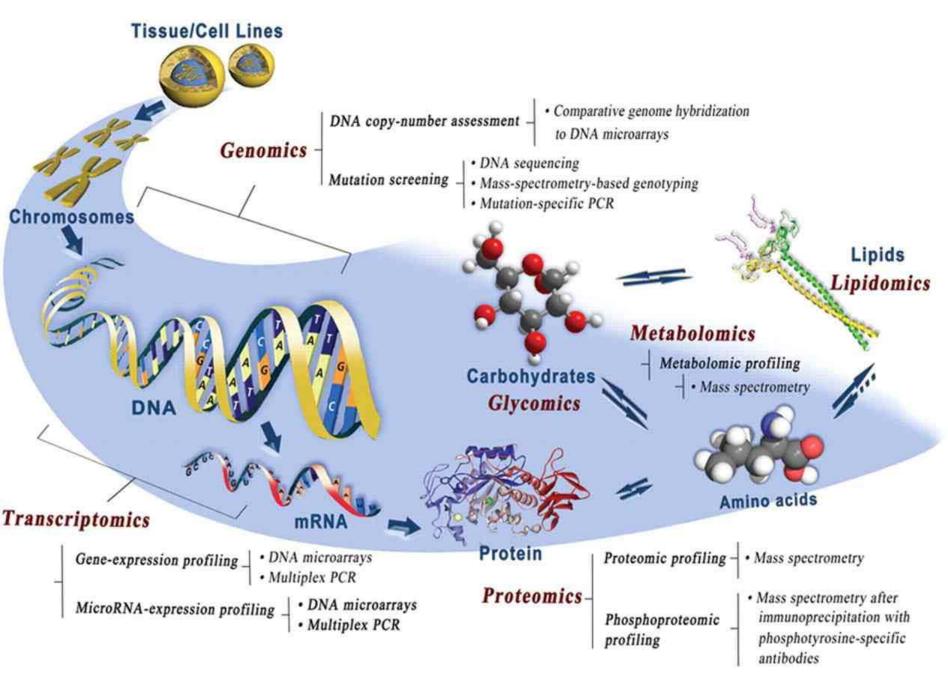
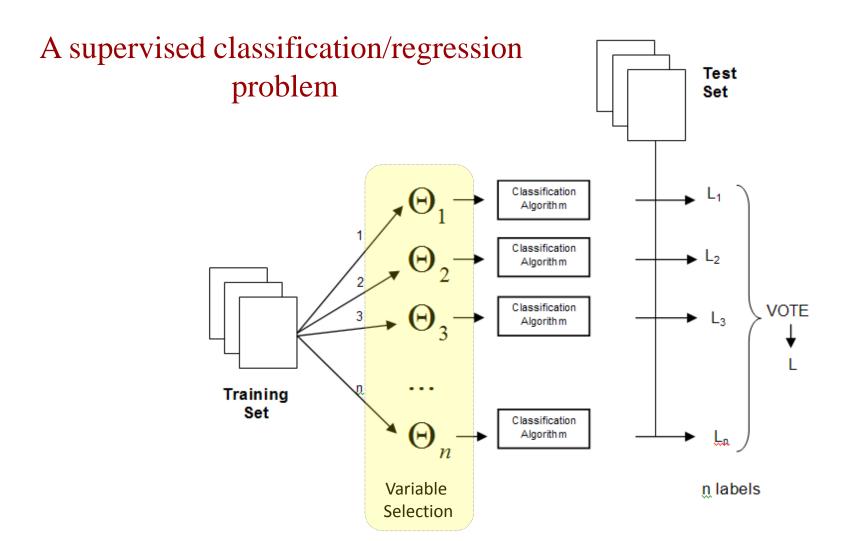
A Systems Biology Approach to Environmental Biology

Philipp Antczak

Why Systems Biology?



How do we deal with that much information?

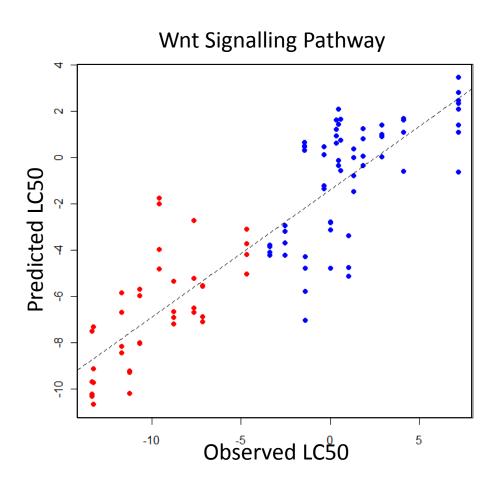


Genetic Algorithms and Bayesian Variable Selection

Trevino, V, & **F Falciani**, 'GALGO: an R package for multivariate variable selection using genetic algorithms.', Bioinformatics vol. 22, no. 9, 2006, pp. 1154-1156.

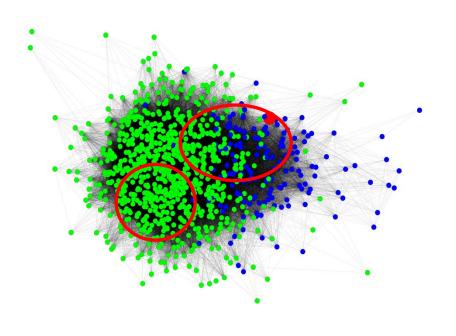
Sha N, Vannucci M, Tadesse MG, Brown PJ, Dragoni I, Davies N, Roberts TC, Contestabile A, Salmon M, Buckley C, **Falciani F**. Bayesian variable selection in multinomial probit models to identify molecular signatures of disease stage. Biometrics. 2004 Sep;60(3):812-9.

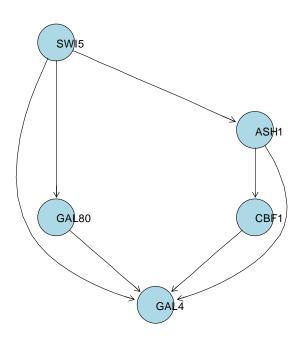
Linking endpoints to molecular response



Regulatory networks

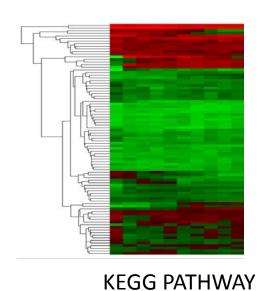
Static Dynamic





Gene-level analyses can be hard to interpret!

