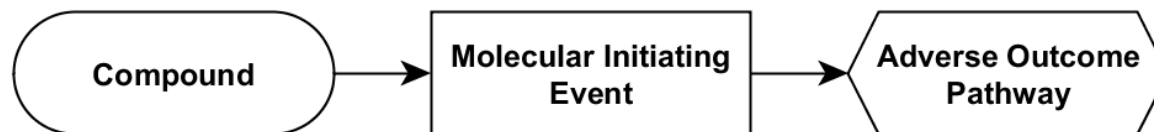


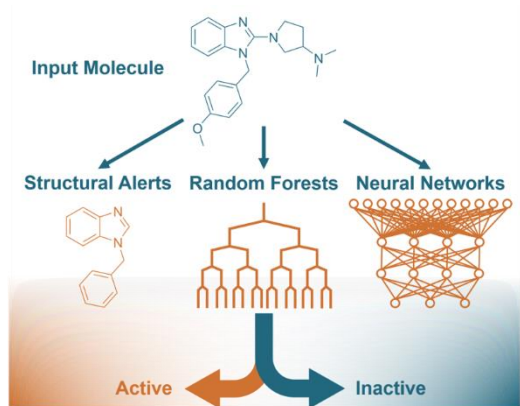
# Use of chemical informatics, quantum chemistry modelling and artificial intelligence algorithms to predict molecular initiating events



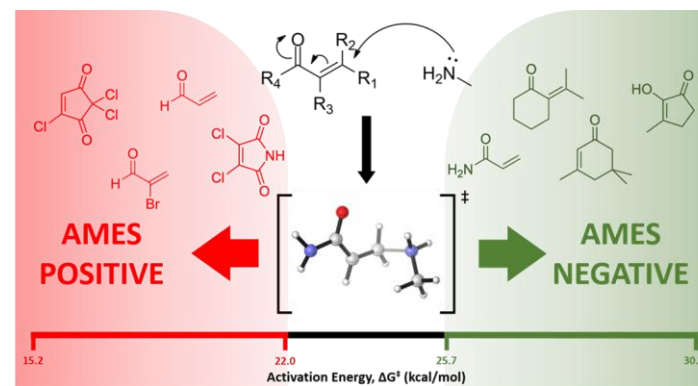
Timothy E H Allen – [teha2@cam.ac.uk](mailto:teha2@cam.ac.uk)

AJ Wedlake, MN Grayson, AM Middleton, M Folia, M Baltazar, P Piechota, E Gelžinytė, JM Goodman, PJ Russell, P Kukic, S Gutsell

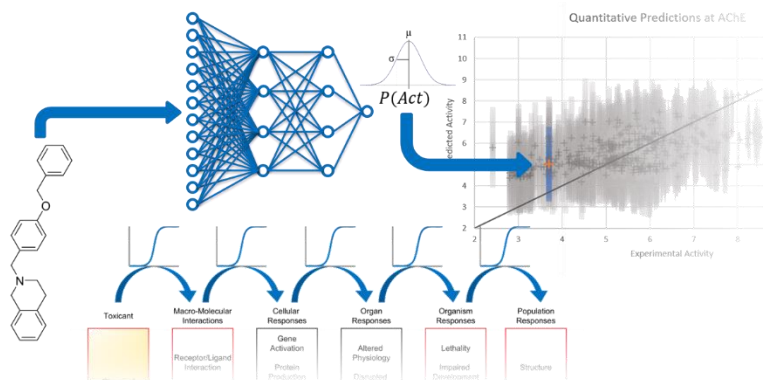
EUROTOX – 27<sup>th</sup> September 2021



