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SC2-PCR++ :An efficient and Robust Point Cloud Registration method

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SC^2-PCR++: Rethinking the Generation and Selection for Efficient and Robust Point Cloud Registration

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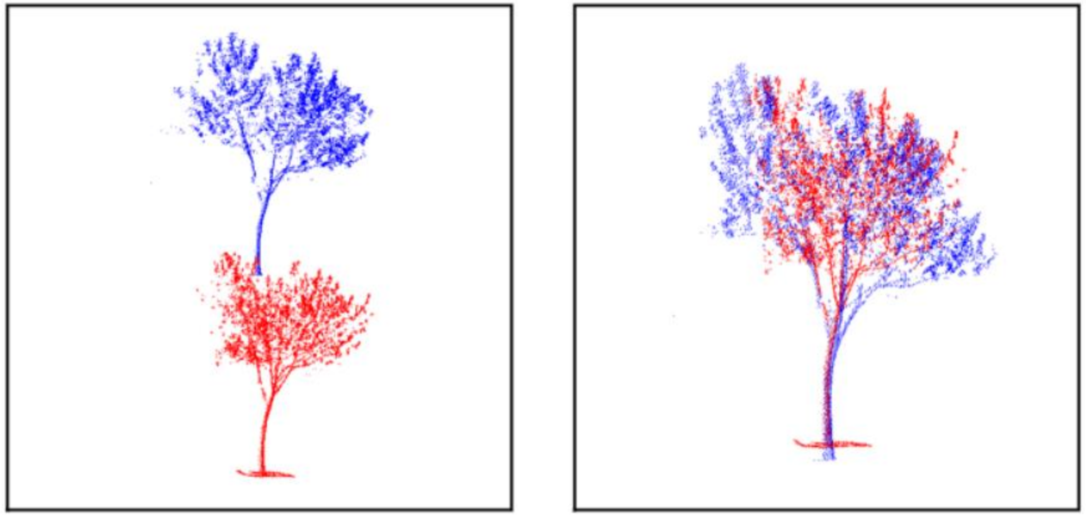
Introduction

Point Cloud Registration (PCR) :The alignment of two 3D scans of the same scene

(1) Establishes feature correspondences

(2) Estimates the 3D rotation and translation that achieve optimal alignment of the common parts.



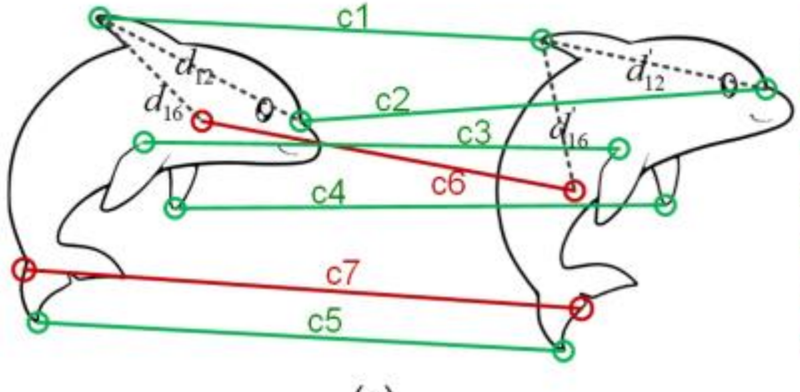
原始点云　　配准后的点云

Challenge : Due to the partial overlap or feature ambiguity, model estimation is prone to outliers in the correspondences, leading to inaccurate or wrong alignment.

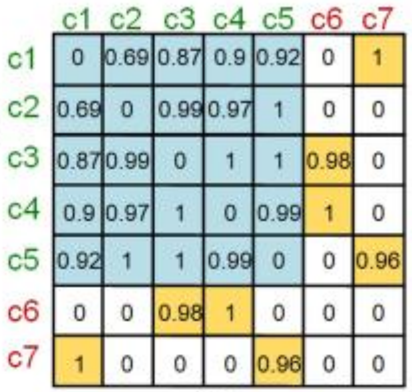
Introduction - sampling process

Spatial Compatibility (SC) : A widely used similarity measure for boosting the robustness and efficiency of the rigid transformation estimation.

$$SC_{ij} = \phi(d_{ij}), d_{ij} = \mid d(x_i, x_j) - d(y_i, y_j) \mid$$



(a)



	c1	c2	c3	c4	c5	c6	c7
c1	0	0.69	0.87	0.9	0.92	0	1
c2	0.69	0	0.99	0.97	1	0	0
c3	0.87	0.99	0	1	1	0.98	0
c4	0.9	0.97	1	0	0.99	1	0
c5	0.92	1	1	0.99	0	0	0.96
c6	0	0	0.98	1	0	0	0
c7	1	0	0	0	0.96	0	0

(b)

Advantage: Sampling from compatible correspondences increases the probability of getting inliers.

Disadvantaged: Such kind of first-order metric still suffers from outliers due to locality and ambiguity. The outliers would be inevitably involved in the model estimation process, leading to performance deterioration.

Introduction - sampling process

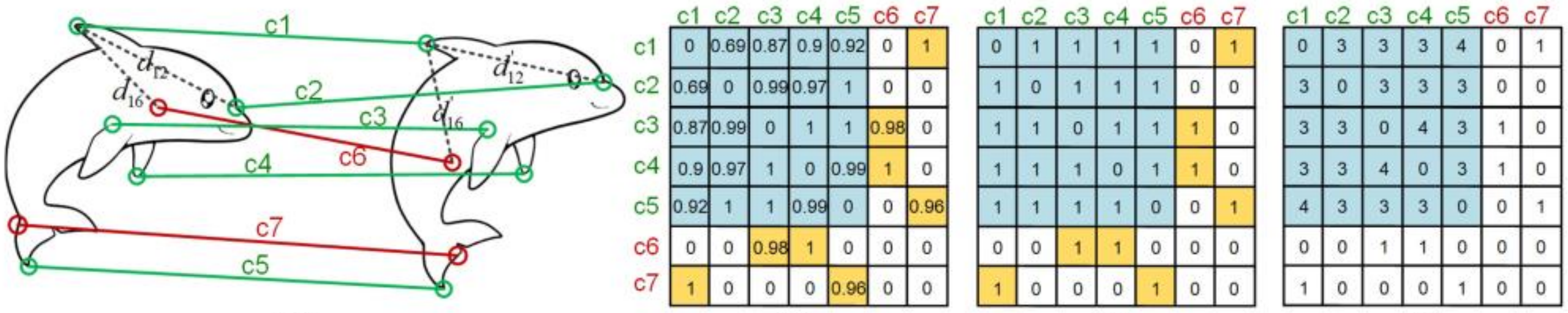
Second-order spatial compatibility (SC2) measure: A new global measure of the similarity between two correspondences.

