

Aligning Transformers with Continuous Feedback via Energy Rank Alignment

Shriram Chennakesavalu, Frank Hu,
Sebastian Ibararan, and Grant M. Rotskoff

NeurIPS 2025

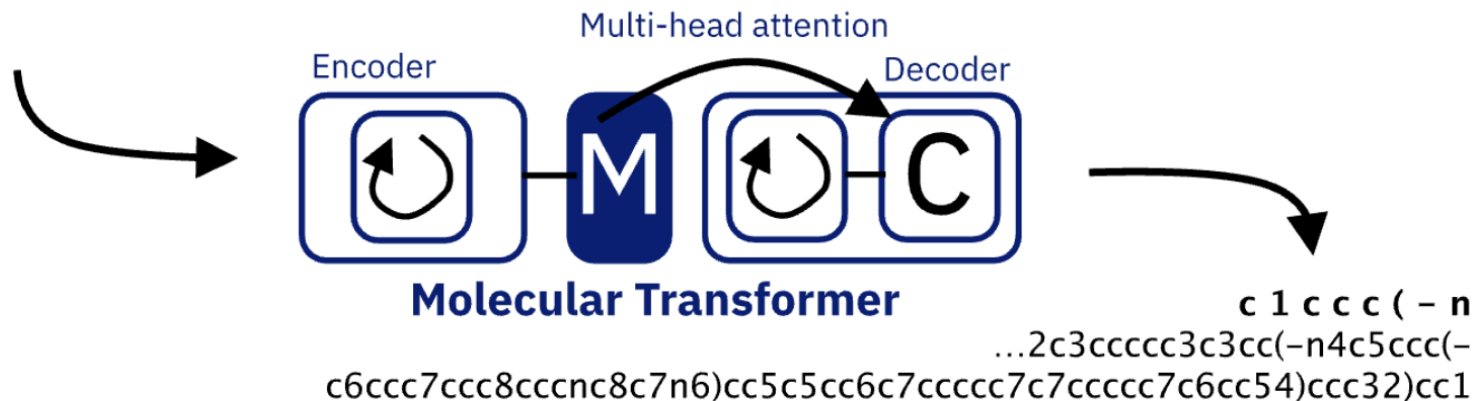
Chemistry Language Models

Foundation Models for Molecular Generation

- Molecular Transformer (2019):

Input: reactants-reagents (atom-wise tokenization)

Br c 1 c c c 2 ...
c(c1)c1cc3c4cccc4c4cccc4c3cc1n2-c1ccc2c(c1)c1cccc1n2-c1cccc1.CCO.
Cc1cccc1.OB(O)c1ccc2ccc3ccnc3c2n1.c1ccc([PH](c2cccc2)(c2cccc2)[Pd]([PH](c2cccc2)
(c2cccc2)c2cccc2)([PH](c2cccc2)(c2cccc2)c2cccc2)[PH](c2cccc2)(c2cccc2)c2cccc2)cc1



