

Complexity of enumeration and a practical example in cheminformatics

Yann Strozecki

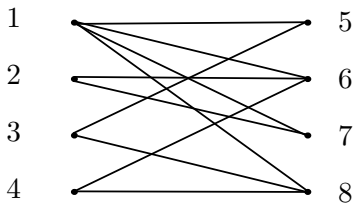
Université de Versailles St-Quentin-en-Yvelines
Laboratoire PRiSM

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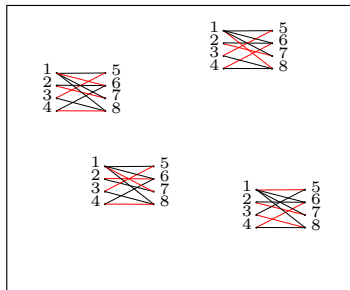
Enumeration problems

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

Perfect matchings:



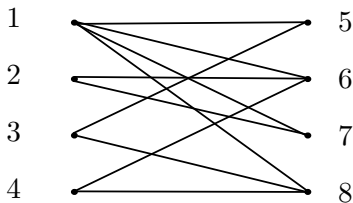
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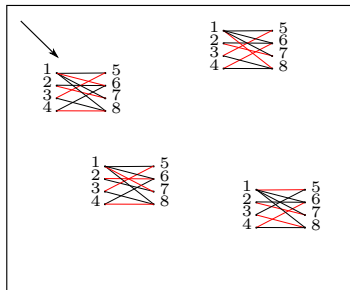
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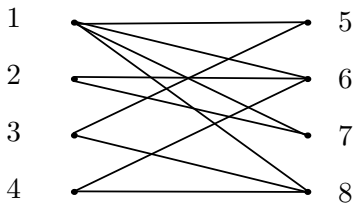
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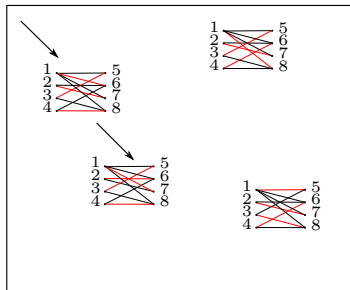
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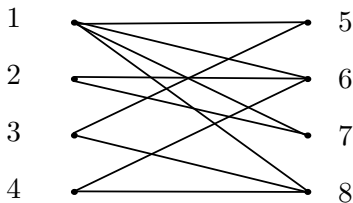
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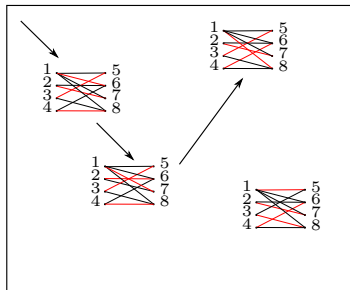
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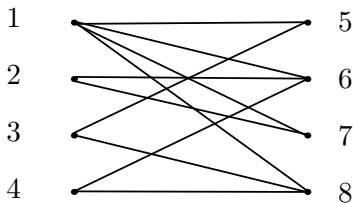
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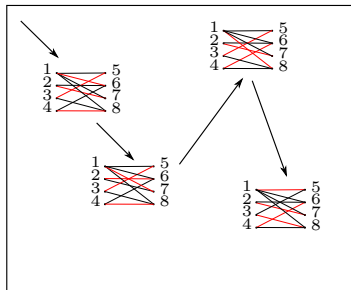
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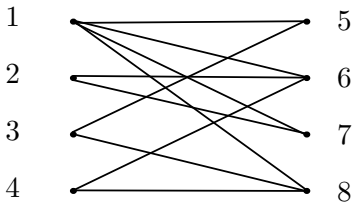
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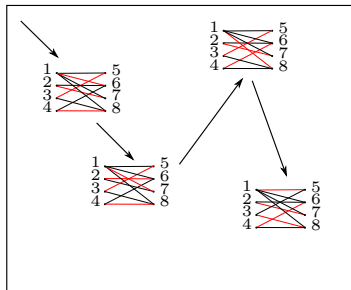
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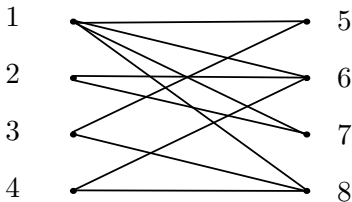
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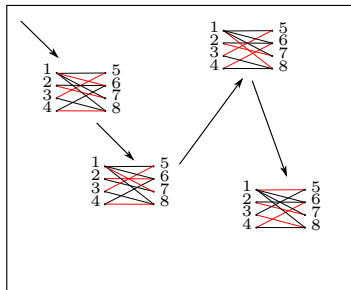
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Enumeration Complexity

Theoretical framework

Methods for enumeration

A practical enumeration problem from cheminformatics

Enumeration of planar maps with constraints

Our algorithm: Kékulé

Framework

Polynomially balanced predicate $A(x, y)$, decidable in polynomial time.

