Subpocket-based fingerprint for structural kinase comparison

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Introduction

Kinases are important and well studied drug targets for cancer and inflammatory diseases. Due to the highly conserved structure of kinases, especially at the ATP binding site, the main challenge when developing kinase inhibitors is achieving selectivity, which requires a comprehensive understanding of kinase similarity. [1] Here, we present our work on a novel fingerprinting strategy designed specifically for kinase pockets, allowing for similarity studies across the structurally covered kinome.

Methods

The kinase fingerprint is based on the KLIFS [2] pocket alignment, which defines 85 aligned pocket residues for all kinase structures. This enables a residue-by-residue comparison across the kinome without a computationally expensive alignment step.

Data preparation. KLIFS dataset was filtered for structures (i) describing human kinases, (ii) in DFG-in conformation, (iii) with the best quality score per kinase-structure pair, and (iv) with a resolution ≤ 4 and a quality score ≥ 4. The resulting kinase dataset consists of 3,875 structures.

Kinase fingerprint. The *pocket fingerprint* consists of 85 concatenated *residue fingerprints*, each encoding a residue's spatial and physicochemical properties (**Fig. 1**). Inspired by the ligand-based USR approach [3], the *spatial properties* describe the residue's position in relation to the kinase pocket centroid and important kinase subpockets, i.e. the hinge region, the DFG region, and the front pocket. The resulting distance distributions per subpocket are reduced in complexity to the first three moments, i.e. the mean, standard deviation and skewness. The *physicochemical properties* encompass for each residue its size, side chain orientation and pharmacophoric features as described by SiteAlign [4] in addition to its solvent exposure as implemented in Biopython's module `Bio.PDB.HSExposure` [5, 6].

Kinase comparison & scoring. Kinase structures are compared pairwise using the inverse, translated and scaled Manhattan distance as implemented for the USR method [3]. Per kinase pair, the best score is used for further analysis, resulting in a 253x253 similarity matrix.

$$d(A,B) = \frac{1}{1 + \frac{1}{N}\sum_{i=1}^{N}|A_i - B_i|} \in]0,1]$$

(inverse; translated; scaled; Manhattan distance)