Simplifying the Problem by previous knowledge



Principal component 1

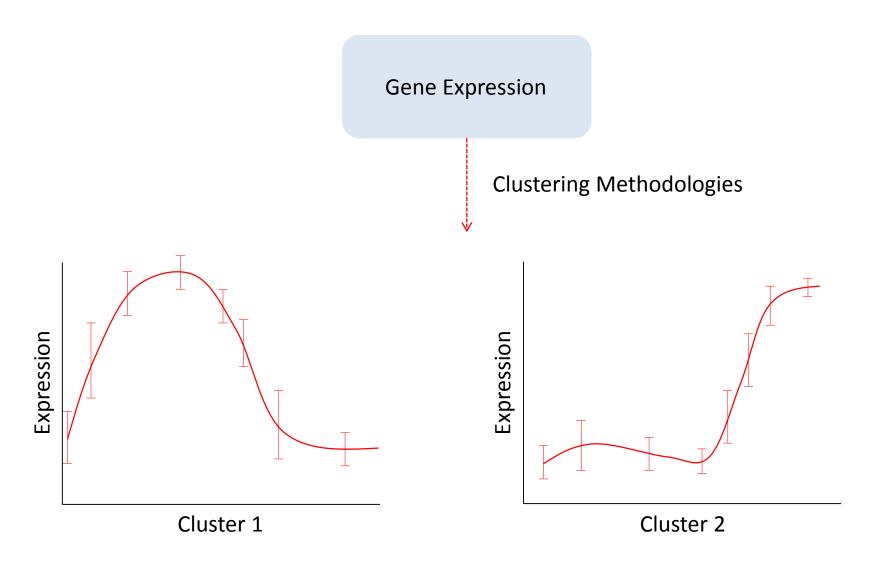
Gene 3 🚩

Gene 1

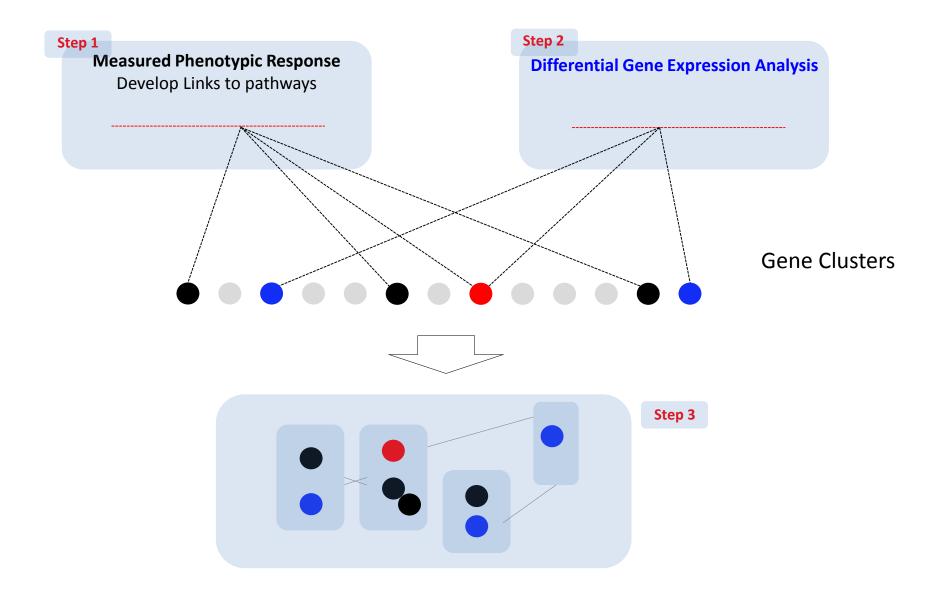
Principal component 2

Gene 2

Simplifying the problem by expression similarity

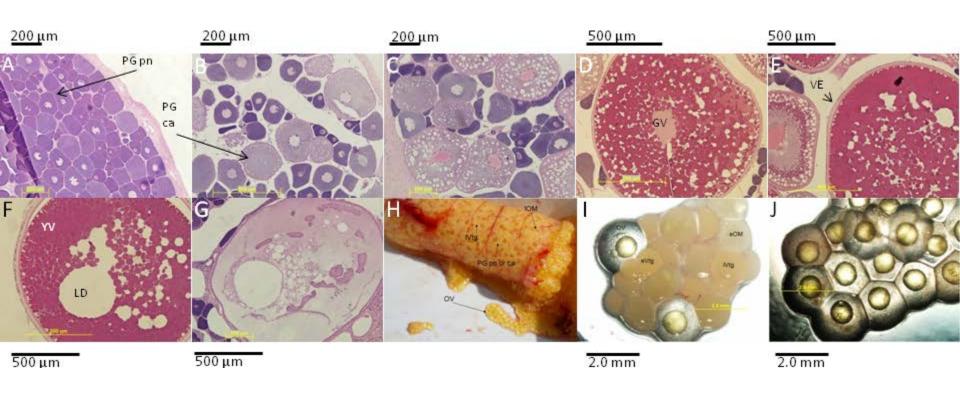


Combination into Workflows



How can we apply these techniques in environmental biology?

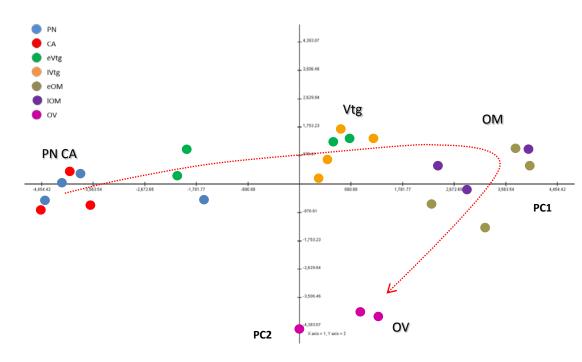
Case Study – Ovarian Maturation



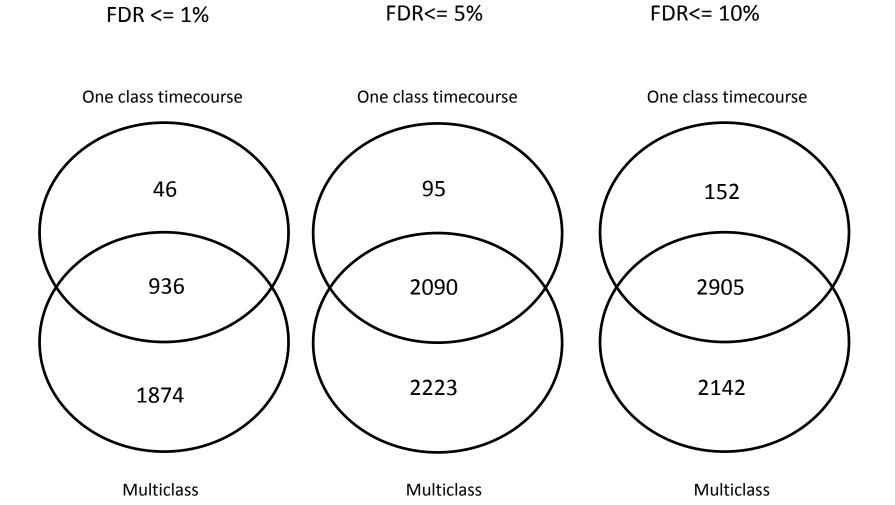
Martyniuk CJ, Prucha MS, Doperalski NJ, Antczak P, Kroll KJ, et al. (2013) Gene Expression Networks Underlying Ovarian Development in Wild Largemouth Bass (*Micropterus salmoides*). PLoS ONE 8(3): e59093. doi:10.1371/journal.pone.0059093

