

On Maximum Clique and Maximum Consensus Formulations in Point Cloud Registration

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Abstract—Maximum clique and maximum consensus are widely used formulations for robust point cloud registration in robotics. Maximum consensus seeks one transformation that aligns as many matches as possible, while maximum clique selects matches through pairwise distance tests. Maximum clique is often used as a substitute for or an approximation to maximum consensus, with empirical evidence suggesting a close relationship. However, how closely the two formulations agree is not fully understood. We study this relationship theoretically. We show that a maximum clique can have arbitrarily large alignment error and be arbitrarily larger than the maximum consensus set at any fixed positive tolerance, and derive geometric conditions that bound this error. When rotation is fixed, we derive sharp error bounds and tests that exactly characterize maximum consensus for the translation subproblem. Finally, we study group- k consistency, which tests groups of k matches, and determine the smallest group sizes that guarantee alignment error bounds independent of point cloud scale and geometry. These are $d + 1$ for rotations and translations and $d + 2$ when reflections are allowed, in dimensions $d \geq 2$. Interactive examples and proof verification using the Lean theorem prover are available at <https://mc-vs-mc.pages.dev>.

I. INTRODUCTION

To build a map or localize within one, a robot needs to align 3D environment scans taken from different viewpoints [3], [4]. Point cloud registration estimates the alignment between the scans when they are represented as point clouds. When no initial alignment is available, registration pipelines begin by matching local features across the scans, providing a set of tentative correspondences [1]. Repeated structures and limited overlap can make many of these matches incorrect, so registration must identify which matches support a reliable alignment.

Maximum consensus and maximum clique are two widely used formulations for selecting reliable matches. *Maximum consensus* seeks one transformation that aligns as many correspondences as possible within a prescribed tolerance. *Maximum clique* selects a largest set that passes all pairwise distance tests, without estimating a transformation. The two are closely related, and **maximum clique is often used as a substitute for maximum consensus, but how far their solutions can differ is not fully understood.**

At matched tolerances, maximum clique is a relaxation of maximum consensus. Any set that one transformation aligns within the point tolerance passes every pairwise test and therefore forms a clique, so maximum clique size gives an upper bound on maximum consensus. The converse does not hold in general [5], [6]. This upper bound alone does not tell us the clique’s alignment error or how many of its matches can be aligned within the prescribed tolerance. Fig. 1

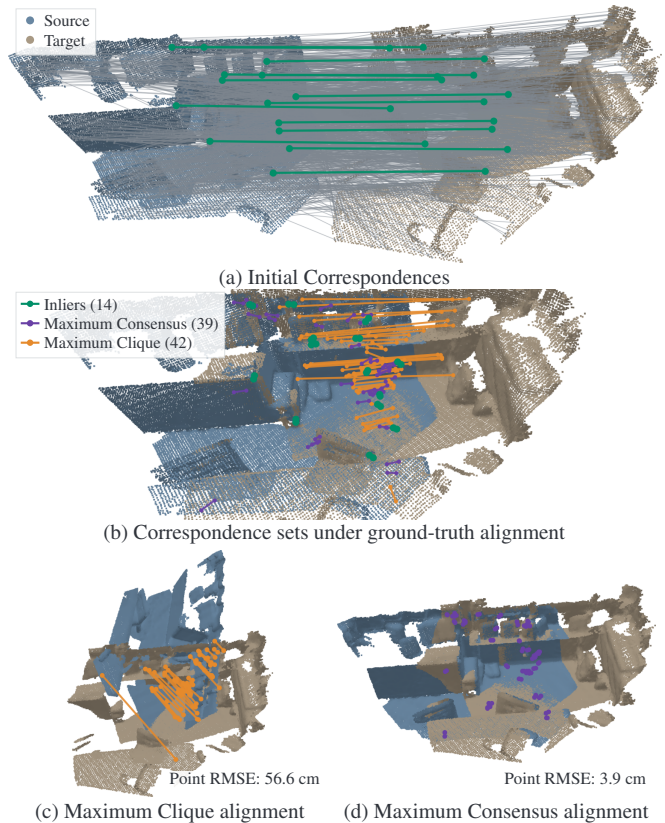


Fig. 1. Maximum clique and maximum consensus can yield very different alignments. (a) Tentative feature correspondences between two 3DMatch [1] scans using FPFH [2] and mutual nearest neighbor matching. (b) Scans aligned using the ground-truth transformation, showing the inlier correspondences, maximum consensus set at tolerance 5 cm, and maximum clique of the pairwise consistency graph at tolerance 10 cm. (c) Fitting the maximum clique produces a poor registration despite its pairwise consistency. (d) Fitting the maximum consensus set closely aligns the scans.

shows an example in practice, where a maximum clique and a maximum consensus set of similar sizes have few matches in common and produce very different registration results.

Testing larger groups offers a way to narrow this gap by detecting inconsistencies that pairwise tests miss. In *group- k consistency*, every group of up to k matches must admit an alignment within the prescribed tolerance, although different groups may use different transformations [7]. Fig. 2 compares these three selection approaches on a small example.

In this paper, we study the theoretical relationship between these three formulations, independently of a specific registration pipeline. We begin with the simpler problem of known rotation, where pairwise tests bound the translation error and testing larger groups gives an exact characterization

