Transforming data into knowledge for intelligent decision-making in early drug discovery

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Chapter four

Analysis of Iterative Screening with Stepwise Compound Selection Based on Novartis In-house HTS Data

Abstract

With increased automation and larger compound collections, the development of high-throughput screening (HTS) started replacing previous approaches in drug discovery from around the 1980s onward. However, even today it is not always appropriate, or even feasible, to screen large collections of compounds in a particular assay. Here, we present an efficient method for iterative screening of small subsets of compound libraries. With this method, the retrieval of active compounds is optimized using their structural information and biological activity fingerprints. We validated this approach retrospectively on 34 Novartis in-house HTS assays covering a wide range of assay biology, including cell proliferation, antibacterial activity, gene expression, and phosphorylation. This method was employed to retrieve subsets of compounds for screening, where selected hits from any given round of screening were used as starting points to select chemically and biologically similar compounds for the next iteration. By only screening ~1% of the full screening collection (~15000 compounds), the method consistently retrieves diverse compounds belonging to the top 0.5% of the most active compounds for the HTS campaign. For most of the assays, over half of the compounds selected by the method were found to be among the 5% most active compounds of the corresponding full-deck HTS. In addition, the stringency of the iterative method can be modified depending on the number of compounds one can afford to screen, making it a flexible tool to discover active compounds efficiently.

Introduction

Early drug discovery traditionally has been the result of a close collaboration between chemists, pharmacologists, and clinical scientists, where knowledge from pharmacology and (medicinal) chemistry was combined to design potentially active molecules for testing.[1,2] From around the 1980s onward, rapid improvements in automation and combinatorial chemistry led to the development and increasing acceptance of high-throughput screening (HTS), which allows rapid screening of large collections of compounds using robotics and automated data processing. This enabled HTS to be used to study relationships between compounds and putative biological targets on a very large scale, so that libraries of 1−2 million compounds are routinely screened in big pharmaceutical companies, several times per year.[2,3] Conceptually, HTS aims to screen large numbers of molecules in a brute-force

approach to identify hits, and the most promising chemical entities are then selected as starting points for further investigation. It is hoped that screening large numbers of molecules increases the chance of finding promising chemical entities. However, the previous often iterative cycles of design–screen–refine in small interdisciplinary project teams were somewhat lost.

Over the past few decades, HTS has hence become increasingly popular and has been augmented in capacity from being able to screen tens of thousands of compounds a day to over 100000 compounds a day and has become – in addition to many other techniques – of crucial importance for early drug discovery.[4–6] However, HTS also has some significant drawbacks. Cell-free HTS campaigns, such as biochemical target-based assays, are not adequately predictive of compounds' ADMET (absorption, distribution, metabolism, excretion, and toxicity) properties, which are important pharmacokinetic parameters for drug development.[7] For cell-based phenotypic HTS assays, which can be more predictive of certain ADMET properties such as bioavailability and cytotoxicity, target deconvolution is an important challenge.[8] Additionally, HTS campaigns sometimes cannot be performed at scale for complex biological systems that cannot be mass-produced (e.g., organoids).[9] Finally, and of most relevance for the current study, HTS remains a resource-intensive endeavor with a large fraction of the compounds screened being inactive or uninteresting. The latter renders the identification of smaller screening sets which lead to a significant fraction of active chemical matter detected very relevant.[4]

The mentioned drawbacks prompted efforts to optimize various aspects of HTS campaigns, such as compound library design (for example, based on chemical diversity, where libraries are chosen on the basis of chemical knowledge),[10–14] post-HTS data analysis for triaging active compounds (in order to select subsets for further validation),[15,16] and selecting novel compounds similar to active compounds detected in the assay for further investigation.[17–21] Given the recent perceived ineffectiveness of target-based HTS,[22] a shift to phenotypic HTS has occurred,[8] hence increasing the need for target identification methods. In this regard, a high-throughput screening fingerprint (HTS-FP) capturing past performance of compounds across a number of screens was developed by Petrone *et al.* at Novartis,[23] which allows the comparison of compounds according to their bioactivity across a range of HTS assays. This approach was used for both similarity searching and various

machine learning methods for target identification of hits from phenotypic screens. Later, a public version of the same fingerprint was developed and analyzed by Dančík *et al.*,[24] who also reported its usefulness in the elucidation of the compound mode of action. However, despite these computational advances in postscreen analysis, HTS campaigns remain an expensive endeavor.

In this study, we aim to address efficient ways of screening subsets of compound libraries, instead of screening entire compound libraries, while at the same time optimizing the retrieval of active compounds. We developed and retrospectively validated an iterative screening method on Novartis in-house HTS data, in which selected hits from any given round of screening were used as starting points to select chemically and biologically similar compounds for the next iteration. This approach was developed with the explicit aim to select much smaller subsets of compounds with enriched activity, by harnessing the bioactivity information on compounds in the previous iteration. While briefly mentioned by Mayr and Bojanic as an idea,[5] and used on a small scale by Keenan *et al.* for the design of plasmodial kinase inhibitors,[25] the concept of iterative screening has not been explored systematically in the published literature. A related concept has been previously described by Schneider *et al.* in the context of iterative virtual synthesis and testing of individual molecules, where molecules are designed automatically using evolutionary algorithms and particle swarm optimization.[26] However, our approach differs considerably, because we iteratively generate sets of molecules instead of individual molecules, hence investigating the concept on a much larger scale.

