

Point Cloud Registration Based on 1-point RANSAC and Scale-annealing Biweight Estimation

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Abstract—Point cloud registration (PCR) is an important task in photogrammetry and remote sensing, whose goal is to seek a 7-parameters similarity transformation to register a pair of point clouds. Traditional iterative closest point (ICP) variants highly rely on the initial parameters and most of them cannot deal with cross-source (multi-source) point clouds with scale changes. In this paper, we propose a flexible correspondence-based PCR method, which is initial-guess free, fast, and robust. We first decompose the full 7-parameters registration problem into three subproblems, i.e., scale, rotation, and translation estimations, based on line vectors. Then, we propose an 1-point random sample consensus (RANSAC) algorithm to estimate the scale and translation parameters. For the rotation estimation, we introduce a graduated optimization strategy into the Tukey’s biweight function and propose a scale-annealing biweight estimator. We evaluate the proposed method on both same-source and cross-source data. Results show that the proposed method is robust against over 99% outliers and is 1~2 orders of magnitude faster than its competitors. The source code of our method will be made public¹.

Index Terms—Point cloud registration, cross-source (multi-source), correspondence, RANSAC, biweight estimator.

I. INTRODUCTION

THREE dimensional measurement such as light detection and ranging (LiDAR) scanning is a basic and important technique, which has been widely applied in the fields of remote sensing, photogrammetry, and computer vision, such as 3D city modeling [1], digital elevation model (DEM) generation [2], simultaneous localization and mapping (SLAM) [3], indoor mapping [4], and archaeology [5], to name a few. Unfortunately, a single point cloud only covers a part of the scene due to viewpoint occlusions and limited field-of-view (FoV). For example, the maximum measuring range of RIGEL VZ-400² scanner is 600m and its vertical FoV is 100°. To cope with this problem, multiple 3D scans recorded from different viewpoints are required to cover the whole scene. Similar to image-based 3D reconstruction, these scans form a scan sequence where each adjacent point cloud pair has overlaps. Point cloud registration (PCR) can merge these individual scans into a 3D panorama, whose basic idea is to seek optimal similarity transformations to convert point clouds with local coordinate systems into the same reference system [6].

Iterative closest point (ICP) [7] is probably the most popular PCR method, which has become a de-facto standard for engineering solutions. However, the performance of ICP highly relies on the initializations for rigid transformations since it establishes correspondences based on nearest distance in each

iteration and only converges to a local minimum. In practice, engineering solutions require additional information to improve the robustness of ICP. For example, RIEGL airborne LiDAR equips a GNSS/INS navigation system to provide real-time pose for accurate point cloud fusion; ground laser LiDARs such as Z+F IMAGER³ scanner use high-reflection targets as control points to estimate initial solutions. However, GNSS/INS systems are expensive and control point layout is labor-intensive. Moreover, ICP cannot deal with cross-source point clouds with scale changes such as multi-view stereo (MVS) and LiDAR point cloud pairs [8], [9]. The MVS-LiDAR registration can reconstruct more realistic and accurate 3D scenes. LiDAR provides accurate geometric information while MVS provides rich spectral information. Both geometric information and spectral information are important for scene interpretation. For example, LiDAR-MVS fusion can improve the accuracies of object detection, classification, semantic segmentation, etc.

Thanks to the development of 3D keypoint technology, correspondence-based PCR methods have received more and more attentions, because they are initialization-free, cheap, and flexible. Unlike ICP, these methods pre-establish correspondences by a 3D feature matching technique such as fast point feature histogram (FPFH) [10] algorithm. Then, a geometric transformation (7-parameters similarity model) is fitted via robust estimation. Perhaps, random sample consensus (RANSAC) [11] is the most widely used method for robust model fitting. Unfortunately, 3D keypoint matching [12] is much more challenging than 2D feature matching like scale-invariant feature transform (SIFT) [13], speeded up robust features (SURF) [14], and radiation-variation insensitive feature transform (RIFT) [15], because of the problems of texture-less, noise, and density variations, which result in extremely high outlier rates in putative correspondences. As point out by [16], the outlier rates of initial correspondences are often higher than 95%. At such high outlier rates, RANSAC and its variants require a huge number of subset sampling trials to obtain a satisfactory result, which dramatically decreases their efficiency. For instance, to obtain an outlier-free minimal size subset with 0.99 confidence for 7-parameters registration at an outlier rate of 99%, RANSAC theoretically requires 4605168 trials (please see Sec. III-B for details), which is too huge to be practical.

In this paper, we aim to design a PCR method with following properties: (1) initialization-free; (2) high efficiency; (3) high robustness (robust against over 99% outliers); (4) 7-

¹<http://www.escience.cn/people/ljiayuan/index.html>

²<http://www.riegl.com/products/>

³<https://www.zf-laser.com>

parameters registration (suitable for cross-source point clouds with scale changes). We extend the concept of line vector to cope with scale changes and use it to decompose the full 7-parameters registration problem into three subproblems, which largely reduces the parameter space. This decomposition lays a foundation for the subsequent model estimation, which makes the 7-DoF registration problem become much easier. We propose a 1-point RANSAC for scale and translation estimations, which dramatically reduces the computational complexity. Our 1-point RANSAC does not require any prior information since the transformation decomposition does not rely on other sensor information or assumptions. To our best knowledge, 1-point RANSAC has never been used in PCR before. We also introduce a graduated optimization strategy into the biweight function to solve the rotation problem, which is fast and robust. These improvements guarantee the high robustness and high efficiency of the proposed method. The proposed method is a correspondence-based method, which does not require initial parameters to establish correspondences like ICP-type methods. The estimations of scale, rotation, and translation also do not rely on initial solutions. Thus, it is an initialization-free method unlike ICP. We conduct two real experiments, i.e., same-source registration and cross-source registration. Both experiments show that the proposed method is much superior to other compared baselines and state-of-the-arts, especially on cases with extremely high outlier rates.

The remainder of this manuscript is organized as follows. Section II briefly reviews some related techniques. Section III describes the details of the proposed PCR method. The experimental setup, datasets, performance metrics, and result discussions are provided in Section IV. Section V presents the conclusions.

II. RELATED WORK

In this section, we briefly review some techniques that are highly related to PCR, including 3D keypoint matching, correspondence-based registration, and point-based registration methods. More comprehensive surveys can be found in [17], [18].

A. 3D Keypoint Matching

The same as image feature matching, 3D keypoint matching also contains three main steps: detection, description, and matching.

Keypoint detectors: Detectors usually analyze the distribution properties of local surfaces to identify distinctive points (keypoints), which can be grouped into two categories, i.e., hand-crafted detectors and learning-based ones. Hand-crafted detectors are mostly driven by mathematical analysis. The representative methods are local surface patches (LSP) [19], intrinsic shape signatures (ISS) [20], MeshDoG [21], and so on. Differently, learning-based ones are driven by data, e.g., KeypointNet [22], unsupervised stable interest point (USIP) [23], and salient keypoint detection (SKD) [24].

Keypoint description: Descriptors encode local patches of keypoints into feature vectors, so that matching patches and non-matching patches can be easily distinguished. Unique

shape context (USC) [25], binary shape context (BSC) [26], [27], fast point feature histogram (FPFH) [10], and rotational projection statistics (RoPS) [28] are representative hand-crafted descriptors. Recently, learning-based descriptors (such as 3DMatch [29], PPFNet [30], and 3DSmoothNet [31]) become popular, which have shown potentials compared with their hand-crafted counterparts.

Feature matching: Establish one-to-one corresponding relationship based on matching scores between feature vectors of keypoints, e.g., the chi-square test method [20] and nearest neighbor distance ratio strategy [13].

B. Correspondence-based Registration

RANSAC-family: RANSAC is the most widely used robust fitting method in computer vision, whose basic idea relies on a hypothesize-and-verify technique. RANSAC alternately performs minimal subset sampling and model fitting until stopping criterion is reached. It has many variants [32]–[41]. For example, maximum likelihood estimation sample consensus (MLESAC) [32] generalizes RANSAC based on a probabilistic interpretation. Group sample consensus (GroupSAC) [34] uses a prior that inliers are more similar to each other to improve the sampling stage. Locally optimized RANSAC (LORANSAC) [33] and fixed LORANSAC (FLORANSAC) [36] do not agree with the assumption that a model fitted by an outlier-free subset is consistent with all inliers. They locally refine the estimated model based on current inlier set. Chum and Matas [35] proposed a model verification strategy called modified sequential probability ratio (SPR) test to reduce the time complexity. Universal RANSAC (USAC) [37] incorporates many practical tricks such as sampling, model checking, model verification, and model refinement into a common framework. Marginalizing sample consensus (MAGSAC++) [39] proposes a scoring function that the inlier threshold parameter is not required and fits model by iteratively reweighted least-squares (IRLS) [42]. Differentiable sample consensus (DSAC) [40] uses a probabilistic-based hypothesis selection to learn good samples in an end-to-end manner. Neural-guided RANSAC (NG-RANSAC) [41] uses prior information to guide hypothesis sampling and combines this strategy with DSAC to build neural networks. As mentioned earlier, the major limitation of these methods is that they require a huge number of iterations to seek a satisfactory solution under high outlier rates.