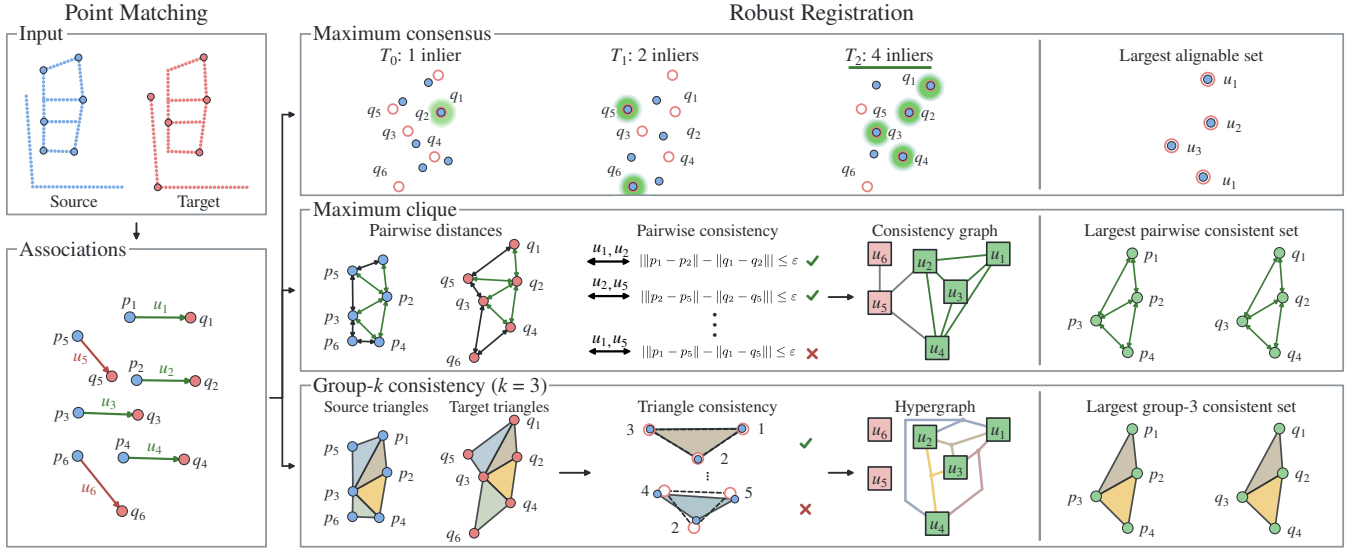


Fig. 2. Point matching followed by correspondence selection. Maximum consensus finds the transformation, T_2 , that aligns the most matches within tolerance among possible transformations such as T_0 , T_1 and T_2 . Maximum clique selects a largest set passing all pairwise distance tests. Group-3 consistency requires every triple in the selected set to be alignable at that tolerance, possibly by different transformations.

of maximum consensus. When rotation must also be estimated, **we show a maximum clique can have arbitrarily large alignment error and be arbitrarily larger than a maximum consensus set.** We derive bounds that explain how this error depends on point cloud geometry. We then show how group- k tests give alignment error guarantees without assumptions on point cloud scale or geometry, and determine the smallest group sizes needed. In summary, the contributions of this paper are as follows:

- We show that maximum clique and maximum consensus methods for point cloud registration can give different results in general. In particular, for certain point clouds, maximum clique can produce matches that cannot be obtained through maximum consensus, regardless of the chosen tolerance.
- When the rotation that aligns two point clouds is fixed, we provide sharp lower and upper bounds on the maximum consensus solution size in terms of the maximum clique size. In particular, in a d -dimensional space, we show that maximum clique using group- $(d+1)$ consistency is equivalent to maximum consensus.
- In the general case with unknown rotation, we show that $d+1$ is the smallest group size for which maximum clique using group consistency can provide lower and upper bounds on the maximum consensus solution size. When reflections are allowed, the smallest such group size is $d+2$.

II. RELATED WORK

Maximum consensus methods jointly estimate a transformation and select the correspondences that it fits within a tolerance. Random sampling can approximate maximum consensus by fitting small subsets and counting their inliers [8]. Deterministic methods use branch-and-bound search to solve

the maximum consensus problem [9] or subproblems based on other robust losses [10]. Geometric pruning methods can reduce this search by removing correspondences while preserving the maximum consensus solution [11].

Clique-based outlier rejection offers practical runtimes and robustness to extreme outlier rates, with reported registration results including cases where over 99% of matches are incorrect [12], [13]. Approaches include exact maximum clique search [12], approximations using large maximal cliques [13], and evaluating multiple candidate cliques before selecting an alignment [5], [6]. Graph structure and effective pruning can make maximum clique search practical despite its worst-case complexity [14], [12]. Clique selection can precede robust fitting [3], [15] or maximum consensus in separate rotation, translation, and scale subproblems [16].

Extensions of pairwise consistency use triangles [17] or shared neighbors [18] to reject matches that pass individual pairwise tests. Group- k consistency generalizes compatibility checks to k measurements and formulates selection as maximum clique in a hypergraph [7]. These tests capture relations among larger groups that pairwise checks can miss.

Beyond point cloud registration, consistency-based selection is used in inter-robot loop-closure selection [4], rotation averaging [15], and object-based localization [19]. These applications share the question of whether locally compatible measurements support one common estimate. A related geometric question arises in global graph rigidity, which asks when edge lengths uniquely determine a point configuration up to rigid motion [20].

This work studies the theoretical relationship between maximum consensus, maximum clique, and group- k consistency in point cloud registration. We use results from classical geometry [21], near-isometry theory [22], [23], and Procrustes analysis [24], [25], [26] to establish when

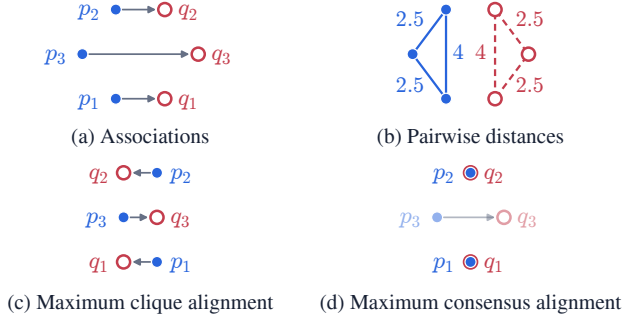


Fig. 3. Two reflected triangles have identical pairwise distances, forming a clique at $\epsilon = 0$. At $\tau = 0.5$, maximum consensus restricted to proper transformations can align only two matches.

consistency tests guarantee a bound on alignment error and when they can fail.

III. PRELIMINARIES

Let $\{(\mathbf{p}_i, \mathbf{q}_i)\}_{i=1}^n$, with $\mathbf{p}_i, \mathbf{q}_i \in \mathbb{R}^d$, be a set of candidate correspondences. A correspondence set $\mathcal{C}$ denotes a subset of the indices $\{1, \dots, n\}$. Registration seeks a rigid transformation $T(\mathbf{p}) = \mathbf{R}\mathbf{p} + \mathbf{t}$, where $\mathbf{t} \in \mathbb{R}^d$ and $\mathbf{R} \in O(d)$. We write $T \in E(d)$ for such transformations. We initially allow reflections to show that pairwise consistency can fail even when reflections are permitted. See Fig. 3. Proper rigid motions are treated separately in Section VI-C.