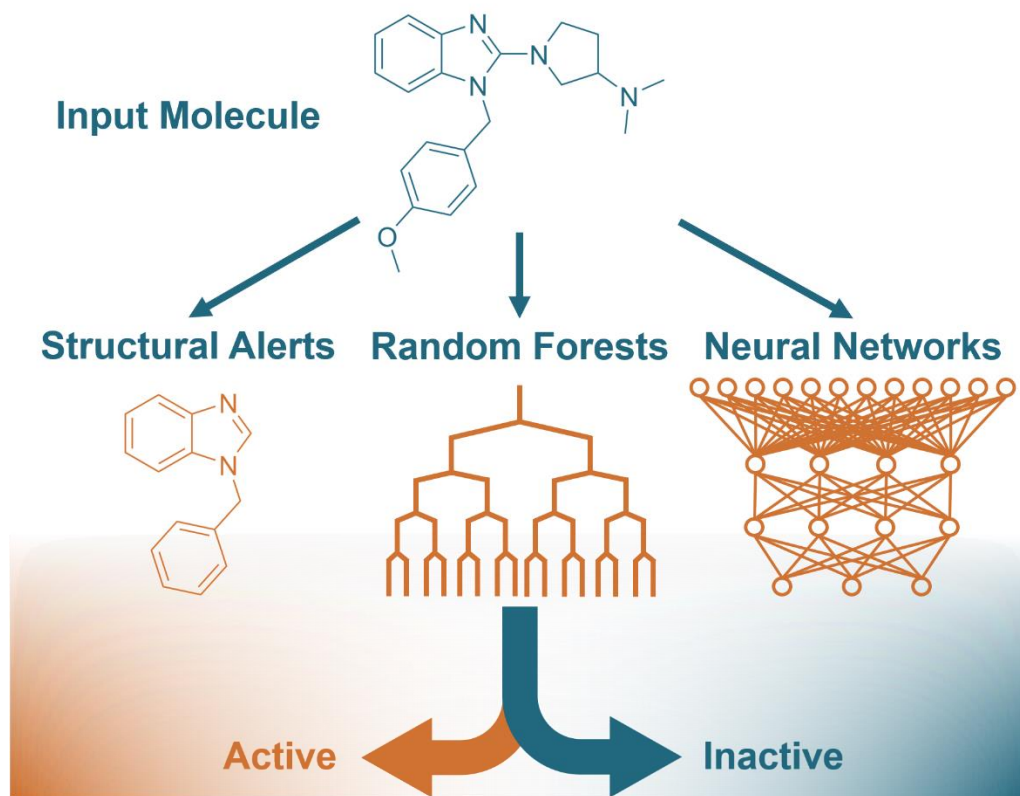
**Mechanistic Toxicity Predictions**



**Quantum Chemistry Predictions**



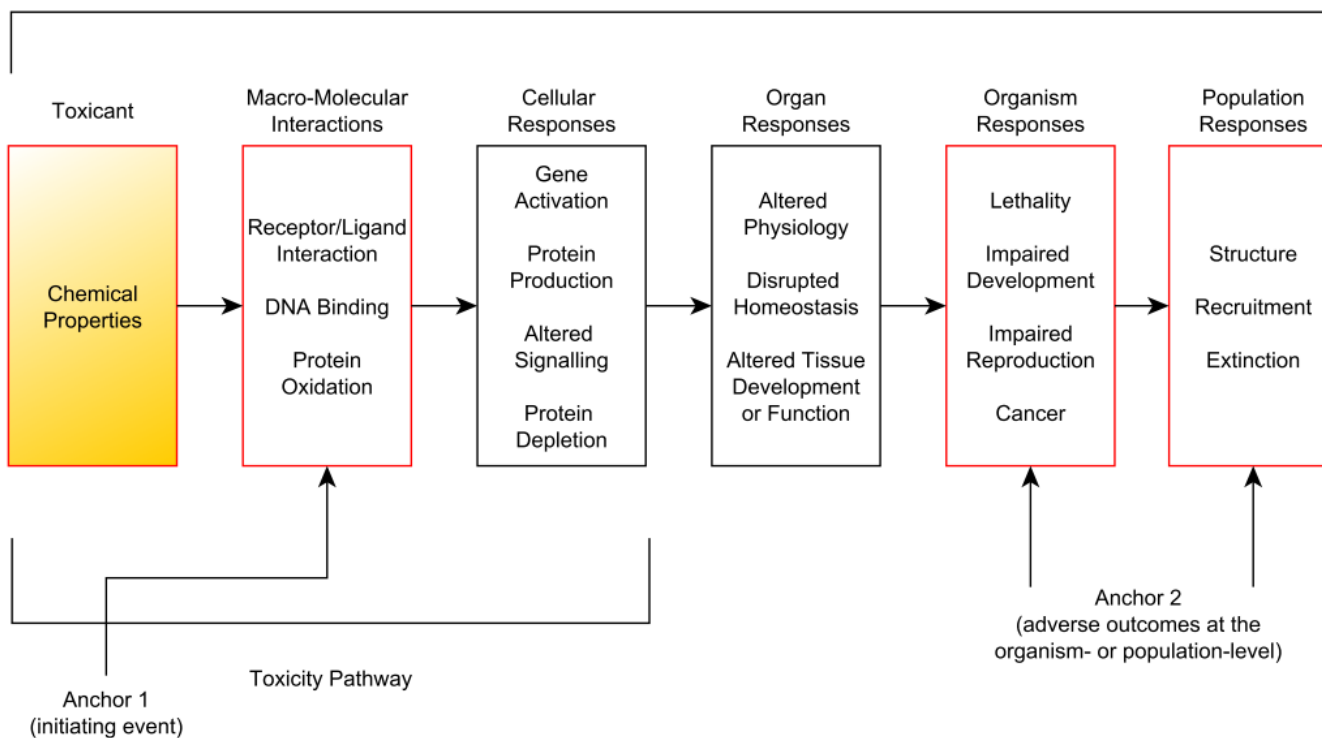
**Bayesian Neural Networks**



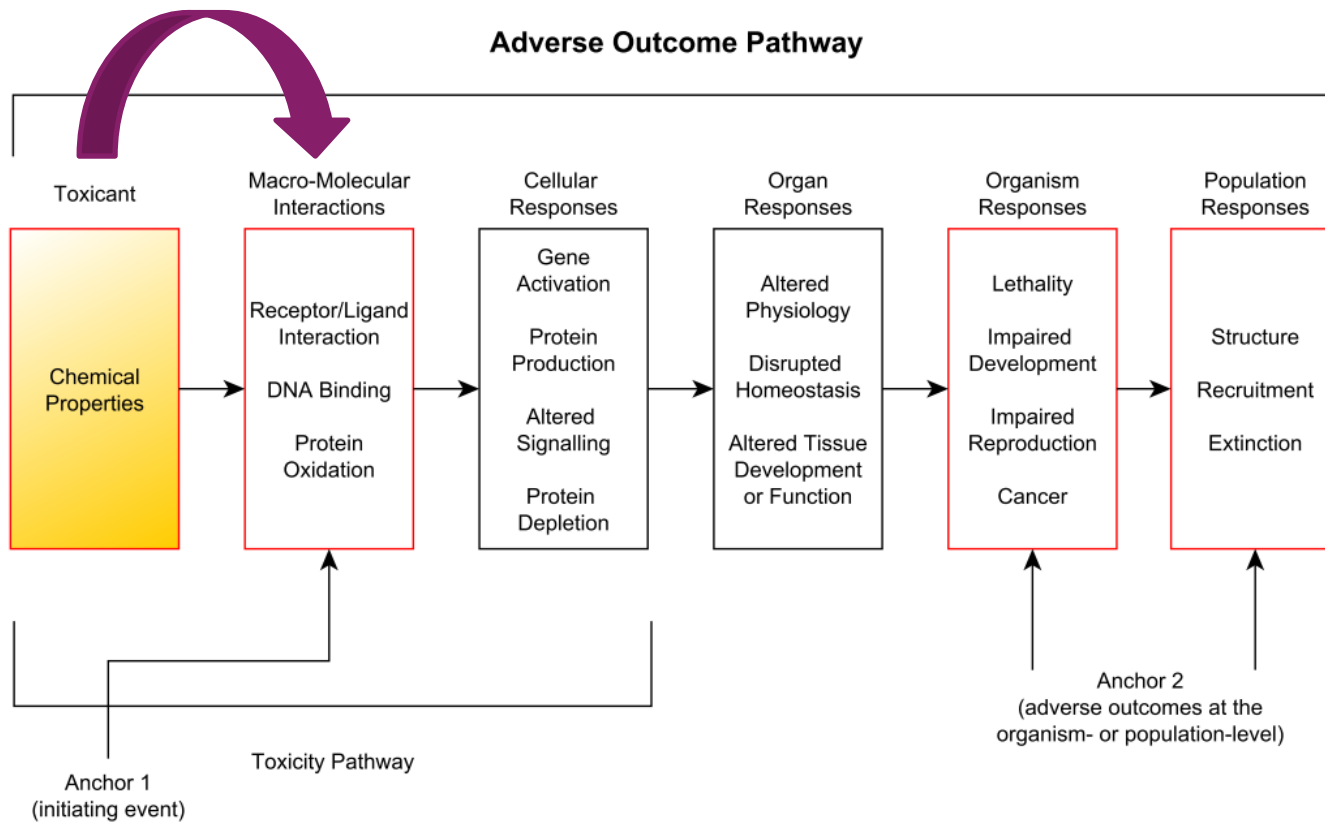
# Mechanistic Toxicity Predictions

# Adverse Outcome Pathway

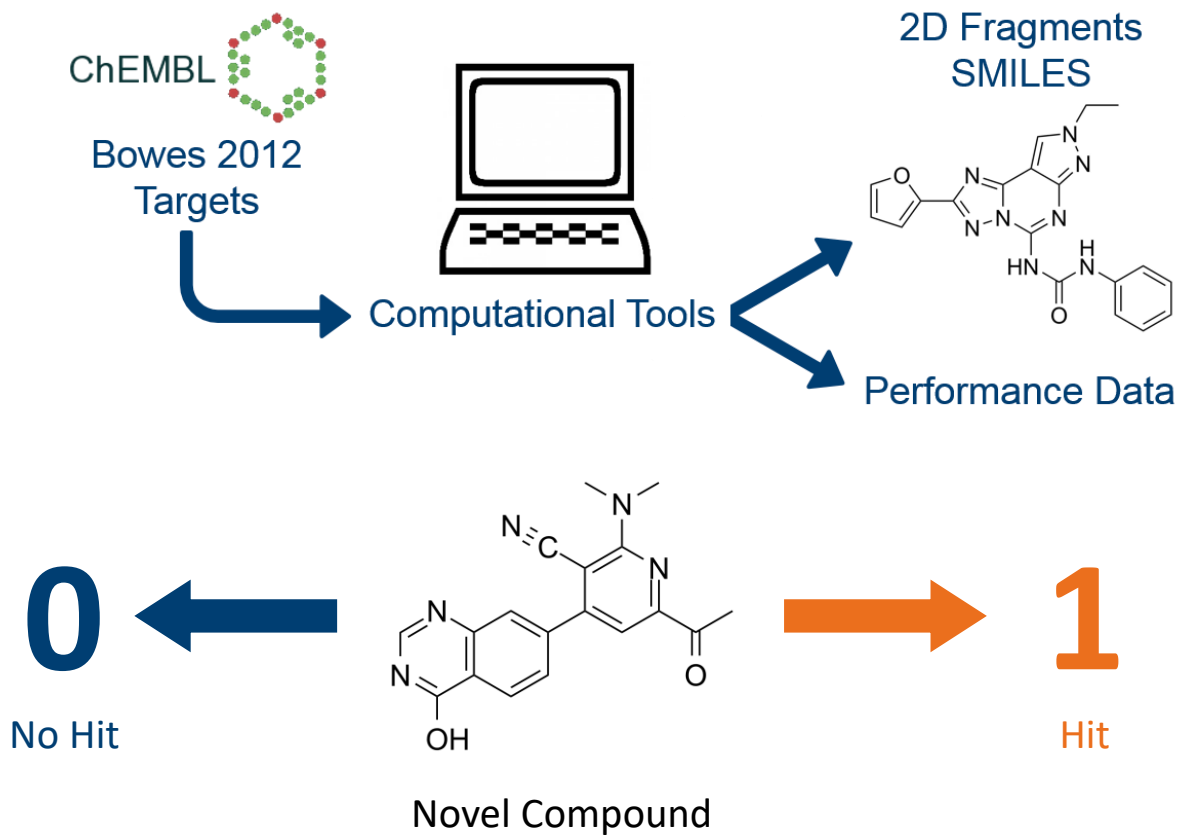
## Adverse Outcome Pathway



# Adverse Outcome Pathway

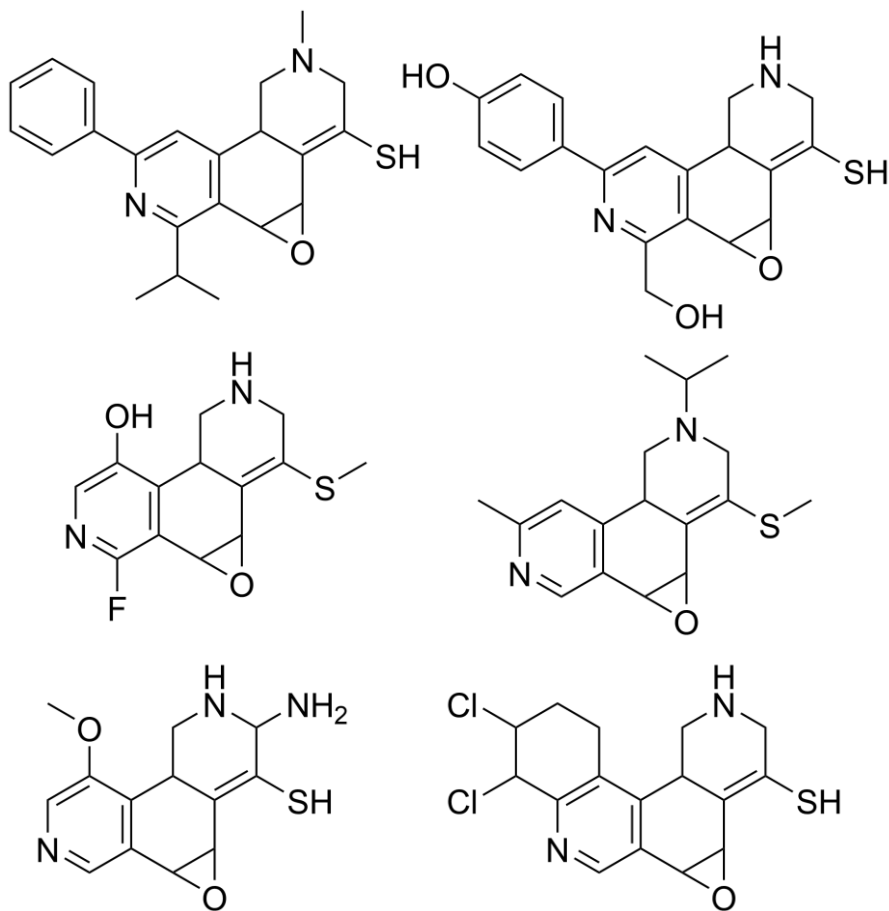


# Structural Alerts



Allen, T.E.H. *et al.* (2018) *Toxicol. Sci.*, 165; 213.  
Wedlake, A.J. *et al.* (2019) *Chem. Res. Toxicol.*, 33; 388.

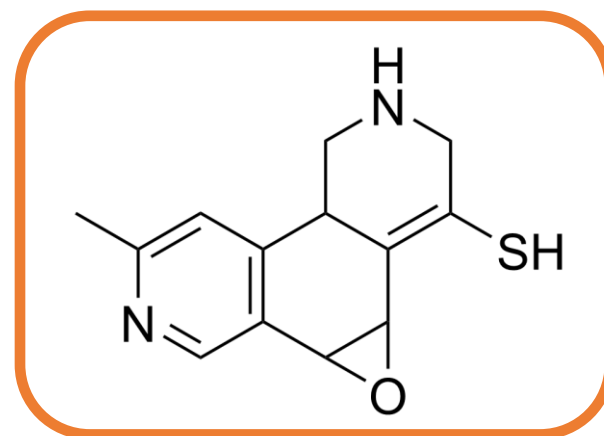
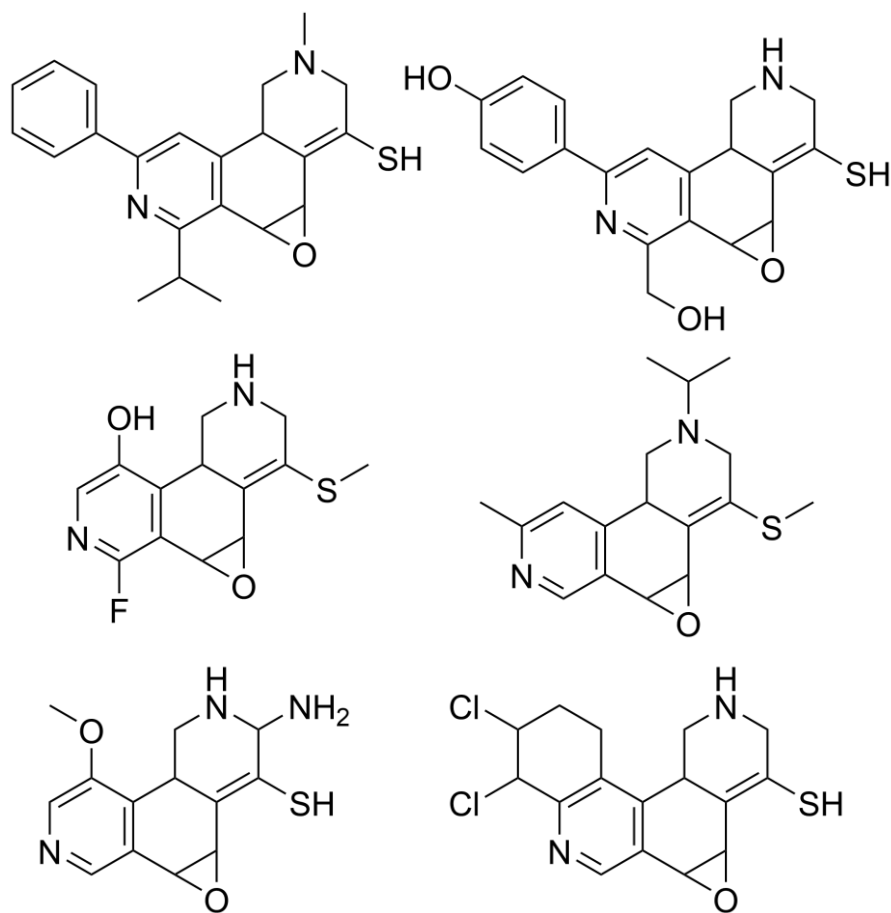
# Maximal Common Substructure



# Maximal Common Substructure

MRC

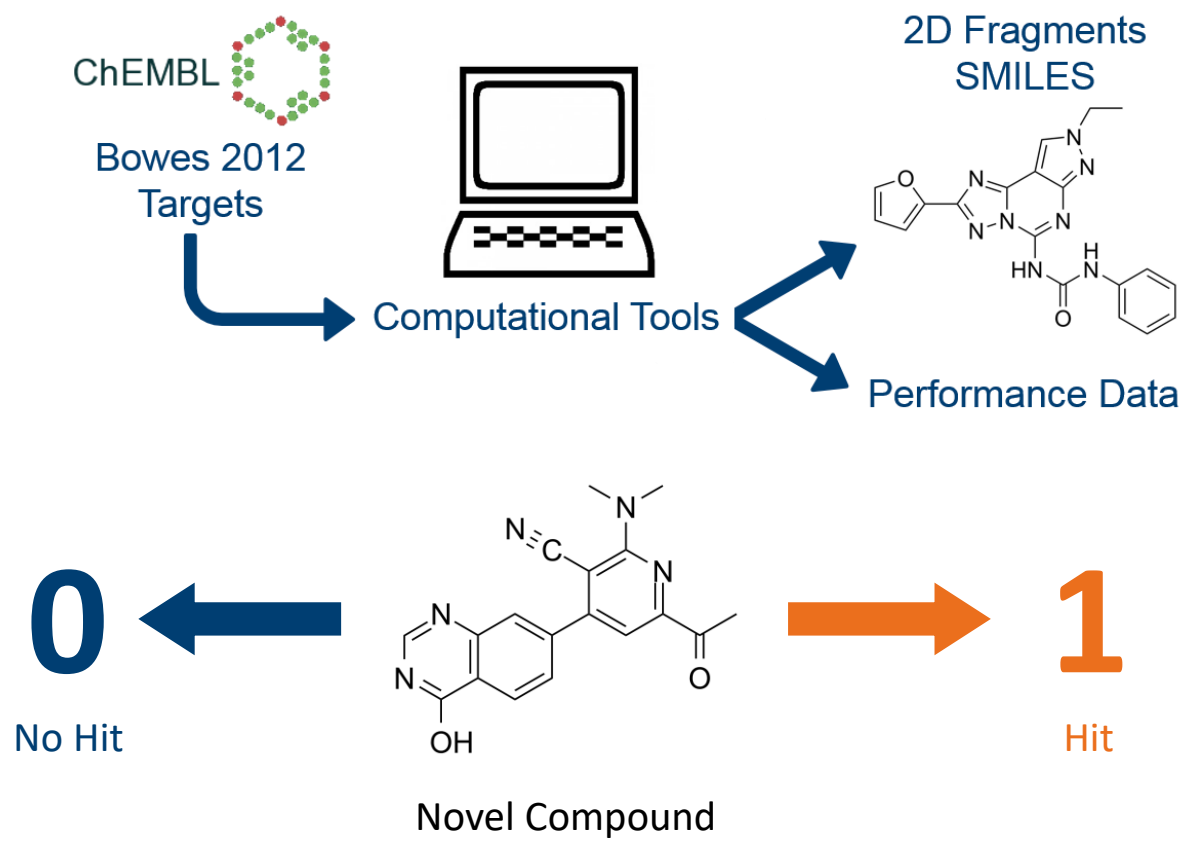
Toxicology  
Unit



Present in 6 of 6  
chemicals

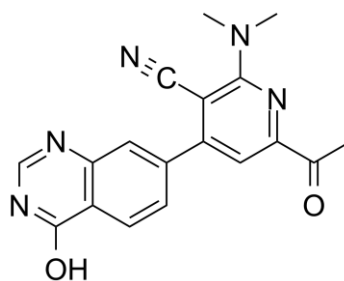


# Structural Alerts

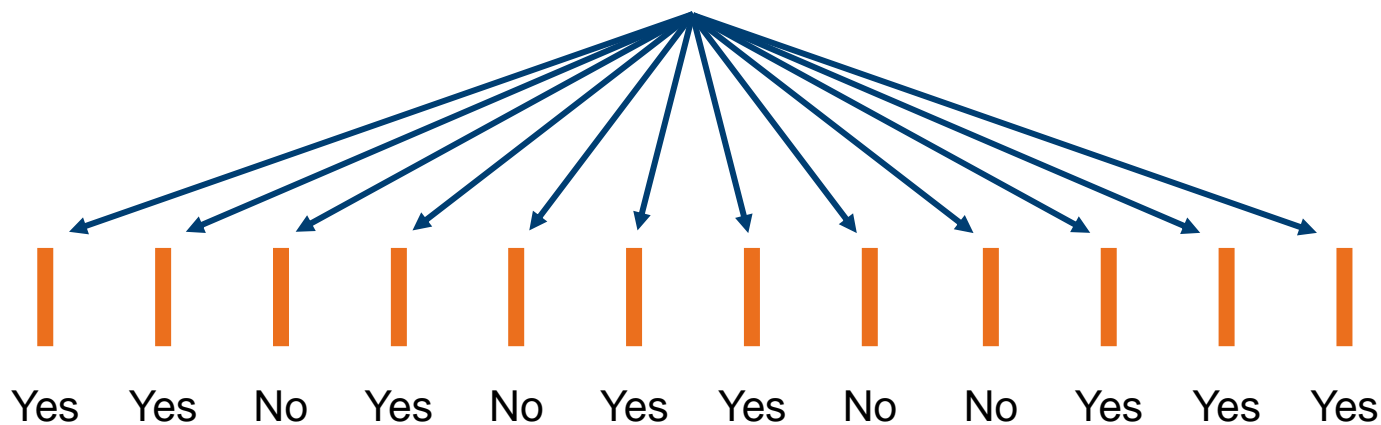


Allen, T.E.H. *et al.* (2018) *Toxicol. Sci.*, 165; 213.  
Wedlake, A.J. *et al.* (2019) *Chem. Res. Toxicol.*, 33; 388.