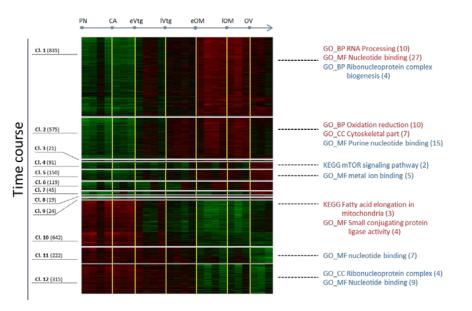


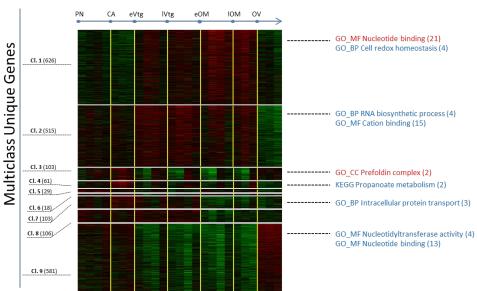


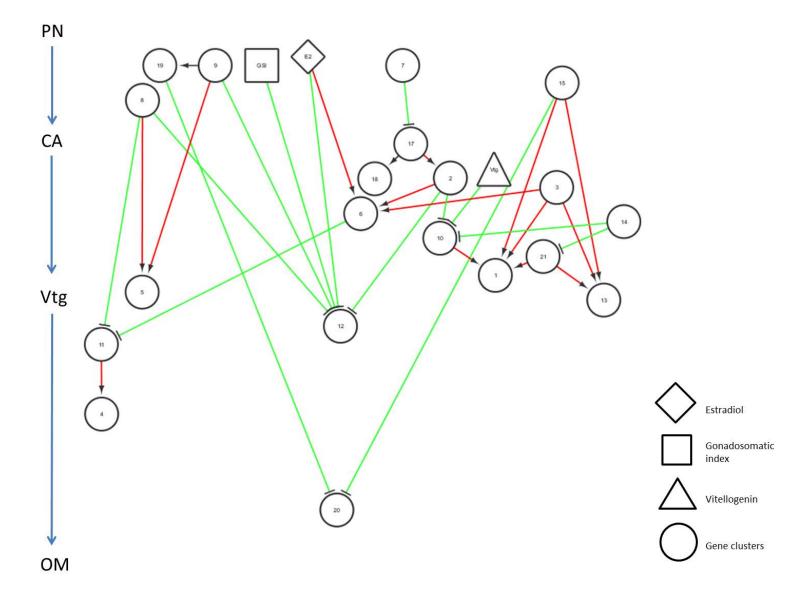


 Vitellogenin (Vtg), estradiol (E2) and Gonadosomatic index (GSI) measurments were taken at the sampling time.

