Solving Atomix with Pattern Databases

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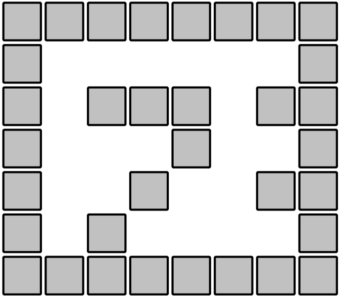

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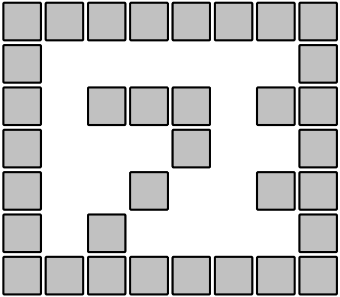

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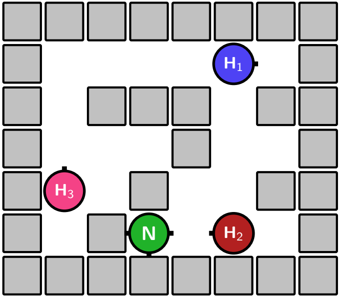

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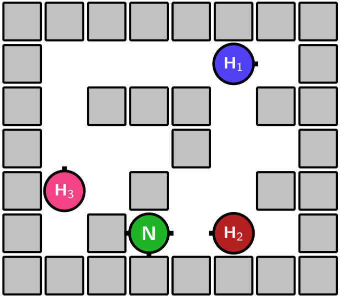

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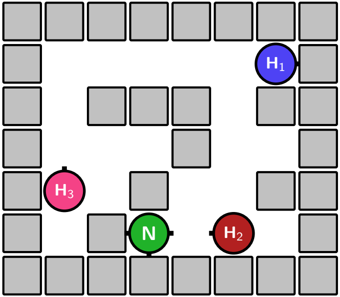

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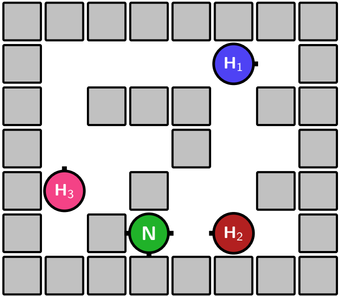

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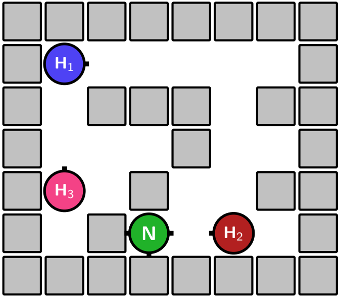

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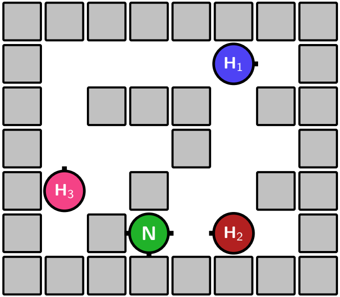

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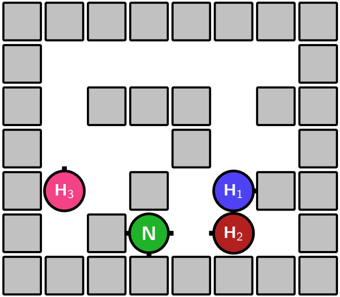

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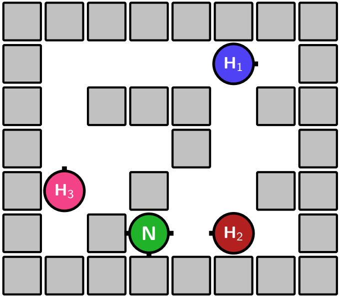

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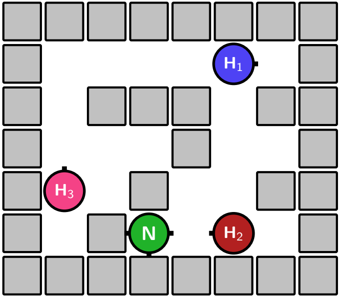

