Bayesian optimisation for additive screening and yield improvements in chemical reactions – beyond one-hot encodings

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Abstract

Reaction additives play a significant role in controlling the reactivity and outcome of chemical reactions. For example, a recent high-throughput additive screening identified a phthalimide ligand additive Ni-catalysed photoredox decarboxylative arylations. This discovery enabled a 4-fold yield improvement by stabilising oxidative addition complexes and breaking up deactivated catalyst aggregates. However, such large-scale screenings are currently inaccessible to most research groups. This work demonstrates how these discoveries can be made under much lower experimental budgets using Bayesian optimisation. We consider a unique reaction screening setting with 720 additives which forces us to go beyond simple one-hot encoding of the reaction components. We investigate a range of molecular representations and demonstrate convincing improvements over baselines. Our approach is not limited to Ni-catalysed reactions but can be generally applied to, for example, achieving yield improvements in diverse cross-coupling reactions or unlocking access to new chemical spaces of interest to the chemical and pharmaceutical industries.

1 Introduction

Artificial intelligence holds the promise to accelerate chemical sciences^{1–3}. In the last decade, we witnessed ground-breaking advances in machine learning for de novo molecular design^{4–8}, synthesis planning^{9–15}, and reaction outcome prediction^{16–23}. More recently, sequential model-based optimisation algorithms have been investigated to efficiently find optimal conditions for chemical reactions^{24–32}. As demonstrated in the space of chemical reactions by Shields et al. ²⁹, Bayesian optimisation (BO) is particularly well suited for trading exploration and exploitation in the low data

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Figure 1: A visualisation of Bayesian optimisation for additive screening. Starting from the HTE dataset³³, we propagate the data through the reaction encoder to obtain suitable reaction representations. Using these representations, we organise the latent space and select the initial data points to set up the Gaussian process surrogate model. The BO loop then runs for a selected number of iterations during which we reach the global optimum in terms of the highest yield.

regime. Most BO studies report one-hot encodings (OHE) of the reaction components, where no chemical information is used, to perform remarkably well^{28,32} even compared to more elaborate quantum mechanical (QM) descriptors²⁹. While small, OHE still incorporate enough information for BO to read and exploit, whereas more complex representations bring additional noise.

In this work, we apply BO to explore an additive screening dataset containing 720 additives³³. The dataset consists of four plates with different Ni-catalised photoredox decarboxylative arylations reactions. Additives are key for altering the reactivity and outcome of chemical reactions^{34,35}. While Prieto Kullmer et al.³³ used those additives through high-throughput experimentation, not all laboratories have access to robotic platforms. Still, synthetic chemists could benefit from efficiently finding the best additives through BO, i.e. improving a reaction without having to run all possible reactions (Figure 1). Compared to existing applications of BO to chemical reactions (e.g., Buchwald-Hartwig reactions with 44 OHE dimensions³⁶), the additive dataset is substantially more challenging. Firstly, using OHE is not suitable as it has a dimensionality of 720, with only one datapoint corresponding to each additive. Indeed, applying BO to this representation fails to improve over random search. Secondly, the additives are structurally more diverse than the components screened in other HTE studies, which makes the computation of human-labelled local QM descriptors more laborious. We overcome those limitations by using reaction fingerprints as a representation and a maximal diversity initialisation scheme. Using as little as 5/10/20 initialisation reactions, we demonstrate that BO efficiently finds high-yielding reactions in less than 100 single-point optimisation iterations.

2 Methods

2.1 Reaction representations

The most straightforward reaction representation is the OHE encoding of the individual reaction components. For instance, if the design space contains 15 aryl halides, 23 additives, 4 catalysts, and 3 bases ³⁶, the components present in a reaction would be represented by a 1 in a binary reaction vector, and as a 0 otherwise. More chemically meaningful representations are mixtures of molecular and atomic QM descriptors as used by Ahneman et al. ³⁶ and Shields et al. ²⁹. However, the local atomic QM descriptors are limited to molecules with similar functional groups. Hence, those representations are not well suited for the additive screening dataset ³³. Instead, we could represent reactions by isolating the additives and encoding them using molecular fingerprints ^{37–39}. Because the additives are the only varying part of the chemical reaction in our dataset, they uniquely represent each data point. The optimisation process remains the same, but by separating them from the rest of the reaction, we lose information intertwined in the reaction components.

