

Toxicological Tipping Points

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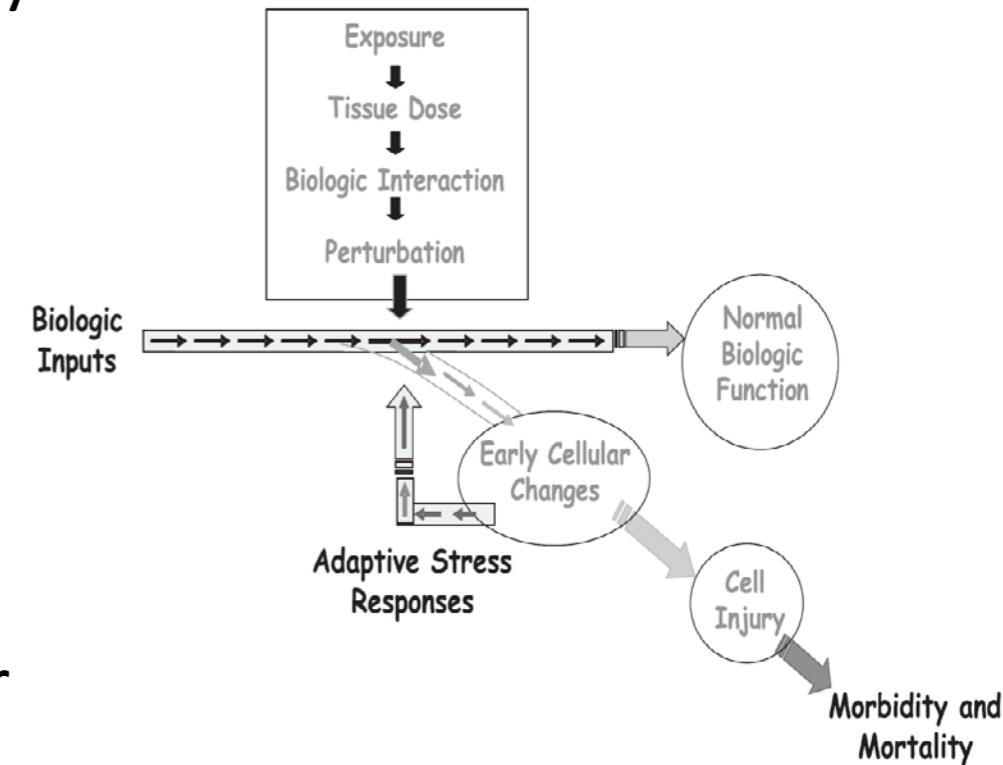
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National Toxicology Program
Laboratory Seminar Series

The views expressed in this presentation are those of the author[s] and do not necessarily reflect the views or policies of the U.S. Environmental Protection Agency.

Toxicological Tipping Points ...

- ❑ Current toxicological tests use apical *in vivo* adversity to define a point of departure (PoD) for risk assessment
- ❑ Biological systems are resilient and adapt to environmental perturbations
- ❑ Threshold between adaptation and adversity:
Tipping point
- ❑ Toxicological tipping points could be used as PoD for risk assessment
- ❑ ***How can we use high-content imaging (HCI) data to find tipping points ?***



Krewski, Daniel, Daniel Acosta Jr, Melvin Andersen, Henry Anderson, John C Bailar 3rd, Kim Boekelheide, Robert Brent, et al. "Toxicity Testing in the 21st Century: a Vision and a Strategy." *Journal of Toxicology and Environmental Health. Part B, Critical Reviews* 13, no. 2–4 (February 2010): 51–138.

High Content Imaging (HCI)

□ Study

- HepG2 cell culture
- 967 chemicals (ToxCast)
- 10 conc (0.1, 3 times)

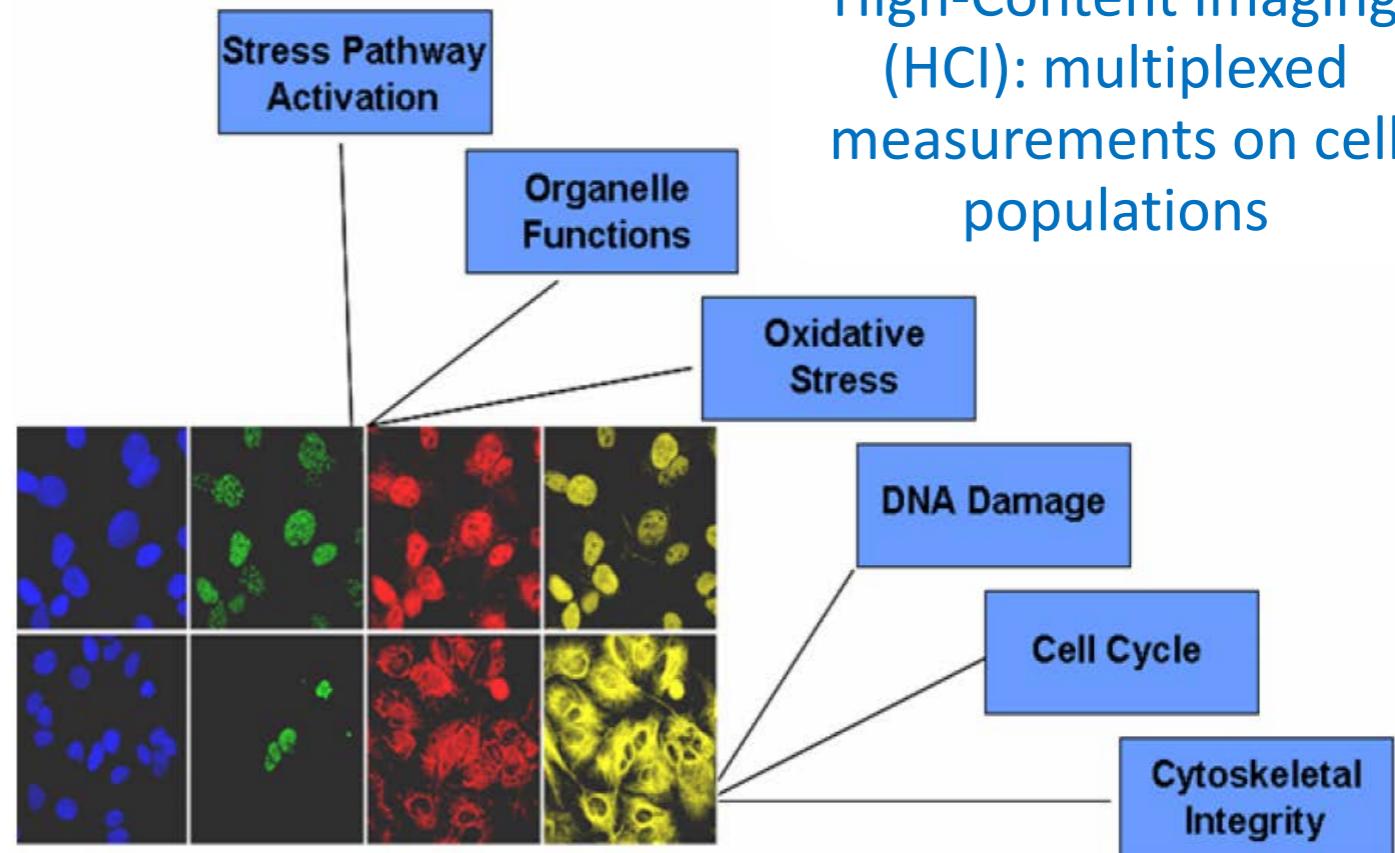
□ HCI Assays

- Health
- Stress
- Cellular perturbations

□ Dynamic phenotypic response of cells to chemicals

□ Large-scale data

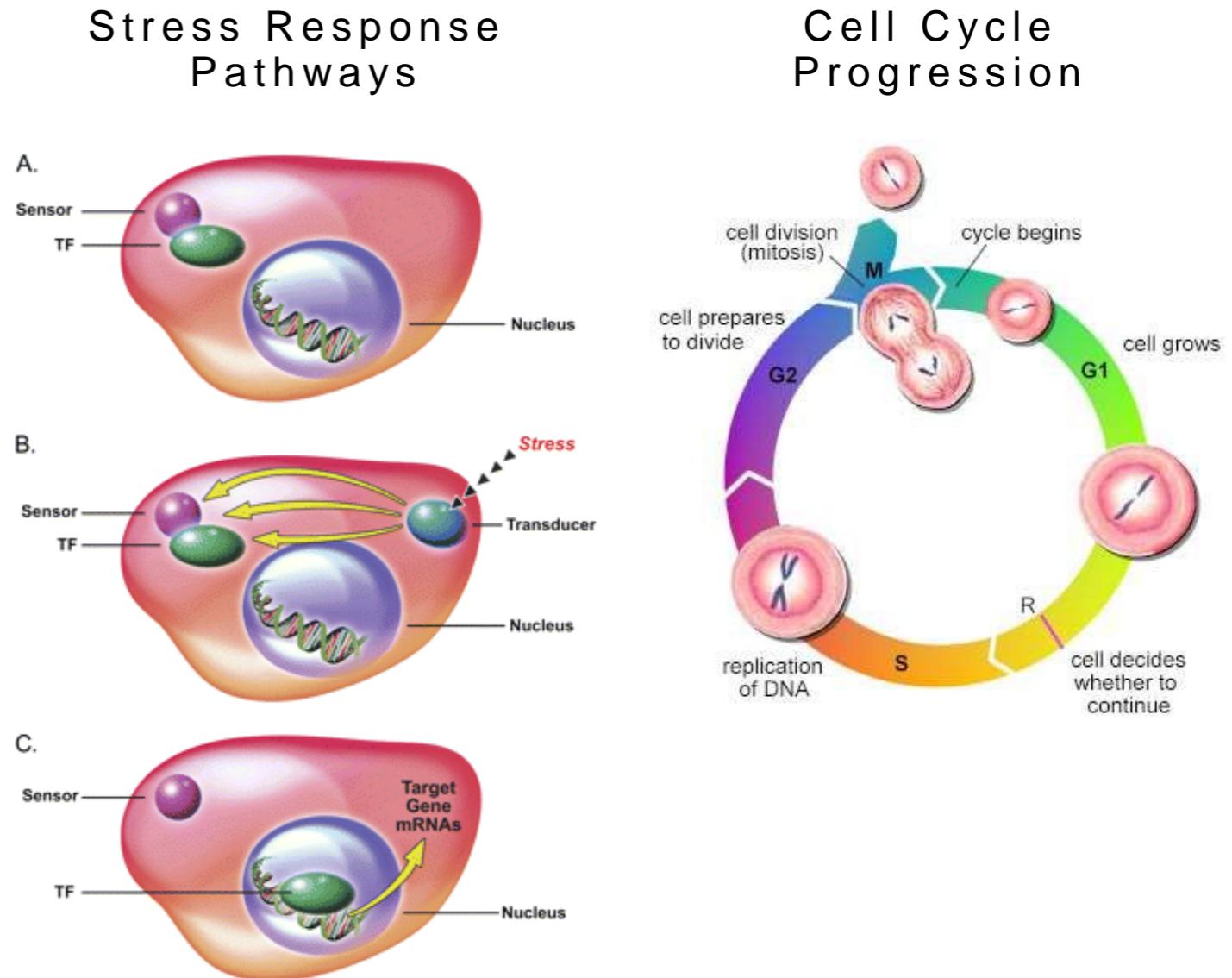
- ~400 plates
- ~100,000 wells
- ~2,400,000 images



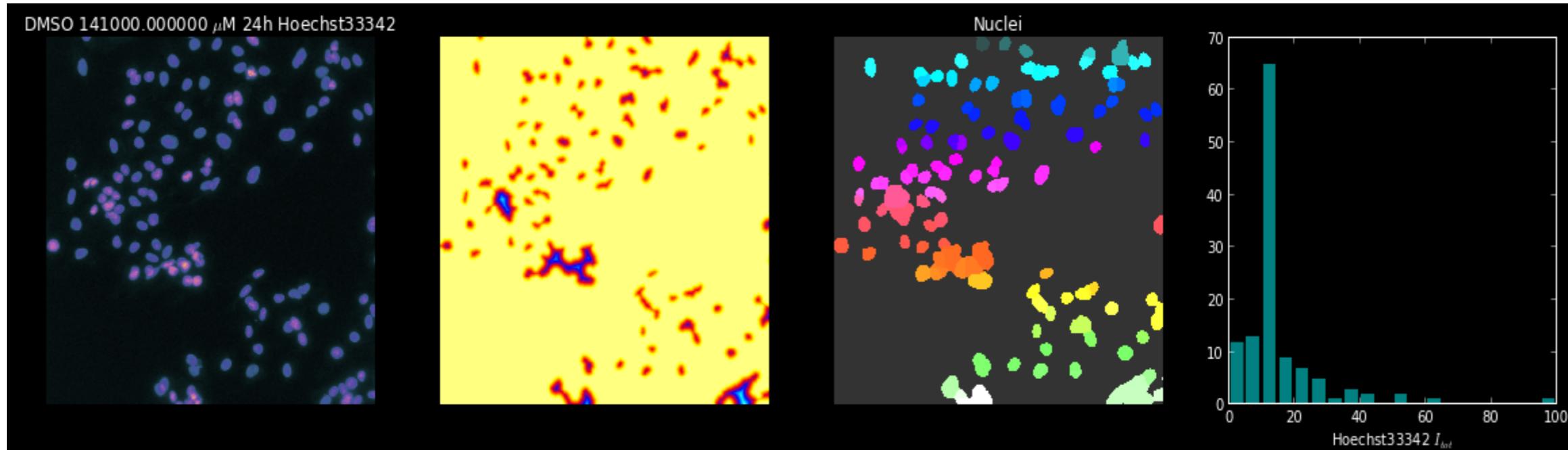
HCI Conducted by Cyprotex, Inc.