M-like estimators: M-like estimators penalize outliers by giving them very small weights based on robust cost functions [43]–[50]. Unfortunately, traditional M-estimators and S-estimators are sensitive to outlier rates. They can not tolerate more than 50% outliers. Recently, several robust methods that are robust to high outlier rates are proposed. For example, Zhou et al. [47] introduced the Geman-McClure estimator loss for PCR and optimized this robust cost based on line processes. Similar to our method, truncated least squares estimation and semidefinite relaxation (TEASER++) first decouples the registration problem into subproblems. Differently, it uses a truncated least-squares (TLS) cost for each subproblem estimation. The complexity of scale estimation in TEASER++ is $O(N^4)$, which is too slow to be practical.

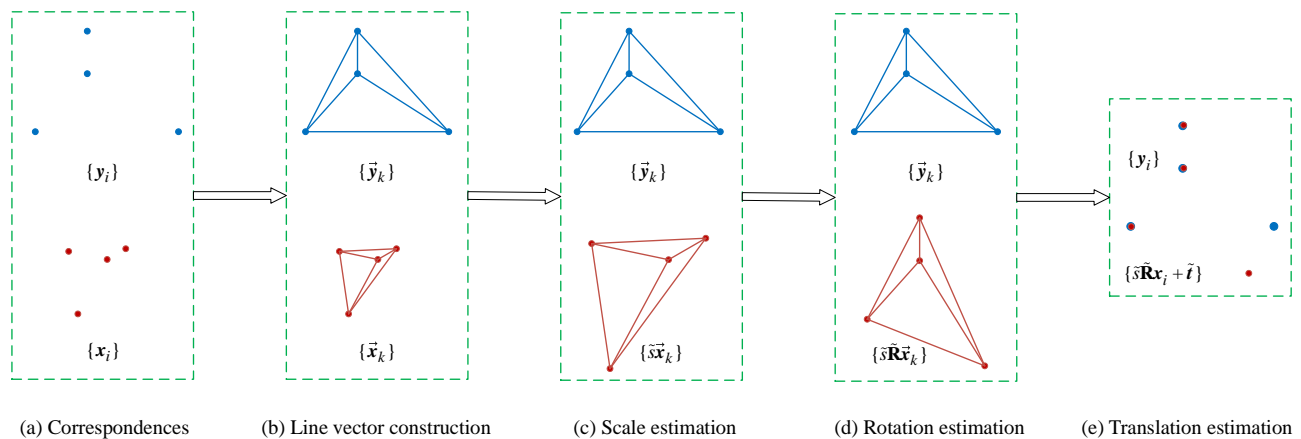


Fig. 1. Illustrating the framework of our proposed 7-parameters PCR method. Given a set of 3D correspondences $\{(\mathbf{x}_i, \mathbf{y}_i)\}_1^N$ (a), we first construct a set of line vector correspondences $\{(\tilde{\mathbf{x}}_k, \tilde{\mathbf{y}}_k)\}_1^K$ (b), which are used for scale estimation based on model (7). The scale difference is eliminated according to \bar{s} (c). Then, the rotation is estimated based on model (4) (d). Finally, a translation estimation step is performed to register these two point sets (e).

C. Point-based Registration

ICP-family: ICP [7] is a milestone for PCR, which simultaneously establishes correspondences and estimates relative pose between point clouds. Specifically, ICP first finds point correspondences based on the criterion of nearest distance; then, a rigid transformation is fitted by using these correspondences. ICP alternates these two stages until converging to a local minimum. Many variants are proposed to improve one or more subtasks (sampling, error metric, outlier rejection, and optimality) of ICP. The sizes of point clouds are huge, an appropriate sampling such as voxel-grid filtering [51] and octree compression [52] can largely improve the efficiency. More accurate error metrics such as point-to-line [53] metric for 2D point clouds, point-to-plane [54] and plane-to-plane [55] metrics for 3D point clouds, are introduced into ICP. Original ICP is sensitive to partial overlaps, which leads to outliers in correspondence establishment stage. To improve the robustness to partial overlaps, many methods introduce robust estimation technique in pose estimation stage. For example, least trimmed squares (LTS) robust estimator is used in Trimmed ICP [56] and Anisotropic ICP [57]; a sparse cost function is introduced by Sparse ICP [58]; and weighted l_q -norm ICP [6] adapts a weighted l_q estimator with high robustness. Yang et al. [59] proposed a global optimal ICP (Go-ICP), which uses a branch-and-bound (BnB) algorithm to globally search the rotation and translation. As aforementioned, ICP-family highly relies on the initializations and is not suitable for cross-source data with scale changes.

Other methods: A representative work is 4-points congruent sets (4PCS) [60], which uses affine-invariant intersection ratios to find coplanar 4-point correspondence bases and estimates an optimal rigid model based on these selected bases. Various variants of 4PCS have been presented. For example, Super 4PCS (S4PCS) [61] introduces a smart index to organize data and converts the original 4PCS as an instance problem to significantly reduce its computational complexity. Ge [62] proposed a non-rigid variant to cope with isometric deformations. Keypoint 4PCS (K4PCS) [63] extracts 3D DoG and Harris keypoints as the input of 4PCS. However, their

computational complexities are still very high at high outlier rates.

III. METHODOLOGY

A. Problem Formulation

Given a set of 3D correspondences $M = \{(\mathbf{x}_i, \mathbf{y}_i)\}_1^N$ without outliers, where $\mathbf{x}_i, \mathbf{y}_i \in \mathbb{R}^3$, such that the geometric relationship between \mathbf{x}_i and \mathbf{y}_i can be exactly modeled by,

$$\mathbf{y}_i = s\mathbf{R}\mathbf{x}_i + \mathbf{t} + \mathbf{n}_i \quad (1)$$

where $s > 0$ is a scale factor, $\mathbf{R} \in SO(3)$ is an orthogonal rotation matrix; $\mathbf{t} \in \mathbb{R}^3$ is a translation vector; and \mathbf{n}_i represents measurement noise, which can be assumed that it is unknown but bounded. However, there must be outliers in the correspondence set M obtained by a 3D keypoint matching technique. Correspondence-based PCR should be formulated as a robust estimation problem,

$$\underset{s, \mathbf{R}, \mathbf{t}}{\text{minimize}} \sum_{i=1}^N \rho(\|\mathbf{y}_i - (s\mathbf{R}\mathbf{x}_i + \mathbf{t})\|) \quad (2)$$

where $\rho(\cdot)$ is a robust function and $\|\cdot\|$ is the l_2 -norm.

B. Transformation Decomposition

Motivation: Probably, RANSAC is the most widely used technique for solving problem (2). It is reliable and efficient in cases with low outlier rates. However, its computational complexity increases exponentially as outlier rate increases. The minimal number of trials N_T required by RANSAC to generate at least one good subset with purely of inliers is computed as follows,

$$N_T = \left\lceil \frac{\log(1-p)}{\log(1-(1-p)^m)} \right\rceil \quad (3)$$

where p is the confidence of good subsets, which is generally set to 0.99; m is the size of minimal subsets ($m = 3$ for 7-parameters registration); and $\lceil \cdot \rceil$ is a ceiling function. At an outlier rate of 99%, RANSAC requires at least 4605168 trials

to get a probably correct solution for registration problem, which is too large to be practical. Fortunately, if we can decompose the full 7-parameters registration problem into scale, rotation, and translation estimation subproblems, the values of m become small, i.e., $m = 1$ for scale and translation estimations and $m = 2$ for rotation estimation. Then, at the same outlier rate, RANSAC only requires 459 trials and 46050 trials for $m = 1$ and $m = 2$, which are the 1/10000 and 1/100 of the original value, respectively. In our method, we use a scale-annealing biweight estimator instead of 2-point RANSAC for rotation estimation, which further speeds up the optimization.

Line vector: In our previous work [6], we present an edge line vector to decompose a six degrees-of-freedom (DoF) rigid transformation into two 3-DoF subproblems. In this paper, we extend this line vector to cope with scale differences and use it to decompose the full 7-parameters registration problem.

Specifically, given a pair of point correspondences $(\mathbf{x}_i, \mathbf{y}_i)$ and $(\mathbf{x}_j, \mathbf{y}_j)$, we can construct a line vector correspondence $(\vec{\mathbf{x}}_{ij} = \mathbf{x}_i - \mathbf{x}_j, \vec{\mathbf{y}}_{ij} = \mathbf{y}_i - \mathbf{y}_j)$. If both $(\mathbf{x}_i, \mathbf{y}_i)$ and $(\mathbf{x}_j, \mathbf{y}_j)$ are inliers, we have,

$$\begin{aligned} \vec{\mathbf{y}}_{ij} &= s\mathbf{R}(\mathbf{x}_i - \mathbf{x}_j) + (\mathbf{n}_i - \mathbf{n}_j) \\ &= s\mathbf{R}\vec{\mathbf{x}}_{ij} + \vec{\mathbf{n}}_{ij} \end{aligned} \quad (4)$$

where $\vec{\mathbf{n}}_{ij} = \mathbf{n}_i - \mathbf{n}_j$ is a noise vector. If the noise bound is τ , then $\|\vec{\mathbf{n}}_{ij}\| \leq 2\tau$. Clearly, the translation term is eliminated in (4). Thus, the line vector is invariant to translation and only related to scale and rotation.