A. Maximum consensus

Given a point-error tolerance $\tau \in \mathbb{R}^+$, maximum consensus seeks a transformation that aligns as many correspondences as possible within τ . To express this objective in terms of subsets, define the alignment error of a correspondence set $\mathcal{C}$ as

$$\rho(\mathcal{C}) = \min_{T \in E(d)} \max_{i \in \mathcal{C}} \|T(\mathbf{p}_i) - \mathbf{q}_i\|. \quad (1)$$

We call $\mathcal{C}$ *alignable at tolerance τ* if a single transformation makes every point-to-point error at most τ , or equivalently $\rho(\mathcal{C}) \leq \tau$. We call the largest such set the maximum consensus set and denote its size by

$$\text{MC}(\tau) = \max\{|\mathcal{C}| : \rho(\mathcal{C}) \leq \tau\}. \quad (2)$$

B. Pairwise consistency

Pairwise consistency uses the fact that rigid transformations preserve distances. Define the distance discrepancy of a pair and its maximum over a correspondence set

$$\delta_{ij} = \left| \|\mathbf{p}_i - \mathbf{p}_j\| - \|\mathbf{q}_i - \mathbf{q}_j\| \right|, \quad (3)$$

$$\delta(\mathcal{C}) = \max_{i,j \in \mathcal{C}} \delta_{ij}. \quad (4)$$

The consistency graph has one vertex per correspondence and an edge between i and j whenever $\delta_{ij} \leq \epsilon$. A clique is a set of vertices in which every pair is connected, and a maximum clique is a largest such set. Let $\omega(\epsilon)$ denote the maximum clique size at tolerance ϵ

$$\omega(\epsilon) = \max\{|\mathcal{C}| : \delta(\mathcal{C}) \leq \epsilon\}. \quad (5)$$

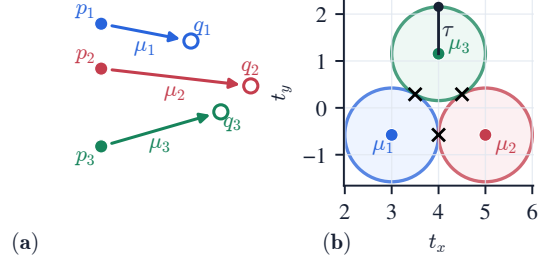


Fig. 4. In the translation subproblem, pairwise consistency does not guarantee a common translation at the same tolerance. (a) Each arrow μ_i is the translation vector that aligns source $\mathbf{p}_i$ and target $\mathbf{q}_i$. (b) Every disk of radius τ centered at μ_i contains all translations that align $\mathbf{p}_i$ and $\mathbf{q}_i$ within τ . Crosses mark pairwise intersections, but no translation aligns all three correspondences.

Note that the edge tolerance ϵ bounds distance disagreement, whereas τ measures point error.

If $\mathcal{C}$ is alignable at tolerance τ , the triangle inequality bounds the distance discrepancy of every pair by 2τ . Consequently,

$$\delta(\mathcal{C}) \leq 2\rho(\mathcal{C}), \quad \text{MC}(\tau) \leq \omega(2\tau). \quad (6)$$

C. Group- k consistency

For two correspondences, the alignment error is exactly half their distance discrepancy: $\rho(\{i, j\}) = \delta_{ij}/2$. A set therefore forms a clique at tolerance 2τ if and only if every pair is alignable at tolerance τ . Group- k consistency extends this requirement to larger subsets [7]. We call $\mathcal{C}$ *group- k consistent at tolerance τ* if every subset of at most k correspondences is alignable at τ , allowing a different transformation for each subset. Equivalently, $\rho_k(\mathcal{C}) \leq \tau$, where the *group- k consistency error* is the largest alignment error among these subsets

$$\rho_k(\mathcal{C}) = \max_{\substack{\mathcal{I} \subset \mathcal{C} \\ |\mathcal{I}| \leq k}} \rho(\mathcal{I}). \quad (7)$$

Increasing k strengthens the tests, giving

$$\delta(\mathcal{C})/2 = \rho_2(\mathcal{C}) \leq \rho_3(\mathcal{C}) \leq \dots \leq \rho(\mathcal{C}). \quad (8)$$

A uniform bound $\rho(\mathcal{C}) \leq c\rho_k(\mathcal{C})$ means that fitting every subset of at most k correspondences within τ/c guarantees one common alignment within τ . Throughout the paper, we therefore derive alignment error bounds, which also give lower bounds on maximum consensus.

IV. TRANSLATION SUBPROBLEM

We begin with the translation subproblem, in which rotation is fixed and only translation is estimated. This setting arises naturally in registration pipelines that estimate rotation and translation separately [3], [16], and provides a geometric baseline for understanding what local consistency can guarantee. Even in this simpler setting, aligning every pair of correspondences within a tolerance does not ensure a common translation at that tolerance. However, the gap is bounded, and we derive sharp alignment error bounds that progressively tighten as larger subsets are tested.

For a fixed rotation $\mathbf{R}$, each correspondence suggests the translation $\boldsymbol{\mu}_i = \mathbf{q}_i - \mathbf{R}\mathbf{p}_i$, illustrated by the arrows in Fig. 4(a). Applying a translation $\mathbf{t}$ gives correspondence i a point error of $\|\mathbf{t} - \boldsymbol{\mu}_i\|$. Therefore, the translations that align correspondence i within τ form a ball of radius τ centered at $\boldsymbol{\mu}_i$, shown in Fig. 4(b). Two correspondences are alignable by a common translation within τ exactly when their disks intersect, or equivalently when $\|\boldsymbol{\mu}_i - \boldsymbol{\mu}_j\| \leq 2\tau$. In the figure, every pair of disks intersects, but no translation belongs to all three, and aligning the entire set requires a larger tolerance.

To determine the tolerance required for a common translation, we define the translation-only alignment error as

$$\rho^{(t)}(\mathcal{C}) = \min_{\mathbf{t} \in \mathbb{R}^d} \max_{i \in \mathcal{C}} \|\mathbf{t} - \boldsymbol{\mu}_i\|. \quad (9)$$

Geometrically, $\rho^{(t)}(\mathcal{C})$ is the radius of the smallest ball enclosing the candidate translations. Jung's theorem [21] bounds this radius in terms of the largest distance between the candidates. Since the pairwise test ensures that these distances are at most 2τ , Jung's theorem bounds the alignment error by

$$\rho^{(t)}(\mathcal{C}) \leq \tau J_d, \quad J_d = \sqrt{\frac{2d}{d+1}}. \quad (10)$$

In one dimension, $J_1 = 1$, so maximum clique under this pairwise test is the same as the maximum consensus. The same equivalence holds for scalar scale estimation [16]. In 2D and 3D, the pairwise test guarantees a common translation within approximately 1.15τ and 1.22τ , respectively.

