

Generating sound molecular cages

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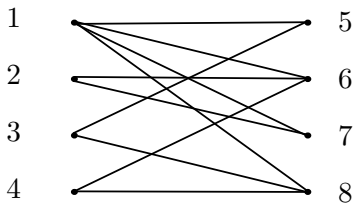
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Laboratoire PRiSM

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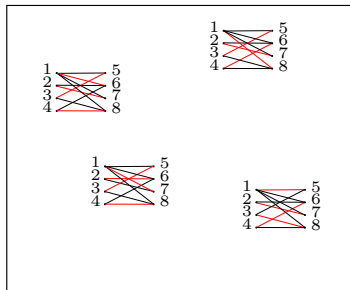
Enumeration problems

- **Enumeration problems:** list all solutions rather than just deciding whether there is one.

Perfect matchings:



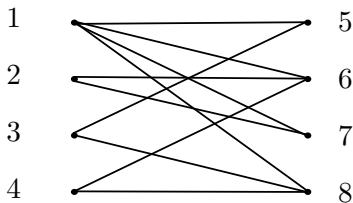
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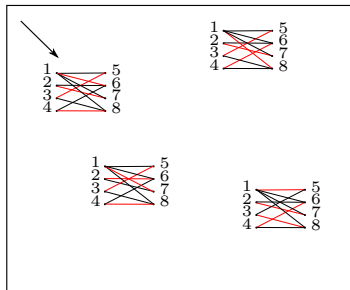
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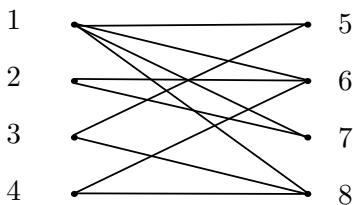
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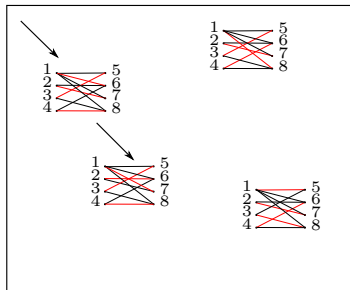
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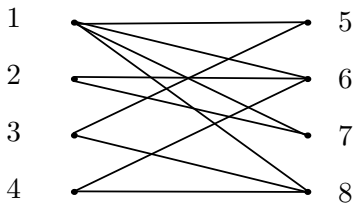
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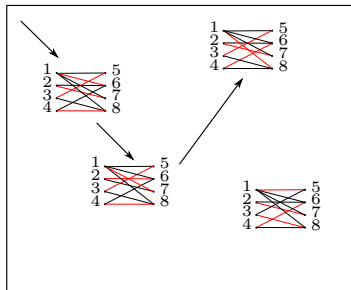
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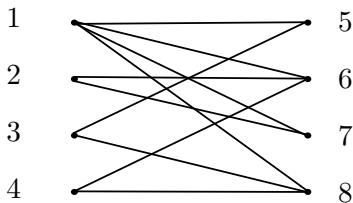
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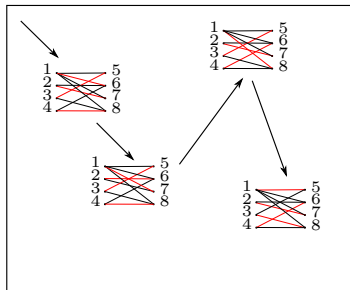
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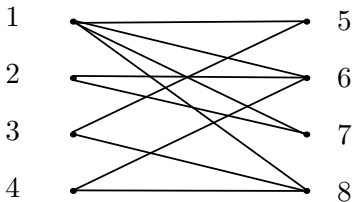
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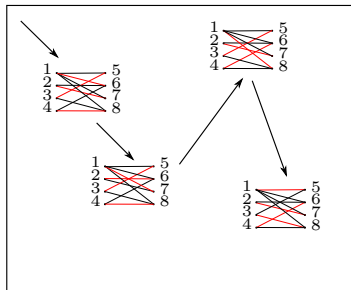
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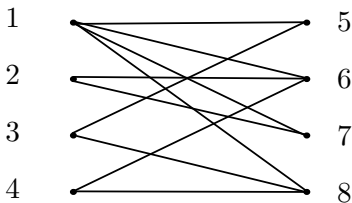
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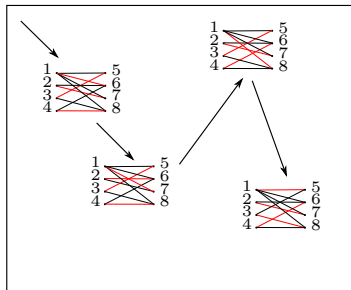
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Modelling

