Dynamic Many-Objective Molecular Optimization: Unfolding Complexity with Objective Decomposition and Progressive Optimization

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Abstract
Molecular discovery has received significant attention across various scientific fields by enabling the creation of novel chemical compounds. In recent years, the majority of studies have approached this process as a multi-objective optimization problem. Despite notable advancements, most methods optimize only up to four molecular objectives and are mainly designed for scenarios with a predetermined number of objectives. However, in real-world applications, the number of molecular objectives can be more than four (many-objective) and additional objectives may be introduced over time (dynamic-objective). To fill this gap, we propose DyMol, the first method designed to tackle the dynamic many-objective molecular optimization problem by utilizing a novel divide-and-conquer approach combined with a decomposition strategy. Additionally, we comprehensively integrate convergence, Pareto diversity, and structural diversity into the optimization process to provide efficient exploration of the search space. We validate the superior performance of our method using the practical molecular optimization (PMO) benchmark. The source code and supplementary material are available online.

1 Introduction
Molecular discovery is foundational to progress in a variety of scientific fields, ranging from the development of new pharmaceuticals to the creation of innovative materials [Bilodeau et al., 2022]. Basically, molecular discovery is a complex process that seeks to identify molecules with desirable properties [Son et al., 2024]. In essence, this process is fundamentally a constrained multi-objective optimization problem, where the objectives are to simultaneously maximize or minimize certain attributes of molecules [Fromer and Coley, 2023].

Unlike single-objective optimization, the multi-objective optimization problem introduces distinct challenges that arise from the necessity to balance multiple and often conflicting objectives [Marler and Arora, 2004]. Therefore, it becomes infeasible to identify a single optimal solution that satisfies all objectives. Instead, the focus shifts to finding Pareto optimal solution sets that represent various trade-offs among these objectives [Gunantara, 2018].

In the context of molecular discovery, the application of multi-objective optimization may exhibit unique characteristics compared to its use in other general domains. First, oracle calls in real-world molecular discovery are expensive, requiring resource-intensive wet-lab experiments or computer simulations to accurately evaluate molecular properties [Huang et al., 2021]. Second, the discrete nature of molecules results in a complex and challenging optimization landscape [Wang et al., 2006]. Lastly, the non-gradual transitions in molecular structures introduce additional complexity by creating an optimization landscape with sharp cliffs [Aldeghi et al., 2022].

To tackle the multi-objective molecular optimization (MOMO) problem, much prior work has employed a range of generative models, including sampling-based methods [Fu et al., 2021; Xie et al., 2021], genetic algorithms [Jensen, 2019; Tripp et al., 2021], probabilistic models [Bengio et al., 2021], and reinforcement learning [Olivercrna et al., 2017; Jin et al., 2020]. However, given the necessity of simultaneously optimizing multiple objectives, they have commonly adopted two multi-objective optimization techniques: scalarization [Eichfelder, 2009] and Bayesian optimization [Laumanns and Ocenasek, 2002]. The scalarization method transforms multiple objectives into a single objective function by aggregating them using weighted sums or other combining strategies [Gunantara, 2018]. On the other hand, the Bayesian optimization method can address multiple objectives concurrently by leveraging acquisition functions to navigate the optimization landscape without needing to quantify the relative weights of each objective [Fromer and Coley, 2023]. While prior frameworks have shown effectiveness in molecular optimization, their applications exhibit distinct constraints. Specifically, they are typically limited to optimizing up to four objectives and they are designed to work with a fixed number of objectives, thereby lacking the capability to adapt to scenarios with varying numbers of objectives.

In real-world applications such as drug discovery, the importance of a dynamic many-objective molecular optimization setting becomes particularly evident [Luukkonen et al., 2023]. From a many-objective perspective, the drug development process is inherently complex and multifaceted, typically requiring optimization of more than four objectives. In
On the other hand, Pareto diversity indicates the spread of solutions across the Pareto front, ensuring a wide range of solutions with varying trade-offs among objectives [Yuan et al., 2015]. Pareto diversity is particularly important in molecular optimization, where the optimal trade-off is often unknown in advance [Fromer and Coley, 2023]. In this paper, we comprehensively address both convergence and Pareto diversity through progressive optimization using the divide-and-conquer approach alongside convergence and Pareto sampling. In addition to Pareto diversity, we also take into account for molecular structural diversity, which refers to the variety in chemical structures within the generated molecules. Promoting structural diversity is vital in molecular discovery fields such as drug design, as it offers multiple candidate molecules that meet desired criteria while exhibiting distinct chemical structures [Mathur and Hoskins, 2017].

