

# A Common Positive Point for Braid Varieties

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## Abstract

We compare two positive subsets of a braid variety: the positive locus of its weave cluster structure and the geometric positive locus defined by the joint nonnegative closure in a twisted product of flag varieties. For every positive braid word of finite crystallographic simple type, with a fixed standard pinning, these subsets agree on the same flag-chain variety. We construct a point at which every variable of the left-inductive seed is one. A root-subgroup stabilizer fixes its entire flag chain, allowing a simultaneous rank-one positive limit that puts the point in the geometric locus. An elementary connected-component criterion for locally acyclic cluster algebras with inverted frozen variables, together with Bao–He’s geometric component theorem, proves the equality. We also distinguish affine from compact closures and give explicit small-rank examples, including a six-component real braid variety. The comparison concerns positive loci, not an identification of two cluster atlases or a classification of all real components.

## 1 Introduction

Braid varieties parametrize chains of flags with prescribed successive relative positions and a fixed endpoint. Their weave cluster structures were constructed by Casals, Gorsky, Gorsky, Le, Shen and Simental [CGGLSS]. Bao and He defined total positivity in twisted products of flag varieties and proved that the corresponding positive strata are connected components of the real strata [BH]. These constructions suggest a comparison on the underlying flag chains. The distinction matters: positivity of the usual affine braid coordinates is not, in general, cluster or geometric positivity.

Fix a split real form of a complex simple algebraic group, a standard pinning, and a positive braid word  $\beta$ . Let  $X(\beta)$  be the flag-chain variety defined in Section 2. Denote by  $C_\beta$  the positive locus of the weave cluster structure, and by  $P_\beta$  the intersection of  $X(\beta)(\mathbb{R})$  with the defining joint nonnegative closure in the flag-chain space.

**Theorem 1.1.** *For every positive braid word  $\beta$  in finite crystallographic simple type, with the conventions of Section 2,*

$$C_\beta = P_\beta.$$

*There is an explicitly recursive point  $q_\beta$  in this common locus at which every extended variable of the left-inductive weave seed is equal to one.*

The comparison is the identity on the flag-chain variety. In particular, it does not pass through an unspecified isomorphism with a Richardson variety. The proof has two parts. First, a positive cell of a locally acyclic cluster algebra with inverted frozen variables is a real connected component.

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Second, we construct a point belonging to both positive loci. The second part uses a stabilizer that fixes every flag simultaneously; positivity of each individual flag would not suffice to place a chain in the defining joint closure.

The cluster construction and its local acyclicity are inputs from [CGGLSS]; the geometric component and compact ball theorems are inputs from [BH]. The rank-one limiting argument is motivated by Marsh–Rietsch [MR, Lemma 11.9]. Our purpose is to give a direct comparison proof with these inputs and the pinning held fixed, without an absolute priority claim for the comparison or the elementary component observation.

There are related, but logically different, comparisons in the literature. Galashin, Lam and Sherman-Bennett construct braid cluster structures by Deodhar geometry [GLSB]; their relation to weave structures is established in [CGSSS]. The Richardson-to-braid maps and positivity conventions in Appendix C of [CGSSS] are specified maps, not an assertion that arbitrary identifications preserve positivity. Bao–Ye construct an upper cluster structure on twisted-product Richardson varieties and identify its positive part [BY, Theorem 6.5 and Propositions 7.4–7.5]. Their Remark 6.6 discusses identification with weave seeds. Equality of positive loci, as here, is weaker than equality of the seed atlases. Mizuno’s cluster-localization and product results provide further structural comparisons [Miz, Theorem 1.1].

The result answers a precise positivity-comparison question associated with the broader request to describe positive braid varieties. It does not exhaust that open-ended geometric agenda. This manuscript is AI-assisted and self-audited. AI assistance was used in the research, writing and exact-check code; no independent review or formal proof-assistant verification is claimed.