(1) Binarize the spatial compatibility matrix into the hard form.

$$C_{ij} = \begin{cases} 1; d_{ij} \leq d_{thr}, \\ 0; d_{ij} > d_{thr}. \end{cases}$$

(2) For two compatible correspondences, we compute the number of correspondences that are simultaneously compatible with both of them as the new similarity between them.

$$SC_{ij}^{2} = C_{ij} \cdot \sum_{k=1}^{N} C_{ik} \cdot C_{kj}.$$



(a) (b) (c) (d)

(b)

	c1	c2	c3	c4	c5	c6	c7
c1	0	0.69	0.87	0.9	0.92	0	1
c2	0.69	0	0.99	0.97	1	0	0
c3	0.87	0.99	0	1	1	0.98	0
c4	0.9	0.97	1	0	0.99	1	0
c5	0.92	1	1	0.99	0	0	0.96
c6	0	0	0.98	1	0	0	0
c7	1	0	0	0	0.96	0	0

(c)

	c1	c2	c3	c4	c5	c6	c7
c1	0	1	1	1	1	0	1
c2	1	0	1	1	1	0	0
c3	1	1	0	1	1	1	0
c4	1	1	1	0	1	1	0
c5	1	1	1	1	0	0	1
c6	0	0	1	1	0	0	0
c7	1	0	0	0	1	0	0

(d)

	c1	c2	c3	c4	c5	c6	c7
c1	0	3	3	3	4	0	1
c2	3	0	3	3	3	0	0
c3	3	3	0	4	3	1	0
c4	3	3	4	0	3	1	0
c5	4	3	3	3	0	0	1
c6	0	0	1	1	0	0	0
c7	1	0	0	0	1	0	0

The global compatibility matrix can better distinguish inliers from outliers.

Second-order spatial compatibility measure

The probability of ambiguity event : Reflect the robustness of a measure-based sampling method.

$$\mathrm{P}_{am}(M) = \mathrm{P}(M_{in,out} > M_{in,in}),$$

M is a specific metric for measuring correspondence-wise similarity

P(Z) is the probability of an event Z

$M_{in,out}$ is the similarity between an inlier and an outlier , $M_{in,in}$ is the similarity between two inliers

we assume that $d_{in,in}$ is uniformly distributed over d_{thr} , get the probability density function (PDF) of the distance difference between two inliers as follows

$$\mathrm{PDF}_{in,in}(l) = 1/d_{thr}, 0 \leq l \leq d_{thr}.$$

$$\mathrm{PDF}_{in,out}(l) = F(l), \mathrm{PDF}_{out,out}(l) = F(l); 0 \leq l \leq d_r, \quad F(l) = f_0, 0 \leq l \leq d_{thr}.$$

$$\begin{aligned}\mathrm{P}(SC_{in,out} > SC_{in,in}) &= \mathrm{P}(d_{in,out} < d_{in,in}) \\ &= \int_0^{d_{thr}} \int_0^l \mathrm{PDF}_{in,in}(l) \cdot \mathrm{PDF}_{in,out}(x) dx dl \\ &= \int_0^{d_{thr}} \int_0^l \frac{1}{d_{thr}} \cdot f_0 dx dl = \frac{d_{thr} \cdot f_0}{2}.\end{aligned}$$

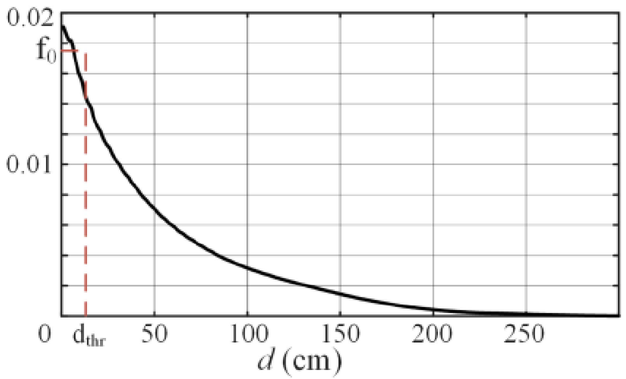


Fig. 3. The empirical probability density function (F) of the distance difference between two unrelated correspondences, i.e., $d_{in,out}$ and $d_{out,out}$.

Second-order spatial compatibility measure

we analyze the ambiguity probability of SC^2, P($SC^2_{in,out} > SC^2_{in,in}$). Suppose there are N pairs of correspondences and the inlier ratio is α,The ambiguity probability of $SC2$ measure, P($SC^2_{in,out} > SC^2_{in,in}$),can be written as follows:

$$\mathrm{P}(SC^2_{in,out} > SC^2_{in,in}) = p \cdot \mathrm{P}(X > (N \cdot \alpha - 2)),$$

$$X \sim S((N\alpha - 1)p + (N(1-\alpha) - 1)p^2, N(1-\alpha)p^2),$$

$$p = d_{thr} \cdot f_0,$$

Ambiguity Probability Comparison：

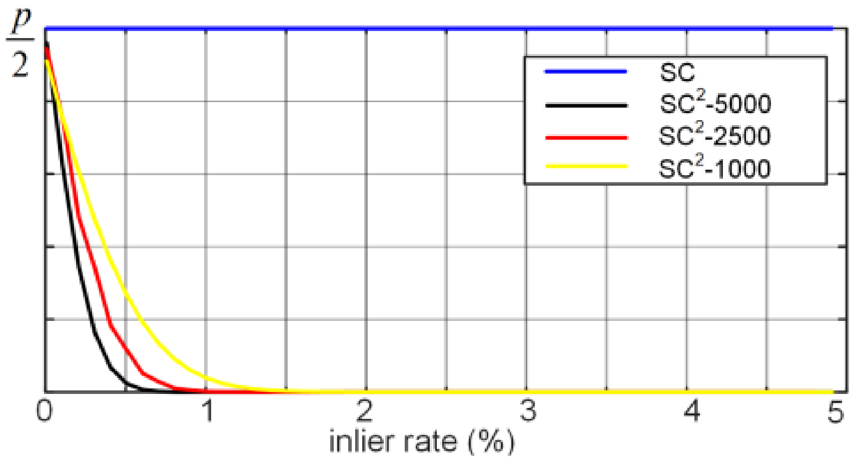


Fig. 4. The probability of ambiguity event. SC is spatial consistency measure. SC^2-N ($N = 5000, 2500, 1000$) is the second-order spatial consistency measure with N correspondences.