Simplified molecular-input line-entry system (SMILES)⁴⁰ have emerged as one of the leading methods of representing the chemical space of diverse molecules and reactions. Using a molecular graph representation of the different components in a reaction, they impose a highly informative reaction depiction suitable for advanced machine-learning models based on textual representation⁴¹. Additionally, their easy conversion to a vectorised form makes them appealing to various computational models^{42–44}. For instance, the reaction fingerprint by Schneider et al.⁴² is computed by subtracting the molecular fingerprints^{37,38} of the reactants from the ones of the products. More recently, Schwaller et al.⁴³ derived data-driven reaction fingerprints directly from the reaction SMILES (RXNFP) and Probst et al.⁴⁴ introduced the differential reaction fingerprint (DRFP), which is based on the symmetric difference of two sets containing the circular molecular *n*-grams generated from the molecules listed left (reactants and reagents) and right (products) from the reaction arrow. We use the RXNFP and DRFP in our experiments.

2.2 Bayesian optimisation

Many problems in scientific discovery may be framed as global optimisation problems of the form

$$\mathbf{x}^{\star} = \arg \max_{\mathbf{x} \in \mathcal{X}} f(\mathbf{x}),\tag{1}$$

where $f : \mathcal{X} \to \mathbb{R}$ is a function over a design space \mathcal{X} . In the case of molecular representations, the design space is discrete and structured, containing graphs, fingerprint vectors and strings. Equation 1 is a black-box optimisation problem as we do not know the analytic form of f or its gradients and may only query f pointwise. Furthermore, evaluations of f require laboratory experiments and so are high-cost and time-consuming. Lastly, our observations of f are subject to a (potentially heteroscedastic⁴⁵) noise process. BO is an adaptive strategy that has recently emerged as a powerful solution method for black-box optimisation problems with proven success in applications including machine learning hyperparameter optimisation⁴⁶, chemical reaction optimisation²⁹, protein design⁴⁷, and as a subcomponent in AlphaGo⁴⁸. The Appendix A.4 provides pseudocode for BO and more details on the algorithm.

2.3 Data initialisation

The BO algorithm relies on sample data to initialise its surrogate model and accelerate the discovery of the needed outcome. Using Gaussian processes as the surrogate models allows us to work in the low data regime due to the well-calibrated uncertainty estimates they provide. See⁴⁹ or⁵⁰ for a description of Gaussian process in the context of structural inputs. However, the common machine learning doctrine where more data brings more clarity still stands. When initiated with more data points, the surrogate model has a better overview of the underlying function of the data, so the uncertainty measures are more precise. On the other hand, the chemist's incentive is to start the optimisation process early and preserve the time needed for running reactions in the laboratory. These two viewpoints collide, and there is a need for a balancing solution. Instead of randomly choosing experiments for initializing the surrogate model, we explore our search space of reactions and select a diverse sample of points achieving good coverage of the space. In particular, we select a random initial point in the latent space and look for its matching pair in terms of the maximal distance (i.e., Jaccard⁵¹). We repeat the process for the identified least similar pair, ensuring we removed its previous match from the distance matrix. This policy allows us to diversify the initial sample of data points and expand the set coverage.

3 Results & Discussion

Our results show that utilizing BO substantially accelerates the discovery of the optimal additives for the highest yield improvement. Most importantly, we can achieve these results with novel priors like the DRFP, an NLP-inspired reaction fingerprint⁴⁴.