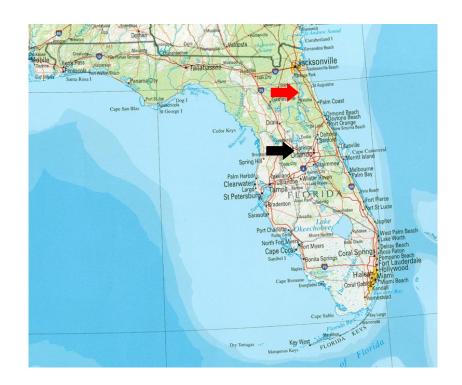


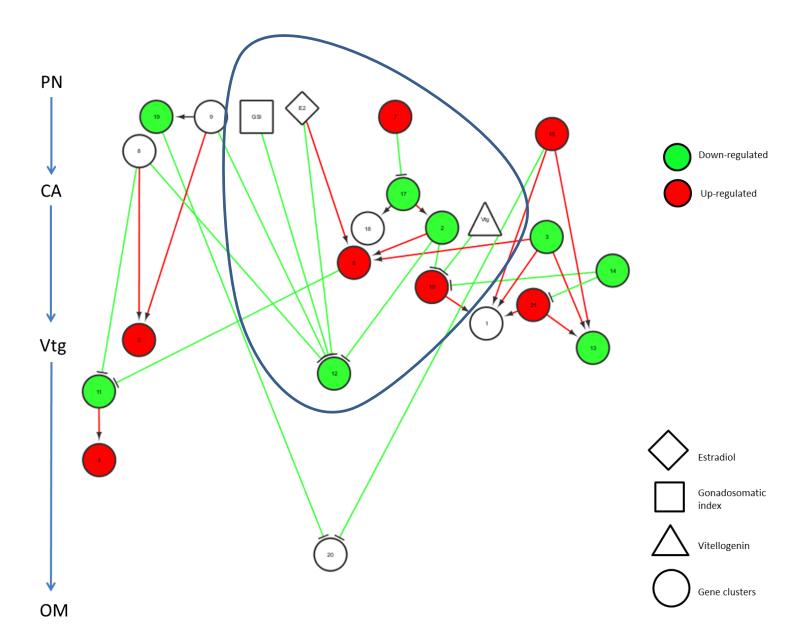


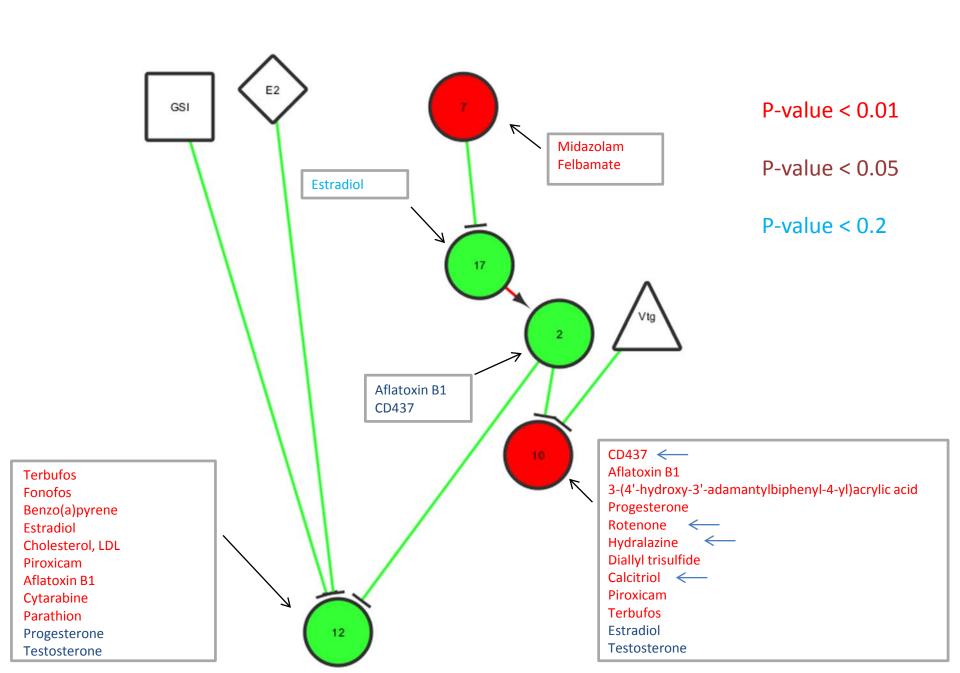


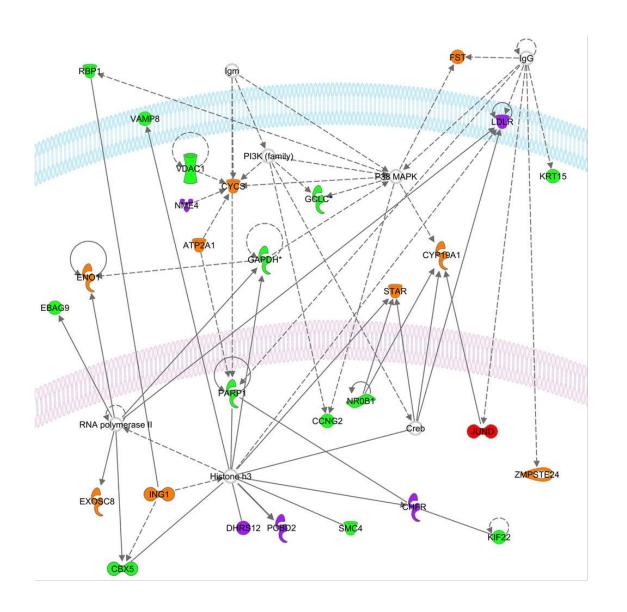


How does pollution perturb this network?

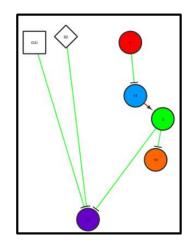








- Cluster 7
 Cluster 17
- Cluster 17
- Cluster 2
- Cluster 10
- Cluster 12

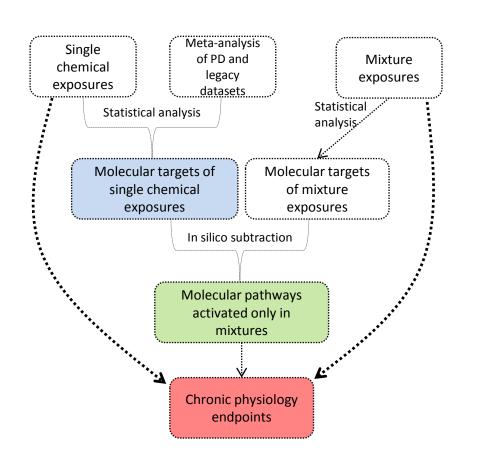


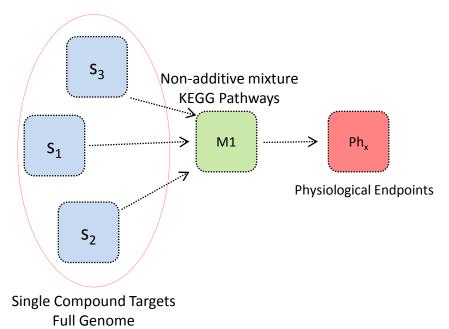
Discovering Adverse Outcome Pathways from molecular data

Example of complexity



High Level approach to pAOPs





Experimental System



Stickleback (*Gasterosteus aculeatus*):

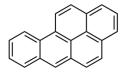
- widespread
- native UK species
- •annual reproductive cycle
- Cefas experience

- microarray and biomarkers developed
- •large enough to dissect tissues
- •small enough to maintain in the laboratory
- •well annotated draft genome sequence



DMSO: 88 mg/l (0.008%)

Solvent



Benzo(a)pyrene: 10μg/l

PAH

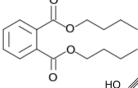
LC50: 1200, HEC: 96 μg/l

Cd²⁺

Cadmium: 65μg/l

Heavy metal

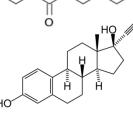
LC50: 6500, HEC: 4000 μg/l



Dibutyl phthalate: 35µg/l

Plasticizer

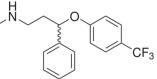
LC50: 350, HEC : 170 μg/l



Ethinyl estradiol: 0.06 μg/l

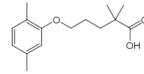
Endocrine disrupter

LC50: 1600, HEC 0.04 μg/l



Fluoxetine: 10μg/l CF₃ SSRI antidepressant

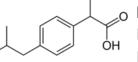
LC50: 700, HEC 1 μ g/l



Gemfibrozil: 50 μg/l

Fibrate

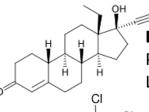
LC50: 22000, HEC : 5 μg/l



Ibuprofen: 50 μg/l

Painkiller

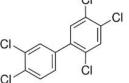
LC50: 7100, HEC : $28 \mu g/l$



Levonorgestrel: 0.05 µg/l

Progestin

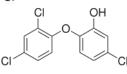
LC50: 6500, HEC : 0.015 μg/l



PCB-118: 1 μg/l

PCB

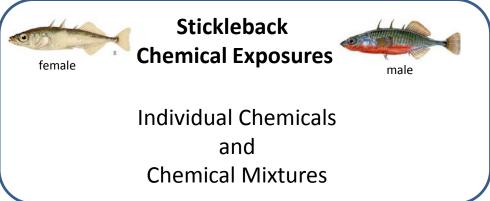
LC50: 15 μ g/l, HEC : 123 μ g/kg (sed)