The main contributions of our method can be summarized:

• To the best of our knowledge, DyMol, our proposed method, is the first to tackle the dynamic many-objective molecular optimization problem in molecular discovery.
• We propose a novel divide-and-conquer approach to decompose many-objective problems into sub-problems by starting with a single objective, then systematically adding over time to enable progressive optimization.
• Due to the incremental nature of adding objectives, our approach can handle dynamic-objective settings, where new objectives are introduced throughout the optimization process. In addition, we develop an objective adaptation technique that aids our model in adjusting more easily and effectively to newly introduced objectives.
• As far as we are aware, our method is the first to comprehensively integrate convergence, Pareto diversity, and structural diversity into molecular optimization by utilizing both convergence sampling and Pareto sampling.

2 Related Work

2.1 Generative Models for Molecular Discovery

In recent years, there has been a growing interest in the use of various generative models for molecular discovery. Generative models employed in molecular discovery can be broadly classified into four categories: 1) sampling-based methods, 2) genetic algorithms, 3) reinforcement learning (RL), and 4) probabilistic models. The sampling-based methods [Xie et al., 2021; Fu et al., 2021] focus on sampling from a distribution of possible molecules with desirable properties. The genetic algorithms [Jensen, 2019; Tripp et al., 2021] employ a population-based approach that evolves molecules through iterative selection, crossover, and mutation guided by a fitness function. The RL-based methods [Olivecrona et al., 2017; Jin et al., 2020] involve an agent that interacts with an environment to generate molecular structures. In this paradigm, the agent receives rewards for taking actions that lead to desirable outcomes, thereby gradually refining its strategy through trial and error to learn an optimal policy [Shin et al., 2024]. The probabilistic models, GFlowNets [Bengio et al., 2021], generate molecular structures by identifying high-potential regions using probability distributions learned from data.
2.2 Multi-Objective Molecular Optimization

In the context of the MOMO problem, the challenge lies in simultaneously optimizing multiple molecular objectives, which often conflict with each other [Luukkonen et al., 2023]. To address this, two prominent multi-objective optimization techniques have been widely adopted: scalarization and Bayesian optimization (BO). For instance, in the case of scalarization, MIMOSA [Fu et al., 2021] has employed straightforward linear scalarization techniques to handle the MOMO problem. These techniques aim to aggregate multiple objectives into a single objective function by using weighted sums or Tchebycheff methods [Lin et al., 2022]. On the other hand, BO offers a black box optimization approach that has been integrated into various molecular generative models to enhance sample efficiency [Laumanns and Ocenasek, 2002].

In particular, GPBO [Tripp et al., 2021] exemplifies the integration of BO within the framework of GraphGA [Jensen, 2019] as the backbone model. Similarly, LaMBO [Stanton et al., 2022] leverages BO on top of denoising autoencoders to address multi-objective sequence design problems. Recently, HN-GFN [Zhu et al., 2023] proposes a multi-objective BO algorithm that leverages hypernetwork-based GFlowNets.

2.3 Dynamic Many-Objective Optimization

Dynamic many-objective optimization, while yet to be widely explored in molecular optimization, has found application in diverse fields such as manufacturing [Quan et al., 2022], environmental management [Liu et al., 2021], and mineral processing [Ding et al., 2018]. Existing approaches in these domains have predominantly employed decomposition-based MOEA/D [Zhang and Li, 2007] and non-dominated sorting NSGA-III [Deb and Jain, 2013] frameworks due to their effectiveness in navigating high-dimensional search space.

3 Preliminary

3.1 Problem Formulation

In this work, we tackle the dynamic many-objective molecular optimization problem, characterized by the introduction of new objectives during the optimization process. In this context, ‘many-objective’ implies optimizing over four or more objectives, presenting a significant increase in complexity and dimensionality compared to a typical multi-objective problem [Hughes, 2005]. The dynamic many-objective molecular optimization problem can be formally defined as:

\[
\begin{align*}
\text{Maximize} & \quad \mathbf{F}(x, t) = \{f_1(x), f_2(x), \ldots, f_i(x)\}, \\
\text{subject to} & \quad g_j(x, t) \leq 0, \quad j = 1, 2, \ldots, k; \\
& \quad h_j(x, t) = 0, \quad j = 1, 2, \ldots, l;
\end{align*}
\]