Methods

HTS Data. Novartis proprietary HTS assays comprising at least 1300000 compounds with an inhibitory assay readout were used, resulting in a total of 34 assays, of which 11 were cell-based assays and 23 were cell-free (biochemical) assays. These assays covered a wide number of biological events, including cell proliferation, antibacterial activity, gene expression, and phosphorylation.

Starting Set for Initial Screening Round. We used a starting set of well-studied and manually curated compounds, many with tested clinical relevance, known to cover a large amount of druggable bioactivity space and of which the mechanism of action (MoA) is known. This set (the MoABox)

comprised 2757 compounds and is used as a starting point for many phenotypic screening projects at Novartis due to the high-quality annotations of each compound. The physicochemical properties and the chemical and biological diversity of the MoABox were calculated using RDKit[27]. The design of the MoABox inherently entails that most compounds have properties favorable for cell-based screening. Owing to operational turnover of the compound archive, not every full-deck HTS contains every compound of the MoABox. Therefore, the starting set for each specific assay was the MoABox compounds present in it at the time it was performed. The smallest starting set comprised 2050 compounds, whereas the largest comprised 2692 compounds.

In order to determine the importance of the starting set for good performance, we repeated our analysis with 10 randomly chosen starting sets and the results were compared to those obtained with the MoABox as a starting set. These sets were obtained by repeatedly selecting a random subset from the entire screening deck of equal size to that of the MoABox present in the corresponding assay, minus any MoABox compounds that might have been coincidentally selected.

Iterative Screening Algorithm (ISA). For any given set of compounds, we are able to look up its activities in a past assay with ~1.3 M compounds. This *in silico* screening allows not only a relative ranking (according to activities within the subset) but also an absolute ranking (according to the 1.3 M compounds). Our aim was to iteratively optimize the absolute ranking of subsets of compounds, thereby efficiently selecting highly active compounds and steering the screening process toward success with much smaller compound sets. Therefore, the method developed in this study consists of three iterative procedures (see **Figure 14**): (1) ranking of compounds based on retrospective activity data, (2) selection/triaging of hits, and (3) expanding from hits to close analogs based on chemical and biological similarity metrics.

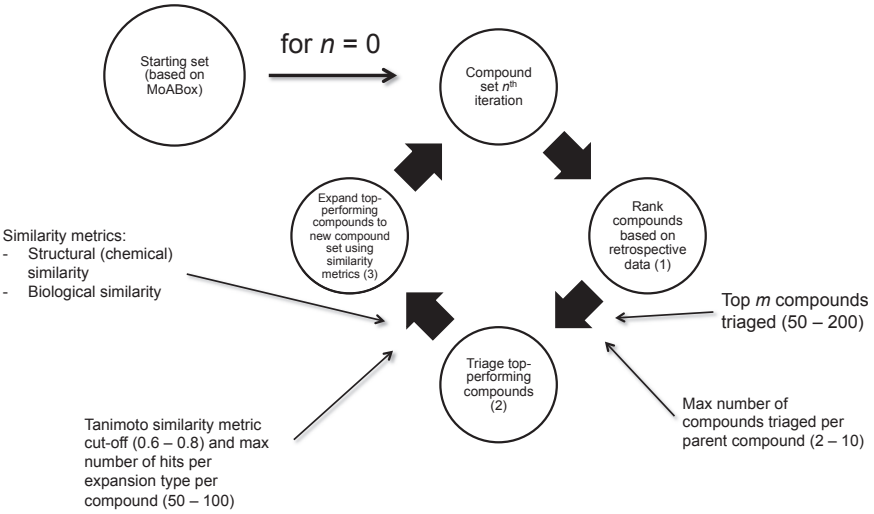

Figure 14. Iterative screening algorithm (ISA) overview. The ISA developed in this study consisted of three iteration steps: (1) ranking of compounds based on retrospective data, (2) triaging of (i.e., selecting) top-performing compounds, and (3) expanding from top-performing compounds to close analogs based on chemical and biological similarity metrics. The starting set comprises the MoABox compounds present in the HTS assay. The ISA allows for adjustment of parameters at the triaging stage (the number of compounds carried forward, and the number of compounds originating from the same parent compound to limit large numbers of closely related analogs). At the expansion stage, the parameters used (chemical and/or biological similarity) can be adjusted, as well as the corresponding similarity cutoff and maximum number of expansions per compound.

Since this study is a retrospective analysis on HTS data, the ranks of the compounds selected correspond to the ranks of the same compounds had they been screened in a full-deck screen. Our method is fundamentally different from a basic similarity search using active probes, because we perform a similarity search iteratively based on active compound information at every round of screening, rather than only once. Circular fingerprints[28] (SciTegic ECFP4-like) were used as features for determining chemical similarity, and HTS fingerprints (HTS-FP)[23] were used as features for determining biological similarity.