The generalized Jung's theorem [21] extends the pairwise bound to group- k consistency tests. Define $\rho_k^{(t)}$ as in (7), using $\rho^{(t)}$ in place of ρ . The alignment error is then bounded by

$$\rho^{(t)}(\mathcal{C}) \leq \rho_k^{(t)}(\mathcal{C}) J_{d,k}, \quad J_{d,k} = \sqrt{\frac{kd}{(d+1)(k-1)}}, \quad (11)$$

for $2 \leq k \leq d+1$. At $k = d+1$, the factor equals one, so aligning every subset of at most $d+1$ correspondences within τ guarantees a common translation at the same tolerance. Selecting a largest set satisfying these tests therefore solves translation-only maximum consensus exactly.

V. PAIRWISE CONSISTENCY WITH UNKNOWN ROTATION

We now consider the case where both rotation and translation are unknown. We first show that pairwise consistency does not guarantee bounded alignment error, and that the maximum clique size can exceed the maximum consensus size by an arbitrarily large factor. We then identify additional geometric conditions under which pairwise consistency guarantees bounded alignment error.

A. Limitations of pairwise consistency

We show that alignment error can grow arbitrarily large while pairwise consistency holds at a fixed tolerance. To simplify the arguments, we exploit the following constraint that pairwise consistency does not capture.

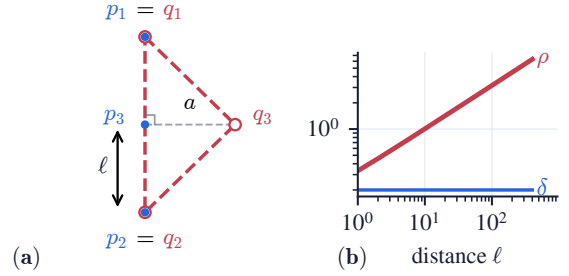


Fig. 5. Unbounded joint error at fixed pairwise discrepancy. (a) Source and target points. (b) Maximum pairwise distance error δ and alignment error ρ as distance ℓ grows.

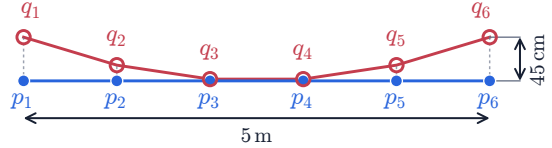


Fig. 6. All six correspondences are pairwise consistent at a distance-discrepancy tolerance of 5 cm, but no triple can be aligned within 2.5 cm. Thus maximum clique has size 6, while maximum consensus has size 2.

Lemma 1 (Zero-sum combination bound). *For a correspondence set $\mathcal{C}$ and coefficients α_i satisfying $\sum_{i \in \mathcal{C}} \alpha_i = 0$,*

$$\left\| \sum_i \alpha_i \mathbf{p}_i \right\| - \left\| \sum_i \alpha_i \mathbf{q}_i \right\| \leq \rho(\mathcal{C}) \sum_i |\alpha_i|. \quad (12)$$

If one transformation aligns all correspondences within τ , it also aligns corresponding midpoints and, more generally, convex combinations within τ . Differences of convex combinations give the zero-sum combinations used in the lemma.

Example 1 (Unbounded alignment error). Consider aligning the point clouds in Fig. 5(a) at tolerance τ , with

$$\begin{aligned} \mathcal{P} &= \{(0, \ell), (0, -\ell), (0, 0)\}, \\ \mathcal{Q} &= \{(0, \ell), (0, -\ell), (a, 0)\}. \end{aligned} \quad (13)$$

The point $\mathbf{p}_3$ is the midpoint of $\mathbf{p}_1$ and $\mathbf{p}_2$, whereas $\mathbf{q}_3$ lies a distance of $|a|$ from the midpoint of $\mathbf{q}_1$ and $\mathbf{q}_2$. Therefore, Lemma 1, with $\boldsymbol{\alpha} = (\frac{1}{2}, \frac{1}{2}, -1)$, gives $\rho(\mathcal{C}) \geq |a|/2$. Translating every source point horizontally by $a/2$ attains this bound, so $\rho(\mathcal{C}) = |a|/2$.

The distance between the first two source points equals the distance between their corresponding target points, and the other two pairwise distances each change by $\delta = \sqrt{\ell^2 + a^2} - \ell$. To keep this discrepancy fixed, choose

$$a = \sqrt{(\ell + 2\tau)^2 - \ell^2} = 2\sqrt{\tau(\ell + \tau)}. \quad (14)$$

As shown in Fig. 5(b), this keeps $\delta = 2\tau$, while

$$\lim_{\ell \rightarrow \infty} \rho(\mathcal{C}) = \lim_{\ell \rightarrow \infty} \frac{a}{2} = \infty. \quad (15)$$

Example 2 (Maximum clique can be arbitrarily larger than maximum consensus). As illustrated in Fig. 6, place n source points on a line and their targets on a parabola

$$\begin{aligned} x_i &= i - \frac{n+1}{2}, & i &= 1, \dots, n, \\ \mathbf{p}_i &= (\ell x_i, 0), & \mathbf{q}_i &= (\ell x_i, a x_i^2). \end{aligned} \quad (16)$$

A distance calculation similar to that in Example 1 gives

$$\delta_{ij} \leq \frac{a^2 |x_i - x_j| (x_i + x_j)^2}{2\ell}. \quad (17)$$

Choosing ℓ sufficiently large ensures $\delta_{ij} \leq 2\tau$ for every pair, forming a complete consistency graph with $\omega(2\tau) = n$.

For indices $i < j < k$, co-linearity of source points gives

$$\mathbf{p}_j = \lambda \mathbf{p}_i + (1 - \lambda) \mathbf{p}_k, \quad \lambda = \frac{k - j}{k - i}. \quad (18)$$

Using Lemma 1 with coefficients $\alpha = (\lambda, -1, 1 - \lambda)$ gives

$$|a|(j - i)(k - j) \leq 2\rho(\{i, j, k\}). \quad (19)$$

Since $(j - i)(k - j) \geq 1$, the alignment error is at least $|a|/2$. Choosing $a > 2\tau$ makes every triple inconsistent. Consequently

$$\omega(2\tau) = n, \quad \text{MC}(\tau) = 2. \quad (20)$$

B. Alignment bounds using point cloud geometry

Both previous counterexamples exploit increasing point cloud diameters to reduce pairwise distance discrepancies. This dependence on scale is captured by classical near-isometry theory, which studies how closely a map that approximately preserves distances can be matched by a rigid transformation [22], [23]. Let $\mathcal{C}$ be pairwise consistent at tolerance ϵ , and let D be the diameter of its source points. For $\epsilon \leq D$,

$$\rho(\mathcal{C}) \leq c_d \sqrt{D} \epsilon, \quad (21)$$

where c_d depends only on dimension. For $\epsilon \leq 0.01D$, the stated constants are $c_2 = 8.73$ in 2D and $c_3 = 18.8$ in 3D [22]. The $\sqrt{D}$ dependence is also unavoidable without additional assumptions such as point cloud spread or thickness, as Example 1 shows.