Introduction - Model Selection

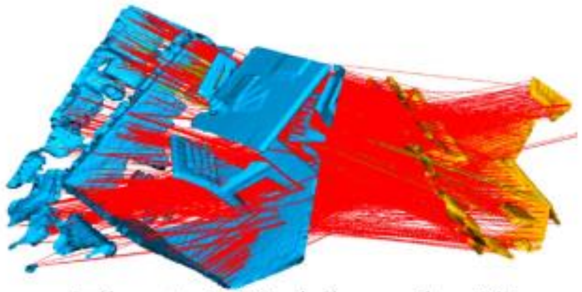
RANSAC: After generating some hypotheses, the inlier count (IC) is adopted as the metric for selecting the best estimation among them.

$$\mathrm{IC}_k = \sum_{i=1}^{N} [\|R_k x_i + t_k - y_i\| < \tau],$$

where *N* is the number of putative correspondences. (*xi*, *yi*) is a pair of correspondence. [·] is the Iverson bracket , Once *Rk* and *tk* are correctly estimated, the IC*k* should be close to the number of inliers.

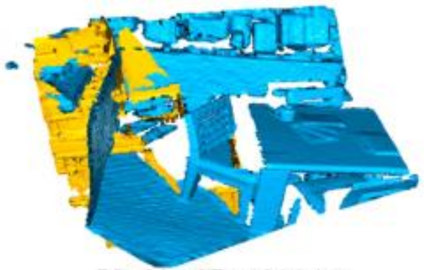
The drawback of the IC metric is the dependence on putative correspondences and the lack of global alignment information . We expect to introduce the Chamfer distance (CD) metric to address the issue of IC metric.

$$\mathrm{CD}_k = \sum_{i=1}^{N} \min_{y_j \in \mathcal{Y}} \|R_k x_i + t_k - y_j\|.$$



Inlier rate: 0.027 inlier number: 77

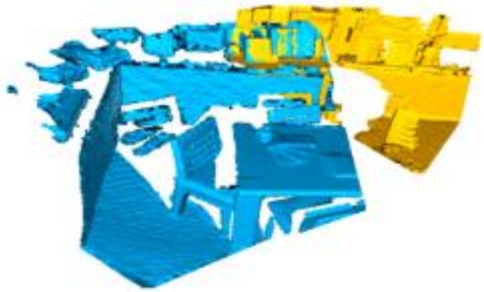
(a) putative correspondences



IC: 89 CD: 1314.1m

TCD: 692 FS-TCD:180

(b) wrong model



IC: 75 CD: 1412.0m

TCD: 634 FS-TCD:282

(c) correct model

FS-TCD Feature and Spatial consistency constrained Truncated Chamfer Distance metric

First reformulate the CD metric as a truncated form (TCD) :

$$\mathrm{TCD}_k = \sum_{i=1}^{N} [(\min_{y_j \in \mathcal{Y}} \|R_k x_i + t_k - y_j\|) < \eta],$$

In TCD, when *Rk* and *tk* are incorrectly estimated, it is still possible that the alignment area is miscounted because some points are incorrectly aligned together by chance. To suppress this situation, we introduce two constraints on the TCD. To build the F-TCD as follows:

$$\text{F-TCD}_k = \sum^{N} [(\min_{H_{ij}=1} \|R_k x_i + t_k - y_j\|) < \eta].$$

