

Consensus Modeling in Support of a Semi-Automated Read-Across Application

Richard Judson
U.S. EPA, National Center for Computational Toxicology
Office of Research and Development



SOT 2016, New Orleans

March 17, 2016

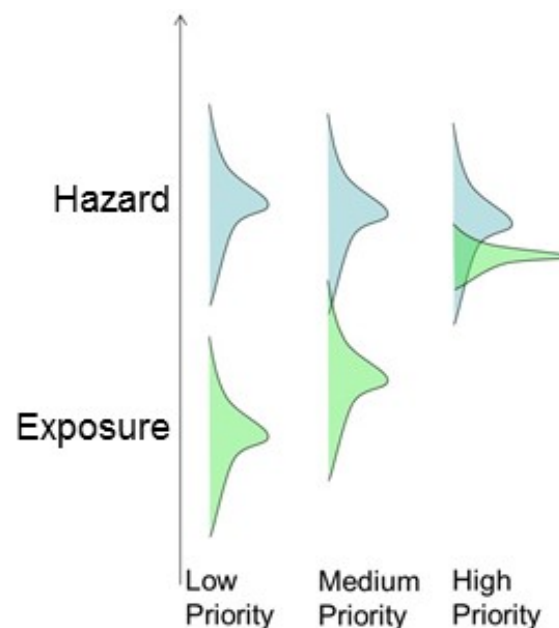
Problem Statement

- Too many chemicals, too little data
 - There are tens of thousands of man-made chemicals in the environment, and few of them are thoroughly tested for potential toxicity
- Need to use data-gap-filling methods / models
 - Read-across, QSAR, QBAR, systems models
- All data and models are subject to errors, uncertainty and noise
- Need to develop methods to manage these issues

Key Points

- Goal is to build predictive models in the presence of noisy data
- Recognize and quantify uncertainty
- Build models on the best (most reproducible) data
- Combine multiple imperfect models together (consensus)
- Build local models where possible

Never despair:
You may not know much but
you never know nothing



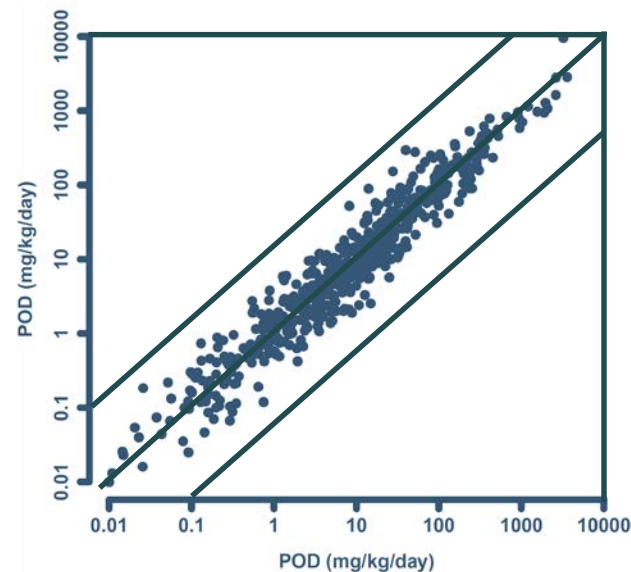
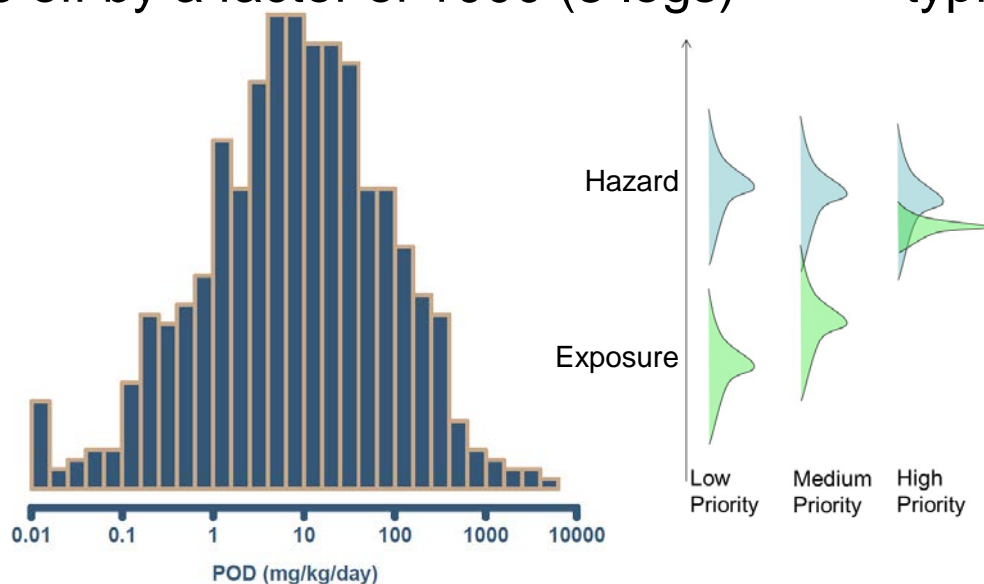
What are the limits on predictivity?