Metrics Used for Performance Assessment. We used two criteria for evaluating compound sets at each iteration: (1) the rank distribution based on compound activity and (2) the cumulative coverage of Murcko scaffolds[29] found in the top 0.5% of compounds ranked by activity. In conjunction, these criteria assess the retrieval of not only active but also structurally diverse sets of compounds. A median rank cutoff of 65000 is sometimes used to assess

performance; this corresponds to 5% of a total screening collection of 1.3 million compounds.

Systematic Exploration of Parameters. The number of compounds triaged per iteration as well as the number and types of expansions affect the size and diversity of the compound sets selected. First, the number of top-performing compounds triaged can be varied. Second, expansions can be adjusted (chemical and/or biological similarity), as well as the corresponding Tanimoto[30] similarity cutoff and maximum number of expansions per compound. Moreover, the maximum number of compounds originating from the same parent compound can be adjusted in order to limit the number of closely related analogs. We systematically explored the influence of these parameters in a number of *in silico* experiments (see **Table 5**), where the influence of each parameter was analyzed individually.

Table 5. Summary of parameters explored over nine *in silico* experiments. Here, experiment 1 was considered as the reference experiment, which was chosen on basis of a trade-off between number of compounds screened over 10 iterations (approximately 1% of screen size) and performance. All other experiments varied one parameter, therefore allowing an assessment of its influence with respect to the reference experiment. For example, a comparison of experiment 3 with experiment 1 shows the effect of doubling (from 100 to 200) the number of compounds triaged per iteration.

Experiment number	**Iteration count**	**Triaged number of compounds**	**Maximum number of expansions (structure-based)**
1	10	100	50
2	10	50	50
3	10	200	50
4	10	100	100
5	10	100	50
6	10	100	50
7	10	100	50
8	10	100	50
9	10	100	50
Tanimoto cutoff (structure-based)	**Maximum number of expansions (HTS-FP-based)**	**Tanimoto cutoff (HTS-FP-based)**	**Maximum number of compounds triaged per parent compound**
0.6	50	0.6	5
0.6	50	0.6	5
0.6	50	0.6	5
0.6	50	0.6	5
0.8	50	0.6	5
0.6	100	0.6	5
0.6	50	0.8	5

0.6	50	0.6	2
0.6	50	0.6	10

Experiment 1 was considered as a realistic reference experiment that balances performance and the number of compounds screened over 10 iterations (~1% of entire collection, ~15000 compounds). All other experiments varied one parameter, therefore allowing an assessment of its influence with respect to the reference experiment. For example, a comparison of experiment 3 with experiment 1 shows the effect of doubling the number of compounds triaged per iteration from 100 to 200.

Data Analysis. The workflow comprised Python and Perl scripts for data analysis and the Indigo toolkit[31] and RDKit[27] for cheminformatics calculations. Spotfire[32] was used for data exploration, and R[33] and Cytoscape[34] were used for the visualization of results.

Results and discussion

Here, we present in detail the results belonging to the reference experiment (experiment 1 in **Table 5**), followed by a comparison to other experiments. Experiments 4, 6, and 7 showed the same results as the reference experiment and are therefore not discussed separately; these experiments highlight, however, that more than 50 expansions or a more stringent HTS-FP similarity cutoff do not change the results.

Iterative Screening Is Highly Effective Across Assay Types. The median rank of the compounds selected was 36101 (excluding the starting set) across all assay types, which corresponds to the top ~2.8% of a collection of ~1.3 M compounds. In other words, half the compounds selected across all iterations (except for the starting set) are found among the top 2.8% of the corresponding 1.3 M compound screen, indicating a clear enrichment in activity of the compounds selected. Of note, the performance is consistent for a large number of different assay types (median rank below 65000, see **Figure 15**).

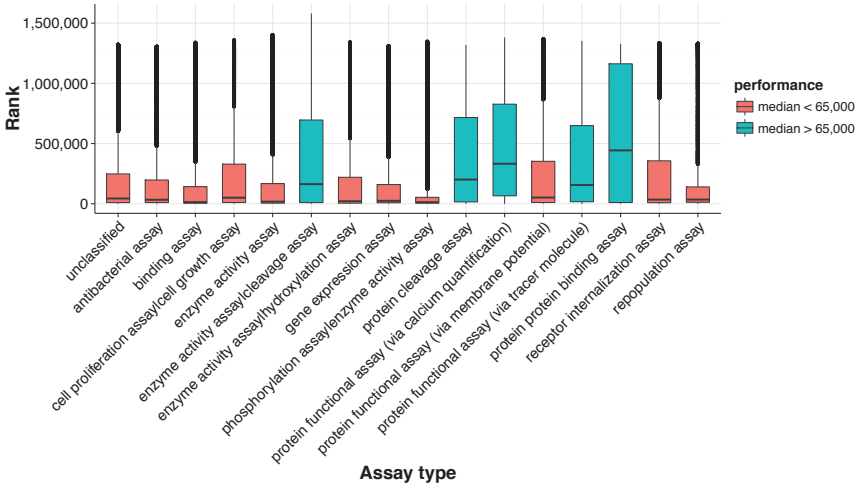

Figure 15. Ranks of compounds from iterations for all assay types. Boxplots of ranks for all compounds selected by the iterative screening algorithm (ISA) for iterations 1–10 (excluding the starting set) are represented for each assay type. The performance for enzyme activity/cleavage assay, protein cleavage assay, protein functional assay, and protein–protein binding assay is much worse (median rank of 200000 on average) compared to other assays, with also a broader rank distribution. Red, median rank below 65000; blue, median rank above 65000. The first 65000 compounds correspond to the top ~5% of 1.3 M.

