

Exploring Chemical Space

Two (still immature) ways of traversing in the molecule space

Nico Domschke

Bioinformatik Uni Leipzig

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Chemical space in numbers

- ▶ New innovative molecules are needed for drug discovery.
- ▶ Only 12267 approved drugs¹
- ▶ How big is the chemical space? 10^{60} drug like molecules[4]
- ▶ Huge untapped potential

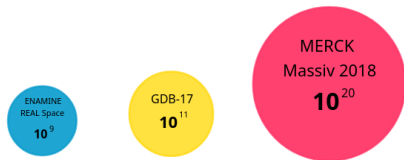


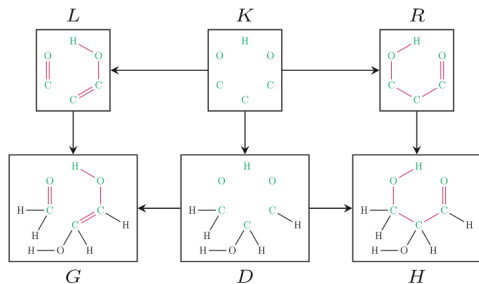
Figure: Chemical Space in Numbers.²

¹on DrugBank 11.02.23

²Hoffmann, Torsten. The next level in chemical space navigation: Going far beyond enumerable compound libraries. Drug Discovery Today, 24(5):1148–1156, 2019

A rule based approach

- ▶ Using MØD as the underlying framework [1]
- ▶ Category theory embedded subgraph matching on molecule graphs
- ▶ A restriction on actual chemistry produces synthesizable molecules [5]
- ▶ Curated collection of 54 organic reactions by Hartenfeller et al.[3]

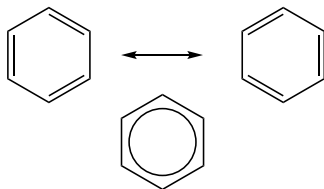


Term-Rewriting

- ▶ Chemical context needs to be explicitly defined
- ▶ `ConstrainLabelAny` gives a lot of flexibility
- ▶ A liberal definition should be the sweet spot
- ▶ Much Needed: Negative Lists and Subgraph Matches

```
1  (...)
2  node [ id 1 label "_U" ]
3  edge [ source u target v label "_A" ]
4  constrainLabelAny [
5      label "Meso(_A,_B,_C,_D,_E,_F)"
6      labels [label "Meso(-,=,-,=,-,=)" label "Meso(=,-,=,-,=,-)"]
7  ]
8  constrainLabelAny [
9      label "Halo(_U)"
10     labels [label "Halo(Cl)" label "Halo(Br)" label "Halo(I)"]
11 ]
12 ]
```

Term-Rewriting

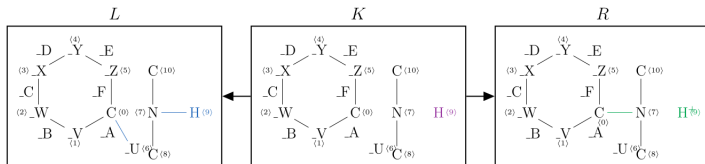


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Term-Rewriting

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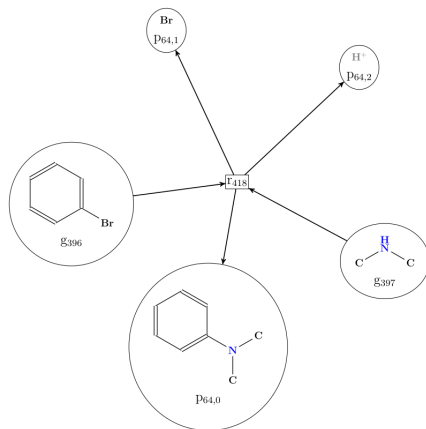
65.1.1 Buchwald-Hartwig-amine