## 2 Pinning and the two positive loci

Let  $G$  be a complex simple algebraic group with a split real form. Choose opposite real Borel subgroups  $B^+, B^-$ , their common torus  $T$ , and pinned root subgroups  $x_i, y_i$ , indexed by the simple roots. We may use the simply connected cover: central isogenies preserve the flag variety and the pinned flag-chain constructions. Write  $\mathcal{F} = G/B^+$ ,  $W$  for the Weyl group and  $\Phi^+$  for the positive roots. For the pinned homomorphism  $\phi_i : \mathrm{SL}_2 \rightarrow G$ , put

$$\dot{s}_i = \phi_i \begin{pmatrix} 0 & -1 \\ 1 & 0 \end{pmatrix}, \quad h_i(t) = \phi_i \begin{pmatrix} t & 0 \\ 0 & t^{-1} \end{pmatrix}, \quad B_i(z) = x_i(z)\dot{s}_i. \quad (1)$$

Thus in rank one  $B_i(z)$  is represented by  $\begin{pmatrix} z & -1 \\ 1 & 0 \end{pmatrix}$ . The lift in (1) is used throughout.

For a word  $\beta = i_1 \cdots i_r$ , its Demazure product is denoted by  $\delta(\beta)$ . In particular, if  $w = \delta(\gamma)$ , then

$$\delta(i\gamma) = \begin{cases} s_i w, & \ell(s_i w) = \ell(w) + 1, \\ w, & \ell(s_i w) = \ell(w) - 1. \end{cases} \quad (2)$$

Choose any lift  $\dot{w} \in N_G(T)$  of each  $w$ . The endpoint flag  $\dot{w}B^+$  does not depend on its torus ambiguity.

**Definition 2.1.** The braid variety  $X(\beta)$  consists of chains  $(F_0, \dots, F_r)$  with

$$F_0 = B^+, \quad \mathrm{pos}(F_{k-1}, F_k) = s_{i_k} \quad (1 \leq k \leq r), \quad F_r = \dot{\delta}(\beta)B^+.$$

The usual affine realization sends  $(z_1, \dots, z_r)$  to  $F_k = B_{i_1}(z_1) \cdots B_{i_k}(z_k)B^+$ , with endpoint condition

$$\dot{\delta}(\beta)^{-1} B_{i_1}(z_1) \cdots B_{i_r}(z_r) \in B^+; \quad (3)$$

see [CGGLSS, Corollary 3.7].

Let  $U_{\geq 0}^-$  be the semigroup generated by  $y_i(a)$  with  $a \geq 0$ . Under the cumulative-product identification of the twisted product with a product of flag varieties, define

$$\mathcal{Z}_{r,\geq 0} = \overline{\{(B^+, u_1 B^+, u_1 u_2 B^+, \dots, u_1 \cdots u_r B^+) : u_j \in U_{\geq 0}^-\}}. \quad (4)$$

The closure is Euclidean in  $\{B^+\} \times \mathcal{F}(\mathbb{R})^r$ . For  $r = 0$  the set is the single flag  $B^+$ . This is the joint nonnegative closure of [BH, Section 3.4], with the constant initial flag included in the notation. Set

$$P_\beta = X(\beta)(\mathbb{R}) \cap \mathcal{Z}_{r,\geq 0}. \quad (5)$$

Bao–He’s Theorem 3.4(1), specialized as in their Section 5.1, says that  $P_\beta$  is a connected component of  $X(\beta)(\mathbb{R})$ .

The weave construction equips  $\mathbb{C}[X(\beta)]$  with a cluster algebra structure whose frozen variables are inverted [CGGLSS, Section 2 and Corollary 6.12]. The pinned construction is defined over  $\mathbb{R}$ . An *extended seed* includes the mutable and frozen variables. Its positive torus is the set where all those variables are positive. Exchange relations are subtraction-free, so this set is independent of the seed; call it  $C_\beta$ .

### 3 A positive component criterion

We use the following elementary consequence of local acyclicity. Its frozen-unit hypothesis and the meaning of “localization” are important.

**Proposition 3.1.** *Let  $\mathcal{A}$  be a finitely generated cluster algebra of geometric type over  $\mathbb{R}$ . Assume that its exchange monomials have coefficient one and that all frozen variables are inverted. Suppose  $X = \text{Spec } \mathcal{A}$  has an open cover by acyclic cluster localizations. Then its positive cell  $X_{>0}$  is a connected component of  $X(\mathbb{R})$ .*

Here a cluster localization freezes and inverts some variables of a global seed, with coordinate ring equal to that localization of  $\mathcal{A}$ . After mutation within the remaining mutable vertices, its mutable exchange quiver is acyclic. All variables in such a chart are restrictions of global cluster variables. An arbitrary cover by varieties abstractly isomorphic to acyclic varieties would not be enough for the assertion.

