

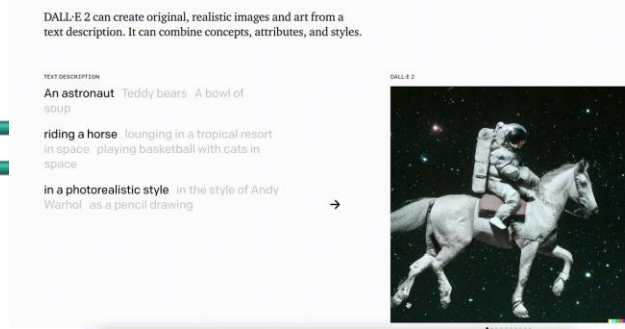
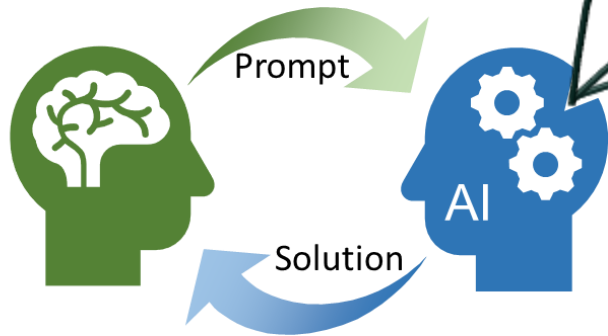
Advancing Toxicology in Drug Discovery using Generative Adversarial Networks – Part II

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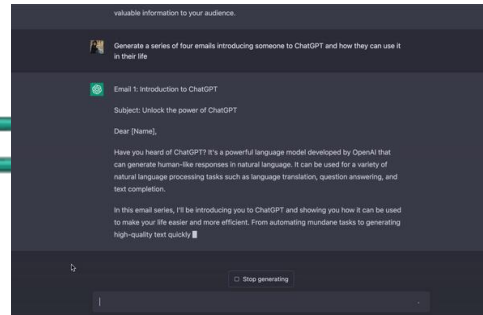


Generative AI (GenAI)



Heterogeneous data translation

- DALL E3
- Stable Diffusion
- Midjourney
- **GANs**



Large language models (LLMs)

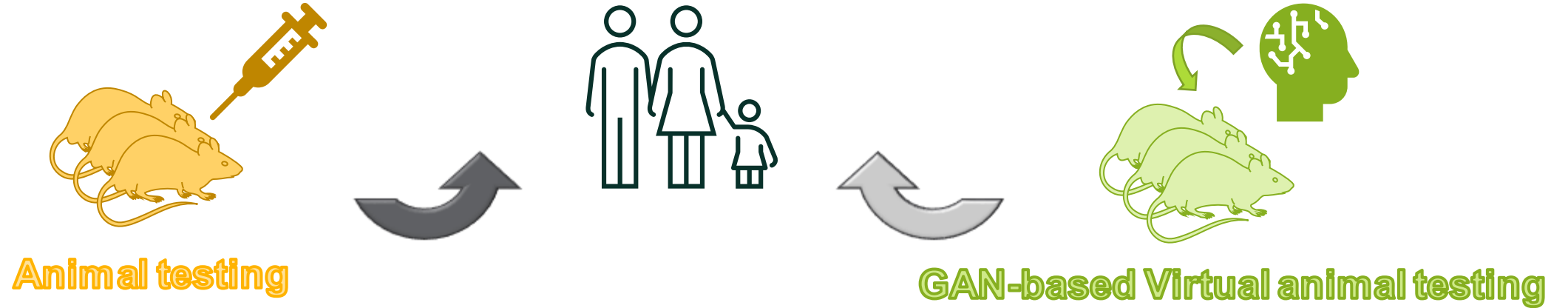
- GPT3/ChatGPT/GPT4
- BARD
- Claude 2
- LLaMA
- Llama 2
- ...



Computer Vision

- Meta-AI Segment Anything Models (SAMs)

Exploring the Use of GAN Models in Generating Animal Testing Results

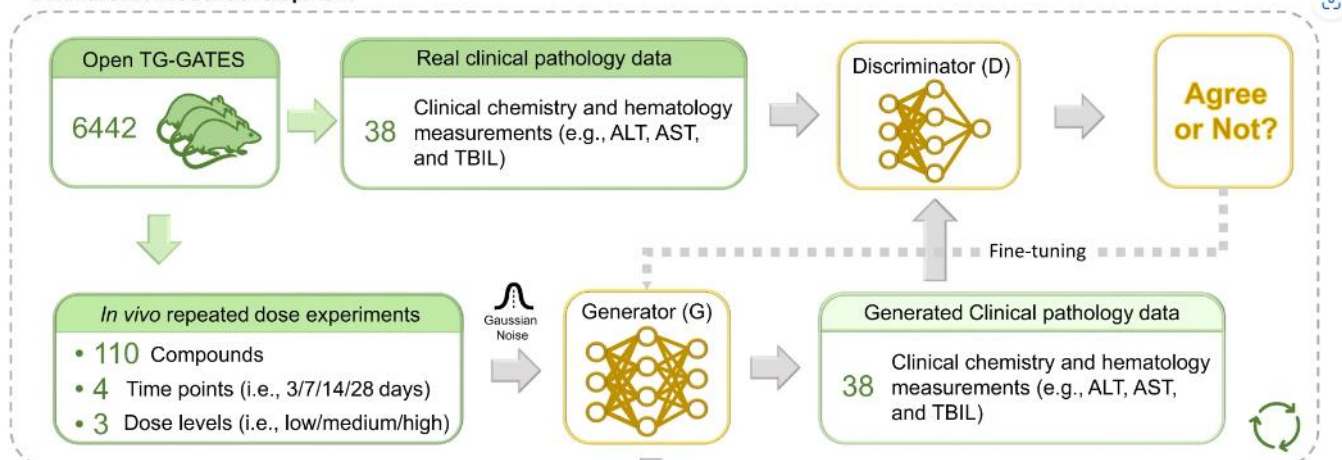


- Disparate animal species and strains
- Variability in animals for study
- Small experimental groups
- Selection of outcome measures
- Variable duration of follow up

