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MUTATIONS AND POINTING FOR BRAUER TREE ALGEBRAS

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Abstract

Brauer tree algebras are important and fundamental blocks in the representation theory of finite dimensional algebras. In this research, we present a combination of two main approaches to the tilting theory of Brauer tree algebras.

The first approach is the theory initiated by Rickard, providing a direct link between an ordinary Brauer tree algebra and the Brauer star algebra. This approach was continued by Schaps-Zakay with their theory of pointing the tree.

The second approach is the theory developed by Aihara, relating to the sequence of mutations from the ordinary Brauer tree algebra to the Brauer star algebra. Our main purpose in this research is to combine these two approaches.

We first find an algorithm based on centers which are all terminal edges, for which we are able to obtain a tilting complex constructed from irreducible complexes of length two [13], which is obtained from a sequence of mutations.

In [1], Aihara gave an algorithm for reducing from tree to star by mutations and showed that it gave a two-term tree-to-star complex. We prove that Aihara's complex is obtained from the corresponding completely folded Rickard tree-to-star complex by a permutation of projectives.

1. INTRODUCTION

This work concerns Brauer tree algebras, a widely studied class of algebras of finite representation type which includes all blocks of cyclic defect group in modular group representation theory. A block of cyclic defect group is a Brauer tree algebra and its Green correspondent is a Brauer star algebra. Rickard proved [10] that every Brauer tree algebra has a tilting complex which makes it derived equivalent to the corresponding Brauer star algebra. Schaps-Zakay [13] , [14] showed that the tilting complexes in the opposite direction can be constructed from irreducible projective complexes of length two. This is the all-at-once approach to the theory.

The other main approach is the step-by-step approach going back to König and Zimmermann [6], later formulated in terms of mutations by Aihara [1] and used recently by Chan [3] and Zvonareva [17]. In this paper we propose to combine and compare the two approaches.

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Most of this work appeared in the M.Sc. thesis of the second author.

2. DEFINITIONS AND NOTATION

2.1. POINTED BRAUER TREES. We first define Brauer tree algebras.

DEFINITION 2.1. Let e and m be natural numbers. A *Brauer tree* of type (e, m) is a finite tree $(V, \mathcal{E})$ where V is the set of vertices, $\mathcal{E}$ is the set of edges, $|\mathcal{E}| = e$, together with a cyclic ordering of the edges at each vertex and a designation of an exceptional vertex which is assigned multiplicity m.

The set of all edges incident to vertex u is denoted by $\mathcal{E}(u)$. By "cyclic ordering" we mean that for each edge E in $\mathcal{E}(u)$ there is a 'next' edge in $\mathcal{E}(u)$ and that edge has a next edge in $\mathcal{E}(u)$, etc., until each edge of u is counted exactly once, in which case E is the next one. We note that if E and F are the only edges of u then F is next after E and E is next after F.

Every Brauer tree can be embedded in the plane in such a way that the cyclic ordering on each $\mathcal{E}(u)$ is the counterclockwise direction. The exceptional vertex will be drawn as a black circle and the other vertices as open circles. Two important examples of Brauer trees are:
(i) The *star* with the exceptional vertex in the center.
(ii) The *linear tree*, which includes, for example, the Brauer trees of blocks of cyclic defect in the symmetric groups.

We relate Brauer trees to the structure of algebras.

DEFINITION 2.2. An algebra A is called a *Brauer tree algebra* if there is a Brauer tree such that the indecomposable projective A-modules can be described by the following algorithm:

(i) There is a bijection between the edges of the tree and the isomorphism classes of simple A-modules, i.e. each edge is labelled by the corresponding isomorphism class.

(ii) If S is a simple A-module and P_S is the projective cover of S then $P_S \supseteq \mathrm{rad}(P_S) \supseteq \mathrm{soc}(P_S) \cong S$ and $\mathrm{rad}(P_S)/\mathrm{soc}(P_S)$ is a direct sum of one or two uniserial modules corresponding to the two vertices of the edge, with composition factors determined by a counterclockwise circuit around the vertex ending at S. When the multiplicity m is greater than 1, the circuit is made m times altogether.

The Brauer tree algebras for a given tree of type (e, m) are Morita equivalent, and this Morita equivance is an isomorphism if there is a map of the tree to itself preserving the cyclic ordering for which the degrees of the simples at corresponding vertices are the same. The skeleton is the Morita equivalent Brauer tree algebra in which every simple has degree 1. Even when the algebra which interests us is the block of a group algebra, we will not use the actual block but rather its skeleton.

DEFINITION 2.3. Let e and m be natural numbers with $e > 1$. Let K be any field containing a primitive eth root of unity ξ. Let $\widehat{n} = em + 1$. Let the cyclic group $C_e = \langle g \rangle$ act on the truncated polynomial ring $A = K[x]/x^{\hat{n}}$, $g : x \longmapsto \xi x$. The *Brauer star algebra* of type (e, m) is the skew group algebra $b = A[C_e]$, in which g and x obey the relation $g^{-1}xg = \xi x$. The algebra b has e distinct simple modules, corresponding to the idempotents

$$f_i = \frac{1}{e}\sum_{j=0}^{e-1} \xi^{-ij} g^j, \quad i = 1, .., e,$$

and satisfying $f_i x = x f_{i+1}$.

The corresponding indecomposable projective left modules are denoted by $P_i = bf_i$, $i = 1, \dots, e$. Each P_i is uniserial, and the projective cover of $\mathrm{rad}(P_{i+1})$ is P_i. We let $\{x^s f_i\}_{s=0}^{em}$ be a basis for P_i, and define the following maps:

$$\varepsilon_i : P_i \to P_i, \quad \varepsilon_i(f_i) = x^e f_i$$

$$\tilde{h}_{ij} : P_i \to P_j, \ \tilde{h}_{ij}(f_i) = x^k f_i, \ k \equiv j - i \mod e, \quad 0 \leq k < e.$$

For $i \neq j$, we denote $\tilde{h}_{ij}$ by h_{ij}, and for $i = j$ by id_i. For any $0 \leq \ell \leq m$ we call a map $\varepsilon_j^\ell \tilde{h}_{ij} \left(= \tilde{h}_{ij}\varepsilon_i^\ell\right)$ *normal homogeneous* of degree $\ell e + k$,
where

$$k \equiv j - i \mod e, \quad 0 \leq k < e.$$

Definition 2.4. A cochain map $l_\bullet$ between $C^\bullet$ and $D^\bullet$ is called *normal homogeneous* if each component l_i of $l_\bullet$ is normal homogeneous.

Definition 2.5. We call the homomorphism $\varepsilon_i^m : P_i \to P_i$ the *socle map*, for the obvious reason that it maps the top of P_i into its socle $\langle x^{em} f_i\rangle$.

Tilting complexes were introduced by Rickard in [9] and a complete treatment of tilting complexes in group representation theory can be found in [7]. Rickard showed [9] that we can work with complexes of projective modules and consider all maps up to equivalence in the homotopy category. A general introduction to complexes, chain maps and homotopy can be found in [15]. The shift $T[n]$ of a complex T shifts it n degrees to the left if n is positive, and $|n|$ degrees to the right if n is negative. A complex T of projective modules is a partial tilting complex if it has no chain maps from itself to a non-trivial shift of itself which are not homotopic to the zero map. A partial tilting complex becomes a tilting complex if it is sufficiently large that all the indecomposable projectives can be obtained from the indecomposable components of the complex by recursively taking mapping cones, direct summands and shifts (Theorem 6.3.3, [7]). The number of indecomposable components in a tilting complex will equal the number of simples in the original algebra.