where \(x\) denotes the molecule vector, with \(\mathcal{X}\) representing the feasible set in \(n\)-dimensional solution space. The \(\mathbf{F}(x, t)\) represents the set of molecular objective functions at time stage \(t \in T\). The objective function \(f_i : \mathcal{X} \times T \rightarrow \mathbb{R}\) maps the molecular space to the real numbers. Constraints are two-fold: inequality constraints \(g_j(x, t)\) set the boundaries for feasible solutions, while equality constraints \(h_j(x, t)\) specify exact conditions that feasible solutions must satisfy. The goal of this problem is to identify and track the evolving Pareto front.

3.2 Key Pareto Principles in Optimization

As mentioned earlier, the Pareto front is a set of solutions that are each Pareto optimal, which indicates that none of these solutions can be dominated by any other solutions. Therefore, we have the following definitions in our problem formulation:

**Definition 1 (Pareto Dominance).** Let \(x^a, x^b \in \mathcal{X}\), \(x^a\) is said to Pareto dominate \(x^b\) (denoted as \(x^a \succ x^b\)) if and only if:

\[
\forall i \in \{1, \ldots, t\}, f_i(x^a) \geq f_i(x^b)
\]

and

\[
\exists j \in \{1, \ldots, t\}, f_j(x^a) > f_j(x^b).
\]

Here, \(f_i(x^a)\) and \(f_i(x^b)\) represent the values of the \(i^{th}\) objective function for solutions \(x^a\) and \(x^b\), respectively.

**Definition 2 (Pareto Optimality).** A solution \(x^* \in \mathcal{X}\) is defined as Pareto optimal if no other solution in the feasible set dominates it such as follows:

\[
\nexists x \in \mathcal{X} : x \succ x^*.
\]

**Definition 3 (Pareto Front).** The Pareto front, denoted as \(\text{PF}\), indicates the boundary of best possible trade-offs within the objective space. It is formally defined as:

\[
\text{PF} = \{f(x^*) \mid x^* \in \mathcal{X}, \nexists x \in \mathcal{X} : x \succ x^*\},
\]

where \(f(x^*)\) denotes the vector of objective function values corresponding to a Pareto optimal solution.

4 Methods

4.1 Objective Decomposition

As shown in Figure 2, at time stage \(t_0\), our method begins by decomposing complex many-objective sets into more manageable sub-problems. This decomposition process is facilitated by our decomposition module, which analyzes the complexities of each objective and automatically determines the order in which they should be prioritized during optimization. Within this decomposition module, the generative module initially optimizes all objectives jointly for a limited number of iterations. The model uses an initial molecule as a starting point and produces an optimized molecule. Once complete, both the optimized and initial molecules are evaluated by objective functions \(F(x, t_0)\), also referred to as oracle functions.

From this evaluation, we calculate ordering scores by subtracting the objective scores of the initial molecules from the optimized molecules. These ordering scores offer insights into the extent of improvement in objective scores accomplished by the model. A lower ordering score indicates that optimizing a specific objective is more challenging, implying the need for early prioritization. It is worth noting that if a preferred order for the optimization process is available, this can be employed as the decomposition order as well.

4.2 Progressive Optimization

The main idea behind our method is to employ a divide-and-conquer approach to provide adaptability and efficiency when dealing with dynamic many-objective optimization. Consider a scenario where we have a total of five molecular objectives: objectives A through E, as shown in Figure 2. Following the
Decomposition order of A → D → E → B → C, our proposed model begins by solely optimizing objective A as follows:

\[
\text{Maximize} \quad F(x, t_1) = \{f_A(x)\},
\]

subject to

\[
\begin{align*}
g_j(x, t_1) & \leq 0, \quad j = 1, 2, \ldots, k; \\
h_j(x, t_1) & = 0, \quad j = 1, 2, \ldots, l;
\end{align*}
\]

where \(f_A(x)\) denotes the value of objective A for a molecule \(x\) at time stage \(t_1\), and \(X_1\) represents the feasible set in the decision space specific to \(t_1\), potentially different from the general decision space \(X\) due to the dynamic nature of the problem. The \(g_j(x, t_1)\) and \(h_j(x, t_1)\) represent inequality and equality constraints, respectively, derived from the physical, biological, or chemical requirements that a molecule must meet to be viable in a real-world environment.

