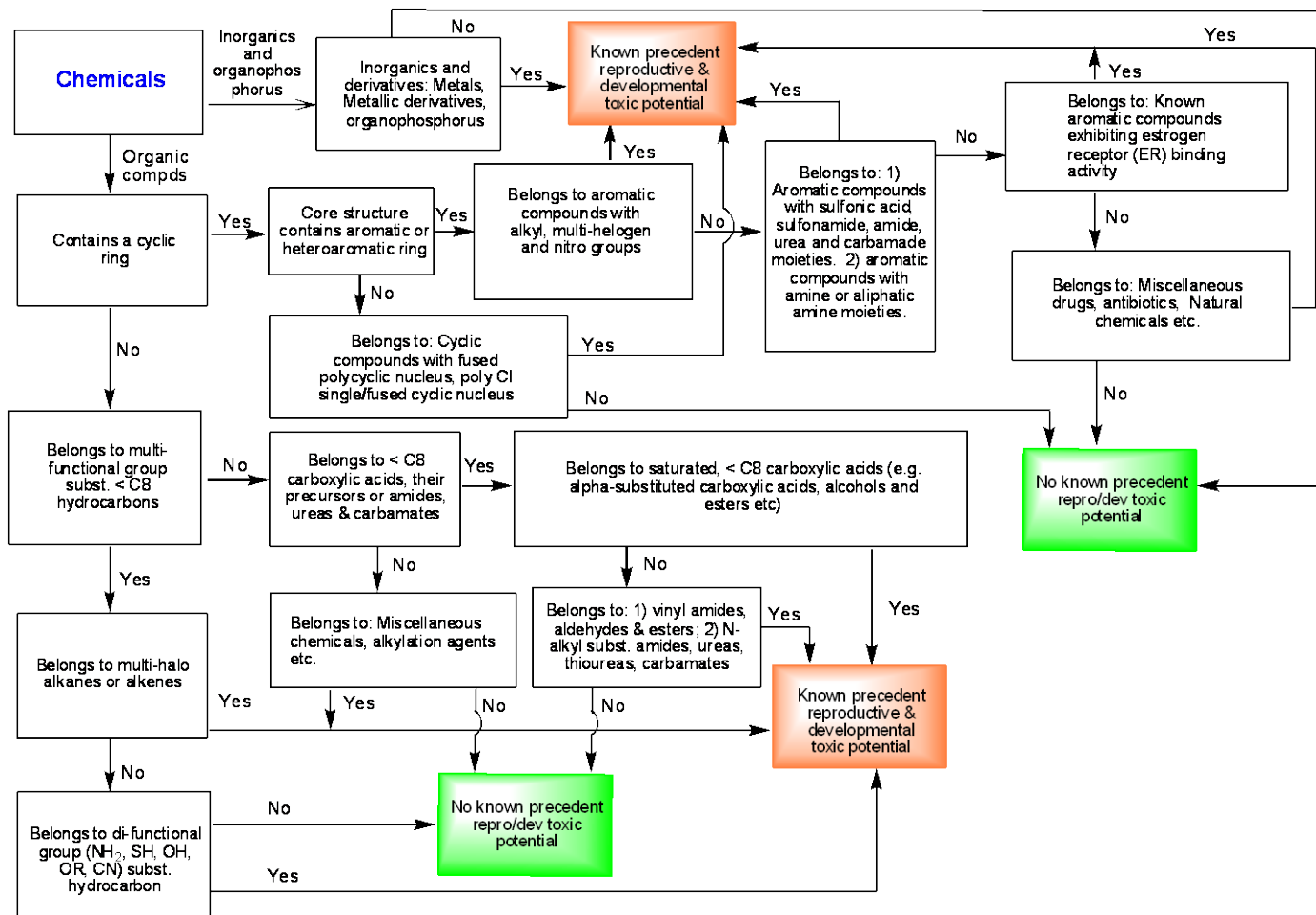
Cheminformatics: Ontology

- Use large database to organize chemicals into mode of action groupings
- Start to estimate the extent of “the universe of toxicity mechanisms”
- This will allow us to design a suite of model systems that is comprehensive