*Proof.* Inverting all variables of a seed gives its Laurent polynomial ring. Thus the positive cell is a nonempty connected open subset of  $X(\mathbb{R})$ , isomorphic to  $(\mathbb{R}_{>0})^N$ , where  $N$  is the size of an extended seed. We show that it is also closed.

Let  $p$  lie in its Euclidean closure. Every cluster variable is a regular function on  $X$ , so has nonnegative value at  $p$ . The original frozen variables, being units, have strictly positive values. Choose an acyclic cluster-localization chart containing  $p$ . Its newly frozen variables are global cluster variables and units on the chart; their values at  $p$  are therefore also positive.

Suppose a nonempty set  $S$  of mutable variables vanishes at  $p$ . For  $i \in S$ , the exchange relation gives

$$0 = x_i(p)x'_i(p) = M_i^+(p) + M_i^-(p).$$

Both monomials are nonnegative and consequently both vanish. No frozen factor vanishes. Hence, within the mutable subquiver on  $S$ , every vertex has a neighbor in each arrow direction. In particular every vertex has an outgoing neighbor. Following arrows in this finite graph produces a

directed cycle, contradicting acyclicity. This argument uses only the signs and positive exponents in the exchange matrix, and applies to skew-symmetrizable seeds as well.

All variables of this seed are therefore positive at  $p$ . Seed independence of positivity gives  $p \in X_{>0}$ . The positive cell is closed, open and connected, hence a connected component.  $\square$

*Remark 3.2.* If frozen variables may vanish, both exchange monomials can vanish through frozen factors, with no mutable directed cycle. The argument does not extend to that partial compactification.

**Corollary 3.3.** *The sets  $C_\beta$  and  $P_\beta$  are connected components of the same real variety. To prove their equality, it suffices to find one point in their intersection.*

*Proof.* For  $C_\beta$ , use Proposition 3.1 and the local acyclicity of [CGGLSS, Theorem 7.13]. Its proof constructs charts by freezing and inverting actual seed variables, so the required cluster-localization condition holds. The statement includes the non-simply-laced types. For  $P_\beta$ , use the component theorem following (5). Two connected components that meet are equal.  $\square$

## 4 Root subgroups fixing an entire chain

Write  $U^+$  for the unipotent radical of  $B^+$ . For  $w \in W$ , define

$$H_w = U^+ \cap \dot{w}U^+\dot{w}^{-1}, \quad R_w = \{\alpha \in \Phi^+ : w^{-1}\alpha \in \Phi^+\}. \quad (6)$$

The group  $H_w$  is generated by the root subgroups  $U_\alpha$  with  $\alpha \in R_w$ . This description is independent of the torus ambiguity in  $\dot{w}$ .

**Lemma 4.1.** *If  $\ell(s_i w) = \ell(w) + 1$ , then*

$$x_i(\mathbb{R}) \subset H_w, \quad \dot{s}_i^{-1} H_{s_i w} \dot{s}_i \subset H_w. \quad (7)$$

*If  $\ell(s_i w) = \ell(w) - 1$ , then, for all  $t \in \mathbb{R}$ ,*

$$y_i(t)^{-1} H_w y_i(t) = H_w. \quad (8)$$

*Proof.* For an ascent,  $w^{-1}\alpha_i$  is positive. This gives the first inclusion in (7). If  $\alpha \in R_{s_i w}$ , then  $\alpha \neq \alpha_i$ , since  $(s_i w)^{-1}\alpha_i = -w^{-1}\alpha_i$  is negative. A simple reflection takes every other positive root to a positive root. Thus  $s_i \alpha$  is positive and  $w^{-1}s_i \alpha$  is positive. Conjugation by  $\dot{s}_i^{-1}$  takes  $U_\alpha$  to  $U_{s_i \alpha} \subset H_w$ . Signs in the root parameters do not affect this subgroup inclusion.