FS-TCD metric : Integrate the spatial consistency constraint into F-TCD

The pipeline of SC2-PCR++

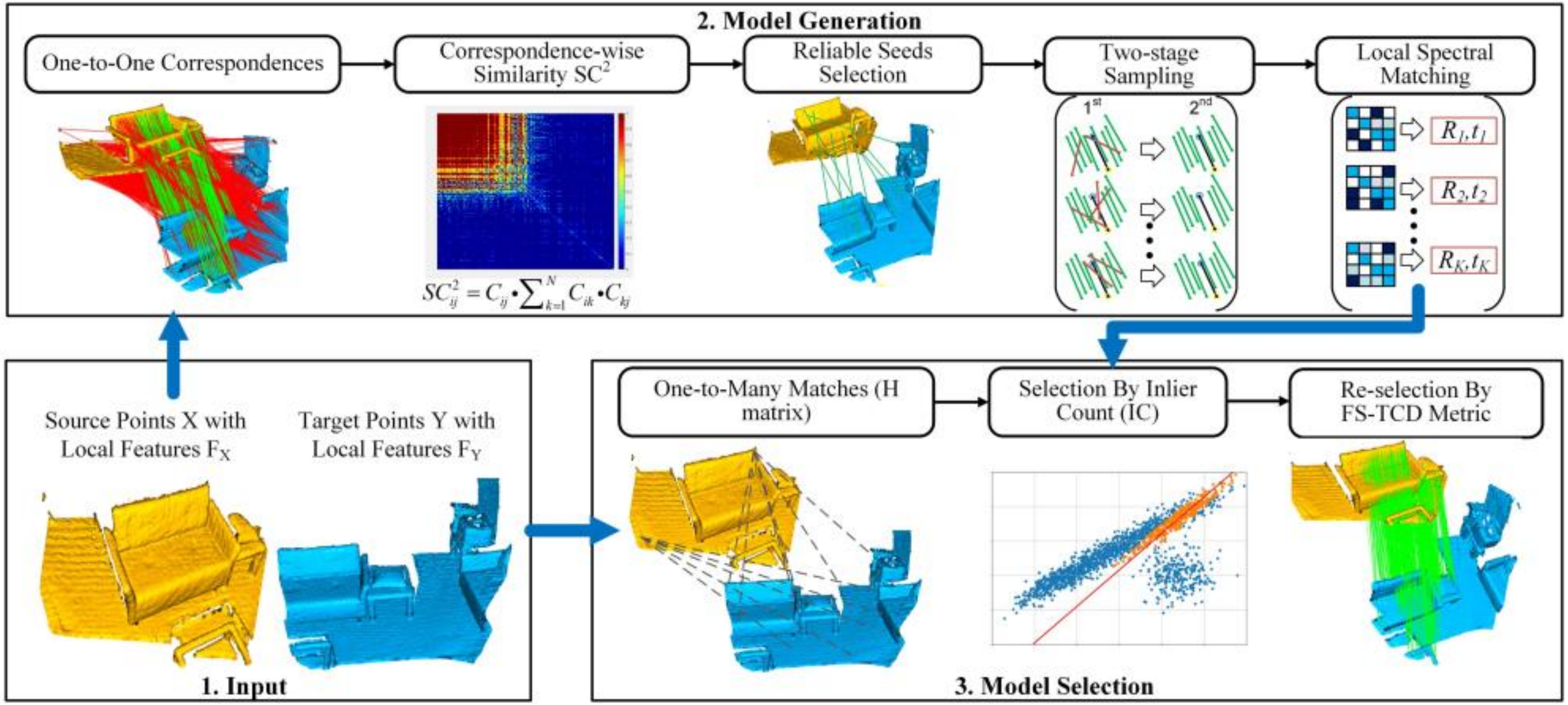


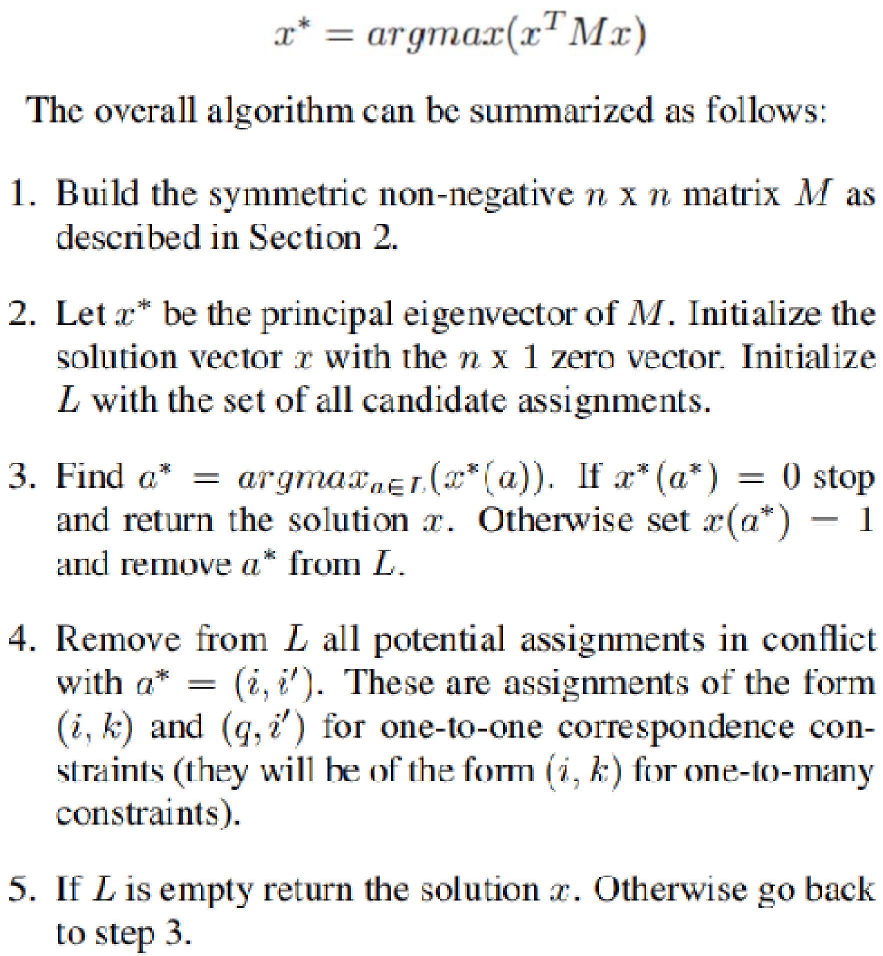
Fig. 6. Pipeline of our method. The input is the source and target points with extracted features. The proposed method rebuilds the model generation and model selection process of the classic RANSAC.

Reliable Seed Selection

We perform the spectral matching technique to select seed points and accelerate the registration process.

(1)We first build the similarity matrix for all of the correspondences and normalize the value in the matrix to 0-1.

(2) Then, the association of each correspondence with the leading eigenvector is adopted as the confidence for this correspondence. The leading eigenvector is solved by the power iteration algorithm



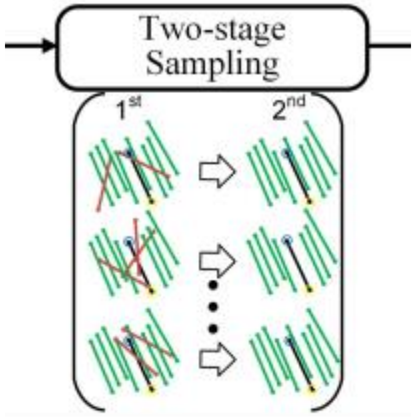
$$x^* = argmax(x^T M x)$$

The overall algorithm can be summarized as follows:

1. Build the symmetric non-negative n x n matrix M as described in Section 2.
2. Let x^* be the principal eigenvector of M. Initialize the solution vector x with the n x 1 zero vector. Initialize L with the set of all candidate assignments.
3. Find $a^* = argmax_{a \in L}(x^*(a))$. If $x^*(a^*) = 0$ stop and return the solution x. Otherwise set $x(a^*) = 1$ and remove a^* from L.
4. Remove from L all potential assignments in conflict with $a^* = (i, i')$. These are assignments of the form (i, k) and (q, i') for one-to-one correspondence constraints (they will be of the form (i, k) for one-to-many constraints).
5. If L is empty return the solution x. Otherwise go back to step 3.

Two-stage Consensus Set Sampling

As some seed points are selected, we extend each of them into a consensus set.



In the first stage, we select *K*1 correspondences for each seed by finding its top-*K*1 neighbors in the SC^2 measure space. The ambiguity probability $P(SC^2_{in,out} > SC^2_{in,in})$ is very small. when a seed is an inlier correspondence, the consensus set also mainly contains inliers.

In the second stage of the sampling operation is adopted to further filter potential outliers in the set obtained in the first stage.
The SC2 matrices are reconstructed within each set produced by the first stage instead of the whole set. We select top-*K*2 ($K2 < K1$) correspondences of the seed by the newly constructed local SC2 matrices.