Generating Planar map with constraints

Overview of the algorithm

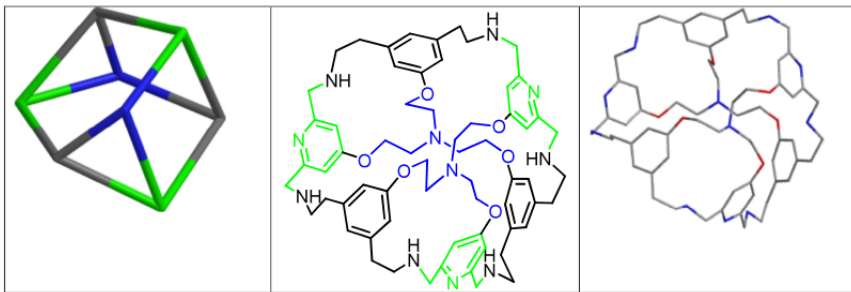
- Generating backbones

- Folding the map

- Computing the indices

Overview of frequent questions

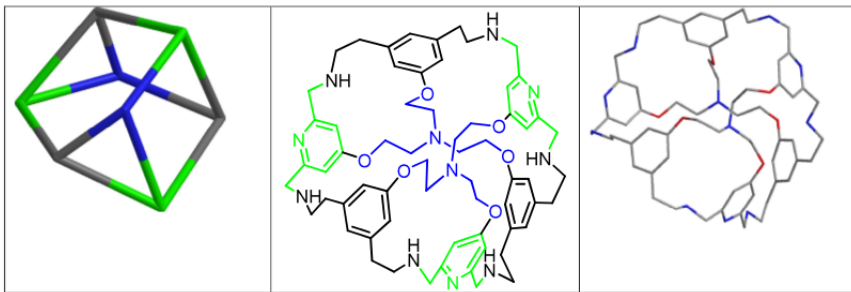
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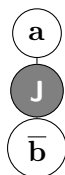
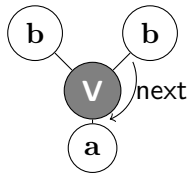
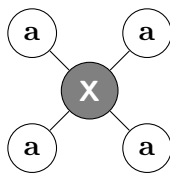
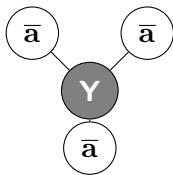
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The motifs

Definition

A map $G = (V_c, V, E, \text{next})$ is a **motif** if

1. V_c contains only one vertex c called the center
2. each vertex in V is colored with a color in \mathcal{A} a fixed alphabet
3. $E = \{(c, u), u \in V\}$
4. next gives an order on the edges of c



Map of motifs

Definition

A connected planar map $G = (V_c, V, E, \text{next})$ is a **map of motifs** based on \mathcal{M} if,

1. each vertex in V is connected to at most one vertex in V , which is of the complementary colour.
2. when all edges between vertices in V are removed, the remaining connected components must all be motifs of \mathcal{M}

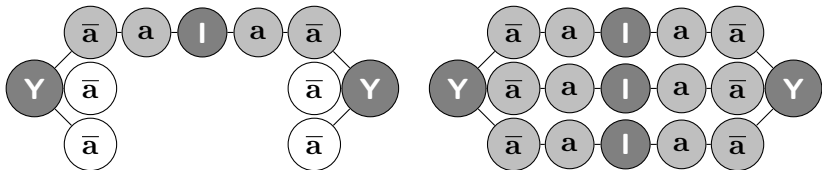


Figure: Example of two maps of motifs based on $\mathcal{M} = \{Y, I\}$, the first map is **unsaturated** while the second map is **saturated**.

Molecular map

Definition

Let $G = (V_c, V, E_G, \text{next}_G)$ be a saturated map of motifs based on \mathcal{M} , we define the **molecular map** $M = (V, E_M, \text{next}_M)$:

1. $V = V_c$
2. $(c_1, c_2) \in E_M$ if it exists a path (c_1, u, v, c_2) in G
3. $\text{next}_M((c, c_1)) = (c, c_2)$ if it exists two paths (c, u_1, v_1, c_1) and (c, u_2, v_2, c_2) in G and $\text{next}_G((c, u_1)) = (c, u_2)$

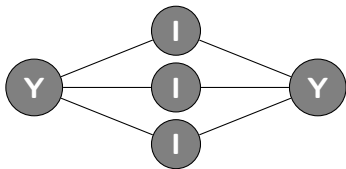


Figure: The molecular map corresponding to the saturated map of motifs in Fig. 1

The indices

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1. Constraint on the edges: possible chemical connections
2. The *size* of a cut $S = (S_1, S_2)$ is the number of edges with one end in S_1 and the other in S_2 .

$$sparsity(S) = \frac{size(S)}{\min(|S_1|, |S_2|)}$$

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We want to generate, given a set of motifs \mathcal{M} and a size n , all molecular maps based on \mathcal{M} and of size n .