Further, the length of a line vector is invariant to both rotation and translation. Thus, we take the l_2 -norm operation on (4) and obtain,

$$\|\vec{\mathbf{y}}_{ij}\| = \|s\mathbf{R}\vec{\mathbf{x}}_{ij} + \vec{\mathbf{n}}_{ij}\| \quad (5)$$

According to the triangle inequality, the above equation can be reformulated as,

$$-\|\vec{\mathbf{n}}_{ij}\| \leq \|\vec{\mathbf{y}}_{ij}\| - \|s\mathbf{R}\vec{\mathbf{x}}_{ij}\| \leq \|\vec{\mathbf{n}}_{ij}\| \quad (6)$$

To eliminate the rotation term, (6) is divided by $\|\vec{\mathbf{x}}_{ij}\|$, which leads to,

$$|s_{ij} - s| \leq \tau_{ij} \quad (7)$$

where $s_{ij} = \frac{\|\vec{\mathbf{y}}_{ij}\|}{\|\vec{\mathbf{x}}_{ij}\|}$ is the scale difference between lines $\vec{\mathbf{x}}_{ij}$ and $\vec{\mathbf{y}}_{ij}$, and $\tau_{ij} = \frac{2\tau}{\|\vec{\mathbf{x}}_{ij}\|}$. Equation (7) is a scalar function, where the scale s is the only unknown.

Therefore, the full 7-parameters registration problem is divided into three subproblems, as illustrated in Fig. 1. First, we estimate the optimal scale parameter \tilde{s} based on the model (7). Then, the scale difference is eliminated according to \tilde{s} and the optimal rotation $\tilde{\mathbf{R}}$ is estimated based on the model (4). Finally, we put \tilde{s} and $\tilde{\mathbf{R}}$ into problem (1) and seek the optimal translation $\tilde{\mathbf{t}}$. Note that the operations on line vectors are the same as the ones on points, since a line vector can also be treated as a 3D-coordinate vector.

C. Scale Estimation

Actually, robust scale estimation based on model (7) is equivalent to a maximum consensus problem, which seeks a scalar scale that maximizes the number of inliers,

$$\begin{aligned} &\underset{s, I^s \subseteq H}{\text{maximize}} \quad |I^s| \\ &\text{subject to} \quad \frac{|s_k - s|}{\tau_k} \leq 1 \quad \forall k \in I^s \end{aligned} \quad (8)$$

where for simplicity we use subscript k instead of ij , $\mathcal{H} = \{1, 2, \dots, K\}$ is an index set of the scale observations $\{s_k\}_1^K$, $\{\tau_k\}_1^K$ is a set of inlier thresholds, subset I^s is a consensus set that consists of inliers and $|I^s|$ denotes the number of inliers (or called the size of inlier set). The optimal scale \tilde{s} corresponds to the largest inlier consensus set \tilde{I}^s . Hereafter, the indices and their corresponding data are treated as equivalent.

This problem can be solved by a straightforward enumeration method. Specifically, for each s_k , we regard it as the solution of the above problem and calculate its corresponding consensus set. Then, we find the consensus set \tilde{I}^s with the largest size and use \tilde{I}^s to estimate an optimal scale \tilde{s} based on the least-squares cost,

$$\tilde{s} = \arg \min_s \sum_{k \in \tilde{I}^s} \left(\frac{s_k - s}{\tau_k} \right)^2 \quad (9)$$

The solution is,

$$\tilde{s} = \left(\sum_{k \in \tilde{I}^s} \frac{1}{\tau_k^2} \right)^{-1} \sum_{k \in \tilde{I}^s} \frac{s_k}{\tau_k^2} \quad (10)$$

This enumeration method suffers from high computational complexity, which is not acceptable in practice. For a correspondence set with N points, we can construct $K = \frac{N(N-1)}{2}$ line vectors. Hence, the computational complexity of the enumeration method is $O(K^2) = O(N^4)$. To reduce the complexity, we present an 1-point RANSAC algorithm for robust scale estimation. Actually, 1-point RANSAC means that the size of minimal subsets $m = 1$, which had been used in pose estimation [64] and visual odometry [65]–[67]. These methods highly rely on prior information to reduce the DoF of parameter space, which limits their applications. For example, Scaramuzza [67] proposed an 1-point RANSAC algorithm for motion estimation. However, it is only suitable for cases that the camera is installed on a nonholonomic wheeled vehicle. Civera et al. [66] used the prior probabilistic information from the extended kalman filter (EKF) to reduce the DoF. Lee et al. [64] used a ground object assumption and a 2D object bounding box as additional observations. Differently, our method does not require any prior information since the transformation decomposition does not rely on other sensor information or assumptions. Moreover, to our best knowledge, 1-point RANSAC has never been used in PCR before.

We also introduce a local optimization strategy in the 1-point RANSAC to refine the solution. First, we randomly sample a scale s_i from $\{s_k\}_1^K$ and find a consensus set I_i^s . Then, I_i^s is used to estimate a refined scale s'_i based on (10) and a refined consensus set I'_i^s is calculated according to s'_i . These two steps are alternated until the stopping criterion is reached and the scale with the largest consensus set is accepted

Algorithm 1 1-point RANSAC for scale estimation

Input: $\{s_k\}_1^K$ and $\{\tau_k\}_1^K$.
Initialize: $p = 0.99$, $i = 0$, $N_T := 10^5$, and $|\tilde{I}^s| := 0$.
1: **while** $i \leq N_T$ **do**
2: Randomly pick a scale s_i from $\{s_k\}_1^K$.
3: Find a consensus set I_i^s according to (8).
4: **if** $|I_i^s| > |\tilde{I}^s|$ **then**
5: Estimate a refined scale s'_i according to (10).
6: Find a refined consensus set $I_i'^s$.
7: $|\tilde{I}^s| := |I_i'^s|$, $\tilde{I}^s := I_i'^s$, $\tilde{s} := s'_i$.
8: Update N_T according to (3).
9: **end if**
10: $i := i + 1$;
11: **end while**
Output: the optimal scale \tilde{s} and the inlier set \tilde{I}^s .

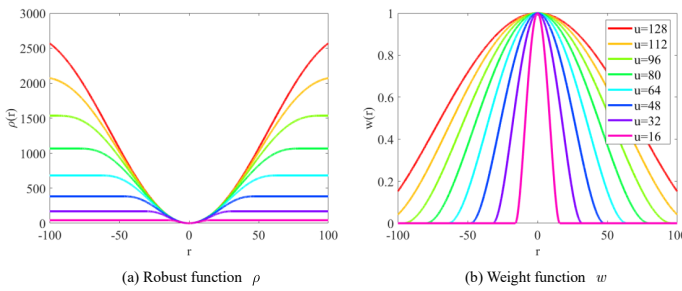


Fig. 2. Visualization of the proposed scale-annealing biweight cost (a) and its weight function (b) with different scale parameters.

as the optimal solution \tilde{s} . The details of the 1-point RANSAC are summarized in **Algorithm 1**.

D. Rotation Estimation

In the scale estimation step, a large portion of outlying line vector correspondences can be filtered. Namely, the inlier set \tilde{I}^s can be used for rotation estimation, which has a much lower outlier rate (generally lower than 80%). Based on this observation, we propose a generalized M-estimation called scale-annealing biweight estimator. It can tolerate 80% ~ 90% outliers and is much faster than a 2-point RANSAC algorithm. The objective function of the proposed estimator is,

$$\underset{\mathbf{R}}{\text{minimize}} \sum_{(\tilde{\mathbf{x}}_k, \tilde{\mathbf{y}}_k) \in \tilde{I}^s} \rho(\|\tilde{\mathbf{y}}_k - \tilde{s}\mathbf{R}\tilde{\mathbf{x}}_k\|) \quad (11)$$

If $(\tilde{\mathbf{x}}_k, \tilde{\mathbf{y}}_k)$ is an inlier, then $r_k = \|\tilde{\mathbf{n}}_k\| \leq 2\tau$, where $r_k = \|\tilde{\mathbf{y}}_k - \tilde{s}\mathbf{R}\tilde{\mathbf{x}}_k\|$ is the residual of $(\tilde{\mathbf{x}}_k, \tilde{\mathbf{y}}_k)$; otherwise, the residual can be $\gg 2\tau$. It means that the energy is dominated by outliers. The robust function $\rho(r_k)$ reflects the influence of r_k towards the total optimization energy, which is critical to robust estimation problems. A good robust function should have a property that minimizes the distances between correspondences, while disabling spurious data. In our method, we adapt a scaled biweight function,

$$\rho(r_k, u) = \begin{cases} \frac{u^2}{6} \left(1 - \left(1 - \frac{r_k^2}{u^2}\right)^3\right) & |r_k| \leq u \\ \frac{u^2}{6} & |r_k| > u \end{cases} \quad (12)$$

Algorithm 2 Scale-annealing biweight for rotation estimation

Input: \tilde{s} and \tilde{I}^s .
Initialize: $u := 1000$, $\alpha = 1.3$, and $\{w(r_k)\} := 1$.
1: **while** not converged **do**
2: Formulate a WLS problem according to (13).
3: Estimate a solution \mathbf{R} via the SVD.
4: Calculate residuals $\{r_k\}$ for \tilde{I}^s .
5: Update weights $\{w(r_k)\}$ according to (14).
6: Anneal the scale by $u := \frac{u}{\alpha}$.
7: **end while**
8: Compute $\tilde{\mathbf{R}}$ via the SVD with the newest weights.
Output: the optimal rotation $\tilde{\mathbf{R}}$.

where u is a scale parameter, which controls the shape of function ρ . Fig. 2(a) visualizes the biweight functions with different scales. As shown, the larger the scale u , the greater the impact of outliers on the total energy.