Local Spectral Matching

In this step, we perform the weighted SVD on the consensus set to generate an estimation of rigid transformation for each seed**.**

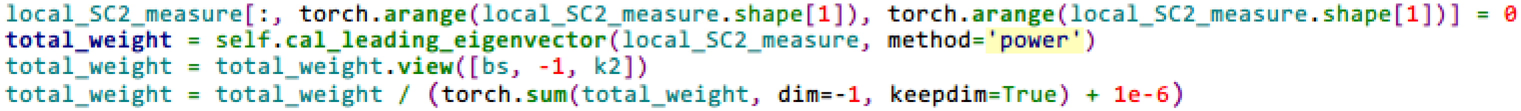
奇异值分解（SVD）：是将任意较复杂的矩阵用更小、更简单的 3个子矩阵的相乘表示， 用这3个小矩阵来描述大矩阵重要的特性。

In order to facilitate matrix analysis, we convert the SC2 measure into soft form (*SC*˜ 2) as follows:

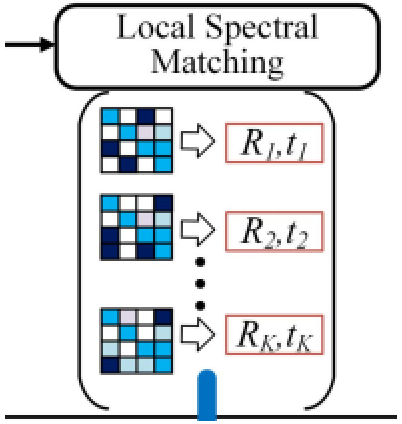
$$S\tilde{C}^2 = \tilde{C} \cdot (\tilde{C} \times \tilde{C}),$$

$$\tilde{C}_{ij} = \mathrm{ReLU}(1 - d_{ij}^2 / d_{thr}^2), (1 \leq i \leq K_2, 1 \leq j \leq K_2)$$

Then we conduct local spectral decomposition on the adjacent matrix of the local graph, i.e., SC˜ 2, to obtain a weight wi for correspondence i.



```
local_SC2_measure[:, torch.arange(local_SC2_measure.shape[1]), torch.arange(local_SC2_measure.shape[1])] = 0
total_weight = self.cal_leading_eigenvector(local_SC2_measure, method='power')
total_weight = total_weight.view([bs, -1, k2])
total_weight = total_weight / (torch.sum(total_weight, dim=-1, keepdim=True) + 1e-6)
```



Experiment

Datasets

Indoor Scenes: Use the 3DMatch benchmark for evaluating the performance on indoor scenes.

Outdoor Scenes: The KITTI dataset is composed of 11 outdoor driving scenarios of point clouds.

Multi-Way Registration Dataset: Use the Augmented ICL_NUIM dataset for testing the performance.

Evaluation Criteria : registration recall (RR) under an error threshold . For a pair of point clouds to be aligned, calculate the errors of translation and rotation estimation separately.

$$\mathrm{RE} = \mathrm{acos}\left(\frac{\mathrm{trace}(\hat{\mathrm{R}}^{-1}\mathrm{R}) - 1}{2}\right), \mathrm{TE} = \|\mathrm{t} - \hat{\mathrm{t}}\|_2,$$

Evaluation on Indoor Scenes

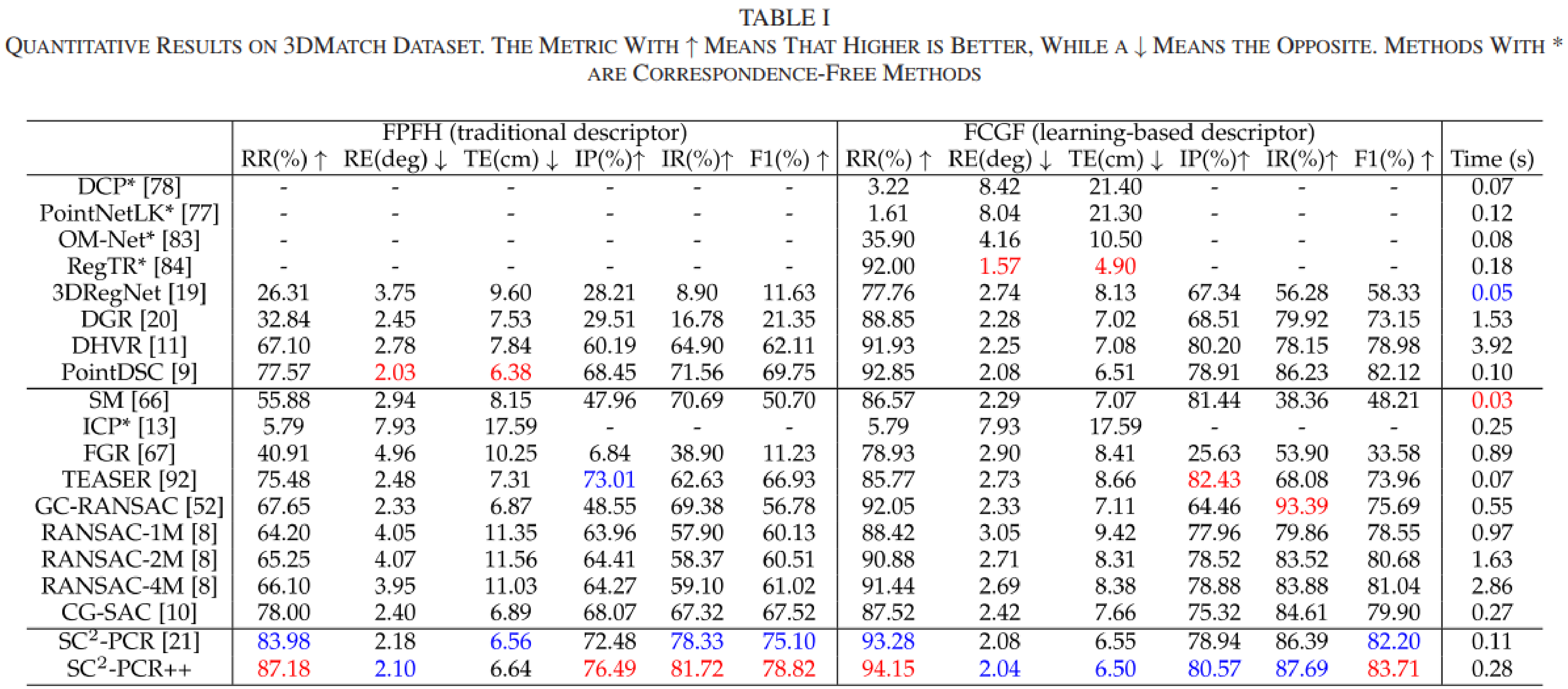


TABLE I

Quantitative Results on 3DMatch Dataset. The Metric With ↑ Means That Higher is Better, While a ↓ Means the Opposite. Methods With * are Correspondence-Free Methods