Example using predictions of PODs

Quantify
uncertainty

Worst case: Predict the mean of all chemicals – at worst a prediction will be off by a factor of 1000 (3 logs)

Best case: RMSE cannot be better on average than 0.3 log units due to typical wide dose spacing



Case Study: Endocrine Disruption

- EPA has to test ~10,000 chemicals in the EDSP
 - Tier 1 battery can run at ~50/year at \$1M/chemical
 - 100+ years, billions of dollars
 - Even the tier 1 guideline studies are imperfect
- Proposed approach is to use a combination of methods
 - Tier 1, in vivo read-across, HTS, in vitro-based models, QSAR
 - Combine staged replacement of tests with prioritization
 - But the new approaches are also imperfect
- Today focus on estrogen receptor activity

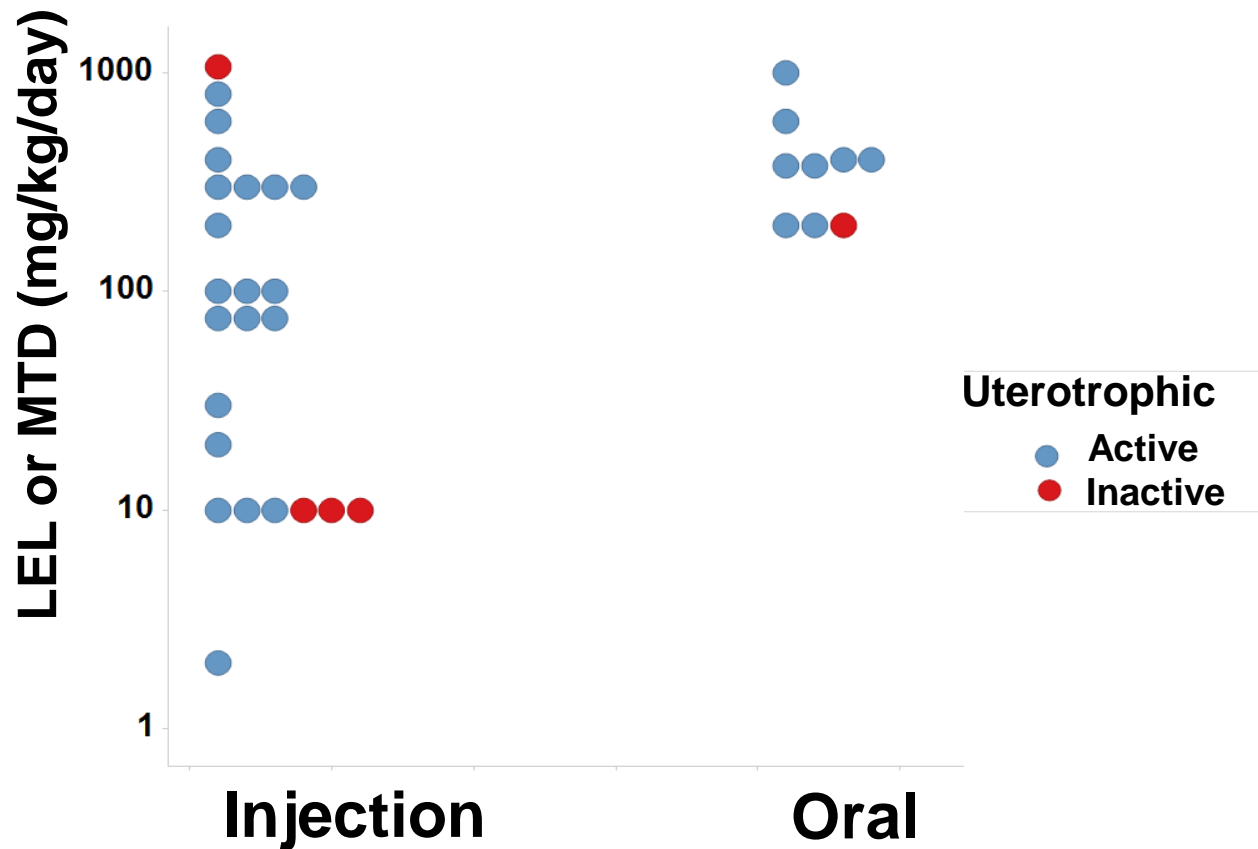
Quantify
uncertainty

Consensus
Model

In vivo guideline study uncertainty

26% of chemicals tested multiple times in the
uterotrophic assay gave discrepant results