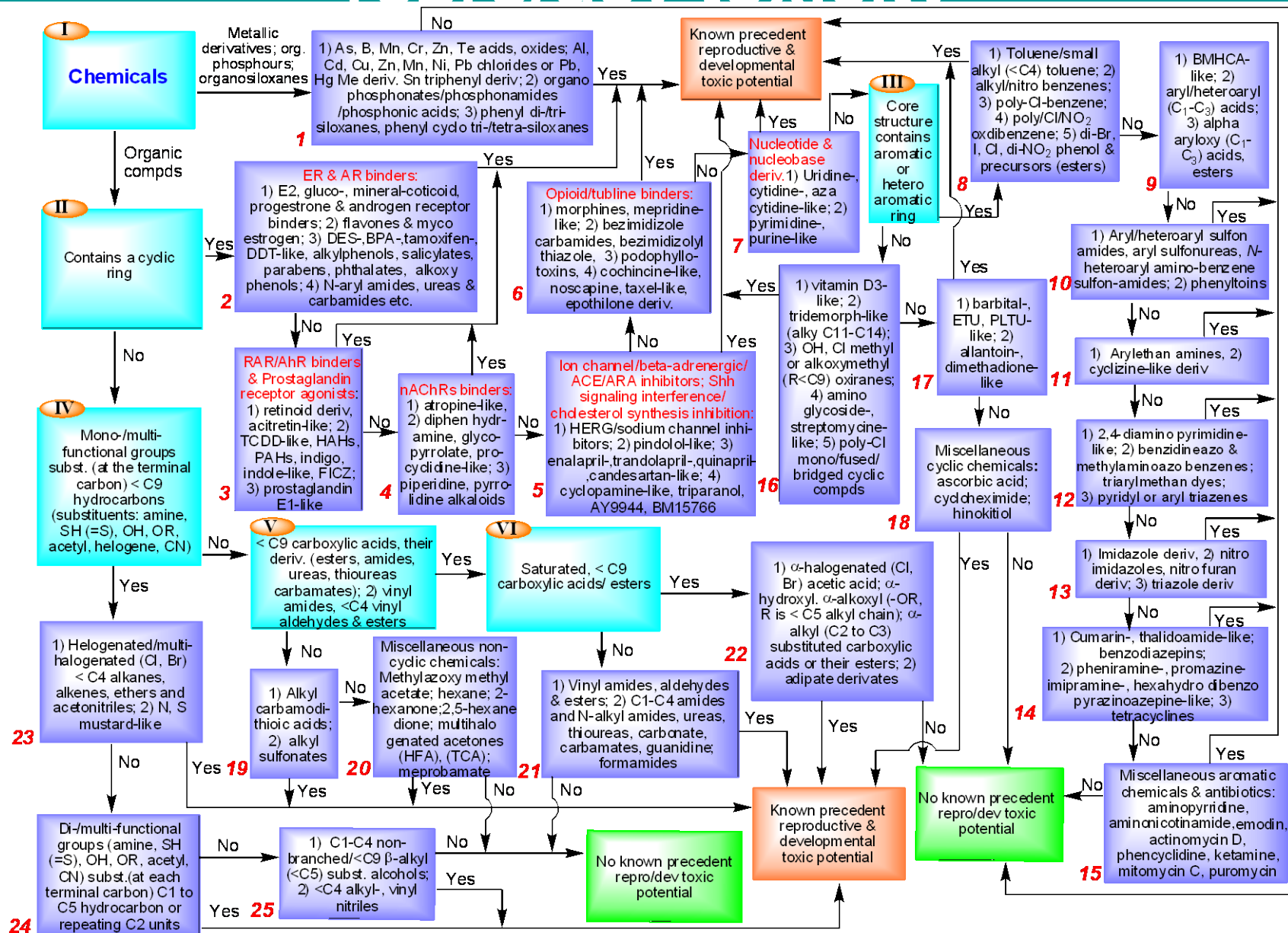
Initial Concept

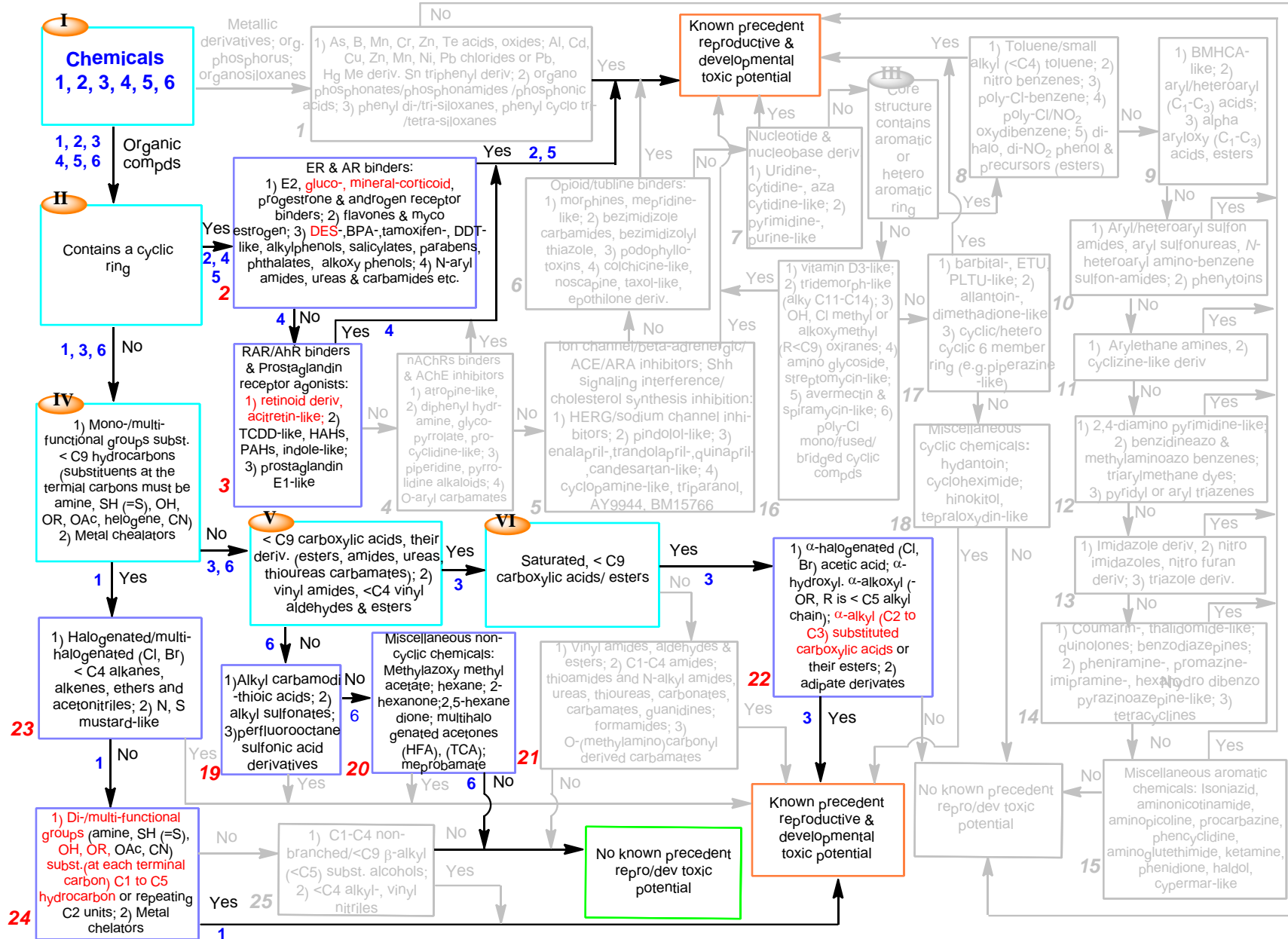
- An initial list of ~ 260 chemicals with DART data was originally developed as part of an evaluation of Threshold of Toxicologic Concern (TTC) (Laufersweiler et al., 2012)
- These chemicals were grouped based on their chemical characteristics and this tree was published in concept in Blackburn et al. (2011)