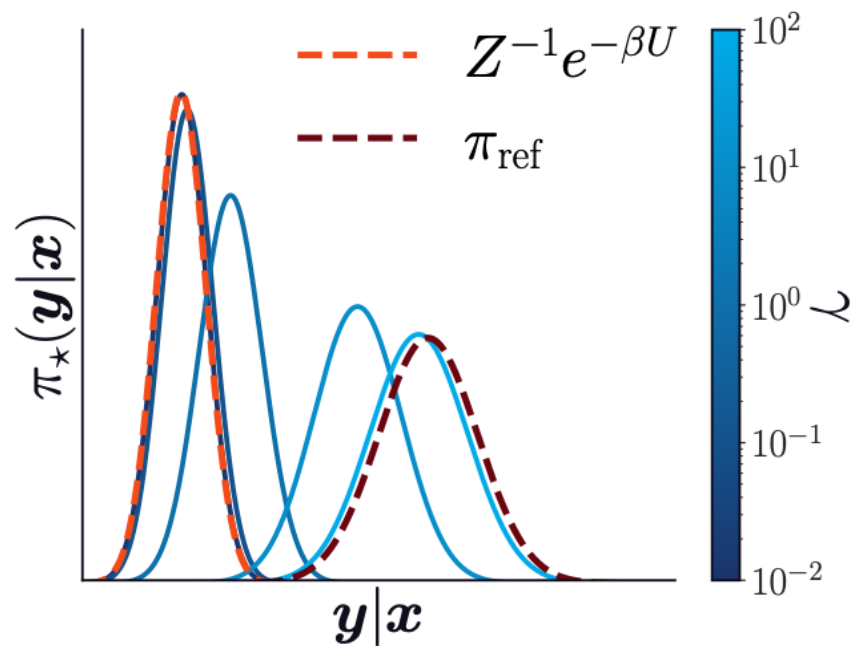
Target: most likely products

Schwaller et al., *ACS Cent Sci*, **2019**

Energy Rank Alignment (ERA)

- Simple gradient-based objective
- Explicitly incorporates a reward/energy function
- Avoids greedy policies
- Controllable regularization
- State-of-the-art performance on molecular generation benchmarks

