

# Higher-dimensional subdiagram matching

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- Formalisation of higher category theory, higher algebra, homotopy theory or combinatorial topology.

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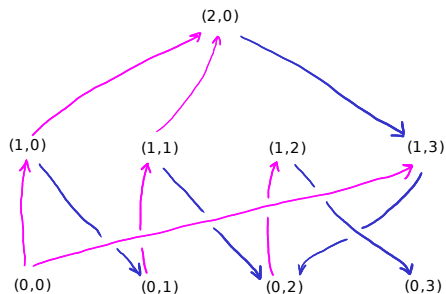
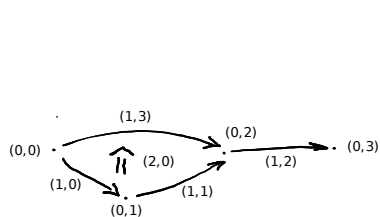
- Formalisation of higher category theory, higher algebra, homotopy theory or combinatorial topology.
- Diagram rewriting as a model of computation.

Goal:

Relate the derivational complexity of a higher-dimensional rewrite system to the worst-case time complexity of an implementation of a machine operating by higher-dimensional diagram rewriting.

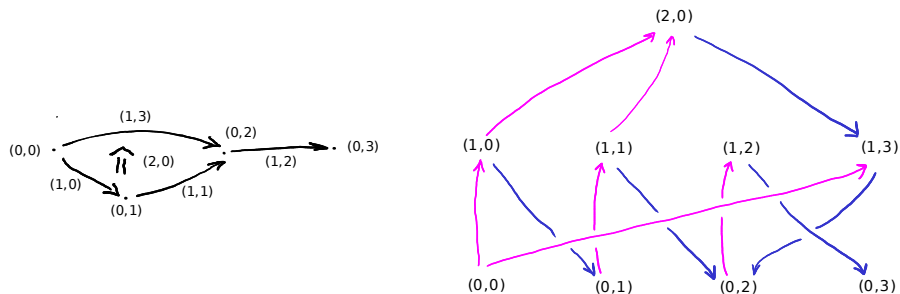
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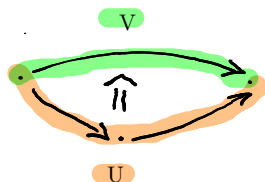
The well-formed shapes of diagrams form an inductive subclass of oriented graded posets called *regular molecules*.

## Regular molecules

- (Point): • is a regular molecule.

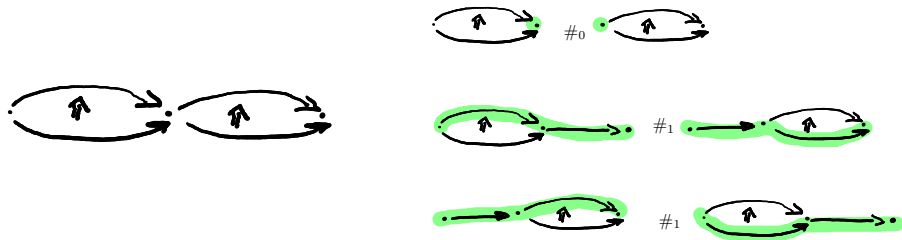
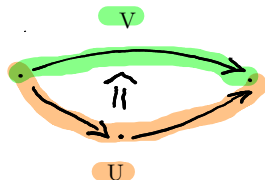
## Regular molecules

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- (Atom): Let  $U$ ,  $V$  be regular molecules satisfying some conditions. Then  $U \Rightarrow V$  is a regular molecule.