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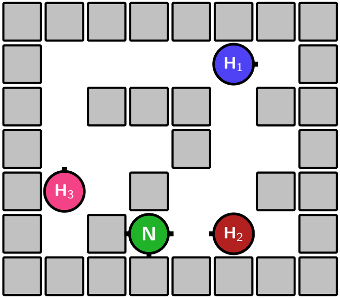

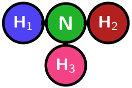

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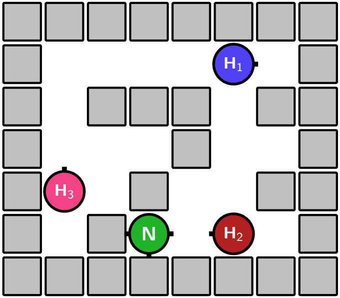

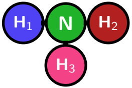

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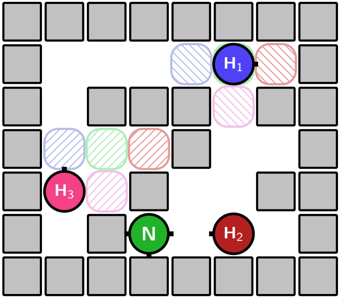

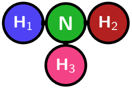

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- This presentation: focus on PDBs, other contributions with more details in the paper

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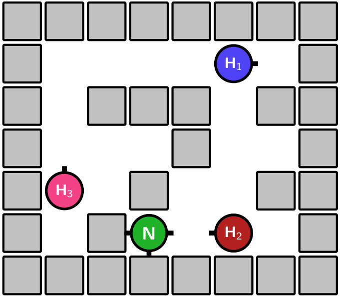

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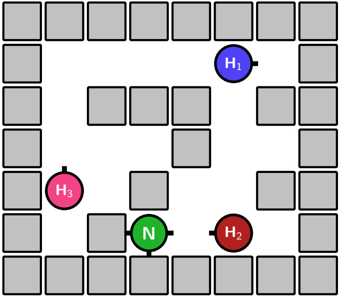

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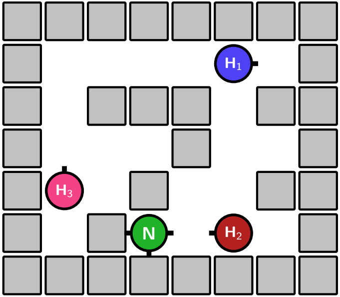

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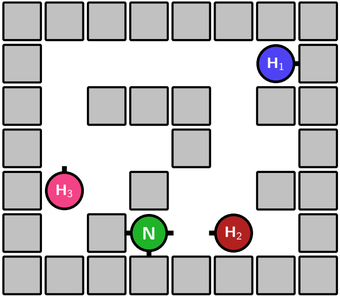

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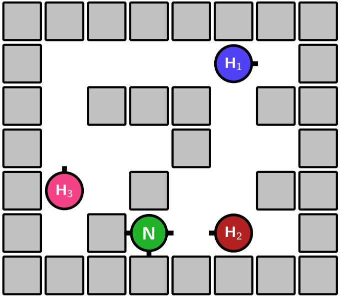

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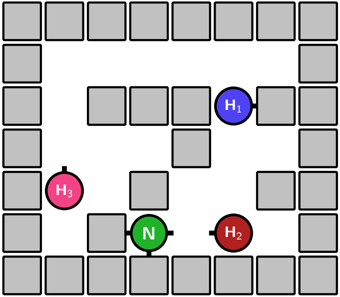

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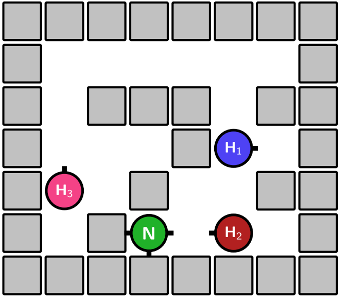

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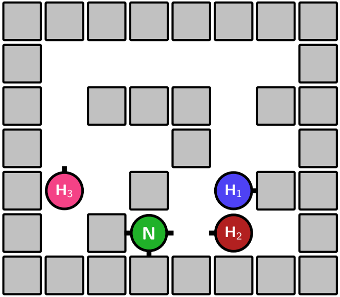