- ▶ $\exists?yA(x, y)$: **decision** problem (class NP)
- ▶ $\#\{y \mid A(x, y)\}$: **counting** problem (class #P)
- ▶ $\{y \mid A(x, y)\}$: **enumeration** problem (class ENUMP)

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1. The total time

- ▶ polynomial total time: TOTALP (Transversal hypergraph)
- ▶ constant amortized time: CAT (Tree enumeration)

2. The delay

- ▶ incremental polynomial time: INCP (Circuits of a matroid)
- ▶ polynomial delay: DELAYP (Perfect Matching)
- ▶ Constant or linear delay
 - ▶ A two steps algorithm: preprocessing + generation
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- ▶ SDelayP: produce the next solution from the last one only in polynomial time
- ▶ QueryP: produce the i^{th} solution in polynomial time

Proposition

Conditional separation under $P \neq NP$ hypothesis:

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Randomized enumeration algorithm

Two ways of introducing randomness:

1. We can allow some randomization in our algorithms. They must satisfy that all solutions are enumerated correctly with probability $1 - \epsilon$.
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If A has a polytime almost uniform random generator, then $\text{ENUM}\cdot A \in \text{INCP}$.

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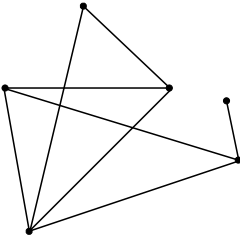
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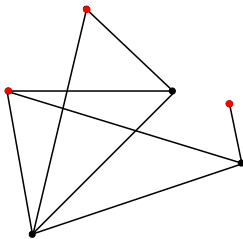
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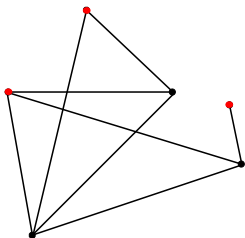
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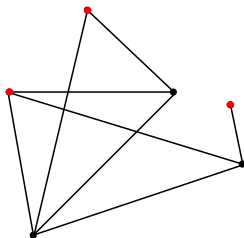
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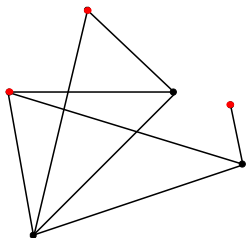
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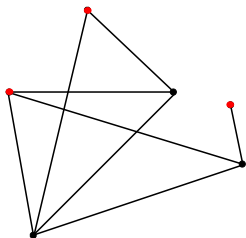
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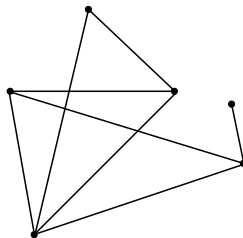
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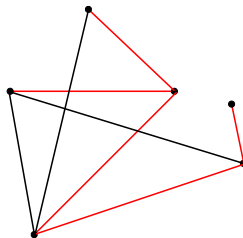
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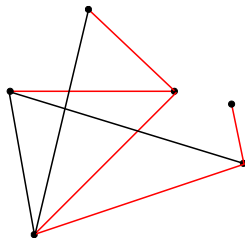
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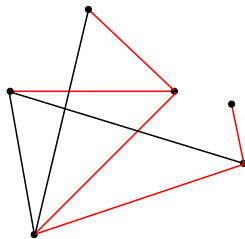
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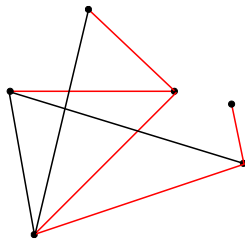
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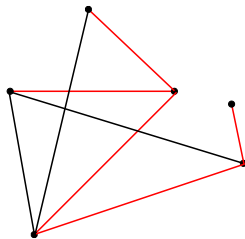
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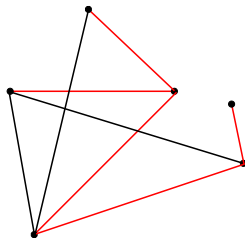


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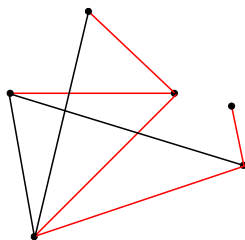


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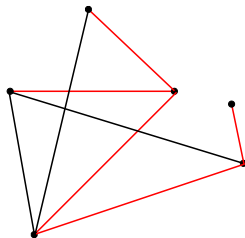