A partial tilting complex T for the Brauer star algebra b is called *two-restricted* if it is a direct sum of shifts of the indecomposable complexes

$$\begin{array}{llllllll} S_i: & 0 & \to & P_i & \to & 0 & & \\ T_{ij}: & 0 & \to & P_i & \to & P_j & \to & 0, \quad i < j \end{array}$$

where the first nonzero component P_i of S_i and T_{ij} is in degree zero, and the second component of T_{ij} is in degree 1. The complexes $S_i[n]$ and $T_{ij}[n]$ are called *elementary.* The map from T_{ij} to T_{ij} which is ε_i^m on P_i and zero on P_j is called the *socle chain map.* It is chain homotopy equivalent to the map which is zero on P_i and $-\varepsilon_j^m$ on P_j. A basis of the endomorphism ring of a two-restricted tilting complex is given by the normal homogeneous

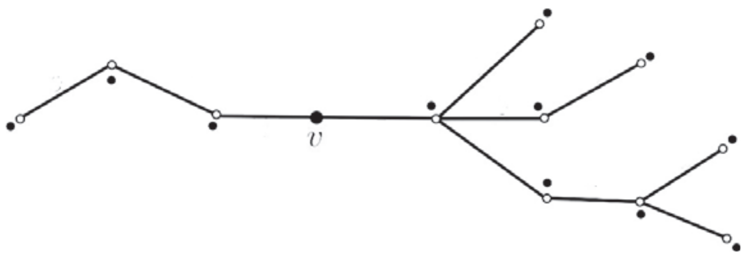

Fig. 1. A pointed Brauer tree

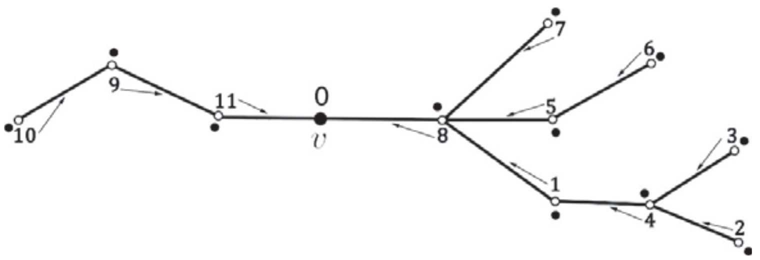

Fig. 2. From vertex numbering to edge numbering

maps defined above [13].

Definition 2.6. Let B be a Brauer tree of type (e, m). A *pointing* on B is the choice, for each nonexceptional vertex u, of a pair of edges (i, j) which are adjacent in the cyclic ordering at u. If there is only one edge i at u, then we take (i, i) as the required pair. The tree B together with a pointing is called a *pointed Brauer tree*.

Remark 2.1. Recall that we have represented each Brauer tree by a planar embedding and the cyclic ordering at each vertex u by counterclockwise ordering of the edges in the plane. We then represent the pointing (i, j) by placing a point in the sector between edge i and edge j in a small neighborhood of each non-exceptional vertex u, as in Fig.1.

Definition 2.7. Let B be a Brauer tree with vertex set V. The distance $d(u)$ of any vertex $u \in V$ from the exceptional vertex v is the number of edges in a minimal path from u to v (and hence in any path without backtracking, since the graph is acyclic). For any edge w, the vertex closest to the exceptional vertex will be called the *near end* and the other vertex will be called the *far end*. The distance of an edge is the distance of the near end.

Definition 2.8. Let B be a Brauer tree with edge set $\mathcal{E}$. A *vertex numbering* of B is a Brauer tree with all its vertices numbered by $0, 1, \ldots, e$. The exceptional vertex is numbered as 0.

An *edge numbering* of B is obtained from a vertex numbering by giving each edge the same number as the vertex at its far end.

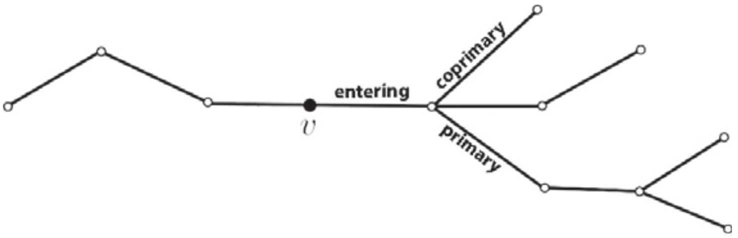

Fig. 3. Primary and coprimary edges at a vertex

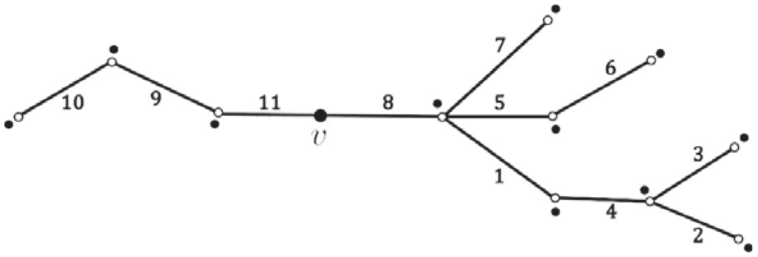

Fig. 4. The left alternating pointing and its edge numbering

DEFINITION 2.9. A *Green's walk* for a planar tree is a counterclockwise circuit of the tree as if one were walking around the tree touching each edge with the left hand. For a Brauer tree, we assume that each Green's walk begins at the exceptional vertex. A *branch* is a connected component of the tree with the exceptional vertex removed. For any branch, let the edge connected to the exceptional vertex be called the *root*.

Each pointing and each choice of an initial branch together determine a vertex numbering and an edge numbering by starting at the exceptional vertex v, taking a Green's walk around the tree which begins with the root of the designated initial branch, and numbering the vertices and corresponding edges as $1, 2, 3, \ldots, e$ as one comes to the points.

DEFINITION 2.10. At any vertex besides the exceptional vertex, we will call the first edge that one would meet on a Green's walk around the tree the *primary edge* of the vertex, and the first edge one would meet on a reversed Green's walk will be called the *coprimary edge*, as in Fig.3.

The pointing which puts the point between the entering edge and the primary edge at each vertex will be called the *ordinary pointing* and the pointing which puts the point between the entering vertex and the coprimary edge will be called the *reversed pointing*. The *left alternating pointing* has the point alternately on the left or right of the entering edge, starting on the left for the edge connected to the exceptional vertex. There is a corresponding dual pointing. In Fig.4 we have the edge numbering corresponding to the vertex numbering in Fig.2, which comes from a left alternating pointing.

As described in [14], each pointing determines a two-restricted star-to-tree tilting complex, in which the projectives of the tilting complex are taken from the Brauer star with the same (e, m) and the opposite algebra of the endomorphism ring in the homotopy category

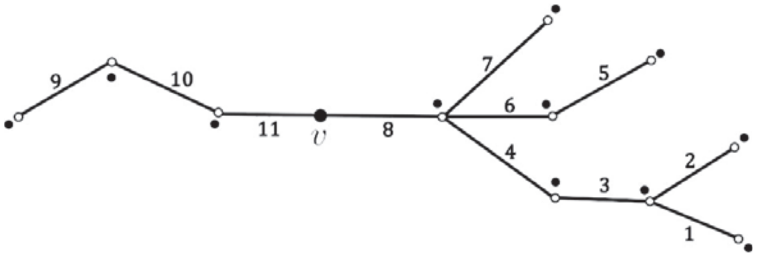

Fig. 5. The reversed pointing and its edge numbering

is isomorphic to the Brauer tree algebra of the tree which was pointed. The components T_i of this star-to-tree complex are stalk complexes for edges at the exceptional vertex and complexes $T_{ij}[-n_i]$ or $T_{ji}[-n_i + 1]$, depending on whether the point is after or before i in the cyclic ordering from the entering edge j. The shifts are adjusted so that every P_i appears in a unique degree n_i.