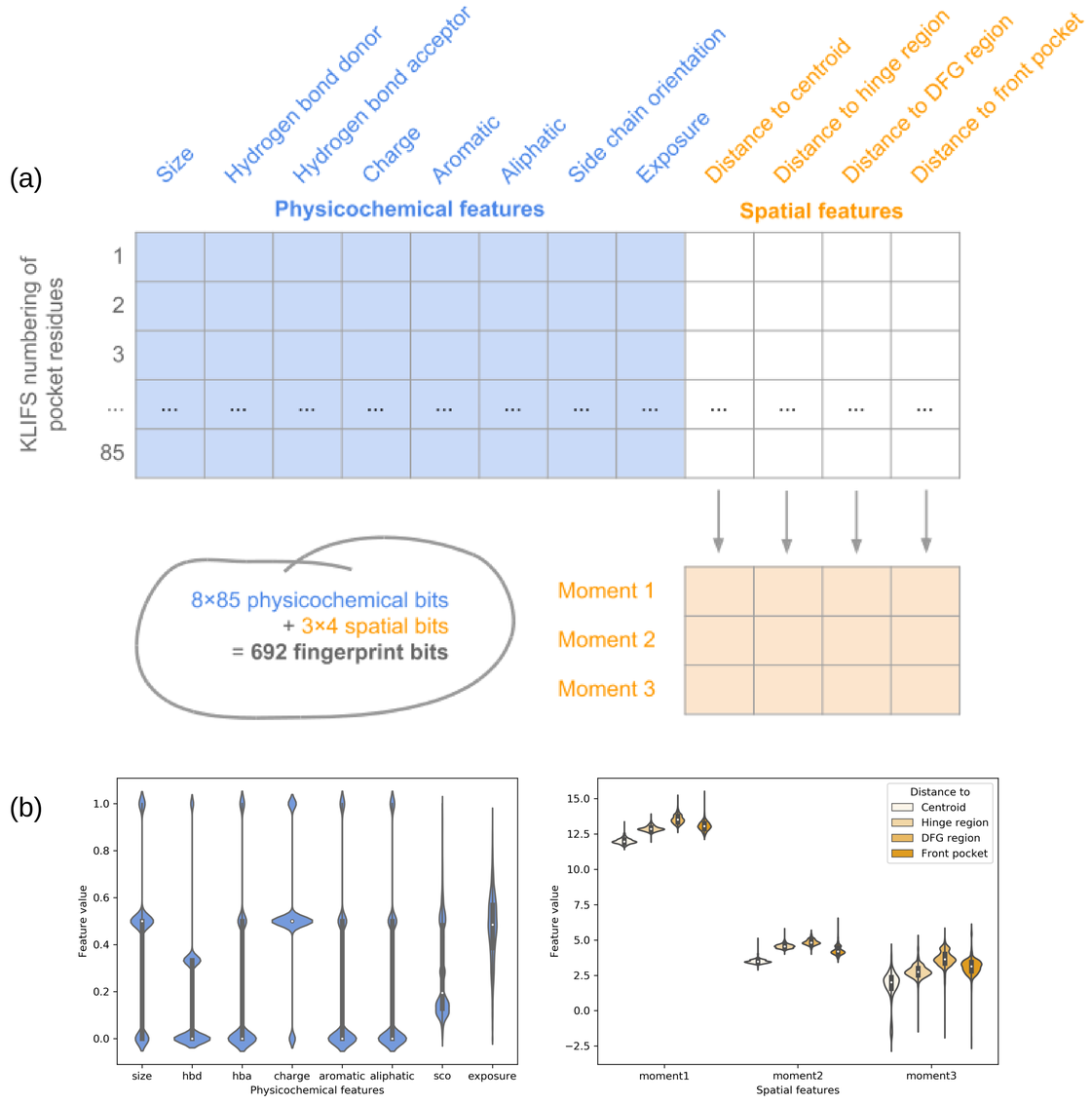

Fig. 1: (a) Composition of 962 bit kinase fingerprint, (b) feature value distribution over all 3,875 kinase structures.

Results

The potential of our subpocket-based kinase comparison is demonstrated by uncovering retrospectively on- and off-targets for EGFR using KinMap [7] (**Fig. 2**).

Compared to profiling data for EGFR inhibitor erlotinib by Karaman et al. [8], our 20 most similar structures to EGFR include many off-targets in the TK group as well as the reported off-target kinases LOK and SLK (STE), though missing the off-target kinase GAK (Other). Similarity score clustering shows that our method can reproduce the Manning classification [9] in large part, however also reveals new groupings such as the aforementioned STE kinases within the TK group or the grouping of DRAK2 (DAPK) with the reported off-target CaMKK2 (Other group) [10] (**Fig. 3**).