Triclosan: 20 μg/l Antibacterial/fungal

LC50: 260, HEC : 5 μg/l

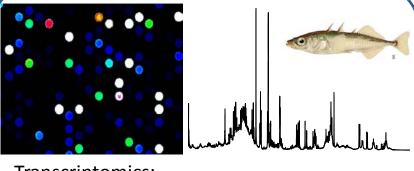
Experimental Scheme



Acute





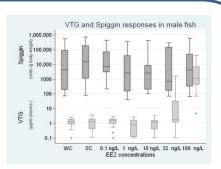


Transcriptomics:

Hepatic 8x15k Agilent stickleback microarray Metabolomics:

Hepatic polar and non-polar FT-ICR Mass Spectrometry



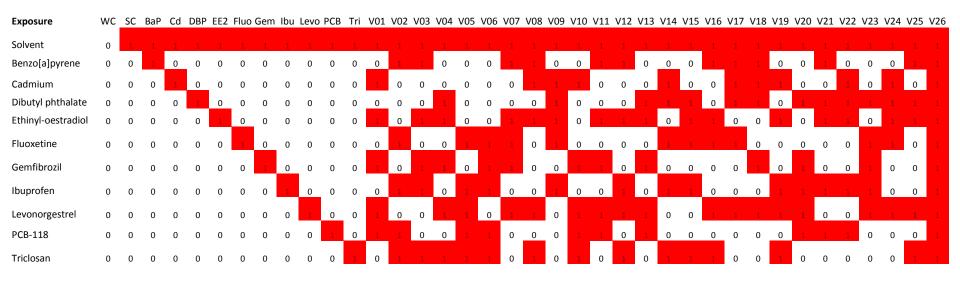


Stickleback morphology
Cortisol assay on tank water
Reproductive behaviour & output
Vitellogenin & Spiggin assays
Immunocompetence by pathogen challenge

Exposures:

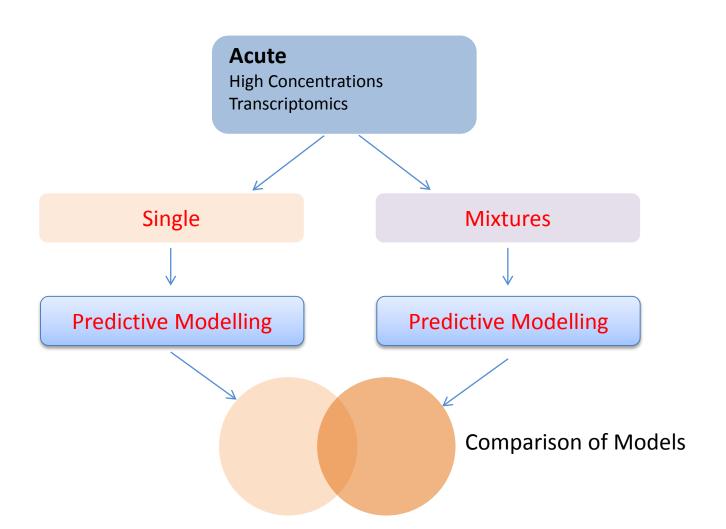
- •Each of 10 compounds singly, plus solvent
- •25 mixtures of 5 components plus solvent, one of all 10
- •10 sticklebacks per tank (mixed male and female)
- Solvent and water controls
- •Duplicate tanks for each exposure = 80 tanks with 800 fish
- •Acute = 4 day exposure (complete)
- •800 sticklebacks sexed, livers dissected and frozen at -80C
- •Chronic = 4 months (2014)
- Chemical analysis: Passive samplers (selected tanks; 2013-14)