HCI Endpoints: Cell State

- P53: p53 activity (**p53**)
- c-Jun: stress kinase (**SK**)
- H2AX: oxidative stress (**OS**)
- MitoTracker Red:
mitochondrial mass (**MM**),
mitochondrial membrane
potential (**MMP**)
- Tubulin: microtubule
organisation (**Mt**)
- Hoechst33342: nuclear size
(**NS**), cell cycle
arrest/progression (**CCA**),
cell number (**CN**)
- PH3: mitotic arrest (**MA**)



Cell-State Data from Images

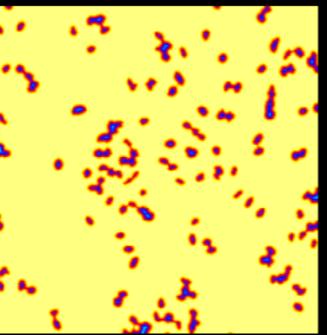
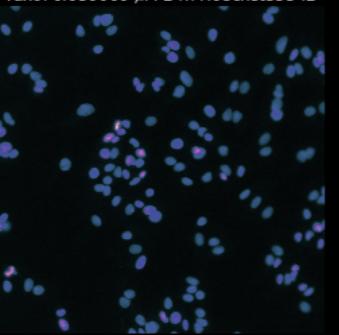


Raw Image (Hoechst) → Intensity Analysis → Object Identification → Nuclear intensity distribution

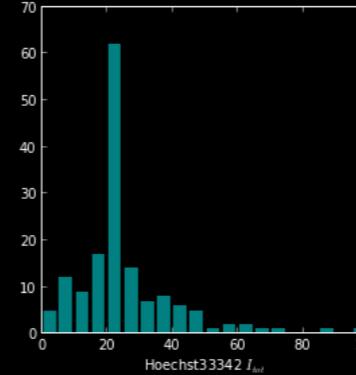
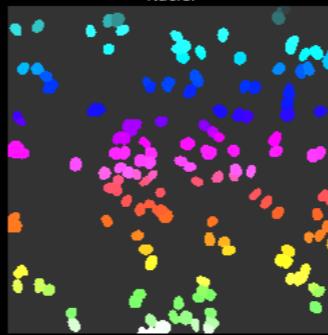
Image analysis and cell level feature extraction conducted by Cyprotex Inc. (proprietary software)

Taxol 0.03uM

Taxol 0.030000 μ M 24h Hoechst33342



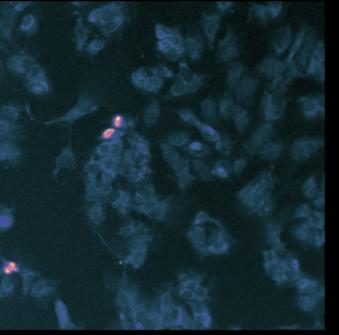
Nuclei



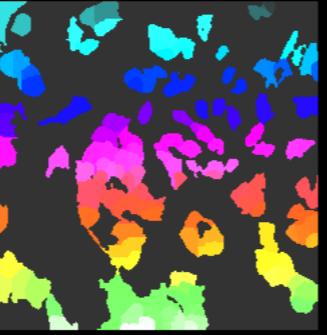
nuclear size (**NS**)
cell cycle arrest (**CCA**)
cell number (**CN**)

Hoechst33342

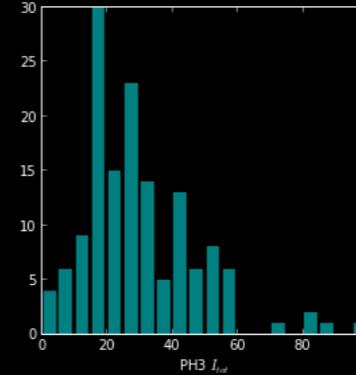
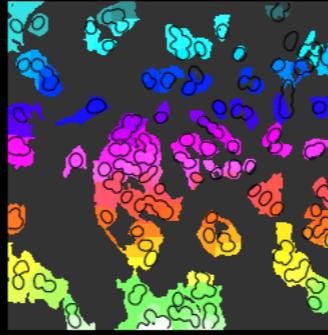
Taxol 0.030000 μ M 24h PH3



Cell PH3



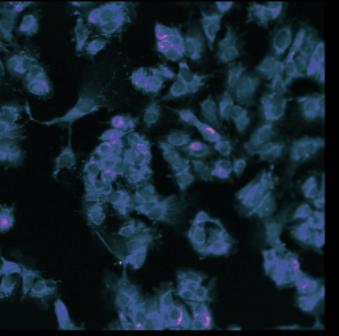
Cell+Nuc PH3



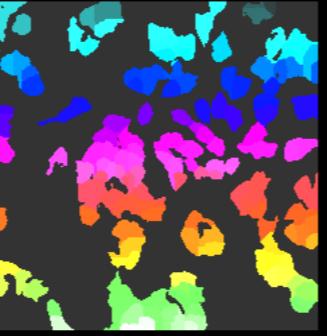
mitotic arrest (**MA**)

Phospho-Histone3

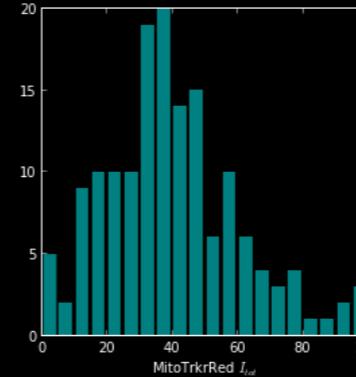
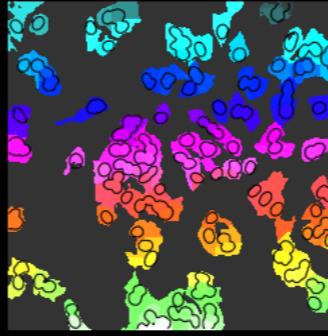
Taxol 0.030000 μ M 24h MitoTrkrRed



Cell MitoTrkrRed



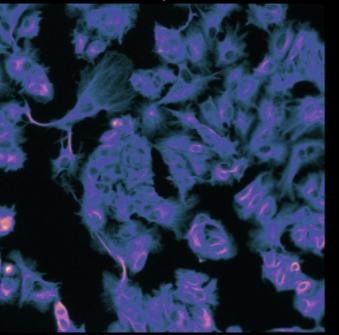
Cell+Nuc MitoTrkrRed



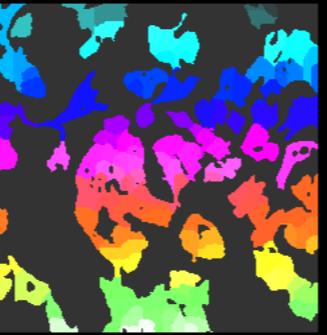
mitochondrial mass (**MM**)
mitochondrial membrane
potential (**MMP**)

MitoTracker Red

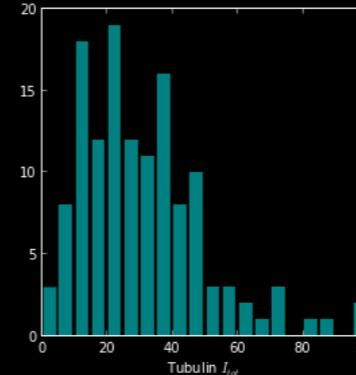
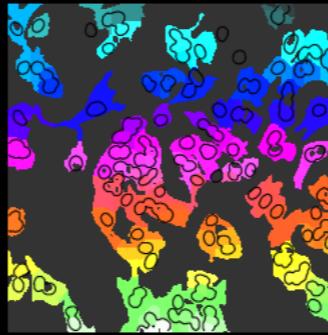
Taxol 0.030000 μ M 24h Tubulin



Cell Tubulin



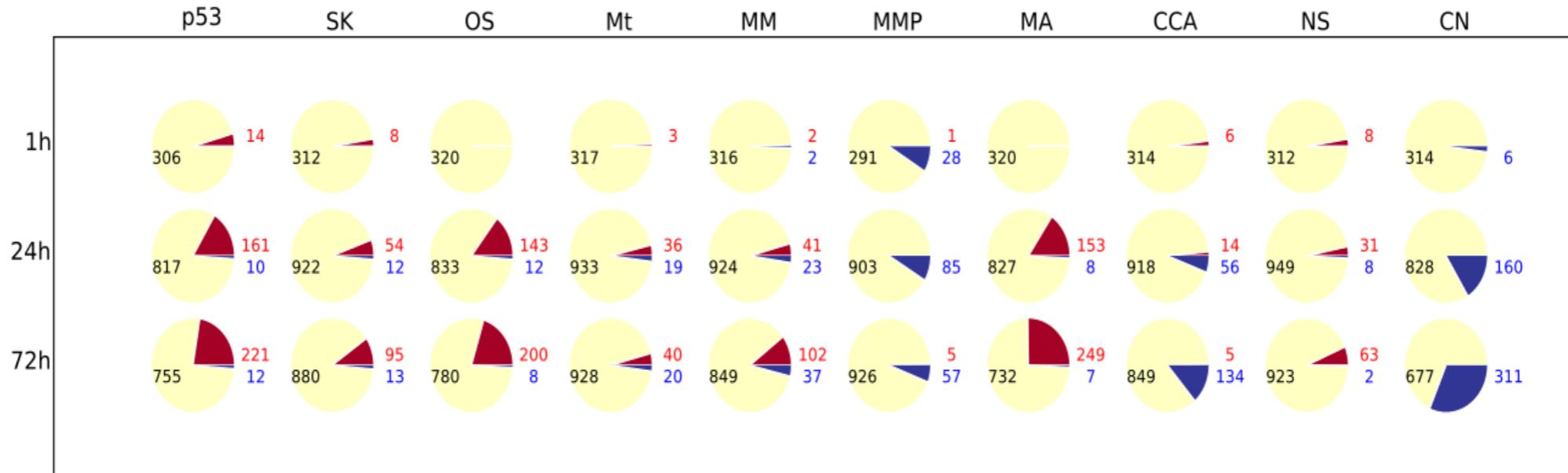
Cell+Nuc Tubulin



microtubules (Mt)