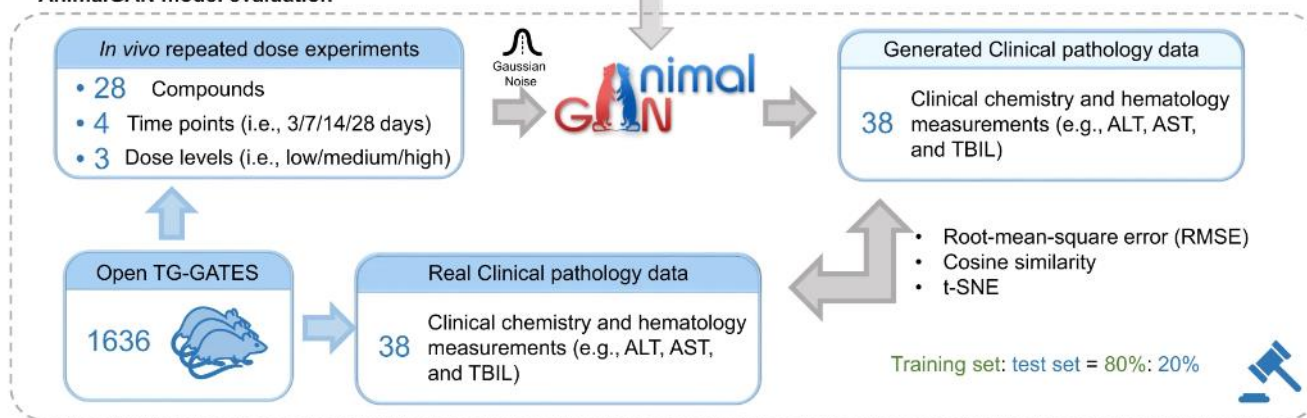
- Learning distribution of data to generate the new data with same characteristics
- Data augmentation
- Versatility
- Improvement over time



AnimalGAN model development



AnimalGAN model evaluation



Input of Generator (3556-length vector)

1828-length Treatment condition vector

- Compound: Mordred descriptor (1826-length)
- Time: 3/7/14/28 days (1-length)
- Dose: low/middle/high - 1:3:10 (1-length)

1828-length Gaussian Noise: mimic animal variance

Input of discriminator (1866-length vector)

- 38 real and generated clinical pathology data
- 1828-length Treatment condition vector

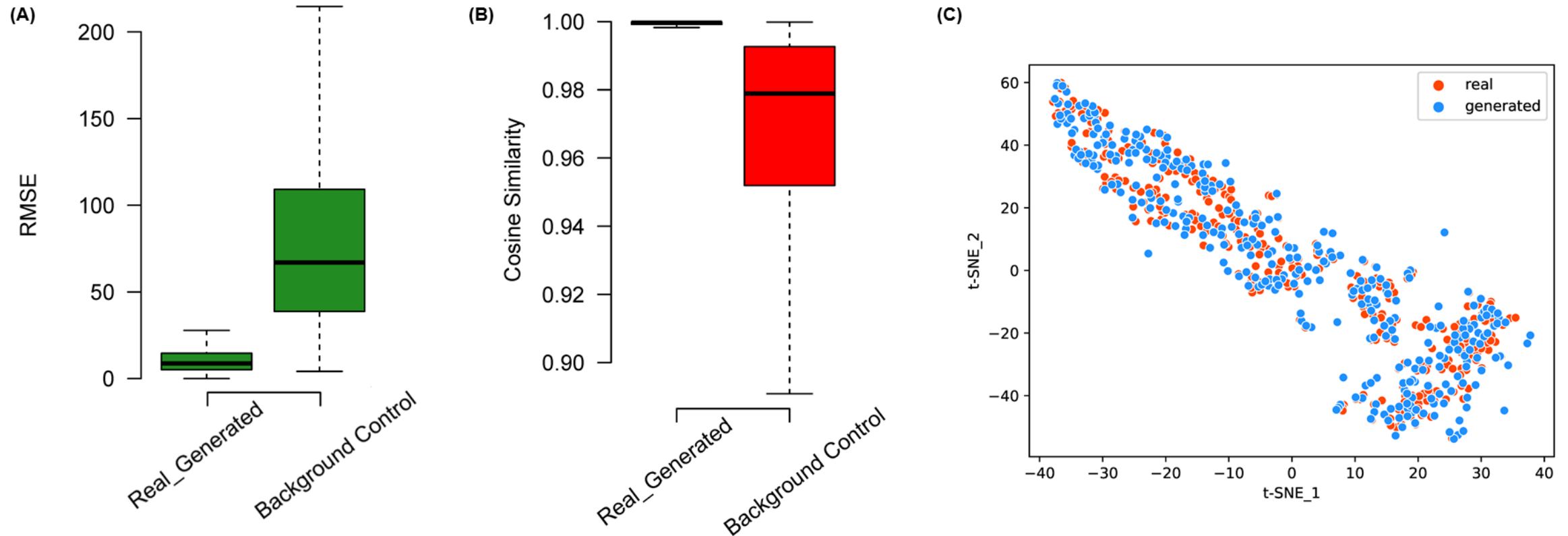
Normalization matters

- [-1,1] for both generator and discriminator

“invalid records” check:

- White blood cells (WBCs) are composed of neutrophils, eosinophils, basophils, monocytes, and lymphocytes, so the total percentages of each type of WBC should not exceed 100%.
- Cut-off: 105% by taking system errors into consideration