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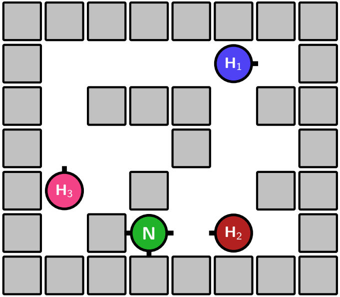

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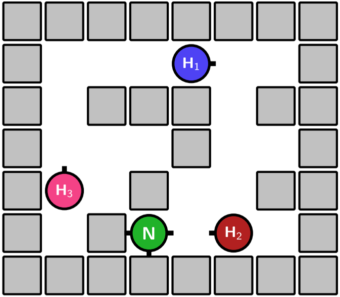

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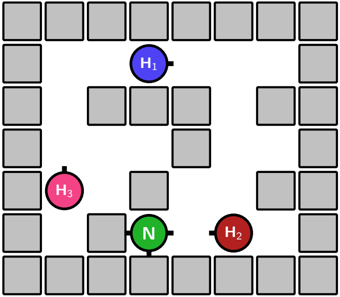

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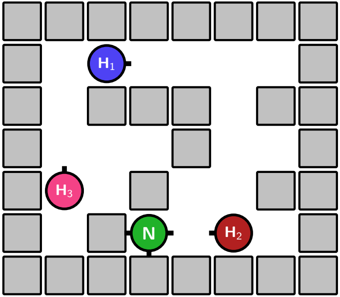

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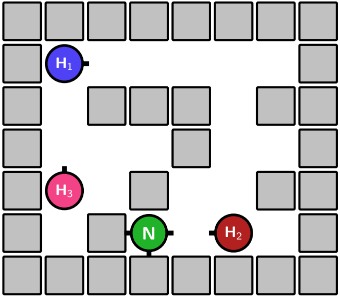

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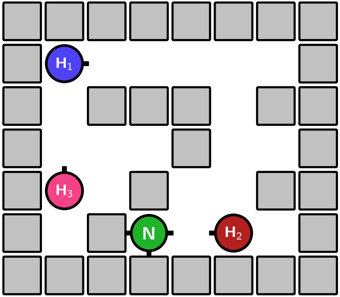

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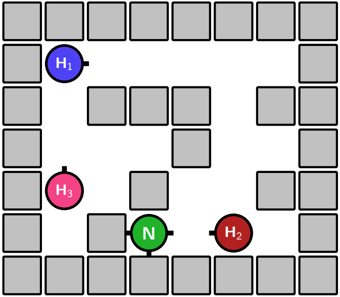
- Generalized distance: minimum number of relaxed moves from one position to another
- **Heuristic value of a state:** sum of generalized distances from every atom, independently, to its final position in a molecule



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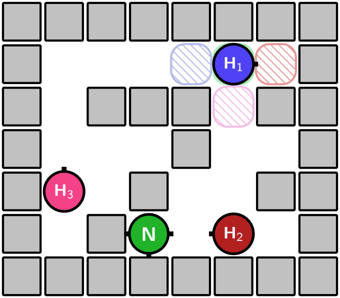

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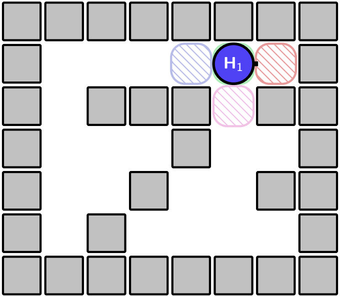

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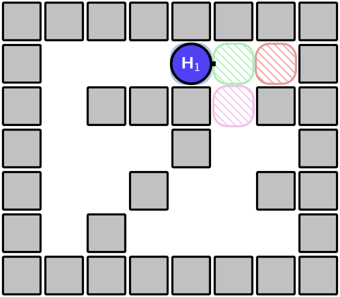

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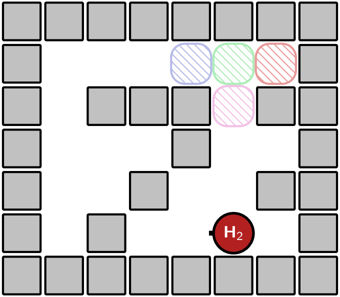