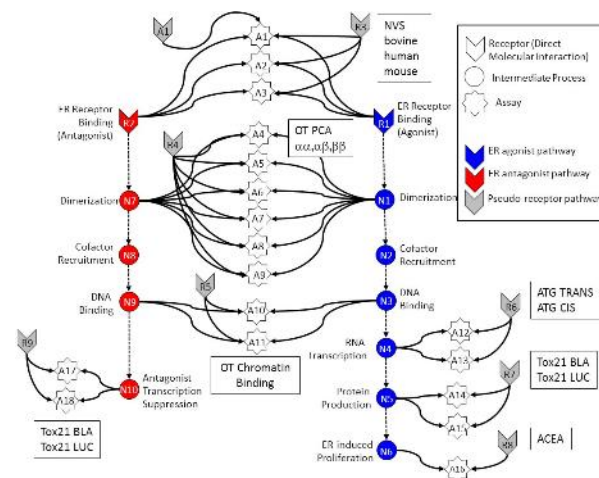
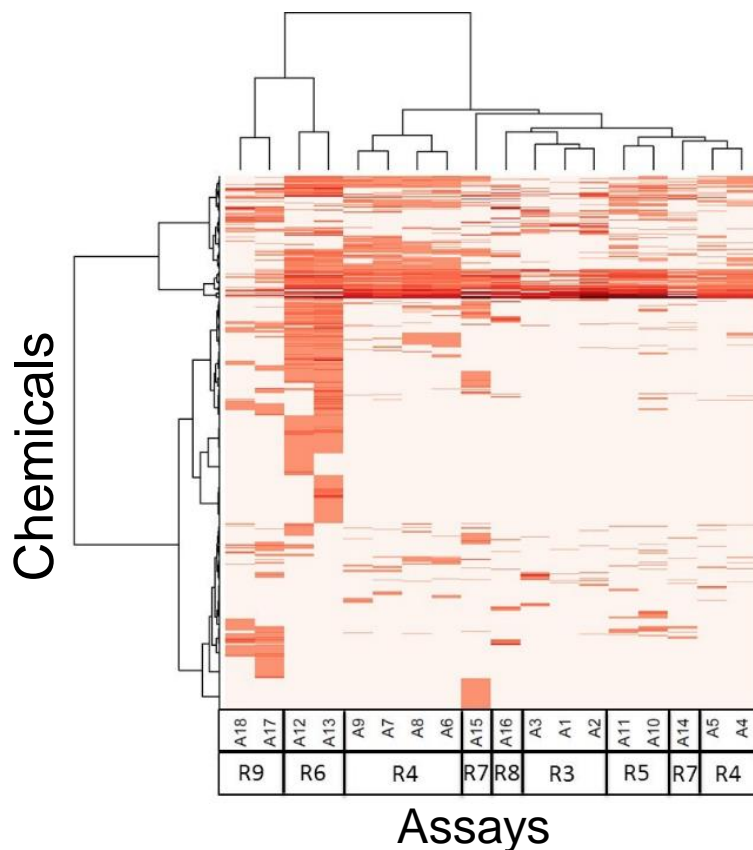
Immature Rat: BPA



Much of this “noise” is reproducible

- “assay interference”
- Result of interaction of chemical with complex biology in the assay

- Solvents
- Surfactants
- Intentionally cytotoxic compounds
- Metals
- Inorganics
- Pesticides
- Drugs



Assay-to-assay variation

Quantify
uncertainty

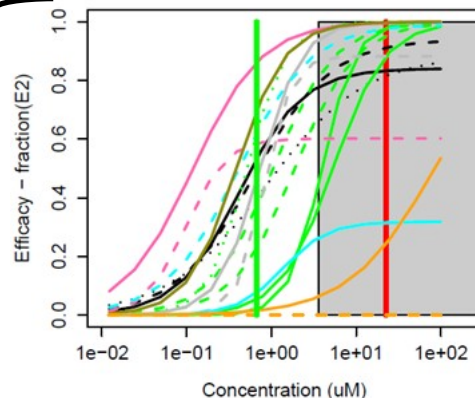
Consensus
Model

All appropriate
assays are active
but efficacy and
potency vary

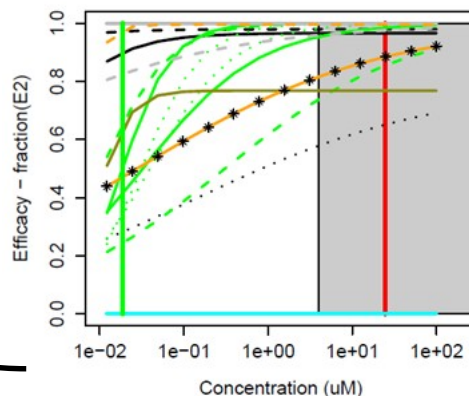
“Noise” or real
variation in biology
between cell types?

