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# DockTDesign

## Deep Generative Models for *de novo* Drug Design

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# Summary

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## 1. Introduction

- 1.1 Generative modelling: variational autoencoders
- 1.2 Multi and *many*-objective optimization

## 2. Methodology

## 3. Results

## 4. Conclusions

# Motivation

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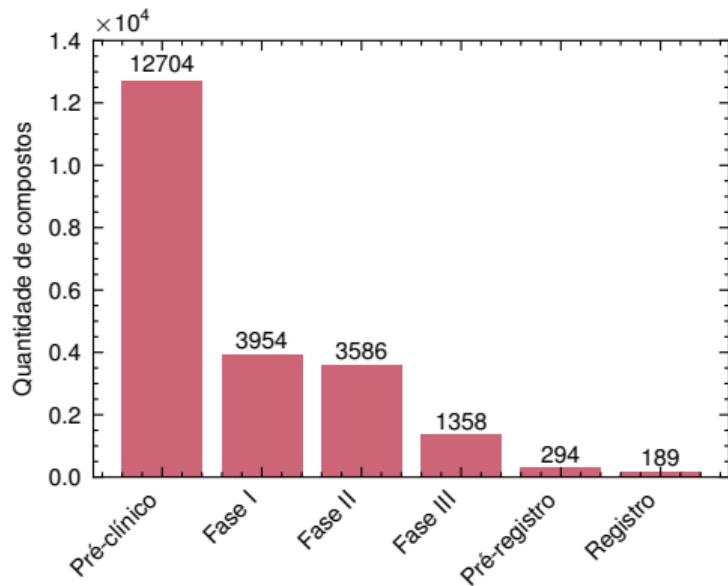


Figure: Number of compounds per development phase in 2025. Source: [Pharmaprojects](#).

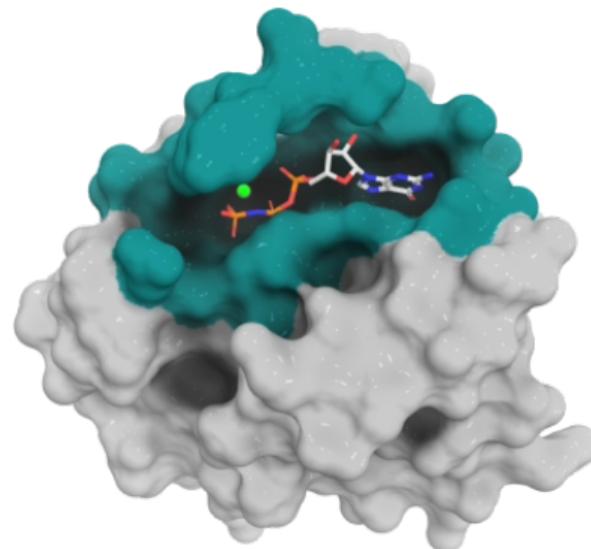
- Drug development: long, costly, and with low success rates ( $\leq 5\%$  in the preclinical phase).
- Increasing the success rate in early phases can have a large economic and public-health impact.
- Computational methods are essential for the early identification of promising molecules (*hits*).

## Objectives

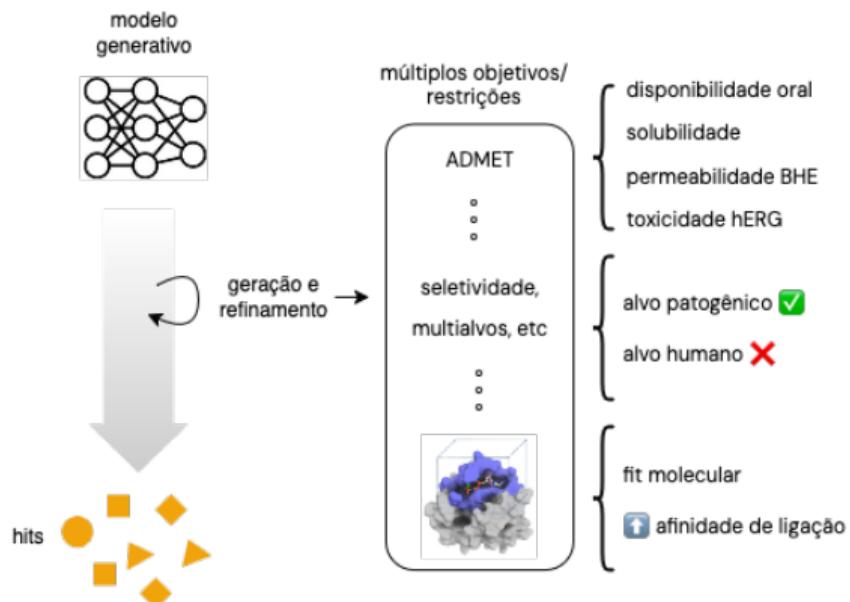
- Pose prediction
- Binding affinity prediction