However, for the types enzyme activity/ cleavage assay, protein cleavage assay, protein functional assay, and protein–protein binding assay, the performance was reduced, as evidenced by a median rank greater than 65000 combined with a higher standard deviation.

Interestingly, performance is better for the cell-free assays than the cell-based assays (rank distributions for both assay formats is shown in **Figure 16**).

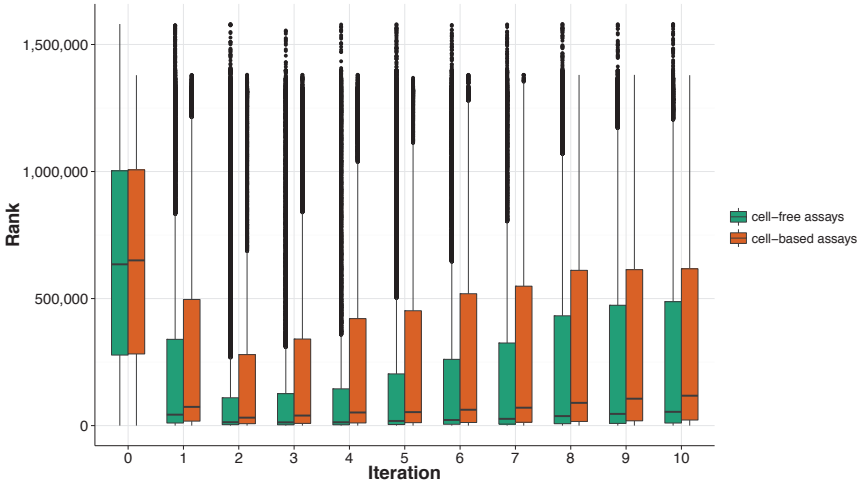

Figure 16. Ranks of iteratively selected compounds for cell-free and cell-based assays. Green, cell-free assays; orange, cell-based assays. There is a consistent difference in median rank (and interquartile range, extension of boxplot) across iterations 1 to 10 between cell-free and cell-based assays. This indicates the relative difficulty in selecting compounds that are able to satisfy cell-based screening requirements (e.g., cell permeability). Median ranks are significantly different (paired *t*–test, *p*-value < 10^{-5}), as are the rank distributions for each iteration (Kolmogorov–Smirnov test, *p*-value < 10^{-5}).

In order to investigate whether this difference was statistically significant, a paired *t*–test was performed for the median ranks across iterations 1 to 10. In addition, a Kolmogorov–Smirnov test was performed for every iteration on compound ranks of different assay formats. All *p*-values were smaller than 10^{-5}, hence indicating a statistically significant difference in distribution of rank between cell-free and cell-based assays. This difference is likely due to the fact that in order for compounds to have an effect in cell-based assays, they have to be able to cross the cell membrane to reach the target of interest (in cases when this target is not membrane-bound). Hence, these compounds must have suitable physicochemical properties (such as permeability), in order to be effective. Since our method on purpose did not distinguish between cell-free and cell-based assays, these results are in line with expectations; however, specific compound criteria for cell-based assays (e.g., incorporation of logP values, past performance in cell-based assays) are likely to diminish this observed gap in performance between the two assay formats in the future. Our starting set, the MoABox (see Methods), is geared toward hypothesis-generating cell-based phenotypic screening; as a result, this set of

compounds performs equally well on cell-based and cell-free assays (**Figure 16**, iteration 0).

Next, median compound ranks were evaluated per assay type (**Figure 17**).

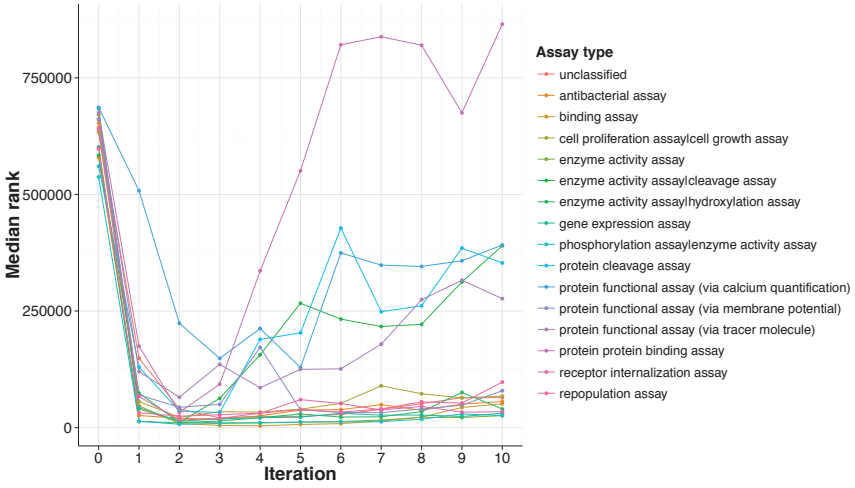

Figure 17. Median rank per iteration across assay types. The median rank of the compounds of the selected subset at each iteration is plotted versus iteration. The iterative screening algorithm (ISA) performs consistently well for most assay types, but there are a number of assays for which the median rank of compounds selected swiftly deteriorates after around iteration 3. These assays are for protein–protein binding, protein cleavage, protein function, and enzyme activity/cleavage and are the same ones shown to have an overall median rank greater than 65000 (**Figure 15**).

