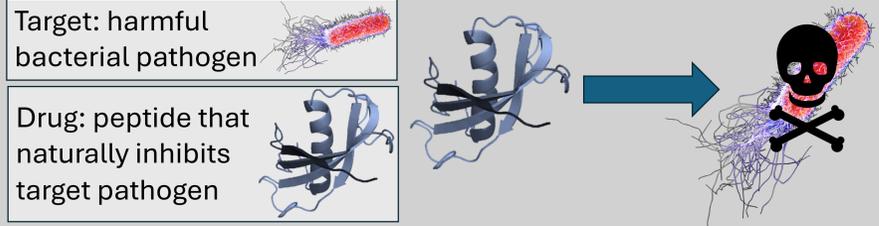


## Abstract

**Traditional multi-objective optimization** returns Pareto solutions balancing trade-offs—but when objectives conflict heavily, no single solution performs well across all. **Coverage optimization** selects a small set of solutions such that each objective is well-addressed (i.e., “covered”) by at least one. **We introduce MOCOBO**, the first Bayesian optimization method for coverage optimization.

## Drug Discovery as Black-Box Optimization

**Goal:** Find a new peptide that works as a drug against a target bacterial pathogen



**Black-box objective function (real-valued):**

$f(x)$  = effectiveness of peptide  $x$  in inhibiting the target

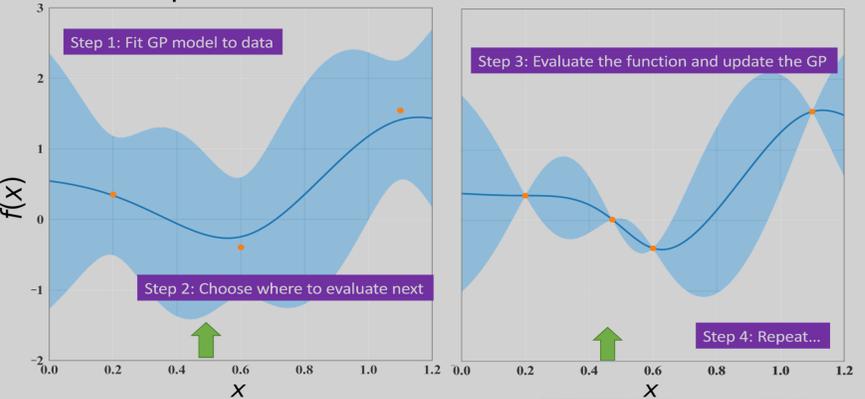
**Goal:** Find a peptide that optimizes  $f(x)$ , formally:

$$\operatorname{argmax}_{x \in X} f(x)$$

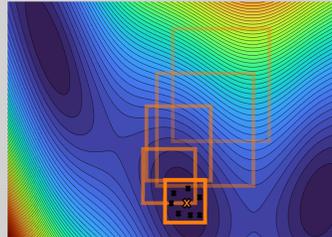
**Multi-objective setting:** Find a peptide  $x$  that optimizes multiple objectives  $f_1, f_2, \dots, f_T$  (e.g., multiple pathogens)

## Bayesian Optimization (BO)

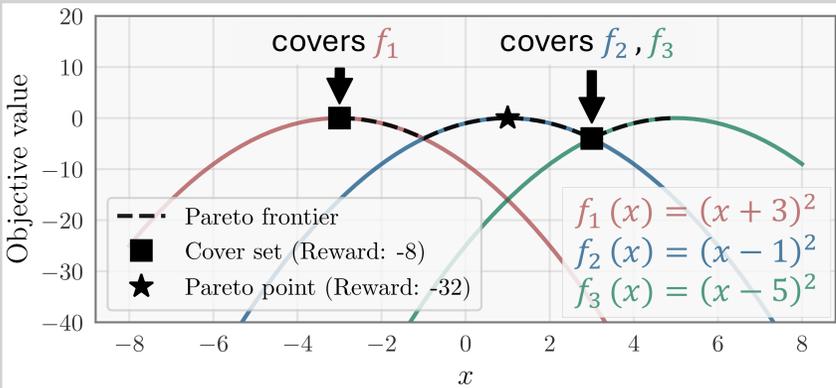
**BO:** A model-based global optimization technique for black-box optimization.