# Random Forest

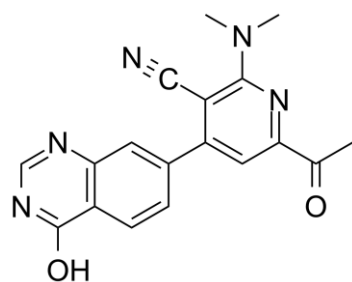


Novel Compound

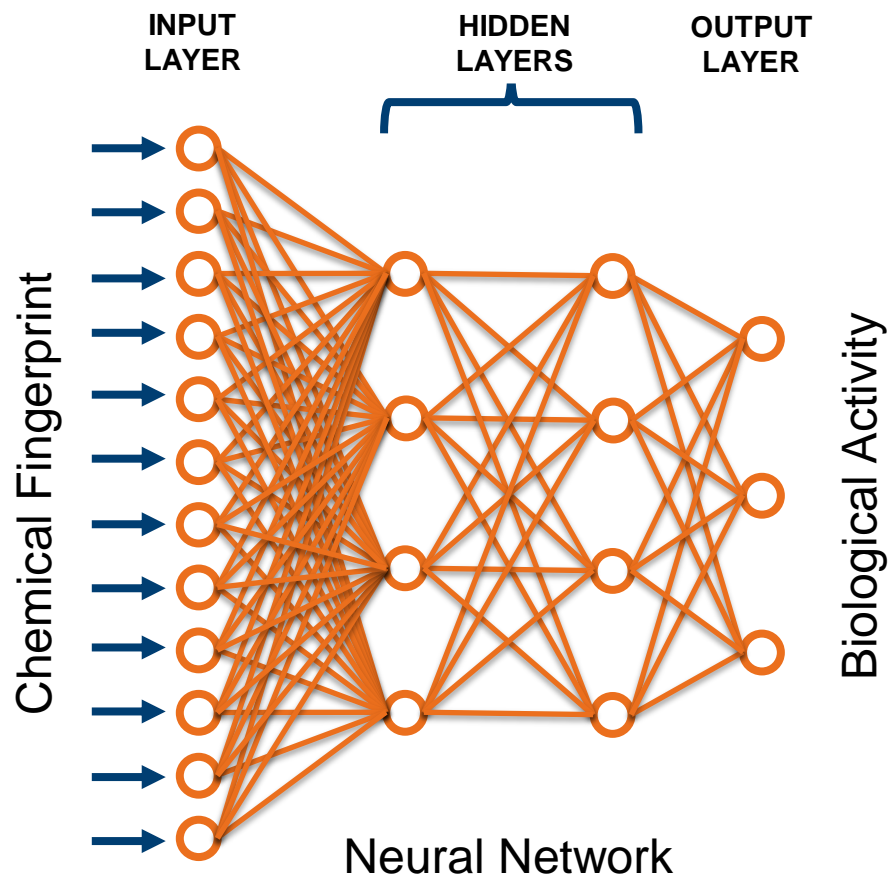


8/ 12 Trees predict Yes  
Therefore overall prediction is Yes

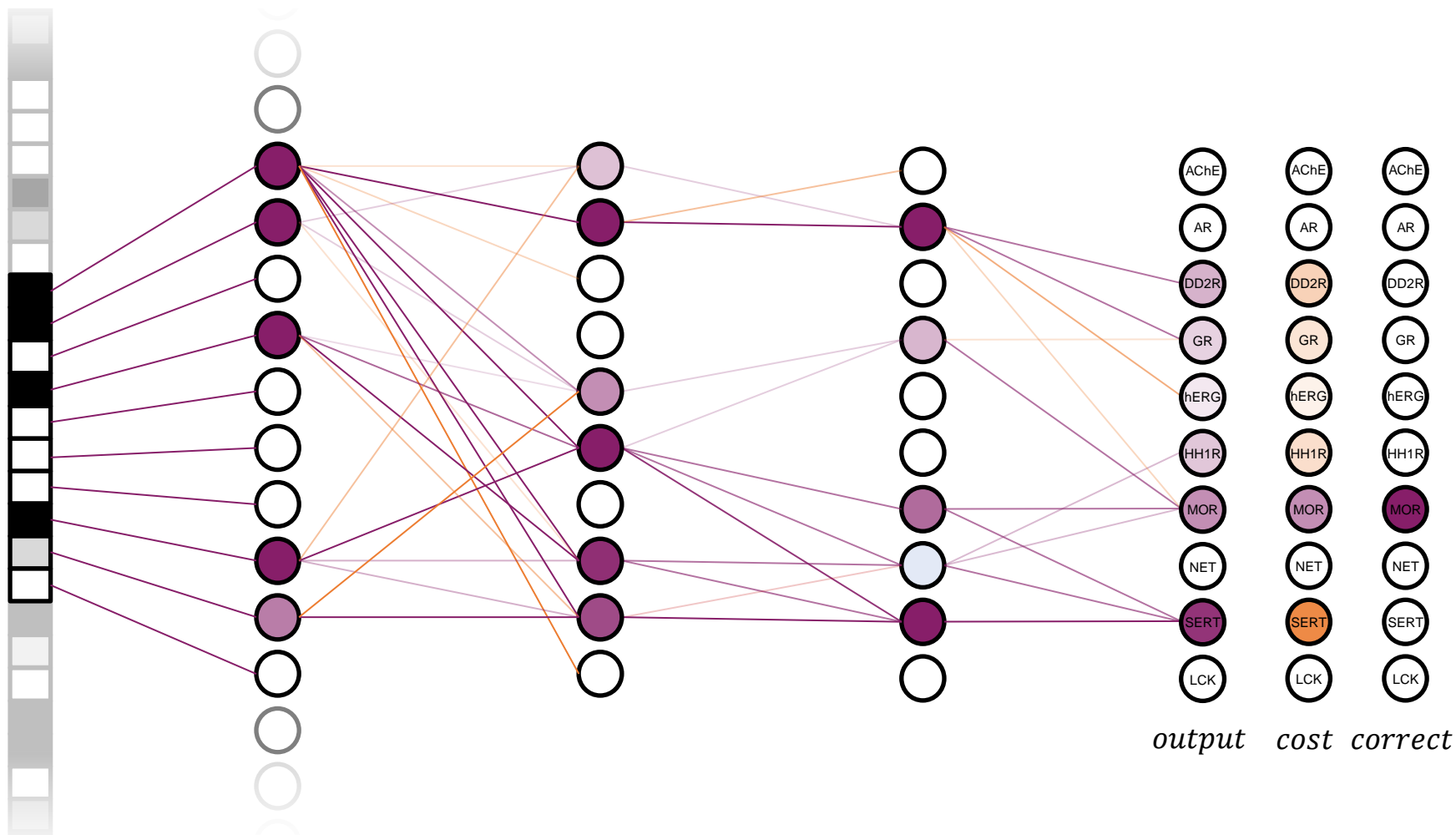
# Neural Network



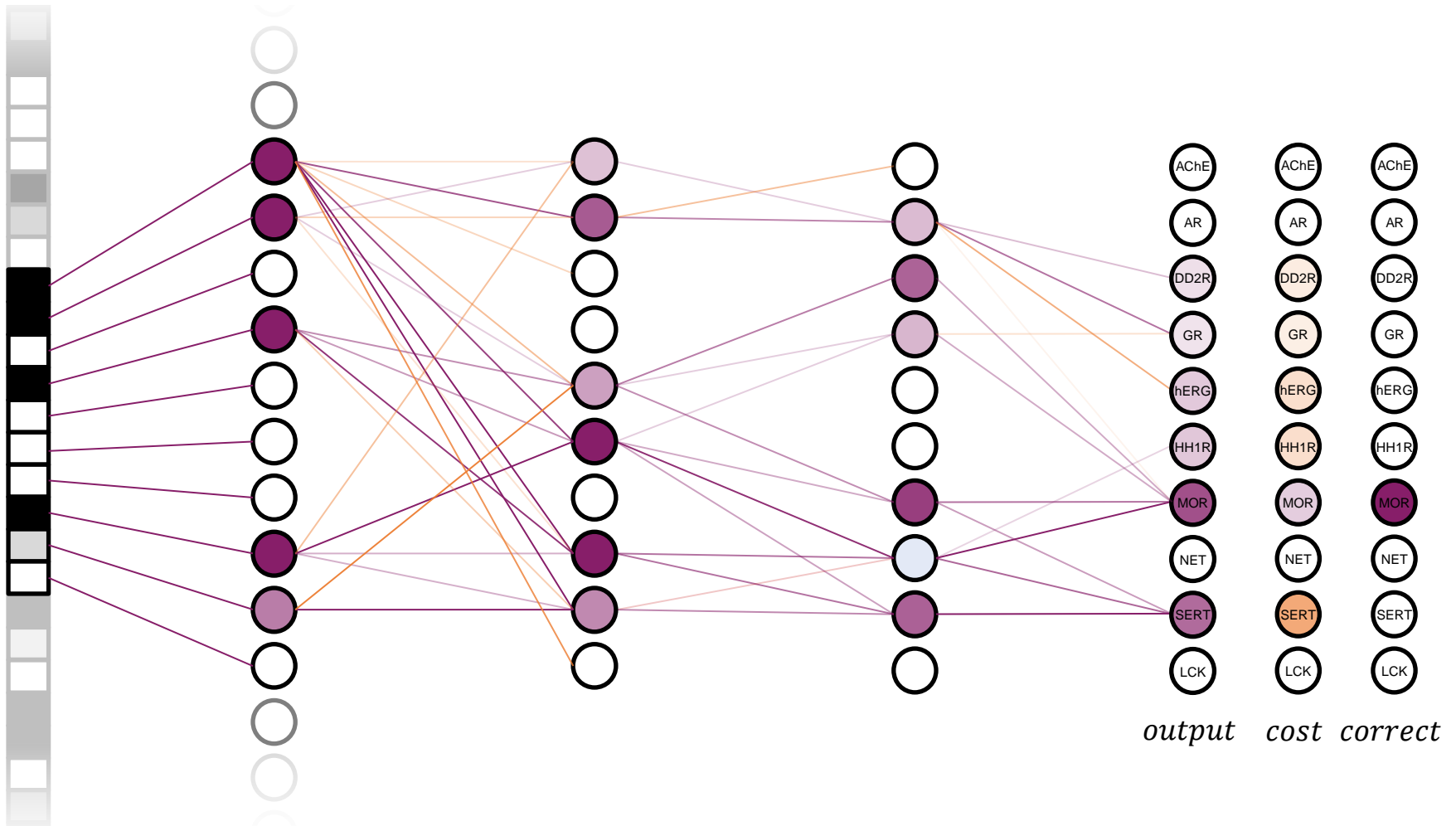
Novel Compound



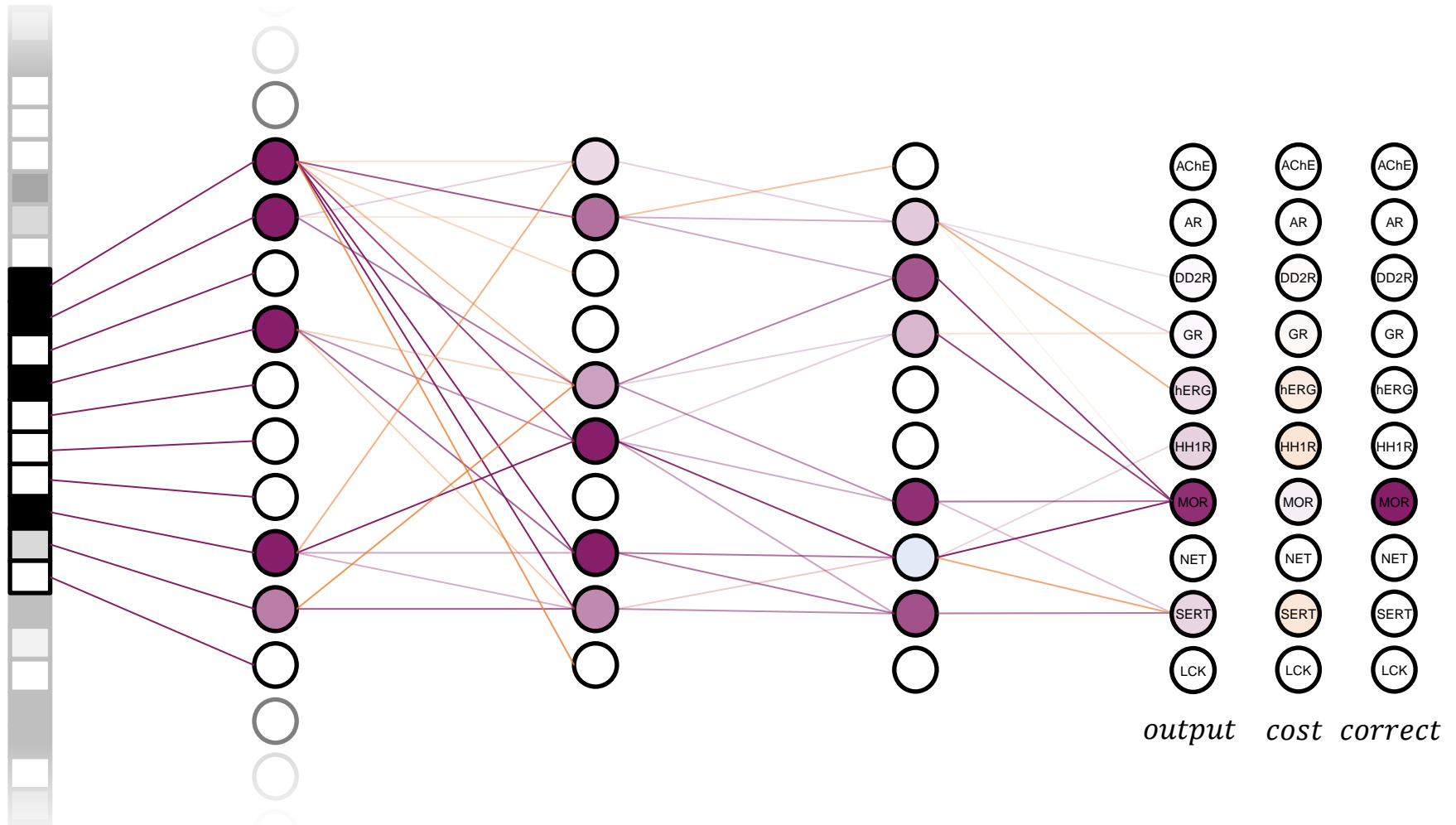
# Neural Network



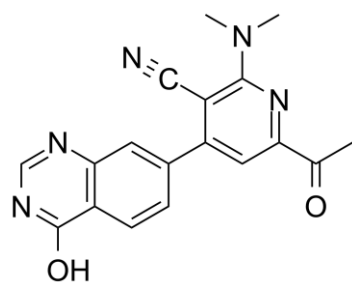
# Neural Network



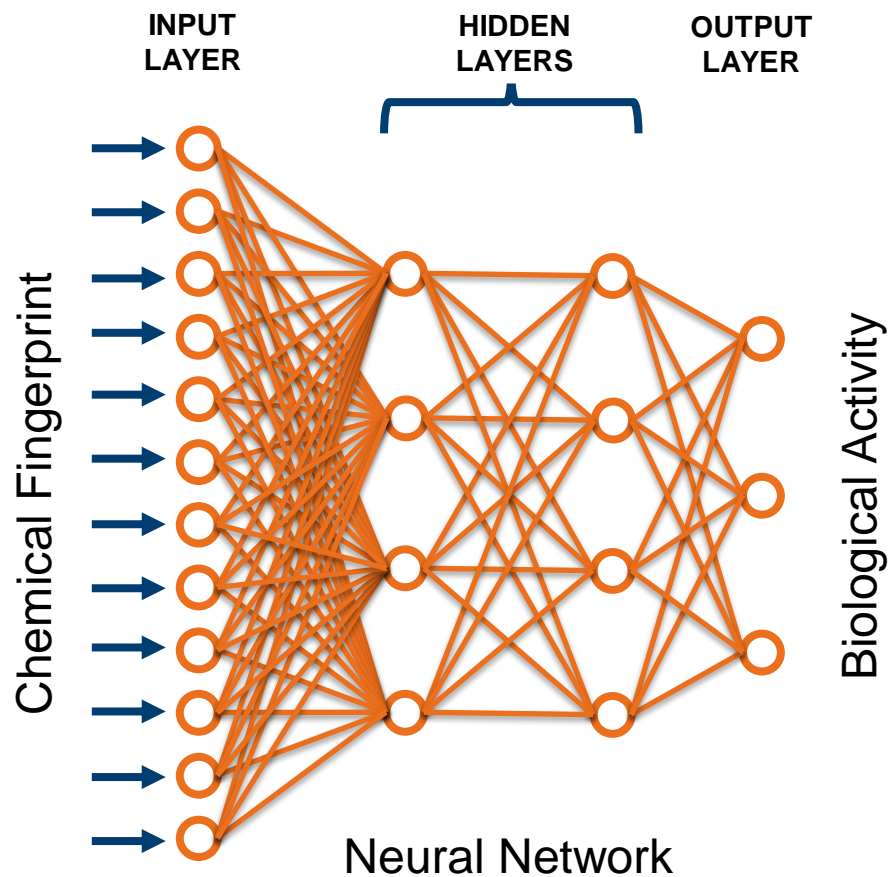
# Neural Network



# Neural Network



Novel Compound



# Model Performance

		Held Out Test Data			
		SE	SP	ACC	MCC
Structural Alerts	Average	84.1	93.5	91.1	0.790
	SD	11.6	4.6	4.2	0.096
Random Forests	Average	89.0	90.4	92.2	0.815
	SD	11.6	8.1	4.0	0.091
Neural Networks	Average	87.8	93.6	92.8	0.832
	SD	10.4	5.9	4.0	0.089

*SE = sensitivity (percentage active chemicals correctly assigned)*

*SP = specificity (percentage negative chemicals correctly assigned)*

*ACC = overall quality (percentage of chemicals correctly assigned)*

*MCC = Matthews correlation coefficient (score from -1 to 1 with a higher score indicating a better model. scores account for imbalance in dataset)*

Wedlake, A.J. *et al.* (2019) *Chem. Res. Toxicol.*, 33; 388.