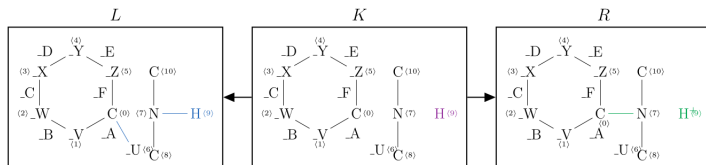
Files: out/819_r_418_10300010_{L, K, R}

`Permut(_V, _W, _X, _Y, _Z) ∈ {'Permut(C,C,C,C,C)', 'Permut(N,C,C,C,C)', 'Permut(C,C,C,C,N)'}`
`Meso(_A, _B, _C, _D, _E, _F) ∈ {'Meso(-, -, -, -, =)', 'Meso(=, -, -, -, -)'}`
`Halo(_U) ∈ {'Halo(Cl)', 'Halo(Br)', 'Halo(I)'}`

Term-Rewriting



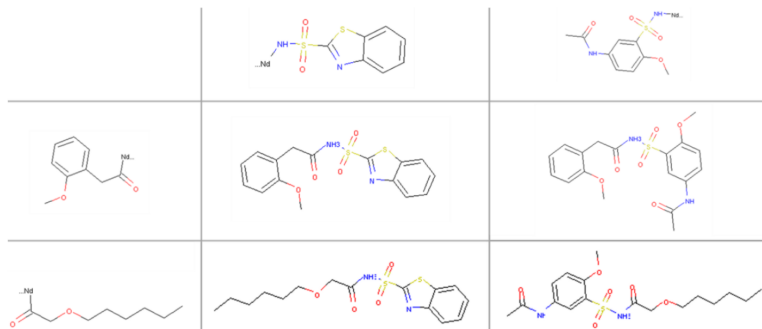
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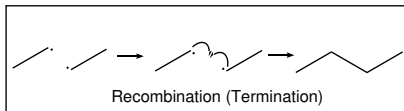
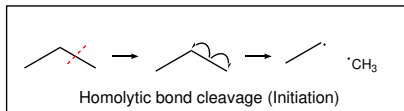
A rule based approach

- ▶ A first test is *planned* using the ENAMINE synthesize-on-demand library



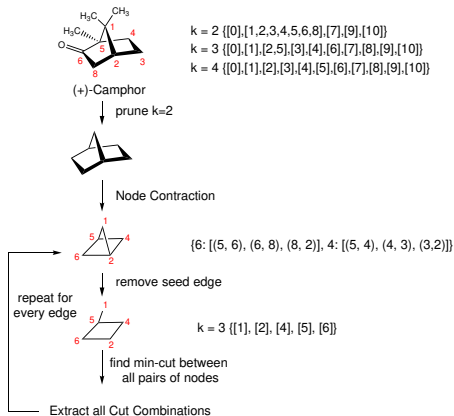
Crossover mutations

- ▶ Two parent molecules each cut into two fragments
- ▶ Corresponds to the formation of radicals in chemistry
- ▶ No restriction by relying on reactions
- ▶ exhaustive graph bipartitioning



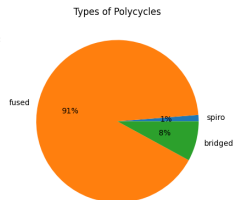
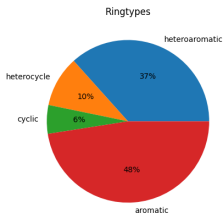
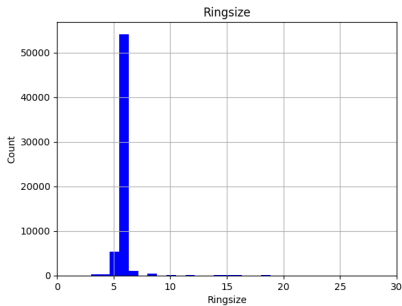
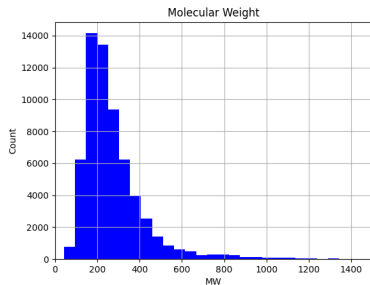
Generating all possible cuts