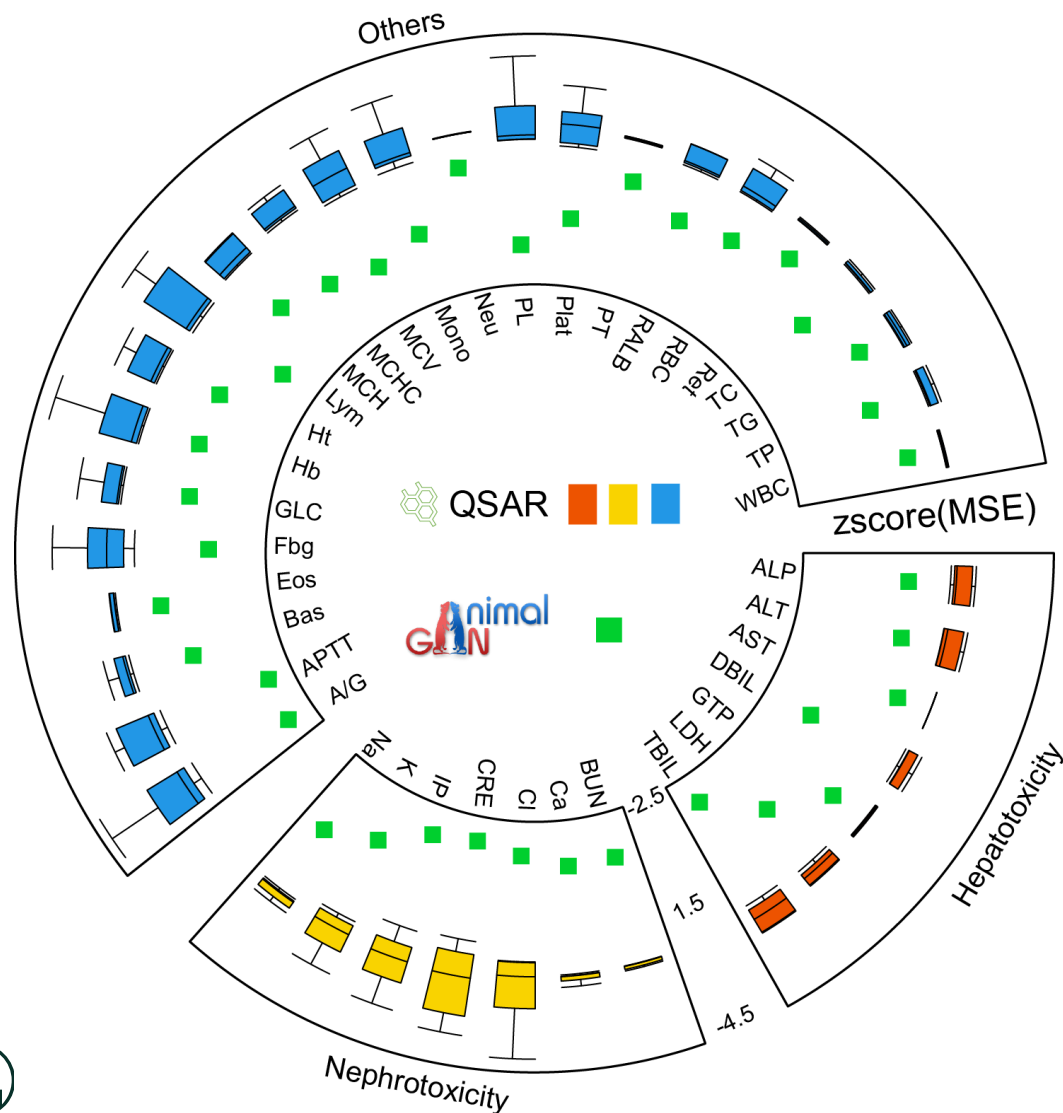
High Concordance between Real Data and Generated Data



Boxplot of (A) RMSE - Root Mean Square Error, (B) Cosine Similarity between generated data and their corresponding animal testing data in the test set, and (C) t-SNE plot of test set.

Average 100 generated clinical pathology measures that passed “invalid records” check were used!!!

AnimalGAN vs. QSAR model

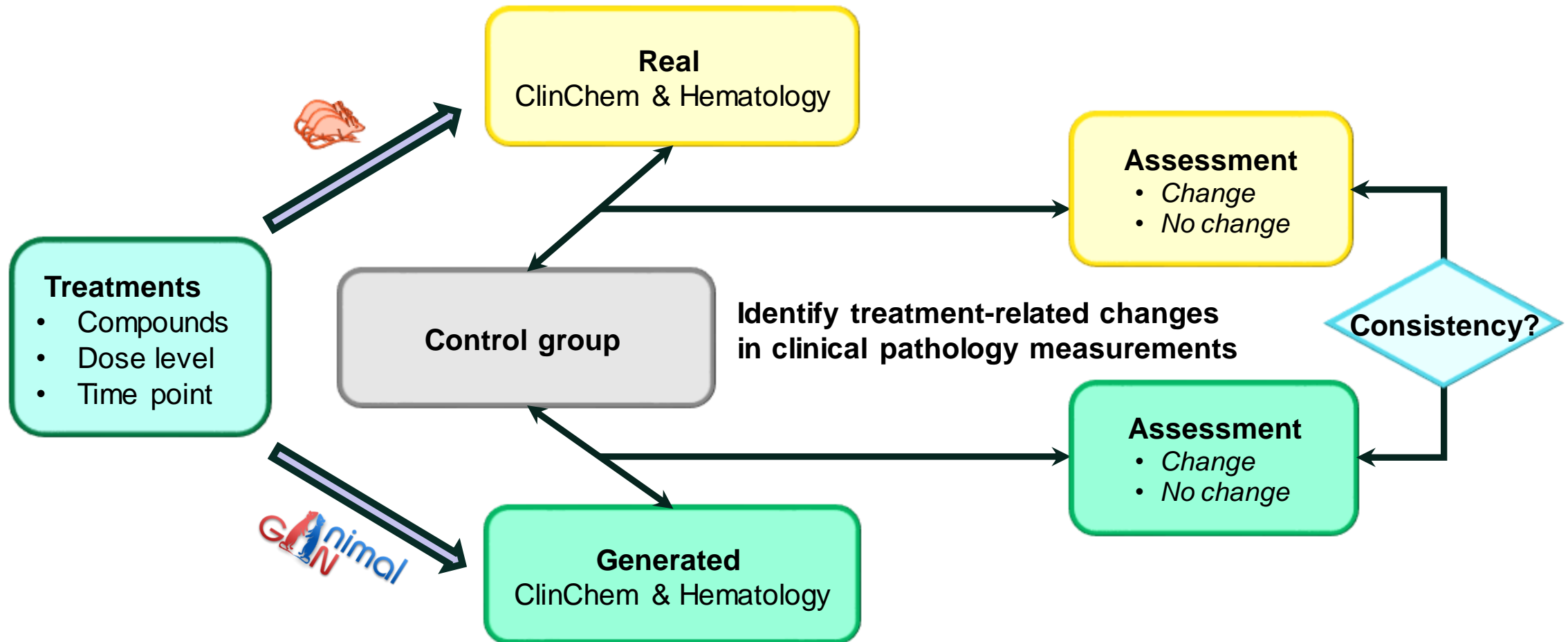


QSARs

- 12 regressors (i.e., k-nearest neighbors, decision tree, extremely randomized tree, random forest, epsilon support vector regression, linear support vector regression, stochastic gradient descent, AdaBoost, gradient boosting, Bayesian ARD regression, Gaussian process regression and multi-layer perceptron)
- 5-fold cross validation for hyperparameter optimization – same training set



A Framework to Evaluate Consistency on Toxicity Assessment



High Consistency Between Real and Generated Results for Hepatotoxicity and Nephrotoxicity-related Clinical Pathology Measurements