The iterative method performs consistently well for the majority of assay types (median ranks are smaller than 100000 for iterations 1–10 for 11 out of the 16 assay types), but there are a number of outlier assay types for which the median rank of compounds selected swiftly deteriorates after around iteration 3. These assays cover the biological events protein–protein binding, protein cleavage, protein function, and enzyme activity/cleavage and are the same ones shown to have an overall median rank above 65000 (**Figure 15**). These results suggest that expansions in chemical and biological space are unable to effectively retrieve the most active compounds for these assay types after the first few iterations.

Chemical Diversity Analysis of Iterative Screening Results. In addition to the rank distribution of the iteratively selected compounds, we also analyzed the percentage of highly active scaffolds cumulatively retrieved. Highly active scaffolds were separately defined for each assay as the Murcko scaffolds[29] belonging to the top 0.5% most active molecules in the assay. While Murcko

scaffolds are useful for assessing structural diversity of cyclic compounds (the definition by Bemis and Murcko[29] is based on ring systems and linkers), this measure of diversity is biased for assays where many aliphatic compounds are hits. In the absence of a more inclusive and/or appropriate definition of scaffold, the following analysis only includes chemical matter with a defined Murcko scaffold.

The average retrieval rate of highly active scaffolds after 10 iterations across all assay types is 41% (~1600 unique scaffolds per assay, ~9 analogs per scaffold), with an average of 14959 compounds screened across all iterations per assay. These results indicate that our method is able to prioritize diverse chemical matter despite much smaller screening sets. In addition, it performs substantially better than a traditional similarity search as the retrieval of highly active scaffolds is only 11% in the first iteration where the similarity search would stop, compared to 41% after 10 rounds of iterative screening.

The percentage of cumulatively retrieved highly active scaffolds steadily increases with the iteration count (**Figure 18**), with the steepest increases occurring in the earliest iterations.

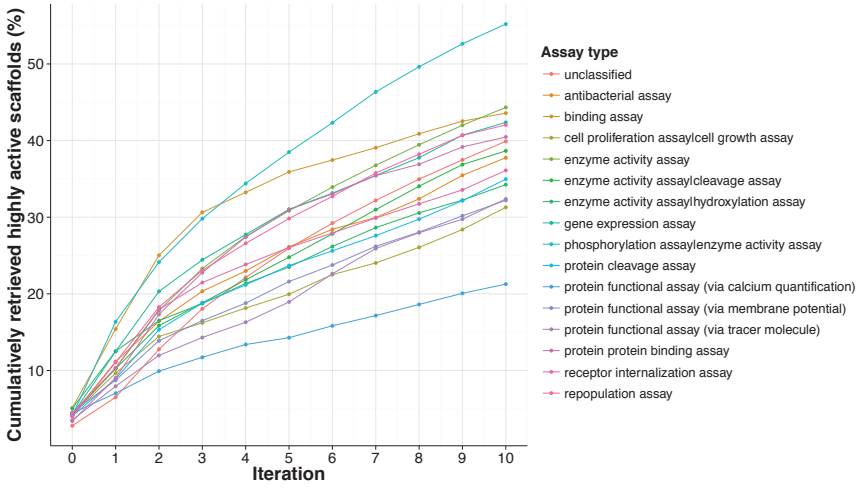

Figure 18. Cumulatively retrieved highly active scaffolds (%). For all assay types, the percentage of cumulatively retrieved highly active scaffolds (scaffolds of the 0.5% most active compounds of the full HTS) steadily increases, with the steepest increases occurring in the earliest iterations. Most assay types display a scaffold retrieval of between 30 and 45% after 10 iterations. The calcium quantification assay showed relatively poor scaffold coverage (~20% after 10 iterations), whereas the phosphorylation assays showed much better scaffold coverage compared to other assay types (~55% after 10 iterations).