Figure 2 provides an overview of BO performance compared to the random search on different reaction plates. We used the first reaction plate as a testing ground for model configurations and their influence on the yield. We ran the experiments on the remaining plates and demonstrated the compelling influence of BO for finding the best reaction conditions. While both DRFP and RXNFP



Figure 2: An overview of the results with different reaction representations. Figures a, d, e, f show the optimisation path towards the optimal parameters with mean observed value at each iteration over twenty different-seed trials (Gaussian Process surrogate model, 10 initialisation points). The shaded regions represent the 95% confidence interval. Figure b shows the distribution of the selected yield between random and BO search. Figure c depicts the latent space of DRFP reaction representations using principal component analysis and emphasises the selected initial data points together with the global optimum.

representations perform well on the first reaction plate, there is an evident divergence in their success when employed on the remaining reactions. Note that DRFP achieves the best results over all reaction plates. More importantly, we clearly differentiate the path that the BO with DRFP takes to reach the optimum, in contrast to the random search. While we cannot equate a chemist's intuition with random exploration, relevant research²⁹ acknowledges that scientists show bias due to their expert knowledge. BO algorithms do not suffer from this favouritism and analyse the search space efficiently, offering practical suggestions to chemists. Figure 2b shows us that, on average, BO models choose parameters with higher output over all iterations compared to the random search. The distribution of BO-selected values is centred around the larger yield increase.

We define a top-n neighbourhood as a set of n reactions with the highest yield for each reaction plate. Searching for the best reaction inside this set is the main goal of the optimisation process. However, it is equally important to uncover a variety of reactions that bring a comparable yield improvement. Table 1 displays the percentage of the top-n yield reactions discovered over all twenty trials for different reaction plates (10 initialisation reactions). A more comprehensive table with additional parameters is presented in the A.4. The table shows that BO performs much better than the random search. The results suggest that BO can help chemists discover relevant conditions for reaction optimisation even in challenging settings such as this additive design space.

Reaction plate	Optimisation	top 1 [%]	top 3 [%]	top 5 [%]	top 10 [%]
Plate 1	BO	55	61.67	50	38
	Random	25	18.33	15	16.5
Plate 2	BO	65	61.67	58	39
	Random	5	10	15	14.5
Plate 3	BO	95	95	76	67
	Random	10	10	10	18
Plate 4	BO	80	76.67	76	54
	Random	10	20	19	19.5

Table 1: [%] of the top *n*-highest yields discovered during the 100 iterations of optimisation, starting from the 10 initial data points.

4 Conclusion

Bayesian optimisation is a powerful optimisation method that steers the exploration of the search space towards promising regions. It is especially valuable in the domain of chemistry as it saves time and resources and allows uncovering of unexplored but high-yielding chemical reactions²⁹. The main goal of this paper was to determine whether BO provides insights into a challenging additive screening HTE dataset³³, where OHE and QM descriptors are not well suited. We demonstrated that exploiting BO using an elaborate initialisation scheme and reaction fingerprints efficiently reveals key additives that lead to yield improvement in chemical reactions.

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A Appendix

A.1 Bayesian optimisation algorithm

The BO algorithm consists of two core components, a surrogate model and an acquisition function. The surrogate is typically a probabilistic model such as a Gaussian process⁵² that captures the prior belief about the nature of $f(\mathbf{x})$. The uncertainty estimates afforded by the surrogate are crucial in representing knowledge about the unobserved values of the black-box function $f\mathbf{x}$ and act to inform further data collection via a policy known as an acquisition function. The acquisition function, $\alpha(f(\mathbf{x}), \mathcal{D})$, is responsible for selecting the next data point on a given iteration of the BO algorithm. The acquisition function achieves this by leveraging the uncertainty estimates of the surrogate to trade off between exploration and exploitation in the black-box objective $f(\mathbf{x})$. The acquisition function should be cheaper to evaluate relative to the black-box and easy to optimise^{53–55}. Modifications to classical BO surrogates, which typically assume design spaces, \mathcal{X} that are compact subsets of \mathbb{R}^d , are necessary to operate on molecular spaces. We utilise such models in this work^{49,50,56}. The pseudocode for BO is given in Algorithm 1.