## Components

- Search algorithm
- Scoring function:
  - pose
  - binding affinity



- Generate molecules with desirable properties without the need for pre-defined structures.
- Essentially multi-objective problem.



# Variational autoencoders (VAEs)

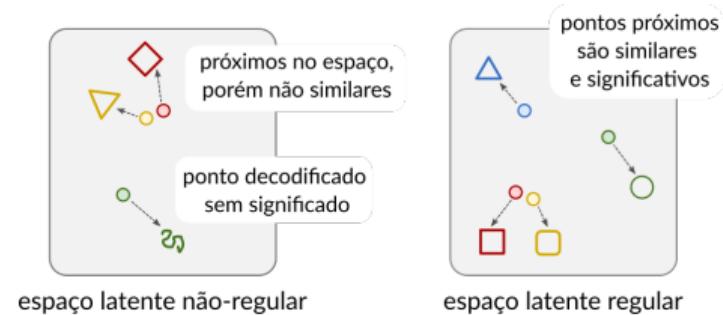
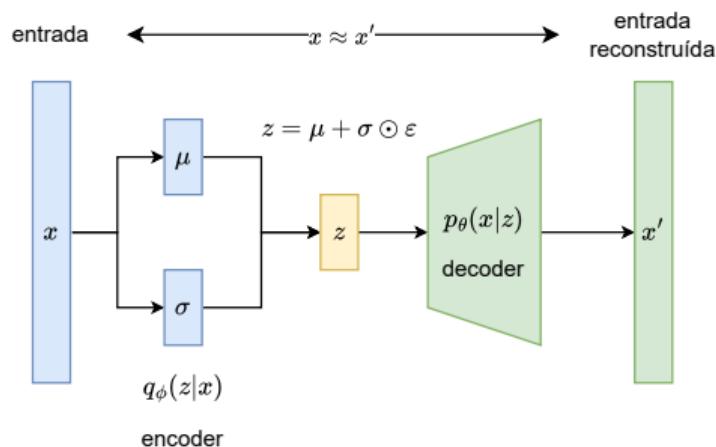


Figure: Properties of the latent space.

Figure: Variational autoencoder (VAE).

# Multi-objective optimization

$$\begin{array}{ll}\text{minimize} & F(x) = (f_1(x), f_2(x), \dots, f_k(x))^T \\ \text{subject to} & g_i(x) \leq 0, \quad i = 1, 2, \dots, m \\ & h_j(x) = 0, \quad j = 1, 2, \dots, p\end{array}$$

$$f_i : \mathbb{R}^n \rightarrow \mathbb{R}$$

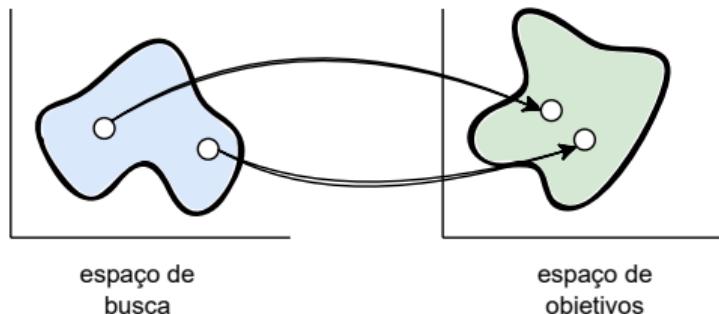


Figure: Different spaces in multi-objective optimization.