As an illustration, we take the reversed pointing in Fig.5. The two edges at the exceptional vertex are 8 and 11, so these are stalk complexes in degree zero, given by T_8 and T_{11} in the two-restricted tilting complex below. Connected to 8 are 4, 6 and 7. These give indecomposable tilting complexes T_{48}, T_{68} and T_{78}. Since 8 and 11 are in degree 0, this requires 4, 6, and 7 to be placed in degree -1 of the complex, and similarly for 10. At the next stage out, 3, 5 and 9 will be in degree -2, and finally, 1 and 2 will be in degree -3. Thus, with a little practice, we can read off from the two-restricted tilting complex both the shape of the tree and the choice of numbering.

The star-to-tree tilting complex of the reversed pointing of the tree given in Fig.5 is as follows:

$$\begin{array}{rccccccccccc}
T_1: & 0 & \to & P_1 & \to & P_3 & \to & 0 & & & & \\
T_2: & 0 & \to & P_2 & \to & P_3 & \to & 0 & & & & \\
T_3: & & & 0 & \to & P_3 & \to & P_4 & \to & 0 & & \\
T_4: & & & & & 0 & \to & P_4 & \to & P_8 & \to & 0 \\
T_5: & & & 0 & \to & P_5 & \to & P_6 & \to & 0 & & \\
T_6: & & & & & 0 & \to & P_6 & \to & P_8 & \to & 0 \\
T_7: & & & & & 0 & \to & P_7 & \to & P_8 & \to & 0 \\
T_8: & & & & & & & 0 & \to & P_8 & \to & 0 \\
T_9: & & & 0 & \to & P_9 & \to & P_{10} & \to & 0 & & \\
T_{10}: & & & & & 0 & \to & P_{10} & \to & P_{11} & \to & 0 \\
T_{11}: & & & & & & & 0 & \to & P_{11} & \to & 0
\end{array}$$

A different pointing would give a different tilting complex with isomorphic endomorphism ring. In the ordinary pointing, as described in [13], projectives corresponding to edges of distance zero lie in degree 0, and every other projective is in a degree corresponding to its distance from the exceptional vertex. In the reversed pointing, we get exactly the opposite, so that all projectives lie in non-positive degrees. We will show below that this reversed pointing will correspond exactly to one of our mutation algorithms.

Let us demonstrate the connection between the tree-to-star complex for a given pointing and the star-to-tree complex for the same pointing. As we see, the star-to-tree complex can be read off from the pointed Brauer tree by associating one row to each edge, connecting it to the edge at its near end, with the direction depending on the numbering. In the tree-to-star complex, we again have one row for each edge, but the projectives appearing in the row are all the projectives leading back to the exceptional vertex, the direction which is the exact opposite of the direction in the star-to-tree complex. The beauty of Rickard's algorithm in [9] was that one can generate all the projectives (the condition distinguishing a tilting complex from a partial tilting complex) by taking the mapping cone of rows corresponding to adjacent vertices along a path to the exceptional vertex. In [11] it was shown that this works as well when the complex is folded and the two tilting complexes are mutually inverse. We will denote the projectives of the tilted algebra by R_j.

Example 1 (Tree-to-star complex, [9]). In the tree with the reversed pointing given in Fig.5, the edge 2 is connected to the exceptional vertex by a path $2, 3, 4, 8$. Then, in the tree-to-star complex, the row corresponding to 2 would be a row T'_2 and the path to the closer vertex 3 would be a shorter row T'_3.

$$\begin{array}{rcccccccc}
T'_2: & 0 & \to & R_8 \to & R_4 & \to & R_3 & \to & R_2 \\
T'_3: & 0 & \to & R_8 \to & R_4 & \to & R_3 & &
\end{array}$$

We then have $R_2 = Cone(T'_3 \to T'_2)$ where the vertical maps are the identity. For comparison, since we gave the entire star-to-tree tilting complex for Fig.5, we will give the entire tree-to-star tilting complex with the same pointing:

$$\begin{array}{rccccccccc}
T'_1: & 0 & \to & R_8 & \to & R_4 & \to & R_3 & \to & R_1 \\
T'_2: & 0 & \to & R_8 & \to & R_4 & \to & R_3 & \to & R_2 \\
T'_3: & 0 & \to & R_8 & \to & R_4 & \to & R_3 & & \\
T'_4: & 0 & \to & R_8 & \to & R_4 & & & & \\
T'_5: & 0 & \to & R_8 & \to & R_6 & \to & R_5 & & \\
T'_6: & 0 & \to & R_8 & \to & R_6 & & & & \\
T'_7: & 0 & \to & R_8 & \to & R_7 & & & & \\
T'_8: & 0 & \to & R_8 & & & & & & \\
T'_9: & 0 & \to & R_{11} & \to & R_{10} & \to & R_9 & & \\
T'_{10}: & 0 & \to & R_{11} & \to & R_{10} & & & & \\
T'_{11}: & 0 & \to & R_{11} & & & & & &
\end{array}$$

The second mutation algorithm that we will consider, that of Aihara [1], will also be connected to a pointing, but in this case the correspondence will not be exact. The pointing we will need will be the left alternating pointing as in Fig.4. The tilting complex of the left alternating pointing is always of length 2, with the degree corresponding to the parity of the distance from the exceptional vertex. The tilting complex of the left alternating pointing of the tree in Fig.4 is as follows:

$$\begin{array}{lccccccc}
T_1: & 0 & \to & P_1 & \to & P_8 & \to & 0 \\
T_2: & 0 & \to & P_2 & \to & P_4 & \to & 0 \\
T_3: & 0 & \to & P_3 & \to & P_4 & \to & 0 \\
T_4: & 0 & \to & P_1 & \to & P_4 & \to & 0 \\
T_5: & 0 & \to & P_5 & \to & P_8 & \to & 0 \\
T_6: & 0 & \to & P_5 & \to & P_6 & \to & 0 \\
T_7: & 0 & \to & P_7 & \to & P_8 & \to & 0 \\
T_8: & & & 0 & \to & P_8 & \to & 0 \\
T_9: & 0 & \to & P_9 & \to & P_{11} & \to & 0 \\
T_{10}: & 0 & \to & P_9 & \to & P_{10} & \to & 0 \\
T_{11}: & & & 0 & \to & P_{11} & \to & 0
\end{array}$$

Our main theorem will be that the tilting complex resulting from composing the mutations in the Aihara algorithm will be a permutation of this tilting complex. However, in order to prove this theorem, we need to gather more information about tilting complexes and mutations.

DEFINITION 2.11. Consider a sequence $\{r_i\}_{i=1}^{\ell}$ of elements of $\{1,\dots,e\}$. Set

$$h = \widetilde{h}_{r_{l-1}r_l} \circ \cdots \circ \widetilde{h}_{r_1 r_2} = \varepsilon_{r_l}^{\alpha}\widetilde{h}_{r_1 r_l}.$$

Then the sequence is *short* if $\alpha = 0$ and *long* if $\alpha > 0$. We generally represent the sequence in the form $r_1 \to r_2 \to \cdots \to r_l$.

EXAMPLE 2. If $e \geq 3$,

- $1 \to 2 \to 3$ is short
- $1 \to 3 \to 2$ is long.

In [13] it was shown that a chain map $l_\bullet : T_{ik} \to T_{jk}$ has the identity map at P_k if $i \to j \to k$ is short and is the socle map if $i \to j \to k$ is long, and similarly for the dual map from T_{ij} to T_{ik}.

2.2. MUTATION. It is, of course, possible to define tilting complexes between two general Brauer tree algebras. Of particular importance are the tilting mutations of [1], which go back to work of Rickard [10] and Okuyama [8], or alternatively, to Kauer [5]. Let A be a finite dimensional symmetric basic algebra, with projective modules P_j. To each j, we can associate an idempotent $\tilde{e}_j$ with $1_A = \sum\limits_{j=1}^{e} \tilde{e}_j$.