Instead of minimising the function ρ directly, it is simpler to solve the following weighted least-squares (WLS) problem,

$$\underset{\mathbf{R}}{\text{minimize}} \sum_{(\tilde{\mathbf{x}}_k, \tilde{\mathbf{y}}_k) \in \tilde{I}^s} w(r_k) \|\tilde{\mathbf{y}}_k - \tilde{s}\mathbf{R}\tilde{\mathbf{x}}_k\|^2 \quad (13)$$

where $w(r_k) = \frac{\partial \rho}{\partial r_k} / r_k$ is a weight. $\frac{\partial \rho}{\partial r_k}$ is the derivative of ρ with respect to the residual r_k . The weight function of robust cost $\rho(r_k, u)$ is,

$$w(r_k, u) = \begin{cases} \left(1 - \frac{r_k^2}{u^2}\right)^2 & |r_k| \leq u \\ 0 & |r_k| > u \end{cases} \quad (14)$$

The weight functions with different scales are displayed in Fig. 2(b). As shown, the larger the scale, the smoother the function curve. Thus, a weight function with a large u allows more observations to take part in the optimization stage, which largely avoids that inliers are disabled by an inaccurate solution of \mathbf{R} . As u decreases, the estimated \mathbf{R} becomes more and more precise. Then, large weights are assigned to data with small residuals while small weights (close to 0) are given to outliers, which disables outliers in the optimization.

Based on this property, we use a graduated optimization strategy instead of fixing the scale in the IRLS. Specifically, the initial scale u is assigned a large value, e.g., $u = 1000$. Then, the scale is decreased by a step-size α , i.e., $u := \frac{u}{\alpha}$, along with iterations. In each iteration, we use a singular value decomposition (SVD) algorithm to solve a solution for \mathbf{R} . This graduated optimization strategy can largely avoid that the solver gets stuck in local minima compared with fixed-scale IRLS. The proposed scale-annealing biweight estimator for robust rotation estimation is summarized in **Algorithm 2**.

E. Translation Estimation

We can obtain an inlier line vector set In based on the optimal scale \tilde{s} and rotation $\tilde{\mathbf{R}}$,

$$In = \{(\tilde{\mathbf{x}}_k, \tilde{\mathbf{y}}_k) \mid \|\tilde{\mathbf{y}}_k - \tilde{s}\tilde{\mathbf{R}}\tilde{\mathbf{x}}_k\| \leq 2\tau; k = 1, \dots, K'\} \quad (15)$$

Since a line vector corresponds to two points in set M , we project the line vector set In to original point space and count

TABLE I
DETAILED SETTINGS OF THE COMPARED ALGORITHMS (MNI REPRESENTS MAXIMUM NUMBER OF ITERATIONS).

Method	Parameters	Implementations	Input	Complexity
FLORANSAC	$m = 3; p = 0.99;$ LO size: 21; LO iterations: 50; $N_T = 10^5$.	MATLAB code; single thread https://zhipengcai.github.io/	Correspondences	$O(N_T N)$
K4PCS	Inlier ratio: 0.5; score bound: 10^{-3} ; maximum time: 10^3 s.	C++ code; single thread https://pointclouds.org/	ISS keypoints	$O(N_{kp}^2 + L)$
FMP+BnB	degrees of freedom: 4; Lower bound: 0; repeat?: true.	C++ code; single thread https://github.com/ZhipengCai/Demo-Practical-optimal-registration-of-terrestrial-LiDAR-scan-pairs	Correspondences	$O(\log(N)N^2)$
TEASER++	GNC factor: 1.4; max clique?: false; kcore heuristic threshold: 0.5; MNI: 100	C++ code; single thread https://github.com/MIT-SPARK/TEASER-plusplus	Correspondences	$O(N^4)$
Ours	$m = 1; p = 0.99; N_T = 10^5; \alpha = 1.3$.	MATLAB code; single thread http://www.escience.cn/people/lijiayuan/index.html	Correspondences	$O(N_T^s N^2)$

the frequency of each point. The higher the frequency of a point, the larger the probability that it is an inlier. Thus, we sort these points according to the frequency and select the best 70% point correspondences M' as potential inliers to estimate the translation. Compared with M , M' has a much lower outlier rate, which speeds up the following optimization.

Essentially, robust translation estimation has the same cost function with scale estimation. It is also a maximum consensus problem,

$$\begin{aligned} & \underset{\mathbf{t}, I^t \subseteq M'}{\text{maximize}} \quad |I^t| \\ & \text{subject to} \quad \|\mathbf{t}_i - \mathbf{t}\| \leq 2\tau \quad \forall i \in I^t \end{aligned} \quad (16)$$

where $\mathbf{t}_i = (\mathbf{y}_i - \tilde{s}\tilde{\mathbf{R}}\mathbf{x}_i)$. We also use the 1-point RANSAC to optimize this problem. The process is almost the same as in **Algorithm 1**. The least-squares solution of \mathbf{t} is just the mean of the consensus set.

F. Computational Complexity

In our method, line vector construction consumes $O(N^2)$ time. The complexity of scale estimation is $O(N_T^s N^2)$, where N_T^s is the minimal number of trials required by RANSAC in scale estimation. Rotation estimation costs $O(|\tilde{I}^s|)$ time ($|\tilde{I}^s| < N^2$). The complexity of translation estimation is smaller than $O(N_T^t N)$ where N_T^t is the minimal number of trials required by RANSAC in translation estimation. Thus, the scale estimation is the most time-consuming step and the total computational complexity of our method can be simplified as $O(N_T^s N^2)$. If the correspondence set is large, then $N^2 \gg N_T^s$ and the complexity becomes $O(N^2)$.

G. Multi-view Scans Registration

Directly using the proposed method to register multiple scans is difficult because of the RANSAC framework. There are two ways to achieve the purpose. First, we can perform pairwise registration to obtain initial poses. These poses are used to initialize a multiple-scans joint registration method like [68]. Second, we can use pairwise registration to construct a pose-graph and optimize this pose-graph based on a SLAM back-end toolbox like g^2o [69].

IV. EXPERIMENTS

This section comprehensively evaluates the proposed method on real experiments. First, we evaluate the proposed method on same-source LIDAR point clouds, which do not suffer from scale changes (In this experiment, scale estimation is disabled). Second, our method is assessed on cross-source point clouds with unknown scales, i.e., MVS and structured light point cloud pairs. Our method is compared with several baselines and state-of-the-arts, including FLORANSAC [36], K4PCS [63], fast match pruning with BnB (FMP+BnB) [70], and TEASER++ [49]. The information of parameters, implementation details, inputs, and time complexity of each compared method is summarized in Table I, where L denotes the number of candidate congruent 4-points and N_{kp} is the number of keypoints. $N_T \gg N$ at high outlier rates.

We use ISS algorithm to detect keypoints and FPFH algorithm for description. A correspondence $(\mathbf{x}_i, \mathbf{y}_i)$ is selected into the initial correspondence set M only if \mathbf{x}_i and \mathbf{y}_i are one of the top- k best matches ($k = 5$ in our experiments) to each other. We regard the average point cloud resolution as the noise bound τ . We use common metrics for quantitative assessment, i.e., translation error E_t and rotation error E_R ,

$$\begin{cases} E_t = \|\mathbf{t}^t - \mathbf{t}^e\| \\ E_R = \arccos \frac{\text{tr}(\mathbf{R}^t(\mathbf{R}^e)^T) - 1}{2} \end{cases} \quad (17)$$

where superscript t and superscript e represent the ground truth one (scale, rotation, or translation) and the estimated one, respectively; $\text{tr}(\cdot)$ is the trace of a matrix. For the second experiment, the scale difference $E_s = |s^e - s^t|$ is also calculated for evaluation. All the results are calculated on a laptop with a single CPU Core i7-8550U @ 1.8GHz, and 8 GB of RAM.