For a descent,  $\alpha_i \notin R_w$  and  $-w^{-1}\alpha_i$  is positive. Take  $\alpha \in R_w$ . Every root occurring in the Chevalley commutator of  $U_\alpha$  and  $U_{-\alpha_i}$  has the form

$$\rho = p\alpha - q\alpha_i, \quad p, q \in \mathbb{Z}_{>0}.$$

The root  $\alpha$  has a positive simple-root coefficient away from  $i$ . So does  $\rho$ ; since a root has simple-root coefficients of only one sign,  $\rho$  is positive. Moreover,

$$w^{-1}\rho = p w^{-1}\alpha + q(-w^{-1}\alpha_i)$$

is a positive combination of positive roots and is itself a root. It is therefore positive, so  $\rho \in R_w$ . All commutator factors lie in  $H_w$ . Conjugation by  $y_i(t)$  preserves  $H_w$ , and the same argument with  $-t$  gives equality. The terms with  $p > 1$  have been retained, so the argument also covers non-simply-laced root strings.  $\square$

We now construct a real point  $q_\beta$  by induction from the right end of the word. For the empty word it is the chain consisting of  $B^+$ . Suppose

$$q_\gamma = (F_0, \dots, F_m), \quad w = \delta(\gamma).$$

Define

$$q_{i\gamma} = \begin{cases} (B^+, \dot{s}_i F_0, \dot{s}_i F_1, \dots, \dot{s}_i F_m), & \ell(s_i w) = \ell(w) + 1, \\ (B^+, y_i(1)F_0, y_i(1)F_1, \dots, y_i(1)F_m), & \ell(s_i w) = \ell(w) - 1. \end{cases} \quad (9)$$

**Lemma 4.2.** *The chain  $q_\beta$  belongs to  $X(\beta)(\mathbb{R})$ , and  $H_{\delta(\beta)}$  fixes every flag of  $q_\beta$ .*

*Proof.* The first new step in either case of (9) has relative position  $s_i$ . Simultaneous left multiplication preserves all later relative positions. The ascent endpoint is  $s_i w B^+$ . In the descent case,  $w^{-1}(-\alpha_i)$  is positive, so  $y_i(1)$  fixes  $\dot{w}B^+$ . The endpoint is therefore the one specified by (2).

For the stabilizer assertion,  $U^+ = H_e$  fixes the initial empty chain. In the ascent case, move an element of  $H_{s_i w}$  across  $\dot{s}_i$  using (7). The resulting element of  $H_w$  fixes every old flag by induction. In the descent case use (8) to move an element of  $H_w$  across  $y_i(1)$ , then apply the same induction. Each of these subgroups also fixes the new initial flag  $B^+$ .  $\square$

In particular, if  $i$  is a left ascent of  $w = \delta(\gamma)$ , then  $x_i(t)$  fixes *every* flag of  $q_\gamma$ , for every real  $t$ . This is stronger than stabilization of the endpoint.

## 5 A simultaneous positive limit

**Lemma 5.1.** *The set  $\mathcal{Z}_{m, \geq 0}$  is preserved by simultaneous left translation by a positive torus element. If  $(B^+, F_1, \dots, F_m) \in \mathcal{Z}_{m, \geq 0}$  and  $a > 0$ , then*

$$(B^+, y_i(a)B^+, y_i(a)F_1, \dots, y_i(a)F_m) \in \mathcal{Z}_{m+1, \geq 0}.$$

*Proof.* For a positive torus element  $h$ , conjugation takes each simple negative root parameter to a positive multiple of that parameter. It preserves  $U_{\geq 0}^-$ . Since  $hB^+ = B^+$ , its action on a cumulative-product chain in (4) conjugates each factor  $u_j$  by  $\bar{h}$ . This proves the first assertion on the defining set and hence on its closure by continuity. The second assertion prefixes the allowed factor  $y_i(a)$  to that defining set and again extends to the closure by continuity.  $\square$

**Proposition 5.2.** *For every positive braid word  $\beta$ , the point  $q_\beta$  of (9) lies in  $P_\beta$ .*

*Proof.* Proceed by induction on word length. The empty case is immediate. In a descent, prefixing  $y_i(1)$  preserves the joint nonnegative closure by Lemma 5.1.