The diameter bound can be conservative because it uses a single global scale for all pairs. We instead derive a bound that combines each pair's discrepancy with its own source and target distances. Define the maximum squared-distance discrepancy of $\mathcal{C}$ as

$$h(\mathcal{C}) = \max_{i,j \in \mathcal{C}} \left| \|\mathbf{p}_i - \mathbf{p}_j\|^2 - \|\mathbf{q}_i - \mathbf{q}_j\|^2 \right|. \quad (22)$$

For a pair with source and target distances u and v , we have $|u^2 - v^2| = |u - v|(u + v)$. Thus, squared-distance discrepancies weight each pair's distance disagreement by the sum of its source and target lengths, penalizing discrepancies on longer pairs more strongly.

Proposition 1 (Squared-distance bound). *For any correspondence set $\mathcal{C}$,*

$$\rho(\mathcal{C})^2 \leq \sqrt{2d} h(\mathcal{C}). \quad (23)$$

The proof is given in the Appendix.

Consider a graph with one vertex per correspondence and an edge whenever the pairwise squared-distance discrepancy is at most η . Let $\omega_h(\eta)$ denote its maximum clique size. At $\eta = \tau^2/\sqrt{2d}$, Proposition 1 guarantees that every clique is alignable at tolerance τ , giving

$$\omega_h\left(\frac{\tau^2}{\sqrt{2d}}\right) \leq \text{MC}(\tau). \quad (24)$$

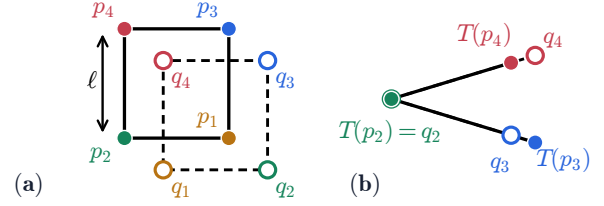


Fig. 7. Group-3 consistency does not bound the alignment error when reflections are allowed. (a) Four correspondences forming a rectangle of width 2 and height ℓ , with the two lower targets exchanged. (b) Every triple can be aligned with maximum point error at most $\sqrt{\ell^2 + 4} - \ell$. As ℓ grows, this error tends to zero, while aligning all four correspondences requires error at least 1.

The same bound also yields a diameter-based guarantee. Pairwise consistency bounds the target diameter by $D + \epsilon$, so $h(\mathcal{C}) \leq (2D + \epsilon)\epsilon$. Proposition 1 therefore gives $c_2 = 2.01$ and $c_3 = 2.22$ in (21) in the same regime.

VI. GROUP- k CONSISTENCY

Group- k consistency strengthens the local tests themselves and can provide alignment error guarantees without controlling point cloud scale or geometric conditioning. We first show that group- $(d + 1)$ consistency can still leave the alignment error unbounded. We then prove that $d + 2$ is the smallest group size that guarantees an alignment error bound. Finally, we separately study proper rigid transformations in $\text{SE}(d)$, where the consistency hierarchy behaves differently.

A. Limits of testing smaller groups

Testing larger groups does not immediately provide an alignment error guarantee.

Example 3 (Group-3 consistency cannot bound the error). Consider aligning two point clouds whose source points are

$$\mathcal{P} = \{(1, 0), (-1, 0), (1, \ell), (-1, \ell)\}, \quad (25)$$

The target points are identical except that the two lower targets are exchanged, as shown in Fig. 7.

Taking $\alpha = (1, -1, -1, 1)$ gives $\sum_i \alpha_i \mathbf{p}_i = 0$ while $\sum_i \alpha_i \mathbf{q}_i = (-4, 0)$. Therefore, Lemma 1 gives $\rho(\mathcal{C}) \geq 1$.

On the other hand, every triple can be aligned as in Fig. 7(b). First, align the unique point in one row with its corresponding target. The angle between its two sides is unchanged, so rotate or reflect the source to make the corresponding sides point in the same directions. These sides have lengths ℓ and $\sqrt{\ell^2 + 4}$, which are exchanged in the target triangle. The other two points therefore each have error $\sqrt{\ell^2 + 4} - \ell$, giving

$$\lim_{\ell \rightarrow \infty} \rho_3(\mathcal{C}) \leq \lim_{\ell \rightarrow \infty} \sqrt{\ell^2 + 4} - \ell = 0. \quad (26)$$

We can extend Example 3 to every dimension. First add zero coordinates to all points to embed them in higher dimensions. In three dimensions, replace $\mathbf{p}_4$ by two matching points whose midpoint is the original $\mathbf{p}_4$. In higher dimensions, use $d - 1$ affinely independent points whose average is the original $\mathbf{p}_4$, with their spread in the additional directions increasing with ℓ . More formally, choose fixed vectors

$\mathbf{v}_1, \dots, \mathbf{v}_{d-1}$ spanning $\mathbb{R}^{d-2}$ and satisfying $\sum_{i=1}^{d-1} \mathbf{v}_i = \mathbf{0}$. Replace the correspondence $\mathbf{p}_4$ by

$$\mathbf{p}_{i+3} = (-1, \ell, \ell \mathbf{v}_i), \quad i = 1, \dots, d-1. \quad (27)$$

Set $\mathbf{q}_1 = \mathbf{p}_2$ and $\mathbf{q}_2 = \mathbf{p}_1$, keeping all remaining target points identical to their sources. This construction gives the following result, which is proved in the Appendix.

Proposition 2 (Limits of group- $(d+1)$ tests). *For every $d \geq 2$, there are correspondence sets $\mathcal{C}_\ell$ in $\mathbb{R}^d$ such that*

$$\lim_{\ell \rightarrow \infty} \rho_{d+1}(\mathcal{C}_\ell) = 0, \quad \rho(\mathcal{C}_\ell) \geq 1 \quad \forall \ell > 0. \quad (28)$$

B. Rigid motions allowing reflections

Proposition 2 shows that group- $(d+1)$ consistency cannot guarantee an alignment error bound. Increasing the group size by one, however, gives a guarantee independent of the number of correspondences and their geometry.