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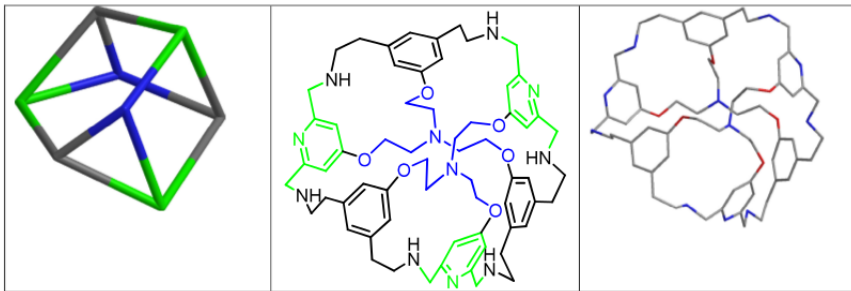
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A practical enumeration problem from cheminformatics

- Enumeration of planar maps with constraints

- Our algorithm: Kékulé

Nice pictures to impress the layman

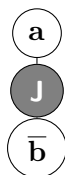
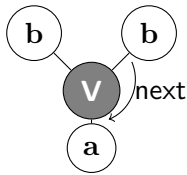
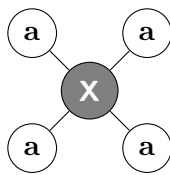
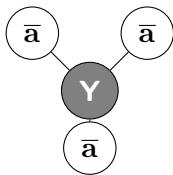


The motifs

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}

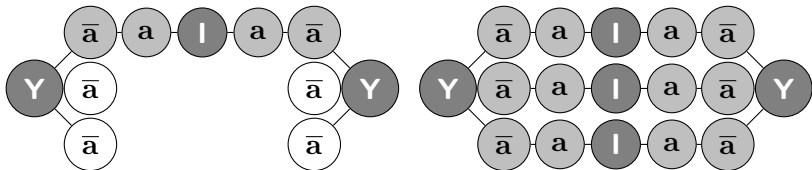


Figure : Example of two maps of motifs based on $\mathcal{M} = \{\mathbf{Y}, \mathbf{I}\}$, the first map is **unsaturated** while the second map is **saturated**.

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 $\text{next}_G((c, u_1)) = (c, u_2)$

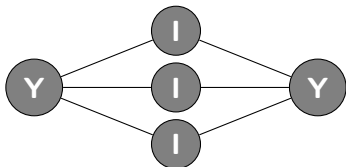


Figure : The molecular map corresponding to the saturated map of motifs in Fig. 1

The indices

Why is a molecular map a **good** representation of a **molecula** ?

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 .

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

Sound molecula have **high minimum sparsity**.

3. Planar graphs and large automorphism groups \equiv spherical shape.
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The problem

Enumeration problem

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 .

The number of maps is **exponential** in n . We would like an algorithm in DELAYP or at least in linear total time.

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We generate different families of **backbones**. Their free vertices (of degree 1) will be folded to get a saturated map.

First idea: generate trees. Since every connected map has a spanning tree, it will make the generation exhaustive.

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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:

1. free
2. of complementary colors
3. in the same face of G

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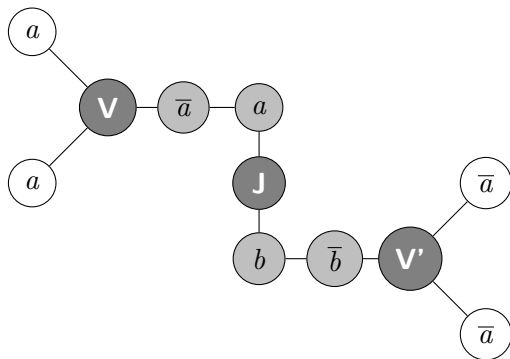
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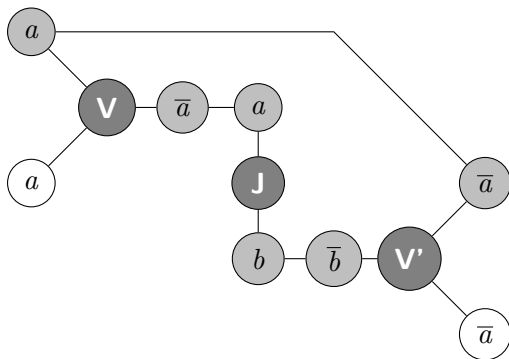
Example



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

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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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} .

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Dynamic programming algorithm:

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We generate a k -dimensional array which allows to decide whether a path can be extended by l motifs and be almost foldable.

Takes $O(n^{k+1})$ but there are about C^n paths and it reduces their number by a large factor.

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Let's all do enumeration

Open Questions

Enumeration:

1. Separate DELAYP from INCP modulo ETH
2. Design a reduction compatible with low enumeration classes.

Cheminformatics:

1. A CAT algorithm to generate maps of motifs which are trees
2. A smaller family of backbones which still make the generation exhaustive.
3. A better fold algorithm (constant delay, linear precomputation).
4. A way to avoid some foldings.