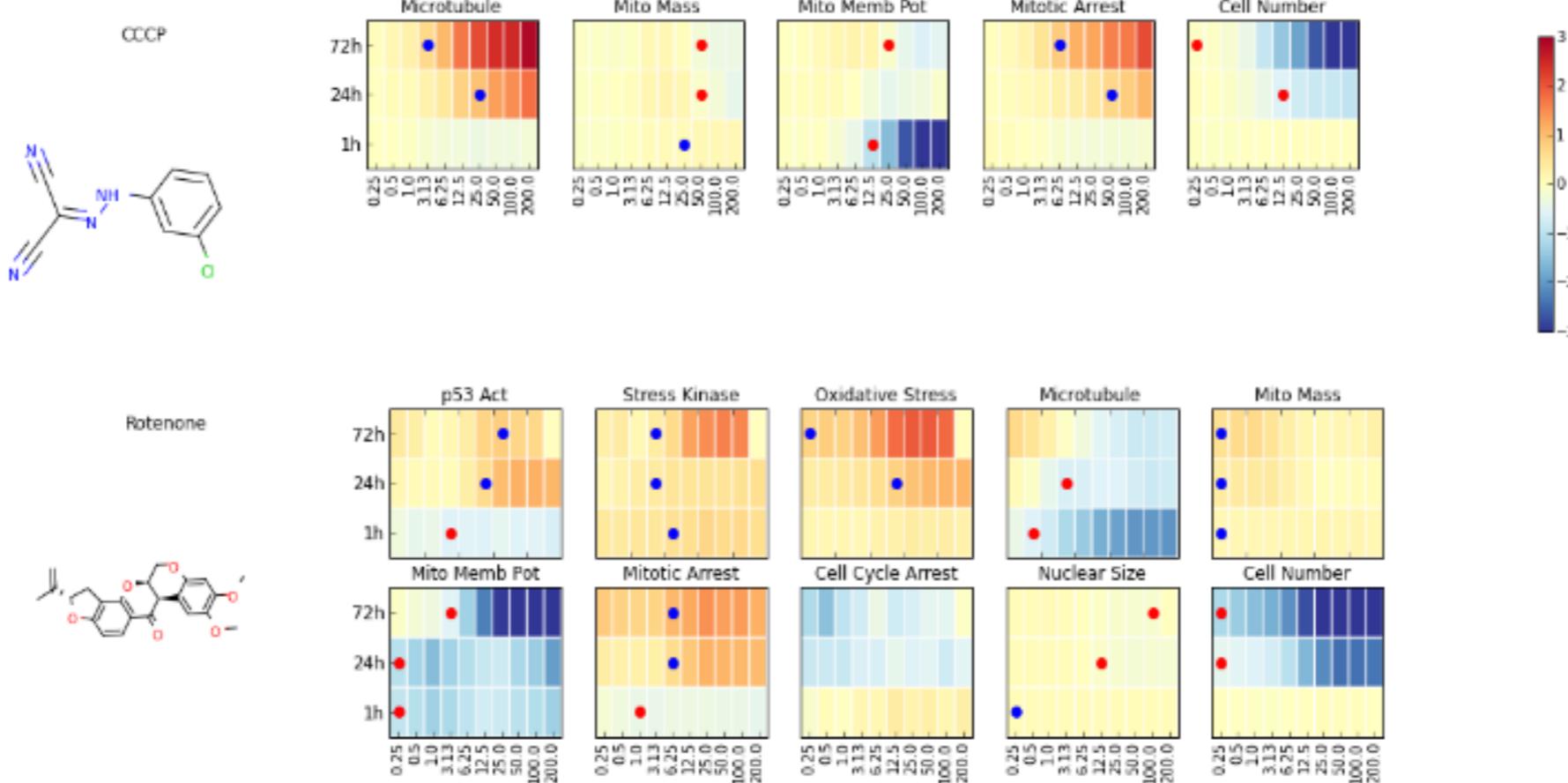
Phospho-Tubulin

Summary of HCI Effects



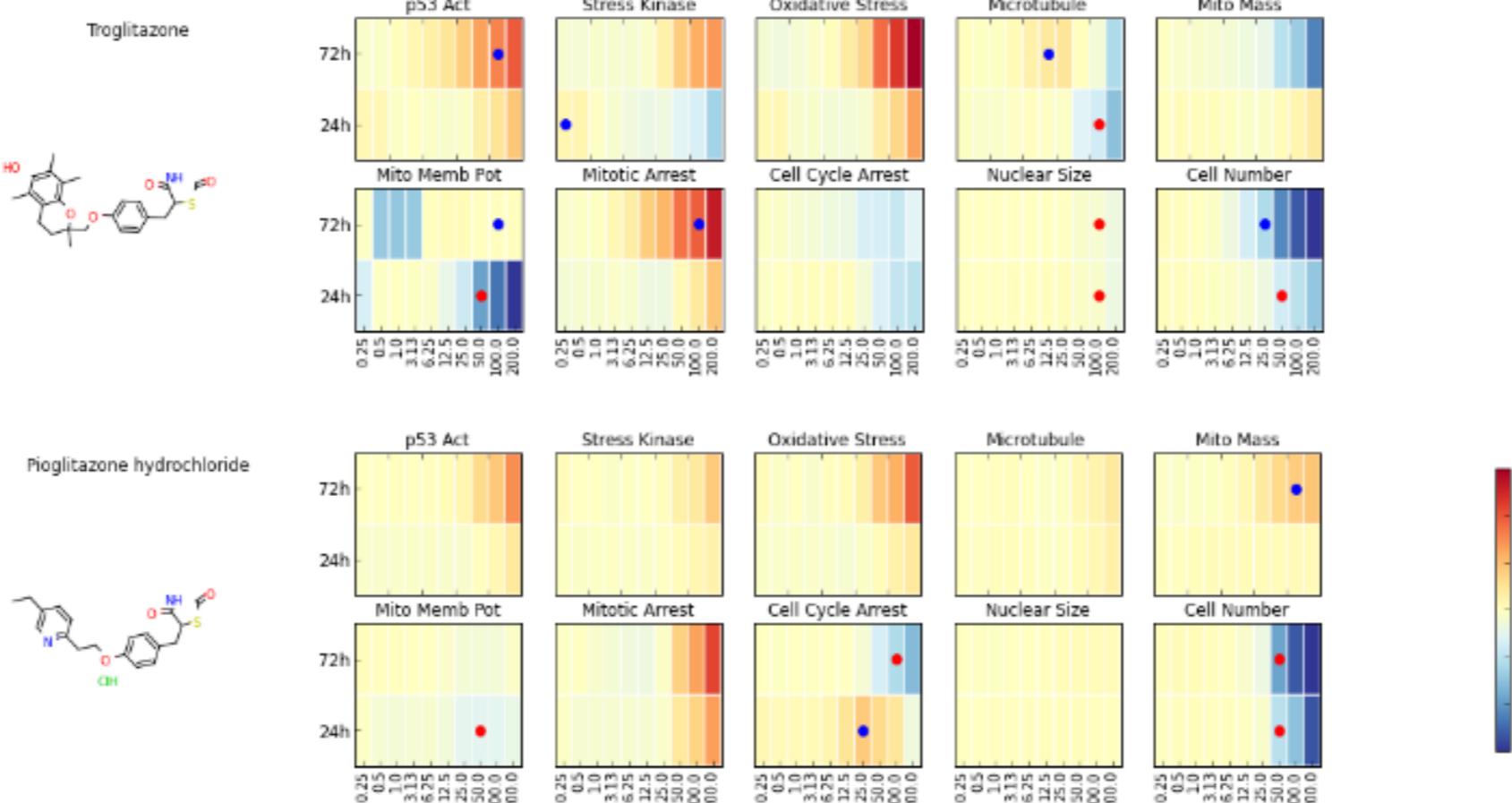
- Early effects: stress pathways & mitochondrial dysfunction
- Intermediate effects: complex
- Late effects: cell number decrease

Mitochondrial disruptors

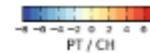


- log₂(fold change): decrease (BLUE), increase (RED) or no effect (YELLOW)
- Bioactivity profile: “deviation from normal state” of HepG2 cells

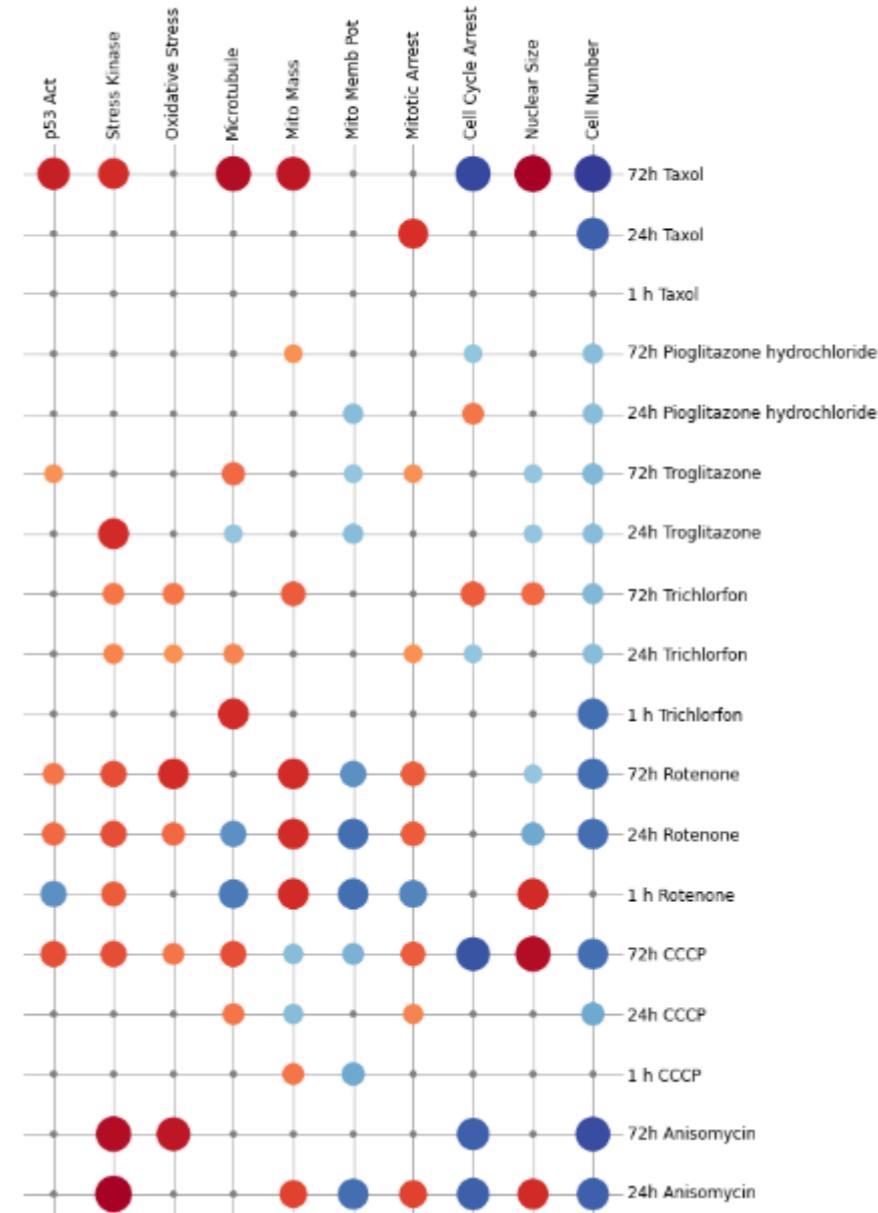
Thiazolidinediones (TZDs)