Allen, T.E.H. *et al.* (2020) *Chem. Sci.*, 11; 7335.



## Structural Alerts and Random Forest Models in a Consensus Approach for Receptor Binding Molecular Initiating Events

Andrew J. Wedlake,<sup>†</sup> Maria Folia,<sup>‡</sup> Sam Piechota,<sup>‡</sup> Timothy E. H. Allen,<sup>†,§</sup> Jonathan M. Goodman,<sup>\*,†</sup> Steve Gutsell,<sup>‡</sup> and Paul J. Russell<sup>‡</sup>

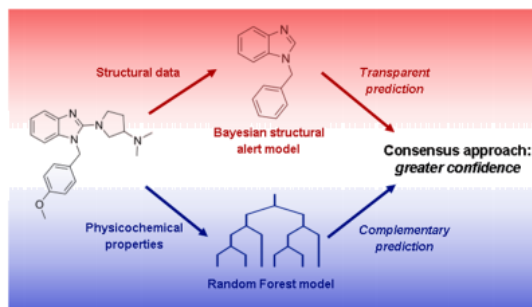
<sup>†</sup>Centre for Molecular Informatics, Department of Chemistry, University of Cambridge, Lensfield Road, Cambridge, CB2 1EW, United Kingdom

<sup>‡</sup>Unilever Safety and Environmental Assurance Centre, Colworth Science Park, Sharnbrook, Bedfordshire, MK44 1LQ, United Kingdom

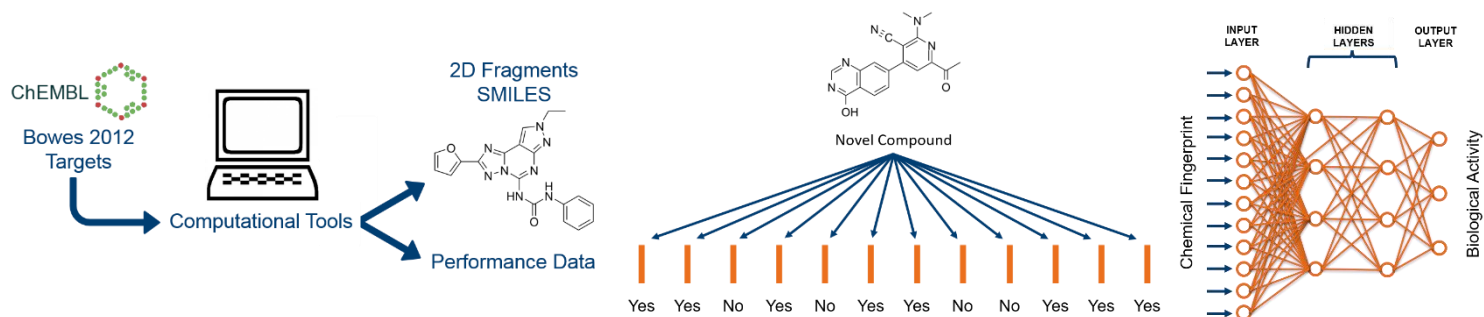
<sup>§</sup>MRC Toxicology Unit, University of Cambridge, Lancaster Road, Leicester LE19HN, United Kingdom

### Supporting Information

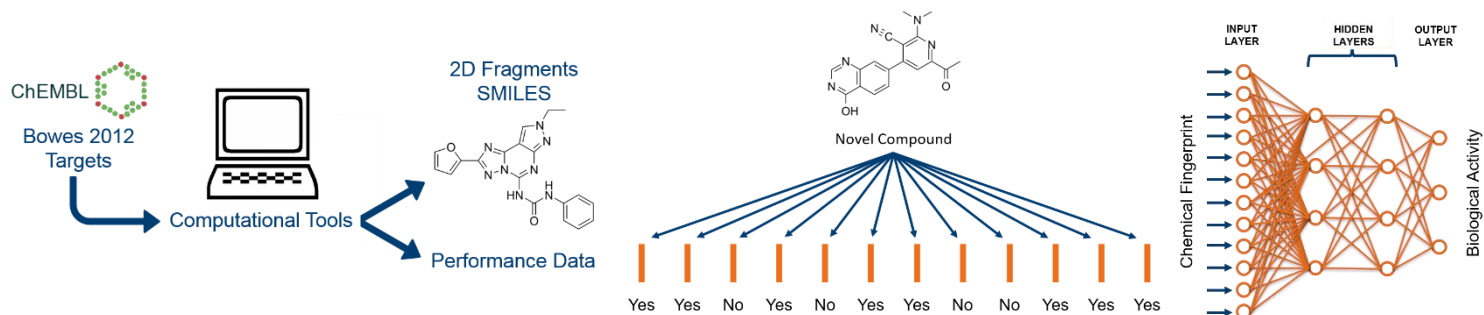
**ABSTRACT:** A molecular initiating event (MIE) is the gateway to an adverse outcome pathway (AOP), a sequence of events ending in an adverse effect. In silico predictions of MIEs are a vital tool in a modern, mechanism-focused approach to chemical risk assessment. For 90 biological targets representing important human MIEs, structural alert-based models have been constructed with an automated procedure that uses Bayesian statistics to iteratively select substructures. These models give impressive average performance statistics (an average of 92% correct predictions across targets), significantly improving on previous models. Random Forest models have been constructed from physicochemical features for the same targets, giving similarly impressive performance statistics (93% correct predictions). A key difference between



# Combined Model



# Combined Model

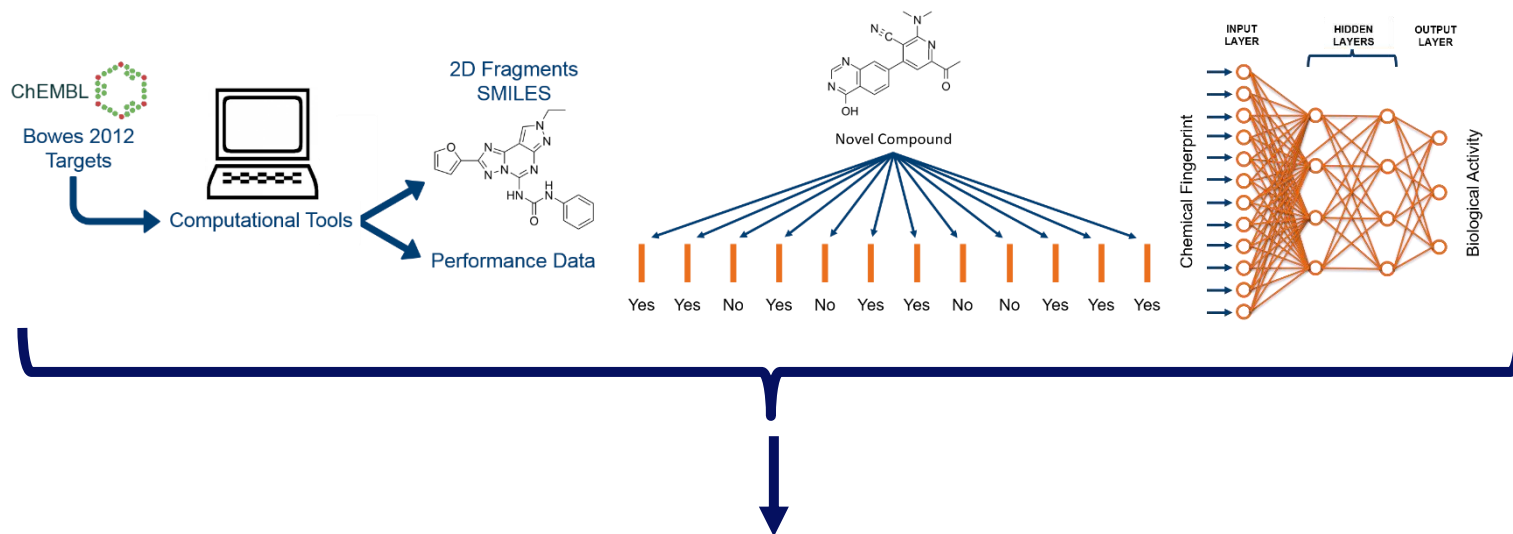


Transparent  
Prediction  
Algorithm

Use of  
Physicochemical  
Descriptors

Highest  
Quality  
Predictions

# Combined Model



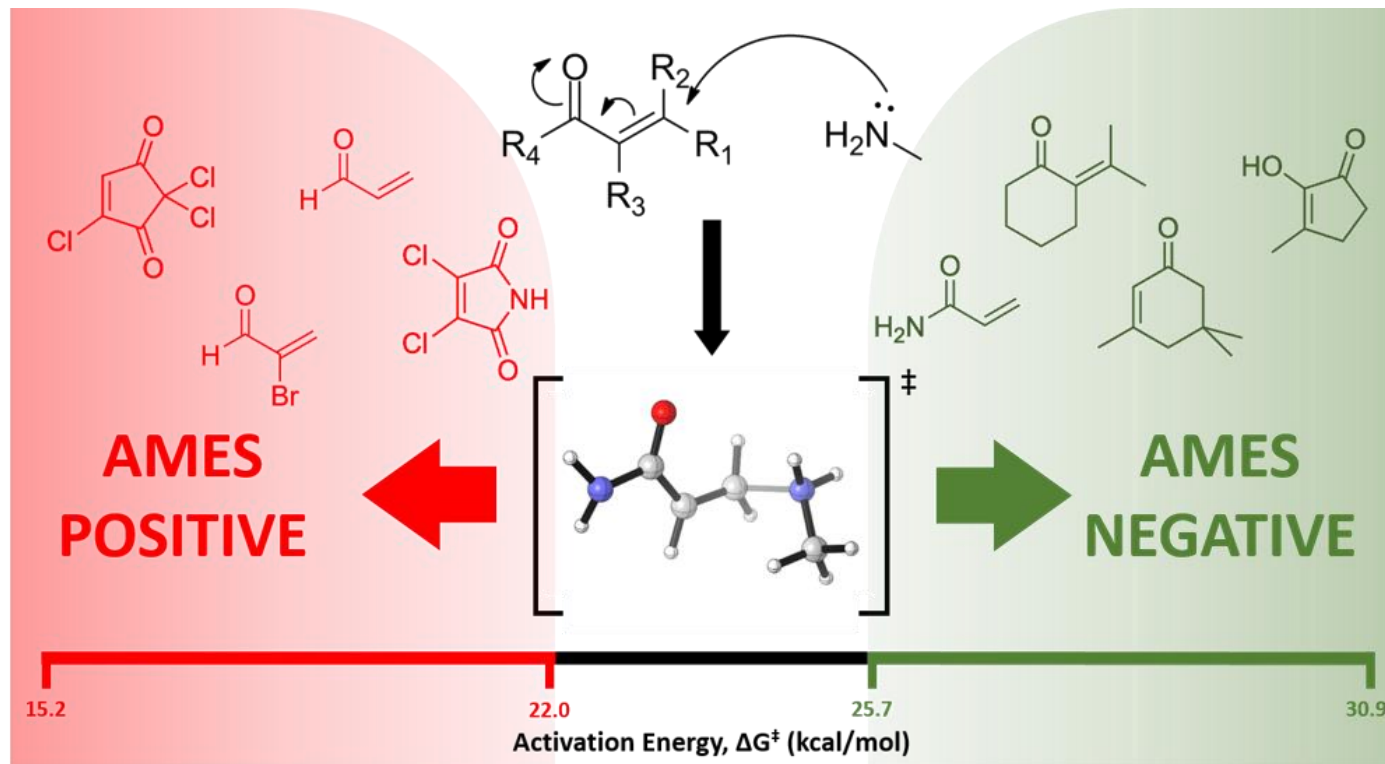
**Consensus approach;  
*Increased confidence***

# Combined Model

Method	SE	SP	ACC	MCC	% Unassigned
<b>Majority Vote</b>	90.7	90.5	92.3	0.827	
<b>ΔSA</b>	4.1	-0.4	2.1	0.045	
<b>ΔRF</b>	-0.8	3.7	1.0	0.023	
<b>ΔNN</b>	0.4	0.4	0.4	0.009	
<b>Unanimous</b>	92.8	93.8	94.9	0.882	9.6
<b>ΔSA</b>	6.2	2.9	4.7	0.100	
<b>ΔRF</b>	1.3	7.0	3.6	0.078	
<b>ΔNN</b>	2.5	3.7	3.0	0.064	

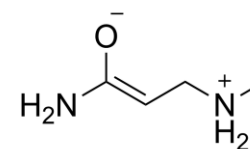
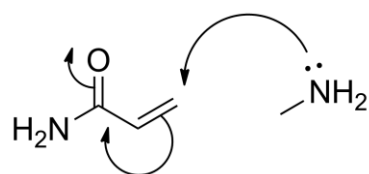
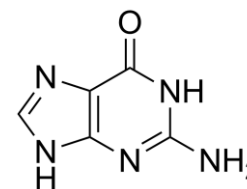
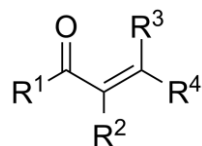
# Conclusions

- MIEs make great targets for *in silico* toxicity predictions based on chemistry
- Structural alerts, random forests and neural networks have all been developed to make these predictions
- Using these algorithms together increases their performance and the confidence we can have in their predictions
- Combining algorithms helps us overcome their specific flaws