A. Same-source registration

Dataset: We use three challenging real datasets for evaluation, i.e., Andreashaus, Bremen_city, and Campus datasets⁴. The Andreashaus is a middle-scale indoor dataset that was collected at 15 different poses inside a residential house. The other two are large-scale outdoor datasets, where the Bremen_city with 13 LIDAR scans was taken in the city center

⁴<http://kos.informatik.uni-osnabrueck.de/3Dscans/>

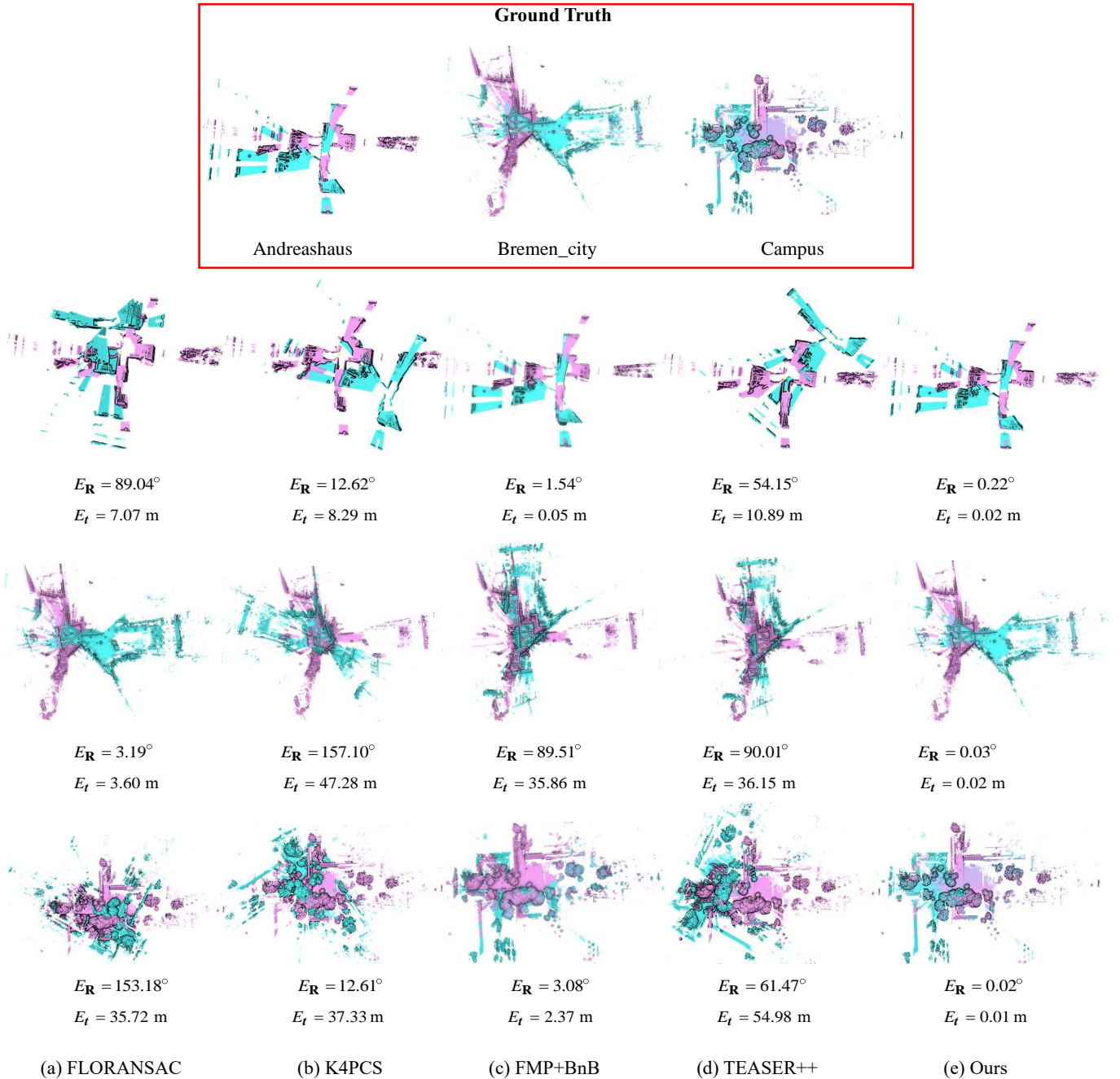


Fig. 3. Qualitative results on three selected scan pairs. The first \sim fifth columns are the results of FLORANSAC, K4PCS, FMP+BnB, TEASER++, and our method, respectively, where magenta point clouds are target point clouds and cyan ones are source point clouds. The registration accuracy (E_R and E_t) of each result is given and the GT registrations are provided in the red box for reference.

of Bremen and the Campus with 74 LIDAR scans was taken on the campus of the Jacobs University Bremen. All these datasets were recorded using a Riegl VZ-400 LIDAR scanner. Since the sizes of original LIDAR scans are huge (more than tens of millions of points in each scan), the voxel-grid filter is applied to downsample the resolutions of these point clouds. The detailed information about these three LiDAR datasets is summarized in Table II, including number of scan pairs N_{pr} , point cloud resolution (it is regarded as the noise bound), average number of points N_{pt} , average number of keypoints N_{kp} , average number of feature correspondences N ,

average overlapping ratio, and average outlier ratio $r_{outlier}$ in the initial correspondences M . Each scan pair of these datasets is assigned an approximate ground truth (GT) rigid transformation $(\mathbf{R}^t, \mathbf{t}^t)$, which is obtained by a coarse-to-fine registration strategy. Specifically, scans are first manually registered by using reflective markers. Then, the 3D Toolkit⁵ (a graph-based pose optimization algorithm) is used to refine the results of manual registration and provide accurate registration parameters. Thus, if a correspondence $(\mathbf{x}_i, \mathbf{y}_i)$

⁵<http://slam6d.sourceforge.net/>

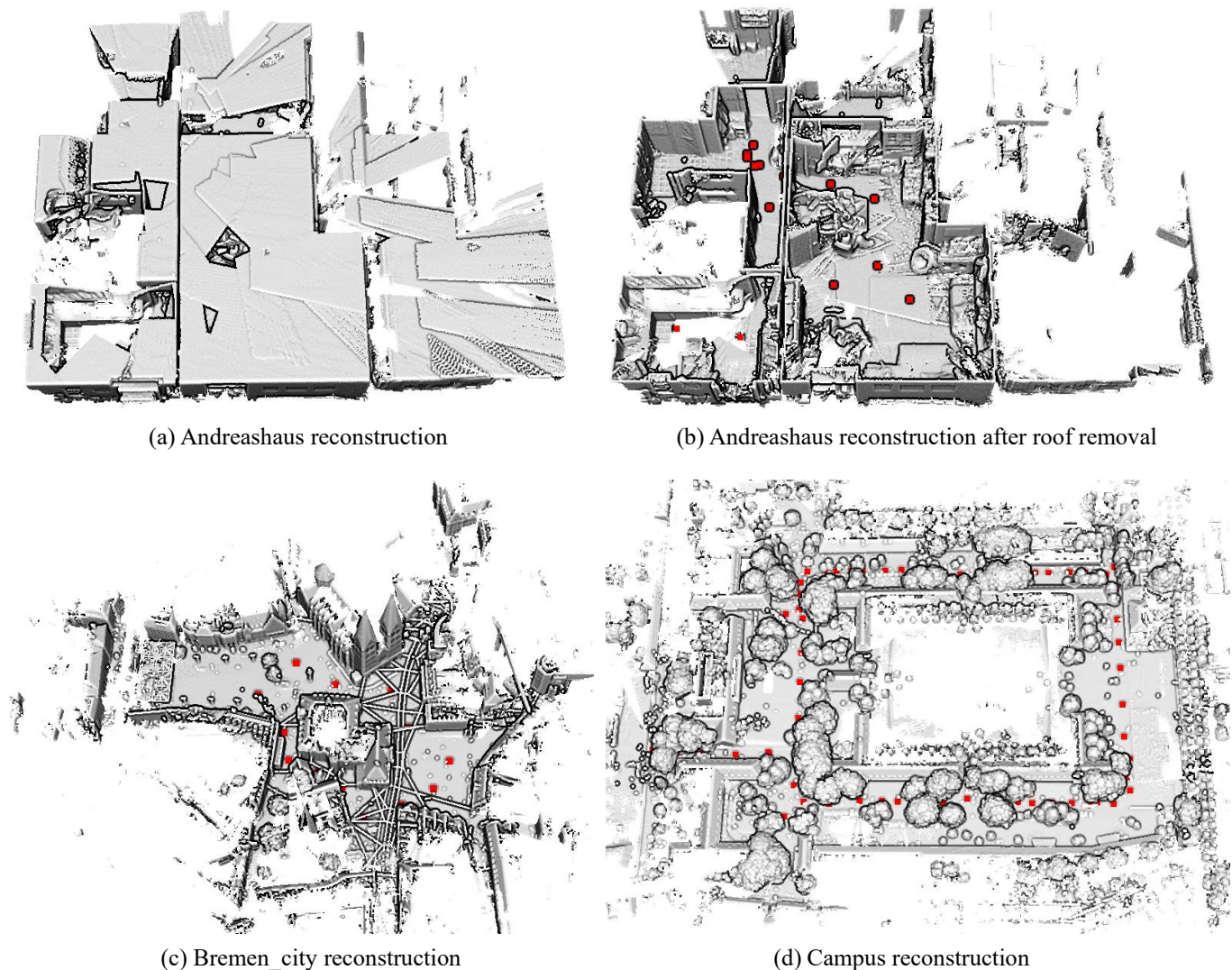


Fig. 4. Scene reconstruction result for each dataset. (a) Andreashaus is reconstructed by 15 LIDAR scans; (c) Bremen_city is reconstructed by 13 LIDAR scans; and (d) Campus is reconstructed by 74 LIDAR scans. Red dots in the figure represent locations estimated by our method where LIDAR scans were recorded.