Theoretical Framework

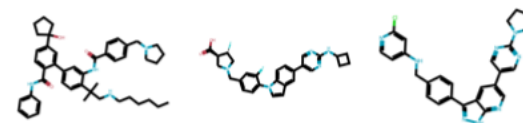


Target Property

Generated Molecules

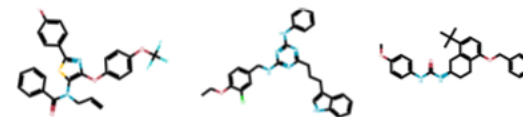
High Ring Count

$y \sim \pi(y|x)$



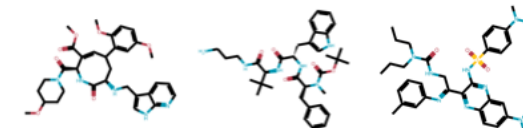
High Hydrophobicity

$y \sim \pi(y|x)$



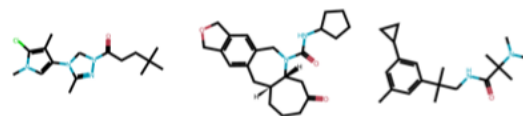
High Polarizability

$y \sim \pi(y|x)$



High Drug-likeness

$y \sim \pi(y|x)$

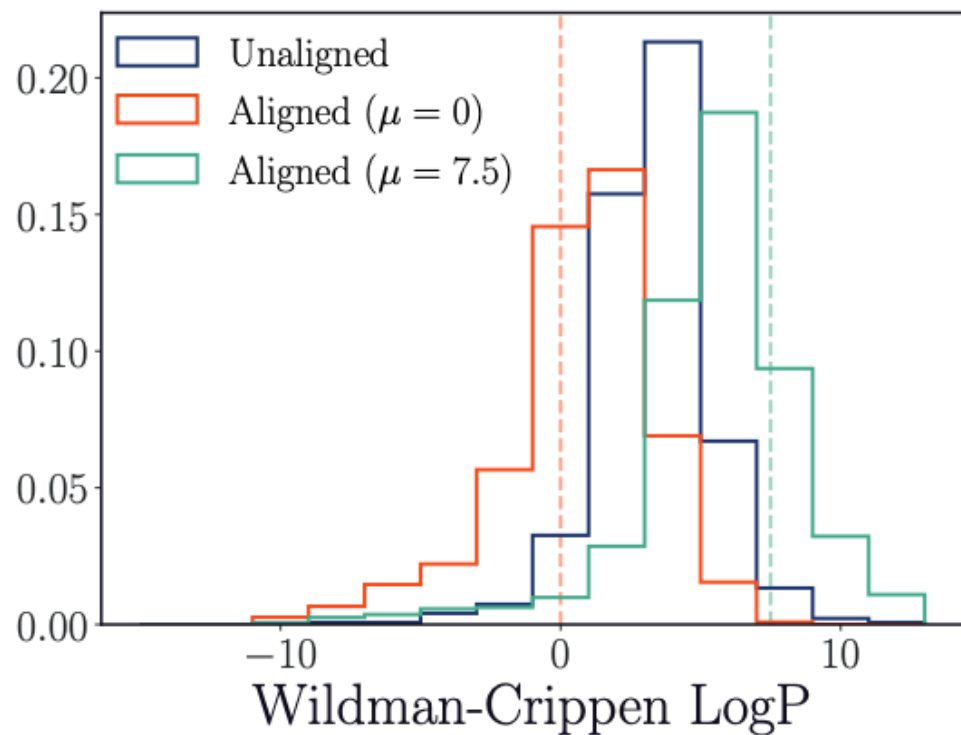
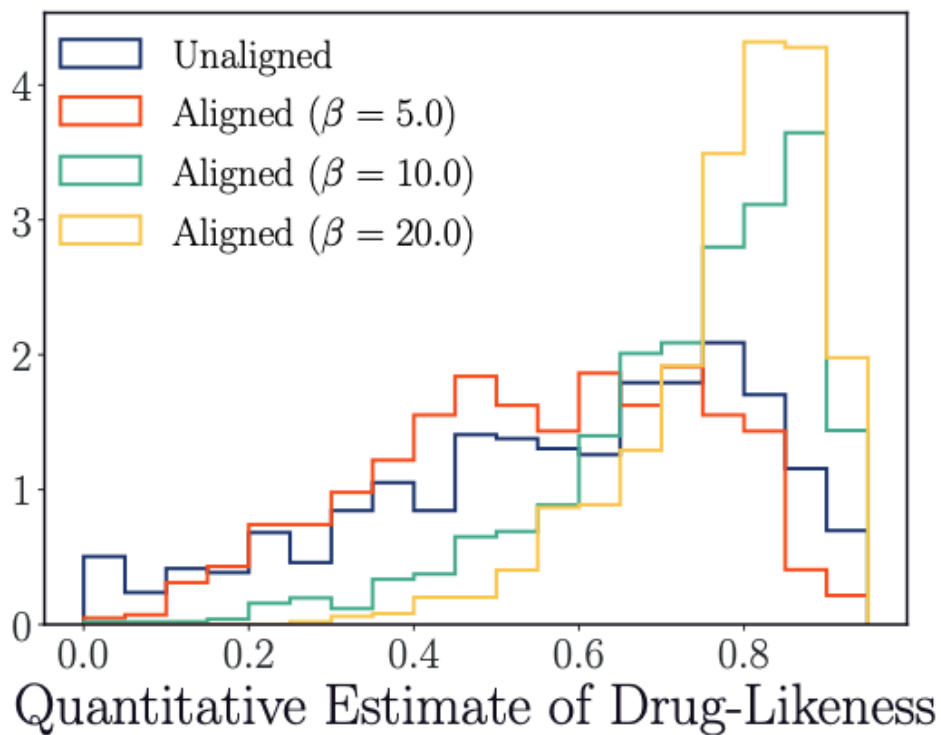