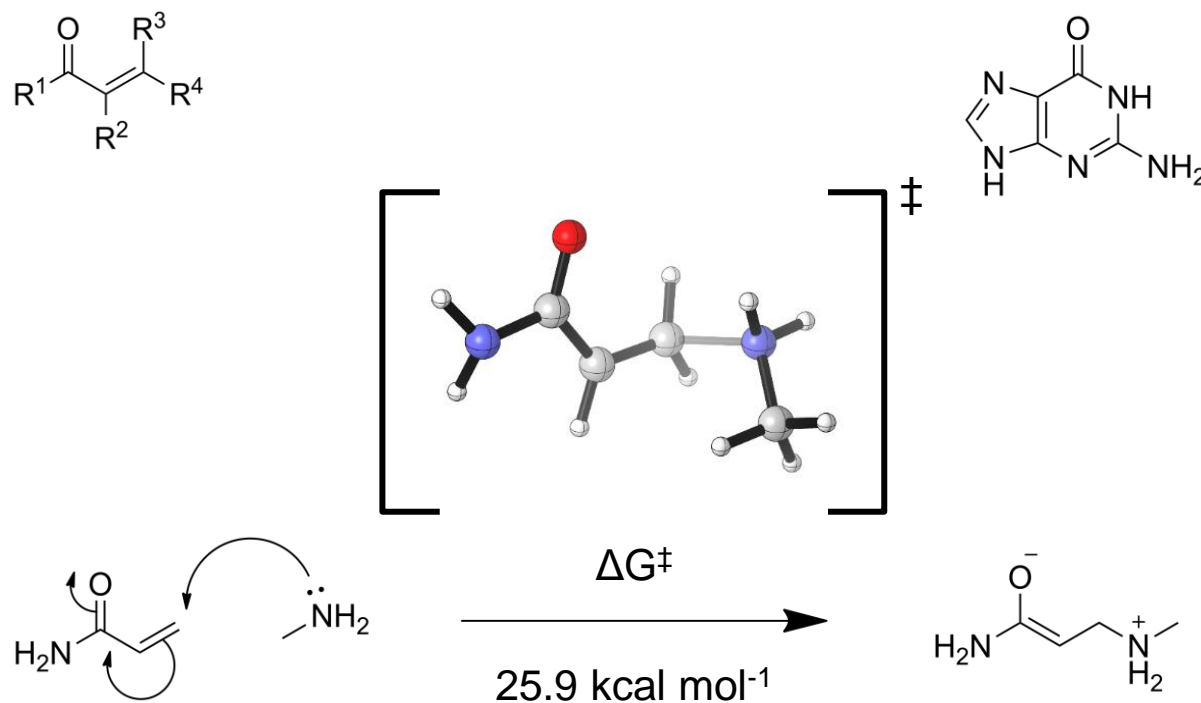
# Quantum Chemistry Predictions

# Modelling the Transition State



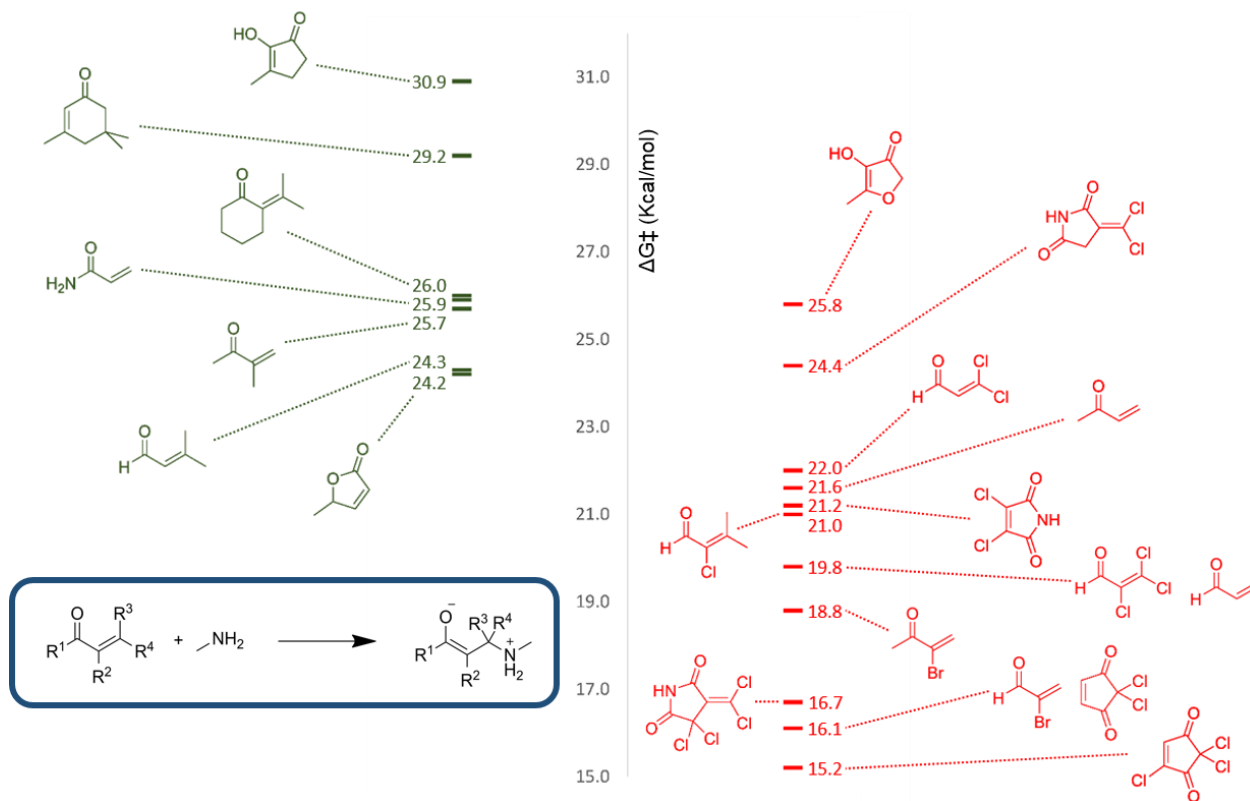


# Modelling the Transition State



# Activation Free Energies

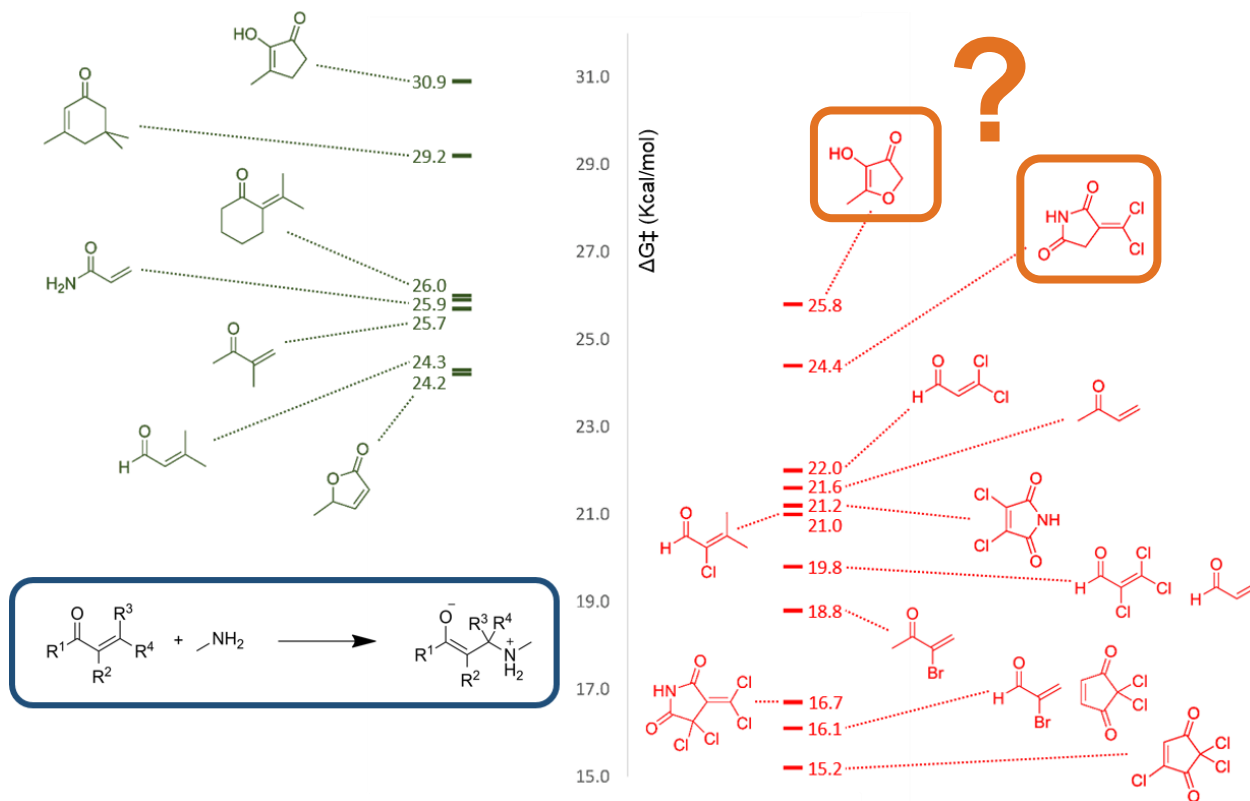
Activation Energies for the reaction of  $\alpha,\beta$  unsaturated carbonyls with methylamine



Allen, T.E.H. *et al.* (2018) *J. Chem. Inf. Model.*, 58; 1266.  
 DFT - Optimization: B3LYP, 6-31+G(d), iefpcm; SPE: M062X, def2tzvpp, iefpcm

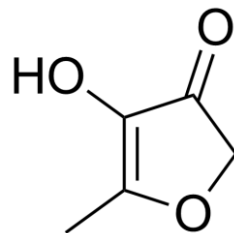
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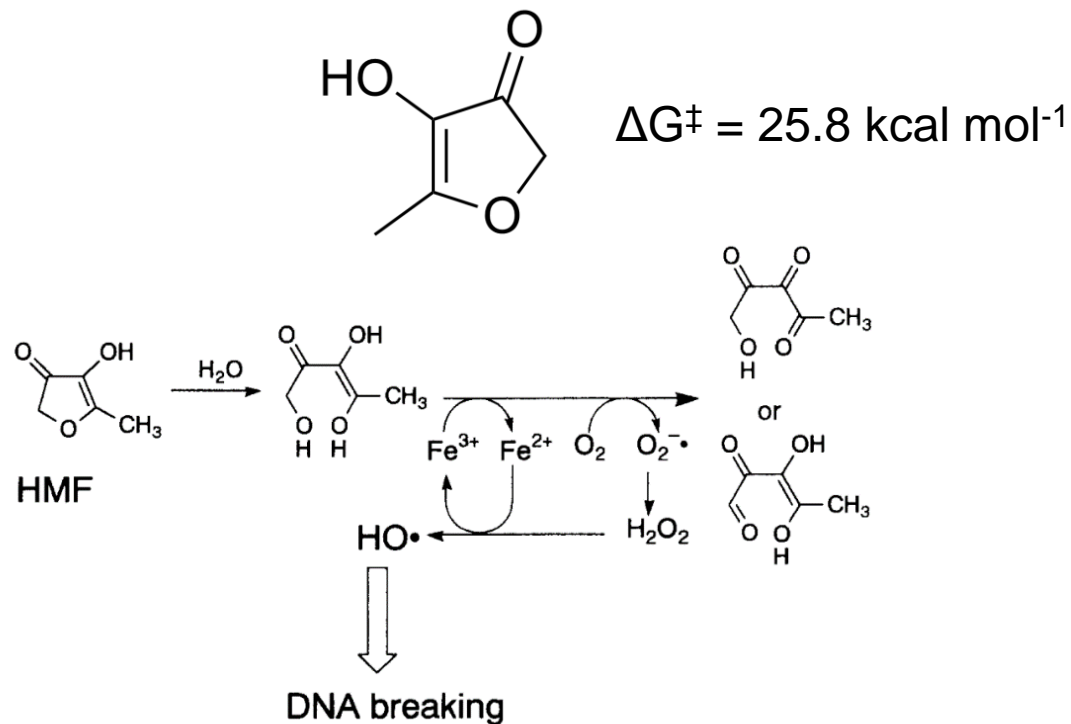
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# 4-Hydroxy-5-methyl-3-furanone



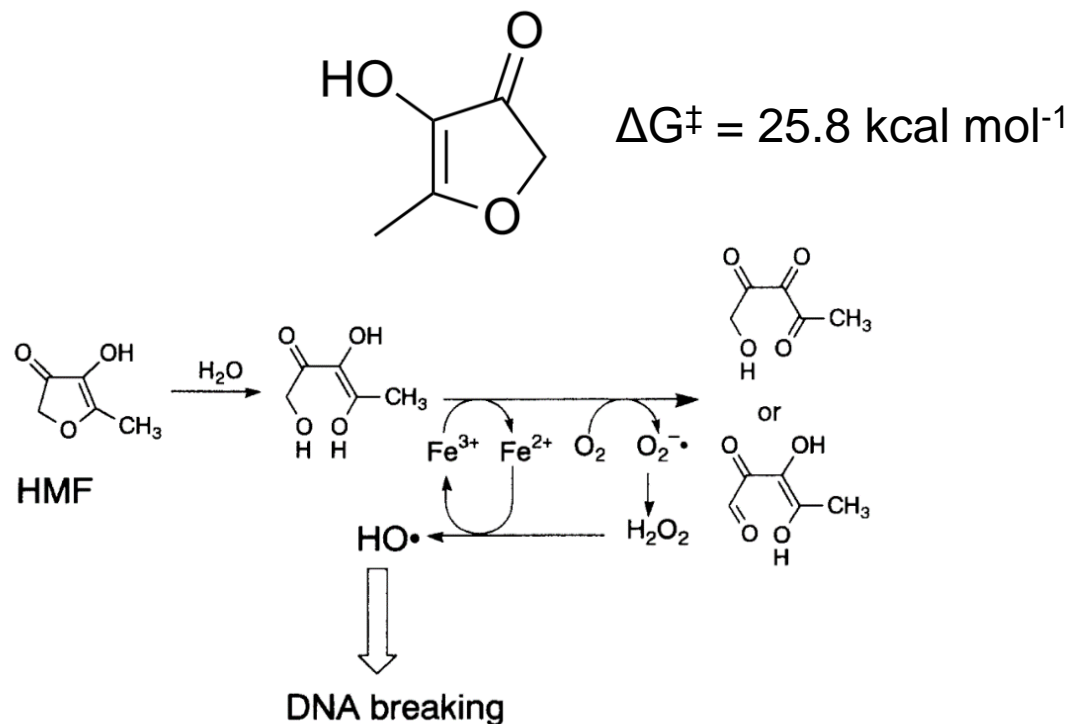
$$\Delta G^\ddagger = 25.8 \text{ kcal mol}^{-1}$$

# 4-Hydroxy-5-methyl-3-furanone



Scheme 2. Possible mechanisms for DNA breaking by HMF.

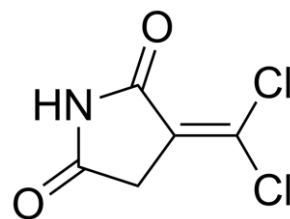
# 4-Hydroxy-5-methyl-3-furanone



Scheme 2. Possible mechanisms for DNA breaking by HMF.

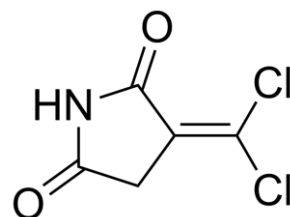
“HMF found to be mutagenic probably due to generation of active oxygen radicals”

# 3-(Dichloromethylene)-2,5-pyrrolidinedione



$$\Delta G^\ddagger = 24.4 \text{ kcal mol}^{-1}$$

# 3-(Dichloromethylene)-2,5-pyrrolidinedione



$$\Delta G^\ddagger = 24.4 \text{ kcal mol}^{-1}$$

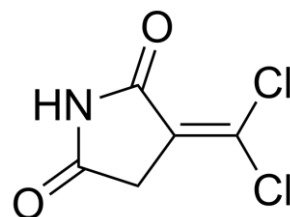
**Table 2. Mutagenicity of Synthesized Chlorinated Imides in *S. typhimurium* TA100<sup>a</sup>**

compound	dose, $\mu\text{g}/\text{plate}$ (nmol/plate)	revertants/plate	molar mutagenicity [slope (rev/nmol)]	$r^b$
DCMI <sup>c</sup>	1 (6)	351; 365	28	0.975
	0.5 (3)	244; 254		
	0.125 (0.75)	233; 201		
solvent control	(0)	179; 178		
<b>B<sup>d</sup></b>	125 (694)	280; 318; 325	0.24	0.971
	50 (278)	190; 230; 218		
	10 (56)	142; 151; 128		
<b>D</b>	10 (47)	451; 533; 513	7.7	0.987
	5 (23)	337; 344; 347		
	1 (4.7)	188; 153; 165		
<b>E</b>	0.1 (0.4)	687; 590; 623	1450 <sup>e</sup>	0.95 <sup>e</sup>
	0.025 (0.1)	260; 295; 278		
solvent control	(0)	152; 148; 148		
<b>E<sup>f</sup></b>	0.1 (0.4)	806; 875; 920		
	0.05 (0.2)	451; 514; 515		
	0.025 (0.1)	383; 333; 361		
solvent control	(0)	193; 221; 158		

<sup>a</sup> The positive control, methyl methanesulfonate, gave >1200 revertants/plate in all assays at 0.4  $\mu\text{L}/\text{plate}$ . <sup>b</sup> Correlation coefficient from linear regression. <sup>c</sup> Assay 1. <sup>d</sup> Assay 2. <sup>e</sup> Data combined from assays 2 and 3. <sup>f</sup> Assay 3.

