Dimer Interpretations in Cluster Algebras: Smashing, Splitting, and Finding the Perfect Match

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Introduction

- Consider cluster variables in cluster algebras of finite types
- Give a new combinatorial interpretation of the f-polynomials of a cluster algebra using mixed dimers.
- We build on previous work about snake graphs



Figure 1: A smashing of two D_n single dimers

Cluster Algebra: The Basics

A **cluster algebra**, denoted as *A*, is a subalgebra of $\mathbb{Q}(x_0, \ldots, x_{n-1})$ defined by generators and relations, starting with the initial cluster $\{x_0, \ldots, x_{n-1}\}$ and a mutation in direction *j*, denoted as μ_j

$$\{x_0,\ldots,x_{j-1},\mathbf{x_j},x_{j+1},\ldots,x_{n-1}\}\xrightarrow{\mu_j}\{x_0,\ldots,x_{j-1},\mathbf{x'_j},x_{j+1},\ldots,x_{n-1}\}$$

generating a new cluster.

We call x_i an initial **cluster variable** of *i*. A cluster algebra is generated by its cluster variables.

A **quiver** is an oriented graph. An **acyclic** quiver refers to a quiver whose underlying graph is acyclic.



Throughout our work, we only consider an unweighted, finite quivers without self-loops or 2-cycles. This quiver defines a cluster algebra!

Quiver: The Mutation - Step 1

Given a quiver Q, a **mutation in direction** j, μ_j , transforms it into a new quiver Q' according to the following rules:

For every 2-path passing j such that k → j → i in Q, add a new edge k → i in Q'.



Quiver: The Mutation - Step 2

• Reverse direction of all edges incident to j in Q'.



Quiver: The Mutation - Step 3

• Delete all 2-cycles in Q'.



Here we go!

Algebraically, the mutation at direction j gives the following relation for a new cluster variable x'_i :

$$x_j x_j' = \prod_{i \to j} x_i + \prod_{j \to k} x_k$$

where the multiplication term is 1 if no edges suit the condition and parallel edges are accounted with multiplicity.

Quiver: The Mutation in Terms of Cluster Variables

In our example, $j \rightarrow k$ twice and $i \rightarrow j$; therefore, we obtain the relation

$$x_j x_j' = x_k^2 + x_i.$$



Quiver: The Mutation-Equivalent Dynkin Diagram

Theorem (Fomin-Zelevinsky 2002)

A connected, unweighted quiver is mutation equivalent to an oriented Dynkin diagram of the following types: A_n, D_n, E_6, E_7 or E_8 .

In other words, mutating a quiver gives rise to a finite cluster algebra exactly when the quiver has an underlying graph that is a Dynkin diagram of type A_n , D_n , E_6 , E_7 or E_8 .



F-Polynomial: The Basic Idea...

The **principal extension** of a quiver Q is formed by adding shadow vertices i' for every vertex i of Q and shadow edges $i' \rightarrow i$.

Each new shadow i' is assigned to a shadow cluster variable y_i .





the principal extension of Q

Given a quiver Q and its principal extension, the **F-polynomial** of a vertex *i* is obtained from the current cluster variable of *i* by setting every initial cluster variable x_i to 1.

By setting every initial cluster variable x_j to 1, the F-polynomial is in fact in the shadow cluster (y_0, \ldots, y_{n-1}) .

F-Polynomial: Example

Suppose we have the following quiver Q and its principal extension:



The initial cluster is $\{x_0, x_1, x_2\}$. Setting every x_i to 1, the initial F-polynomial for every vertex is simply 1.

F-Polynomial: Example cont.

We mutate at vertex 1 and obtain the following quiver:



This mutation gives us the expression:

$$x_1 x_1' = \prod_{i \to 1} x_i + \prod_{1 \to k} x_k = x_2^2 y_1 + x_0.$$

By setting every x_i to 1, we have that the F-polynomial of vertex 1 is now $\frac{1^2y_1+1}{1} = y_1 + 1$.

F-Polynomial: Combinatorial Interpretation

Following previous works, we are able to find a bijection between a quiver of finite type and its square-free F-polynomials with the hexagon-square model, whose edges have a single dimer covering.

This bijections maps the F-polynomial of a quiver, as a consequence of mutation, with a specific transformation of the matching of the hexagon-square model.



F-Polynomial: Combinatorial Interpretation cont.

Another example where the F-polynomial is $1 + y_1 + y_2$.



F-Polynomial: Single Dimer

Given a graph G, a **single dimer**, or equivalently a **perfect matching**, on G is a set of edges such that each vertex is touched exactly once.



F-Polynomial: The Flip

Given a square or hexagon graph and its perfect matching, the **flip** of the graph is a transformation that changes the initial perfect matching to another perfect matching.



the two perfect matchings of the square graph



the two perfect matchings of the hexagon graph

F-Polynomial: The Account Factor for The Flip

For each square/hexagon graph, we assign it the **account factor**, denoted here as y, to keep track of the number of flips applied to the graph. Then,

- A minimal matching is the dimer covering of a graph that allows us to flip in given sequence in order to reach all possible dimer coverings, without having to perform flips that are involutions in this sequence. We assign it a value of 1.
- We flip a minimal matching to get another perfect matching, assigned with a value y.