Summarizing Large-Scale HCl Data

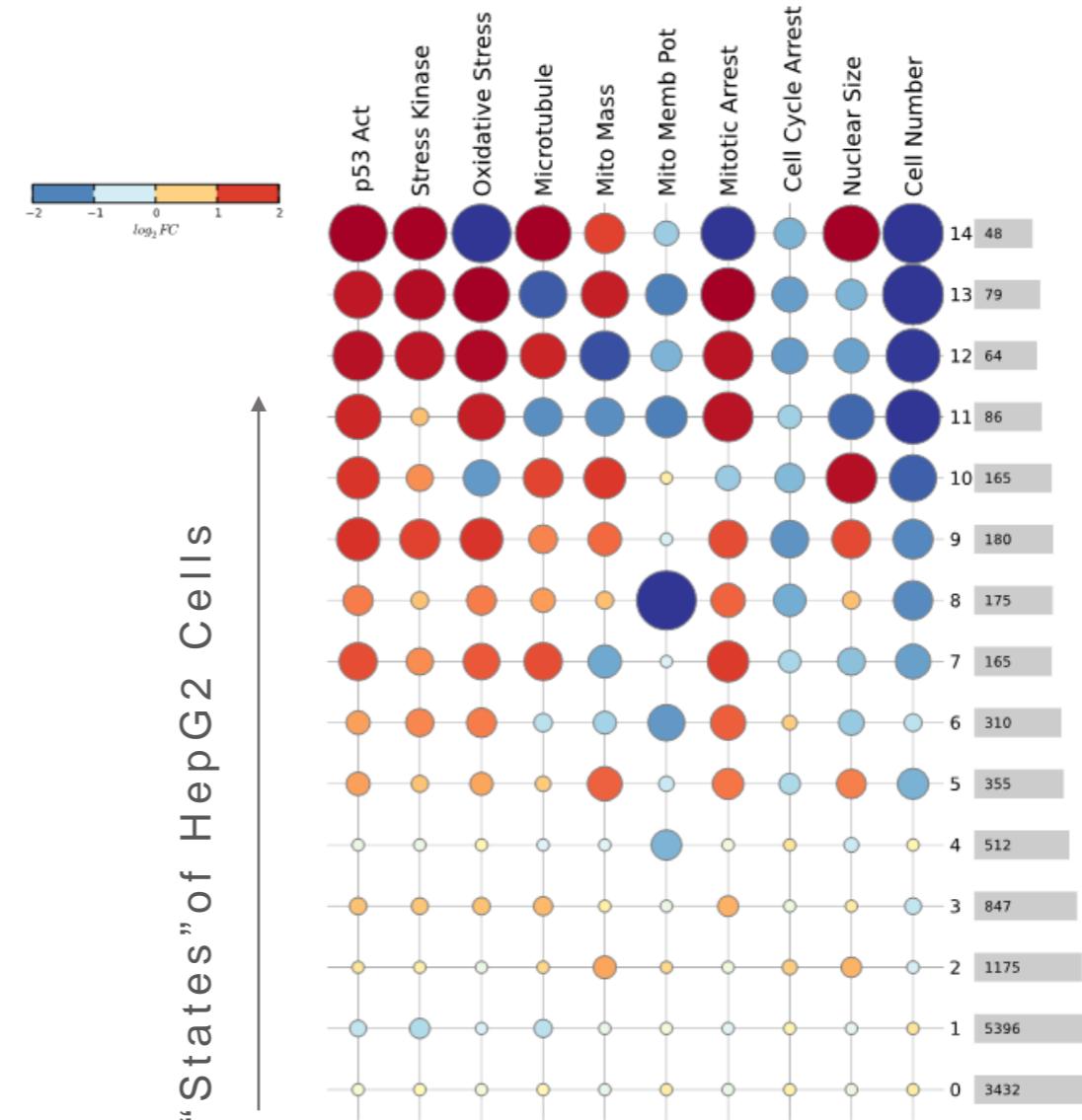


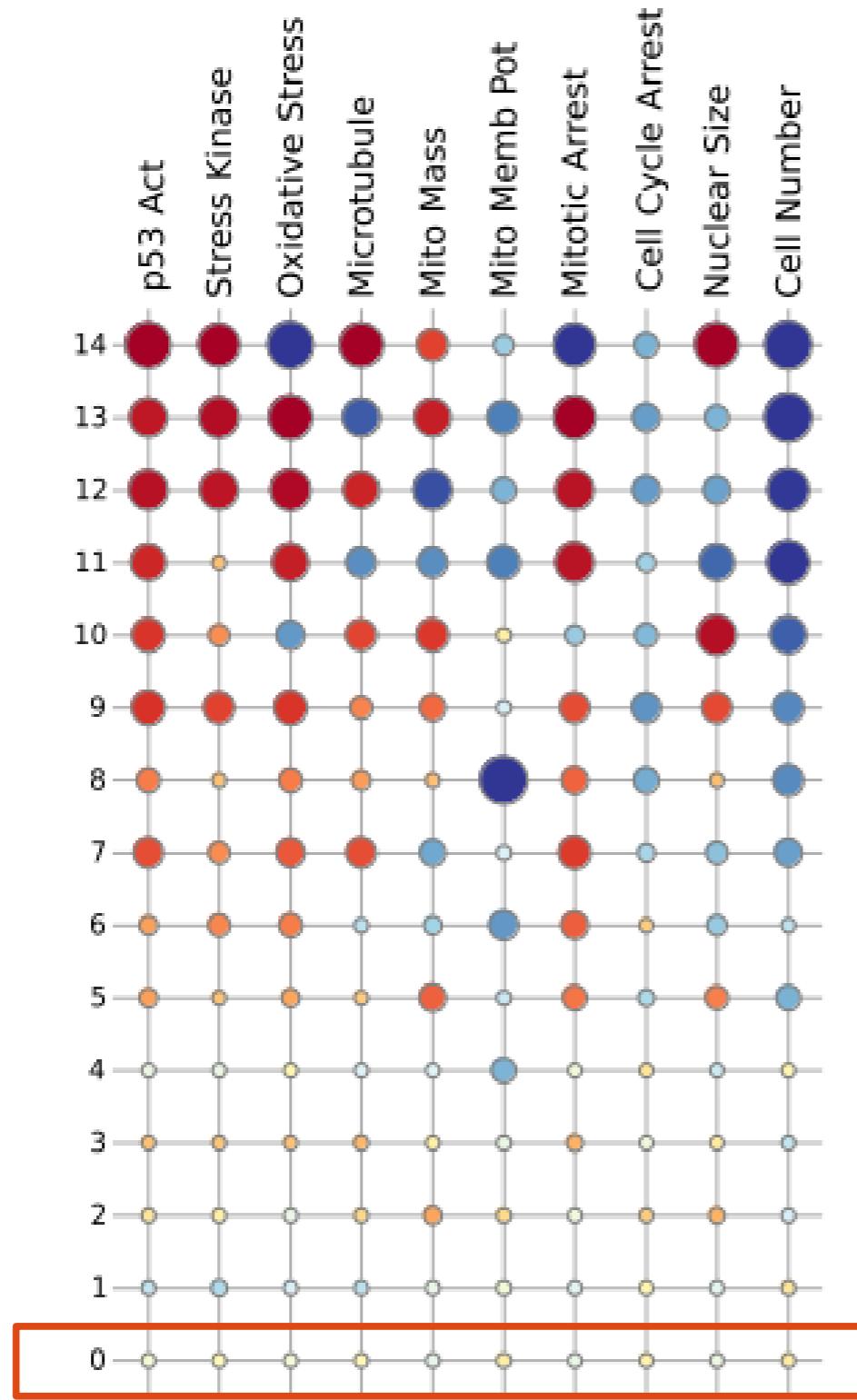
- Each chemical produces a 10 dimensional HCl response for each treatment (concentration & time)
- Results in close to 10^5 data points or 10^4 vectors
- How do we summarize and interpret such data?
- How can we find patterns in the data?
- How do we predict toxicity using these data ?



HCI to Phenotypic States

- We used unsupervised learning (clustering)
- Cluster all 10^4 treatment responses
- Derive phenotypic “states” of HepG2 cells
- Phenotypic states *could* represent canonical behaviours of cells
- We could use these phenotypic states to understand the dynamic response to chemicals

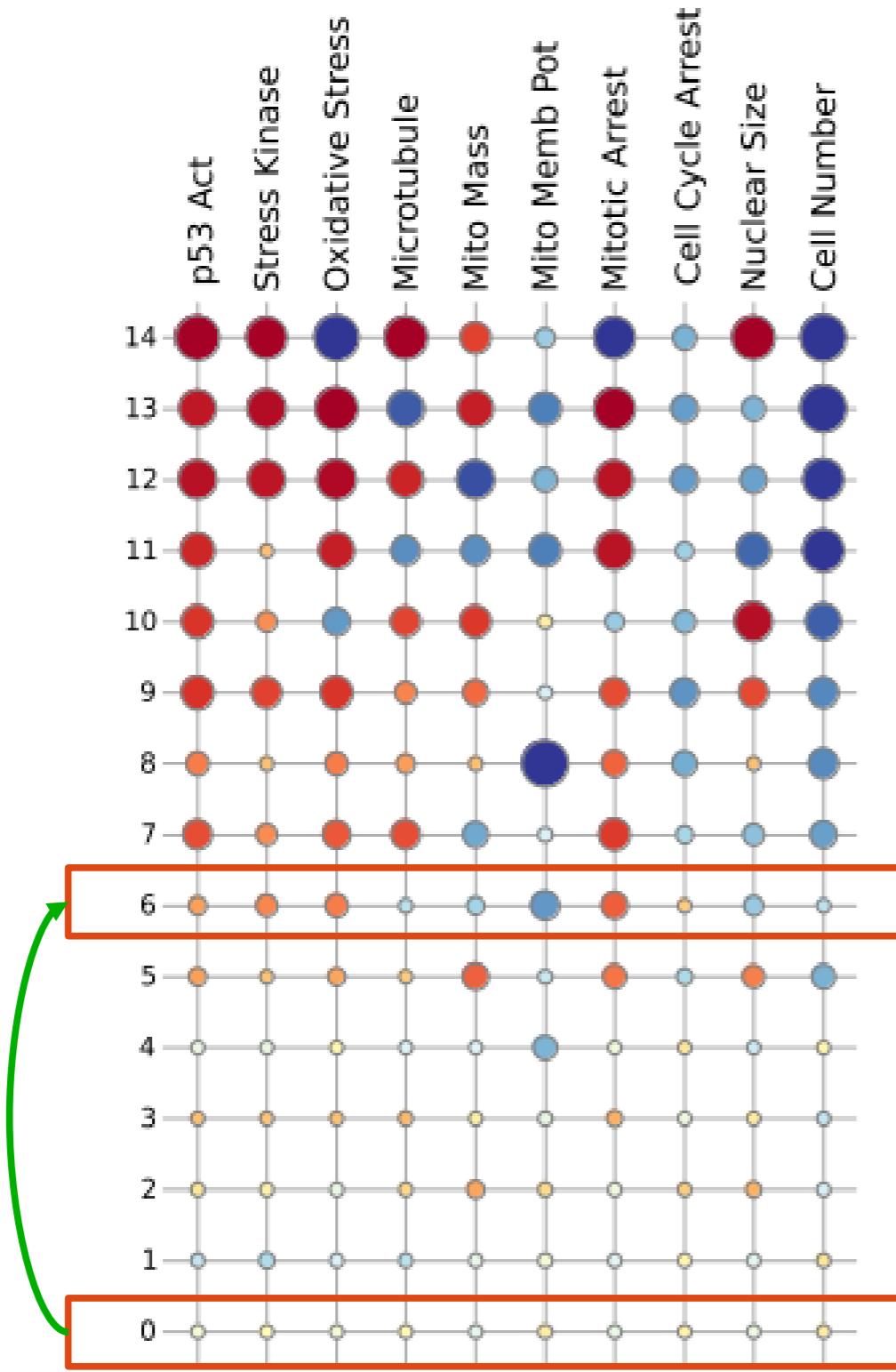




“Normal” State

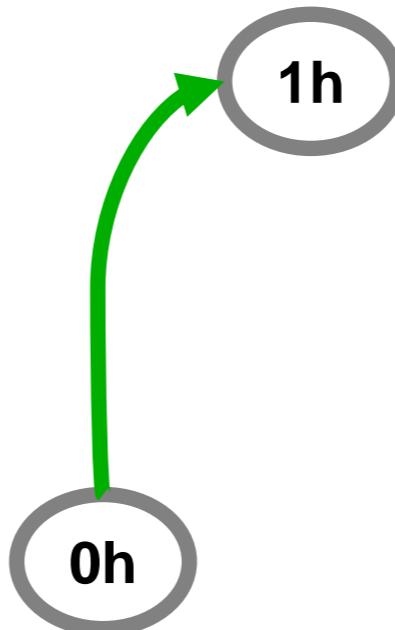
Fluazinam 0.78 uM

0h



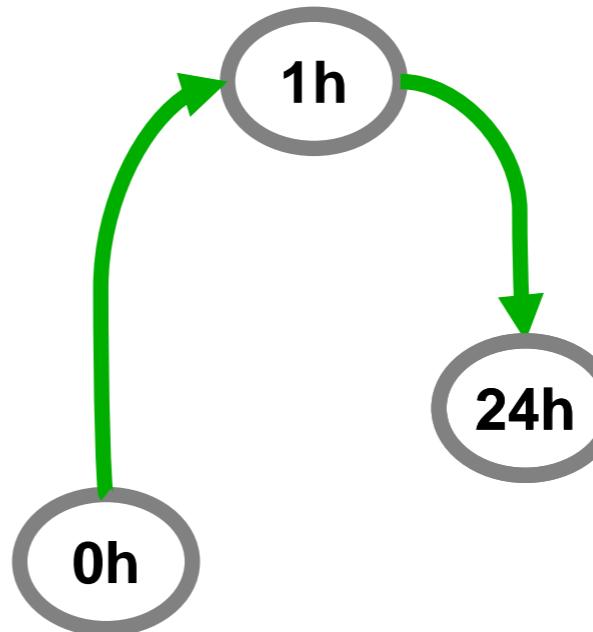
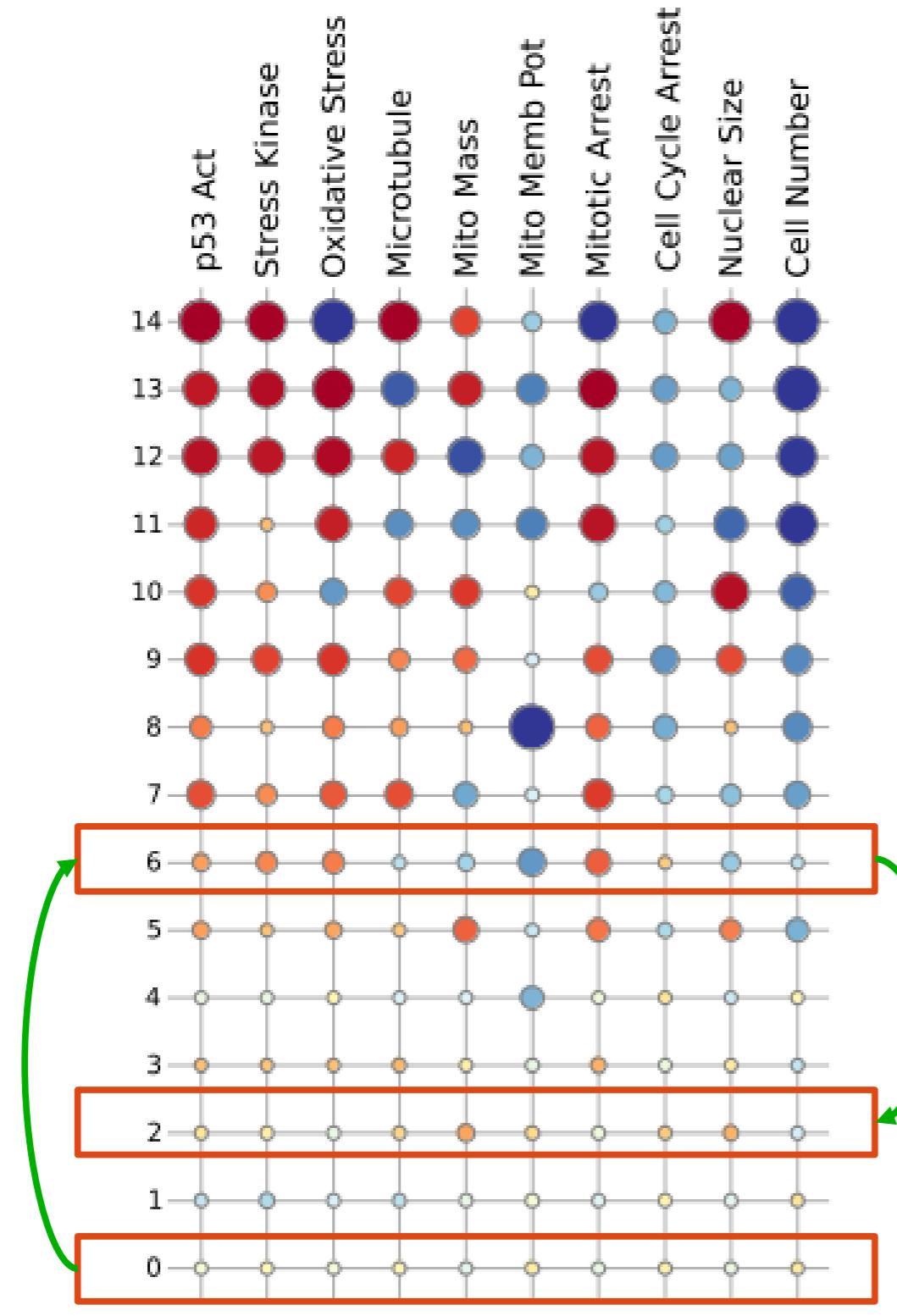
State Transition