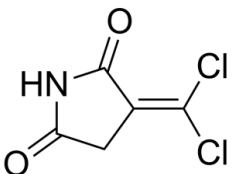


# 3-(Dichloromethylene)-2,5-pyrrolidinedione



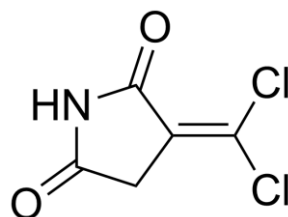
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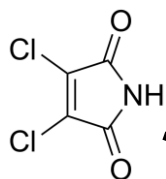


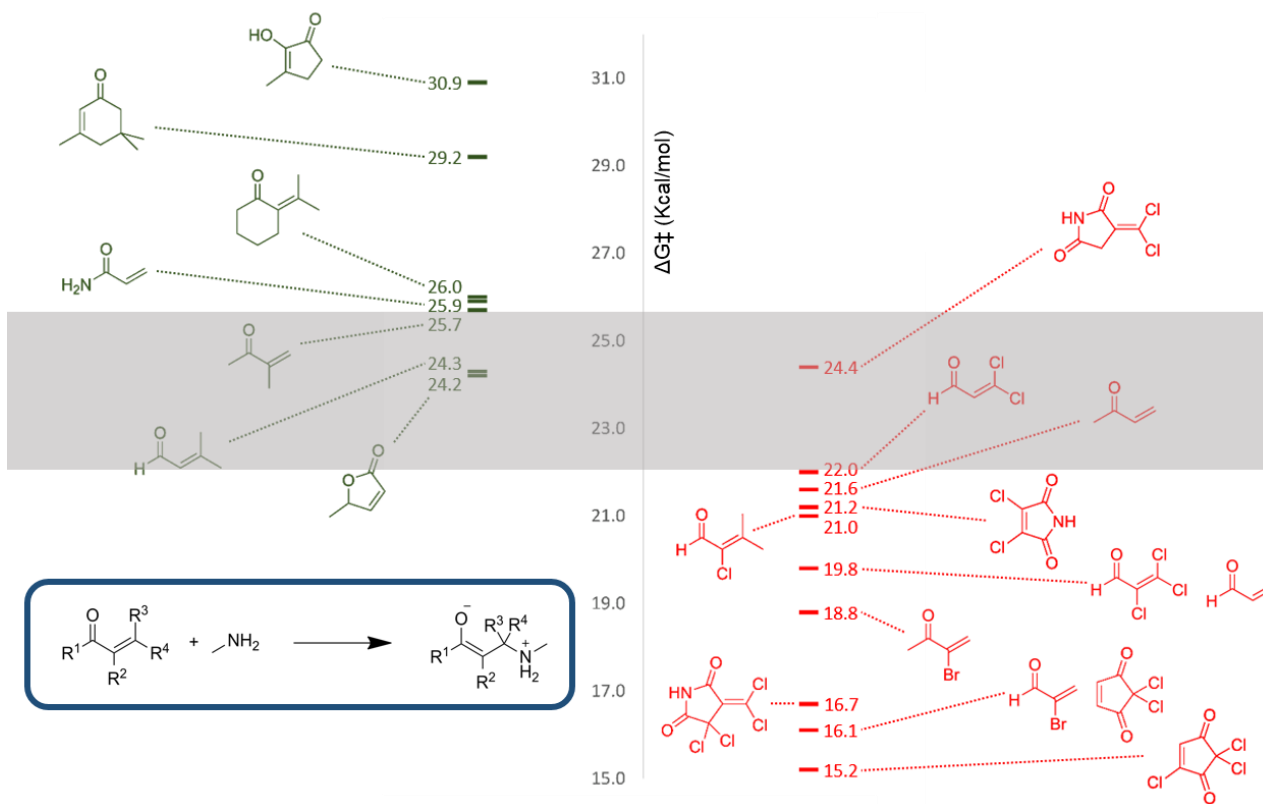
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# The Final Picture

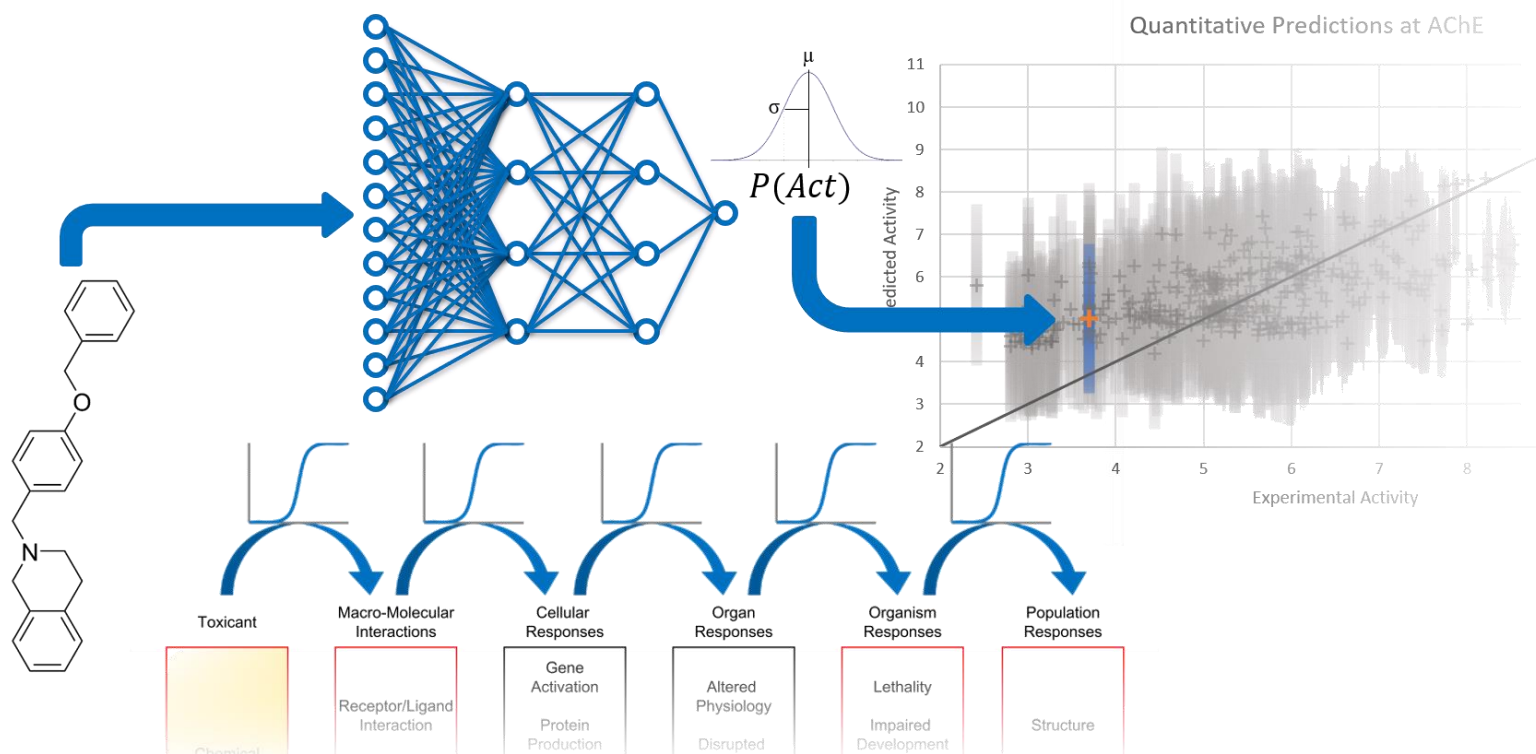
Activation Energies for the reaction of  $\alpha,\beta$  unsaturated carbonyls with methylamine



Allen, T.E.H. *et al.* (2018) *J. Chem. Inf. Model.*, 58; 1266.  
 DFT - Optimization: B3LYP, 6-31+G(d), iefpcm; SPE: M062X, def2tzvpp, iefpcm

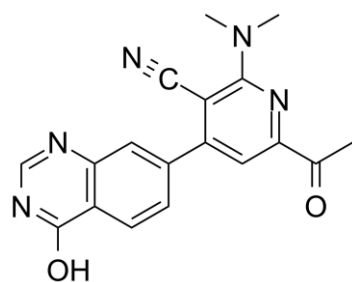
# Conclusions

- DFT calculations provide a window into the molecular interactions driving some Ames positive results
- DFT allows direct modelling of the MIE in this case, and may also be useful for other covalent bond forming MIEs
- This approach helps increase understanding in how and why specific molecules covalently modify DNA

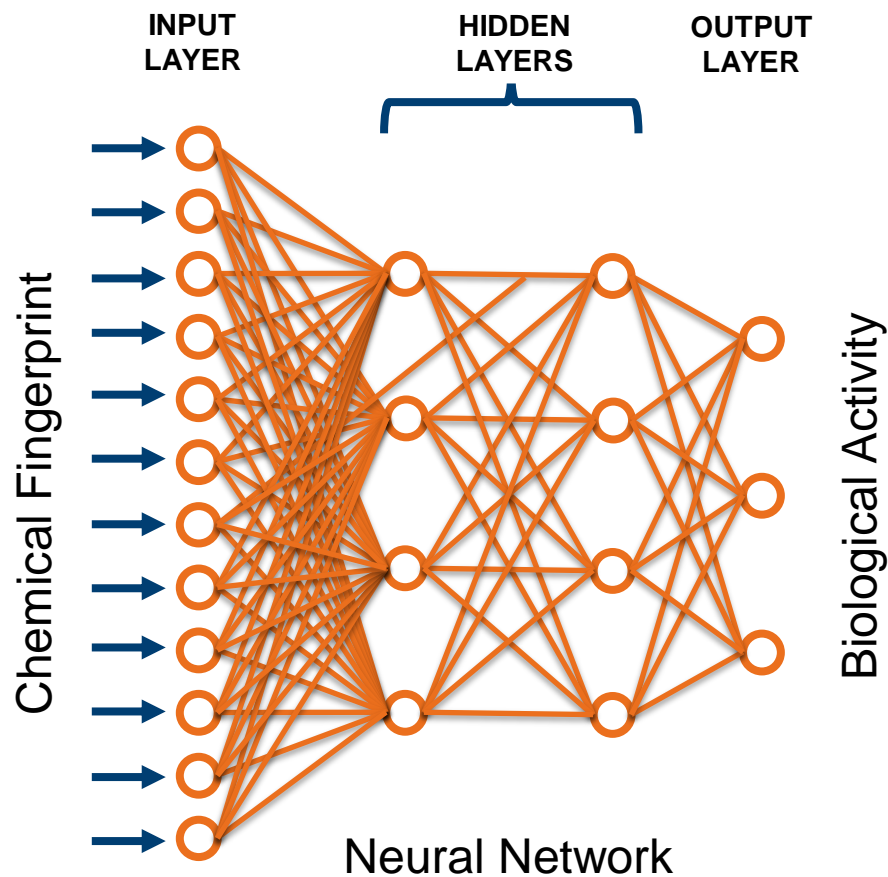


# Bayesian Neural Networks

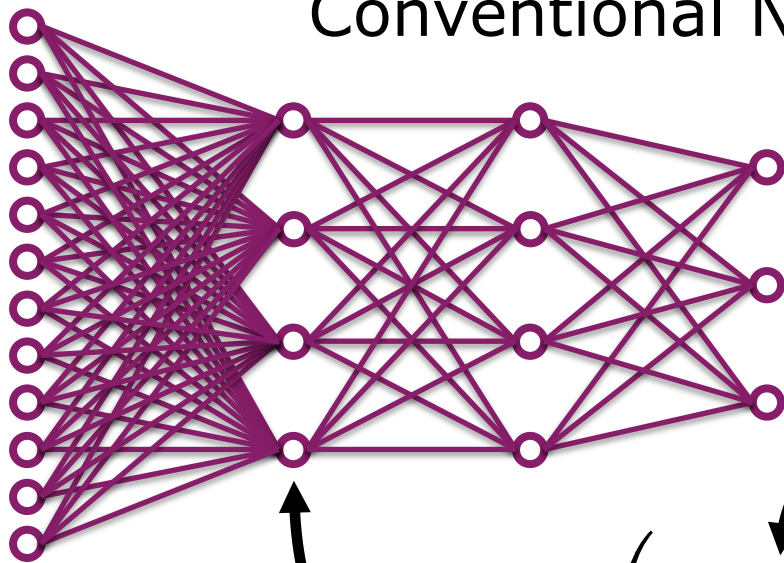
# Quantitative Neural Network?



Novel Compound



## Conventional Neural Network

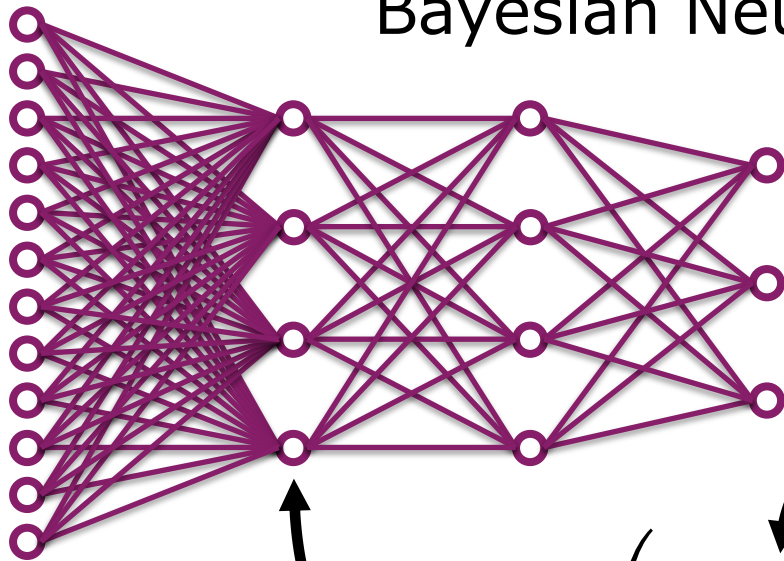


Weights and biases as fixed values

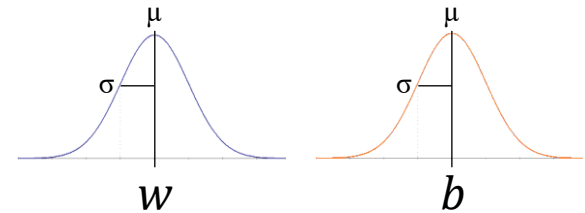
Therefore predictions are fixed values

$$f(\mathbf{x}) = K\left(\sum_i w_i(x_i)\right) + \mathbf{b}$$

## Bayesian Neural Network



Weights and biases defined as probability distributions



Gives predictions meaningful errors

$$f(\mathbf{x}) = K\left(\sum_i w_i(x_i)\right) + \mathbf{b}$$



# Best Models

	<b>Train MAE</b>	<b>Valid. MAE</b>	<b>Test MAE</b>	<b>Ext. Val. MAE</b>
<b>AVERAGE</b>	0.487	0.613	0.621	0.943
<b>SD</b>	0.030	0.051	0.051	0.223
	<b>Train R<sup>2</sup></b>	<b>Valid. R<sup>2</sup></b>	<b>Test R<sup>2</sup></b>	<b>Ext. Val. R<sup>2</sup></b>
<b>AVERAGE</b>	0.743	0.586	0.572	0.128
<b>SD</b>	0.067	0.089	0.094	0.437