**Pareto dominance:**  $x \succ y$  if  $f_i(x) \leq f_i(y)$  for all  $i$  and  $f_j(x) < f_j(y)$  for some  $j$ .

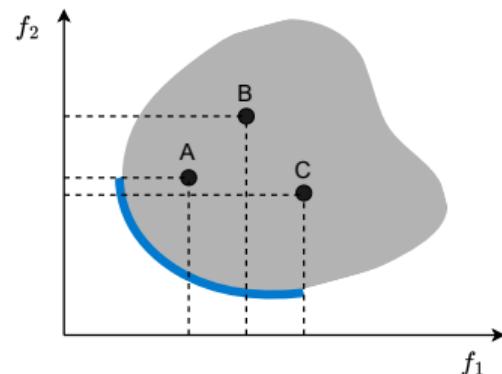


Figure: Dominance and Pareto front.

# Literature review: *de novo* design

Three main approaches are employed for the *de novo* design of molecules using generative models:

- Distribution learning
- Conditional generation
- Objective-guided learning

## Current limitations

Methodologies that handle  $k \geq 4$  objectives are still little explored, especially integrating appropriate techniques and generative models [?].

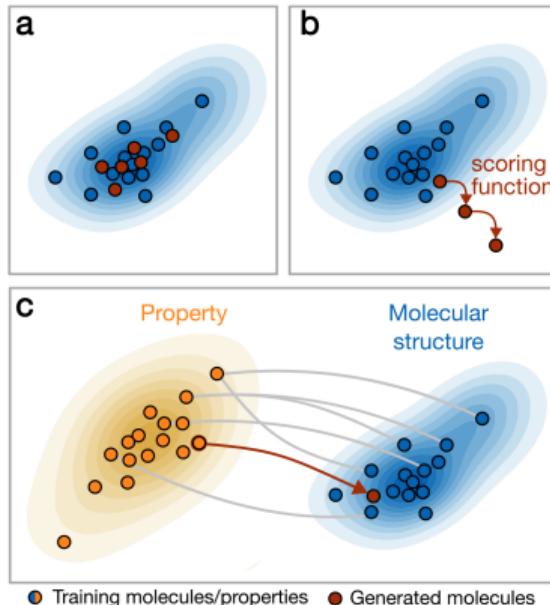


Figure: Generative approaches: (a) distribution learning, (b) objective-guided learning, and (c) conditional generation [?].

# Proposed generative platform

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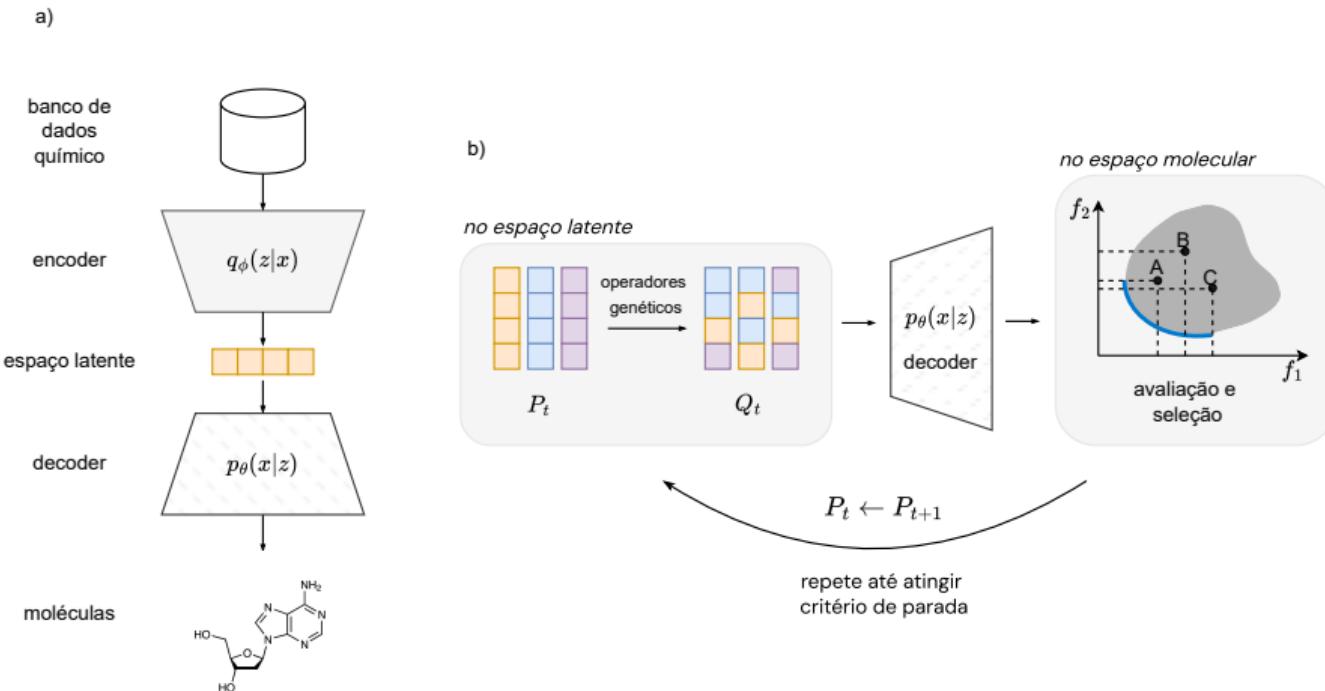