Original Tree

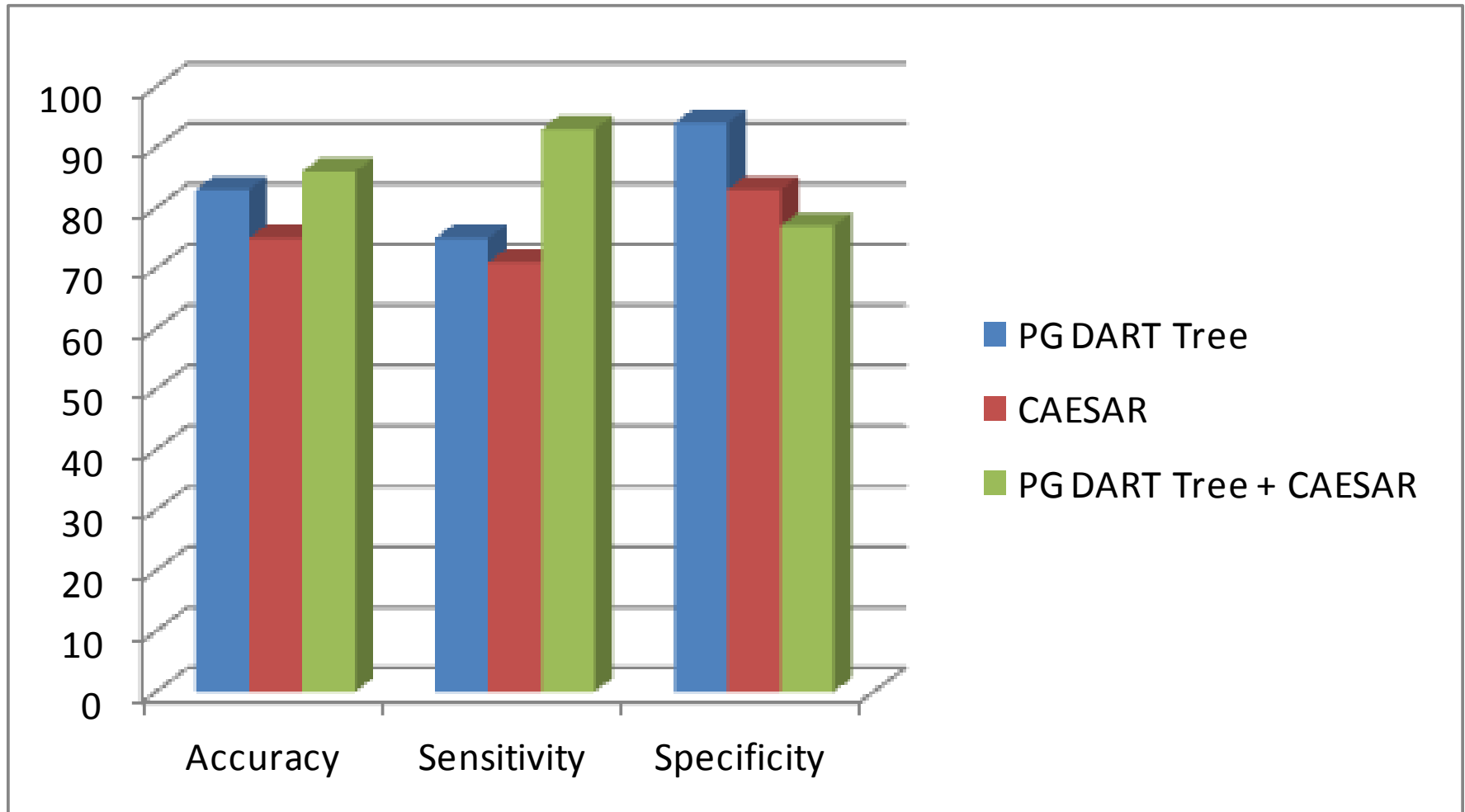


Expert system decision tree for repro/dev toxicity





P&G DART tree + CAESAR for test set (106 active, 73 non-active)



Accuracy: ~86%, Sensitivity: 93% and Specificity: 77%

Putative MOA Grouping by Chemical Structure

- 25 major categories, multiple sub-categories
- Highest level of confidence has
 - Similar structures
 - Identified molecular target
 - Similar DART outcome (e.g., common syndrome or highly specific effect)
- Along with toxicogenomics, has the potential to accelerate assigning MOA to DART compounds

Hierarchy Examples

- Nuclear hormone receptor ligands
- Prostaglandin receptor ligands
- Nicotinic ACh receptor ligands and AChesterase inhibitors
- Shh signaling interference/ cholesterol synthesis inhibitors
- Nucleotide derivatives

Nuclear Hormone Receptor Ligands

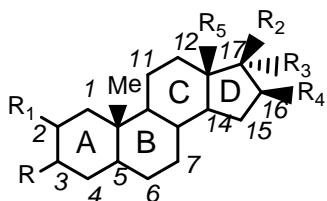
- Estrogen and androgen receptor ligands
- Glucocorticoid receptor ligands
- Retinoic acid receptor ligands
- Thyroid hormone receptor ligands
- Ah receptor ligands

Nuclear hormone receptor ligands

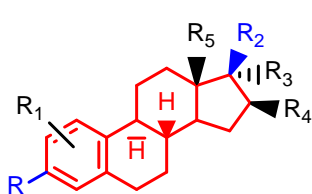
- Estrogen and androgen receptor ligands
 - steroid nucleus-derived compounds
 - Estradiol-like
 - Progesterone, androgens, steroidal anti-androgens
 - Non-steroidal compounds
 - Flavones and mycoestrogens
 - Alkylphenols
 - N-aryl-substituted ureas, carbamides, amides
 - other

