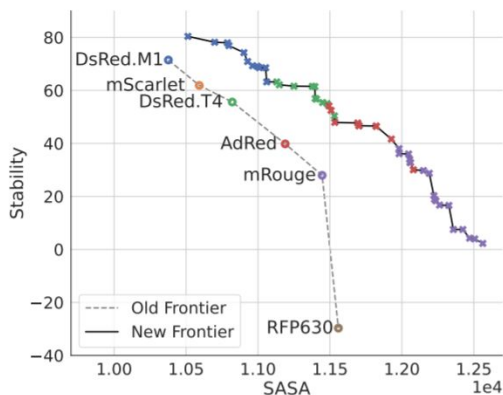


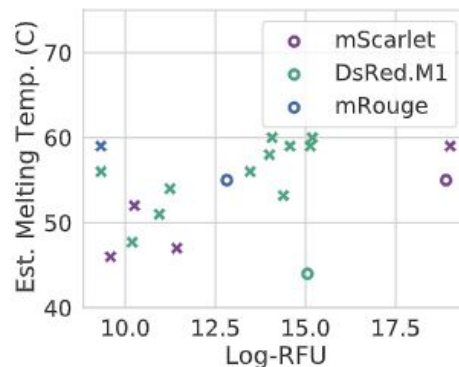
# Accelerating Bayesian Optimization for Biological Sequence Design with Denoising Autoencoders

Samuel Stanton, Wesley Maddox, Nate Gruver, Phillip Maffettone, Emily Delaney, Peyton Greenside, Andrew Gordon Wilson

*in silico*



*in vitro*



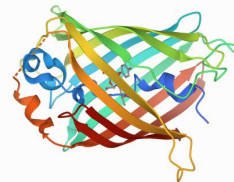
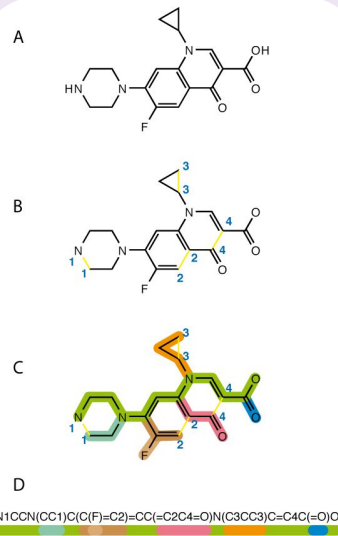
# Biological Sequence Design

intractable combinatorial  
optimization problem

slow/impossible to  
compute

$$\max_{\mathbf{x} \in \mathcal{X}} (f_1(\mathbf{x}), \dots, f_k(\mathbf{x}))$$

- Discrete, high-dim. inputs
- Multiple black-box objectives
- Batched experiments
- Noisy labels



	10	20	30	40	50
MVSKGEELFT	GVVPILVELD	GDVNGHKFSV	SGEGEGDATY	GKLTCLKFICT	
60	70	80	90	100	
TGKLPVPWPT	LVTTLTYGVQ	CFSRYPDHMK	QHDFFKSAMP	EGYVQERTIF	
110	120	130	140	150	
FKDDGNYKTR	AEVKFEGDTL	VNRIELKGID	FKEDGNILGH	KLEYNYNSHN	
160	170	180	190	200	
VYIMADKQKN	GIKVNFKIRH	NIEDGSVQLA	DHYQQNTPIG	DGPVLLPDNH	
210	220	230			
YLSTQSALSK	DPNEKRDMHV	LLEFVTAAGI	TLGMDELYK		

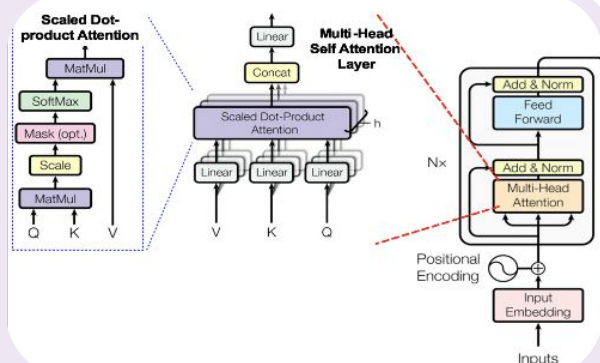
# Deep Generative Models (DGMs)

optimize over small  
DGM-generated subset

ad-hoc proxy objective

$$\max_{\mathbf{x} \in \mathcal{X}'} ???$$

- How do we rank generated sequences, accounting for multiple objectives, explore-exploit, etc.?
- How do we generate good subsets for ranking?