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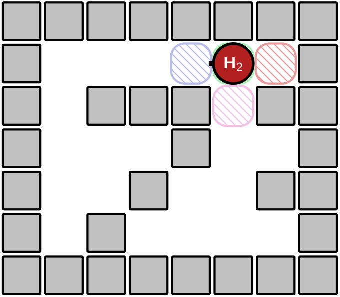

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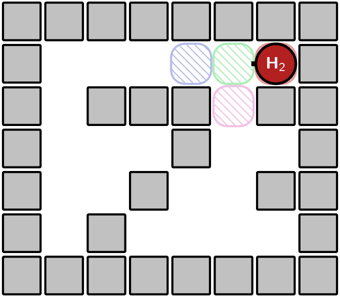

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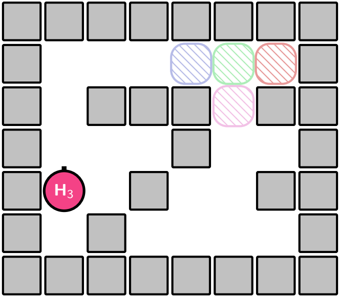

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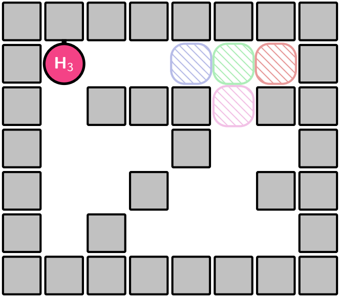

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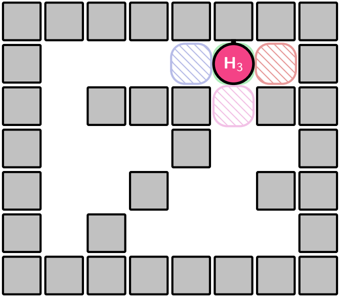

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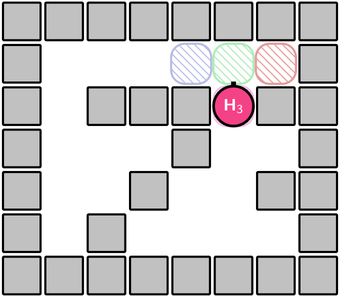

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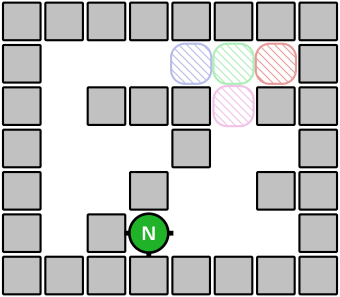

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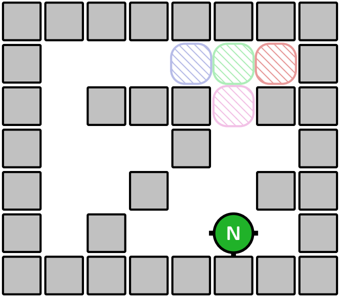

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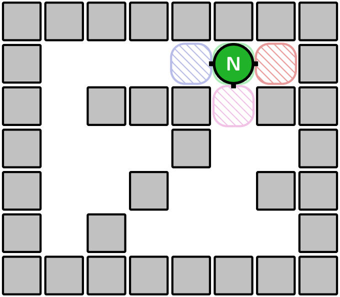

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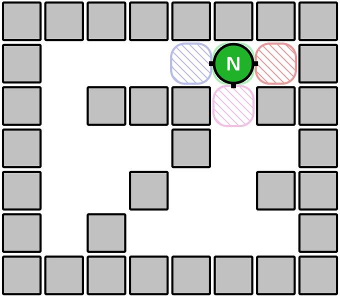

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- Distances are pre-computed before search starts by an all-pairs-shortest-paths algorithm

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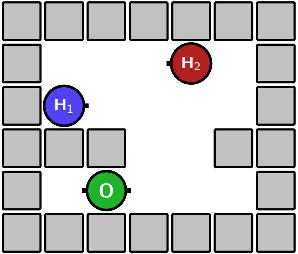
- Normally, in puzzles like Atomix, abstraction is done by removing some pieces