Theorem 1 (Group- k consistency). *For every correspondence set $\mathcal{C}$ of points in $\mathbb{R}^d$,*

$$\rho(\mathcal{C}) \leq 2\sqrt{d} \rho_{d+2}(\mathcal{C}). \quad (29)$$

In 3D, if every subset of up to five correspondences can be aligned within τ , possibly by different transformations, then one rigid transformation aligns the entire set within $2\sqrt{3}\tau$.

The remainder of this subsection develops the proof of Theorem 1. We first relate the alignment error to weighted least-squares fitting, then show how local consistency bounds these weighted errors. Proofs of the intermediate lemmas are given in the Appendix.

For weights $\mathbf{w}$ with $\|\mathbf{w}\|_2 = 1$, define the optimal weighted least-squares error

$$E(\mathbf{w}) = \min_{T \in \text{E}(d)} \sum_{i \in \mathcal{C}} w_i^2 \|T(\mathbf{p}_i) - \mathbf{q}_i\|^2. \quad (30)$$

This is a weighted orthogonal Procrustes problem, solvable using singular value decomposition [27]. Maximizing $E(\mathbf{w})$ over the weights gives the Lagrangian dual problem of $\rho(\mathcal{C})^2$

$$\rho(\mathcal{C})^2 = \max_{\|\mathbf{w}\|_2=1} E(\mathbf{w}). \quad (31)$$

Lemma 2 (Duality gap bound). *For every correspondence set $\mathcal{C}$,*

$$\underline{\rho}(\mathcal{C}) \leq \rho(\mathcal{C}) \leq \sqrt{2} \underline{\rho}(\mathcal{C}). \quad (32)$$

To bound $E(\mathbf{w})$ using local consistency, we return to the zero-sum point combinations from Lemma 1, such as vectors between midpoints. The following lemma expresses the weighted fitting error as a sum of squared length differences between corresponding source and target combinations.

Lemma 3 (Weighted error as length differences). *For every $\mathbf{w}$ with $\|\mathbf{w}\|_2 = 1$, there exist orthonormal vectors $\mathbf{v}_1, \dots, \mathbf{v}_r$, with $r \leq 2d$, such that, setting $\boldsymbol{\alpha}^{(j)} = \mathbf{w} \odot \mathbf{v}_j$,*

$$E(\mathbf{w}) = \sum_{j=1}^r (\|\sum_i \alpha_i^{(j)} \mathbf{p}_i\| - \|\sum_i \alpha_i^{(j)} \mathbf{q}_i\|)^2, \quad (33)$$

$$\mathbf{v}_j^\top \mathbf{w} = 0, \quad j = 1, \dots, r. \quad (34)$$

Here $\odot$ denotes the elementwise product.

We next bound these length differences using local consistency, extending Lemma 1.

Lemma 4 (Local zero-sum combination bound). *For a correspondence set $\mathcal{C}$ and coefficients satisfying $\sum_{i \in \mathcal{C}} \alpha_i = 0$,*

$$\|\sum_i \alpha_i \mathbf{p}_i\| - \|\sum_i \alpha_i \mathbf{q}_i\| \leq \rho_{d+2}(\mathcal{C}) \sum_i |\alpha_i|. \quad (35)$$

Although the coefficients can involve the entire set, the bound depends on at most $d+2$ correspondences at a time.

Proof of Theorem 1. Lemma 4 bounds each length difference in Lemma 3 by $\rho_{d+2}(\mathcal{C})$. With at most $2d$ squared terms, $E(\mathbf{w}) \leq 2d\rho_{d+2}(\mathcal{C})^2$ for every $\mathbf{w}$. Maximizing over $\mathbf{w}$ gives $\underline{\rho}(\mathcal{C})^2 \leq 2d\rho_{d+2}(\mathcal{C})^2$, and Lemma 2 gives (29). $\square$

C. Proper rigid motions

So far, allowing reflections has strengthened the counterexamples by allowing a larger transformation class. For group- k consistency, however, proper rigid motions behave differently. Restricting orientation changes the first k that guarantees a bounded alignment error. We write $\rho^+(\mathcal{C})$ for (1) with the optimization restricted to $\text{SE}(d)$, and define $\rho_k^+(\mathcal{C})$ analogously.

Lemma 5 (Local orientation equivalence). *For a correspondence set $\mathcal{I}$ with $|\mathcal{I}| \leq d$, $\rho^+(\mathcal{I}) = \rho(\mathcal{I})$. Consequently, $\rho_k^+(\mathcal{C}) = \rho_k(\mathcal{C})$ for every $k \leq d$.*

Together with Proposition 2, this rules out an alignment error bound for $k \leq d$. By Lemma 5, Example 3 gives

$$\lim_{\ell \rightarrow \infty} \rho_d^+(\mathcal{C}_\ell) = 0, \quad \rho^+(\mathcal{C}_\ell) \geq \rho(\mathcal{C}_\ell) \geq 1 \quad \forall \ell > 0. \quad (36)$$

At $k = d+1$, the orientation restriction becomes useful. Comparing two proper rigid motions on at most d well-chosen source points is enough to bound their disagreement over the entire cloud.

Lemma 6 (Anchor control). *For every set of source points $\mathcal{P} \subset \mathbb{R}^d$, there is a subset $\mathcal{A} \subseteq \mathcal{P}$ with $|\mathcal{A}| \leq d$ such that any two transformations $T, U \in \text{SE}(d)$ satisfy*

$$\max_{\mathbf{p} \in \mathcal{P}} \|T(\mathbf{p}) - U(\mathbf{p})\| \leq d \max_{\mathbf{a} \in \mathcal{A}} \|T(\mathbf{a}) - U(\mathbf{a})\|. \quad (37)$$

In 2D, we can choose a farthest pair of source points, and in 3D, the vertices of a maximum-area triangle suffice. The proof is given in the Appendix.