When the model satisfies a certain score threshold related to objective A or reaches a predetermined number of iterations, it progresses to the next time stage \(t_2\) and incrementally incorporates additional objective D. Consequently, the optimization problem is expanded to maximize:

\[
F(x, t_2) = \{f_A(x), f_D(x)\}.
\]

However, the introduction of a new objective function \(f_D(\cdot)\) necessarily alters the optimization landscape by expanding the dimensions of the objective space. In this context, our objective adaptation technique plays a crucial role by enabling the model to adapt to this evolving optimization landscape. Specifically, it detects changes in the composition of objective scores, which provide learning feedback for model training and updates. For instance, at stage \(t_1\), the objective scores are solely based on the value of objective A. However, at \(t_2\), they evolve to encompass a composite value of both objectives A and D. The major role of the objective adaptation technique is to retrain the model using these updated objective scores, enabling the model to adjust to the evolving Pareto front, which is defined as:

\[
\text{PF}(t) = \{f(x^*) \mid x^* \in X, \exists x \in X : x > x^* \text{ w.r.t. } F(x, t)\}.
\]

As time stages progress, the model systematically incorporates each new subsequent objective in line with the decomposition order and sequentially adjusts to the evolving Pareto front. Eventually, at the end of the time stage, the model can address the complete set of objectives. Thus, our method can be considered as a divide-and-conquer approach, as it strategically divides the complex optimization task into a series of simpler sub-problems, each focusing on a specific subset of the objectives. However, distinct from conventional divide-and-conquer methods that solve sub-problems independently and then combine their solutions, our approach is characterized by its sequential adaptation and refinement of solutions. As new objectives are introduced, the model dynamically adjusts its search process and integrates the incremental sub-problem solutions into a comprehensive solution that addresses all objectives. This adaptive nature of our method can make it effective in the dynamic-objective settings, where the optimization landscape progressively evolves over time.

**Theoretical Analysis on Divide-and-Conquer**

Here, we present a theoretical analysis demonstrating that our divide-and-conquer method, despite being incremental in nature, progressively converges toward solutions to those of the original complex problem that addresses all objectives jointly.

**Theorem 1** (Convergence of the Divide-and-Conquer Approach to Global Near-Optimal Solutions). Let \(P\) be an original problem with objectives \(\{f_1, \ldots, f_i, \ldots, f_n\}\), and \(P_i\) be a sub-problem of \(P\) focusing on \(\{f_1, \ldots, f_i\}\). The solution \(\{x_1^*, x_2^*, \ldots, x_i^*\}\) obtained at each stage \(i\) can be served as effective initial points for the next stage \(i + 1\) to progressively converge towards a globally near-optimal solution for \(P\).

**Lemma 1** (Initial Convergence). For the initial base case of the divide-and-conquer approach where \(i = 1\), the solution \(x_1^*\) for the sub-problem \(P_1\) can converge to a near-optimal solution for the objective \(f_1\) even in cases of non-convexity. Let \(x_1^* = \arg\max_{x \in X_1} f_1(x)\). Then, by the Bolzano-Weierstrass theorem [Brattka et al., 2012], there exists a sequence \(\{x_k\} \subset X_1\) such that \(x_k \rightarrow x_1^*\), and \(\lim_{k \rightarrow \infty} \frac{f_1(x_k) - f_1(x_1^*)}{\|x_k - x_1^*\|} \geq 0\).
These generated molecules are evaluated by $F(x, t)$ to obtain objective scores. To provide learning feedback, we define the reward scores $R(x, t)$ at each time stage $t$ by computing the weighted sum of objective scores from $F(x, t)$ such as:

$$R(x, t) = \sum_{i=1}^{n} w_i(t) f_i(x),$$

where $n$ is the total number of objective functions and $w_i(t)$ denotes the relative weight for $f_i(x)$ at time stage $t$.

To further enhance the training efficiency, we utilize experience replay $B$ that stores previously optimized molecules with high reward scores. In contrast to traditional approaches that primarily emphasize score-convergence, we develop the Pareto sampling technique to also consider Pareto diversity.

Specifically, we perform two types of sampling: convergence sampling, where we sample molecules $x_c$ with high reward scores from $B$ to promote score-convergence, and Pareto sampling, where we sample molecules $x_p$ from the Pareto front to encourage Pareto diversity. Finally, the generative model parameters $\theta$ are optimized by the following loss function:

$$L(\theta, t) = [-\log P_\theta(x) + \log P_{prior}(x) + R(x, t)]^2,$$

where $P_{prior}$ is the likelihood of a pre-trained model that imposes additional constraints based on the chemical grammar. It should be noted that $x$ encompasses a set of molecules $x_g, x_r, x_p$, represented as $x = \{x_g, x_r, x_p\}$.