**Trust Region BO:** A popular high-dimensional BO method which limits the the large, high-dim search space to a hyper-rectangular trust region  $\tau$ . The size and location of the trust region are updated dynamically.



## Coverage Optimization



**Goal:** Cover  $T$  pathogens with a set of  $K < T$  peptides.

**Idea:** Each target pathogen is inhibited by at least one peptide in the “covering set”.

**Search Space  $X$  (All Peptides)**

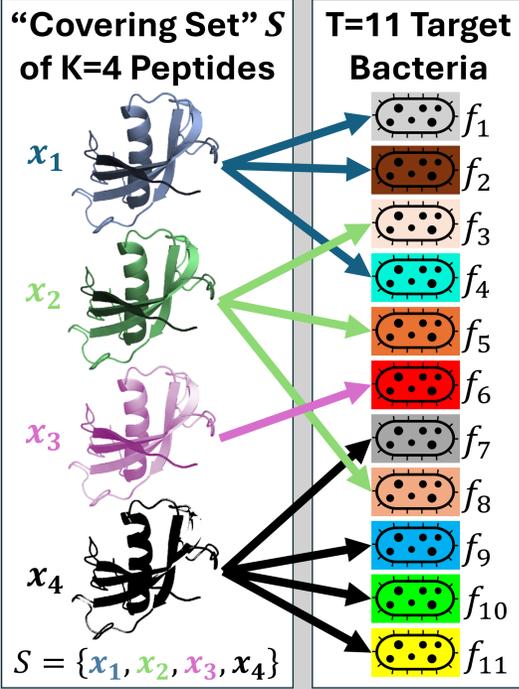
**Coverage score:**

$$c(S) = \sum_{i=1}^T \max_{x \in S} f_i(x)$$

The quantity we seek to optimize

**Goal (formally):**

$$S^* = \operatorname{argmax}_{S \subseteq X, |S|=K} c(S)$$



## Our Method: Multi Objective Coverage BO (MOCOBO)

MOCOBO is a Bayesian optimization algorithm for coverage optimization. To select new candidates for evaluation, MOCOBO introduces ECI, a new acquisition function tailored to the coverage optimization setting.

**Expected Coverage Improvement (ECI):**

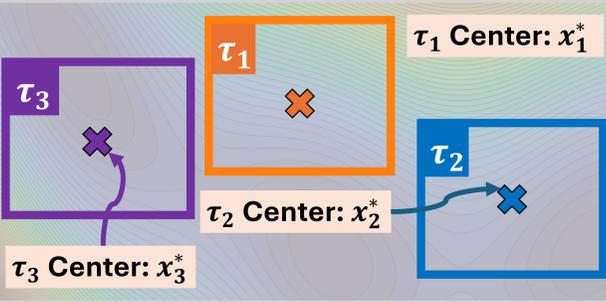
$$ECI(x) = E_{p(y|x, D)} [\max(0, c(S_{DU\{(x,y)\}}^*) - c(S_D^*))]$$