Assay Data

80-05-7 : Bisphenol A

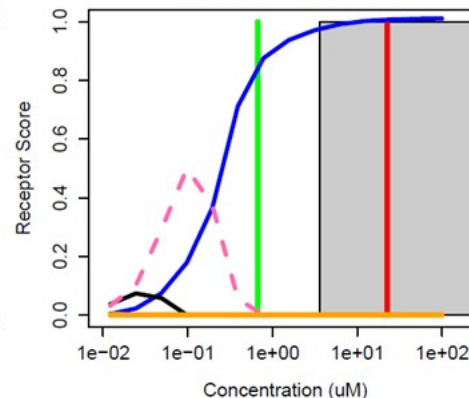


82640-04-8 : Raloxifene hydrochloride



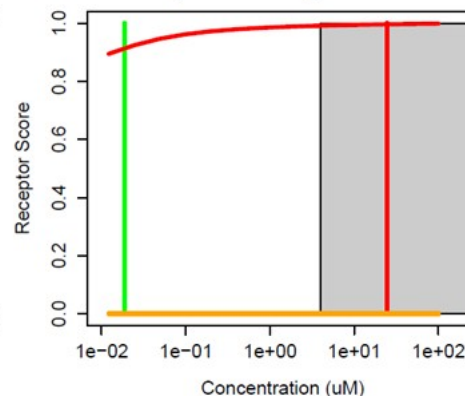
Integrated Model

80-05-7 : Bisphenol A
Agonist: 0.65 Antagonist: 0



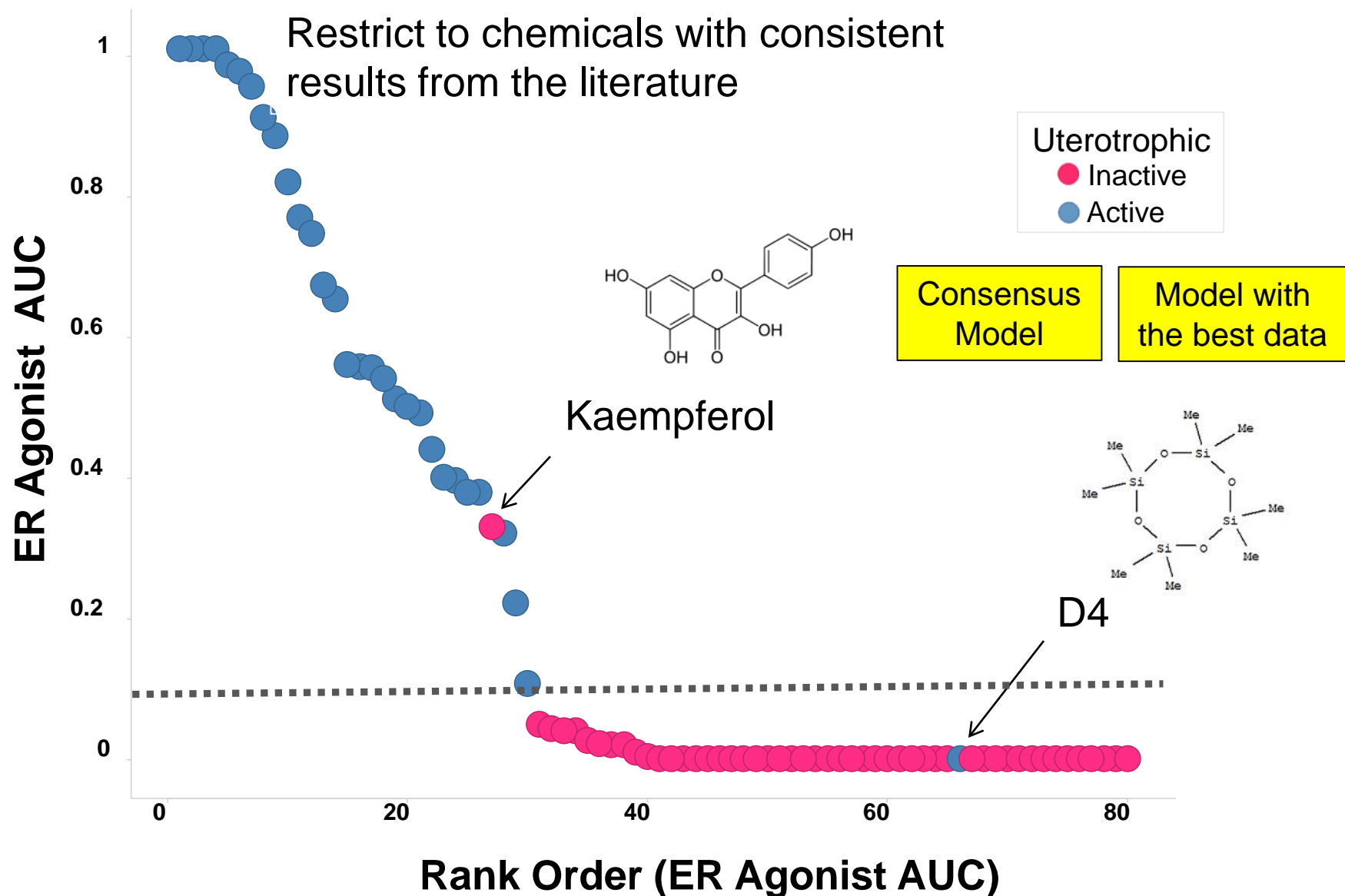
Agonist

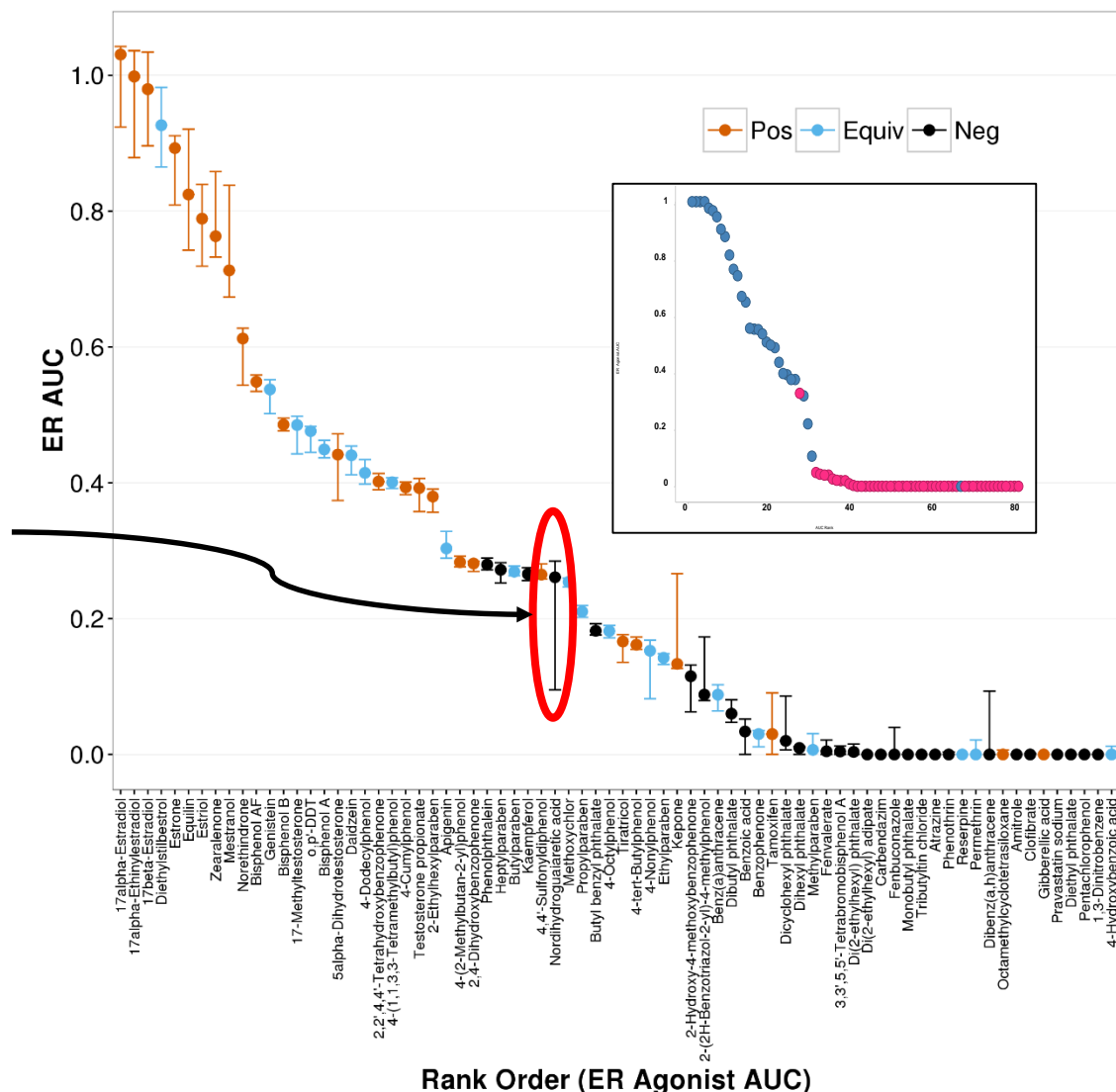
82640-04-8 : Raloxifene hydrochloride