DEFINITION 2.12. Fix an i and define $e_0 = \sum\limits_{j \neq i} \tilde{e}_j$. For any j with $1 \leq j \leq e$, we define a complex by

$$T_j^{(i)} = \begin{cases} (0th) & & (1st) & \\ P_j & \longrightarrow & 0 & j \neq i \\ Q_i & \xrightarrow{\pi_i} & P_i & j = i \end{cases}$$

where $Q_i \xrightarrow{\pi_i} P_i$ is a minimal projective presentation of $\tilde{e}_j A / \tilde{e}_j A e_0 A$. Now we define $T^{(i)} :=$

$\oplus_{j=1}^{e} T_j^{(i)}$. The *mutation* μ_i^+ of A is $A' \cong \mathrm{End}_{D^b(A)} T^{(i)}$. We will also consider the dual variant, as in [12].

$$T_j^{(i)-} = \begin{cases} (-1st) & & (0th) & \\ 0 & \longrightarrow & P_j & j \neq i \\ P_i & \xrightarrow{\pi_i} & Q_i & j = i \end{cases}$$

where Q_i is the minimal injective hull of the quotient of P_i by the largest submodule containing only components isomorphic to the simple module S_i. This injective hull will be a direct sum of injective modules (which are also projective) whose irreducible socles give the socles of this quotient. We will denote this by μ^- [2] (see, e.g., [17] for more detail in the case of Brauer trees).

Since A is a symmetric algebra, either version of the mutation will give a tilting complex.

Now let A be the algebra of an edge-numbered Brauer tree. (We recall that the algebra does not depend on the numbering.) Aihara showed in [1] that there is a simple combinatorial operation on edges which corresponds to the mutation: The edge j is detached from both of its endpoints, and each vertex reattached to the tree at the farther end of the edge which is next before it in cyclic ordering at that vertex. If the edge j is a leaf, then there is only one reattachment made.

By dualizing Aihara's main theorem, [1] Theorem 2.2, the mutation μ^- would correspond to the dual version of Aihara's operation on the Brauer tree, namely, reattaching to the farther end of the edge which is *after* it in the cyclic ordering. The diagrams to demonstrate this can be found in [17].

3. MUTATION REDUCTION

The first algorithm for reducing from a general Brauer tree to the star by a series of mutations is apparently that given in [6]. They operate at each step using a mutation centered on a leaf, chosen so that, after the mutation, the total distance between all the edges will be lower. In this procedure, the exceptional vertex, if we are in the case $m > 1$ where it is uniquely defined, plays no special role. By their algorithm, if a Brauer tree had the exceptional vertex at one end, all the edges would be moved to the center and the exceptional vertex would remain terminal.

Since the purpose of this paper is to compare the step-by-step mutation algorithms with Rickard's all-in-one algorithm, for which the Brauer star must have the exceptional vertex in the middle, we will use a lightly modified version of the algorithm in [6], for which the recursion is by the distance of all other vertices from the exceptional vertex.

Assume we are given a Brauer tree G, with multiplicity m, as in Def. 2.1. If $m > 1$, then there is a designated exceptional vertex v. For $m = 1$, we assume that one of the vertices has been chosen as the exceptional vertex v.

Definition 3.1. A *mutation reduction* is a mutation or sequence of mutations such that the distance of each vertex from the exceptional vertex does not ever increase, and such that at least one such distance actually decreases. A mutation reduction which ends at the Brauer star is called *complete*.

Lemma 3.1. *Assume we are given a Brauer tree.*

(1) *A mutation which is a mutation reduction must be centered at a primary edge.*

(2) *A mutation centered at a primary edge connected to an edge adjacent to the exceptional vertex is a mutation reduction.*

(3) *After a complete mutation reduction, all the edges from a given branch form an interval around the Brauer star, and these intervals follow the counterclockwise ordering of the branches.*

Proof. (1) If the mutation is not centered at a primary edge, then the mutation reattaches the center at the far end of the edge before it in the cyclic ordering, which is at greater distance from the exceptional vertex, in contradiction to our assumption that we have a mutation reduction.

(2) The only mutation which can change the branch structure under a mutation reduction is a mutation by a primary edge w connected to an edge u adjacent to the exceptional vertex. Let U be the remaining branches at u. The effect of such a mutation is to create a new branch by lopping off w and the subgraph S of all edges connected to the exceptional vertex through the center w of the mutation.

Let t be the coprimary edge at w, and let T be the set of branches at the far end of t. Let W be the remaining branches connected to the far end of w. After the mutation of type μ^+, the original branch rooted at u will now be replaced by two branches, one rooted at w and now connected directly to T, while t, which has become coprimary, now has W at its far end. The other branch will be rooted at u, now connected only to U at its far end, and will follow the branch rooted at w immediately in the counterclockwise ordering at v.

It remains to show that this operation was actually a mutation reduction. The edge w, once at distance 1, is now at distance 0. The edge t, once at distance 2, is now at distance 1, and every edge of T, originally connected to t and thus connected to the exceptional vertex via three edges, u, w, t, is now connected to v via w and therefore every vertex is at distance two less than before. Finally, the vertices of W, now all connected to the exceptional vertex via w, t instead of u, w, all remain at exactly the same distance that they had before, as will all the vertices in U.

(3) In any complete mutation reduction, each branch is eventually split entirely into separate leaves attached to the exceptional vertex. However, since this is always done, as described above, by separating one branch into two adjacent branches with the same labels as the original branch, the end result is that all the edges in the original branch correspond to an interval around the star. □

We will examine two different mutation reduction algorithms, one a version of the original algorithm given by Aihara [1] and the other our own from [16].

Aihara's Algorithm [1]

(1) Choose an initial branch.

(2) In a Green's walk starting at the root of the initial branch choose the first primary edge w attached to an edge adjacent to the exceptional vertex. If the tree is not a star, there must be such an edge w. (The edge w need not lie in the initial branch, which could have been badly chosen as an edge attached to the exceptional vertex with no other edges attached to it.)

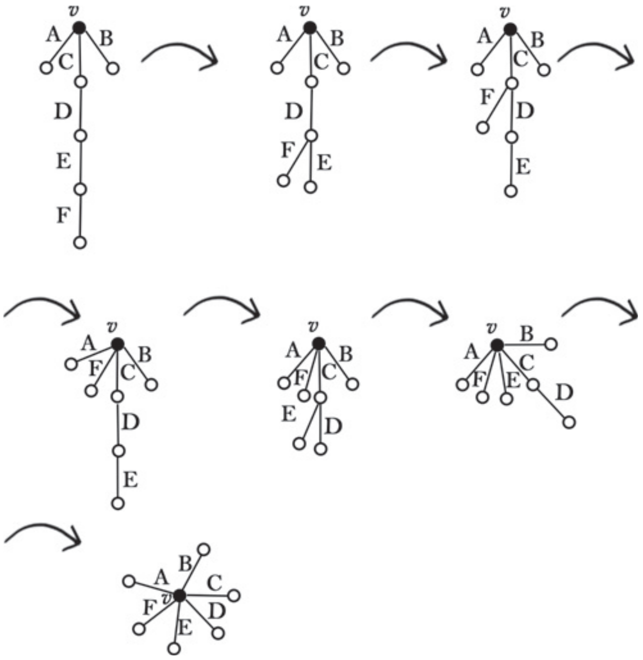

Fig. 6.

(3) By Lemma 3.1(2), the mutation centered on this edge w is a mutation reduction, and from the proof we see that it creates two adjacent branches from the original, the first of which in counter-clockwise order is rooted at w.