Pattern Databases

- Idea: map state space to a smaller, abstract state space that can be fully explored (with backward BFS from goal) and keep the optimal distances to each abstract state in a look-up table, called a PDB
- Solution to abstract state must be a lower bound to the solution of the original state
- Normally, in puzzles like Atomix, abstraction is done by removing some pieces
- In particular, we are interested in **additive PDBs**: if the abstract states use disjoint sets of pieces, we can add their distances and still be admissible

PDBs for Atomix: cannot remove pieces

In Atomix, an abstraction that only removes pieces is inadmissible:



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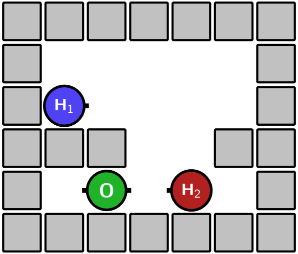

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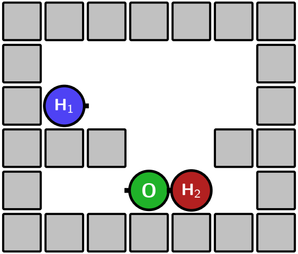

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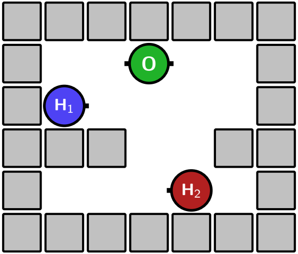

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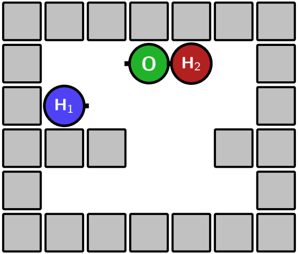

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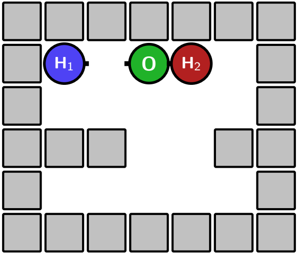

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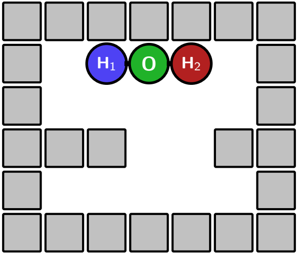

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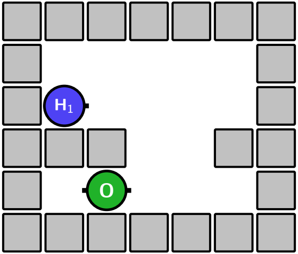

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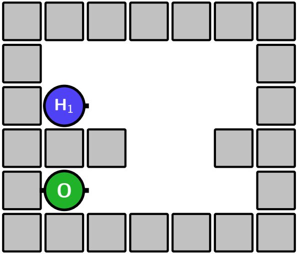

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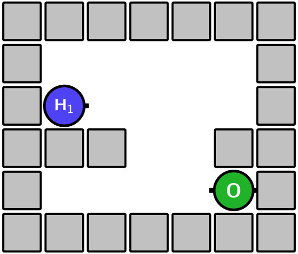

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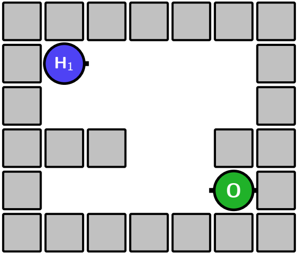

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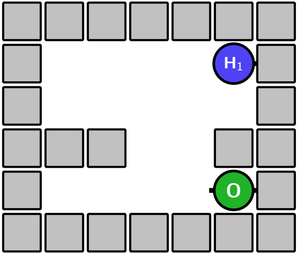

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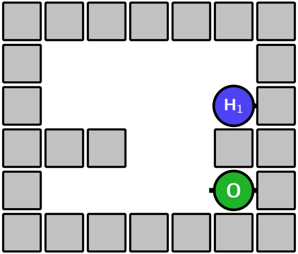

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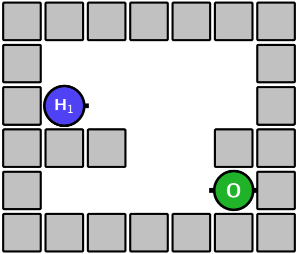