Figure: DockTDesign generative platform.

Two antimicrobial targets were selected as a case study for generating multitarget inhibitors:

- **LpxC<sup>a</sup>** (antimicrobial target involved in LPS synthesis).
- **gshA<sup>b</sup>** (antimicrobial target essential for glutathione biosynthesis).

<sup>a</sup>UDP-3-O-acyl-N-acetylglucosamine deacetylase

<sup>b</sup>Glutamate–cysteine ligase

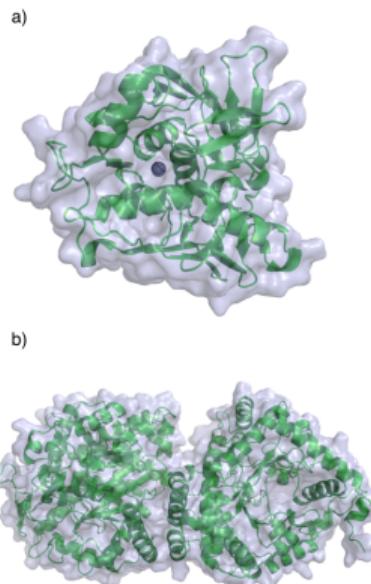


Figure: Receptors (a) LpxC and (b) gshA.

## Experimental design

**Algorithms:** Single-objective GA, NSGA-II and NSGA-III.

## Objectives:

1. maximize QED;
2. minimize SA;
3. minimize complexity;
4. maximize similarity against molecule BDBM50074960 (active LpxC);
5. minimize similarity against molecule BDBM50478376 (active LpxC, active MMP-9).

Work resulted in a publication in an international conference [?].