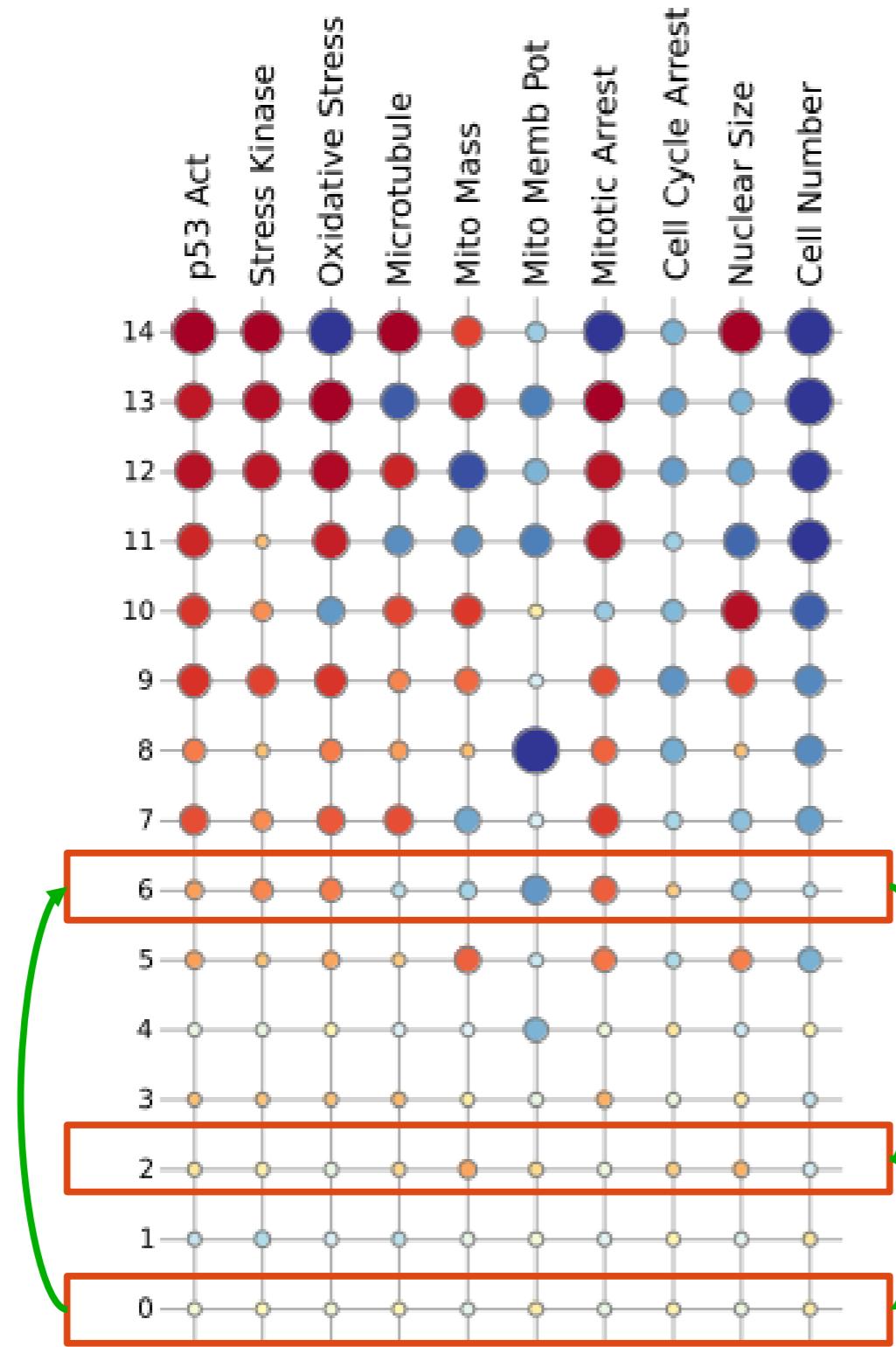
Fluazinam 0.78 uM



System trajectory

Fluazinam 0.78 uM

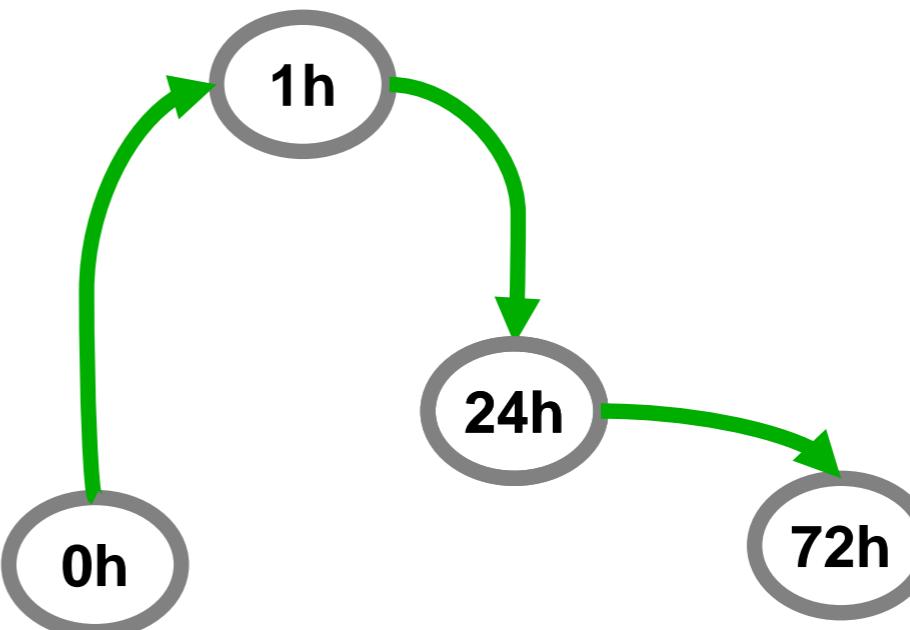




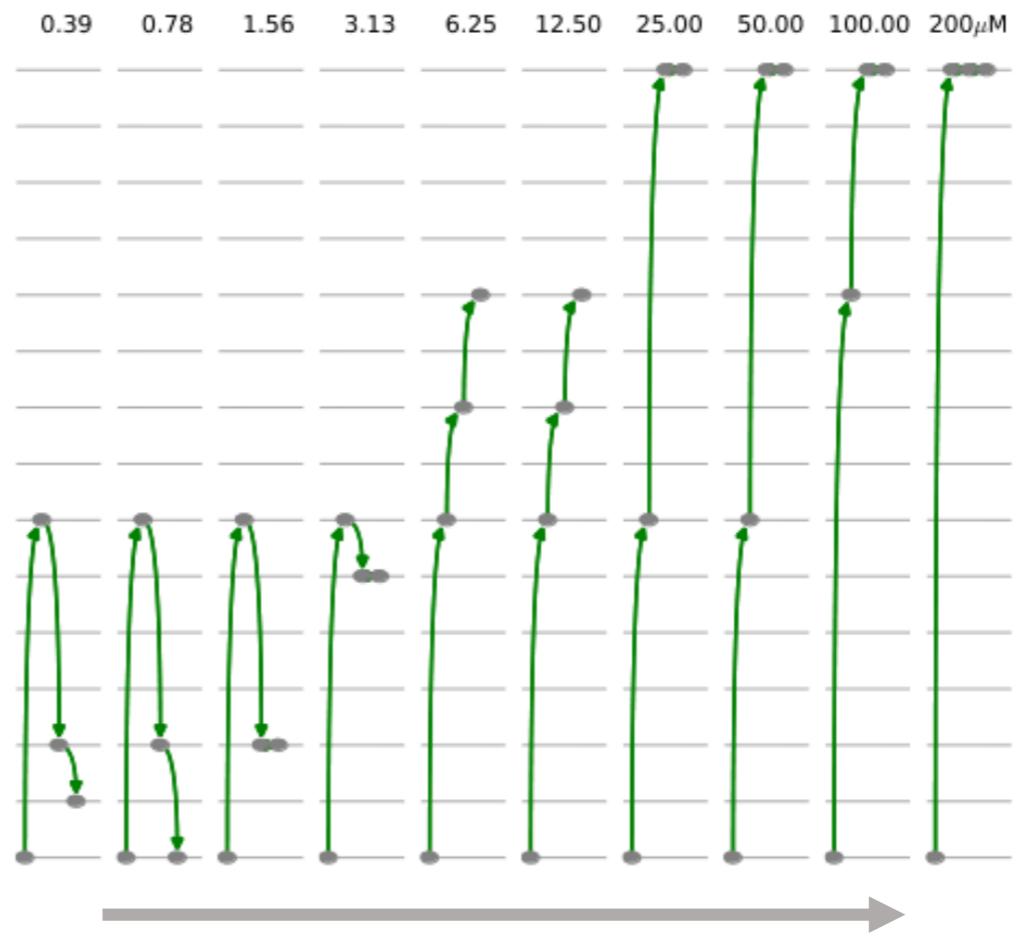
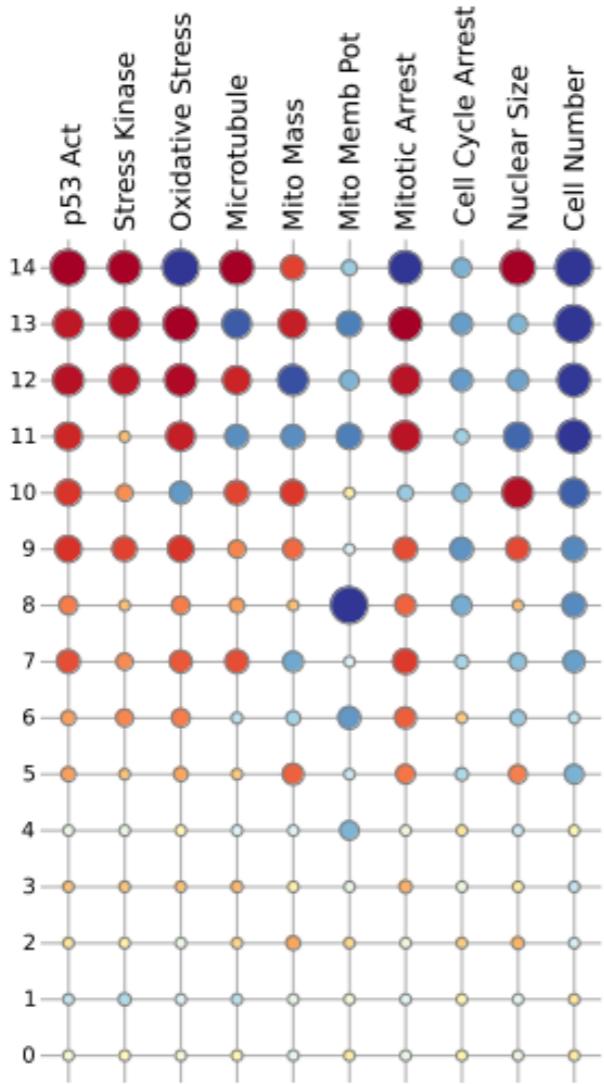
System trajectory