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Constructing PDBs for Atomix

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- Using the generalized moves relaxation, atoms do not need positive interactions to reach places: they can stop anywhere they want
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- An admissible heuristic for the relaxed version is also admissible for the standard version
- A PDB on relaxed Atomix penalizes negative interactions (such as linear conflicts) between atoms within the PDB's set of pieces

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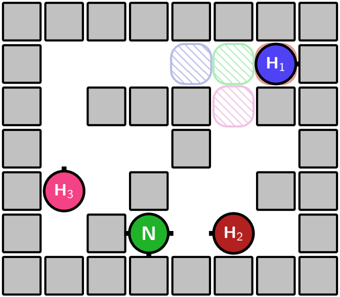
- Chosen patterns of k of atoms stay the same during search
  - Some partitions may yield better overall lower bounds than others
  - Would be good to pick a partition that captures more conflicts within the patterns

Statically-partitioned PDB: example



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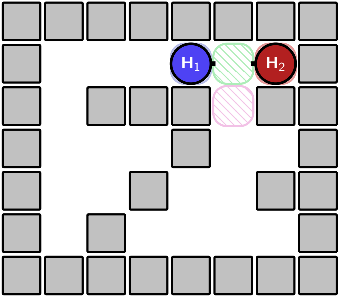

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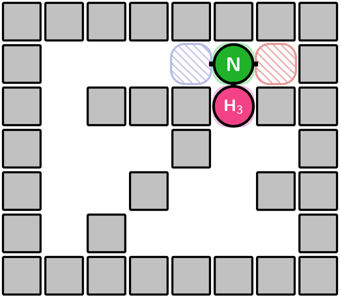

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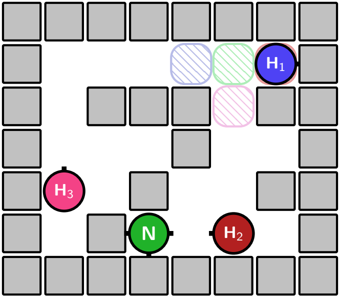

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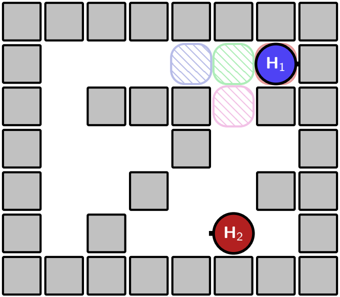

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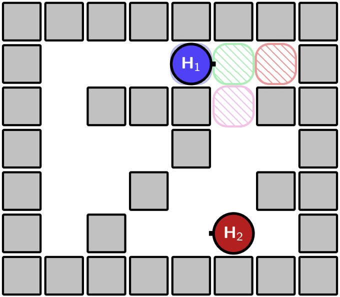

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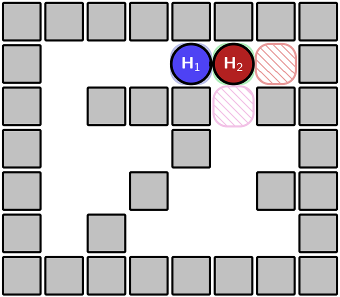

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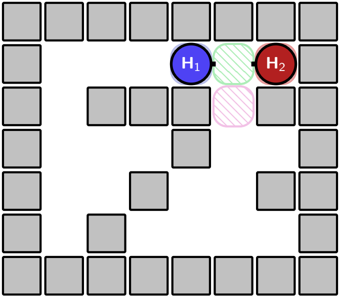

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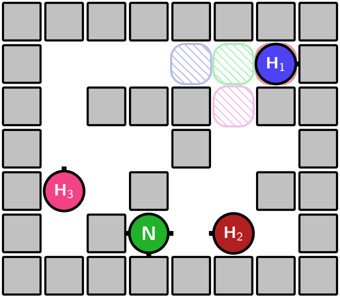

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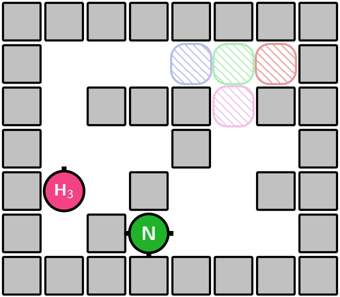