Nuclear hormone receptor ligands

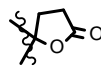
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$R = \text{OH, OMe}$
 $R_1 = \text{OH @ C-2 or C-4}$
 $R_2 = \text{OH}$
 $R_3 = \text{H, alkyne}$
 $R_4 = \text{H, OH}$
 $R_5 = \text{Me, H}$
 $17\text{-OH } (R_2, R_3) \text{ also can be C=O, H}$



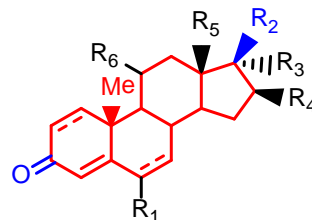
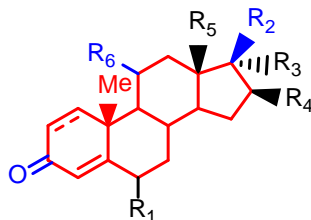
$R_1 = \text{H, F}$
 $R_2 = -\text{COCH}_2\text{OH, } -\text{COCH}_2\text{Cl}$
 $R_3 = \text{OH, CO, H}$
 $R_4 = \text{H, Me}$
 $R_2, R_3 \text{ can form}$



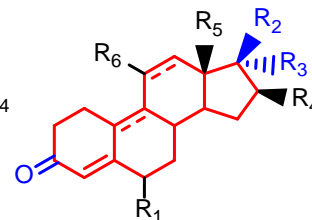
$R_3, R_4 \text{ can form an acetal/ketal}$
 $R_5 = \text{Me, } -\text{CHO}$
 $R_6 = \text{H, OH, } -\text{CO}$
 $\text{C-1, C-2 can be C=C/C-C bond}$
 $\text{C-3 contains H or OH - in very few cases.}$

Key functional groups:

$\text{C=O at C-3; } -\text{COCH}_2\text{OH}$
 $\text{and } -\text{COCH}_2\text{Cl at C-17;}$
 OH, C=O at C-11



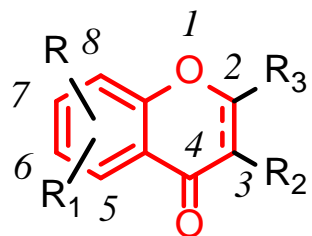
$R_1 = \text{H, Cl, Me}$
 $R_2 = -\text{COCH}_3$
 $R_3 = \text{OH, H, OCOCH}_3, \text{ OCOCH}_2\text{CH}_3$
 $R_4 = \text{H}$
 $R_5 = \text{Me}$
 $R_6 = \text{H}$
 $\text{C-1, C-2 and C-6, C-7 can be saturated/unsaturated}$
 $\text{C-1, C-2 can form cyclopropane}$
Key functional groups:
 $\text{C=O at C-3; } -\text{COCH}_3$
 $\text{and OH, OAc at C-17}$



$R_1 = \text{H}$
 $R_2 = \text{OH}$
 $R_3 = \text{H, Me, Et, ethyn or allyl, actonitrile etc.}$
 $R_4 = \text{H}$
 $R_5 = \text{Me, Et}$
 $R_6 = \text{H}$
 $\text{C-9, C-10 and C-11, C-12 can be C=C/C-C bond}$
Key functional groups:
 $\text{C=O at C-3; } -\text{OH}$
 $\text{and alkyl (C1-C3 carbons), ethyn at C-17}$

Nuclear hormone receptor ligands

- Estrogen and androgen receptor ligands
 - steroid nucleus-derived compounds
 - Estradiol-like
 - Progesterone, androgens, steroidal anti-androgens
 - Non-steroidal compounds
 - Flavones and mycoestrogens
 - Alkylphenols
 - N-aryl-substituted ureas, carbamides, amides
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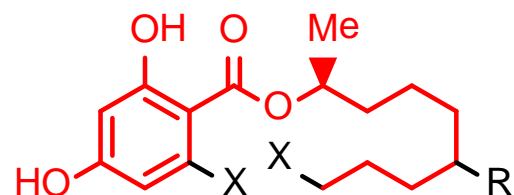


$R=OH, H; R_1=OH$

$R_2=\text{mono-, di-, tri-, OH-Ph, MeO-Ph}$

$R_3=\text{mono-, di-, tri-, OH-Ph}$

R_2 and R_3 can not be present
at C-2 and C-3 simultaneously

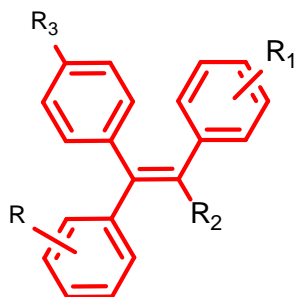


$R=OH, =O$

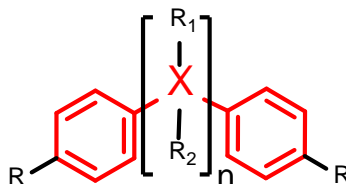
$X-X=C-C, C=C$

Nuclear hormone receptor ligands

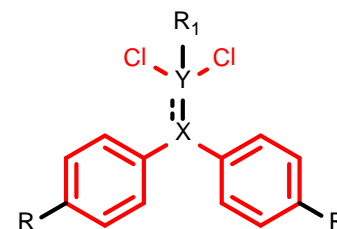
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 - Flavones and mycoestrogens
 - Alkylphenols
 - N-aryl-substituted ureas, carbamides, amides
 - other



$R = H, 4-OH$
 $R_1 = H, OMe$
 $R_2 = Cl, Me, Et$
 $R_3 = H, (Me)_2CH_2CH_2O-$



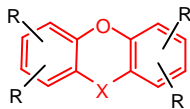
$R = OH, NH_2$
 $n = 1, X = C, R_1 = \text{Alkyl (C1-C4)}$
 $R_2 = Me$
 $R_1, R_2 = \text{isobenzofuranone}$
 $n = 2, R_1 \text{ and } R_2 \text{ are on different C's}$
 $n = 2, X = C-C, R_1, R_2 = H, Me, Et$
 $n = 2, X = C=C, R_1, R_2 = H, Me, Et$
 $n = 1, X = O, S, SO_2, R_1 = R_2 = \text{none}$



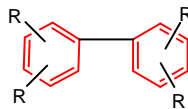
$X-Y = C-C$
 $R = OH, Cl, OMe$
 $R_1 = H, Cl$
 $X-Y = C=C$
 $R = OH, Cl, OMe$
 $R_1 = \text{none}$

Ah Receptor Ligands

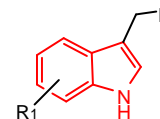
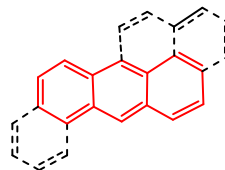
- TCDD-like chemicals
 - cleft palate, hydronephrosis and reproductive system defects
- Indole-related compounds: repro system
- Polycyclic aromatics
- Halogenated aromatics (e.g., PCBs)
 - Liver cyp induction leads to DART effects?