Best coverage score after observing  $(x, y)$  Best coverage score so far

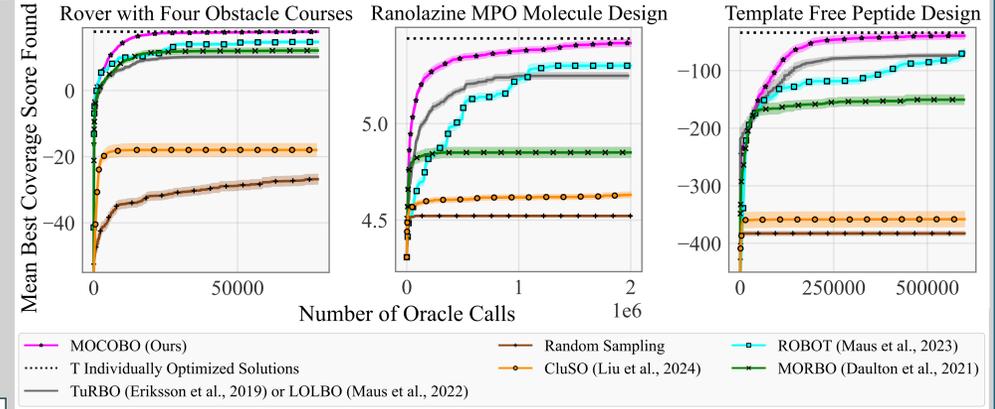
MOCOBO uses  $K$  trust regions  $\tau_1, \tau_2, \dots, \tau_K$  to find  $K$  “covering” solutions. On each step, trust

regions are centered on  $S_D^* = \{x_1^*, x_2^*, \dots, x_K^*\}$ : the best covering set of  $K$  solutions in the observed dataset  $D$ .

$$S_D^* = \operatorname{argmax}_{S \subseteq D, |S|=K} c(S)$$

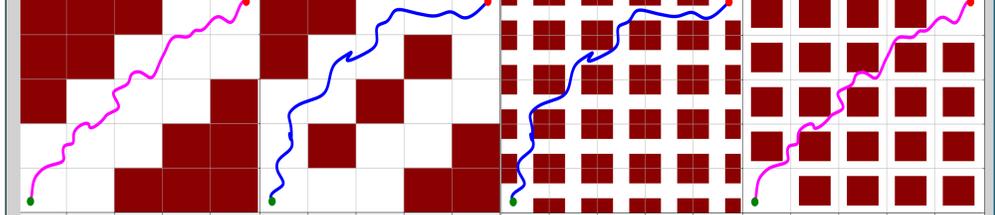


## Optimization Results



## Rover with Four Obstacle Courses Task

The  $K=2$  trajectories (magenta, blue) found by one run of MOCOBO allow the rover to successfully navigate all  $T=4$  unique obstacle courses.



## Ranolazine MPO Molecule Design Task

$T=6$  objectives: add six target elements to Ranolazine (F, Cl, Br, Se, S, P).  $K=3$  covering molecules found by one run of MOCOBO:

- CC=C(C)C(OC(=O)C(O)CCCCCCC(=O)O)=CC=CCCCCCC[Se]CC(=O)NCI=CC=CC=CIC
- CC=C(C)C(OC(=O)CCCCCCC(O)C(=S)Cl)=CC=CCOCCCCC(O)CC(=O)NCI=CC=CC=CIC
- CC=C(C)C(OC(=O)C(O)CCCCCCC(=O)CBr)=CC=COCPCCCCN(C)CC(=O)[NH]Cl=CC=C(P)C=CIC

## Antimicrobial Peptide Design Task

$\{x_1^*, x_2^*, x_3^*, x_4^*\}$ : Covering set of  $K=4$  peptides found by one run of MOCOBO

**B1-B11:** The  $T=11$  target bacteria. (-): Gram-negative (+): Gram-positive  
**MIC (minimum inhibitory concentration):** concentration of peptide needed to inhibit bacterial growth (lower is better)

**In silico MICs:** MOCOBO successfully covers all  $T=11$  target bacteria.

	B1(-)	B2(-)	B3(-)	B4(-)	B5(-)	B6(-)	B7(-)	B8(+)	B9(+)	B10(+)	B11(+)
$x_1^*$	1.017	1.040	1.893	0.999	8.613	0.966	1.039	65.999	38.361	338.692	1.393
$x_2^*$	0.999	15.565	1.860	1.952	404.254	486.860	406.034	1.233	1.318	7.359	0.981
$x_3^*$	2.654	3.268	3.113	4.854	4.923	12.967	14.610	22.631	29.685	254.306	3.947
$x_4^*$	0.939	0.906	1.124	1.310	10.909	1.384	1.711	12.776	32.884	434.193	1.037

**In vitro MICs:** 9 out of 11 bacterial targets are covered *in vitro*.