	FPFH (traditional descriptor)						FCGF (learning-based descriptor)						
	RR(%) ↑	RE(deg) ↓	TE(cm) ↓	IP(%)↑	IR(%)↑	F1(%) ↑	RR(%) ↑	RE(deg) ↓	TE(cm) ↓	IP(%)↑	IR(%)↑	F1(%) ↑	Time (s)
DCP* [78]	-	-	-	-	-	-	3.22	8.42	21.40	-	-	-	0.07
PointNetLK* [77]	-	-	-	-	-	-	1.61	8.04	21.30	-	-	-	0.12
OM-Net* [83]	-	-	-	-	-	-	35.90	4.16	10.50	-	-	-	0.08
RegTR* [84]	-	-	-	-	-	-	92.00	1.57	4.90	-	-	-	0.18
3DRegNet [19]	26.31	3.75	9.60	28.21	8.90	11.63	77.76	2.74	8.13	67.34	56.28	58.33	0.05
DGR [20]	32.84	2.45	7.53	29.51	16.78	21.35	88.85	2.28	7.02	68.51	79.92	73.15	1.53
DHVR [11]	67.10	2.78	7.84	60.19	64.90	62.11	91.93	2.25	7.08	80.20	78.15	78.98	3.92
PointDSC [9]	77.57	2.03	6.38	68.45	71.56	69.75	92.85	2.08	6.51	78.91	86.23	82.12	0.10
SM [66]	55.88	2.94	8.15	47.96	70.69	50.70	86.57	2.29	7.07	81.44	38.36	48.21	0.03
ICP* [13]	5.79	7.93	17.59	-	-	-	5.79	7.93	17.59	-	-	-	0.25
FGR [67]	40.91	4.96	10.25	6.84	38.90	11.23	78.93	2.90	8.41	25.63	53.90	33.58	0.89
TEASER [92]	75.48	2.48	7.31	73.01	62.63	66.93	85.77	2.73	8.66	82.43	68.08	73.96	0.07
GC-RANSAC [52]	67.65	2.33	6.87	48.55	69.38	56.78	92.05	2.33	7.11	64.46	93.39	75.69	0.55
RANSAC-1M [8]	64.20	4.05	11.35	63.96	57.90	60.13	88.42	3.05	9.42	77.96	79.86	78.55	0.97
RANSAC-2M [8]	65.25	4.07	11.56	64.41	58.37	60.51	90.88	2.71	8.31	78.52	83.52	80.68	1.63
RANSAC-4M [8]	66.10	3.95	11.03	64.27	59.10	61.02	91.44	2.69	8.38	78.88	83.88	81.04	2.86
CG-SAC [10]	78.00	2.40	6.89	68.07	67.32	67.52	87.52	2.42	7.66	75.32	84.61	79.90	0.27
SC^2-PCR [21]	83.98	2.18	6.56	72.48	78.33	75.10	93.28	2.08	6.55	78.94	86.39	82.20	0.11
SC^2-PCR++	87.18	2.10	6.64	76.49	81.72	78.82	94.15	2.04	6.50	80.57	87.69	83.71	0.28

Combined With FPFH: The SC2-PCR greatly outperforms all of the other methods.
Compared with the SC2-PCR, SC2-PCR++ further achieves a significant performance improvement.

Combined With FCGF: SC2-PCR++ still achieves the best performance over all the methods, with 2.71% improvement over RANSAC on registration recall.

Evaluation on Indoor Scenes

Qualitative results on 3DLoMatch dataset

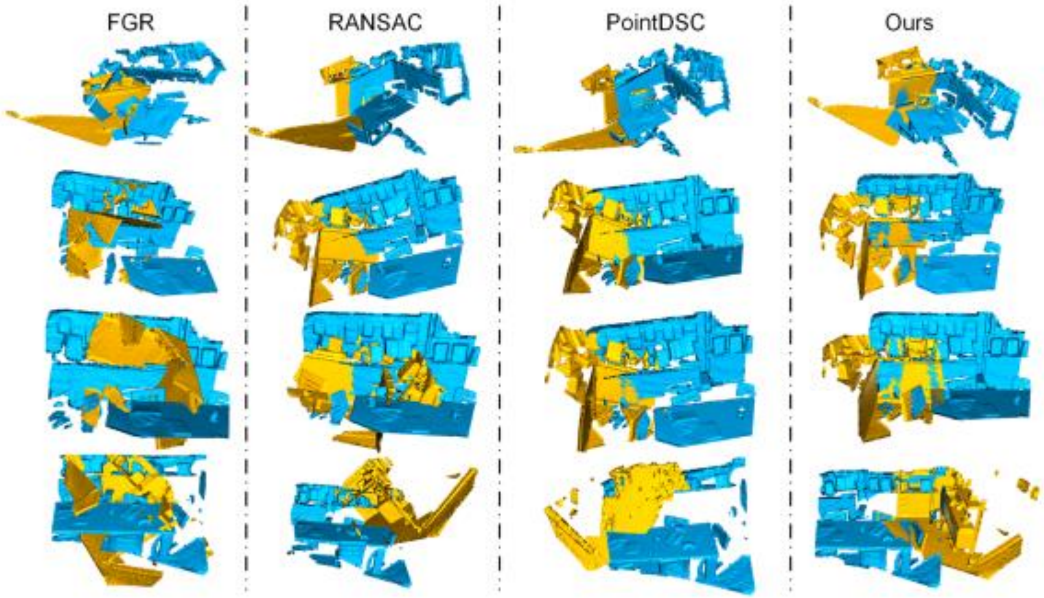


Fig. 7. Qualitative comparison on 3DMatch and 3DLoMatch dataset. From left to right are: FGR [67], RANSAC [8], PointDSC [9] and Ours.