Agonist: 0 Antagonist: 0.97



Antagonist

Model also predicts *in vivo* uterotrophic assay as well as uterotrophic predicts uterotrophic





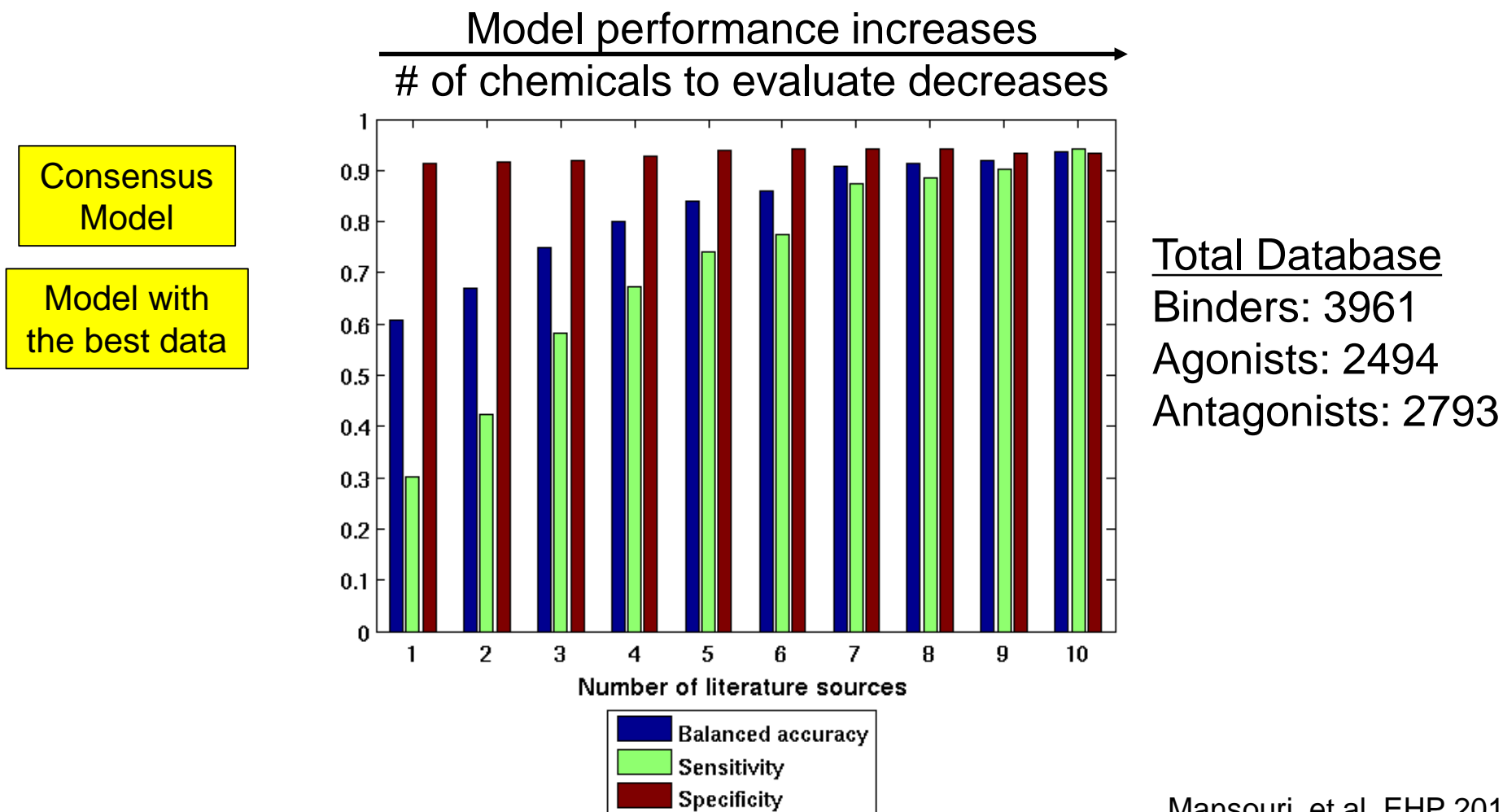
- Collaborative Estrogen Receptor Activity Prediction Project
- Goals:
 - Use ToxCast ER score (or other data) to build many QSAR models
 - Use consensus of models to prioritize chemicals for further testing
- Assumptions
 - ToxCast chemicals cover enough of chemical space to be a good “**global**” training set
 - Consensus of many models will be better than any one individually
- Process
 - Curate chemical structures
 - Curate literature data set
 - Build many models
 - Build consensus model
 - Evaluate models and consensus