TABLE II
DETAILED INFORMATION OF DATASETS (K HERE MEANS THOUSANDS)

Info	Andreashaus (Mean±Std)	Bremen_city (Mean±Std)	Campus (Mean±Std)
N_{pr}	14	12	73
Noise τ	0.02m	0.1m	0.1m
N_{pt}	3122K±1014K	1295K±523K	1232K±301K
N_{kp}	5919±1433	6335±2549	6988±1021
N	8644±2827	8670±2938	9865±1162
Overlap	45%±18%	49%±13%	75%±7%
$r_{outlier}$	99.39%±0.62%	98.74%±0.47%	98.98%±0.52%

satisfies $\|y_i^t - (\mathbf{R}^t x_i + t^t)\| \leq 2\tau$, it is an inlier; otherwise, it is an outlier. As shown in Table II, the lowest $r_{outlier}$ is still higher than 98%, which makes the correspondence-based or keypoint-based registration very difficult.

Qualitative Assessment: One scan pair is selected from each dataset for qualitative evaluation. The pair from An-

dreashaus and the one from Bremen_city have very low overlapping ratios, which are only 25.72% and 33.18%, respectively. The overlap of the pair from Campus is relatively large, i.e., 71.52%. All these pairs are partially overlapping. Therefore, they are challenging for K4PCS. The outlier rates of these three pairs are 99.83%, 99.51%, and 99.56%, respectively. Such high outlier rates bring great challenges to current correspondence-based registration methods, such as RANSAC-type methods and TEASER++. The comparison results are displayed in Fig. 3.

As shown, none of these four compared methods obtain satisfactory results on all the three scan pairs. FLORANSAC and TEASER++ can not handle cases with extremely high outlier rates, e.g., > 99%. Since the outlier rates of initial correspondences are extremely high, they are also extremely high in the keypoints. K4PCS is sensitive to the outlier rates of keypoints. FMP+BnB performs better than aforementioned methods. However, FMP+BnB only solves a 4-DoF registration problem. Its registration accuracy is not very high since it

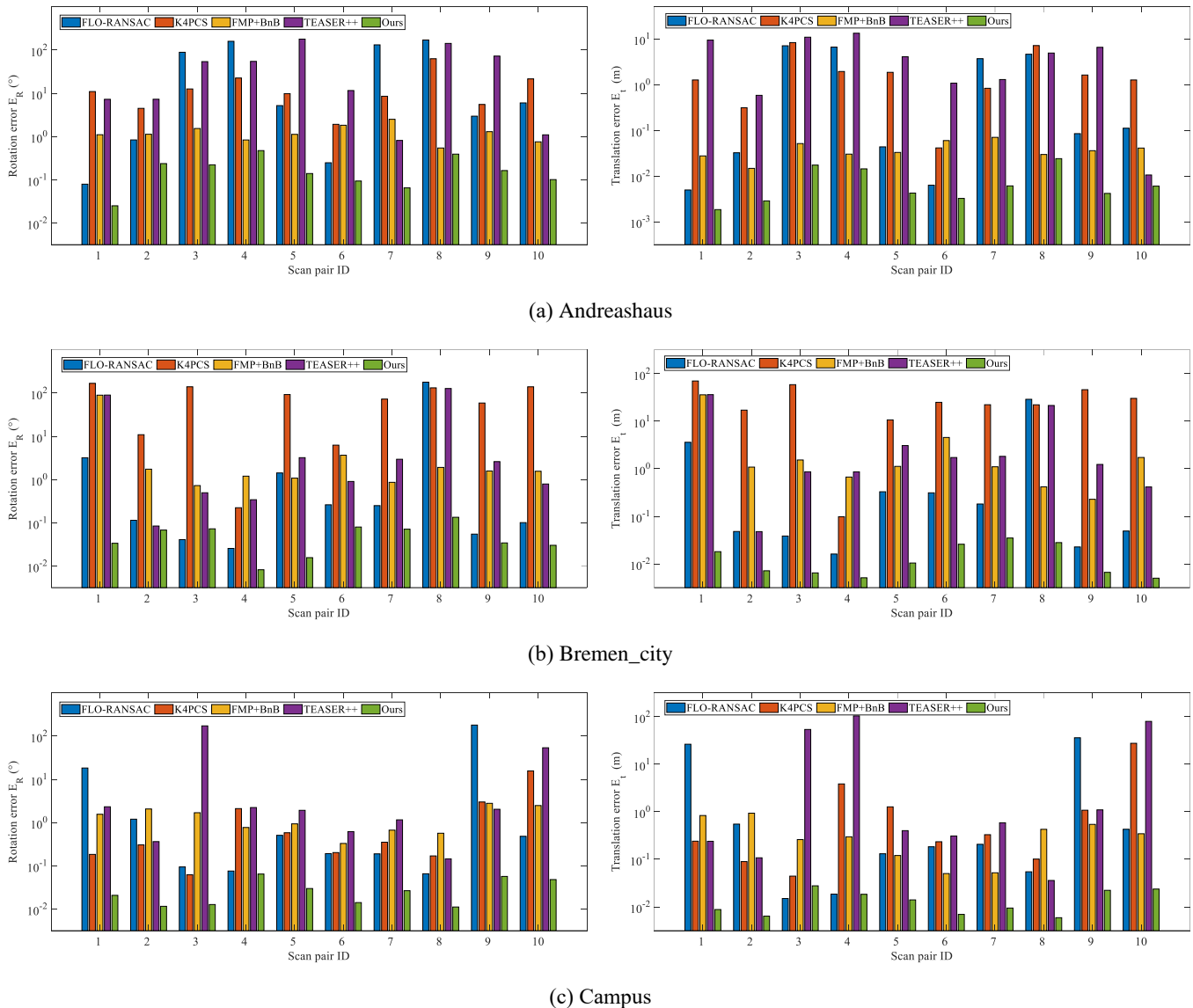


Fig. 5. Individual evaluations on same-source LIDAR datasets. Subfigures (a)~(c) show the results on the Andreashaus, Bremen_city, and Campus, respectively. Left column shows the rotation errors E_R and figures in the right are the translation errors E_t . For better visualization, only the first ten scan pairs for each dataset are displayed.

relies on an accurate level compensator. As a result, it is not suitable for registration of point clouds captured by hand-hold laser scanners. In contrast, the proposed method achieves good alignments on all these scan pairs. Our results are very close to the GT, i.e., the rotation accuracy is better than 0.3° and the translation errors are smaller than 0.05m . Our method is able to tolerate more than 99% outliers, which is more robust than FLORANSAC and TEASER++.

Actually, each dataset is a LIDAR scan sequence, which can be sequentially registered to reconstruct the 3D scene. Thus, we first estimate a rigid transformation for each two adjacent scans. Then, we regard the first scan as the base and transform other scans into the basic coordinate system based on the estimated transformations. This process is called a laser odometry. Campus dataset consists of 74 LIDAR scans. To reduce error accumulation in Campus, we treat 10 scans as a group and use our laser odometry to get a submap. Then,

we use the proposed method to register consecutive submaps to obtain the final 3D scene map. The reconstructed results are displayed in Fig. 4. As shown, our results are impressive. There is almost no “ghosting” in all 3D maps. We calculate the mean absolute error (MAE) between our estimated trajectory and the one of 3D Toolkit for evaluation. The MAEs of the Andreashaus, Bremen_city, and Campus are 0.05m , 0.12m , 0.18m , respectively. Our method can be a good scan matcher of the front-end of a 3D laser SLAM.