SC2-PCR++ can successfully align two point clouds where the low overlap ratio is clearly visible

Evaluation on Outdoor Scenes

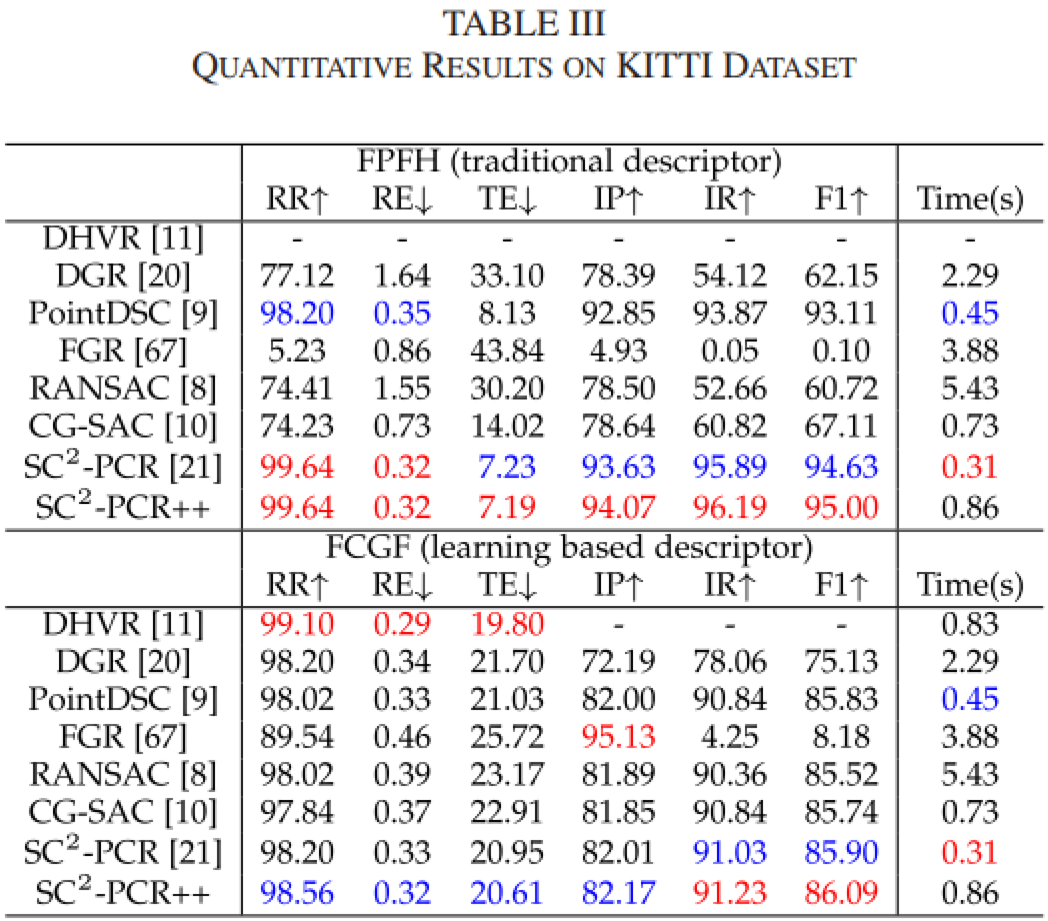


TABLE III
QUANTITATIVE RESULTS ON KITTI DATASET

	FPFH (traditional descriptor)						
	RR↑	RE↓	TE↓	IP↑	IR↑	F1↑	Time(s)
DHVR [11]	-	-	-	-	-	-	-
DGR [20]	77.12	1.64	33.10	78.39	54.12	62.15	2.29
PointDSC [9]	98.20	0.35	8.13	92.85	93.87	93.11	0.45
FGR [67]	5.23	0.86	43.84	4.93	0.05	0.10	3.88
RANSAC [8]	74.41	1.55	30.20	78.50	52.66	60.72	5.43
CG-SAC [10]	74.23	0.73	14.02	78.64	60.82	67.11	0.73
SC^2-PCR [21]	99.64	0.32	7.23	93.63	95.89	94.63	0.31
SC^2-PCR++	99.64	0.32	7.19	94.07	96.19	95.00	0.86
	FCGF (learning based descriptor)						
	RR↑	RE↓	TE↓	IP↑	IR↑	F1↑	Time(s)
DHVR [11]	99.10	0.29	19.80	-	-	-	0.83
DGR [20]	98.20	0.34	21.70	72.19	78.06	75.13	2.29
PointDSC [9]	98.02	0.33	21.03	82.00	90.84	85.83	0.45
FGR [67]	89.54	0.46	25.72	95.13	4.25	8.18	3.88
RANSAC [8]	98.02	0.39	23.17	81.89	90.36	85.52	5.43
CG-SAC [10]	97.84	0.37	22.91	81.85	90.84	85.74	0.73
SC^2-PCR [21]	98.20	0.33	20.95	82.01	91.03	85.90	0.31
SC^2-PCR++	98.56	0.32	20.61	82.17	91.23	86.09	0.86

The SC2-PCR and SC2-PCR++ with FPFH descriptor obtain the results with the highest registration recall and lowest error of rotation and translation.