As time stages advance $t \rightarrow t + 1$, the introduction of new objective changes the composition of objective scores and the reward scores. Although the generative model is initially unaware of these changes, we introduce the objective adaptation technique to update $\theta$. This involves retraining the model using updated reward scores to account for the impact of new objectives. The objective adaptation loss can be expressed as:

$$L_{OA}(\theta, t) = [-\log P_\theta(x_b) + \log P_{prior}(x_b) + R(x_b, t + 1)]^2,$$

where $x_b$ denotes all molecules from $B$. Note that we employ REINVENT [Olivecrona et al., 2017] as our backbone generative model due to its superior performance. The pseudo-code for the entire process is in the supplementary material 7.2.

### 5 Experiments

#### 5.1 Experimental Setup

We evaluated the performance of our proposed method using the practical molecular optimization (PMO) benchmark [Gao et al., 2022]. In this setup, oracle call budgets are strictly limited to 10,000 evaluations to reflect the real-world constraints of molecular discovery. For the oracle functions in our experiments, we adopted the most commonly used molecular objective functions in previous MOMO studies [Jin et al., 2020; Xie et al., 2021]. These include biological objectives such as DRD2, JNK3, and GSK3β, which represent inhibition scores against two target proteins related to Alzheimer’s disease, as well as non-biological objectives like QED and SA that quantify drug-likeness and synthesizability, respectively. To extend our approach to many-objective settings, we included further objectives such as Osimertinib MPO and Fexofenadine MPO objectives for discovering new therapeutics that optimize existing drugs with multiple desirable attributes.
Table 1: Performance comparison in many-objective optimization scenarios with Four objectives (GSK3β+JNK3+QED+SA), Five objectives (GSK3β+JNK3+Osimertinib MPO), and Six objectives (GSK3β+JNK3+QED+SA+DRD2+Osimertinib MPO) using 10 different seeds.

Figure 4: Average HV improvement curves for the top 8 methods.

5.3 Experimental Results

The performances of our proposed method and the competing methods were assessed by two evaluation metrics: the hypervolume indicator (HV) [Zitzler et al., 2003] and the R2 indicator [Brockhoff et al., 2012]. The HV measures the volume of the objective space dominated by the Pareto front, while the R2 evaluates the quality of a solution set based on user-defined reference points. A higher HV value indicates a better solution set, while a lower R2 value is more desirable. Refer to the supplementary material 7.4 for detailed explanations of evaluation metrics. Note that each experiment was conducted with 10 different seeds to ensure result reliability.

Table 1 presents the HV and R2 performance with standard deviations for each method across many-objective optimization scenarios with different numbers of objectives as follows:

- **Four objectives**: GSK3β+JNK3+QED+SA;
- **Five objectives**: GSK3β+JNK3+Osimertinib MPO;
- **Six objectives**: GSK3β+JNK3+QED+SA+DRD2+Osimertinib MPO.

As shown in Table 1, our method outperforms all competing methods across all scenarios. Notably, in scenarios with Five and Six objectives, our method demonstrates a substantial performance improvement. This highlights the effectiveness of our divide-and-conquer approach, which successfully handles the inherent complexity of many-objective problems by decomposing them into manageable sub-problems. However, other competing methods struggle with exponential increases in complexity. Additional experiments for many-objective scenarios are provided in the supplementary material 7.5.

Figure 4 displays the average HV improvement curves for the top 8 methods in Four objective scenarios. As depicted, our method consistently outperforms others after reaching 2500 oracle calls. Genetic-based algorithms like MOEA/D, NSGA-III, and GPBO demonstrate rapid initial performance improvements but typically reach a plateau beyond 3000 oracle calls. In contrast, RL-based algorithms such as REINVENT and AugMem exhibit more consistent and continual improvement over time. Additional HV improvement curves and analyses can be found in supplementary material 7.6.