Another example:





the single dimers of the hexagon graph

F-Polynomial: Summing up the Values

 F-polynomial is the sum of values obtained from every possible flip sequence.

We reproduce our earlier example here where the F-polynomial is $1 + y_1 + y_2$.



Different minimal matchings usually represent different F-polynomials.

Compare the following example of a two-square graph to the above example.



the single dimers of the two-square graph

Introducing a Hexagon for our Model

We focus on vertex 2 of the D_n case:



The Attachment Rule: Where to Place Squares and Hexagons

Based on directions of edges. For the "head" of the D_n :



The Attachment Rule: Where to Place Squares and Hexagons cont.

Based on directions of edges. For the "tail" of the D_n :



Attachment Rule: Cont.



Attachment Rule: Cont.



Working with our model: Terms we need

An **A-type tail** (or simply *tail*) is the portion of a dimer matching that corresponds to indices ≥ 3 in a given quiver. The *length* of a tail refers to the highest indexed vertex in the quiver.

Interior edges are edges in the perfect matching of the A-type tail that occur between two squares in a snake graph. All other edges of the tail are deemed *boundary edges*. (Rabideau)



Figure 2: Interior edges in purple, boundary in blue for a tail of length 8

Double Dimers: Remove Limitation of Single Dimer

Applying a flip twice to a single dimer square or hexagon yields the original matching. This means that we **cannot** use a single dimer model to represent F-polynomials with squared terms.

We introduce a new matching: a **double dimer** is the matching in which each vertex is touched by exactly two edges. A term y_i^2 in the f-polynomial corresponds to a double dimer matching of *i*:



For the D_n case, we need to use both single and double dimers, giving rise to a **mixed dimer**.

Mixed Dimers: Additional Rule

Our mixed dimer model has to obey **connectivity rules**: the vertices labeled with the same colored circles must be connected by the red edges of our matching.



Figure 3: Using our rules for a D_4 quiver

Working with our model: Terms we need

A **revolution** is a source-inducing mutation sequence through every vertex in the quiver. Going through n-revolutions of the quiver produces all possible f-polynomials (Schiffler).

A **batch** is the set of F-polynomials obtained after a revolution, numbered in order. The *kth* batch is produced by the *kth* revolution

Let's Make a Table

We want to know all possible dimer configurations for any f-polynomial for this D_n "all right" quiver, where we use a source-inducing mutation sequence along the A-type tail:



Figure 4: D_n quiver with all arrows pointing right

Table

Suppose we want to make a table of the f-polynomials we can generate by mutating our D_n "all right" quiver through n-1 revolutions.

Figure 5: The first few entries of a table of f-polynomials corresponding to a specific vertex and a batch

A-type Tail- Solved



Figure 6: The upper right triangle of the dimer table for D_n "all right"

How do we complete the table?

From examining the f-polynomials, we know the last row of the table is single dimers



Figure 7: The tail length decreases by one square as we move left to right

What about the rest of the table?

Do we know anything about what these mixed dimers look like?



Figure 8: We need to focus on the mixed dimers in this table

Splitting and Smashing

Suppose S is a mixed dimer. We can split S into two single dimers, so that when we smash them together, we get S back.

We want to show that M # N = S, where M and N are dimers from our table according to specific rules.



Figure 9: S is a mixed dimer we want to split

What do N and M look like?

Suppose S has I as its highest indexed square with a doubled covering, and that S has a length of j, where $j \ge l + 1$. Then S=M#N, where we have:



Figure 10: N has length j, M has length l

Mixed Dimers and Diamonds

We want to look at a diamond of mixed dimers in our table. From the f-polynomials, $AD - BC = Y_{term}$. We are able to split each mixed dimer in this diamond into these specific single dimers:



Figure 11: A diamond recurrence within our table

Helper Lemmas

Lemma

Consider the D_n quiver with all arrows pointing to the right. Let α and β refer to possible source-inducing flip-sequences for two single dimers, M_{α}^{l} and N_{β}^{j} respectively, where M_{α}^{l} has length l and N_{β}^{j} has length j, and $j \ge l + 1$. The smashings $M_{\alpha}^{l} \# N_{\beta}^{j}$ violate connectivity only if $N_{\beta}^{j} = N_{max}^{j}$; when $\beta = \{j, ..., 1, 0\} = max_{N}$ and $\alpha \ne \{l, ..., 3, 2\} = max_{M}$.



Figure 12: We flip M at I, ..., k and smash with N_{max}

Bad Smash!

There is no path of edges to get from one orange vertex to the other! Same problem for purple vertices!



Figure 13: We flip M at I, ..., k and smash with N_{max} to get this mixed dimer

The Forbidden Split

Lemma

AD has one extra matching that cannot be split into B and C. This matching is the one that corresponds to $A_{min} # D_{max}$.

Theorem

The unsplittable matching $A_{min} \# D_{max}$ corresponds to the extra Y term in the f-polynomial recurrence in our diamond.



Figure 14: $A_{min} \# D_{max}$ results in a split that violates connectivity



Our goal for future work is completing more tables for different orientations of the quiver (not just all arrows pointing to the right).

Given an acyclic D_n quiver, we want to prove the rules for drawing its minimal matching.