Most assay types display a scaffold retrieval of 30–45% after 10 iterations. The calcium quantification assay showed relatively poor scaffold coverage (~20% after 10 iterations), whereas the phosphorylation assay, typically used for kinase inhibitors, showed much better scaffold coverage compared to other assay types (~55% after 10 iterations). Given the presence of many series of high-quality kinase inhibitors from past drug discovery programs in the Novartis screening archive, in combination with the promiscuity of kinase inhibitor binding,[35,36] it is likely that many active inhibitors retrieved are structurally/biologically similar. Hence, this is a possible explanation for the preferred retrieval of a higher number of active scaffolds for phosphorylation assays. Another interesting observation is that the assays for protein–protein binding, protein cleavage, and enzyme activity show mediocre median ranks (> 65000), while having average scaffold retrieval rates (30–40% retrieval after 10 iterations). This suggests that while our iterative screening algorithm (ISA) is able to retrieve many compounds present in the top 0.5% of most active compounds (to an extent comparable with the majority of other assays), many inactive compounds are retrieved as well, resulting in a higher standard deviation in rank (see **Figure 15**). The hypothetically best scaffold retrieval among the top 0.5% of compounds screened would be achieved by sorting the top 0.5% of compounds by activity and picking their scaffolds. We observed that after picking 5000 compounds, this best possible performance retrieves ~75% of highly active scaffolds, compared to ~10–25% of highly active scaffolds (depending on assay type) retrieved iteratively and ~0.4% that would be retrieved if selection was random. In other words, iterative screening of ~15000 compounds recovers a third of the structural diversity of the top 5000 compounds of a 1.3 M compound screen.

The fraction of highly active scaffolds retrieved was also analyzed across all assay types. Here, we determined the fraction of highly active scaffolds for each iteration (see **Figure 19**).

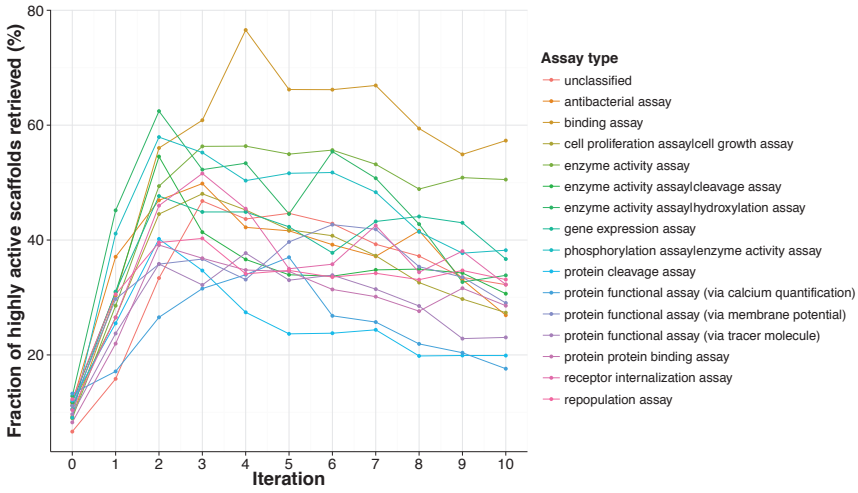

Figure 19. Fraction of highly active scaffolds retrieved (%). The iterative screening algorithm (ISA) exhibits a general trend for all assays: for the first two or three iterations, the fraction of highly active scaffolds retrieved per iteration sharply increases from ~10% to 30–80% depending on assay type (the active scaffolds which are easy to identify are quickly retrieved), after which it slowly decreases, as it becomes increasingly difficult to find the remaining highly active scaffolds. Nevertheless, active scaffolds are still retrieved at the last iterations.

We observed that, in general, the active scaffolds which are easily identified are quickly retrieved: for the first few iterations, the fraction of highly active scaffolds retrieved sharply increases from ~10% to 30–80%, after which it slowly decreases, indicating the progressive difficulty in finding the remaining highly active scaffolds. A possible explanation is the presence of unreachable singletons in the screening archive that are beyond the expansions we implemented thus far.

Visualization of Stepwise Exploration of Chemical Space. In order to illustrate the iterative compound selection in more detail, we showed the expansions for an inhibitory cell-free kinase assay in a network graph (see **Figure 20**).