- ▶ k-connected-components for $k = 2, 3, 4$ [6]
- ▶ remove sidechains ($k=2$)
- ▶ contract nodes
- ▶ remove random seed-edge of graph
- ▶ check k-connected-components after removal
- ▶ get minimum-cut of every pair of atoms in these connected components



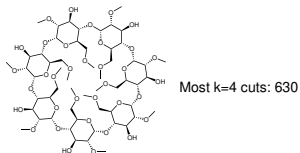
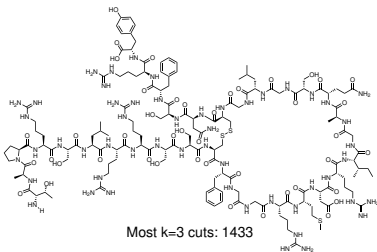
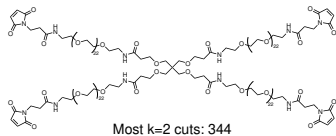
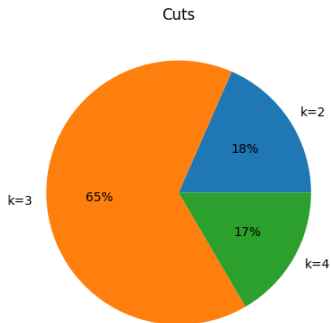
A superficial look at Sigma Aldrich catalog

- ▶ At least 1 Ring, 1 Carbon-Atom, no disconnected components
- ▶ 117k \rightarrow 62k compounds
- ▶ High diversity



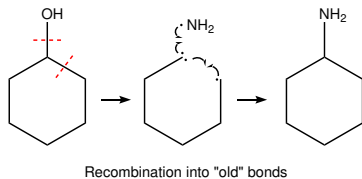
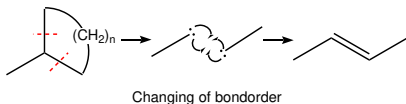
A superficial look at Sigma Aldrich catalog

- Found 3.1 M cut combinations



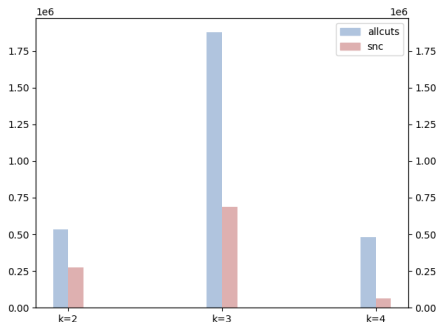
Open Questions of the fragment recombination

- ▶ Allow Termination of multiple radicals at the same atoms?
- ▶ How to proceed with fragments having a mismatched number of radicals?
- ▶ Allow Recombination to previous bond pattern?
- ▶ Matching of single-node-fragments?
- ▶ Essentially point mutations, takes a lot of space (~ 32%) in the cut space



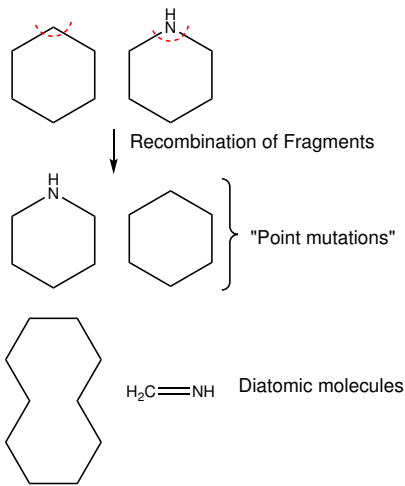
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How to ensure chemical meaningfulness?

- ▶ Possible Restrictions and filters:
- ▶ Remove unstable functional groups (violating Erlenmeyer-Rule etc.)
- ▶ Account for ring strain (violating Bredts-Rule, etc.)
- ▶ Most lead compounds are in range $100 < MW < 350$ Da
- ▶ Empiric MedChem rules: Lipinski Ro5, Lily Medchem [2]

Thanks to my Supervisors
Peter and xtof

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Thank You!

Nico Domschke

Bioinformatik Uni Leipzig

dnico@bioinf.uni-leipzig.de

www.bioinf.uni-leipzig.de



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