(4) If w was on the initial branch, let the new initial branch be the new branch rooted at w, and otherwise let the initial branch remain as before. Begin again from (2).

Algorithm Z [16]

(1) Choose an initial branch. Let $d > 1$ be the maximal distance of a vertex from the exceptional vertex v.

(2) In a Green's walk starting on the initial branch choose the first leaf at distance d, necessarily a primary edge, as center, and perform a series of mutations centered on the edge with this label, for as long as it remains a primary edge or until it reached the exceptional vertex. The distances of all other vertices from the exceptional vertex will be unchanged.

(3) Choose the next leaf at distance d and proceed as in the previous item.

(4) When there are no leaves left at distance d, then we find the new maximal distance d'. If $d' = 1$ we are finished, and otherwise we set $d = d'$ and begin again at (2).

In terms of number of steps, this is as inefficient as a mutation reduction algorithm can be, because at each step, only one edge has its distance reduced by one.

We now construct a numbering on a Brauer tree depending on which algorithm we use. We number the star by starting with the interval coming from the chosen initial branch and numbering the edges in order. Since each mutation gives a one-to-one correspondence of edges, we can pull this numbering back to the Brauer tree. This numbering will be called the *natural numbering* corresponding to this algorithm and this choice of initial branch.

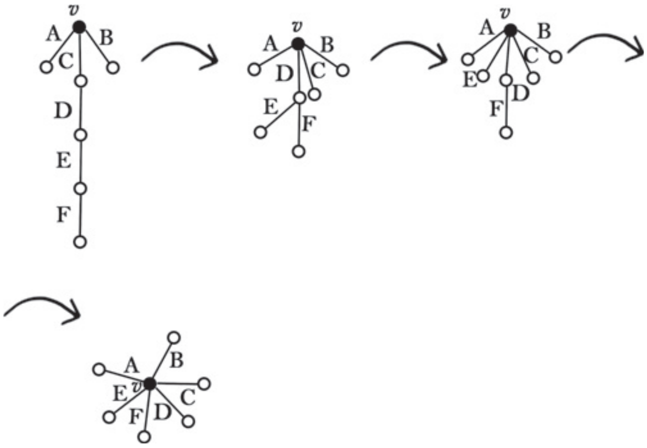

Fig. 7.

Example 3. In Fig.6, we got to the Brauer star using Algorithm Z. Taking the branch with the vertex farthest from the exceptional vertex as initial branch, we get as natural numbering

$$A = 6, B = 5, C = 4, D = 3, E = 2, F = 1.$$

Example 4. Now, we follow Aihara's Algorithm for the same original Brauer tree. In Fig.7, using the same initial branch, we get a different natural numbering. First we chose w to be the first primary edge attached to an edge adjacent to the exceptional vertex, which gives $w = D$. After performing the mutation with center D, we take a new initial branch rooted at w, which is to say, at D. As the next step, we take the first primary edge in this new initial branch, which is E. Since E was already a leaf, it just moves down to the exceptional vertex and is the new initial branch, as described in the algorithm. Now the leaf F becomes a primary edge, and the last step is to move it down to the exceptional vertex. However, since it is not in the initial branch, the leaf E remains the initial branch and thus the numbering begins with $E = 1$.

$$A = 6, B = 5, C = 4, D = 3, E = 1, F = 2$$

The numbering gives a pointing and this pointing gives us a corresponding star-to-tree tilting complex as described in §2. We will prove that from Algorithm Z we get a tilting complex corresponding to the natural numbering derived from the reversed pointing. From Aihara's Algorithm we obtain a tilting complex which comes from a pointing but we will show that it is not usually the pointing corresponding to the natural numbering.

4. MUTATION BY LEAVES

In what follows, given a mutation reduction algorithm, we will label each edge by its number in the natural numbering. The basic step in Algorithm Z is to take a leaf i which is a primary edge in a Brauer tree and to do a mutation centered on this leaf, which will be a mutation reduction to a tree whose algebra is A'. Letting A'' be the algebra of the original Brauer tree, the tilting complex of this mutation is expressed in terms of the projectives P''_s

of $A^{''}$, given by a functor $G : D^b(A^{'}) \to D^b(A^{''})$. Since i is a primary edge attached to some edge j which is closer to the exceptional vertex, the functor G will act as the identity for every projective $P^{'}_{\ell}$ of $A^{'}$ except $P^{'}_i$, and for $P^{'}_i$ itself we will have the projective cover of its radical, which is $P^{'}_j$ because j is a primary edge adjacent to i.

$$\begin{array}{lcccccccl} G\left(P^{'}_s\right): & & 0 & \to & P^{''}_s & \to & 0, & & s \neq i \\ G\left(P^{'}_i\right): & & 0 & \to & P^{''}_j & \to & P^{''}_i & \to & 0 \end{array}$$

Theorem 4.1. *For any complete mutation reduction whose centers are always leaves which are primary edges, the star-to-tree tilting complex of the composed mutations is the star-to-tree complex of the original tree with the reversed pointing.*

Proof. Let $A_{\ell}, A_{\ell-1}, \ldots, A_1$ be the Brauer tree algebras in the complete mutation reduction to the Brauer star algebra A_0. We number each of the corresponding Brauer trees by the natural numbering corresponding to this mutation reduction. For each k between 1 and ℓ, we let

$$F_k : D^b(A_0) \to D^b(A_k)$$

$$F_k^{-1} : D^b(A_k) \to D^b(A_0)$$

be the functors obtained by composing the functors G^+ of the mutations μ^+ and, respectively, the functors G^- of the dual mutations μ^- in the opposite order. We want to show that the star-to-tree tilting complex given by F_{ℓ}^{-1} is the star-to-tree complex given by the reversed pointing, from which it will follow that the tilting complex inducing F_{ℓ} is Rickard's tree-to-star complex for the same reversed pointing, since by the results of [11] the star-to-tree and tree-to-star complexes are inverse to each other.

Let us prove the theorem by induction on ℓ. If ℓ is 1, then the Brauer tree has only one edge w not attached to the exceptional vertex v, but rather to some u attached to v. If w is numbered i after mutation, then u will be numbered by $i+1$ since it comes after the new w in the cyclic ordering of the star. In the tilting complex of μ_i^- we will have $Q_i = P_{i+1}$, and thus it coincides with the star-to-tree complex of the reversed pointing.

Now assume that the theorem is true for $\ell - 1$, so that $F_{\ell-1}^{-1}$ gives the star-to-tree complex of the reversed pointing of the Brauer tree. Let the $\{P^{'}_s\}$ be the projective left modules of $A_{\ell-1}$ and let the $\{P^{''}_s\}$ be the projective left modules of A_{ℓ}. Let i be the number of the center of the mutation in the Brauer tree of $A_{\ell-1}$ and let j be the number of the next edge after it in the cyclic ordering. By the rules for numbering edges at a vertex, we must have $j > i$. Furthermore, since i is a leaf, $P^{'}_i$ is uniserial, so the injective hull $Q^{'}_i$ of $P^{'}_i/soc(P^{'}_i)$ is $P^{'}_j$.

$$\begin{array}{lcccccccl} G^-\left(P^{''}_j\right): & & & & 0 & \to & P^{'}_s & \to & 0, \quad s \neq i \\ G^-\left(P^{''}_i\right): & 0 & \to & P^{'}_i & \to & P^{'}_j & \to & 0 & \end{array}$$

Case 1. The edge j is not attached to the exceptional vertex:

Let k be the entering edge of the vertex at which i and j meet in the Brauer tree of $A_{\ell-1}$, and assume that it is in degree n_k in the tilting complex. Then by the assumption of reversed pointing, we have $i < j < k$, and thus $F_{\ell-1}^{-1}(P^{'}_i) = T_{ik}[n_k + 1]$ and $F_{\ell-1}^{-1}(P^{'}_j) = T_{jk}[n_k + 1]$. In this case we will get that the composition

$$F_{\ell}^{-1}\left(P^{''}_i\right) = F_{\ell-1}^{-1} \circ G^{-1}\left(P^{''}_i\right)$$

$$= F_{\ell-1}^{-1}\left(Cone\left(P_i' \to P_j'\right)\right)$$
$$= Cone\left(F_{\ell-1}^{-1}(P_i') \to F_{\ell-1}^{-1}(P_j')\right).$$

$$= Cone\left(\begin{tikzcd}
0 \arrow[r] & P_i \arrow[r, "h_{ik}"] \arrow[d, "h_{ij}"'] & P_k \arrow[r] \arrow[d, "id"] & 0 \\
0 \arrow[r] & P_j \arrow[r, "h_{jk}"] & P_k \arrow[r] & 0
\end{tikzcd}\right)$$

Denote the chain map in the cone by $l_\bullet$. We compute $Cone(l_\bullet)$ and get:

$$P_i \xrightarrow{(-h_{ik},h_{ij})} P_k \oplus P_j \xrightarrow{(\pi_k+h_{jk}\circ\pi_j)} P_k$$

where P_k is in degree n_k. We want to show that $Cone(l_\bullet)$ is homotopy equivalent to $T_{ij}[-n_k+2]$, which is to say, T_{ij} shifted so that the P_i is in degree n_k-2.

The vertical maps $f_\bullet$ and $g_\bullet$ in the following diagram are actually chain maps. This can be checked by composition or by diagram chasing.

$$\begin{tikzcd}
P_i \arrow[r, "(-h_{ik},h_{ij})"] \arrow[d, "id"] & P_k \oplus P_j \arrow[r, "(\pi_k+h_{jk}\circ\pi_j)"] \arrow[d, "\pi_j"] & P_k \arrow[d, "0"] \\
P_i \arrow[r, "h_{ij}"] \arrow[d, "id"] & P_j \arrow[r] \arrow[d, "(-h_{jk},id)"] & 0 \arrow[d, "0"] \\
P_i \arrow[r, "(-h_{ik},h_{ij})"] & P_k \oplus P_j \arrow[r, "(\pi_k+h_{jk}\circ\pi_j)"] & P_k
\end{tikzcd}$$

The composition $f_\bullet \circ g_\bullet$ is the identity, so we need only prove that the composition $h_\bullet = g_\bullet \circ f_\bullet$ is homotopic to the identity of the mapping cone. We need to find $T_1 : P_k \oplus P_j \to P_i$, $T_2 : P_k \to P_k \oplus P_j$ such that:

$$\begin{tikzcd}
P_i \arrow[r, "(-h_{ik},h_{ij})"] \arrow[d, shift right, "id"'] \arrow[d, shift left, "id"] & P_k \oplus P_j \arrow[r, "(\pi_k+h_{jk}\circ\pi_j)"] \arrow[dl, "T_1"'] \arrow[d, shift right, "(-h_{jk}\circ\pi_j,\pi_j)"'] \arrow[d, shift left, "id"] & P_k \arrow[dl, "T_2"'] \arrow[d, shift right, "0"'] \arrow[d, shift left, "id"] \\
P_i \arrow[r, "(-h_{ik},h_{ij})"] & P_k \oplus P_j \arrow[r, "(\pi_k+h_{jk}\circ\pi_j)"] & P_k
\end{tikzcd}$$

To get the equality we want, we choose $T_1 = 0$ and $T_2 = (-id, 0)$.

Case 2. Near the exceptional vertex: i is adjacent to the exceptional vertex after doing the mutation. When we compute the tilting complex of the mutation, the component of P_i'' also is two-restricted. In this case we will get that the composition

$$F_{\ell-1}^{-1} \circ G^{-1}\left(P_i''\right) = Cone\left(\begin{tikzcd} 0 \arrow[r] & P_i \arrow[r] \arrow[d, "h_{ij}"'] & 0 \\ 0 \arrow[r] & P_j \arrow[r] & 0 \end{tikzcd}\right)$$

which is homotopy equivalent to $T_{ij}[-n_j + 1]$, and equal to $F_\ell^{-1}\left(P_i''\right)$, which is precisely what we need for the star-to-tree tilting complex of the reversed pointing. □

5. AIHARA'S ALGORITHM

In Cor. 2.6 of [1], Aihara shows that the tree-to-star functor obtained by composing the mutations in his algorithm gives a tilting complex of length two. We will compare Aihara's functor with the completely folded two-term version of Rickard's tree-to-star functor given in [11].

Proposition 5.1. *We consider an arbitrary Brauer tree algebra. Let σ be the permutation of $1, \ldots, e$ sending each number in the natural numbering of the tree by Aihara's Algorithm to the number of the corresponding edge in the left alternating numbering. Then*

(1) *The star-to-tree complex obtained by composing the mutations of Aihara's Algorithm in reverse order can be obtained from the star-to-tree complex of the left alternating pointing by permuting the rows by σ.*

(2) *The tree-to-star complex corresponding to Aihara's Algorithm is the completely folded Rickard tree-to-star complex for the left alternating pointing, except that the projectives are permuted by σ.*

Proof. (1) We let ℓ be the number of mutations in the complete mutation reduction. In the case $\ell = 1$, the center of the mutation is a leaf, so the natural numbering is the reversed numbering, and for a linear tree of length 2, this coincides with the left alternating numbering, so the permutation is the identity. We let F_ℓ^{-1} be the star-to-tree functor obtained by composing the inverse mutations, and let H_ℓ^{-1} be the star-to-tree functor given by the left alternating numbering, with σ_ℓ the permutation mapping the natural number of an edge to its number in the left alternating numbering.

We assume, by induction, that the proposition is true for $\ell-1$. Let the P_i' be the projectives for $\ell-1$ in the natural numbering, and let P_i'' be the projectives for ℓ in the natural numbering. Let the Q_i' be the projectives for $\ell - 1$ in the left alternating numbering, and let Q_i'' be the projectives for ℓ in the left alternating numbering. For every i, where $1 \leq i \leq e$, $F_{\ell-1}^{-1}(P_i')$ is the star-to-tree complex obtained by composing the mutations of Aihara's Algorithm and for every j, where $1 \leq j \leq e$, $H_{\ell-1}^{-1}(Q_j')$ is the star-to-tree complex obtained from the left alternating pointing. By our induction hypothesis, we get

$$F_{\ell-1}^{-1}(P_i') = H_{\ell-1}^{-1}(Q_{\sigma_{\ell-1}(i)}')$$

We recall that for any branch, by Def. 2.9, the edge connected to the exceptional vertex is called the root. We are now going to perform an inverse mutation centered at a root w, which will join the branch with root w to the next branch, with root u, where, as stated in Lemma 3.1(3), we have $u > w$. Let $B_{\ell-1}$ be the Brauer tree before the branches rooted at u and w are joined, and let B_ℓ be the Brauer tree after they are joined. We let t be the primary edge connected to w in $B_{\ell-1}$, and Lemma 3.1(3) shows that w is the numerically highest number in the branch, so that $w > t$. We note that for the left alternating numbering the number of the root is also the highest in the branch, so that the permutation σ always acts as the identity on roots.