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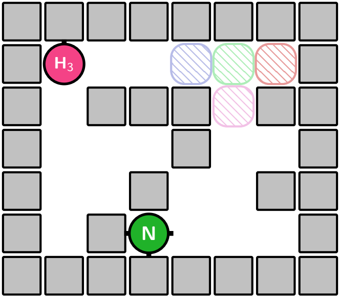

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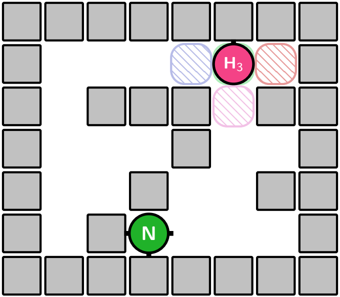

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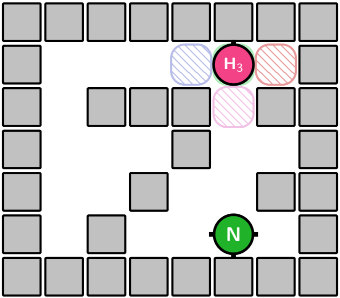

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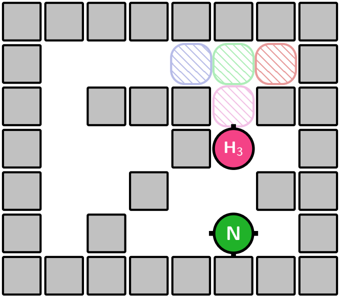

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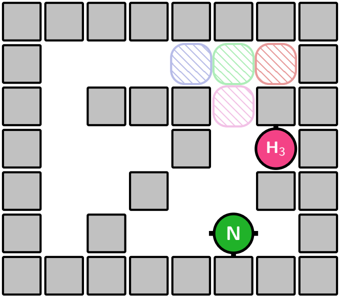

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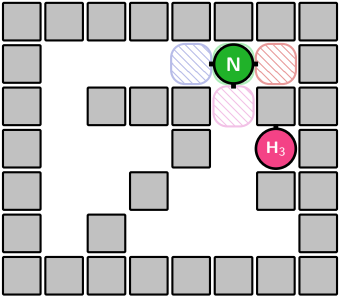

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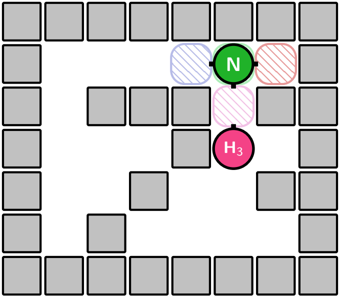

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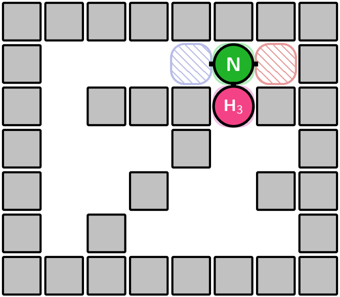

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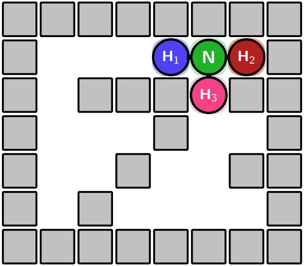

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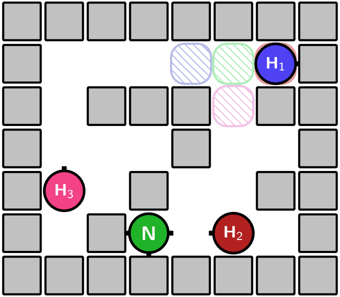
- Final heuristic: 3 for $\{\mathbf{H}_1, \mathbf{H}_2\}$ and 8 for $\{\mathbf{H}_3, \mathbf{N}\}$, total 11. Recall that without PDBs it was 8

Dynamically-partitioned PDB

- Build PDB for all possible $\binom{n}{k}$ partitions of the n atoms
- At every heuristic call, choose the partition with maximum heuristic value
- For $k = 2$, the best heuristic is obtained by a maximum weight perfect matching