Quantitative Assessment: Fig. 5 reports ten individual quantitative results of each dataset. FLORANSAC performs better on the Bremen_city and Campus than on the Andreashaus, since the outlier rate of Andreashaus is higher. FLORANSAC generally can not seek a satisfactory solution within 10^5 iterations at an outlier rate above 99%. For example, it is completely fail on the seventh and eighth scan pairs of Andreashaus (the rotation errors of FLORANSAC are

TABLE III
QUANTITATIVE REGISTRATION RESULTS ON SAME-SOURCE DATA

Method	Andreashaus (Mean±Std)			Bremen_city (Mean±Std)			Campus (Mean±Std)		
	E_R (°)	E_t (m)	time (s)	E_R (°)	E_t (m)	time (s)	E_R (°)	E_t (m)	time (s)
FLORANSAC	47.36±66.44	1.66±2.64	186.05±25.02	15.38±51.53	2.79±8.27	179.82±14.35	12.75±42.30	4.33±11.13	194.58±44.66
K4PCS	26.80±46.72	2.02±2.53	112.46±74.01	71.71±61.91	27.94±21.56	625.30±364.52	10.46±36.79	7.11±23.22	819.56±279.37
FMP+BnB	1.33±0.24	0.05±0.06	2.49 ±0.71	9.27±25.29	4.69±9.93	2.16 ±0.65	1.15±0.86	0.45±0.55	2.21 ±0.89
TEASER++	59.77±68.70	4.43±4.40	8.11±2.74	19.25±42.61	5.78±11.22	8.69±2.46	28.88±52.86	30.28±46.32	9.46±4.93
Ours	0.24 ±0.24	0.01 ±0.01	9.30±2.54	0.05 ±0.04	0.02 ±0.01	9.65±2.44	0.03 ±0.03	0.01 ±0.01	10.44±1.22

TABLE IV
TOTAL SUCCESS RATES ON SAME-SOURCE DATA

Method	Success rate (%)	
	$E_R < 0.5^\circ$, $E_t < 0.2m$	$E_R < 5^\circ$, $E_t < 2m$
FLORANSAC	51.52	74.75
K4PCS	25.25	54.55
FMP+BnB	32.32	83.84
TEASER++	16.16	35.35
Ours	100.00	100.00

larger than 100°). K4PCS is sensitive to overlapping ratios. It achieves better performance on the Campus than on the other two datasets, since the overlap of Campus ($\approx 75\%$) is much higher than the others ($< 25\%$). TEASER++ performs worse than FLORANSAC and K4PCS. The reason may be that truncated least squares used in TEASER++ becomes unreliable at high outlier rates. The proposed method obtains the best performance, which gets good alignments on all these scan pairs. Our method decomposes the full registration problem into subproblems. As a result, our 1-point RANSAC only requires small number of trials to obtain satisfactory solutions. We also introduce a graduated optimization strategy to avoid local minima in the rotation estimation. Both strategies guarantee the high robustness of the proposed method, i.e., it is suitable for cases with extremely high outlier rates ($> 99\%$).

Table III summarizes the average quantitative results of each compared method. Clearly, the proposed method achieves the best registration accuracy, which is far better than others. Its average rotation error is smaller than 0.25° and its translation accuracy is better than $0.02m$. Our method can be directly used in practical applications without any fine registration step such as ICP refinement. The success rates are reported in Table IV. Under a stringent criterion ($E_R < 1^\circ$ and $E_t < 0.2m$), the success rate of our method is 100%, which gains a growth rate of 48.48% compared with the second best method, i.e., FLORANSAC. If we relax the criterion to $E_R < 5^\circ$ and $E_t < 2m$, the success rate of our method is still 16.16% higher than the one of FMP+BnB.

Another major advantage of the proposed method is its high efficiency. Table III also reports the running time of each method. Note that the time of point cloud reading and feature extraction is not included. FMP+BnB is the fastest, because it is only a 4-DoF registration solution while others solve the 6-DoF registration problem. The parameter space of 4-DoF registration is much smaller than the one of 6-DoF registration.

Our method consumes about 10 seconds to register a correspondence set with 9000 points and an outlier rate of 99%, which is much faster than FLORANSAC, and K4PCS. For example, our method is 18+ times faster than FLORANSAC and 60+ times faster than K4PCS on the Bremen_city dataset. Actually, the complexity of the proposed method ($O(N_T^s N^2)$) is close to the one of FMP+BnB ($O(\log(N)N^2)$). FMP+BnB is 4 times faster than our method in the table because of the C++ implementations. TEASER++ is slightly faster than our method, which benefits from the C++ implementation. In our method, all the three subproblems are solved by iteration-based methods. Thus, the time efficiency can be further improved by a programming language that is more suitable for iterative calculation such as C++. Even considering the time required for data reading and feature extraction, our method can still register a point cloud pair in less than 1 minute. For instance, the time of preprocessing (data reading and feature extraction) on the Andreashaus dataset is 22.81 ± 7.18 seconds and it costs 32.95 ± 11.16 seconds on the Bremen_city dataset.

With/Without Scale Estimation: In the above, we disabled the scale estimation since the scale is known, i.e., 1. To evaluate the performance of our full 7-parameters registration method on same-source dataset, we perform a simple experiment that enables the scale estimation on the Bremen_city dataset. The rotation and translation errors are $0.053^\circ \pm 0.037^\circ$ and $0.034m \pm 0.035m$, respectively, which are comparable to the ones without scale estimation. The major difference is that with scale estimation is much slower (running time is 148.29 ± 69.86 seconds). As analysed, the scale estimation is the most time-consuming part of our method.

B. Cross-source registration

In this section, we consider scale differences between point clouds and evaluate the proposed method on a cross-source point cloud dataset. The proposed method is compared with FLORANSAC, which ranks second under the stringent criterion in the same-source registration experiment. K4PCS and FMP+BnB cannot deal with point clouds with scale changes. The computational complexity of TEASER++ is $O(N^4)$, which is too slow to be practical. For example, TEASER++ requires more than 10^{14} iterations for scale estimation with 5000 correspondences, which takes more than one day in our computational environment. Thus, these methods are excluded from comparison.

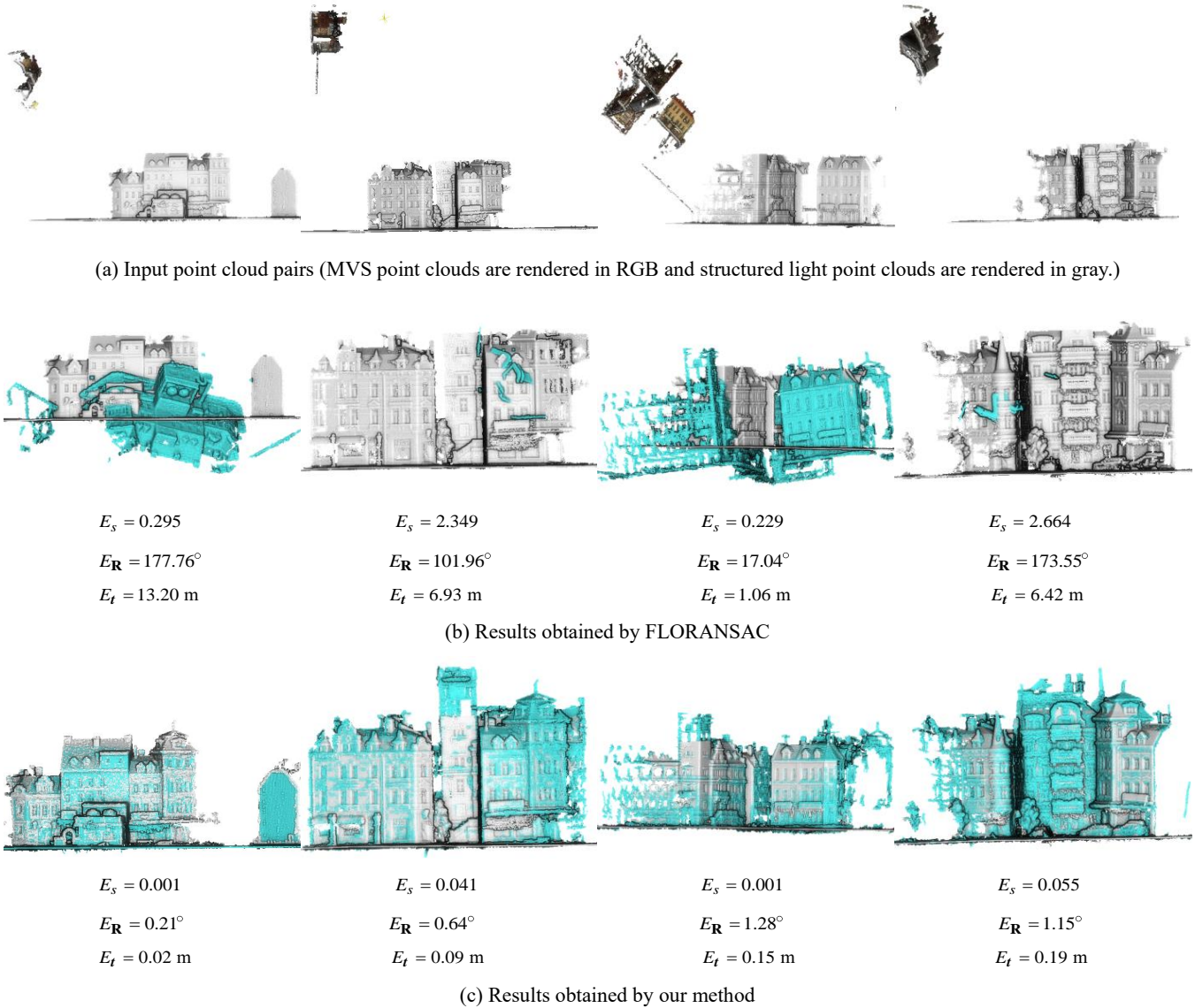


Fig. 6. Qualitative results on cross-source dataset. (a) Input MVS and structured light point cloud pairs; (b) Results of FLORANSAC; and (c) Results of our method. The gray point clouds are captured by a structured light sensor and the cyan ones are generated by a MVS technique. The scale, rotation, and translation errors are provided below each result.