Algorithm 1 Bayesian optimisation (BO)				
input : initial dataset \mathcal{D} repeat select x by optimizing the acquisition function of	⊳ possibly empty			
$\mathbf{x} \leftarrow \underset{\mathbf{x} \in \mathcal{X}}{\operatorname{argm}}$	$\max_{\mathbf{x}} \alpha(\mathbf{x}; \mathcal{D})$			
$y \leftarrow \text{Evaluate}(\mathbf{x}) \\ \mathcal{D} \leftarrow \mathcal{D} \cup \{(\mathbf{x}, y)\} \\ \textbf{until termination condition} \\ \textbf{return } \mathcal{D}$	 evaluate the black-box at the selected input update dataset and surrogate e.g. evaluation budget exhausted 			

A.2 Data preprocessing

We extracted the reactions on the four Ni-catalysed photoredox decarboxylative arylations reaction plates from the supplementary information of the study by³³. We combined all columns containing molecular SMILES to form a reaction SMILES. The reactants and reagents were added on the left side of the "»" and the products on the right side. We canonicalised the reactions with RDKit⁵⁷. When a reaction with the same additive was run multiple times within a plate we averaged the values. Prieto Kullmer et al. ³³ approximated the yields using "UV210_Prod AreaAbs" and estimated the yield improvements by dividing through a baseline reaction without additive.

A.3 Reproducibility

We implemented the code in Python. We used PyTorch⁵⁸, PyTorch Lightning⁵⁹, Gauche⁵⁰ and BoTorch⁶⁰. Different trials were set using a set of seeds ranging from 1 to 20 with PyTorch Lightning's seed_everything function. The surrogate model used is a Gaussian process implemented with SingleTaskGP from Botorch. We used the Tanimoto kernel^{49,61} from Gauche. Reaction representations were defined with DRFP⁴⁴, RXNFP⁴³ and CDDD³⁹ libraries. The acquisition function is UpperConfidenceBound from BoTorch. We tested beta values [0.1, 0.5, 0.9]. The results presented in the main paper use UpperConfidenceBound with beta equaling to 0.1. We will release the code in open source.

A.4 Additional results for initialisation sample sizes

The Table A.4 shows additional results for different initialisation sample sizes.

Reactions	Init size	Optimisation	Beta	top-1 [%]	top-3 [%]	top-5 [%]	top-10 [%]
	5	ВО	0.1	35	40	35	33
			0.9	45	51.67	44	36.5
		Random		5	13.33	14	15.5
Plate 1	10	ВО	0.1	55	61.67	50	38
			0.9	55	61.67	50	37.5
		Random		20	20	20	18
	20	BO	0.1	10	10	9	15
			0.9	15	15	14	16.5
		Random		10	20	18	16.5
Plate 2	5	BO	0.1	33.33	40.73	47.78	36.11
			0.9	25	33.33	43	34
		Random		10.53	10.53	20	18.95
		RO	0.1	65	61.67	58	39
	10	DO	0.9	55	50	48	33
		Random		5	10	15	14.5
	20	BO	0.1	55	43.33	45	32
		DO	0.9	55	46.67	47	33.5
		Random		10.53	10.53	20	18.95
	5	BO	0.1	60	58.33	51	47
			0.9	60	61.67	53	48
		Random		15	10	15	17.5
Plate 3	10	BO	0.1	95	95	76	67
			0.9	35	26.67	25	28
		Random		10	10	10	18
	20	BO	0.1	75	75	60	53.5
			0.9	75	75	61	54
		Random		25	18.33	13	20
Plate 4	5	BO	0.1	80	46.67	40	28
			0.9	80	46.67	40	28.5
		Random		10	21.67	16	13.5
	10	BO	0.1	80	76.67	76	54
			0.9	50	50	49	40
		Random		10	20	19	19.5
	20	BO	0.1	65	28.33	21	24.5
			0.9	60	26.67	20	24.5
		Random		20	26.67	22	18.5

Table 2: [%] of the top n-highest yields discovered during the 100 iterations of BO with different initial sample size and beta values using DRFP fingerprints. Comparison with the random search. Lower beta values correspond to data exploitation while higher values define an exploration strategy.