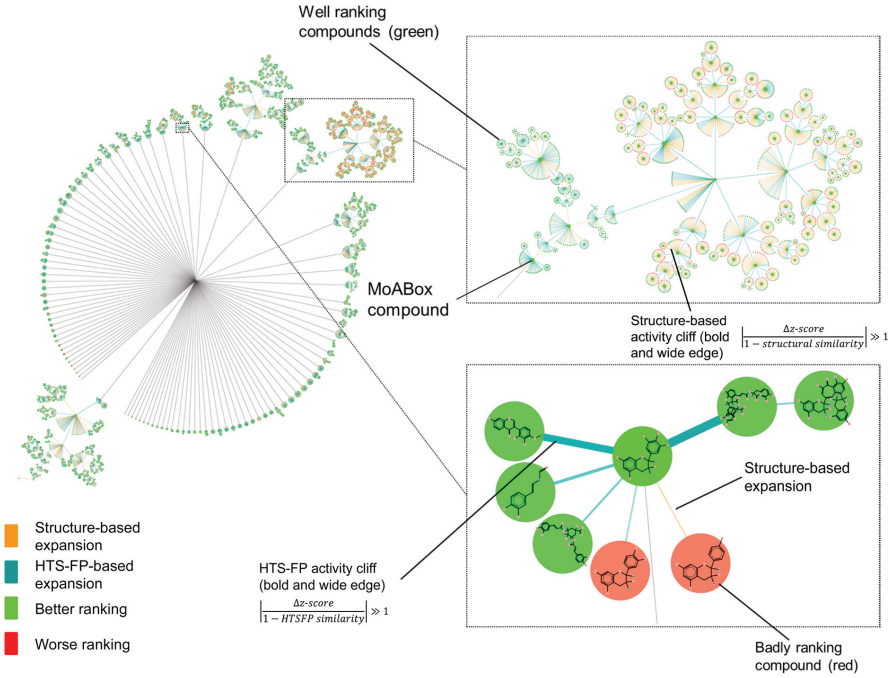

Figure 20. Visualization of stepwise exploration of chemical space for an inhibitory cell-free kinase assay. Expansions for an inhibitory cell-free kinase assay are shown in a network graph. All compounds from the starting set (zeroth iteration) leading to no further expansions have been omitted from the network graph, whereas those that led to at least one further expansion are depicted on the large circle on the left part of the figure. All the compounds present in the subnetwork in the upper-right corner of the figure represent expansions from one single compound from the starting set (MoABox). In the lower-right corner of the figure, we show an example of scaffold hopping, which is commonly caused by expansions based on biological similarity (HTS-FP), enabling the method to explore chemical space that is not reachable via expansions based on chemical similarity. In addition, the depiction of activity cliffs[37] (represented by bold and wide edges) allows the identification of scaffold hopping leading to relatively sharp increases in activity.

All compounds from the starting set (zeroth iteration) leading to no further expansions have been omitted from the network graph, whereas those that lead to at least one further expansion are depicted on the large circle on the left part of the figure. Compounds are color-coded according to their rank (lower/ better and higher/worse ranks are represented by green and red nodes, respectively), and edges are colored according to the expansion type (chemical similarity expansions are orange and biological similarity expansions are turquoise). Certain compounds from the starting set lead to very few further expansions, and hence produce very few branches. Other compounds lead to a larger number of expansions, as can be seen in the upper-right corner of the figure: all the compounds present in that

subnetwork represent expansions from one single compound of the starting set. In the lower-right corner of the figure, we show an example of scaffold hopping, which is commonly observed for biological similarity (HTS-FP) expansions, enabling the method to explore chemical space that is not reachable *via* chemical similarity. In addition, the depiction of activity cliffs[37] (represented by bold and wide edges) allows the identification of scaffold hopping indicative of a relatively sharp increase in activity.

Tuning Iterative Screening to Assay Requirements. The number of compounds triaged per iteration has a large effect: as more compounds are carried forward, both the median ranks and the scaffold retrieval for compounds selected in iterations 1−10 increase (comparison of experiments 2 and 3 with reference, see **Figure 21** and **Figure 22**).

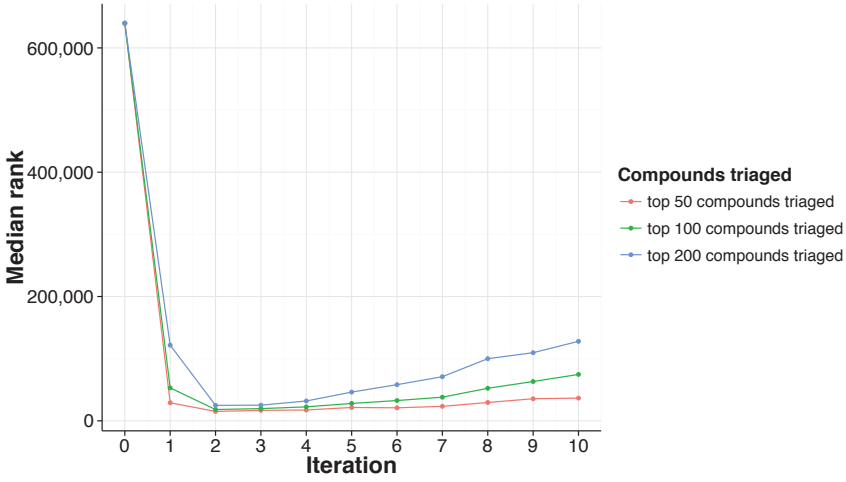

Figure 21. Effect of varying the number of compounds triaged per iteration in terms of median compound rank. As the number of compounds triaged increases, the median ranks consistently increase for iterations 1 to 10. These results are in accordance with our expectations: as the number of triaged compounds is increased (i.e., a less stringent selection criterion is applied for compound triaging), more expansions take place and more compounds are screened overall.