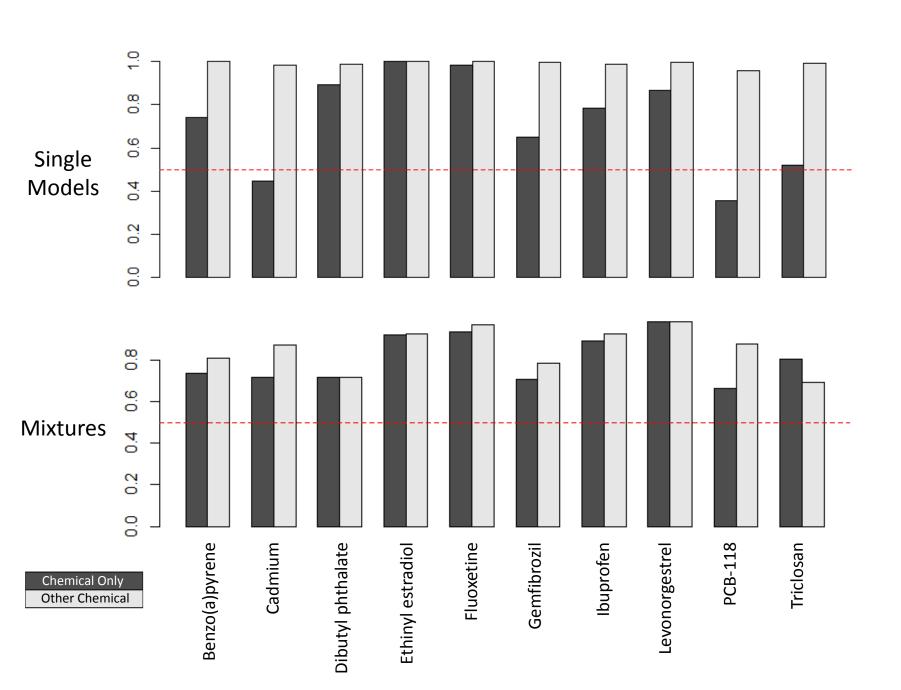




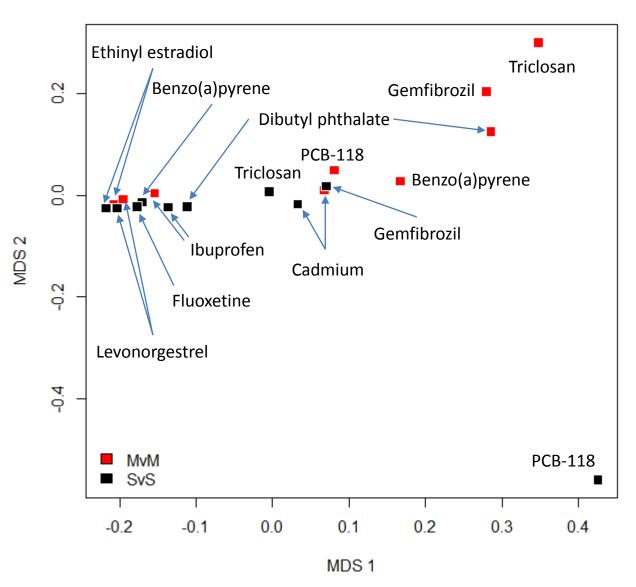
Multi-Step Modelling Procedure

Model 1 – Prediction of Compound presence



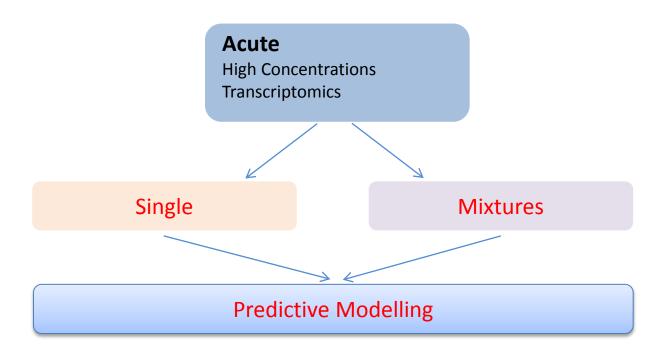


Comparing Model Space



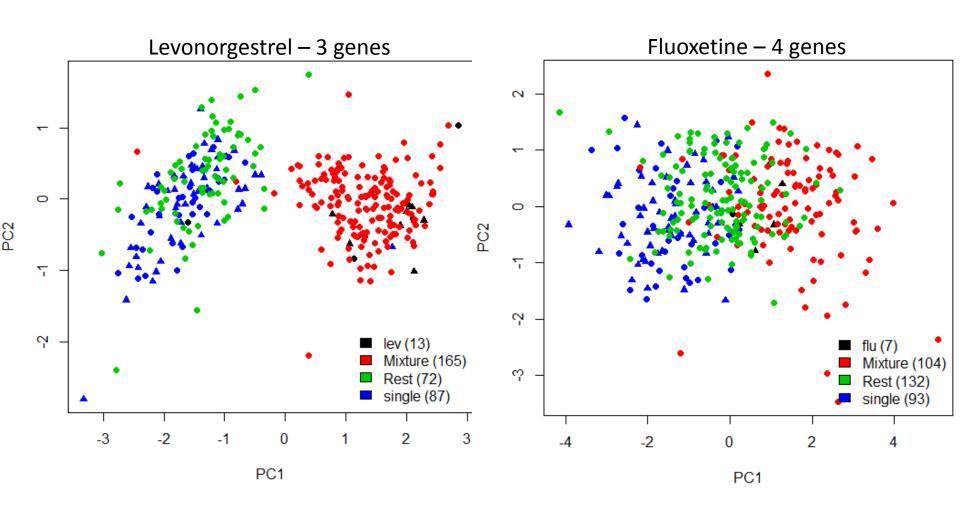
Multi-Step Modelling Procedure

Model 2 – Model Refinement

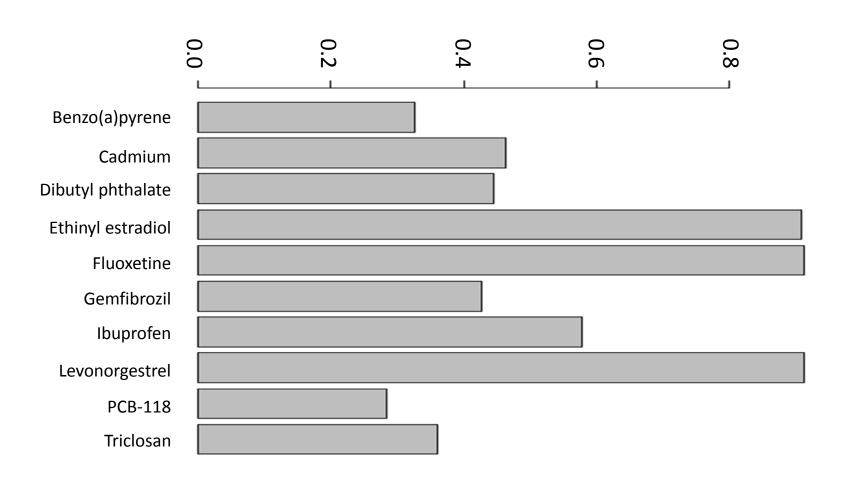


Building Models Predictive in both Single and Mixtures

Predicting exposure to single and mixture exposures

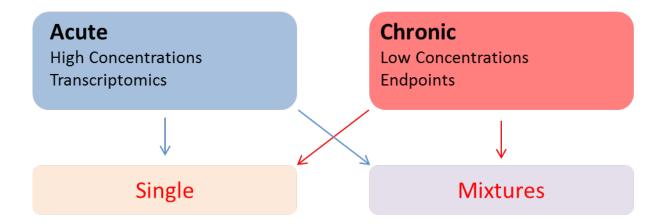


Models predictive of both Single and Mixtures

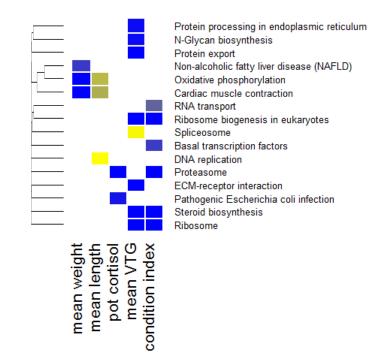


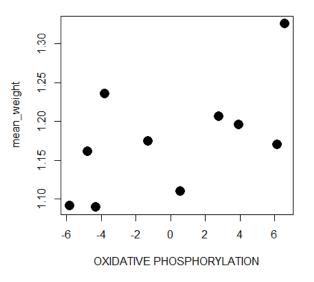
Multi-Step Modelling Procedure

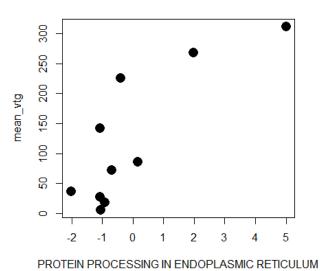
Model 3 – Linking Chronic phenotypes to early molecular response