R=Cl, Br
X=O, none



R=Cl, Br



R=OH
R₁=H

Problems with the chemical approach

- Promiscuous chemicals that have more than one molecular target
- Seemingly similar compounds that have different developmental outcome
 - PK differences?
 - More than one target?
 - Insufficient potency against target?

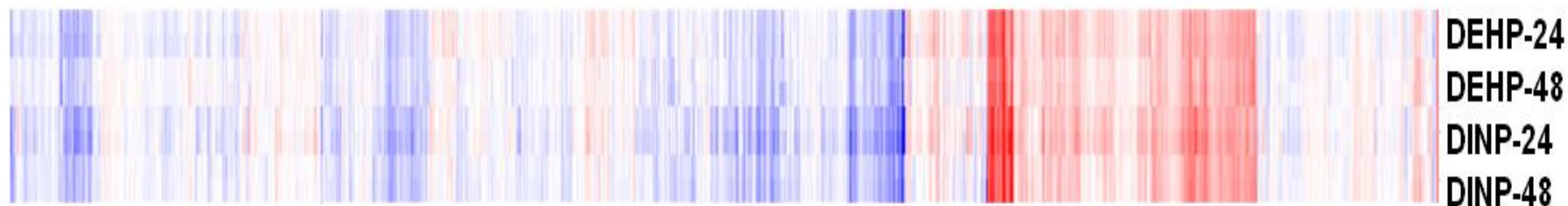
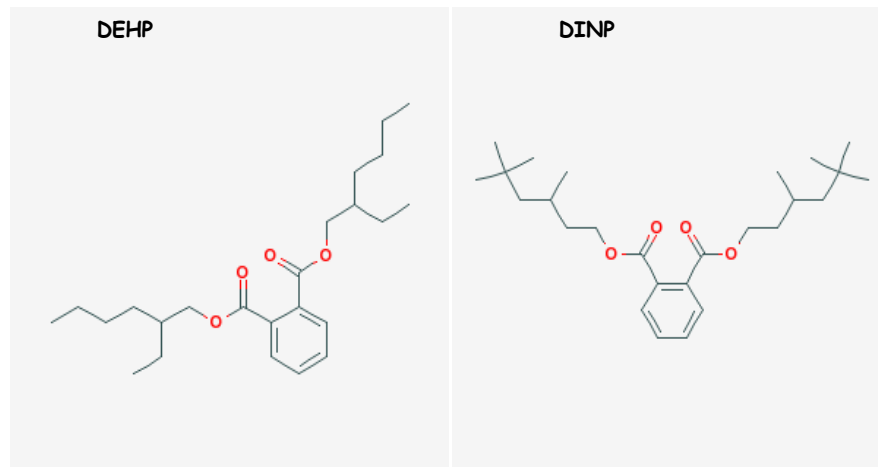
Outcome of chemistry assessment is hypothesis generation

- Chemical is metabolized to a tested chemical, or to a known active metabolite
 - Currently, assessment is done by wet lab metabolism
- Chemical is sufficiently similar in structure to analogs of known toxicity that similar biological activity is inferred
 - Currently, assessment is done by MOA-specific evaluation
 - Add ToxCast and other PubChem data to our databases and our expert considerations about mechanism
 - Global analysis of gene expression

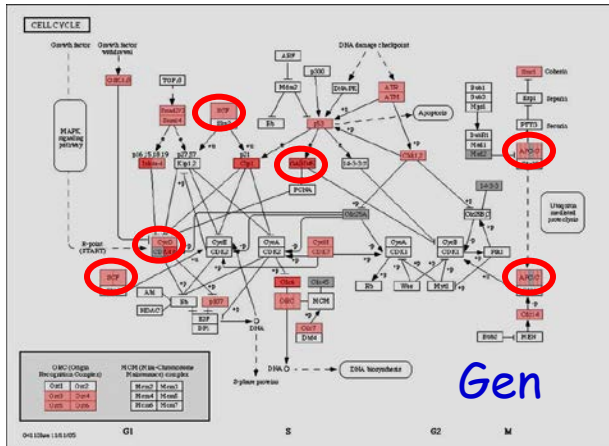
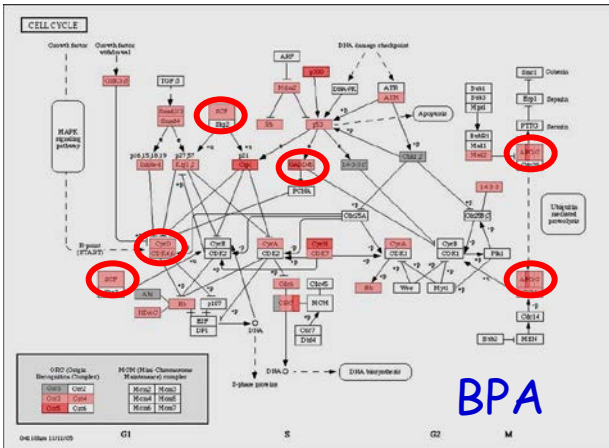
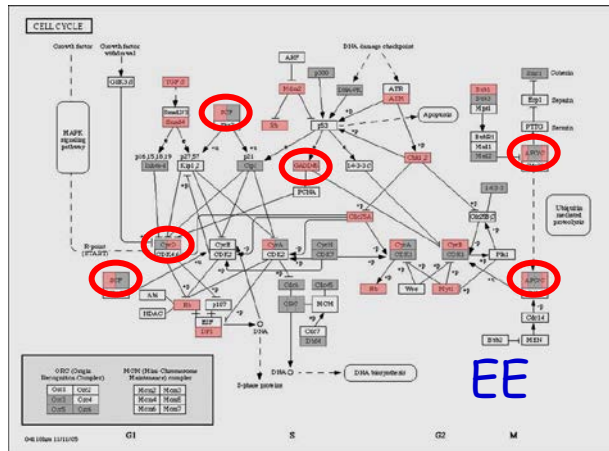
Using Gene Expression Analysis to Inform MOA and AOP