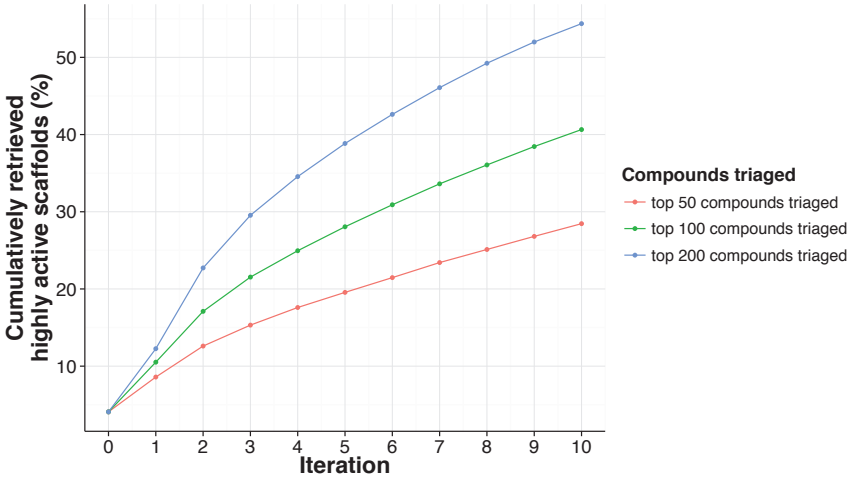

Figure 22. Effect of varying the number of compounds triaged per iteration in terms of percentage cumulatively retrieved highly active scaffolds. As the number of compounds triaged increases, scaffold retrieval is higher as well. These results are in accordance with our expectations: as the number of triaged compounds is increased (i.e., a less stringent selection criterion is applied for compound triaging), more expansions take place and more compounds are screened overall.

When the number of compounds triaged was increased from 50 to 100 and from 100 to 200, median ranks of the compounds selected in iterations 1–10 increased significantly from 23517 to 36101 in the first case and from 36101 to 63721 in the second case (paired *t*–test *p*-values of 1.2×10^{-3} and 3.4×10^{-4}, respectively). Scaffold retrieval increased from 20% to 28% and from 28% to 38% for the same comparisons, with respective paired *t*–test *p*-values of 1.1×10^{-5} and 9.9×10^{-6}. Less stringent hit selection during triaging leads to more subsequent expansions and increases the total number of compounds screened. The overall net result is an increased retrieval of active scaffolds at the cost of screening more inactive compounds as evidenced by higher median ranks.

When investigating the dependence of scaffold coverage on fingerprint type, we found that HTS-FP-based and structure-based expansions accounted for 90% and 50%, respectively, of total highly active scaffold retrieval after 10 iterations. Since HTS-FPs capture the biological profile of compounds, HTS-FP similarity leads to more structurally diverse sets of biologically similar compounds compared to structure-based expansions.

Increasing the Tanimoto[30] cutoff from 0.6 to 0.8 (comparison of experiment 5 to the reference experiment) for structure-based expansions decreased both

median compound ranks from 36101 to 16831 (paired *t*–test *p*-value of 9.4×10^{-4}) and scaffold retrieval from 28% to 16% (paired *t*–test *p*-value of 2.6×10^{-6}). The maximum number of compounds triaged per parent compound did not have a clear effect on the diversity nor the ranks of the compounds screened. Lowering this number from 5 (reference experiment) to 2 (experiment 8) resulted in a 2% higher scaffold retrieval (paired *t*–test *p*-value of 0.047), whereas an increase to 10 (experiment 9) had no significant effect on either median ranks or scaffold retrieval. In summary, the number of compounds triaged was the most influential factor, which can be adjusted depending on the number of compounds one intends (or can afford) to screen.

Finally, iterative screening was repeated with 10 randomly chosen starting sets, and the results were compared to those obtained with the MoABox as a starting set. The latter resulted in better median ranks only until the first iteration, virtually identical median ranks from iteration two onward, and slightly higher scaffold retrieval throughout all iterations. While minor differences across starting sets can be observed, the key findings presented in this study are independent of the precise composition of the starting set. However, the availability of a high-quality starting set, as the MoABox for us, can provide biological insight early on through comprehensive compound annotations.

Conclusions

Even though alluded to in the literature and theoretically appealing, no comprehensive practical evaluation of iterative screening was published. In this study, we have performed an unequaled large-scale validation of iterative screening on 34 HTS assays comprising at least 1300000 compounds and showed greatly improved efficiency over conventional HTS campaigns. For most assays, half of the compounds found by iterative screening of only 1% (~15000 compounds) of the entire collection correspond to the top 5% of the full collection screen. Put differently, screening only 1% of the collection provides ~7500 top-quality hits for further optimization. On average, the compounds selected covered over 40% of the scaffolds belonging to the top 0.5% most active compounds for each assay, hence also ensuring structural diversity. Our method allows for exit points during the iterative screening process: performing large numbers of iterations is not necessary in order to retrieve active compounds, as they are retrieved starting from the first

iteration already, and therefore, a large investment in resources upfront is not required. As expected, the method in its current state performs better for cell-free assays compared to cell-based assays; a future improvement can gear toward physicochemical properties more adapted to cell-based screens.

We used network graphs to visualize the compound selection process, and to highlight activity cliffs,[37] scaffold hopping, and the effect of changing the number of compounds triaged (which was found to have the largest influence on compound selection). As an outlook for further refinement of our method, we propose (1) investigating activity cliffs[37] (to be able to prioritize expansion types) and (2) employing iteratively retrained machine-learning methods[20] to rank the screening collection in parallel to the structure-based and HTS-FP-based expansions currently performed. We believe that the iterative method developed here can easily be fine-tuned for specific assay types, provides multiple exit points, and can potentially lead to considerable savings in both time and resources.

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