We compute the functor G^{-1}, the inverse of the mutation μ^+_w centered at w.

$$\begin{array}{lccccccl} G^{-1}\left(P^{''}_s\right): & & & 0 & \to & P^{'}_s & \to & 0, \quad s \neq w \\ G^{-1}\left(P^{''}_w\right): & 0 & \to & P^{'}_w & \to & P^{'}_u \oplus P^{'}_t & \to & 0 \end{array}$$

Since w and u are both roots, and $\sigma_{\ell-1}$ is the identity on roots, we have

$$\begin{array}{lccccc} F^{-1}_{\ell-1}\left(P^{'}_u\right) = H^{-1}_{\ell-1}\left(Q^{'}_u\right): & 0 & \to & P_u & \to & 0 \\ F^{-1}_{\ell-1}\left(P^{'}_w\right) = H^{-1}_{\ell-1}\left(Q^{'}_w\right): & 0 & \to & P_w & \to & 0 \end{array}$$

It remains to calculate $F^{-1}_{\ell-1}\left(P^{'}_t\right)$.

By the definitions, t is the number assigned to the primary edge at w in the natural numbering. In the left alternating pointing, since the point is on the left at the far end of w, it is the highest number appearing on the branch rooted at w, and since the point at the far end of t is on the right, the primary edge which we have labelled by t in the natural numbering will correspond to the lowest number in the branch, which we will denote by i. Thus by the definition of $\sigma_{\ell-1}$, we have $\sigma_{\ell-1}(t) = i$ and by the definition of the star-to-tree tilting complex of a given numbering, we get a simple complex of length 2 joining P_i with P_w in numerical order, so we have

$$F^{-1}_{\ell-1}\left(P^{'}_t\right) = H^{-1}_{\ell-1}\left(Q^{'}_i\right): \quad 0 \to P_i \to P_w \to 0$$

We now calculate F^{-1}_{ℓ} as the composition $F^{-1}_{\ell-1} \circ G^{-1}$. We first make a general claim that if $i \to j \to k$ is short, then $P_j \oplus P_i \to P_k \oplus P_j$ is homotopy equivalent to $T_{ik}[1]$, where the map is given by $(-h_{jk} \circ \pi_j, \pi_j + h_{ij} \circ \pi_i)$. The chain maps are obvious and the composition from T_{ij} to itself is the identity, so we need only find a homotopy from the opposite composition to the identity:

$$\begin{tikzcd}
P_j \oplus P_i \arrow[r, "(-h_{jk}\circ\pi_j{,}\pi_j+h_{ij}\circ\pi_i)"] \arrow[d, "\pi_i"] & P_k \oplus P_j \arrow[d, "\pi_k+h_{jk}\circ\pi_j"] \\
P_i \arrow[r, "h_{ik}"] \arrow[d, "(-h_{ij}{,}id)"] & P_k \arrow[d, "(id{,}0)"] \\
P_j \oplus P_i \arrow[r, "(-h_{jk}\circ\pi_j{,}\pi_j+h_{ij}\circ\pi_i)"] & P_k \oplus P_j
\end{tikzcd}$$

The needed homotopy is given by $T = (-\pi_j, 0)$. With this result in hand, and noting that $i \to w \to u$ is short because $i \leq t < w < u$, we make our calculation.

$$\begin{aligned} F^{-1}_{\ell-1} \circ G^{-1}\left(P^{''}_w\right) &= F^{-1}_{\ell-1}\left(Cone\left(P^{'}_w \to P^{'}_u \oplus P^{'}_t\right)\right) \\ &= Cone\left(F^{-1}_{\ell-1}(P^{'}_w) \to F^{-1}_{\ell-1}(P^{'}_u) \oplus F^{-1}_{\ell-1}(P^{'}_t)\right) \end{aligned}$$

$$= Cone\left(\begin{tikzcd} 0 \arrow[r] & P_w \arrow[r] \arrow[d, "{(h_{wu},id)}"] & 0 \\ P_i \arrow[r, "{(0,h_{tw})}"] & P_u \oplus P_w \arrow[r] & 0 \end{tikzcd}\right)$$

$$= P_w \oplus P_i \to P_u \oplus P_w$$

$$\equiv P_i \xrightarrow{h_{iu}} P_u$$

The resulting star-to-tree complex is clearly in a two restricted tilting complex. Because G^{-1} is almost everywhere trivial, the only differences between F_ℓ and $F_{\ell-1}$ are:

$$\begin{array}{rccccccc} F_{\ell-1}^{-1}\left(P_w'\right) = H_{\ell-1}^{-1}\left(Q_w'\right): & & & 0 & \to & P_w & \to & 0 \\ F_\ell^{-1}\left(P_w''\right) = H_\ell^{-1}\left(Q_i''\right): & 0 & \to & P_i & \to & P_u & \to & 0 \end{array}$$

and

$$\begin{array}{rccccccc} F_{\ell-1}^{-1}\left(P_t'\right) = H_{\ell-1}^{-1}\left(Q_i'\right): & 0 & \to & P_i & \to & P_w & \to & 0 \\ F_\ell^{-1}\left(P_t''\right) = H_\ell^{-1}\left(Q_w''\right): & 0 & \to & P_i & \to & P_w & \to & 0 \end{array}$$

Thus σ_ℓ is identical with $\sigma_{\ell-1}$ except on w and t. We have $\sigma_\ell(w) = \sigma_{\ell-1}(t) = i$ and $\sigma_\ell(t) = \sigma_{\ell-1}(w) = w$. It remains only to show that H_ℓ^{-1} is indeed the star-to-tree functor for the left alternating pointing.

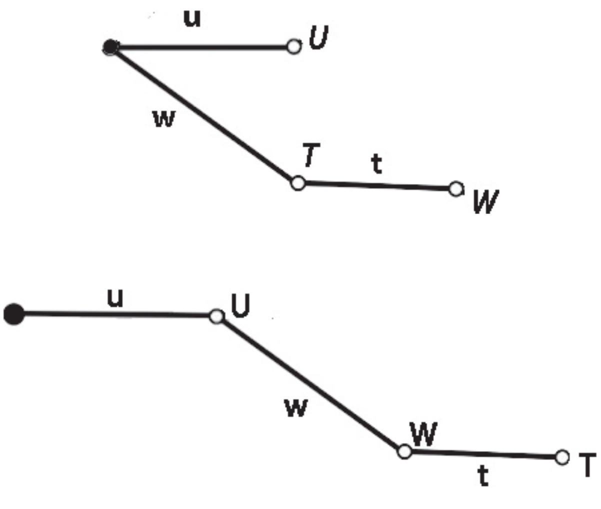

Fig. 8.

We use the same notation as in the proof of Lemma 3.1(2), except that now our mutation is going in the opposite direction, so that t will go from being primary to coprimary. In $B_{\ell-1}$, the top graph in Fig.8, let W be the collection of branches at the far end of t, let T be the remaining branches connected to w, and let U be the collection of branches at the far end of u. The interval in the natural numbering corresponding to T is $[i, \dots, t-1]$, the interval corresponding to W is $[t+1, \dots, w-1]$, and the interval corresponding to U is $[w+1, \dots, u-1]$.

In B_ℓ, the bottom graph in Fig.8, w is attached to u before U, t has become coprimary, with T attached to its far end, and W is now attached directly to w. The distances of U and of W from the exceptional vertex v remain as they were, and the distance of T is increased by two, since it was originally attached directly to w, and now u, w and t intervene. Since the intervals remain the same, and the alternating pointing remains the same, the left alternating numbering for each is the same, and thus σ_ℓ and $\sigma_{\ell-1}$ are identical on U, W and T, and also on u, where both are fixed.

Thus, for every edge except w and t, the left alternating pointing is exactly as it was. At the far end of w, the point is on the right, and thus the left alternating pointing assigns to w the lowest number in the united branches, which was the lowest number in the branch with root w, which we called i. In the united tree B_ℓ, the edge t is coprimary going out from w and has the point between it and w. Since the edge w has been assigned a low number, the alternating numbering assigns to t the largest number in the branch originally rooted at w, which is w. The alternating numbering then gives to every other edge exactly the same number as before. This proves (1).