Dynamically-partitioned PDB: matching example



- Build a full graph where:

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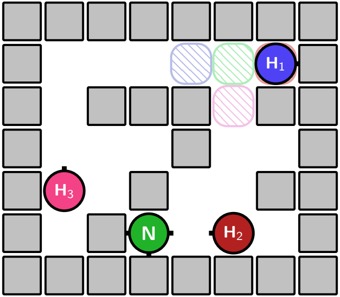
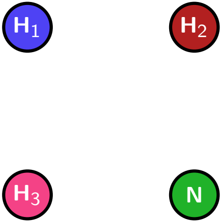
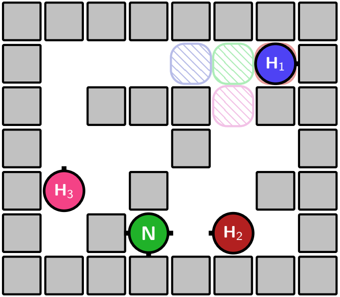
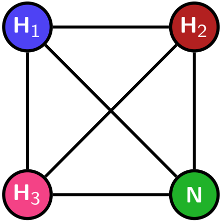




- Build a full graph where:
- Each atom is a node

Dynamically-partitioned PDB: matching example





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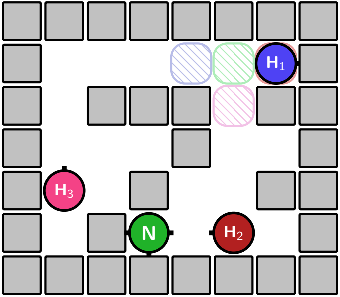

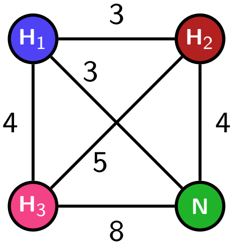

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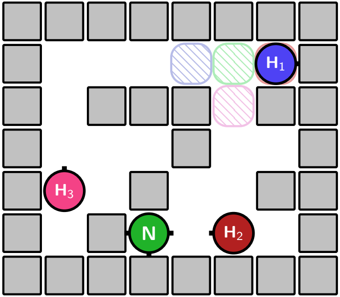

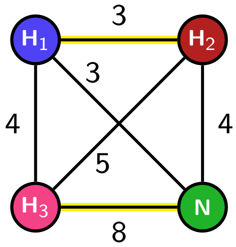

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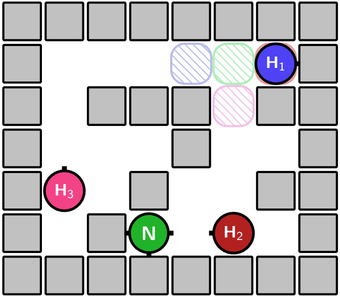

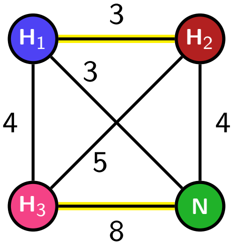

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- Each atom is a node
- Weight of each edge is the solution of the abstract state using only the two atoms that edge connects
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- If $k \geq 3$, matching is NP-hard: better use heuristic methods

Experimental setup

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- 10 replications of each run

PDB Results

	Static $k = 3$	Dynamic $k = 2$	No PDB
# Solved	**82.8**	71	77
Avg. rel. deviation (%)	**0.58**	1.72	1.47
Avg. initial heuristic (%)	24.04	**23.39**	26.23
Time (s)	**2,952**	17,405	3,420
Nodes expanded ($\times 10^8$)	3.39	**2.39**	8.72

Comparison with Hüffner et al. (2001)

	This work (w/ static PDB)	Hüffner et al.
# Solved	**82.8**	75
Avg. rel. deviation (%)	**0.56**	1.67
Time (s)	**9,211**	12,962
Nodes expanded ($\times 10^8$)	**6.79**	47.18

Conclusions

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- Static PDB yields better lower bounds than standard heuristic and in same time $O(n)$
- Dynamic PDB yields even better lower bounds, even with smaller k, but is very slow to compute ($O(n^3)$)
- Static PDB solves 7.8 more instances and expands, on average, 6.94 times fewer nodes compared to previous state of the art

Questions?