- Gene expression is specific for MOA
- In vitro models may have great potential to identify MOA via gene expression

Two Close Structural Analogs



KEGG Cell cycle Example



Connectivity Mapping: High-throughput toxicogenomics

- Concept developed by Lamb in 2006
 - A relatively small number of carefully selected cell types contained all of the pathways necessary to define gene expression profiles for all therapeutic agents in current use
- Can we do the same for toxicants?
 - Cell types: rich in either small molecule receptors or metabolizing enzymes

MOAs to Interrogate with CMAP

- Estrogens, environmental estrogens
- Anti-estrogens
- PPAR agonists
- Anti AndrogenAndrogens
- CAR/PXR agonists
- RAR agonists
- TR agonists
- AhR agonists
- Vitamin D agonist
- Glucocorticoid receptor agonists
- EGFR receptor agonists
- FXR receptor agonists
- Progesterone receptor agonists
- EGFR antagonist
- Steroid synthesis inhibitors
- HDAC inhibitors
- Folate/one-carbon metabolism inhibitor
- Glycolytic inhibitors
- Oxidative phos/mitochondrial inhibitors
- Iron chelators
- Microtubule inhibitors
- Liver cholestasis inducers

Genes Significantly Changed

Chemical	MCF7	Ishikawa	HepG2
Bisphenol A	76	5262	9247
Trenbolone	188	18	3
methotrexate	3296	16	5376
vorinostat	17342	19432	21798
RU486	106	4	22
Vitamin D3	519	93	2
Amoxicillin	6	29	810

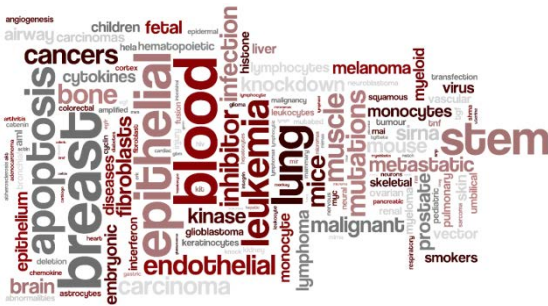
Connectivity Mapping: Example

Bisphenol A comparisons

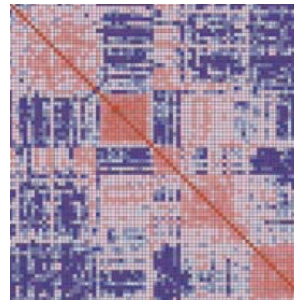
DES
resveratrol
epitiostanol
equilin
genistein
genistein
estrone
genistein
estradiol
levonorgestrel
resveratrol
equilin

landmark genes

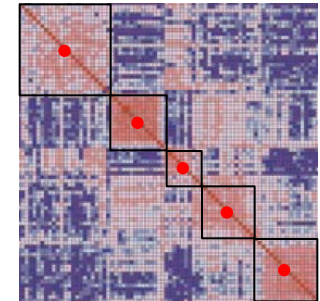
- **expression of 978 *landmark* genes measured**
 - selected from large, diverse, high-quality microarray dataset
 - orthogonal expression and validated predictive power
- **inputs for genome-wide inference model**
 - compute expression of transcripts not explicitly measured
 - flagged as *LM* (rather than *INF*) in output data file