Hepatotoxicity-related measurements

Consistency between  and  Animal



GTP



LDH



TBIL



DBIL



ALT



AST



ALP



Nephrotoxicity-related measurements



BUN



K



CRE



Na



Cl

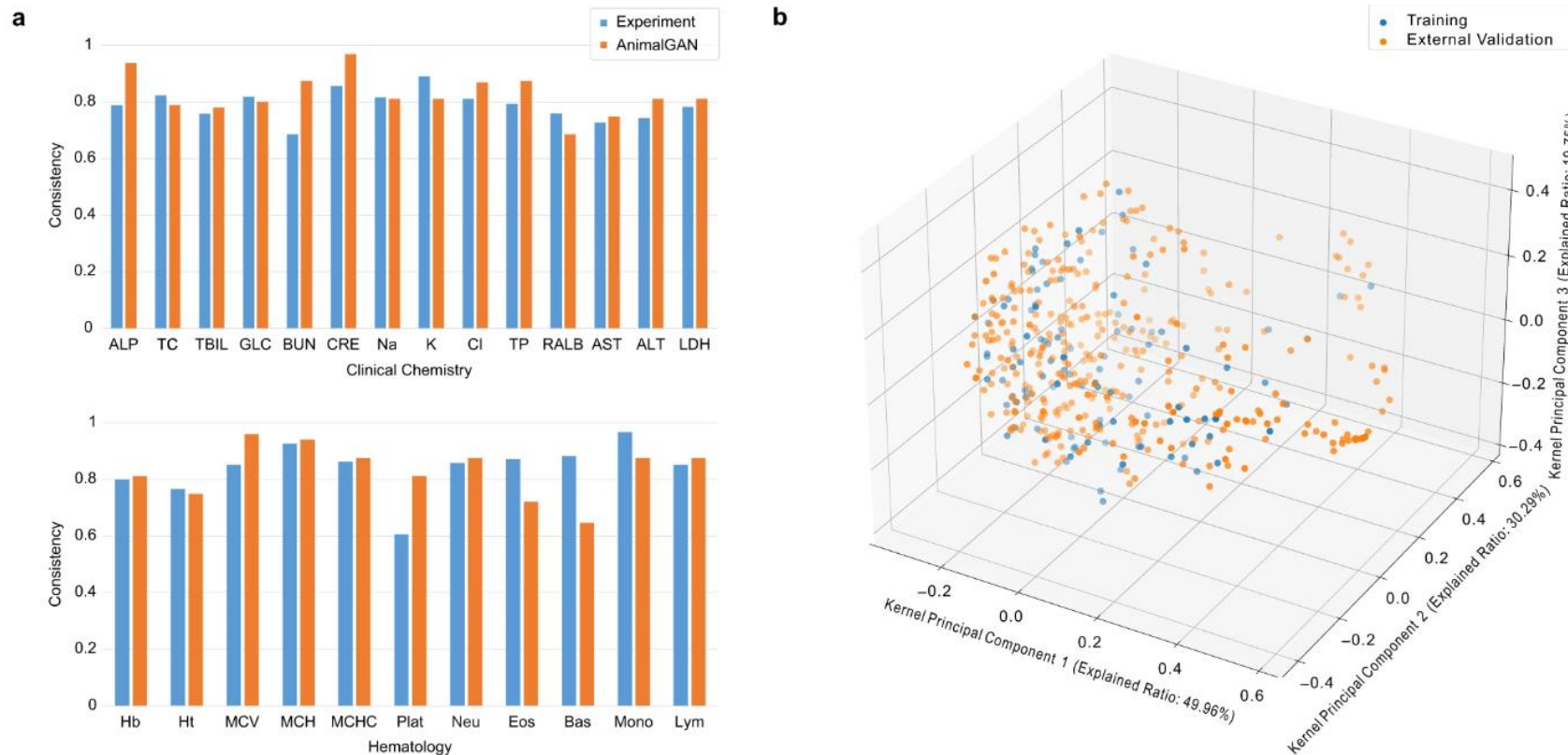


Ca



IP

External validation with DrugMatrix



Criteria for validation set

- Same rat strain and sex
- A similar repeated dose study design as TG-GATEs
- Common compounds tested by TG-GATEs to establish a baseline in comparison
- Contained clinical pathology measurements that significantly overlapped with those tested by TG-GATEs.

- 70 common compound (175 treatment) for baseline: 81.20%
- 355 external validation (717 treatment condition): 82.85%

AnimalGAN for iDILI Detection – Enhancing the Statistical Power of Small Experimental Groups through Data Augmentation with AnimalGAN

Criteria	Troglitazone	Pioglitazone	Rosiglitazone
ALT>ULN	1230	1820	1467
AST>ULN	7413	4315	4591
TBIL>ULN	3421	2083	2215
ALT>ULN or AST>ULN, and TBIL>ULN	375	161	158

The number of rats exhibiting drug-induced liver injury estimated by AnimalGAN for the three thiazolidinediones under the 28-day study with high dose in 100,000 rats

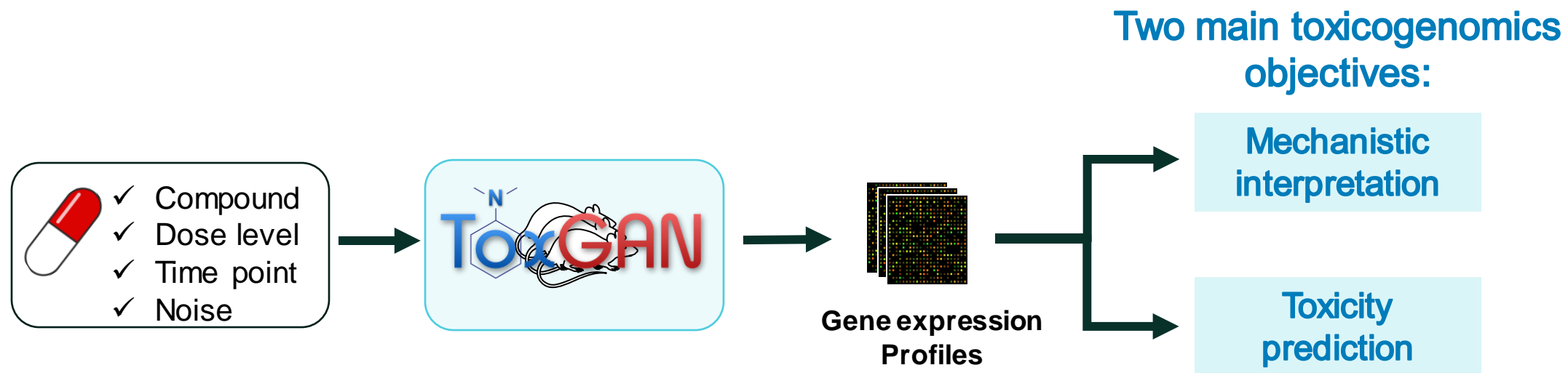
Potential Improvement and Context of Use