Dataset: We collect 19 scenes from the MVS dataset⁶ for assessment. Each scene of this dataset consists of a structured light point cloud, an image sequence, and a calibration file. We use the visualSFM software⁷ and patch-based multi-view stereo software (PMVS) [71] to generate a MVS point cloud for each image sequence. For each scene, we manually pick 4 correspondences and estimate an initial 7-parameters similarity transformation. Then, ICP algorithm is used to refine the initial parameters (rotation and translation) and estimate an accurate transformation, which is regarded as the GT. To reduce the sizes of point clouds, we downsample their resolutions to 0.05m. The detailed information of this dataset is summarized as follows: $N_{pr} = 19$, $N_{pt} = 5.42 \times 10^5$, $N = 3391$, $r_{outlier} = 98.86\%$, $overlap > 80\%$, $resolution = 0.05m$.

Qualitative Assessment: Four difficult scenes are selected for qualitative evaluation (see Fig. 5(a)). Although the overlaps of these point cloud pairs are large, the outlier rates in the initial correspondence sets are still very high. Their outlier rates are 99.16%, 99.47%, 99.33%, and 99.48%, respectively. The reasons may be two-fold: First, MVS methods cannot generate points in textureless images, which result in holes in the point clouds. Then, many keypoints in structured light point cloud do not have corresponding points in the MVS point cloud. Second, MVS point cloud suffers from geometric distortions. Error accumulations cannot be eliminated completely even with a bundle adjustment step. High outlier rates and large scale changes make registration on these pairs challenging. Fig. 6 shows the results of the proposed method and FLORANSAC. As can be seen, our method achieves good results while FLORANSAC fails to register any point cloud

⁶<http://roboimagedata.compute.dtu.dk/>

⁷<http://ccwu.me/vsfm/>

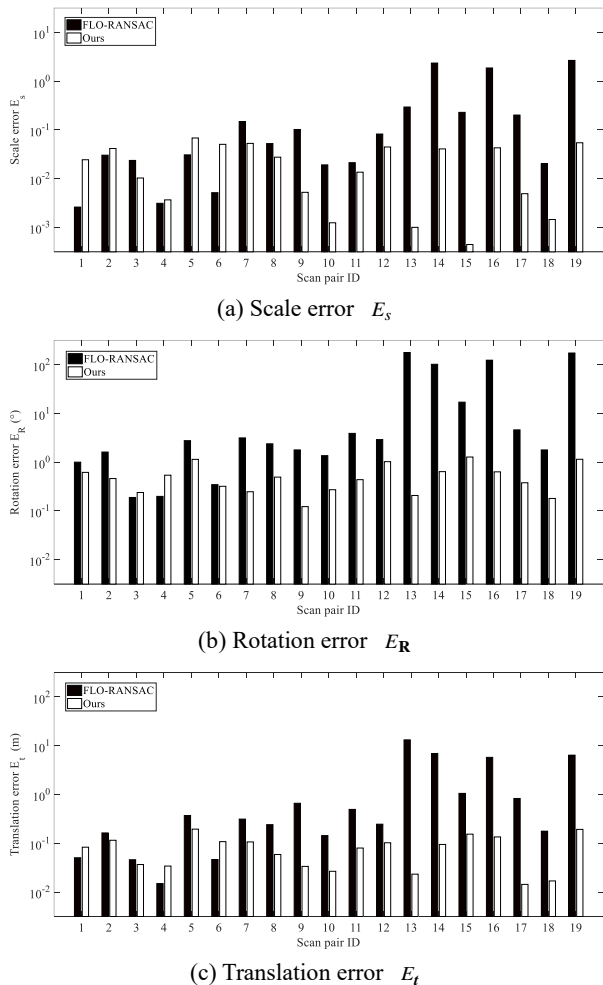


Fig. 7. Individual evaluations on cross-source data. Subfigures (a)~(c) show the results of scale, rotation, and translation errors, respectively.

pair. As aforementioned, the proposed method is more robust than FLORANSAC and suitable for cases with extremely high outlier rates. Generally, the registration accuracy of our method on cross-source data is slightly lower than the one on same-source data. The reasons are as follows: First, MVS point clouds and structured light point clouds cannot be perfectly registered due to geometric distortions. Second, same-source point clouds have an exact scale of one. However, the scales between cross-source point clouds are estimated, which are only optimal approximations. The scale errors will decrease the accuracy of rotation and translation estimations.

Quantitative Assessment: The individual quantitative results are plotted in Fig. 7. As shown, our method performs much better than FLORANSAC on most of the scenes. For example, FLORANSAC gets rotation errors that are even larger than 100° on the last several scenes. In contrast, the maximum rotation error and maximum translation error of our method are 1.28° and 0.19m , respectively.

The quantitative results are reported in Table V. Our method achieves much higher registration accuracy than FLO-RANSAC. Due to the scale errors, the rotation and translation accuracies of the proposed method are less impressive than

TABLE V
DETAILED INFORMATION OF DATASETS (K HERE MEANS THOUSANDS)

Method	E_s (Mean \pm Std)	E_R ($^\circ$) (Mean \pm Std)	E_t (m) (Mean \pm Std)
FLORANSAC	0.429 ± 0.844	32.74 ± 61.20	1.96 ± 3.55
Ours	0.026 ± 0.022	0.55 ± 0.36	0.09 ± 0.05

TABLE VI
TOTAL SUCCESS RATES ON THESE THREE DATASETS

Method	Success rate (%)	
	$E_s < 0.05$ $E_R < 1^\circ, E_t < 0.2\text{m}$	$E_s < 0.1$ $E_R < 5^\circ, E_t < 1\text{m}$
FLORANSAC	15.79	57.89
Ours	68.42	100.00

the ones in the above section. Fortunately, under a stringent criterion ($E_s < 0.05$, $E_R < 1^\circ$, and $E_t < 0.2\text{m}$), our method still obtains a success rate of 68.42%, which is 52.63% higher than the one of FLORANSAC. Under a relaxed criterion ($E_s < 0.1$, $E_R < 5^\circ$, and $E_t < 1\text{m}$), the success rate of our method becomes 100%.

C. Advantages and Limitations

As a highly practical method, the advantages of the proposed method are as follows:

- **High robustness:** Our method is robust against over 99% outliers. The 1-point RANSAC inherits the advantages of RANSAC, such as robustness and interpretability. Moreover, the proposed graduated optimization strategy large improves the robustness of IRLS.
- **High efficiency:** The time complexity of our method is $O(N^2)$. We decompose the full 7-parameters registration problem into three subproblems. The parameter space is largely reduced. Thus, 1-point RANSAC can be very efficient even at extremely high outlier rates.
- **Good scalability:** Our method solves the full 7-parameters registration problem. It is suitable for both same-source data such as LIDAR point cloud registration and cross-source data such as MVS-LIDAR registration.

The limitations of the proposed method are two-fold:

- **Dependence on correspondences:** Our method needs to establish an initial correspondence set M . It cannot take original point clouds as input. Thus, its registration accuracy relies on the location accuracy of 3D keypoint detectors to some extent. Moreover, too few inliers (e.g., < 10) in M may cause the proposed method to fail.
- **Maximum consensus assumption:** In our method, the scale and translation estimation rely on an assumption that the optimal solution corresponds to the maximum consensus. However, if point clouds contain multiple geometric structures (generally occur in non-rigid point clouds), this assumption may not hold any more. For example, if point clouds contain moving objects, the proposed method may align the moving objects instead of static environment.

V. CONCLUSION

In this paper, we propose a highly practical 7-parameters point cloud registration method that is initial-guess free, accurate, fast, and robust. Compared with most of current methods, the proposed approach is suitable for both same-source data and cross-source data. To reduce parameter space and improve efficiency, we decompose the full 7-parameters registration into three subproblems based on the concept of extended line vector. We propose a fast 1-point RANSAC algorithm for scale and translation estimations. We also propose a scale-annealing biweight estimator for rotation estimation and introduce a graduated optimization strategy to largely alleviate the effect of local minima. These improvements ensure the high robustness and high efficiency of our method. Both the same-source and cross source registration experiments demonstrate that our method is much superior to current methods, i.e., it is robust against over 99% outliers and much faster than its competitors.

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