>100,000 Affy U133 scans



gene gene correlation

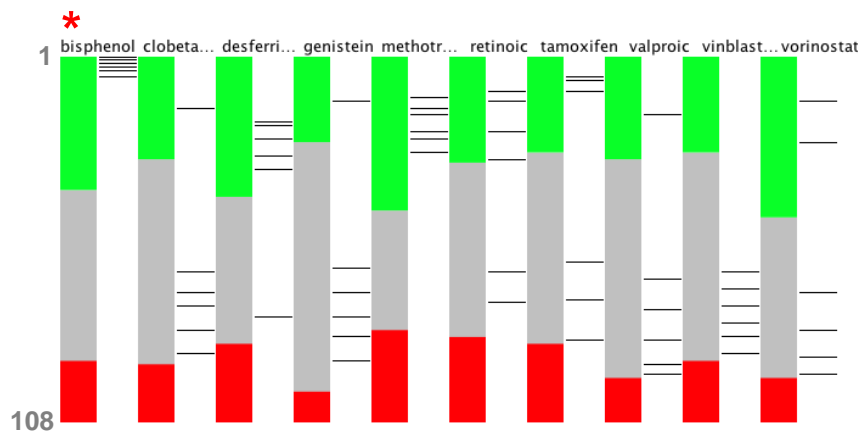


landmarks

AFFX *versus* L1000

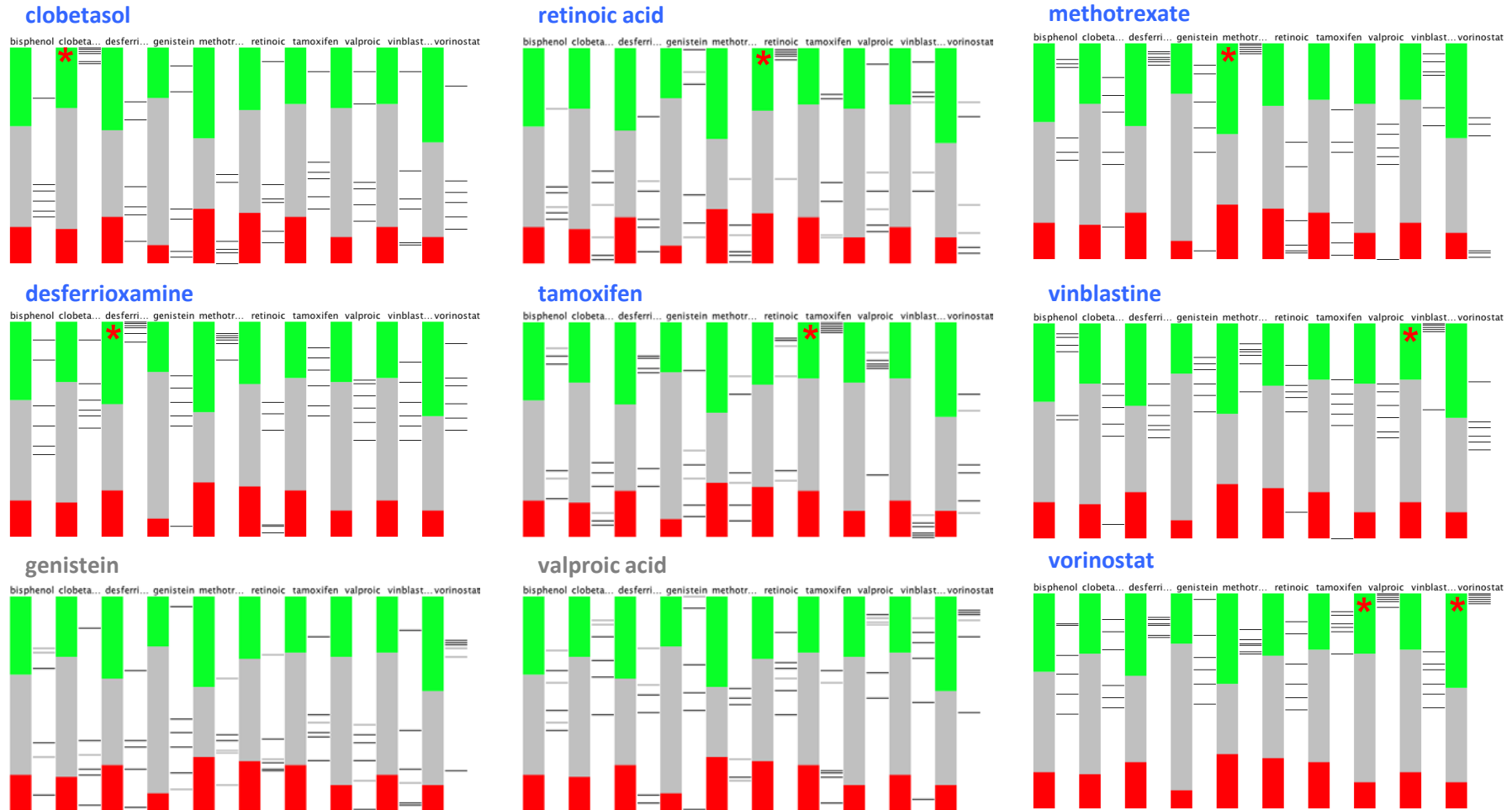
- create *signatures* for each treatment from AFFX data
 - treatment (n=1) *versus* corresponding vehicle control (n=1)
 - 50 up- and 50 down- regulated genes by signal-to-noise
- create *instances* for each treatment from L1000 data
 - rank all features by extent of differential expression
 - treatment compared with matched control sample
- compute enrichment of each signature in each instance
 - rank instances based on these connectivity scores
 - AFFX signature finds expected L1000 instances in 9 of 10 tests

signature: bisphenol A



AFFX *versus* L1000

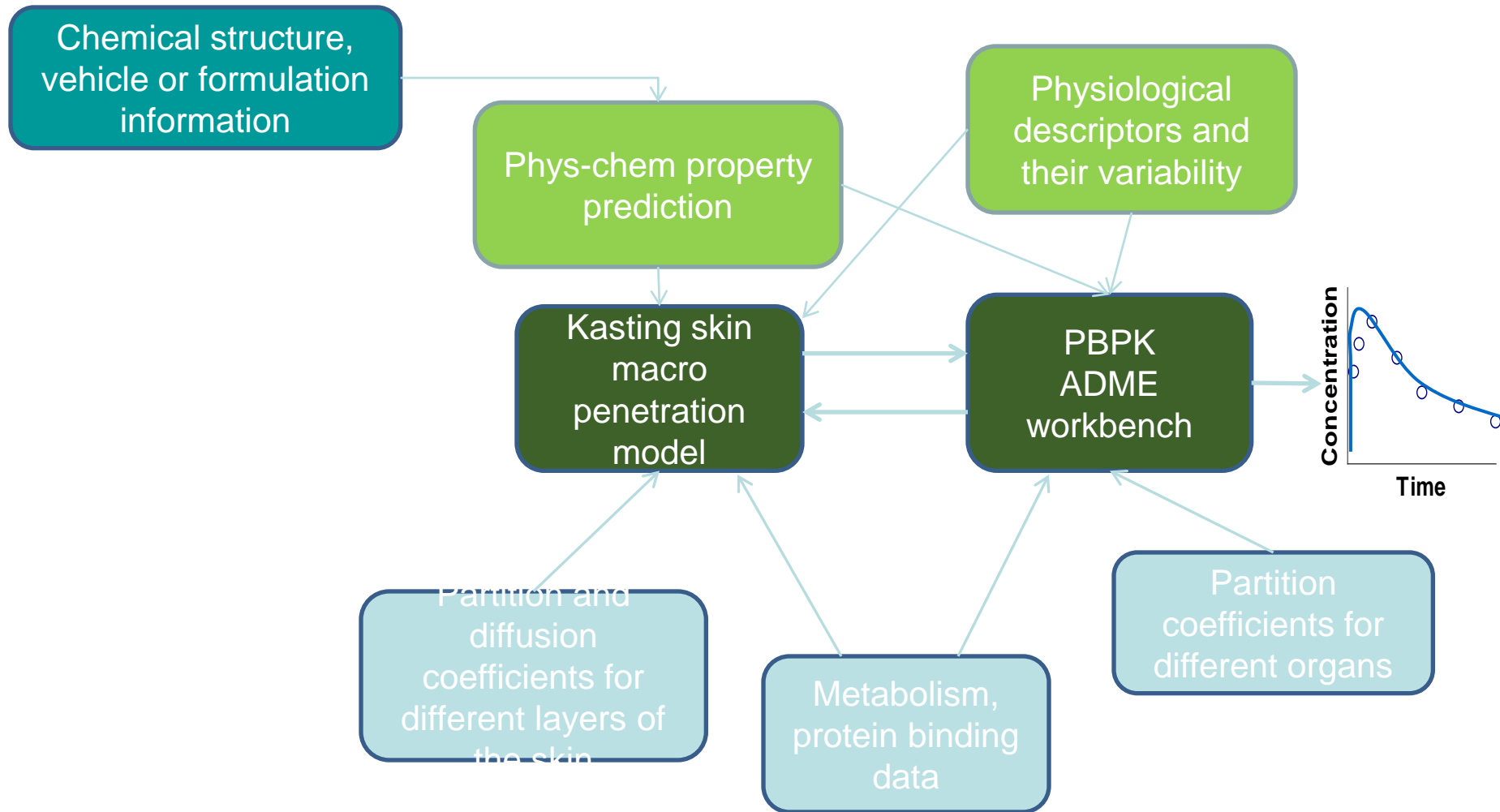
rankings of L1000 *instances* of each treatment with specified AFFX *signature*