Problems	Potential improvement
Input (compounds descriptor 1826 + dose 1 + time + 1)	<p>Strategies to emphasize the wight of dosage</p> <ul style="list-style-type: none">• Embedding-based representation• Attention is all you need <p>Chemical descriptors matter?</p> <ul style="list-style-type: none">• Chemical embedding from large chemical-based language models
Controls (matched control in TG-GATEs)	<p>How to deal with new compound without matched control?</p> <ul style="list-style-type: none">• Toward implementing virtual control groups in nonclinical safety studies (PMID: 38043132)
Model architecture	<p>How to adjust loss functions are more for toxicology applications?</p> <ul style="list-style-type: none">• Adjust Loss function + biological-based criteria
Data sets	<p>How to develop more robust AnimalGAN model?</p> <ul style="list-style-type: none">• SEND data

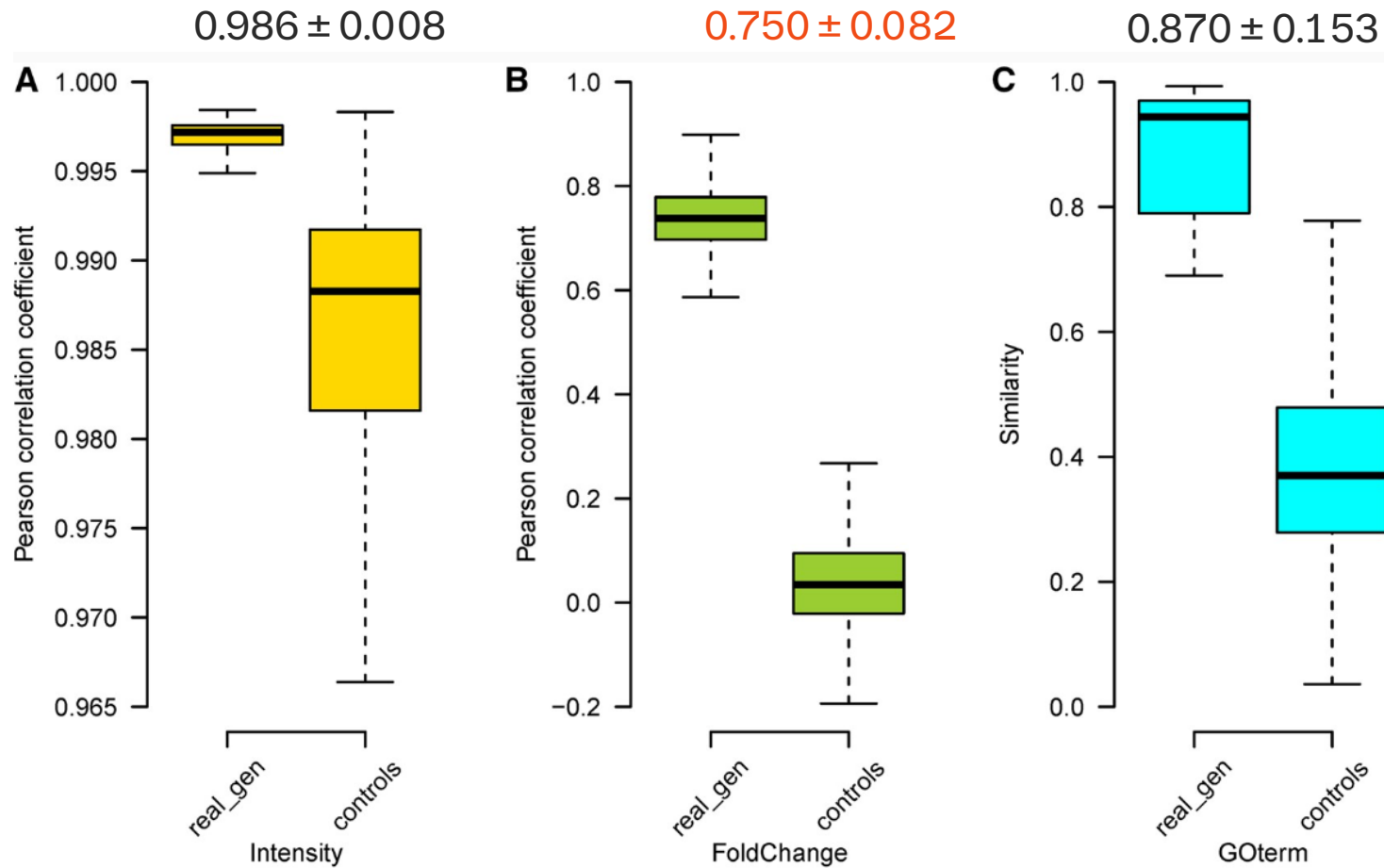
Context of Use

- Experiment design specific model – repeated dose experiment design of Open TG-GATEs
- AnimalGAN is particularly suitable for screening purposes, excelling in the detection of toxicology signals and iDILI