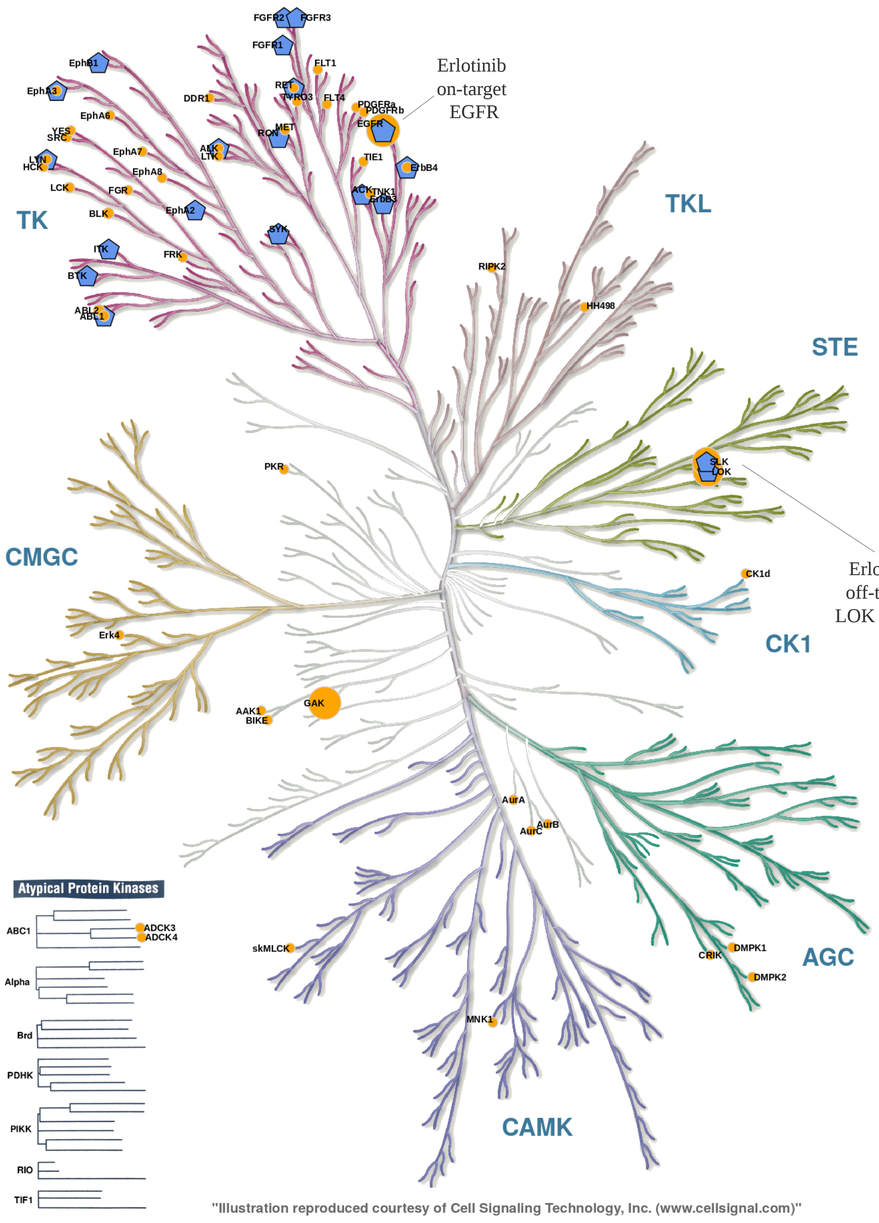

Fig. 2: Ligand-based on-/off-target prediction for EGFR inhibitor erlotinib based on our kinase fingerprint similarity: the 20 most similar structures to EGFR (blue pentagons) and erlotinib profiling data (orange circles).

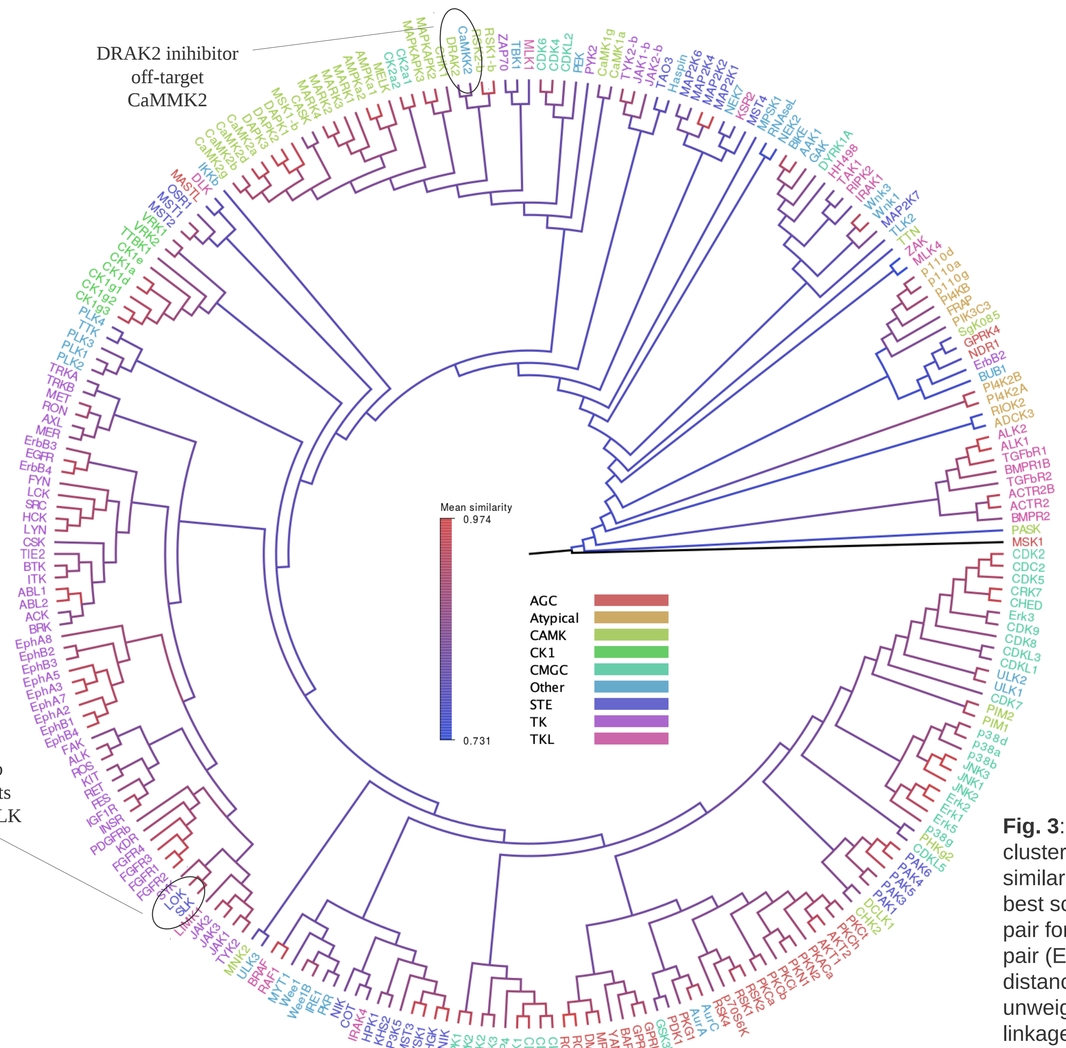

Fig. 3: Hierarchical clustering of pairwise similarity scores for best scoring structure pair for each kinase pair (Euclidean distance with unweighted average linkage clustering).

Conclusion

We believe that our subpocket-based kinase fingerprint can help researchers (i) to detect potential promiscuities and off-targets at an early stage of inhibitor design and (ii) to conduct structure-informed polypharmacology studies.

References

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