Fluazinam 0.78 uM

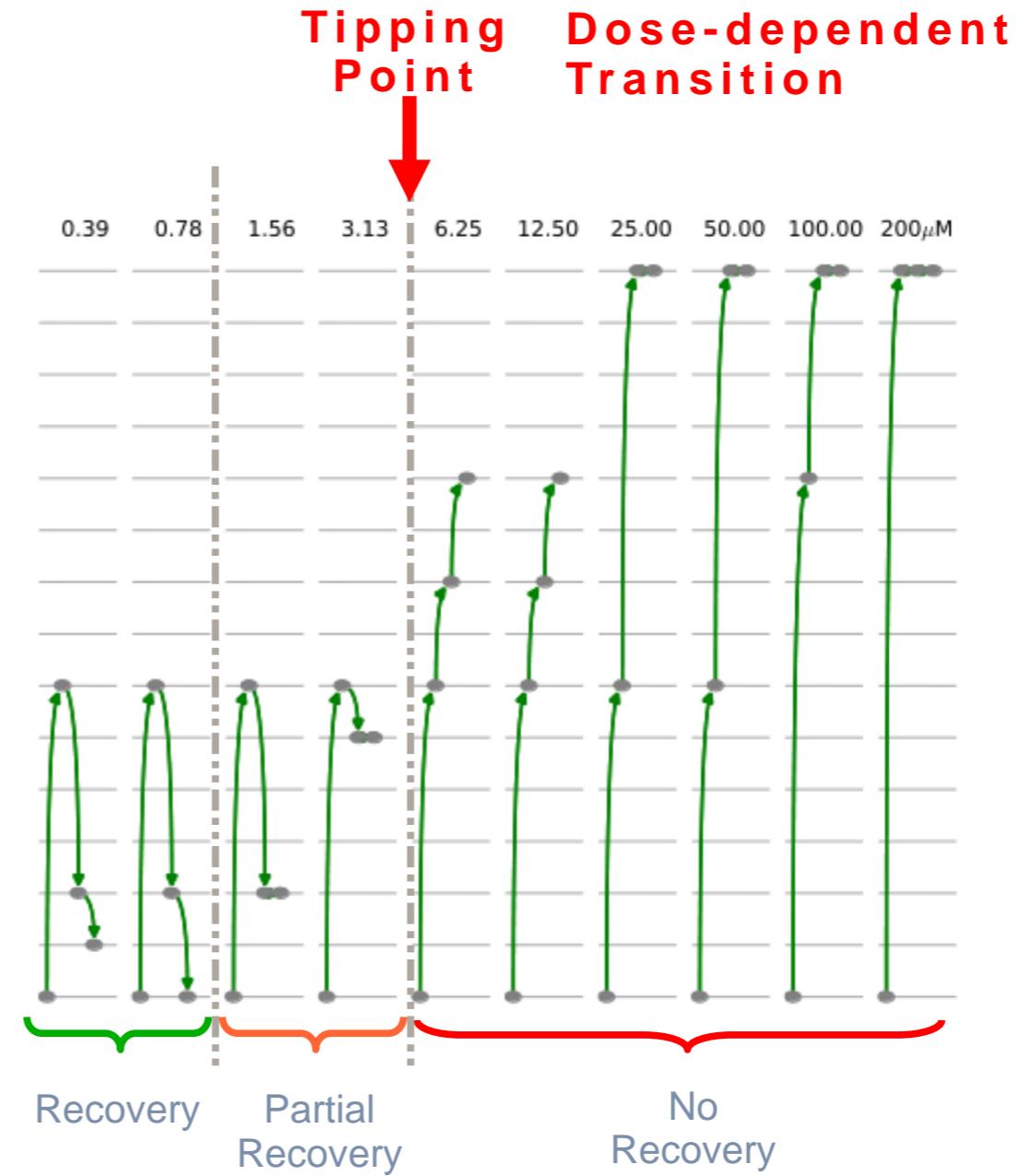
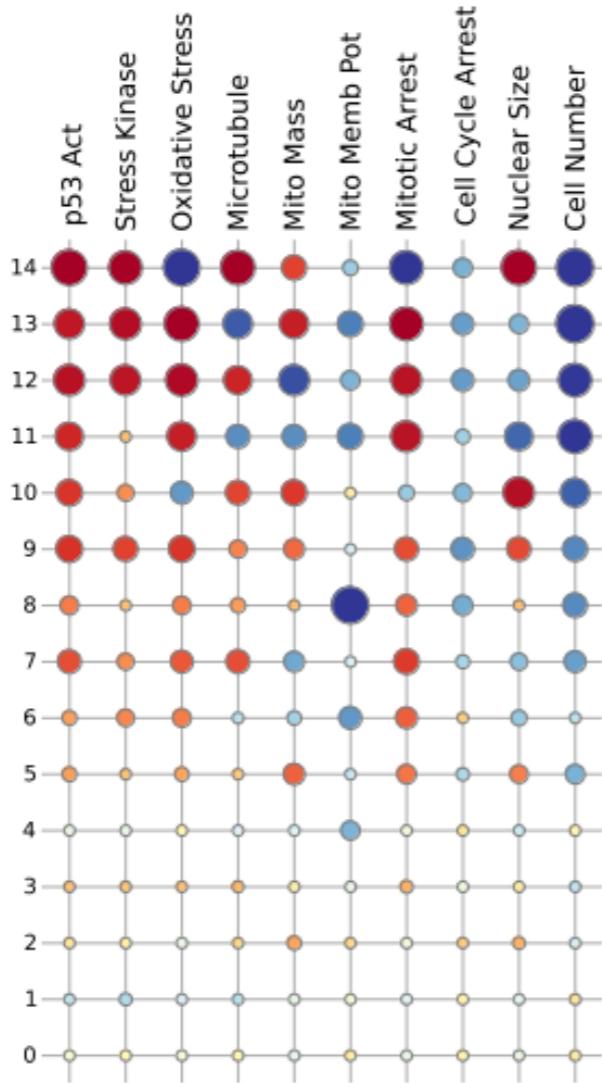
Trajectory=Sequence of states



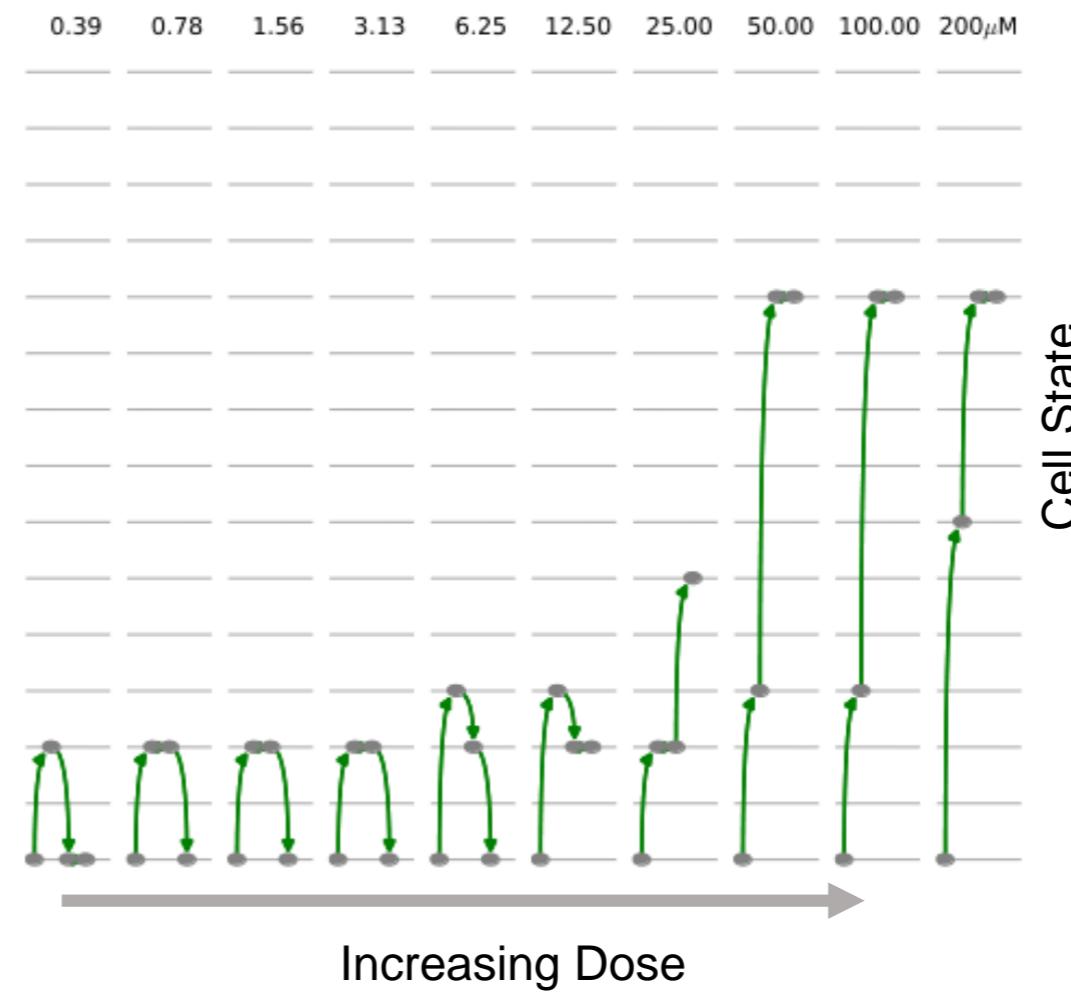
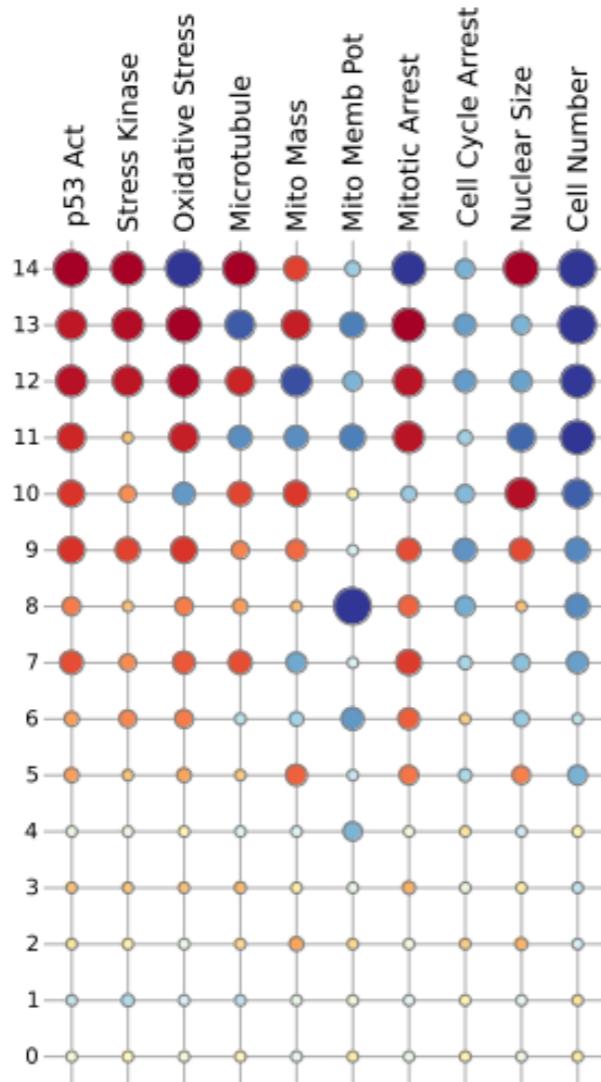
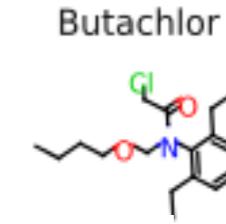
Fluazinam “Trajectories”



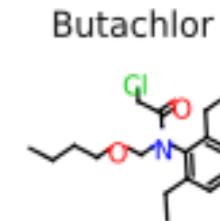
Fluazinam “Trajectories”



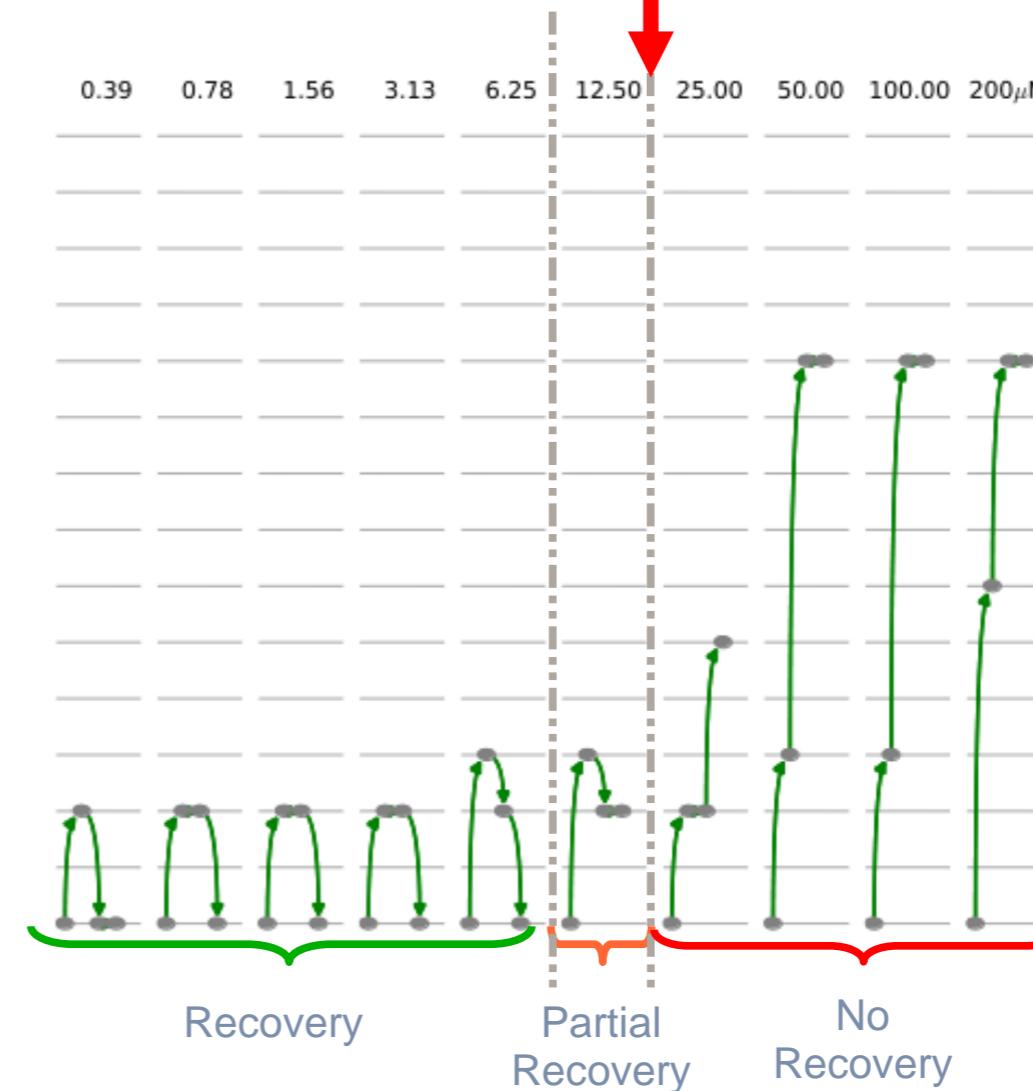
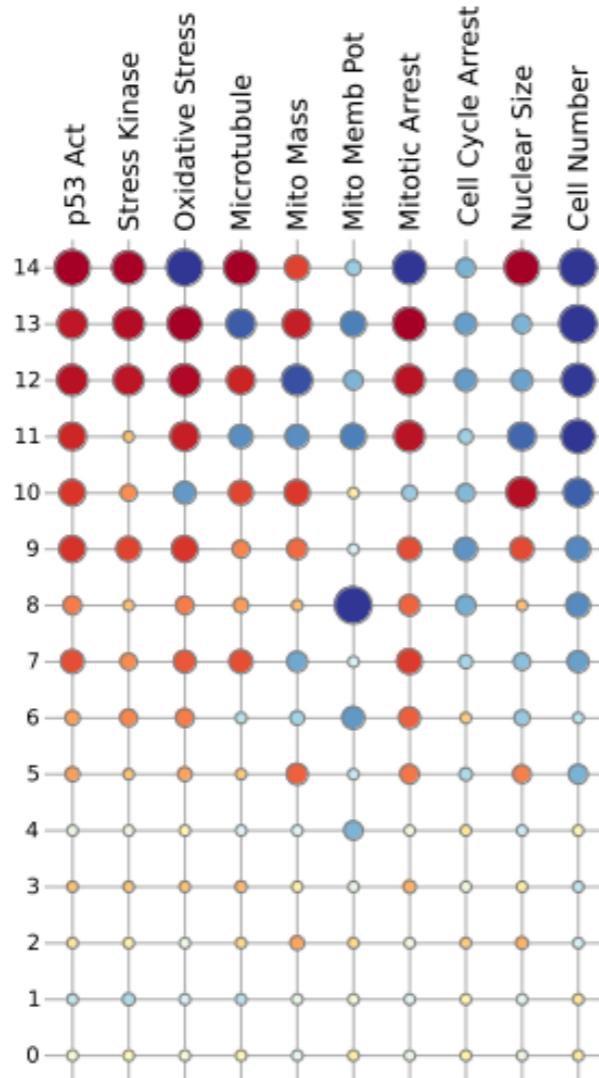
Butachlor Trajectories