ToxGAN for Toxicogenomics



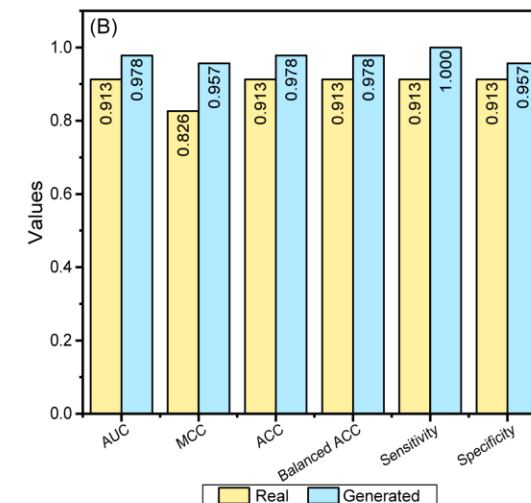
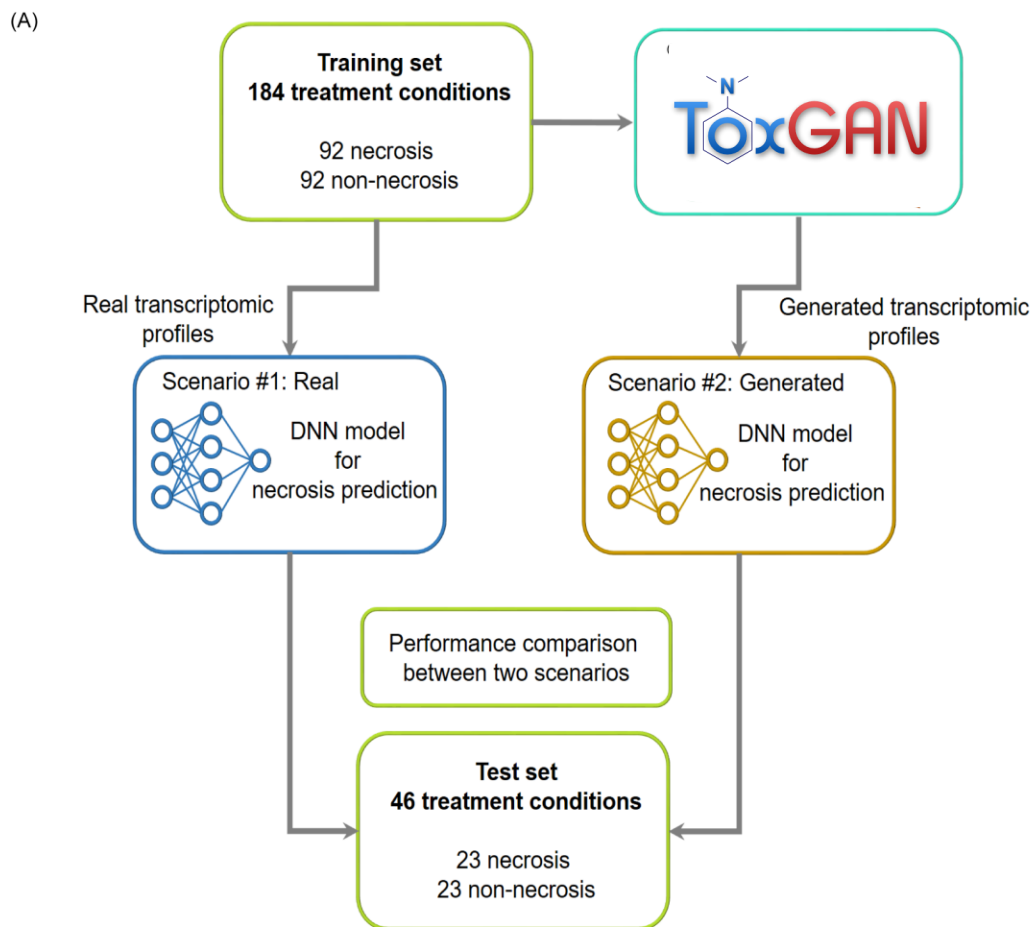
Concordance between Real Data and Generated Data



- High concordance in the intensity level
- Suboptimal concordance in fold change level
- Acceptable concordance in the functional level

#1: ToxGAN for Biomarker Development

Q1: Can ToxGAN generate a reliable biomarker?

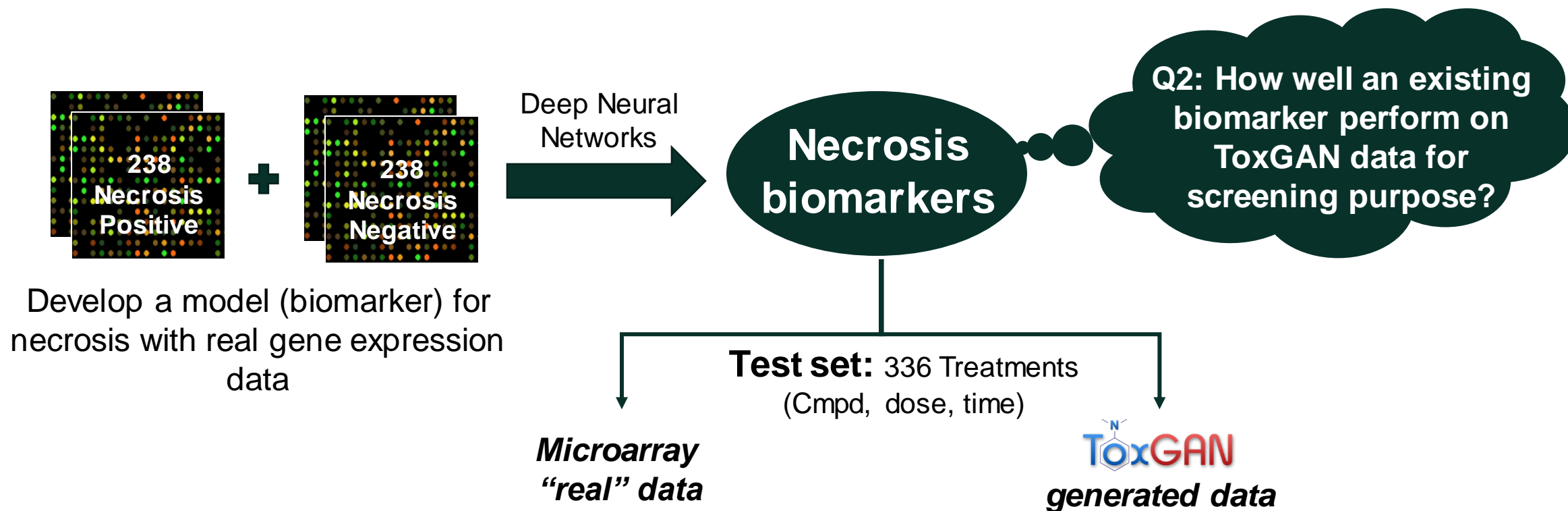


(C)

		DNN_real	
		positive	negative
DNN_gen	positive	21	2
	negative	1	22

Concordance = 0.935

#2: ToxGAN for Biomarker Application



Data	Real	Generated
Accuracy	0.73	0.79
MCC	0.43	0.60

ToxGAN Recapitulated Significant GO Terms

Study Design: to compare significant GO terms from gene expression data in 28-day repeated dose studies:

- Real data from microarray exp
- ToxGAN generated data

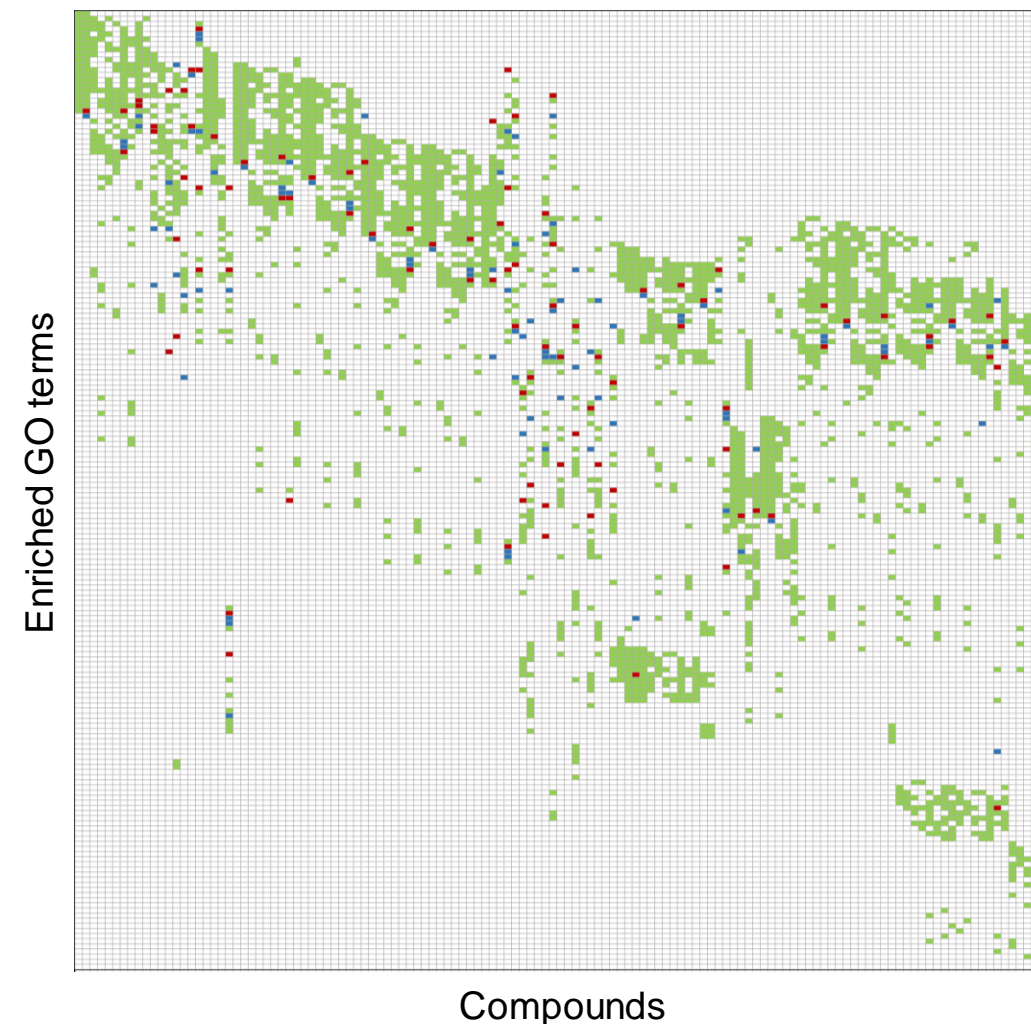
Findings: GO concordance between real and generated gene expression profile were high

GO terms found in

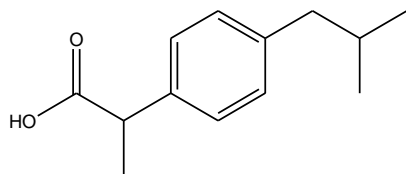
■ Both real and generated data

■ Generated data only

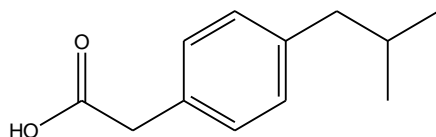
■ Real data only



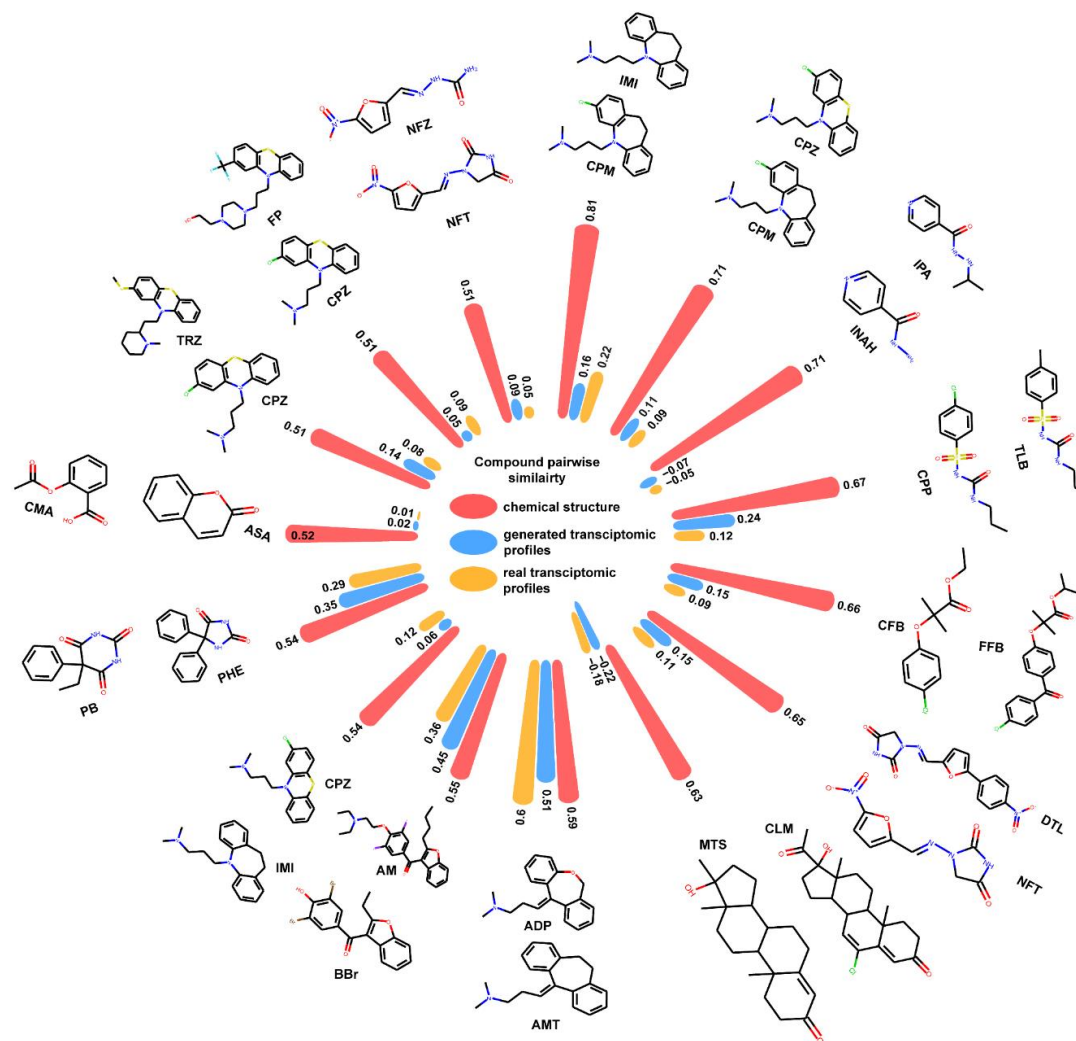
ToxGAN for Improved Read Across



Ibuprofen – OTC drug
On the market >30 yrs with
not much hepatotoxicity



Ibufenac – withdrawal
Marketed in 1966 and withdrawn in
1968 due to hepatotoxicity (no facts
given). Late study demonstrated
elevated ALT in 12/36 patients and
jaundice in 5/400 cases