Proposition 3 (Proper group- k consistency). *For every correspondence set $\mathcal{C}$ of points in $\mathbb{R}^d$, with $\tau = \rho_{d+1}^+(\mathcal{C})$*

$$\rho^+(\mathcal{C}) \leq (2d+1)\tau. \quad (38)$$

Proof. Choose anchor indices $\mathcal{A}$ as in Lemma 6. Let T_0 fit $\mathcal{A}$ within τ , and let T_i align $\mathcal{A} \cup \{i\}$ within τ . They differ by at most 2τ on every anchor, so for all i

$$\|T_0(\mathbf{p}_i) - \mathbf{q}_i\| \leq \|T_0(\mathbf{p}_i) - T_i(\mathbf{p}_i)\| + \tau \leq (2d+1)\tau. \quad (39)$$

$\square$

VII. CONCLUSION

We have shown that maximum clique can differ arbitrarily from maximum consensus in both selected-set size and alignment error. For fixed rotation, classical geometry provides a bound on alignment error and establishes the equivalence between maximum consensus and selecting a largest group- k consistent set at $k = d + 1$. For full registration, our squared-distance bound accounts for the scale of each pair, while group- k tests can remove dependence on point cloud scale and geometry altogether. The smallest sufficient group sizes are $d + 1$ for proper rigid motions and $d + 2$ when reflections are allowed. These results establish theoretical guarantees and limitations of pairwise and subset consistency, independent of any particular registration pipeline.

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APPENDIX

We present proofs of the results discussed in the main text. All proofs have been formally verified using the Lean theorem prover [28]. The corresponding Lean formalization is available at <https://mc-vs-mc.pages.dev>.

Proof of Lemma 1. Choose a transformation with residuals $\mathbf{e}_i = \mathbf{R}\mathbf{p}_i + \mathbf{t} - \mathbf{q}_i$ satisfying $\|\mathbf{e}_i\| \leq \rho(\mathcal{C})$. Since $\sum_i \alpha_i = 0$, we have $\mathbf{R}\sum_i \alpha_i \mathbf{p}_i - \sum_i \alpha_i \mathbf{q}_i = \sum_i \alpha_i \mathbf{e}_i$. The triangle inequality gives (12), since $\mathbf{R}$ preserves lengths. $\square$

Proof of Proposition 2. A fit of the replacement points also fits their centroid, the original $\mathbf{p}_4$, within the same tolerance. Lemma 1 therefore gives $\rho(\mathcal{C}_\ell) \geq 1$. If a $(d + 1)$ -point subset omits $\mathbf{p}_1$ or $\mathbf{p}_2$, apply the planar fit in the first two coordinates and leave the others unchanged. The replacement points share their planar coordinates, so every residual is at most $\sqrt{\ell^2 + 4} - \ell \rightarrow 0$. Otherwise, the subset contains $\mathbf{p}_1, \mathbf{p}_2$ and $d - 1$ points whose targets are unchanged. Take the hyperplane through the origin and these fixed points. Their last $d - 1$ coordinates, divided by ℓ , are $(1, \mathbf{v}_i)$, possibly with

one vector replaced by their average $(1, \mathbf{0})$. The spanning and zero-sum conditions make $(1, \mathbf{v}_i)$ a basis; replacing one vector by their average preserves independence. The first coordinates remain bounded, so this hyperplane tends to $x_1 = 0$ as ℓ grows. Reflection in this hyperplane fixes those points and swaps $\mathbf{p}_1, \mathbf{p}_2$ with vanishing error for large ℓ . $\square$

Proof of Lemma 2. For any transformation, the weighted mean squared error is at most its largest squared residual, giving $\underline{\rho} \leq \rho$. Put $b = \rho(C)^2$ and $\lambda_i = w_i^2$. All vectors $\mathbf{q}_i - \mathbf{R}\mathbf{p}_i$ lie in one fixed ball. Projecting translations onto this ball cannot increase residuals, so the transformations may be restricted to a compact set. The expected squared error is linear in the weights and in a probability distribution over transformations. The minimax theorem [29] therefore gives optimal weights $\boldsymbol{\lambda}^*$ and a random fit T satisfying

$$\mathbb{E}\|T(\mathbf{p}_i) - \mathbf{q}_i\|^2 \leq b \quad \forall i. \quad (\text{A1})$$

The $\boldsymbol{\lambda}^*$ -weighted error is at least b for every fit and has mean at most b , so the distribution uses only weighted minimizers. Every such minimizer aligns the $\boldsymbol{\lambda}^*$ -weighted centroids $\bar{\mathbf{p}}, \bar{\mathbf{q}}$. Thus $T(\mathbf{p}) = \mathbf{U}(\mathbf{p} - \bar{\mathbf{p}}) + \bar{\mathbf{q}}$ for a random $\mathbf{U} \in O(d)$.

Take an SVD $\mathbb{E}\mathbf{U} = \mathbf{N} = \mathbf{A}\boldsymbol{\Sigma}\mathbf{B}^\top$ and set $\mathbf{R} = \mathbf{A}\mathbf{B}^\top$. The singular values σ_j of $\mathbf{N}$ lie in $[0, 1]$, so $|2\sigma_j - 1| \leq 1$ and $\|\mathbf{2N} - \mathbf{R}\|_2 \leq 1$. Hence $\mathbf{y}^\top(\mathbf{2N} - \mathbf{R})\mathbf{x} \leq \|\mathbf{x}\|\|\mathbf{y}\| \leq (\|\mathbf{x}\|^2 + \|\mathbf{y}\|^2)/2$. Expanding the squared errors then gives

$$\frac{1}{2}\|\mathbf{R}\mathbf{x} - \mathbf{y}\|^2 \leq \mathbb{E}\|\mathbf{U}\mathbf{x} - \mathbf{y}\|^2. \quad (\text{A2})$$

Taking $\mathbf{x} = \mathbf{p}_i - \bar{\mathbf{p}}$ and $\mathbf{y} = \mathbf{q}_i - \bar{\mathbf{q}}$ proves (32). $\square$

Proof of Lemma 4. Put $\varepsilon = \rho_{d+2}(C)$, $L = \sum_i |\alpha_i|$, and $\mathbf{x} = \sum_i \alpha_i \mathbf{p}_i$. Fix a unit vector $\mathbf{u}$ and maximize $\mathbf{u}^\top \sum_i \beta_i \mathbf{q}_i$ subject to $\sum_i \beta_i \mathbf{p}_i = \mathbf{x}$, $\sum_i \beta_i = 0$, and $\sum_i |\beta_i| \leq L$. Writing each β_i as the difference of two nonnegative variables gives a bounded linear program with $d+1$ equalities and one bound on their sum. Adding a slack variable for this bound gives $d+2$ equality constraints. An optimal basic solution has at most $d+2$ nonzero variables, and therefore uses at most $d+2$ correspondences. Since $\boldsymbol{\alpha}$ is feasible, applying Lemma 1 to those correspondences gives

$$\mathbf{u}^\top \sum_i \alpha_i \mathbf{q}_i \leq \mathbf{u}^\top \sum_i \beta_i \mathbf{q}_i \leq \|\mathbf{x}\| + \varepsilon L. \quad (\text{A3})$$