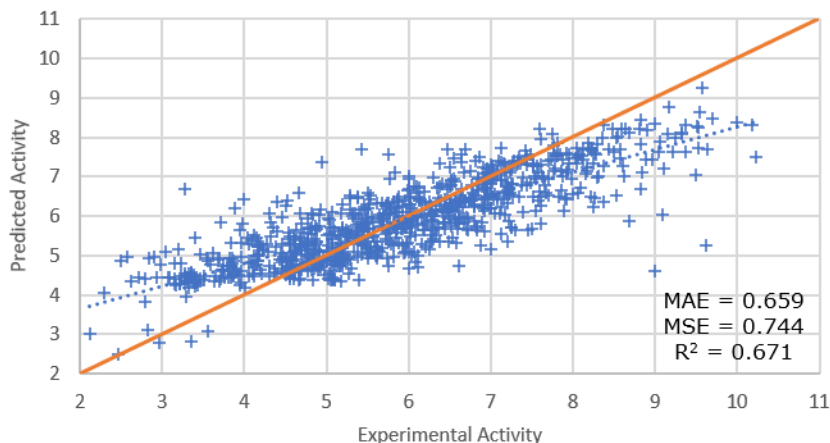
*MAE = Mean Absolute Error*

*SD = Standard Deviation*

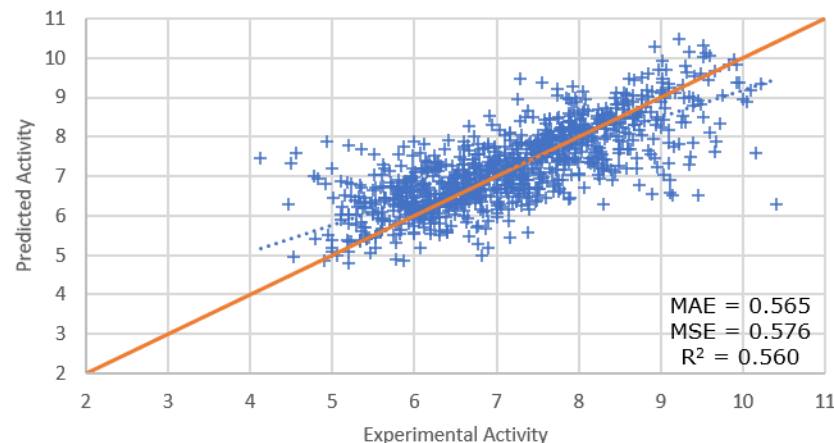
*R<sup>2</sup> = Coefficient of Determination for Linear Correlation*

# Some Models (Test Set)

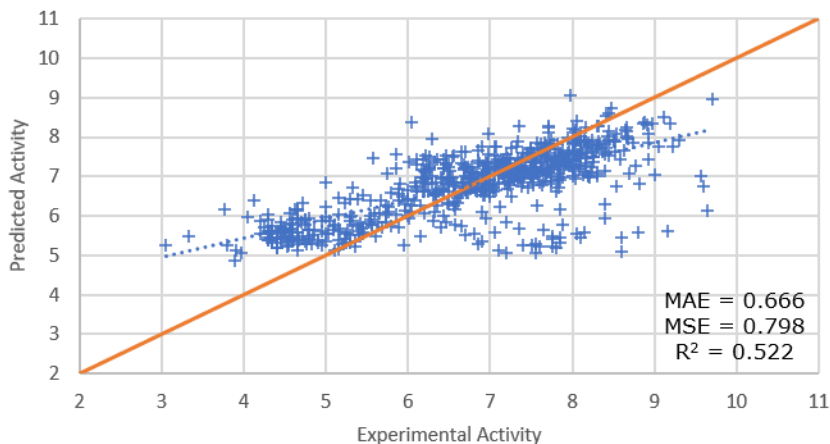
### ACHe Quantitative Predictions (Test)



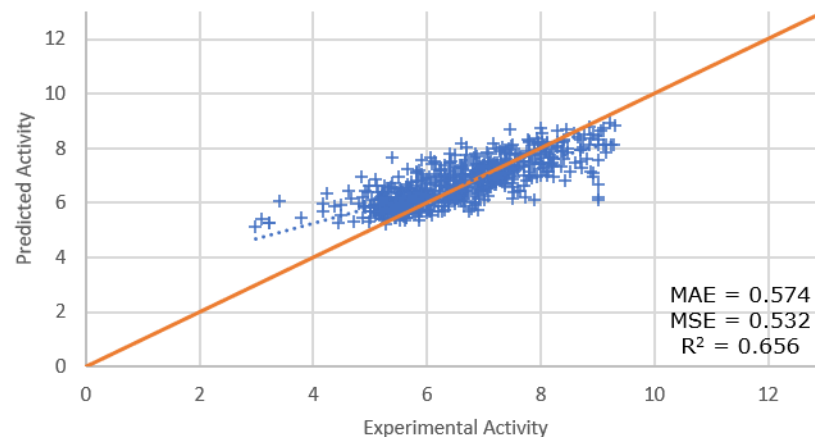
### HTR2A Quantitative Predictions (Test)



### NR3C1 Quantitative Predictions (Test)

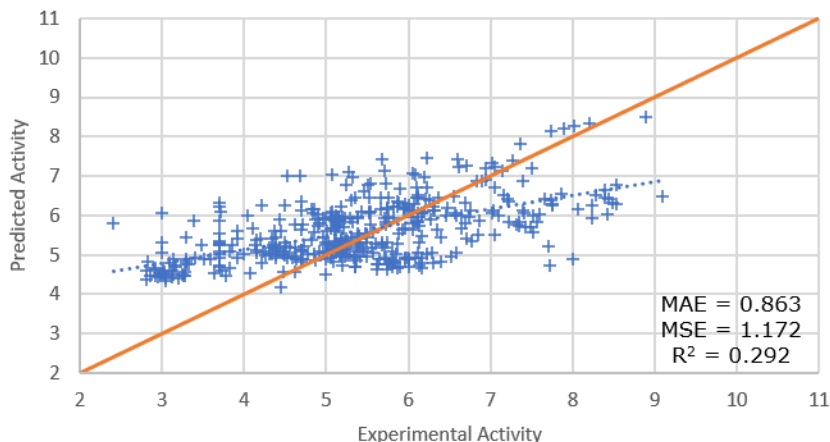


### SLC6A3 Quantitative Predictions (Test)

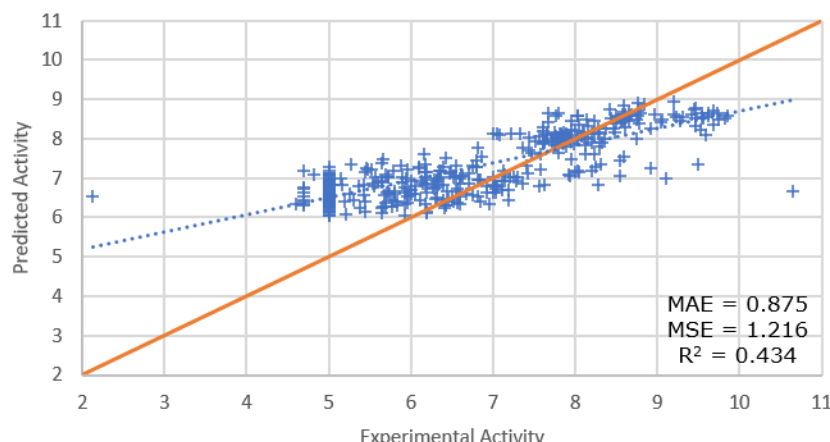


# Some Models (Ext. Valid. Set)

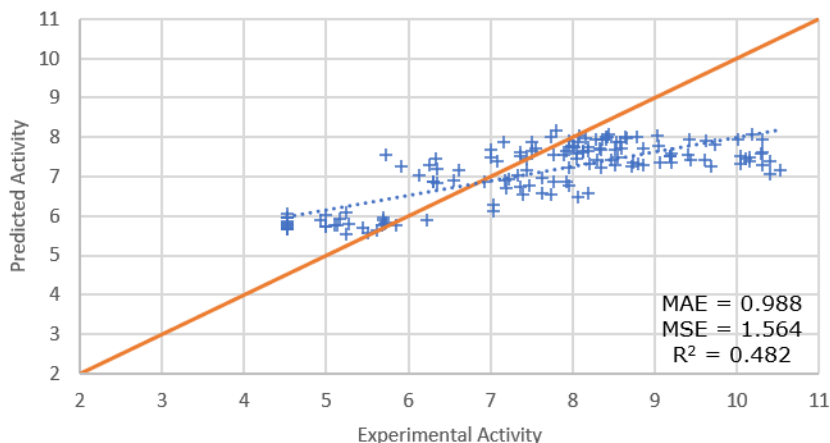
AChE Quantitative Predictions (Ext. Valid.)



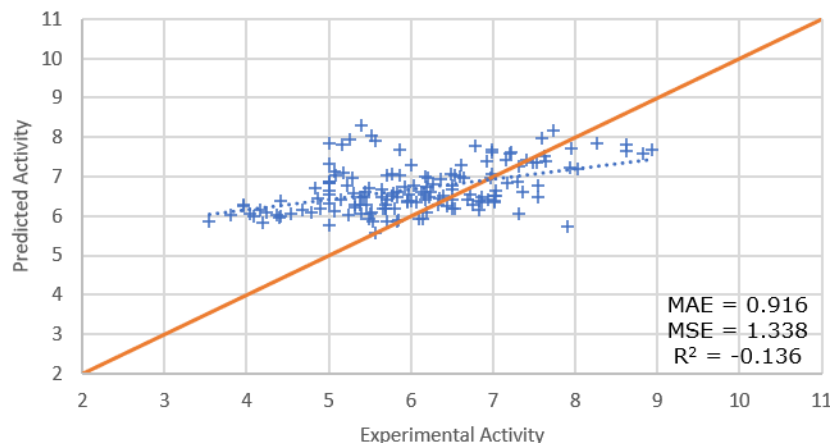
HTR2A Quantitative Predictions (Ext. Valid.)



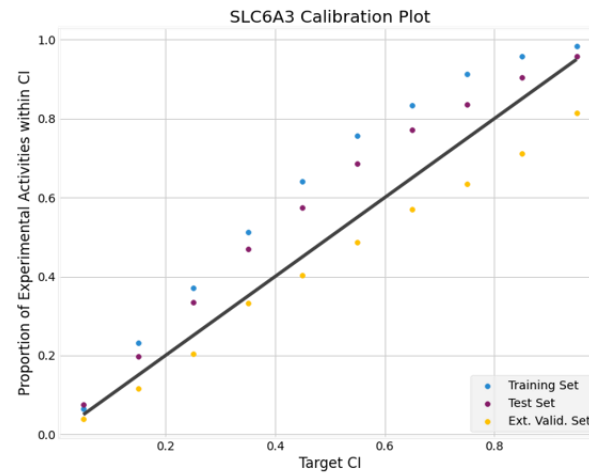
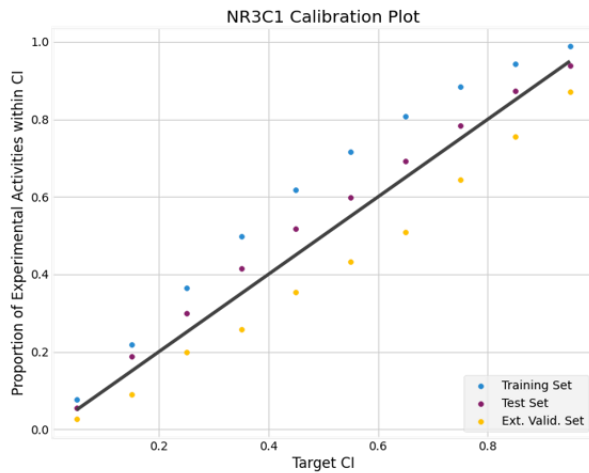
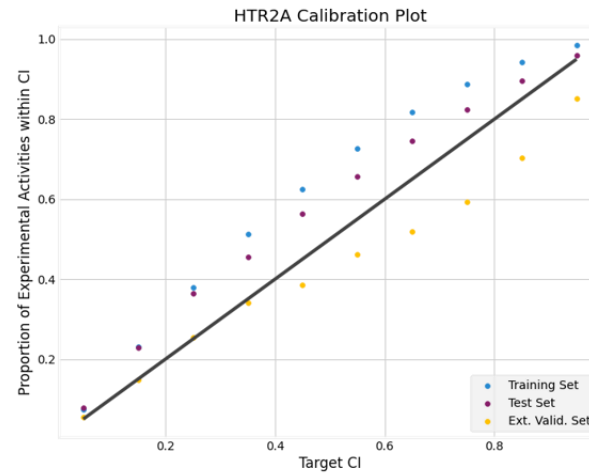
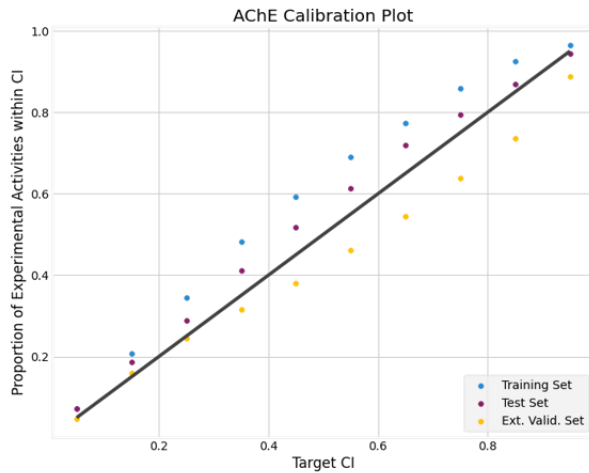
NR3C1 Quantitative Predictions (Ext. Valid.)