Experiments

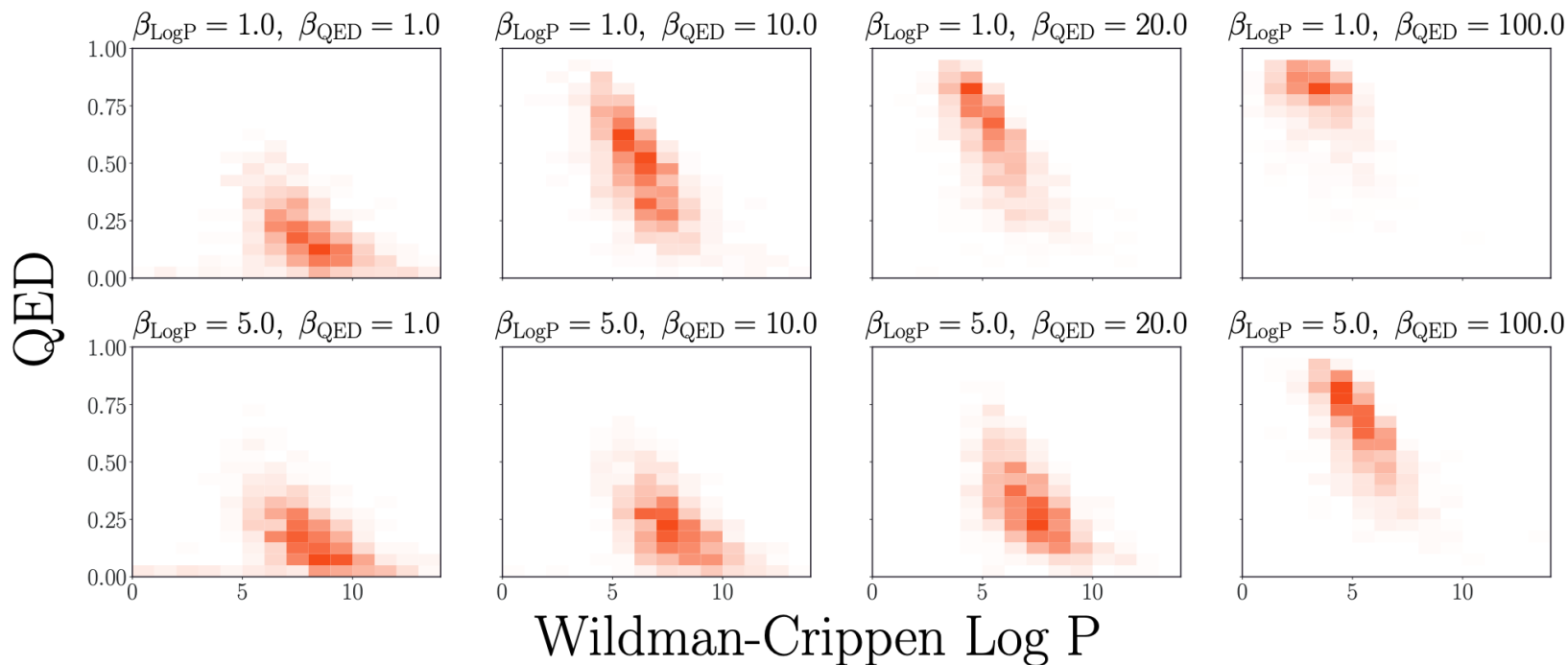
Molecular Generation

- Foundation model: transformer trained on 2.4M ChEMBL SMILES
- Focused on easily computed *in silico* oracles
 - RDKit: QED, hydrophobicity, ring count, Tanimoto similarity
 - Docking: random forest predictors of docking scores against two kinase targets – GSK3 β and JNK3
- Tested both unprompted (BOS token only) and prompted (conditioned on a SMILES) alignment