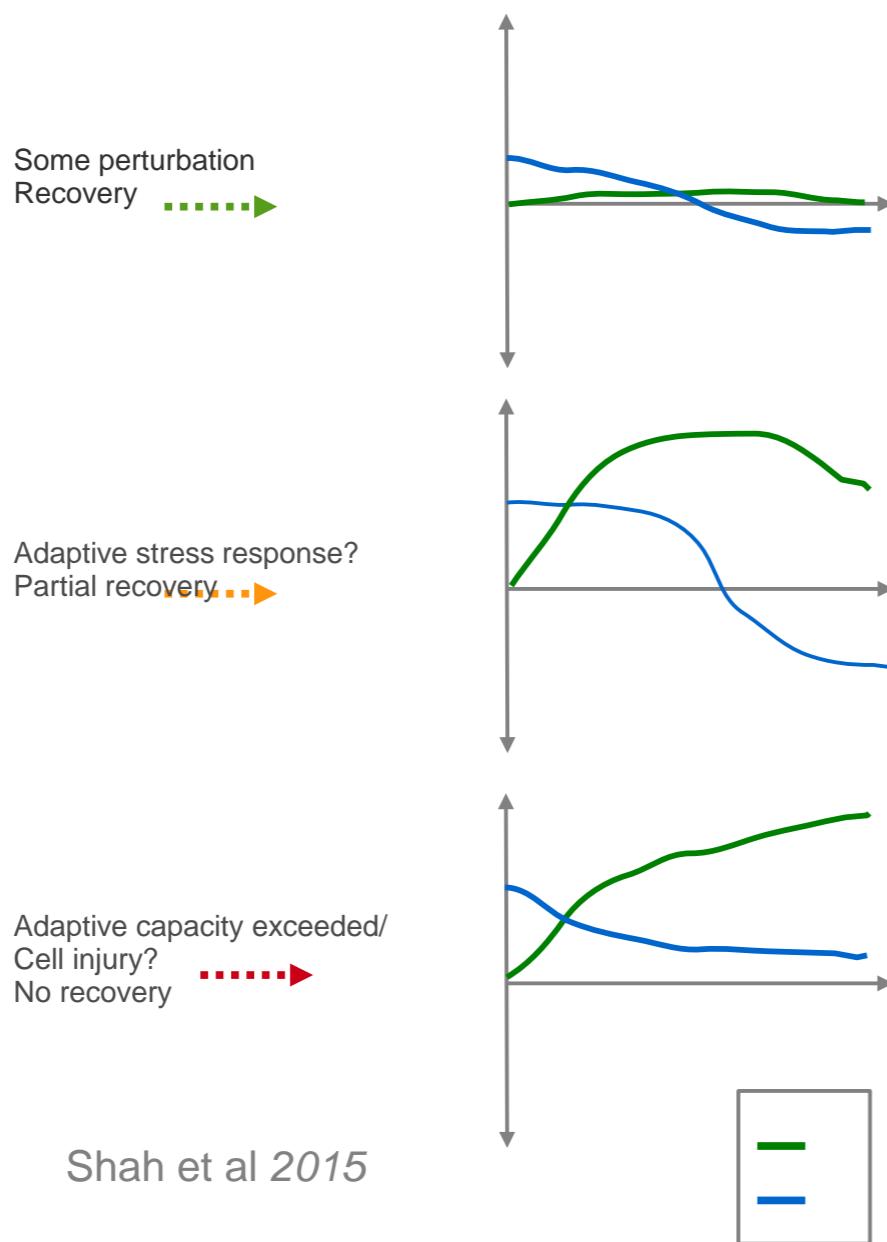
Butachlor Trajectories



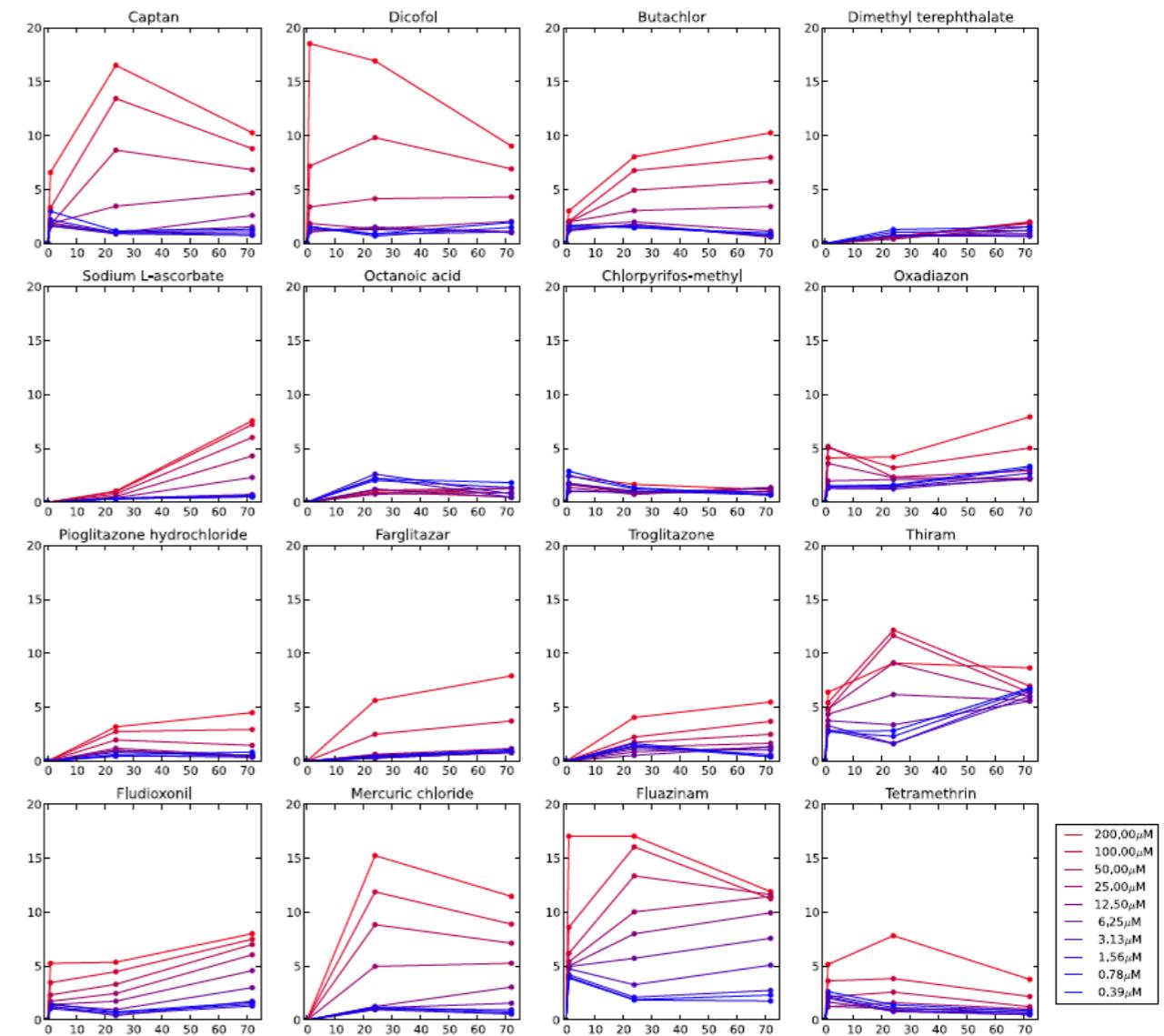
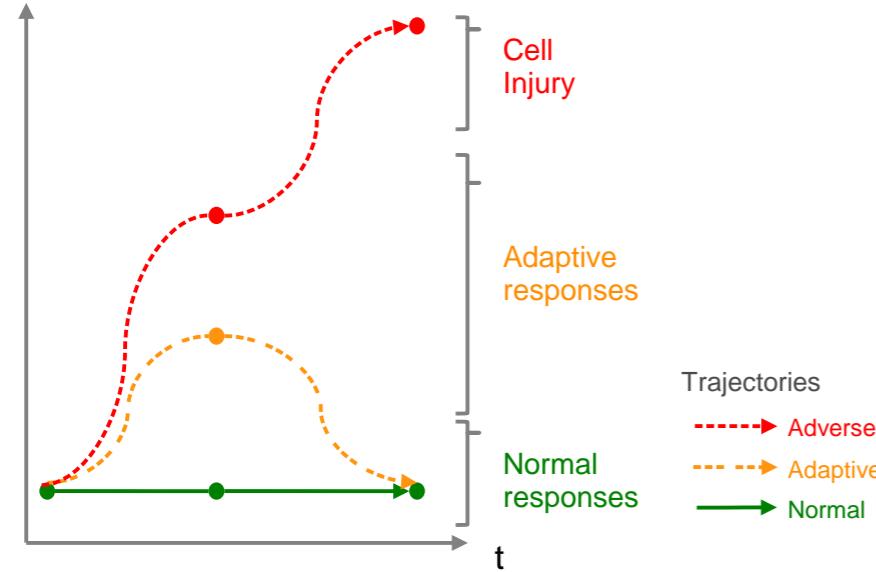
Tipping Point **Dose-dependent Transition**