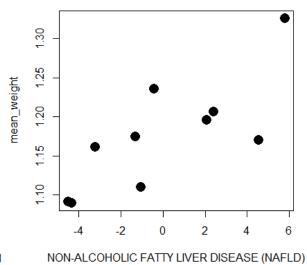


Pathway to Phenotype Association

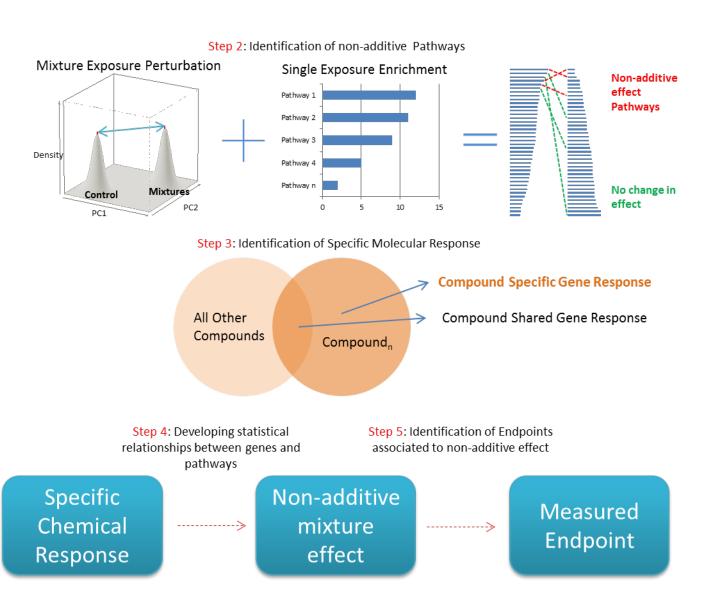




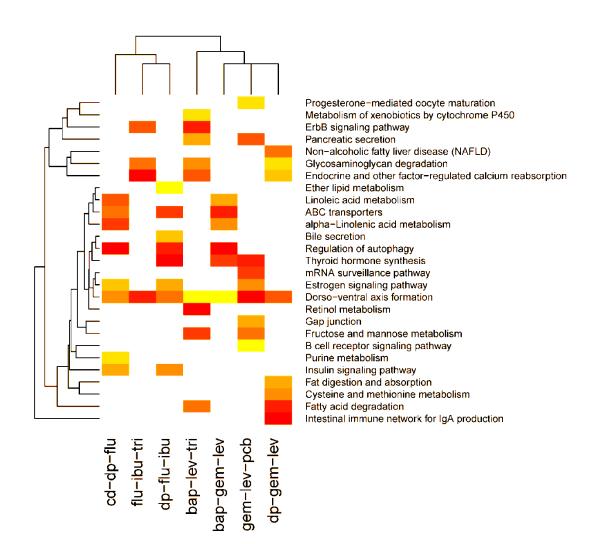




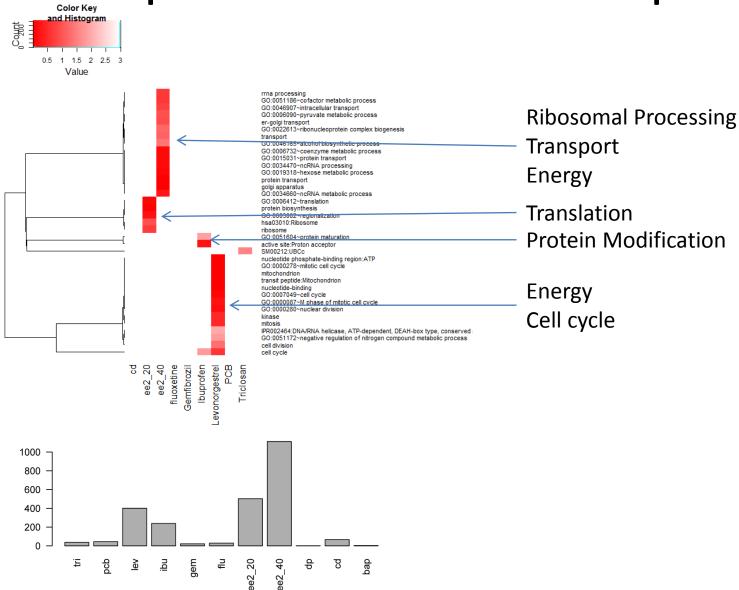
Multi-Step Modelling Procedure



Non additive effect Pathways



Specific Molecular Response



Underlying model

- Genetic Algorithm based optimization technique (GALGO library R)
 - RandomForest regression

$$\begin{aligned} & PC_{i,k} \\ &= gene_{Compound1} + gene_{Compound2} \\ &+ gene_{Compound3} + d + \epsilon \end{aligned}$$

Putative mixture AOPs

Identify differentially expressed genes from Single exposures



Identify Pathways only expressed in mixtures



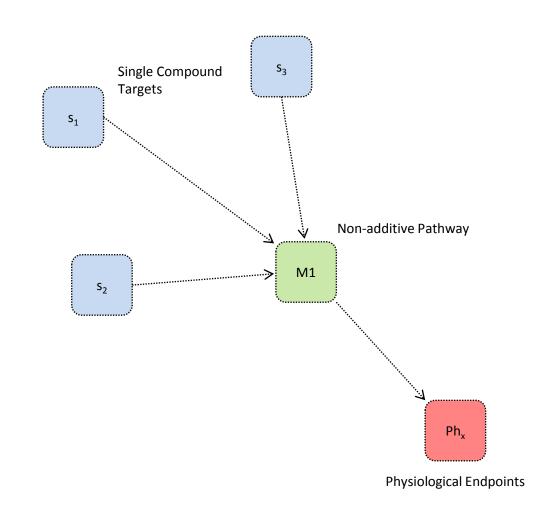
Link genes from single exposures (1 per compound) to pathways



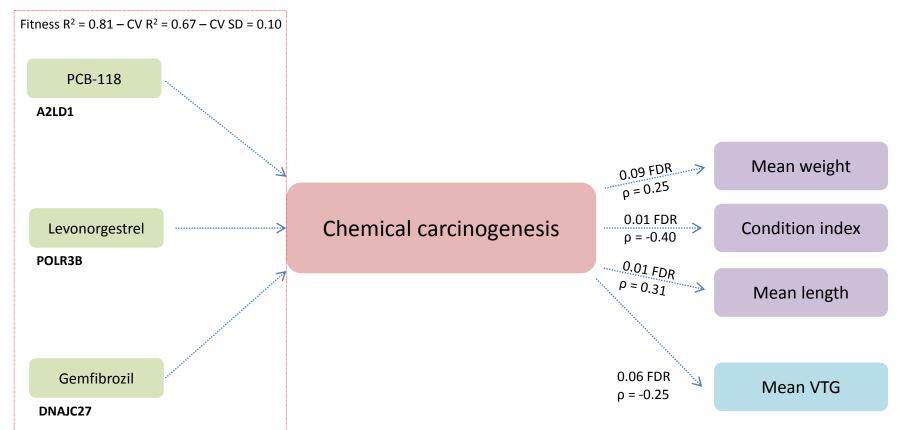
Link physiological endpoints to pathways