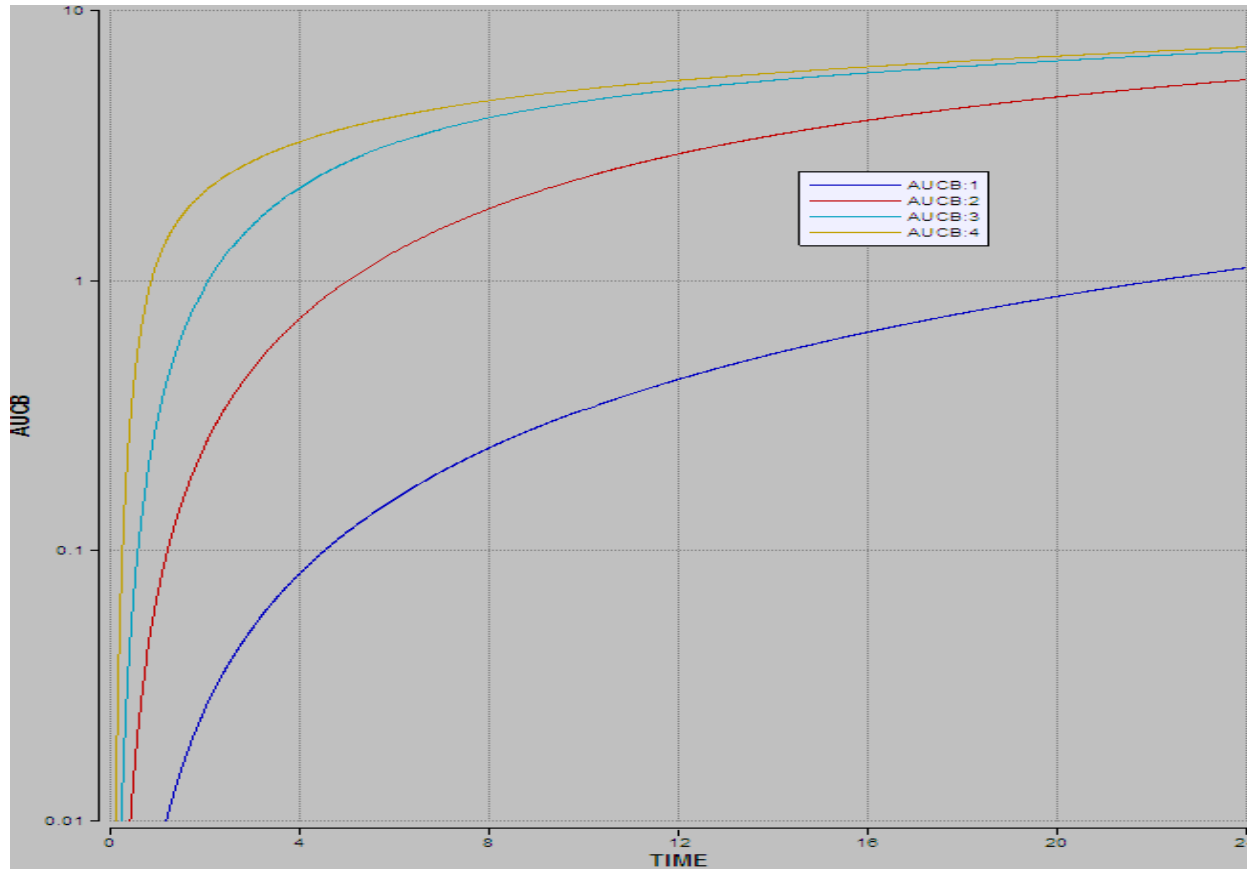
Modeling PK to Ensure the Right In Vitro Concentration

- Dose matters: data obtained in vitro at irrelevant concentrations is also irrelevant in predicting risk
- Active concentrations at the target tissue in vivo are predictable

PK workflow



Modeling AUC for a Range of Absorption Values



Conclusions

- Chemical ontology can aid in assigning chemicals to groups with same putative MOA
- It is possible to estimate the size of the MOA universe
- Linking initial molecular event with outcome will require considerable hypothesis testing, aided by gene expression data, modeling and simulation
- It is already possible to estimate tissue dose using computation, phys chem parameter estimation, and judicious data generation

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