Maximizing over $\mathbf{u}$ bounds the target norm. Exchanging source and target gives the reverse inequality. $\square$

Proof of Lemma 3. Let $\bar{\mathbf{p}} = \sum_i w_i^2 \mathbf{p}_i$ and $\bar{\mathbf{q}} = \sum_i w_i^2 \mathbf{q}_i$ be the weighted centroids, and form matrices with columns

$$\mathbf{F}_i = w_i(\mathbf{p}_i - \bar{\mathbf{p}}), \quad \mathbf{G}_i = w_i(\mathbf{q}_i - \bar{\mathbf{q}}). \quad (\text{A4})$$

The optimal translation is $\bar{\mathbf{q}} - \mathbf{R}\bar{\mathbf{p}}$ [27], giving

$$E(\mathbf{w}) = \min_{\mathbf{R} \in O(d)} \|\mathbf{R}\mathbf{F} - \mathbf{G}\|_F^2. \quad (\text{A5})$$

On $S = (\ker \mathbf{F} \cap \ker \mathbf{G})^\perp$, the Fuchs–Caves identity [30] and the Procrustes trace formula give an orthonormal basis $\mathbf{v}_1, \dots, \mathbf{v}_r$ such that

$$E(\mathbf{w}) = \sum_{j=1}^r (\|\mathbf{F}\mathbf{v}_j\| - \|\mathbf{G}\mathbf{v}_j\|)^2. \quad (\text{A6})$$

For positive-definite real Gram matrices, the identity is attained by an eigenbasis of a real symmetric matrix; rescaling removes its trace-normalization requirement. For singular Gram matrices, add $\eta \mathbf{I}_S$ to both restrictions to S . As $\eta \downarrow 0$, compactness gives a convergent subsequence of orthonormal bases, and continuity preserves the identity.

Finally, $r = \dim S \leq 2d$ and $\mathbf{F}\mathbf{w} = \mathbf{G}\mathbf{w} = 0$, so $\mathbf{v}_j^\top \mathbf{w} = 0$. Thus $\boldsymbol{\alpha}^{(j)} = \mathbf{w} \odot \mathbf{v}_j$ has zero sum, centering cancels, and (A6) gives the stated point combinations. $\square$

Proof of Proposition 1. Use the centered matrices in (A4), set $\mathbf{H} = \mathbf{I} - \mathbf{w}\mathbf{w}^\top$, and define

$$\Delta_{ik} = w_i w_k (\|\mathbf{p}_i - \mathbf{p}_k\|^2 - \|\mathbf{q}_i - \mathbf{q}_k\|^2). \quad (\text{A7})$$

Expanding squared distances gives

$$\mathbf{F}^\top \mathbf{F} - \mathbf{G}^\top \mathbf{G} = -\frac{1}{2} \mathbf{H} \boldsymbol{\Delta} \mathbf{H}. \quad (\text{A8})$$

Since $\mathbf{H}$ is an orthogonal projection and $\|\mathbf{w}\|_2 = 1$ gives $\|\boldsymbol{\Delta}\|_F \leq h(C)$, the Procrustes bound [25] yields

$$\begin{aligned} E(\mathbf{w}) &\leq \sqrt{2d} \|\mathbf{F}^\top \mathbf{F} - \mathbf{G}^\top \mathbf{G}\|_F \\ &\leq \frac{\sqrt{2d}}{2} \|\boldsymbol{\Delta}\|_F \leq \frac{\sqrt{2d}}{2} h(C). \end{aligned} \quad (\text{A9})$$

Maximizing over $\mathbf{w}$ and applying Lemma 2 gives (23). $\square$

Proof of Lemma 5. Because there are at most d source points, they lie in an affine hyperplane. Reflection J across this hyperplane fixes them all. If an optimal unrestricted fit T is improper, $T \circ J$ is proper and has the same residuals. Thus restricting the fit to proper motions does not change the optimal error. $\square$

Proof of Lemma 6. If $\mathcal{P}$ has affine dimension $r < d$, choose the vertices of a maximum-volume r -simplex as anchors. Each point has coordinates $\mathbf{p} = \sum_j \beta_j \mathbf{a}_j$ with $\sum_j \beta_j = 1$. Replacing vertex j multiplies its volume by $|\beta_j|$, hence $|\beta_j| \leq 1$. The affine map $T - U$ therefore gives $\|T(\mathbf{p}) - U(\mathbf{p})\| \leq (r+1) \max_j \|T(\mathbf{a}_j) - U(\mathbf{a}_j)\|$, with $r+1 \leq d$.

For full-dimensional $\mathcal{P}$ and $d \geq 2$, choose the d vertices of a maximum-volume $(d-1)$ -simplex $\mathcal{A}$. For the rotations $\mathbf{R}, \mathbf{S} \in \text{SO}(d)$ of T, U , halving the planar rotation angles gives an orthogonal square root $\mathbf{Q}^2 = \mathbf{R}^\top \mathbf{S}$. The map $f = \mathbf{Q}^\top \mathbf{R}^\top (T - U)$ preserves disagreement lengths and has skew-symmetric linear part $\mathbf{K} = \mathbf{Q}^\top - \mathbf{Q}$. Choose the origin in the anchor hyperplane and let $\mathbf{n}$ be its unit normal. Write $\mathbf{x} = \mathbf{v} + h\mathbf{n}$, with $\mathbf{v} \perp \mathbf{n}$. Let $\beta_j(\mathbf{v})$ be the barycentric coordinates of $\mathbf{v}$ and $\mathbf{g}_j$ their gradients within the hyperplane. Interpolation and $\mathbf{K}^\top = -\mathbf{K}$ give

$$f(\mathbf{x}) = \sum_{j=1}^d [\beta_j \mathbf{I} + h(\mathbf{n}\mathbf{g}_j^\top - \mathbf{g}_j \mathbf{n}^\top)] f(\mathbf{a}_j). \quad (\text{A10})$$

The j th coefficient matrix has norm $\sqrt{\beta_j^2 + h^2 \|\mathbf{g}_j\|^2}$. Since $\|\mathbf{g}_j\|$ is the reciprocal of the altitude at $\mathbf{a}_j$, this is also the volume ratio when $\mathbf{a}_j$ is replaced by $\mathbf{x}$. For $\mathbf{x} \in \mathcal{P}$, maximality bounds each factor by one, giving $\|f(\mathbf{x})\| \leq \sum_j \|f(\mathbf{a}_j)\| \leq d \max_j \|f(\mathbf{a}_j)\|$. $\square$