Single-Property Alignment

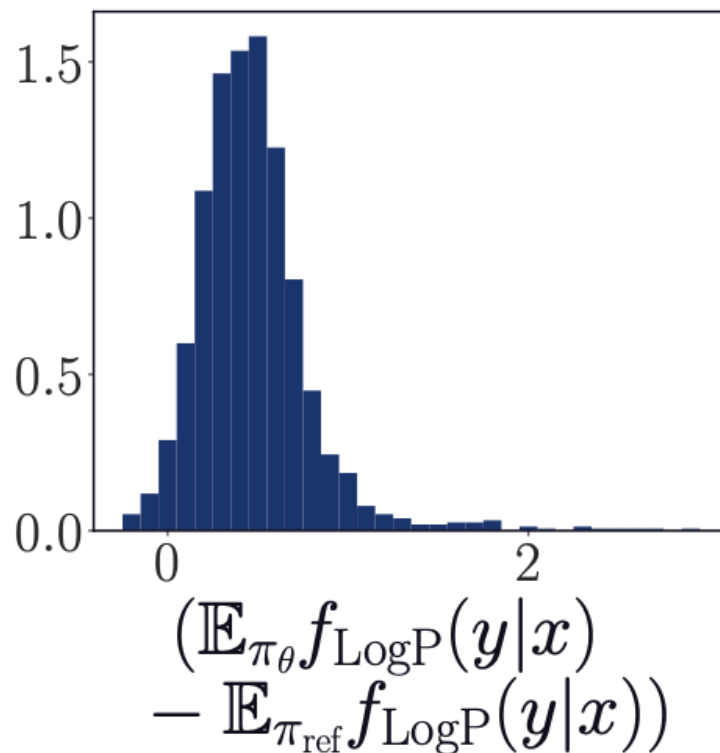
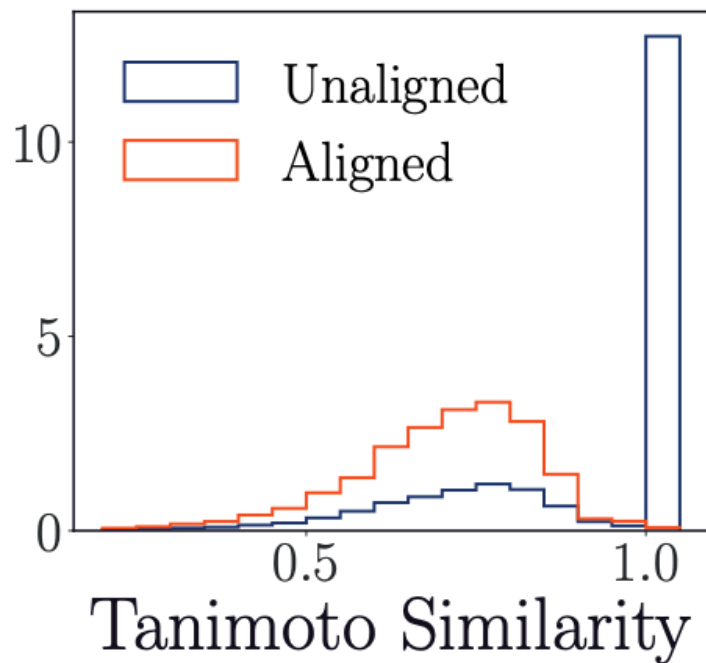


Multi-Property Alignment



Prompted Multi-Property Alignment

Multienergy Alignment (LogP and Tanimoto)



Docking Benchmarks

- Generate more diverse molecules (lower IntDiv) with higher bioactivities

	GSK3 β top-100		JNK3 top-100	
	mean score	IntDiv	mean score	IntDiv
ERA	0.996 \pm 0.000	0.219 \pm 0.002	0.987 \pm 0.001	0.264 \pm 0.005
MolRL-MGPT	1.000 \pm 0.000	0.362 \pm 0.015	0.961 \pm 0.010	0.372 \pm 0.025
GFlowNet	0.649 \pm 0.072	0.715 \pm 0.104	0.437 \pm 0.219	0.716 \pm 0.145
GraphGA	0.919 \pm 0.016	0.365 \pm 0.024	0.875 \pm 0.025	0.380 \pm 0.015
JT-VAE	0.235 \pm 0.083	0.770 \pm 0.067	0.159 \pm 0.040	0.781 \pm 0.127
REINVENT	0.965 \pm 0.011	0.308 \pm 0.035	0.942 \pm 0.019	0.368 \pm 0.021

Acknowledgements



Yinuo Ren

Ph.D. (Institute for Computational and
Mathematical Engineering)



Andy Mitchell

Ph.D. (Chemistry)



Grant Rotskoff

Assistant Professor of Chemistry



Jérémie Klinger

Postdoc



Abigail Park

Ph.D. (Chemistry)



Sherry Li

Ph.D. (Chemistry)



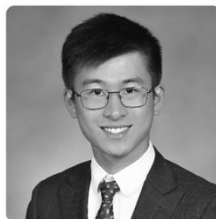
Frank Hu

Ph.D. (Chemistry, Markland Lab)



Emmitt Pert

Ph.D. (Chemistry)



Josh Liu

Ph.D. (Biophysics)



Nick Juntunen

Ph.D. (Chemistry)



Steven Dunne

Ph.D. (Biophysics)



Wenhao Gao

Postdoc