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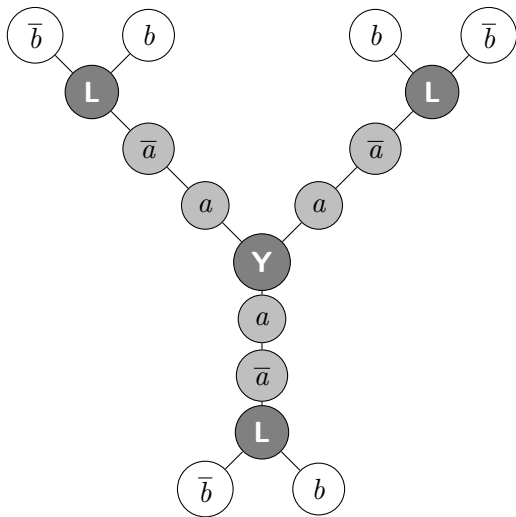
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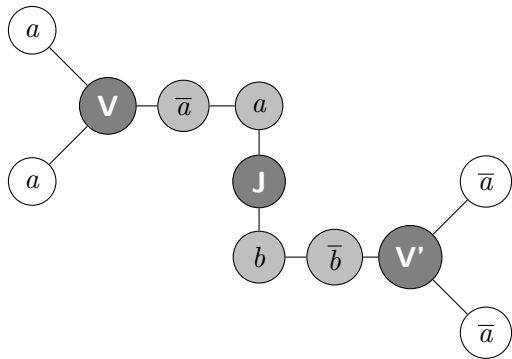
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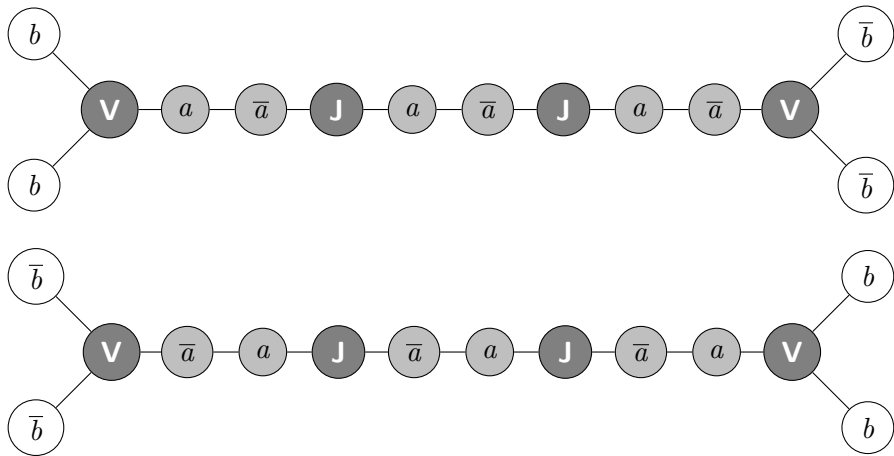
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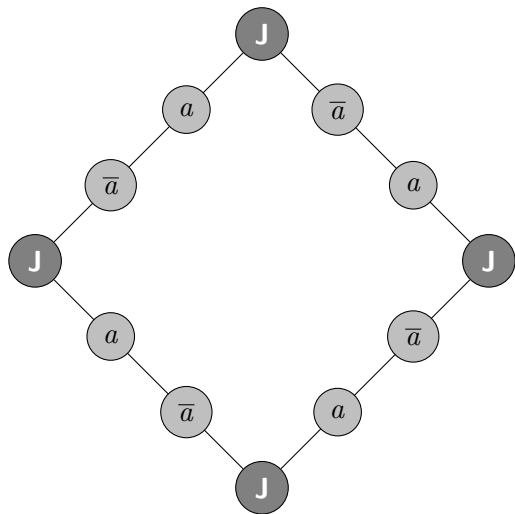
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Fold and outline

The **fold** operation on the vertices u and v is adding the edge (u, v) to G . Valid when u and v are:

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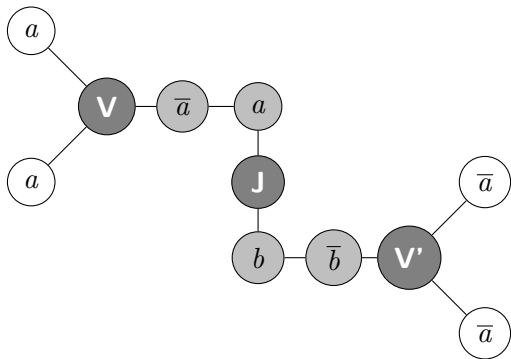
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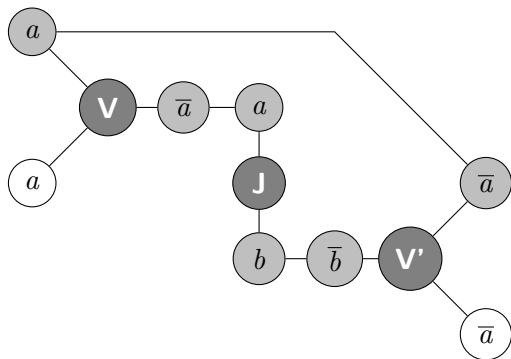
Example



$$\text{outline} = \{a, \bar{a}, \bar{a}, a\}$$

Figure: A map of three motifs on $\mathcal{A}_M = \{\mathbf{V}, \mathbf{V}', \mathbf{J}\}$ and its outline before a fold operation.

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When is a map foldable?

The outline is a circular sequence of vertices. The fold remove two vertices of compatible colours.

Enough to work with the sequence of colours of the vertices. In the previous example $a\bar{a}\bar{a}a$.

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A map is almost foldable if for every letter in $a \in \mathcal{A}$, there are as many vertices labeled with a and \bar{a} .

Since a foldable backbone is always almost foldable, we would like to enumerate **almost foldable backbones only**.

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Another dynamic programming algorithm:

- ▶ Build the matrix M such that $M_{i,j}$ is true if and only if the subword $w_i \dots w_j$ is foldable.
- ▶ In the enumeration algorithm a partially folded word is a **set of subwords**.
- ▶ At each step reduce the **first non folded letter** with all possible letters given by M .
- ▶ The preprocessing is in $O(n^2)$ and the delay is linear.

How to fold a map?

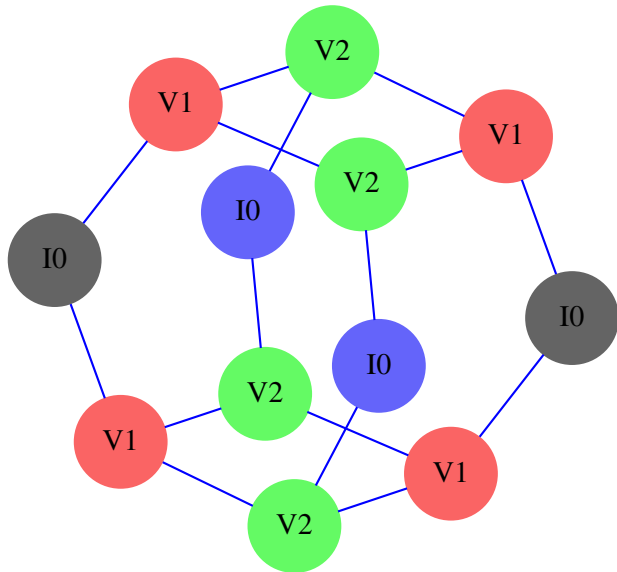
We call **result** of a sequence of reductions the set of pairs (i, j) such that the sequence has paired i and j .

Problem: given a word, we want to generate the results of all sequences of reductions which yield an empty word.

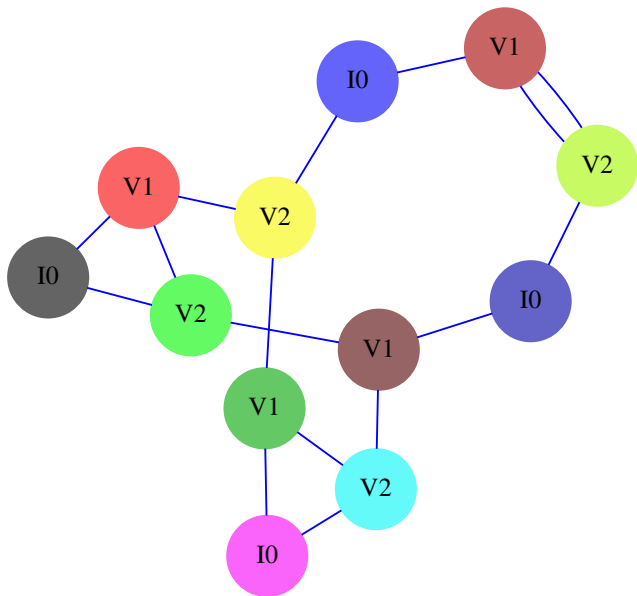
Another dynamic programming algorithm:

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The algorithm generates many **duplicates**.

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