Consider an ascent and write  $q_\gamma = (F_0, \dots, F_m)$ . For  $t > 0$ , the rank-one identity

$$y_i(t)h_i(t)^{-1} = x_i(t^{-1})\dot{s}_i x_i(t) \quad (10)$$

follows by applying  $\phi_i$  to

$$\begin{pmatrix} 1 & 0 \\ t & 1 \end{pmatrix} \begin{pmatrix} t^{-1} & 0 \\ 0 & t \end{pmatrix} = \begin{pmatrix} 1 & t^{-1} \\ 0 & 1 \end{pmatrix} \begin{pmatrix} 0 & -1 \\ 1 & 0 \end{pmatrix} \begin{pmatrix} 1 & t \\ 0 & 1 \end{pmatrix}.$$

Lemmas 4.1 and 4.2 show that  $x_i(t)$  fixes all  $F_j$ . Hence

$$y_i(t)h_i(t)^{-1}F_j = x_i(t^{-1})\dot{s}_i F_j \quad (0 \leq j \leq m). \quad (11)$$

Act on the old nonnegative chain by  $h_i(t)^{-1}$ , then prefix  $y_i(t)$ . Lemma 5.1 places the entire chain

$$(B^+, y_i(t)h_i(t)^{-1}F_0, \dots, y_i(t)h_i(t)^{-1}F_m)$$

in  $\mathcal{Z}_{m+1, \geq 0}$ . Its first nonconstant flag is  $y_i(t)B^+$  because  $h_i(t)$  fixes  $F_0 = B^+$ . As  $t \rightarrow +\infty$ , equation (11) gives simultaneous convergence to  $(B^+, \dot{s}_i F_0, \dots, \dot{s}_i F_m)$ . The joint nonnegative set is closed, so this is the required ascent chain in it. Lemma 4.2 already gives the braid endpoint and relative positions; therefore  $q_\beta \in P_\beta$ .  $\square$

*Remark 5.3.* The products on the left of (10) need not converge in  $G$ . The assertion is convergence of their actions on the flags fixed by  $x_i(t)$ , using the right side of (11). Nor is this an argument that individually nonnegative flags automatically form a jointly nonnegative chain. The whole chain lies in the defining closed set before taking the limit.

## 6 The all-one left-inductive seed

We recall precisely the part of the weave recursion that is needed to evaluate the cluster variables. This avoids any need to compare two complete positive parameterizations.

**Proposition 6.1.** *Every extended variable of the left-inductive weave seed has value one at  $q_\beta$ .*

*Proof.* The assertion is empty for the empty word. Suppose it holds for  $\gamma$  and put  $w = \delta(\gamma)$ .

In an ascent, [CGGLSS, Lemmas 5.24(1) and 5.25] identifies  $X(i\gamma)$  with  $X(\gamma)$  by prefixing  $\dot{s}_i$ . The first braid coordinate is zero, the inductive weave gains a disjoint line, and its old cluster variables are unchanged. This is exactly the first case of (9), so their values remain one.

In a descent, for  $z \neq 0$  there is the factorization

$$\begin{aligned} B_i(z) &= L_i(z)U_i(z), \\ L_i(z) &= y_i(z^{-1})h_i(z), \quad U_i(z) = x_i(-z^{-1}). \end{aligned} \tag{12}$$

In rank one these factors are

$$\begin{pmatrix} z & 0 \\ 1 & z^{-1} \end{pmatrix} \begin{pmatrix} 1 & -z^{-1} \\ 0 & 1 \end{pmatrix} = \begin{pmatrix} z & -1 \\ 1 & 0 \end{pmatrix}.$$

The isomorphism  $X(\gamma) \times \mathbb{C}^* \simeq \{z \neq 0\} \subset X(i\gamma)$  in [CGGLSS, Lemma 5.24(2)] takes the cumulative old flags  $F_j$  to  $L_i(z)F_j$ . Indeed, moving the upper-unipotent factor  $U_i(z)$  through the old braid product is the coordinate change in that lemma. At  $z = 1$ , these flags are  $y_i(1)F_j$ , exactly the descent case in (9).

For a simply-laced group, [CGGLSS, Lemma 5.26(3)] says that the old cluster variables are preserved by this isomorphism. Let  $A_v$  be the new trivalent variable. Equation (32) there reads

$$z = A_v^{-1} \prod_u A_u^{c_u}, \tag{13}$$

where the  $A_u$  are old variables and the exponents are the corresponding cycle weights. At  $z = 1$ , with all  $A_u = 1$ , it follows that  $A_v = 1$ .