Potential Improvement and Context of Use

Problems	Potential improvement
Input (compounds descriptor 1826 + dose 1 + time + 1)	Strategies to emphasize the wight of dosage <ul style="list-style-type: none"> • Embedding-based representation • Attention is all you need Chemical descriptors matter? <ul style="list-style-type: none"> • Chemical embedding from large chemical-based language models
Suboptimal performance of TG-GAN _{fold_change}	<ul style="list-style-type: none"> • Extra bias taken from autoencoder • Biological variance is enlarged in fold change level
Model architecture	How to adjust loss functions are more for toxicology applications? <ul style="list-style-type: none"> • Adjust Loss function + biological-based criteria
Data sets	How to develop more robust ToxGAN model? <ul style="list-style-type: none"> • LINCS data

Context of Use

- Experiment design specific model – repeated dose experiment design of Open TG-GATEs
- ToxGAN is particularly suitable for (1) genomics-based prediction model; (2) biological data-based ReadAcross; and (3) Initial prioritization of key functions or AOPs

Take-home Messages

- No one-fit-all AI solution – context of use
- Position different GAN models into specific toxicological questions
- Beyond GANs – Diffusion models??

Denoising diffusion models

- **Forward / noising process**



- **Reverse / denoising process**

- Sample noise $p_T(\mathbf{x}_T) \rightarrow$ turn into data

Acknowledgement

NDS US

- Charles Wood
- Matthew Bogdanffy

FDA/NCTR

- Weida Tong
- Xi Chen
- Ting Li

External Collaborators

- Ruth Roberts (Apconix and U of Birmingham at UK)
- Scott Auerbach (NIEHS)

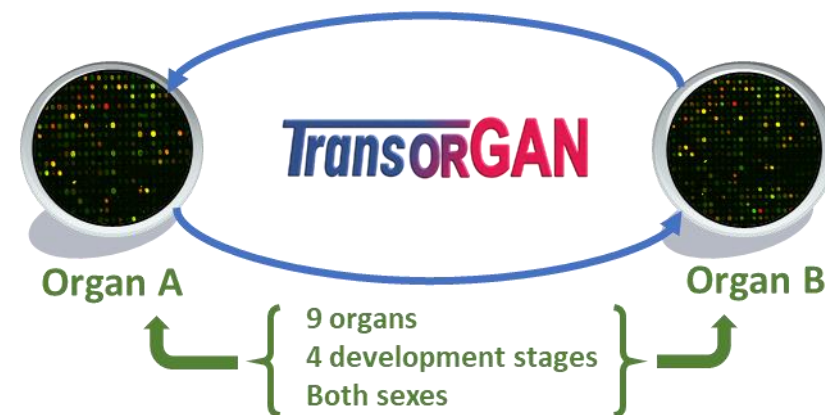
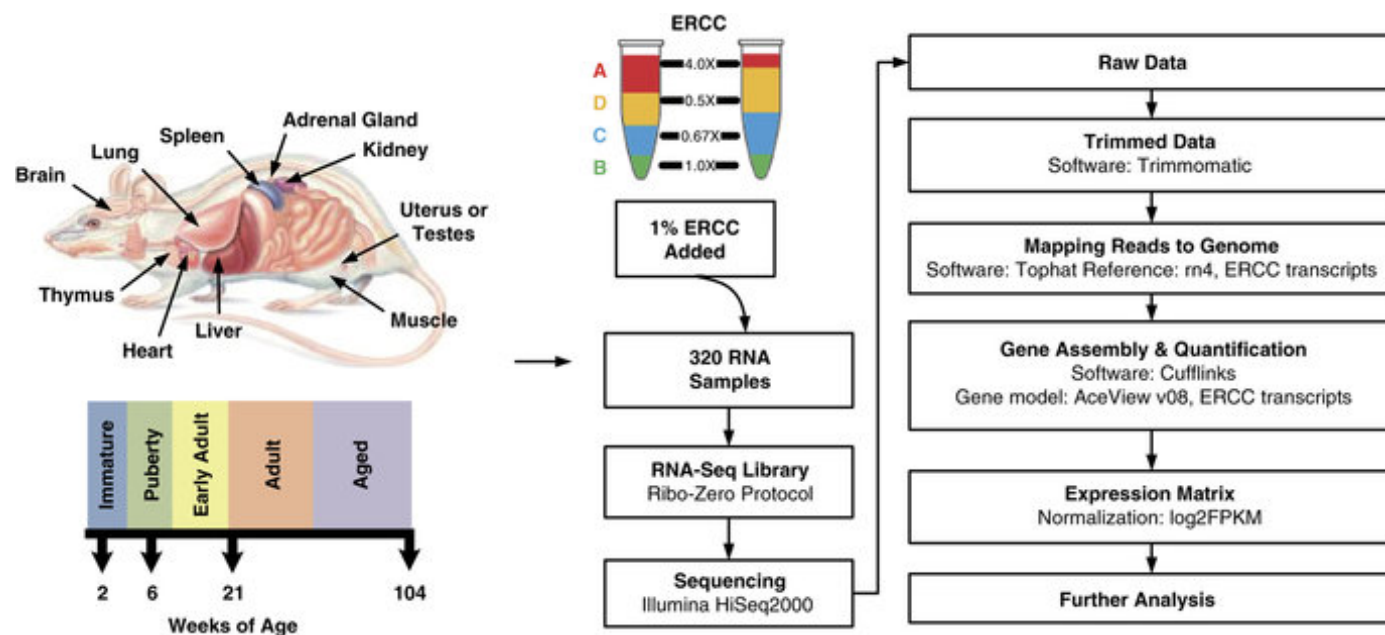


*Thank
you*



Backups

TransORGAN Mapping of Rat Transcriptomic Profiles Between Organs, Ages, and Sexes



Rat BodyMap: Nature Communications volume 5, 3230 (2014)

TransOrGAN could Translate Transcriptomic Profiles from One Organ to Another