5.2 Competing Methods

We compared the performance of our method against a range of competing methods, including Random ZINC [Sterling and Irwin, 2015], SMILES-VAE [Gómez-Bombarelli et al., 2018], MIMOSA [Fu et al., 2021], GFLOWNet [Bengio et al., 2021], and GraphGA [Jensen, 2019]. Additionally, we evaluated against BO methods such as GPBO [Tripp et al., 2021], LaMBO [Stanton et al., 2022], and HN-GFN [Zhu et al., 2022]; well-known many-objective optimization algorithms like MOEA/D [Zhang and Li, 2007] and NSGA-III [Verhellen, 2022]; and RL-based methods, including REINVENT [Olivecrona et al., 2017], REINVENT BO [Tripp et al., 2021], and AugMem [Guo and Schwaller, 2024]. Note that REINVENT was acknowledged as the best-performing algorithm for molecular optimization, as evidenced by the PMO benchmark results [Gao et al., 2022]. Hence, as mentioned earlier, we employed REINVENT as our backbone generative model. However, we distinctively developed it for a dynamic many-objective setting. More information on competing methods, experimental settings, and hyperparameter configurations is available in the supplementary material 7.3.
Four objectives

Six objectives

HV

BM

PS

DC

OA

Table 2: Ablation study for each technique: Pareto Sampling (PS), Divide-and-Conquer (DC), and Objective Adaptation (OA).

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<th>Ablation</th>
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Figure 5: Finetuning performance of the top 4 methods in dynamic-objective scenarios, which introduce a new molecular objective.

5.4 Ablation Study

As shown in Table 2, we have conducted an ablation study to investigate the impact of key techniques on the performance of our method: Pareto Sampling (PS), Divide-and-Conquer (DC), and Objective Adaptation (OA). We observed that each of these techniques significantly contributes to improved performance. DC primarily focuses on improving convergence, bringing solutions closer to the optimal Pareto front values. PS enhances performance through emphasis on Pareto diversity. Remarkably, OA leads to substantial performance gains, especially in Five-objective scenarios, highlighting its capability to adapt effectively to newly introduced objectives.

5.5 Dynamic-Objective Scenarios

To assess our method’s adaptability in dynamic-objective scenarios, we propose a novel experimental setup where a model has initially been fully optimized for a set of Five objectives. Subsequently, a new, sixth objective (Osimertinib MPO) is introduced, requiring additional optimization. Instead of re-optimizing all objectives from scratch, we implement a finetuning approach that leverages the model already optimized for the initial Five objectives, and further optimizing the new objective. As depicted in Figure 5, our method effectively reaches the baseline performance of the Six objectives within fine-tuning 2000 oracle calls and continues to improve beyond that. This achievement can be attributed to our OA technique and the incremental nature of adding objectives within our method. Details on dynamic-objective scenarios and additional experiments are in the supplementary material 7.7.

5.6 Visualization of the Pareto Front

To evaluate solution quality in our method, we have attempted to visualize the Pareto front. However, visualizing the Pareto front in settings with more than three objectives is challenging due to the human limitations in interpreting high-dimensional data [Tušar and Filipič, 2014]. Thus, we only focus on visualizing biological objectives in Five objective scenarios, as they are considered to be more important in drug discovery [Sun et al., 2022]. Figure 6 illustrates the 2D and 3D Pareto fronts, comparing our method with baseline REINVENT method. In both cases, the solutions of our method dominate the baseline method by approaching the optimal Pareto front more closely. Moreover, our method exhibits a broader distribution of solutions along the Pareto front, suggesting a better exploration.

5.7 Structural Diversity Analysis

In the realm of drug discovery, structural diversity plays a pivotal role as it substantially enhances the chances of discovering compounds with distinctive and potent biological activities [Walters and Namchuk, 2003]. To quantitatively assess the structural diversity among the molecules generated by our method, we adopted a diversity metric based on the number of unique Bemis-Murcko scaffolds (BM) and carbon skeletons (CS). As shown in Table 3, our method outperforms other methods in terms of BM and CS, indicating a higher average structural diversity.

6 Conclusion

In this work, we propose DyMol as a novel and first method to address the dynamic many-objective molecular optimization problem by leveraging the divide-and-conquer approach. DyMol decomposes complex many-objective sets into manageable sub-problems for progressive optimization. Our results demonstrate that DyMol outperforms competing methods in both many-objective and dynamic-objective scenarios. Future work can include extending research to material science.
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Contribution Statement
Tae-Eui Kam is the corresponding author. Dong-Hee Shin and Young-Han Son contributed equally to this work as co-first authors. Deok-Joong Lee assisted with figure preparation and data analysis. Ji-Wung Han proofread the manuscript. All authors have read and approved the final manuscript.

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