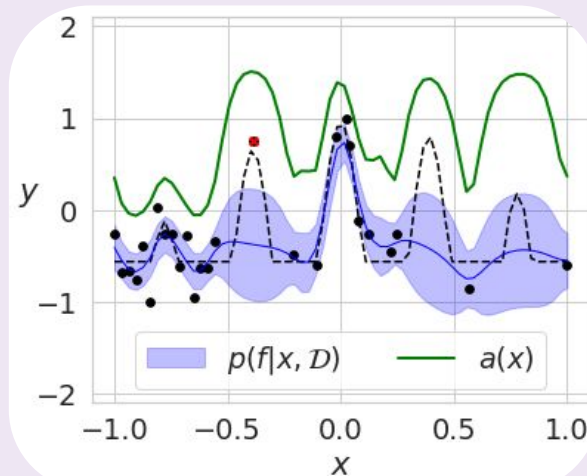
# Bayesian Optimization (BayesOpt)

intractable combinatorial  
optimization subproblem

principled proxy objective

$$\max_{\mathbf{x} \in \mathcal{X}} \mathbb{E}[u(\mathbf{x})]$$

- Strategy 1: solve subproblem with genetic algorithms (inefficient).
- Strategy 2: use a frozen pretrained generative model, solve in latent space (data-hungry).

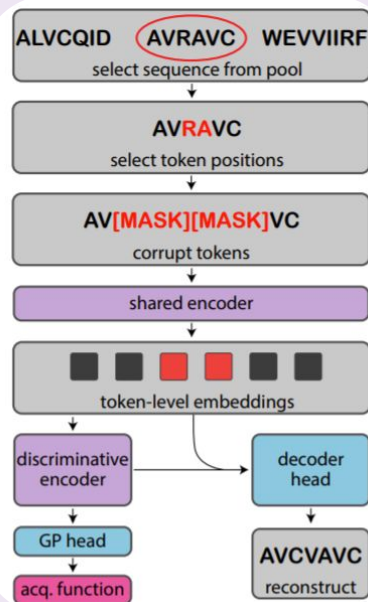


# Latent Multi-Objective BayesOpt (LaMBO)

**LaMBO** is designed from the ground up to combine the best attributes of DGMs and BayesOpt.

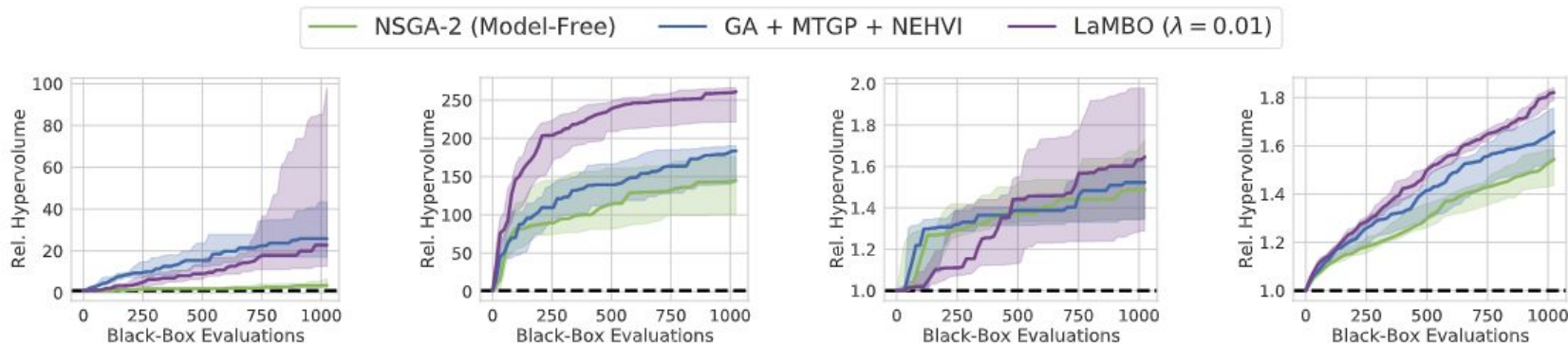
# The LaMBO architecture

- Jointly train a denoising autoencoder and a discriminative deep kernel GP.
- Rank samples with the NEHVI acquisition function, optimize in latent space.
- Pretraining is optional!



# Previewing the results

Comparing **LaMBO** to model-free and model-based genetic algorithms



(a) Bigrams

(b) logP + QED

(c) DRD3 Docking + SA

(d) Stability + SASA

small molecule

large molecule

# Collaborators



**Samuel Stanton**



**Wesley Maddox**



**Nate Gruver**



**Andrew Wilson**



**Phil Maffetone**



**Emily Delaney**



**Peyton Greenside**



# Thanks, come check out the poster!

**Thursday, July 21, 6PM - 8PM**  
**Poster Session 1, Hall E #533**



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Paper



Code