(2) By [11] the Rickard tree-to-star complex for the left alternating pointing is the inverse of the star-to-tree complex for the same pointing. Since the star-to-tree for Aihara's algorithm differs from the star-to-tree for the left alternating pointing only in the order of the components, the Aihara complex differs from the Rickard complex only by the same permutation of the projectives, replacing P''_j by $Q''_{\sigma(j)}$ $\square$

In order for Proposition 5.1 to be truly useful, we would like to give a description of the permutation σ which does not require us to perform the entire Aihara algorithm and find the natural numbering. This we do in the following corollary, which we first illustrate by giving the natural numbering of the tree in the example of Fig.4 when we have done the Aihara algorithm. This numbering can be obtained from a pointing, which we give, but the tilting complex corresponding to this pointing is not the tilting complex resulting from the Aihara algorithm. The natural numbering is given in Fig.9 below.

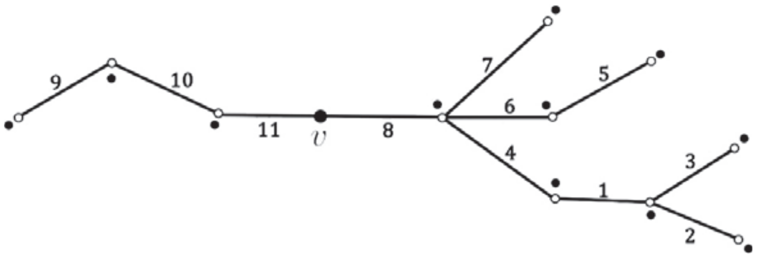

Fig. 9.

The vertices at even distance from the exceptional vertex are those numbered $4, 6, 10$. There are only two edges at each of these vertices, so the cyclic permutation of the edges is just a set of three transpositions, giving $\sigma = (1,4)(5,6)(9,10)$.

Corollary. *The permutation σ is given by the cyclic ordering of edges on the vertices at non-zero even distance from the exceptional vertex.*

Proof. As in the proof of the proposition, we do an induction on ℓ, assuming that the result holds for $\ell - 1$. Thus in $\sigma_{\ell-1}$, the edges at the far end of t are permuted according to the cyclic ordering at the vertex, from the primary edge i through the numerically increasing

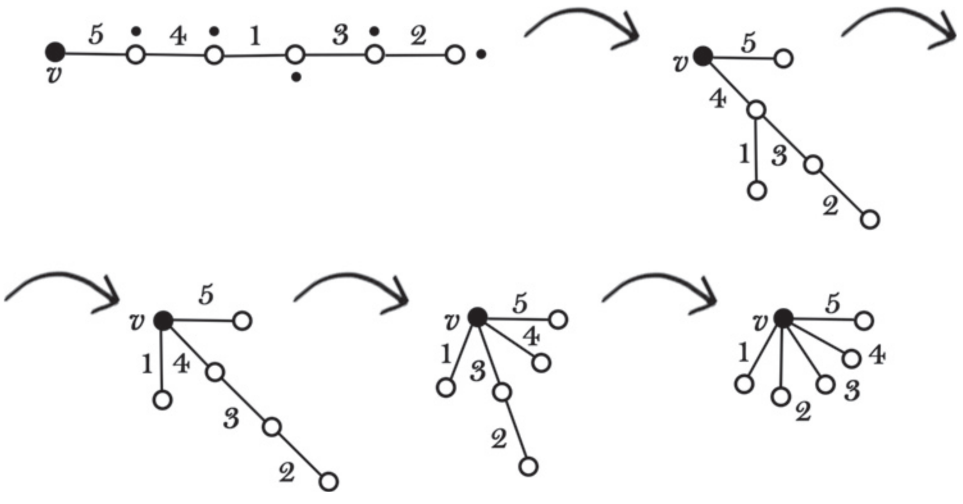

Fig. 10.

starting edges of the branches in T, and then to t, and finally from t back to i. In B_ℓ, this vertex now has an extra edge. The cyclic ordering goes from i though the same sequence of starting edges in T, to the coprimary edge t, and finally to w. This is precisely the change we documented in σ_ℓ, where now w goes to i and t to w, increasing the length of the cycle by one. □

Example 5. We illustrate Proposition 5.1 with a simple example. In Fig.10, we have a linear Brauer tree, which we reduce using Aihara's Algorithm to a Brauer star with $e = 5$. Now we compare this result with the composition of mutations as in Proposition 5.1:

$$\begin{array}{rccccccc}
F_4^{-1}(P_1''): & 0 & \to & P_1 & \to & P_4 & \to & 0 \\
F_4^{-1}(P_2''): & 0 & \to & P_2 & \to & P_3 & \to & 0 \\
F_4^{-1}(P_3''): & 0 & \to & P_2 & \to & P_4 & \to & 0 \\
F_4^{-1}(P_4''): & 0 & \to & P_1 & \to & P_5 & \to & 0 \\
F_4^{-1}(P_5''): & & & 0 & \to & P_5 & \to & 0
\end{array}$$

This differs from the folded star-to-tree complex for the pointed Brauer tree in Fig.10, constructed as in [11], by the ordering of the images. The images of P_1'' and P_4'' are exchanged, as are the images of P_2'' and P_3''.

$$\begin{array}{rccccccc}
H_4^{-1}(Q_1''): & 0 & \to & P_1 & \to & P_5 & \to & 0 \\
H_4^{-1}(Q_2''): & 0 & \to & P_2 & \to & P_4 & \to & 0 \\
H_4^{-1}(Q_3''): & 0 & \to & P_2 & \to & P_3 & \to & 0 \\
H_4^{-1}(Q_4''): & 0 & \to & P_1 & \to & P_4 & \to & 0 \\
H_4^{-1}(Q_5''): & & & 0 & \to & P_5 & \to & 0
\end{array}$$

For completeness, we give the corresponding tree-to-star complexes.

$$\begin{array}{llcccccc}
H_4(P_1): & 0 & \to & Q_5'' & \to & Q_1'' & \to & 0 \\
H_4(P_2): & 0 & \to & Q_5'' \oplus Q_4'' & \to & Q_1'' \oplus Q_2'' & \to & 0 \\
H_4(P_3): & 0 & \to & Q_5'' \oplus Q_4'' \oplus Q_3'' & \to & Q_1'' \oplus Q_2'' & \to & 0 \\
H_4(P_4): & 0 & \to & Q_5'' \oplus Q_4'' & \to & Q_1'' & \to & 0 \\
H_4(P_5): & 0 & \to & Q_5'' & \to & 0 & &
\end{array}$$

$$\begin{array}{llcccccc}
F_4(P_1): & 0 & \to & P_5'' & \to & P_4'' & \to & 0 \\
F_4(P_2): & 0 & \to & P_5'' \oplus P_1'' & \to & P_4'' \oplus P_3'' & \to & 0 \\
F_4(P_3): & 0 & \to & P_5'' \oplus P_1'' \oplus P_2'' & \to & P_4'' \oplus P_3'' & \to & 0 \\
F_4(P_4): & 0 & \to & P_5'' \oplus P_1'' & \to & P_4'' & \to & 0 \\
F_4(P_5): & 0 & \to & P_5'' & \to & 0 & &
\end{array}$$

Since the underlying Brauer trees are the same, the Brauer tree algebras are isomorphic, and we get isomorphisms of projectives according to the permutation σ, namely $P_j'' \equiv Q_{\sigma(j)}''$. In fact, both algebras are endomorphism rings of tilting complexes which differ only in the order of the terms. In Fig.11, we give the linear tree with the left alternating pointing.

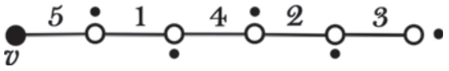

Fig.11.

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