Consensus
Model

Model with
the best data

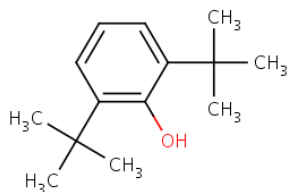
Consensus of models and data helps QSAR model accuracy

Key point: As greater consistency is required from literature sources, model performance improves

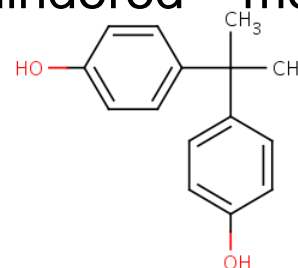


Issue with global models: Phenols are mostly predicted positive

Hindered – mostly inactive

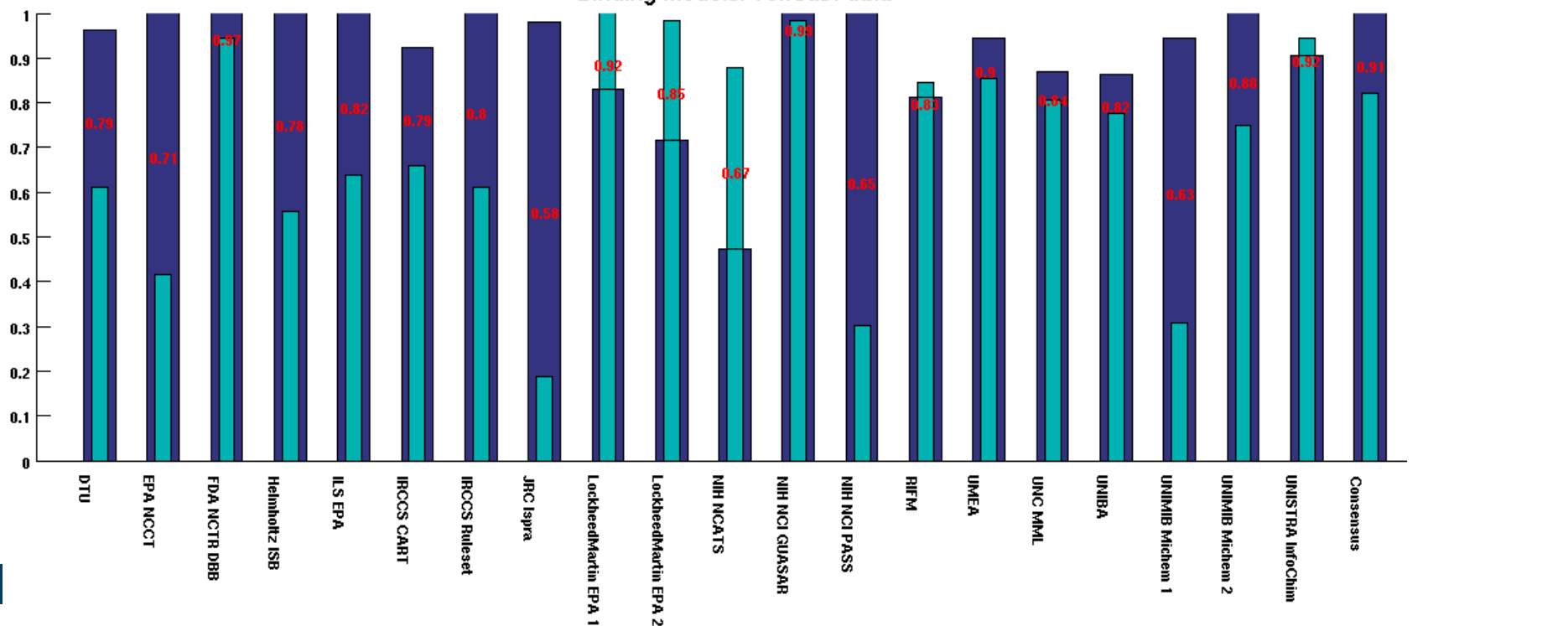


Non-hindered – mostly active



Build Local
Models

Binding models. ToxCast data



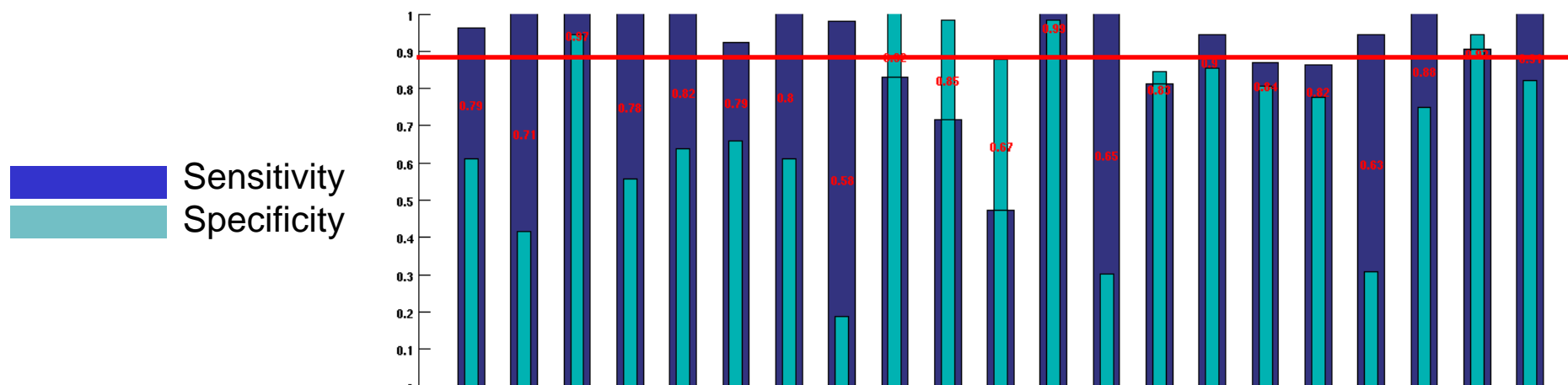
By building a local QSAR model, we can improve local accuracy

PLSDA model: 30 Descriptors, 3 Latent variables

Build Local
Models

Local model has better
balanced accuracy than 17/21
global models and about same
as global consensus

	Training set (483)		Test set (120)
	Calibration	5-Fold CV	validation
SN	0.89	0.88	0.91
SP	0.86	0.85	0.88
BA	0.88	0.87	0.89



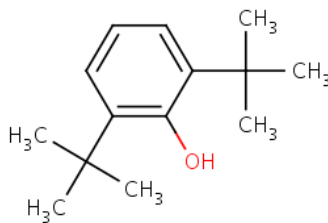
I'm finally getting to read-across!

- Need to focus locally in chemistry and bioactivity
 - Phenols / estrogen
- Need to be conscious of messiness of training and test data
 - All assays are noisy
 - And there is real biological variations between cell types, etc.
- Need to have a goal
 - Can read-across beat a “thoughtless” QSAR model?

Build Local
Models

HINDERED PHENOL CASE STUDY - Health Canada and US EPA

Hindered phenols are phenols with one or more bulky functional groups ortho to the hydroxyl group.



Build Local
Models

Goal: Risk assessment and categorization of 21 Hindered Phenols (HP) under the Chemicals Management Plan. One of the issues is to investigate whether particular HPs have the potential to be estrogenic or not, and if so, their relative potency using read-across and/or (Q)SAR methods.