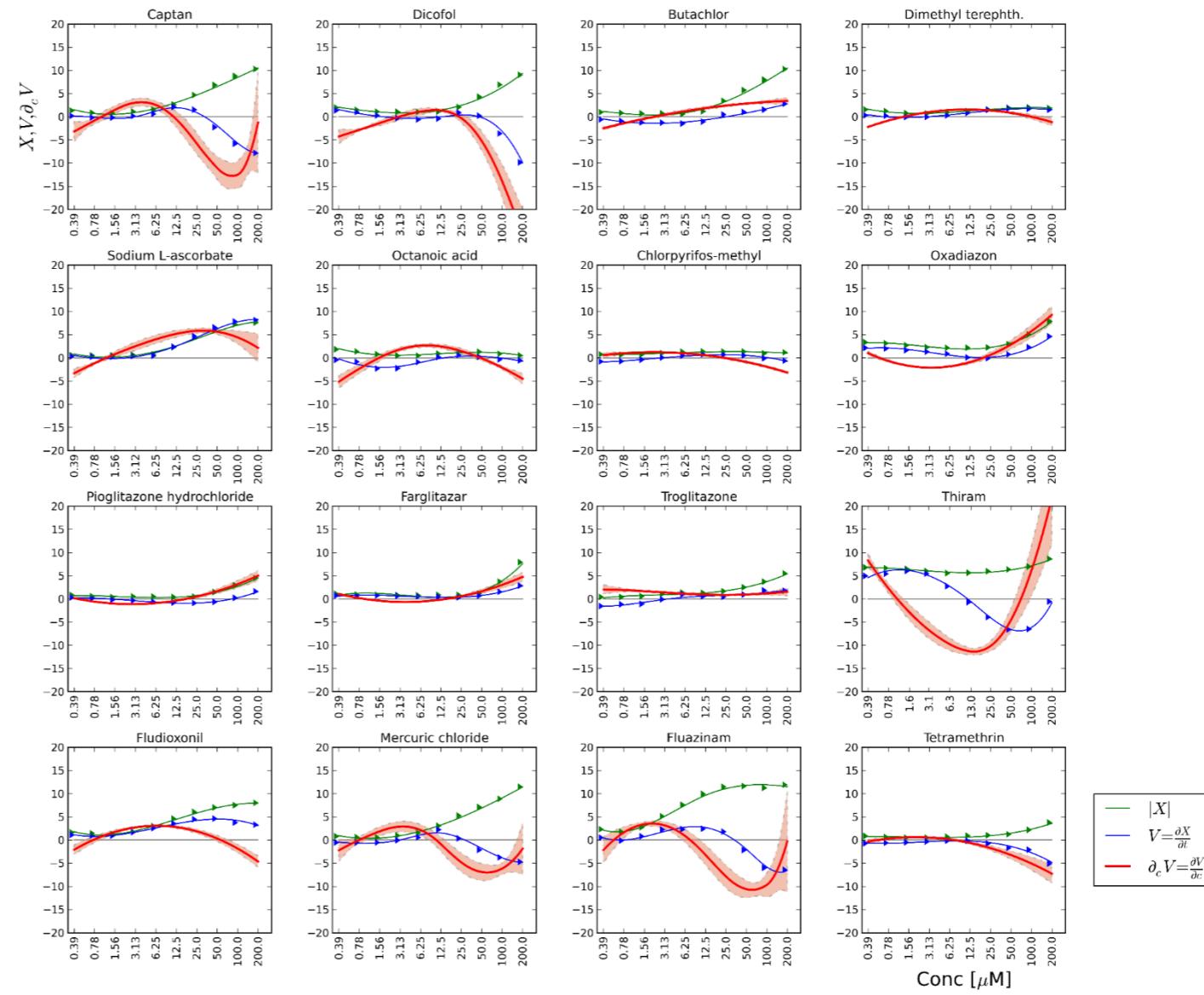
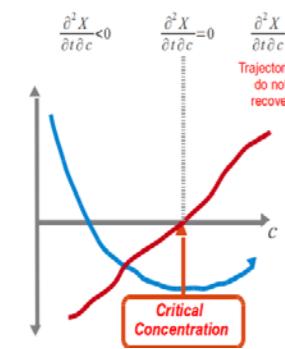
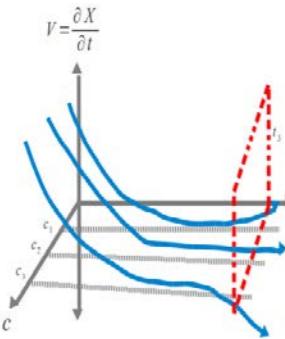
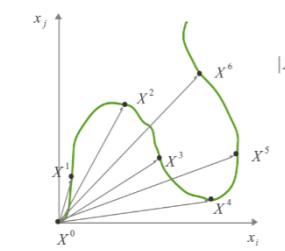
Analyzing Trajectories Quantitatively

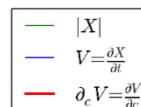


Quantitative Trajectories



Dose-Dependent Transition

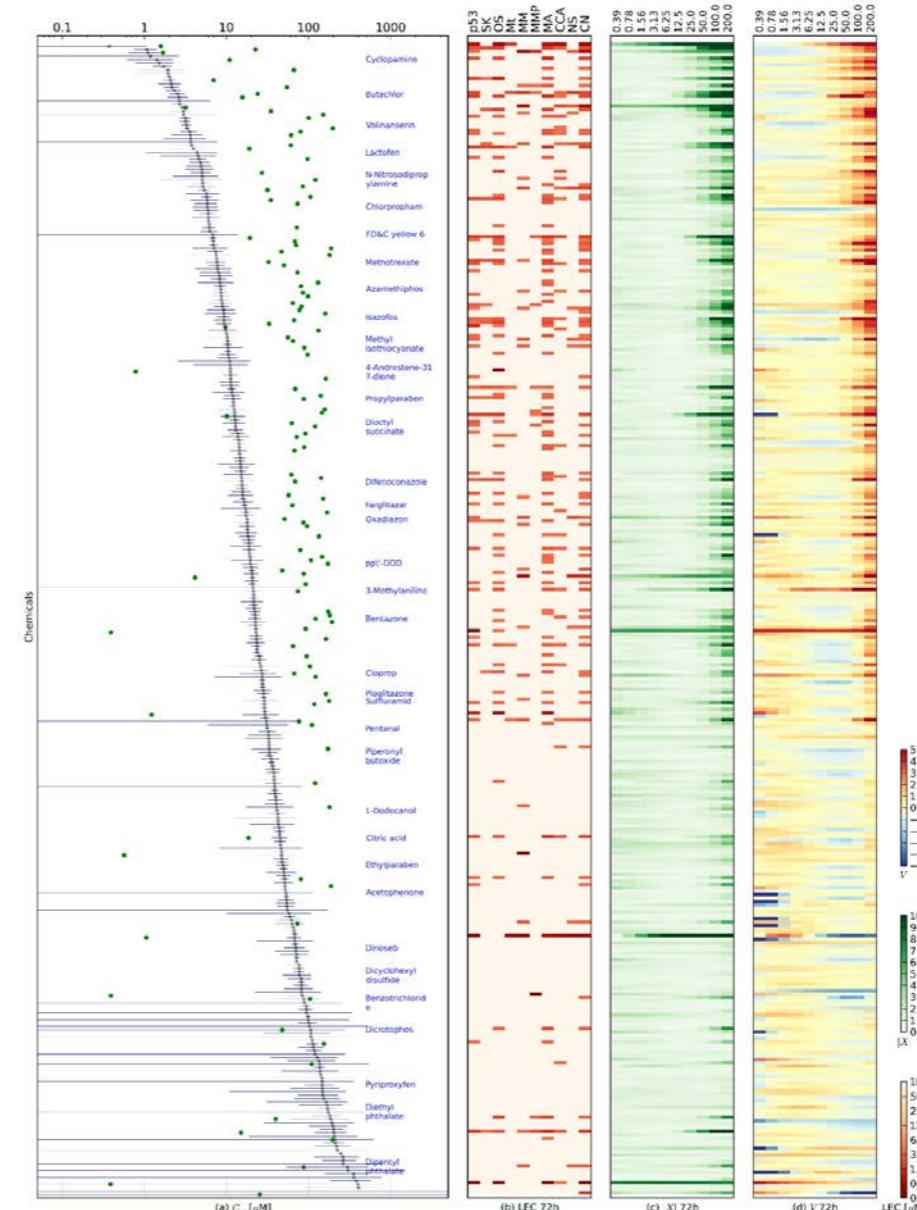




 $|X|$
 $V = \frac{\partial X}{\partial t}$
 $\partial_c V = \frac{\partial V}{\partial c}$

Critical Concentrations

- Can systematically identify critical concentrations- “tipping points”
- Tipping point precedes concentration that produces significant cell loss



MANY CHALLENGES...

□ Study design

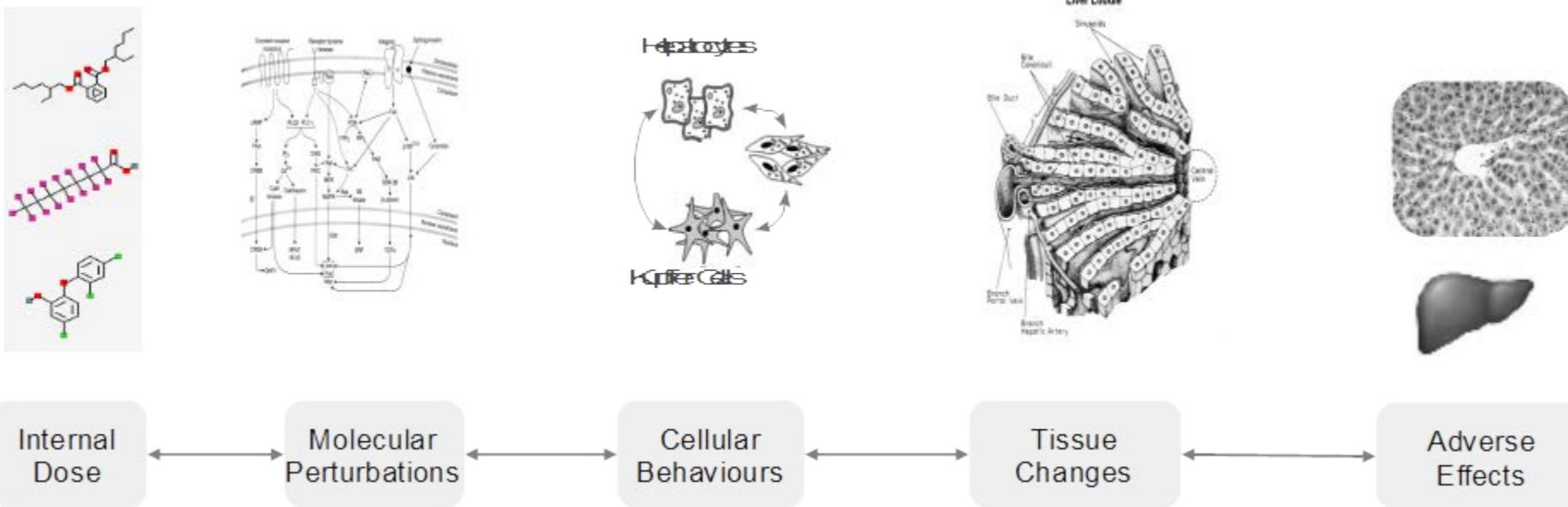
- More time points !
- More stress-response markers !
- How to define critical window to identify tipping points ?
- More physiologically-relevant cell model

□ Tipping point evaluation

- Is it just PK or is there real adaptation ?
- Are they reproducible ?
- Are they biologically relevant (ie. mechanisms)?

New study underway to address some of these challenges ...

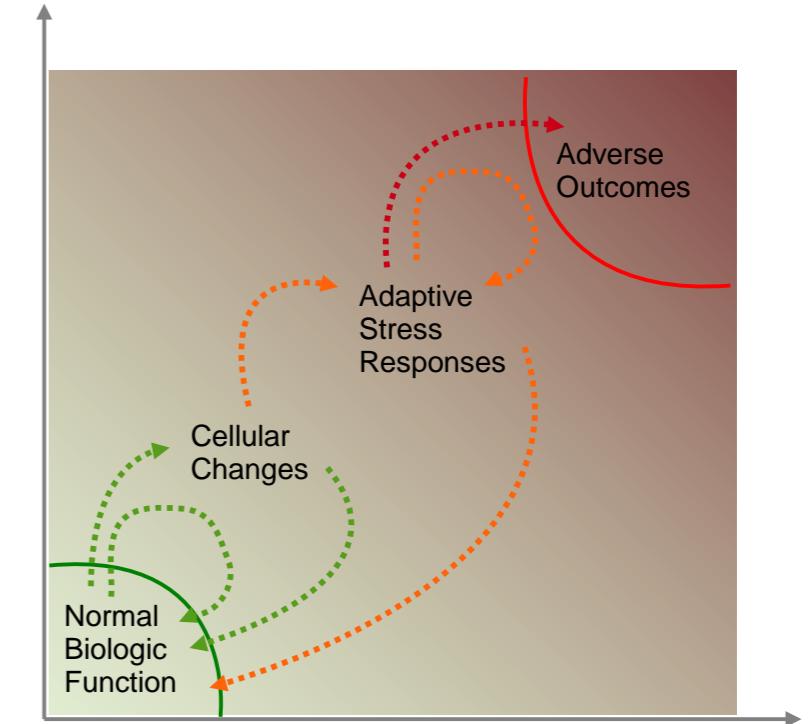
Translation: *in vivo* Tipping Points ?



- ❑ Adverse effects depends on a complex sequence of events
- ❑ Consider *in vivo* lesions:
 - ❑ Hypertrophy
 - ❑ Necrosis
 - ❑ Inflammation
 - ❑ Steatosis
- ❑ These can be acute effects of chemical exposure or intermediate steps towards chronic injury
- ❑ Differentiating adaptation and adversity is difficult !
- ❑ **Transient effects are more likely to be adaptive**

Summary

- Complex biological data: system state
- State perturbations define trajectory
- Trajectory analysis → Tipping Point
- Threshold for homeostatic adaptation
- Linked with adversity
- Could be used as point of departure for risk assessment



Biologic Perturbations:

System Trajectories:

- ➡ Some perturbation/
Recovery
- ➡ Adaptive stress response/
Recovery
- ➡ Adaptive capacity exceeded/
Cell injury/
No recovery

Acknowledgements

- HCI Experiment Analysis
 - Keith Houck
 - David Dix
 - Cellumen/Apredica/Cypr
otex
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 - Kevin Crofton
 - Rusty Thomas
 - Richard Judson
 - Thomas Knudsen
 - Robert Kavlock
- Data Processing
 - Matt Martin
 - David Reif (NSCU)
 - Woodrow Setzer
 - John Jack (NSCU)
 - Jie Liu