# Results: molecular docking (protocol I)

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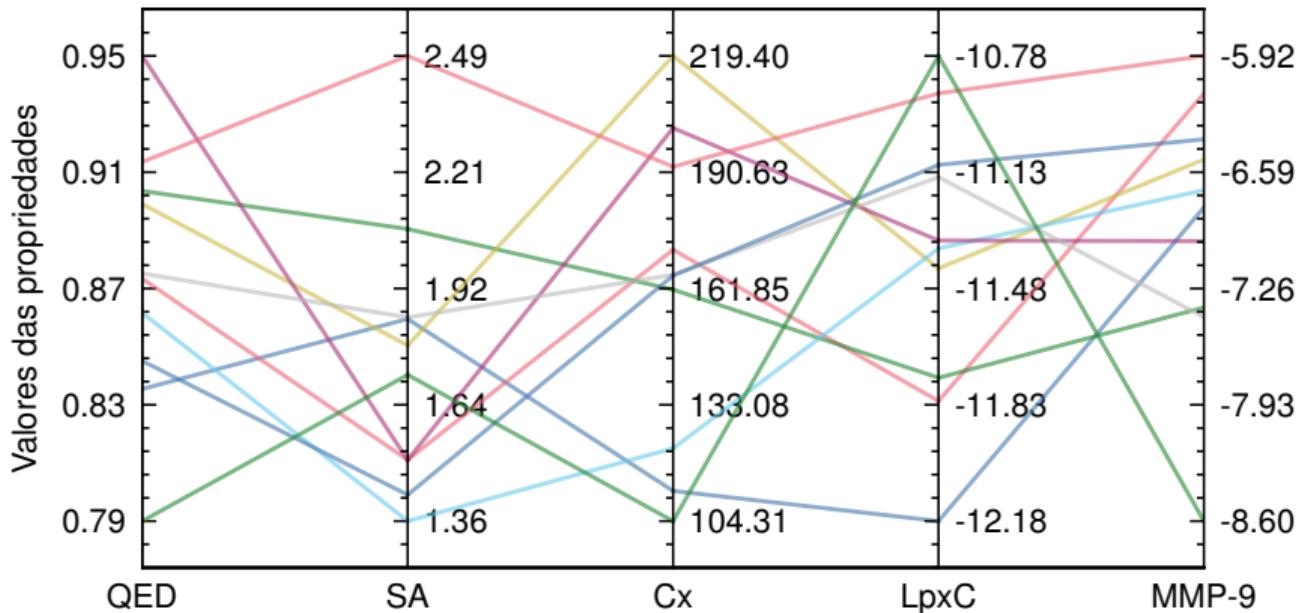
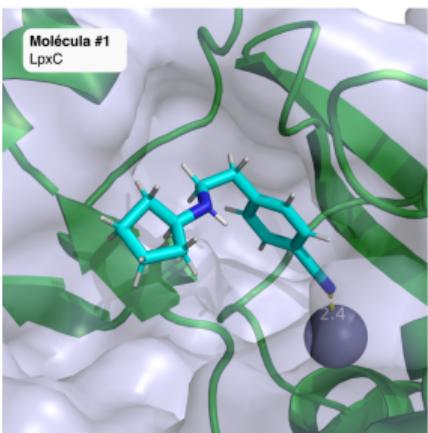


Figure: Parallel coordinates plot for the solutions obtained with protocol I.

# Results: molecular docking (protocol I)

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a)



b)

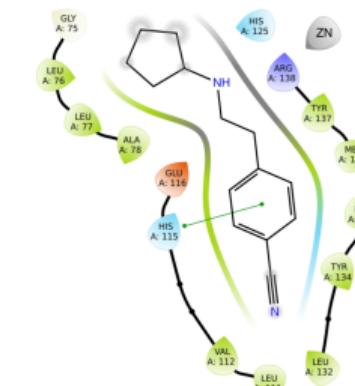
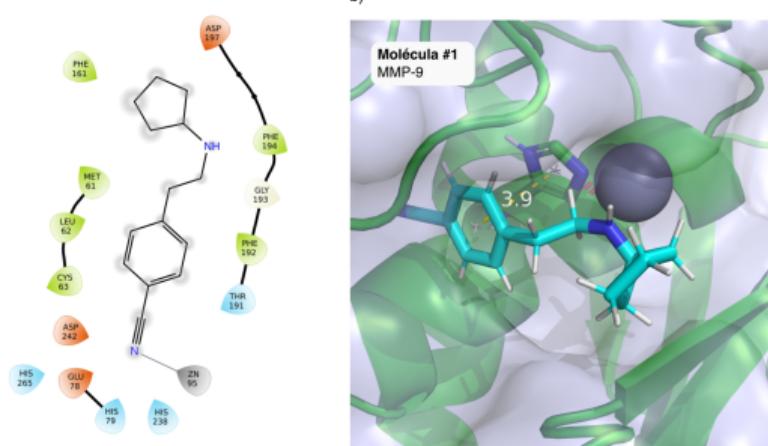


Figure: Compound 1 from protocol I in the active sites of (a) LpxC and (b) MMP-9. LpxC: -12,176 kcal/mol; MMP-9: -6,795 kcal/mol; QED: 0,836; SA: 1,85; Cx: 111,781.

- **DockTDesign**, together with **DockThor** and **DockTDeep**, presents itself as a promising and flexible platform for hit identification, capable of suggesting to the specialist a set of molecules that simultaneously meet multiple objectives.

# Thank you!



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