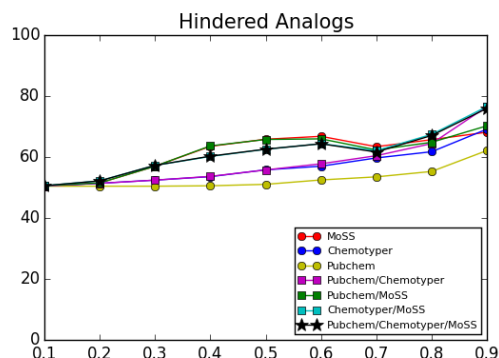
READ-ACROSS PREDICTIONS

Build Local
Models

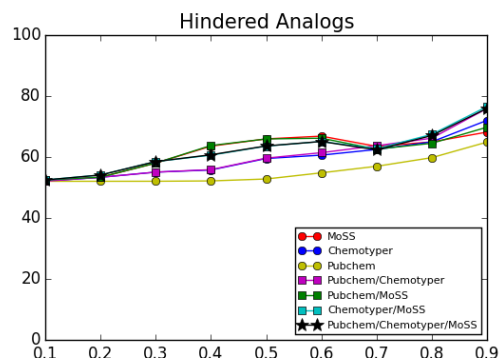
Model with
the best data

Accuracy increases as

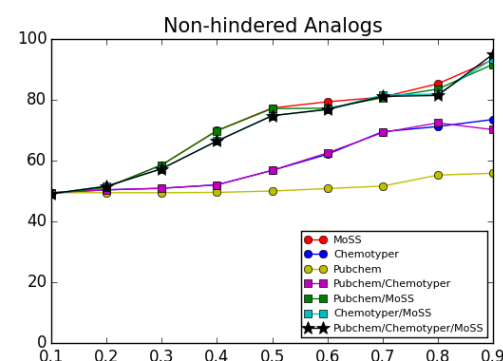
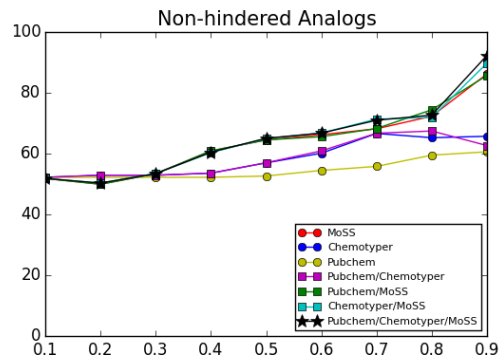
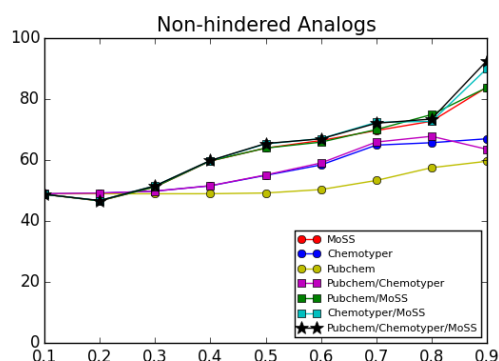
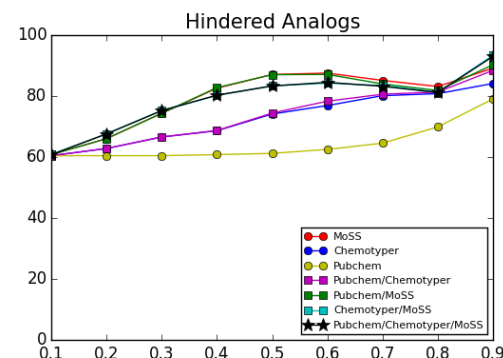
1. Better data is used in the evaluation
2. Neighbors are closer (structure and physchem)



Filtering 1 (Log P_{kow} & MV)



Filtering 2 (No. of Literature Sources ≥ 3)



- Goal: To make ER and AR data easily available to all stakeholders
 - Assay-by-assays concentration-response plots
 - Model scores – AUC agonist and antagonist
 - ER QSAR calls
 - Other relevant data
- <http://actor.epa.gov/edsp21>

The screenshot displays the EDSP21 Dashboard interface. On the left, a sidebar shows 'Chemical Selection' with a search bar and a list of chemicals, including Bisphenol A. The main panel is titled 'EDSP21 Dashboard' and 'Endocrine Disruption Screening Program for the 21st Century'. It features a 'Chemical Structure and Data' section with a chemical structure of Bisphenol A and a table of properties. Below this is a 'PhysChem Properties' table.

Property	Model Name	Raw Result	Result (Mean)	Result (min)	Result (max)	Result Unit
Source: Alfa Aesar (4 Results)						
Source: EPI SURTE (126 Results)						
Source: J and K Scientific (1 Result)						
Source: Jean-Claude Bradley Open Melting Point Dataset (2 Results)						
Source: Merck Millipore (1 Result)						
Source: QikProp (51 Results)						
Source: TCI (3 Results)						

ToxCast Model Predictions		
Model	Agonist AUC	Antagonist AUC
ER	0.45	0
AR	0	0.136

Consensus CERAPP QSAR ER Model Predictions			
Class	Agonist (Potency Level)	Antagonist (Potency Level)	Binding (Potency Level)
from Literature	Active (Weak)	-	Active (Weak)
QSAR Consensus	Active (Weak)	Active (Strong)	Active (Weak)

Summary

- Goal is to build predictive models in the presence of noisy data
- Recognize and quantify uncertainty
- Build models on the best (most reproducible) data
- Combine multiple imperfect models together (consensus)
- Build local models where possible

Acknowledgements

Kamel Mansouri
Nicole Kleinstreuer
Eric Watt
Prachi Pradeep
Patience Browne
Grace Patlewicz
Imran Shah

NCCT Staff Scientists

Rusty Thomas
Kevin Crofton
Keith Houck
Ann Richard
Richard Judson
Tom Knudsen
Matt Martin
Grace Patlewicz
Woody Setzer
John Wambaugh
Tony Williams
Steve Simmons
Chris Grulke
Jim Rabinowitz

NCCT

Nancy Baker
Jeff Edwards
Dayne Filer
Parth Kothiya
Doris Smith
Jamey Vail
Sean Watford
Indira Thillainadarajah

NCCT Postdocs

Todor Antonijevic
Audrey Bone
Kristin Connors
Danica DeGroot
Jeremy Fitzpatrick
Jason Harris
Dustin Kapraun
Agnes Karmaus
Max Leung
Kamel Mansouri
LyLy Pham
Prachi Pradeep
Caroline Ring
Eric Watt



NIH/NCATS

Menghang Xia
Ruili Huang
Anton Simeonov

NTP

Warren Casey
Nicole Kleinstreuer
Mike Devito
Dan Zang