For completeness, the evaluation is unchanged in the non-simply-laced types. The framing and definition of the cluster variables in [CGGLSS, Section 6.1] are the same as in its Section 5. The unipotent gauge  $U_i(z)$  has diagonal entries one, so the old right incoming trivalent parameters, and hence the old cluster variables, are unchanged. The northeast parameter at the new trivalent vertex

is  $z^{-1}$ . Formula (25) expresses  $A_v$  as that parameter times a monomial in the old variables. Thus all-one input still gives  $A_v = 1$ , independently of root lengths and of those monomial exponents. Theorem 6.10 of [CGGLSS] establishes that the double-inductive seeds used here are cluster seeds in every finite type. This verifies the all-type extension of the evaluation, rather than imposing a simply-laced exchange matrix convention.

Induction proves the assertion for every extended variable, including the frozen ones.  $\square$

*Proof of Theorem 1.1.* Proposition 6.1 gives  $q_\beta \in C_\beta$ ; Proposition 5.2 gives  $q_\beta \in P_\beta$ . Corollary 3.3 then gives equality.  $\square$

The value-one assertion refers to the displayed left-inductive seed. Variables in another seed need not all evaluate to one. Their values are positive by mutation, which is the property used in the theorem.

## 7 Closures and small-rank examples

**Corollary 7.1.** *The common positive part is closed in the affine real variety  $X(\beta)(\mathbb{R})$ . Its closure in the projective flag-chain compactification is the geometric nonnegative closed braid variety; by Bao–He’s theorem, that closure is a regular CW complex homeomorphic to a closed ball.*

*Proof.* The first assertion follows from Proposition 3.1. The comparison theorem identifies the two positive subsets in the same compactification, so their closures agree. The second assertion is [BH, Theorems 3.4(2) and 5.1].  $\square$

The compact ball and its boundary structure in Corollary 7.1 are attributed results, not new ball theorems. A compact boundary need not arise by setting finite affine braid coordinates to zero.

*Example 7.2* (Raw positive coordinates). In type  $A_1$ , put

$$B(z) = \begin{pmatrix} z & -1 \\ 1 & 0 \end{pmatrix}, \quad P_{-1} = 0, \quad P_0 = 1, \quad P_j = z_j P_{j-1} - P_{j-2}.$$

For a word of length four the braid equation is  $P_4 = 0$ . The positive tuple

$$(z_1, z_2, z_3, z_4) = (1/2, 1/2, 1/2, 6/7)$$

has prefix continuants  $(P_0, P_1, P_2, P_3, P_4) = (1, 1/2, -3/4, -7/8, 0)$ . It is not geometrically positive. In rank one the flags are lines in  $\mathbb{R}^2$ , and cumulative products of  $y(a)$ ,  $a \geq 0$ , give weakly increasing slopes in  $[0, \infty]$ . This property persists in the defining closure. At the displayed tuple the first flag has slope 2, whereas the second has slope  $-2/3$ . Thus coordinatewise positivity does not characterize  $P_\beta$ , and, by Theorem 1.1, does not characterize  $C_\beta$ . The same tuple occurs in the rank-one research attempt attached to the source record in [UM]; it is used here as an illustration, not as a new counterexample.

**Proposition 7.3.** *For  $G = \mathrm{SL}_3$  and  $\beta = 121121$ , the real braid variety has six contractible connected components. Its cluster and geometric positive part is exactly the locus where all six affine braid coordinates are positive.*

*Proof.* With upper triangular  $B^+$  and the pinning (1), write

$$B_1(a) = \begin{pmatrix} a & -1 & 0 \\ 1 & 0 & 0 \\ 0 & 0 & 1 \end{pmatrix}, \quad B_2(b) = \begin{pmatrix} 1 & 0 & 0 \\ 0 & b & -1 \\ 0 & 1 & 0 \end{pmatrix}.$$

Set

$$M(a, b, c) = B_1(a)B_2(b)B_1(c) = \begin{pmatrix} ac-b & -a & 1 \\ c & -1 & 0 \\ 1 & 0 & 0 \end{pmatrix}, \quad \dot{w}_0 = M(0, 0, 0) = \dot{w}_0^{-1}.$$