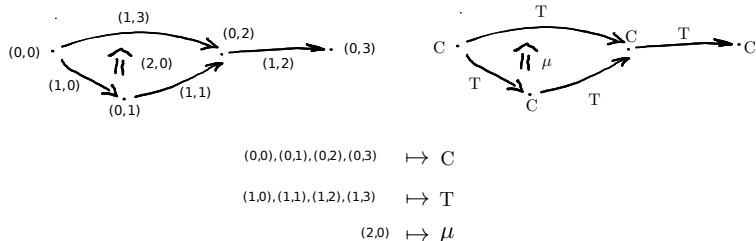
# Regular molecules

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- (Atom): Let  $U, V$  be regular molecules satisfying some conditions. Then  $U \Rightarrow V$  is a regular molecule.
- (Paste): Let  $U, V$  be regular molecules satisfying some conditions. Then the pasting  $U \#_k V$  is a regular molecule.

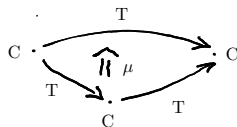


# Diagrams

A diagram in our setting is a labelling of a regular molecule into a set of variables.



A cell is a diagram whose shape has one maximal element. This represents a basic rewrite.



# Constructing regular molecules

Joint work with Amar Hadzihasanovic.

- Data structures for topologically sound higher-dimensional diagram rewriting.
  - ACT 2022, arXiv: 2209.09509.
  - Traversal algorithm for solving the isomorphism problem for regular molecules, running in time  $O(n^2 \log n)$ .
  - Already implemented in **rewalt** - <https://rewalt.readthedocs.io>.

# Diagrammatic machines

A machine that operates by higher-dimensional rewriting works as follows:

- It has a list of  $(n + 1)$ -dimensional rewrites whose input and output are  $n$ -dimensional diagrams.
- Given an  $n$ -dimensional diagram  $t$  as input, the machine tries to match one of the input boundaries of a rewrite rule to a rewritable subdiagram (portion) of  $t$ .
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Question: Is the obvious cost model that attributes constant cost to each rewrite step a “reasonable” cost model?

## Higher-dimensional subdiagram matching

Given diagrams  $s : V \rightarrow \mathbb{V}$  and  $t : U \rightarrow \mathbb{V}$  such that  $\dim(V) = \dim(U) = n$  and  $V$  is round, find if any all the inclusions  $\iota : V \hookrightarrow U$  such that:

- $\iota(V) \sqsubseteq U$   
( $\iota(V)$  is a factor in a pasting decomposition of  $U$ ),
- $s = \iota; t$   
(the labels match).

## Higher-dimensional subdiagram matching

Given diagrams  $s : V \rightarrow \mathbb{V}$  and  $t : U \rightarrow \mathbb{V}$ , the subdiagram matching problem can be split into three subproblems:

- 1 (Molecule matching problem) find, if any, the inclusions of  $V$  into  $U$ ;
- 2 (Rewritable submolecule problem) decide if an inclusion is a *submolecule* inclusion;
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Problem 1 admits an algorithm that has a low-degree polynomial time bound in the sizes of  $U$  and  $V$ .

Problem 3 is trivial and should take linear time in the size of the diagram.

Problem 2 turns out to be more challenging.

# Rewritable submolecule problem

## Theorem

*The problem of deciding if an inclusion is a rewritable submolecule inclusion in dimension  $n$  can be solved in time*

$$O\left(\prod_{k \leq n} |U_k|! |U_k|\right),$$

*where  $U_k$  is the set of  $k$ -dimensional elements of  $U$ .*

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### Theorem

*Every diagram of dimension  $\leq 3$  is stably frame-acyclic.*

## Rewritable submolecule problem

**Goal:** Find if  $V$  is a factor in a pasting decomposition of  $U$ .

**Problem:** There are many possible decompositions. We need to “constrain” the space of possible decompositions.

**The algorithm for arbitrary  $n$ :** “Parametrise” this space by topological sorts of a DAG with at most  $|U_n|$  number of vertices.

**For stably frame-acyclic regular molecules:** Either all topological sorts work or none works.

## Future work

- Is there a PTIME algorithm for subdiagram matching in dimension 4?
- Is the problem of subdiagram matching in dimension 4 NP-complete?

Thank you!