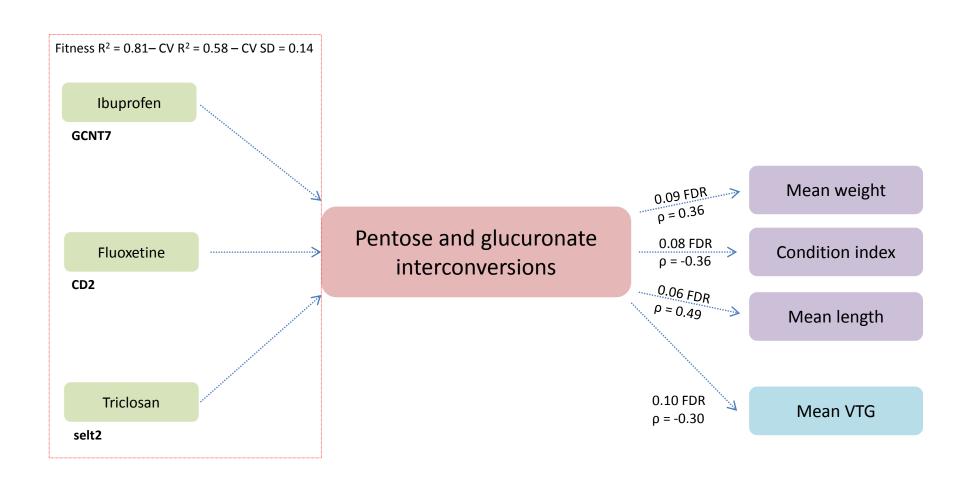


Derive mixture AOP based on best model fit

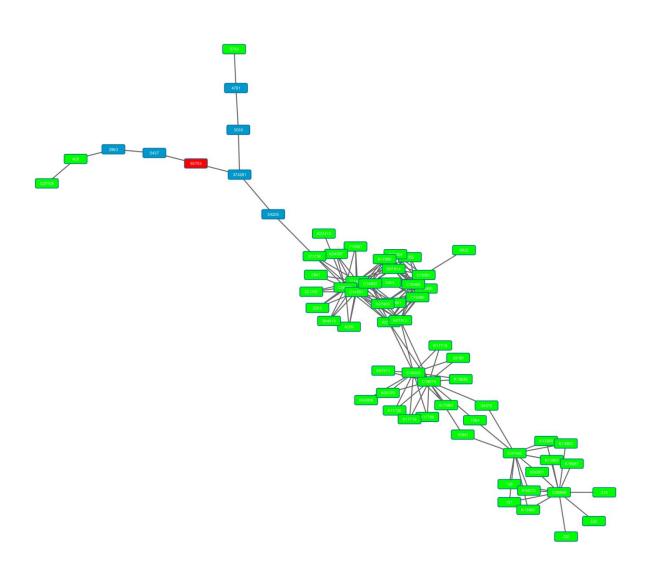


Integrating and identifying pAOPs

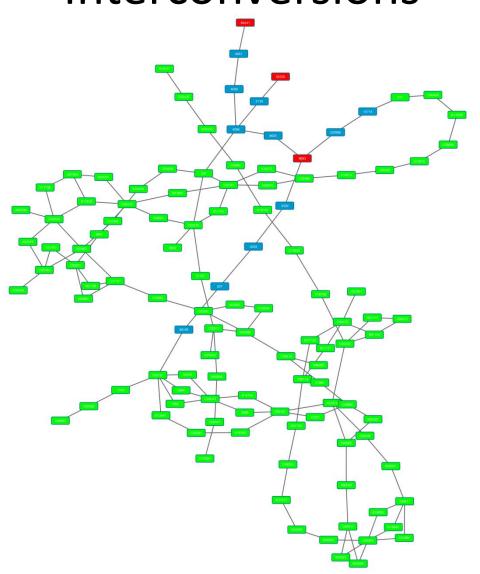




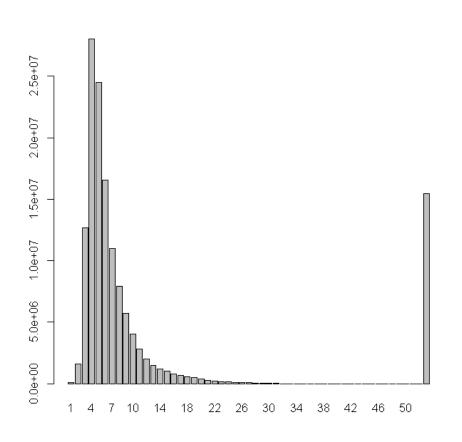
Chemical Carcinogenesis

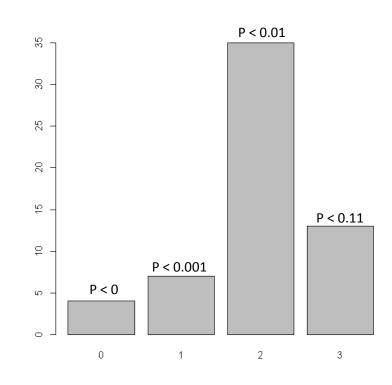


Pentose and glucuronate Interconversions



Shortest Paths within KEGG+MiMI





Summary

- Molecular data can be used as a predictive tool to identify and classify samples
- We are able to develop models linking single chemical exposure, non-additive mixture effect and phenotypic endpoints to develop putative mixture adverse outcome pathways
- We need to develop more quantitative/predictive Adverse Outcome Pathways to support risk assessment.

The next challenge

- Predictive/quantitative Adverse Outcome Pathways
- Cross species extrapolation of adverse outcome pathways
- Interactions between chemicals and a changing environment
- Robust molecular models for mTIE (molecular toxicity identification and evaluation) across large numbers of compounds
- Mixture AOPs linking single exposures to expected phenotypic effect and population outcome

Acknowledgements

University of Liverpool

Prof. Francesco Falciani

Kim Clarke

Jaanika Kronberg

John Herbert

John Ankers

Peter Davidsen

Cefas

Ioanna Katsiadaki

Marion Sebire

Jessica Tasker

Jenni Prokkola

Brett Lyons

Tim Bean







University of Birmingham

Prof. Mark Viant

Tom White

Prof. Kevin Chipman