The endpoint condition on  $M(a, b, c)M(d, e, f)$  is

$$(ac - b)(df - e) - af + 1 = 0, \quad (14)$$

$$c(df - e) - f = 0, \quad (15)$$

$$a - d(ac - b) = 0. \quad (16)$$

Put  $q = df - e$  and  $h = ac - b$ . If  $q = 0$ , equation (15) gives  $f = 0$ , then  $e = 0$ , contradicting (14). Equation (16) gives  $a = dh$ ; substitution in (14) gives  $eh = 1$ . The resulting formulas are

$$e, q \neq 0, \quad a = d/e, \quad b = 1/q, \quad c = f/q, \quad df = e + q. \quad (17)$$

Conversely these formulas imply all three endpoint equations. This identifies the variety with

$$\{(d, e, f, q) : e, q \in \mathbb{C}^*, d, f \in \mathbb{C}, df = e + q\}.$$

No division by  $d$  has been used, so the model retains  $d = 0$ .

Here 121 is a reduced lift of  $w_0$ . The right-inductive seed for the trailing word 121, computed by the principal-minor rule in [CGGLSS, Section 3.7 and Proposition 5.20], is

$$d, \quad e, \quad q = df - e.$$

The last occurrences of the two simple indices are frozen, so  $e, q$  are frozen units and  $d$  is mutable. The exchange relation is  $df = e + q$ . Cluster positivity is therefore  $d, e, q > 0$ . Formula (17) then makes all six original coordinates positive. Conversely, positive  $a, b, c, d, e, f$  give  $d, e > 0$  and  $q = 1/b > 0$ . Theorem 1.1 supplies equality with geometric positivity.

It remains to count real components. The signs of  $e$  and  $q$  cannot change on a connected component. If both are positive, then  $df = e + q > 0$ , giving two components distinguished by the sign of  $d$ ; each is parametrized by  $(|d|, e, q) \in (\mathbb{R}_{>0})^3$ . If both are negative, there are again two components, now with  $d$  and  $f$  of opposite signs, parametrized by  $(|d|, -e, -q)$ .

If  $e > 0$  and  $q < 0$ , set  $D = d/\sqrt{e}$ ,  $F = f/\sqrt{e}$ . This sign region is parametrized by

$$(e, D, F) \in \mathbb{R}_{>0} \times \{(D, F) \in \mathbb{R}^2 : DF < 1\}, \quad q = e(DF - 1).$$

The planar region is star-shaped about the origin: replacing  $(D, F)$  by  $(tD, tF)$ ,  $0 \leq t \leq 1$ , multiplies the product by  $t^2$  and preserves  $DF < 1$ . It is one contractible component. For  $e < 0$ ,  $q > 0$ , use  $E = -e$  and  $D = d/\sqrt{E}$ ,  $F = f/\sqrt{E}$ . The analogous region is  $\mathbb{R}_{>0} \times \{DF > -1\}$ , also star-shaped in the last two coordinates and contractible. The count is  $2 + 2 + 1 + 1 = 6$ .  $\square$

## 8 Verification and scope

The proofs above are analytic and algebraic. The accompanying Python standard-library code supplies exact finite regressions for the common-point construction and the small-rank identities. For the common point, 299,141 checks cover 1,742 type- $A$  flag chains and specified finite root-system calculations. The root systems include the exceptional finite types; the largest Weyl groups are sampled, not exhaustively enumerated. Full flags, endpoints, stabilizer actions and the rank-one

identity are checked. An intentional inverse-lift substitution is detected as a negative control. The separate rank-two script checks the polynomial model and flag-coordinate identities. The saved reports specify their domains.

Ordinary and optimized Python executions are required to return identical outputs. These are executions of the same code, not two independent implementations. They do not mechanically verify the topological limit, the imported cluster construction or the general comparison theorem, and they do not replace the written proofs.

Theorem 1.1 uses finite crystallographic type and the pinned split real form. No assertion is made for an infinite Kac–Moody weave structure, for an arbitrary Richardson identification, or for a partial compactification in which frozen variables may vanish. Nor is every real component asserted to be positive or to come from a compatible signed seed. The examples illustrate these distinctions without claiming a new classification of all real braid varieties.

## References

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