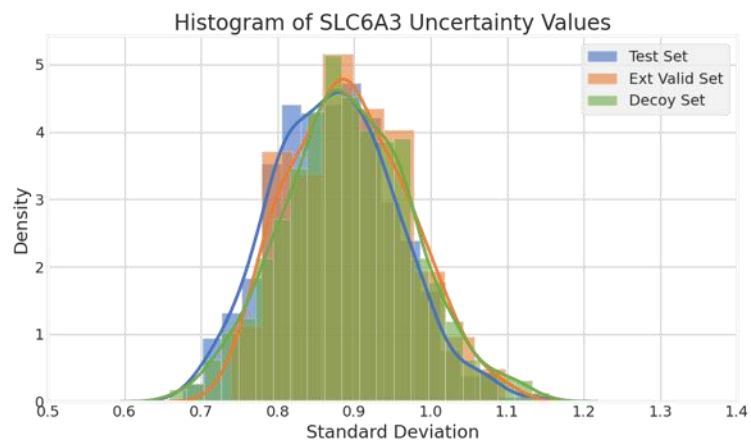
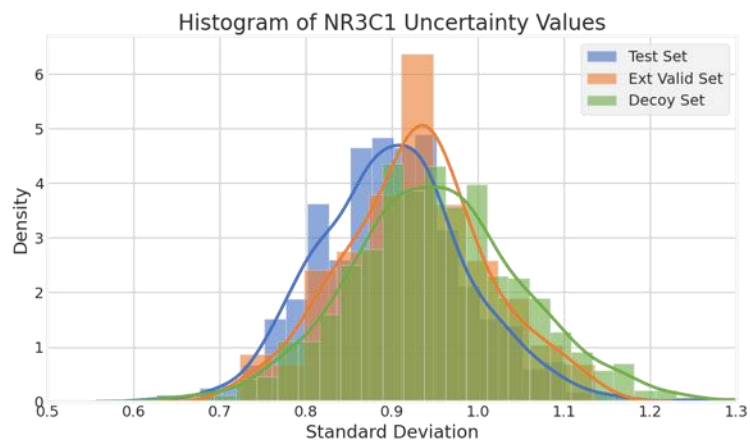
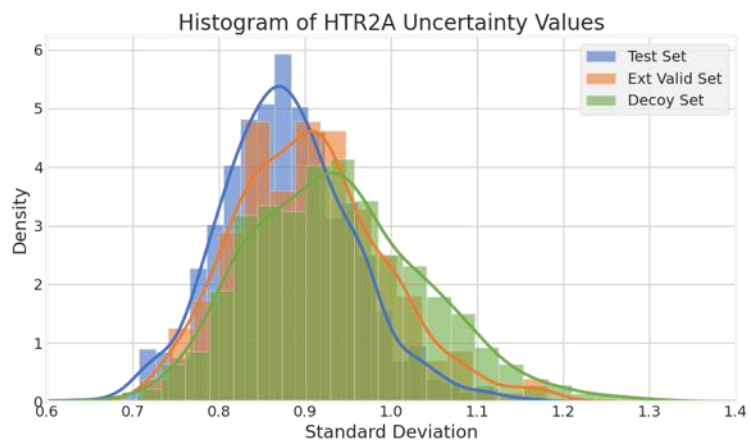
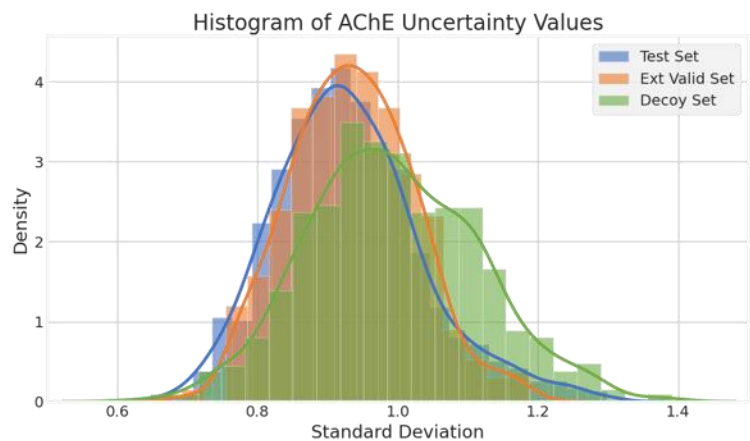
SLC6A3 Quantitative Predictions (Ext. Valid.)



# Calibration of Uncertainties

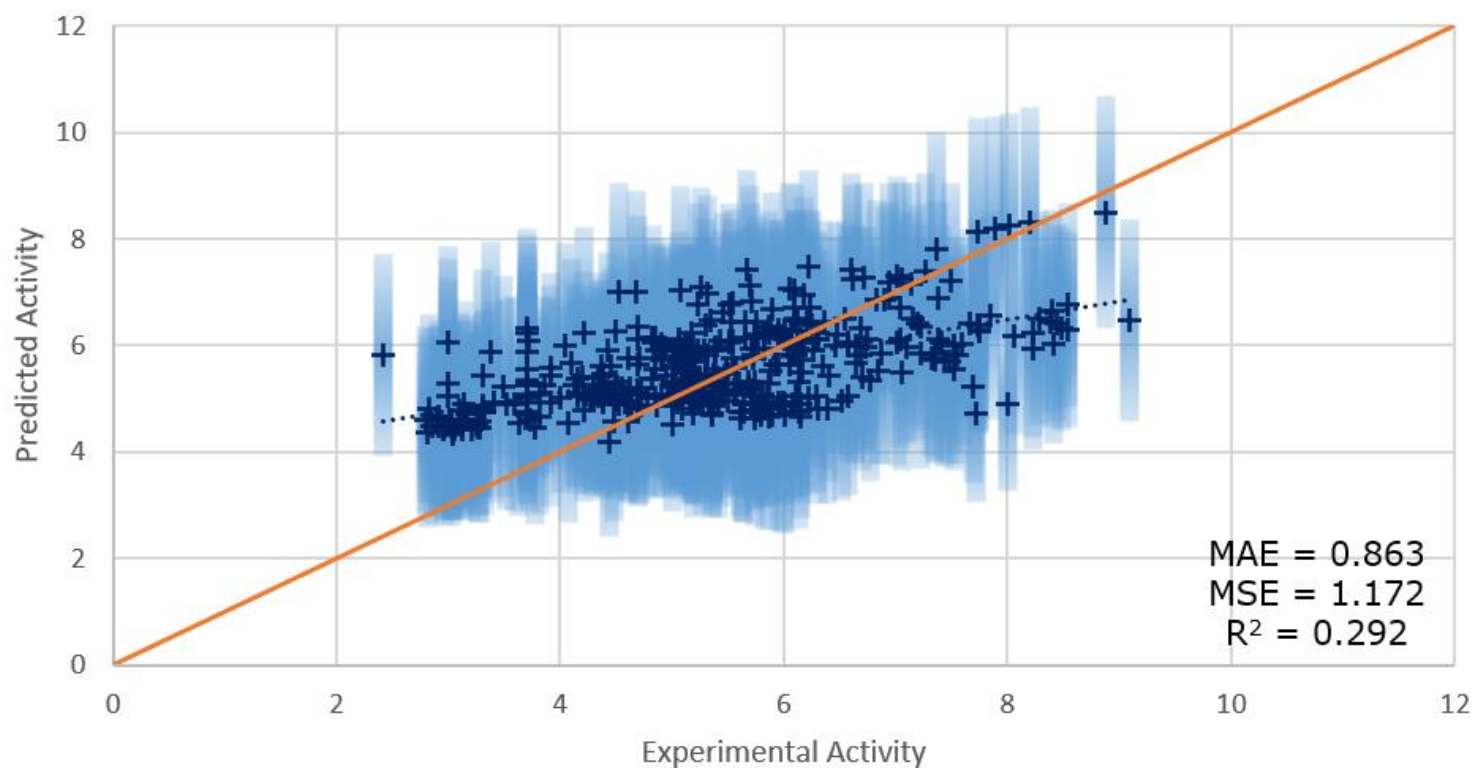


# Distribution of Uncertainties

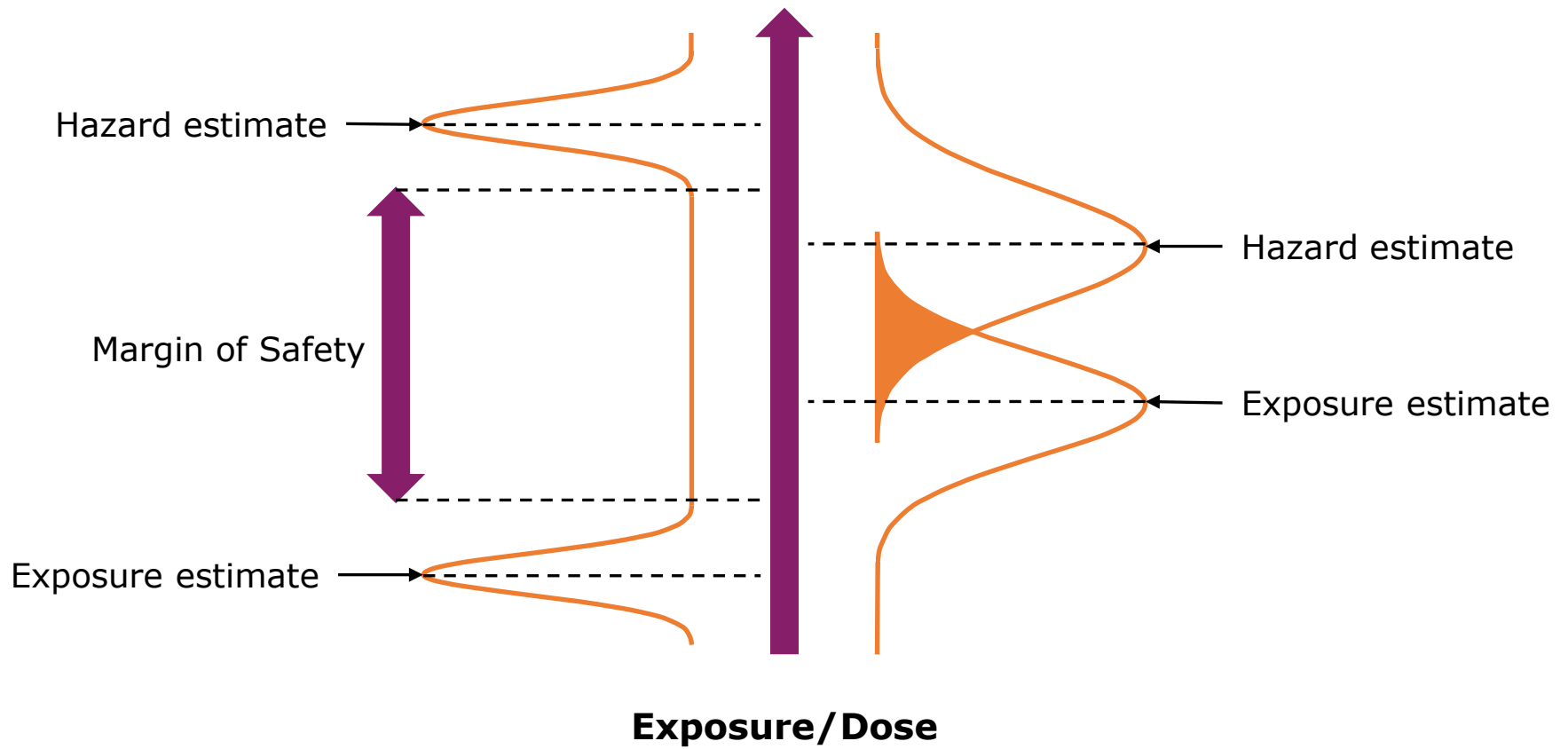


# Predictions with Uncertainties

## AChE Quantitative Predictions (Ext. Valid.)



# Safety Decision Making

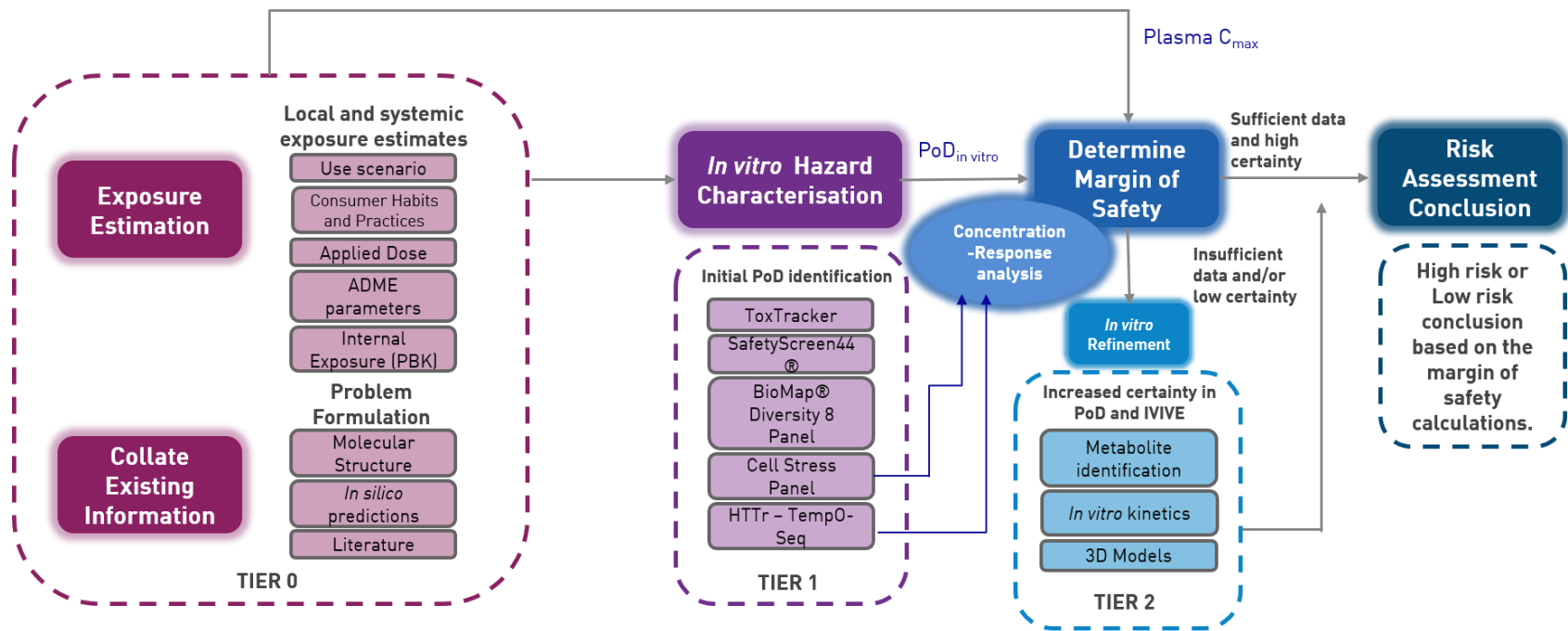


# Conclusions

- Bayesian learning regression neural networks provide the ability to both make quantitative predictions and understand the uncertainty in those predictions
- These algorithms have been shown to be useful in the prediction of molecular activity at human MIEs



# Ab Initio NGRA Framework



Uncertainty

Mechanistic understanding

# Acknowledgements

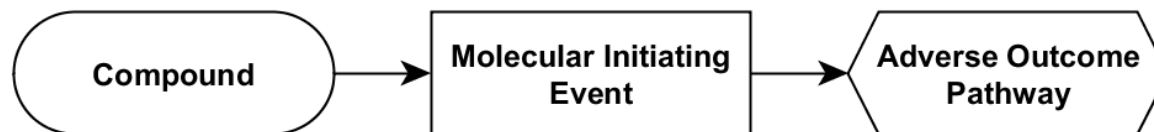
- Professor Jonathan Goodman
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- **Quantitative Predictions for Molecular Initiating Events using 3D Quantitative Structure-Activity Relationships.** Allen, T.E.H.; Goodman, J.M.; Gutsell, S.; Russell, P.J. *Chem. Res. Toxicol.* **2020**, 33(2), pp 324-332. DOI: 10.1021/acs.chemrestox.9b00136
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- **Confidence in Inactive and Active Predictions from Structural Alerts.** Wedlake, A.J.; Allen, T.E.H.; Goodman, J.M.; Kukic, P.; Gutsell, S.; Russell, P.J. *Chem. Res. Toxicol.* **2020**, 33(12), 3010-3022. DOI: 10.1021/acs.chemrestox.0c00332

# Use of chemical informatics, quantum chemistry modelling and artificial intelligence algorithms to predict molecular initiating events



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