Multi-Way Registration

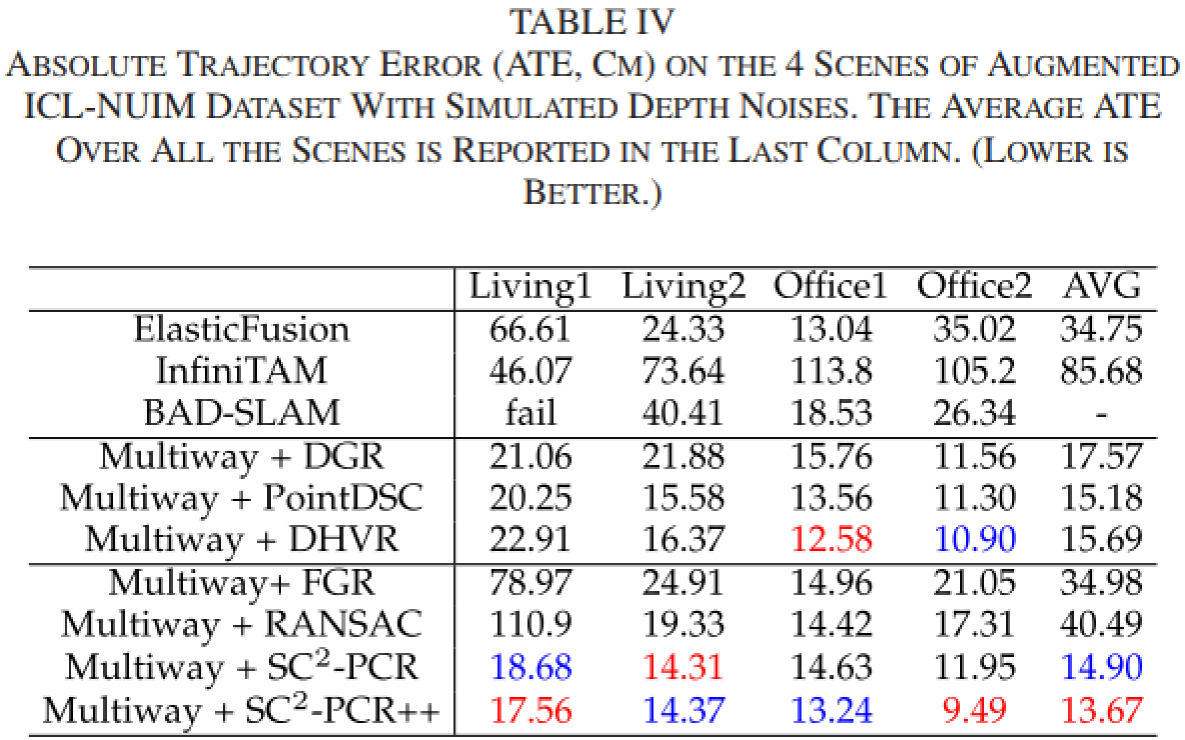


TABLE IV

ABSOLUTE TRAJECTORY ERROR (ATE, CM) ON THE 4 SCENES OF AUGMENTED ICL-NUIM DATASET WITH SIMULATED DEPTH NOISES. THE AVERAGE ATE OVER ALL THE SCENES IS REPORTED IN THE LAST COLUMN. (LOWER IS BETTER.)

	Living1	Living2	Office1	Office2	AVG
ElasticFusion	66.61	24.33	13.04	35.02	34.75
InfiniTAM	46.07	73.64	113.8	105.2	85.68
BAD-SLAM	fail	40.41	18.53	26.34	-
Multiway + DGR	21.06	21.88	15.76	11.56	17.57
Multiway + PointDSC	20.25	15.58	13.56	11.30	15.18
Multiway + DHVR	22.91	16.37	12.58	10.90	15.69
Multiway+ FGR	78.97	24.91	14.96	21.05	34.98
Multiway + RANSAC	110.9	19.33	14.42	17.31	40.49
Multiway + SC^2-PCR	18.68	14.31	14.63	11.95	14.90
Multiway + SC^2-PCR++	17.56	14.37	13.24	9.49	13.67

SC2-PCR and SC2-PCR++ achieve great performance among all the methods.
The SC2-PCR++ achieves the best performance on the Living1 and Office2 scenes and the lowest average ATE over the four test scenes

Generalization and Robustness

Generalization Experiments

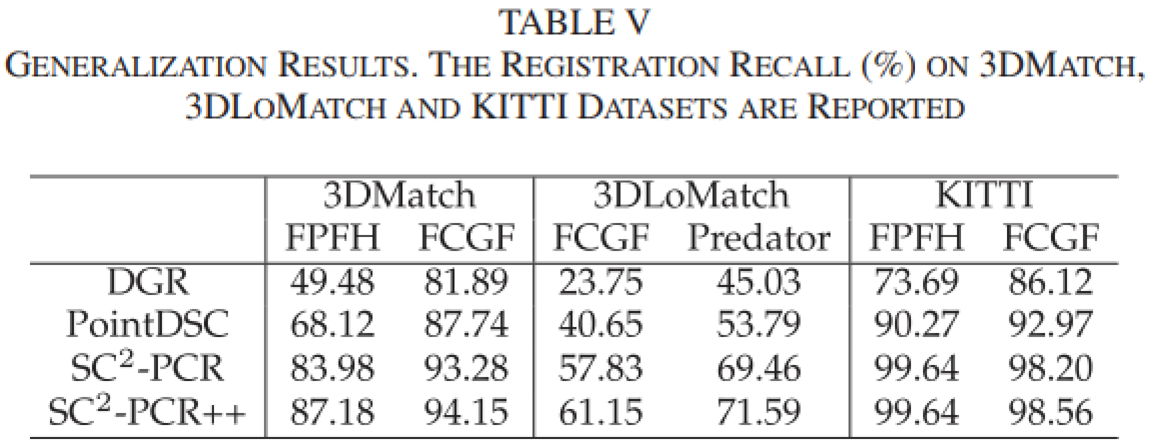


TABLE V

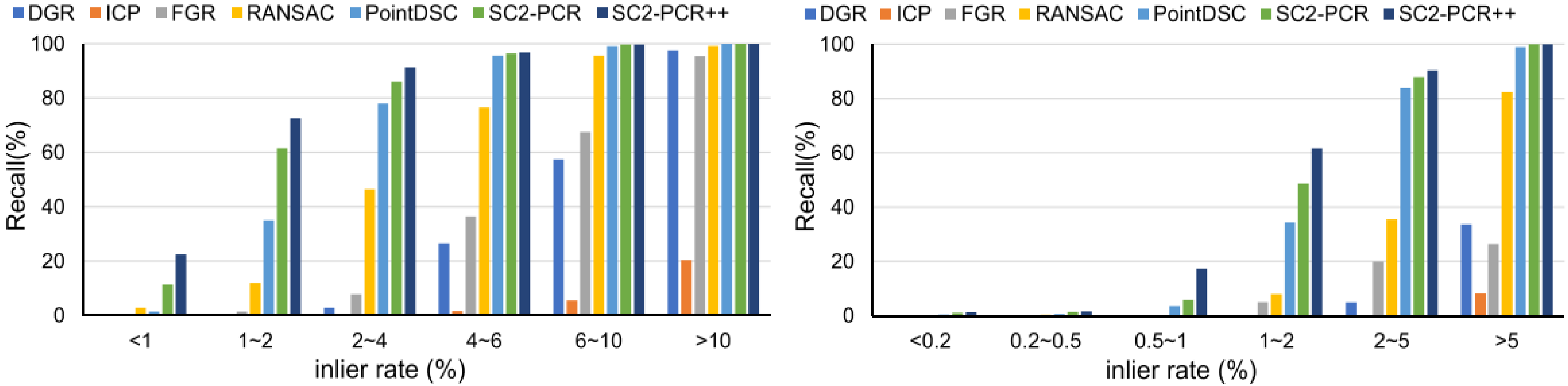
GENERALIZATION RESULTS. THE REGISTRATION RECALL (%) ON 3DMATCH, 3DLOMATCH AND KITTI DATASETS ARE REPORTED

	3DMatch		3DLoMatch		KITTI	
	FPFH	FCGF	FCGF	Predator	FPFH	FCGF
DGR	49.48	81.89	23.75	45.03	73.69	86.12
PointDSC	68.12	87.74	40.65	53.79	90.27	92.97
SC^2-PCR	83.98	93.28	57.83	69.46	99.64	98.20
SC^2-PCR++	87.18	94.15	61.15	71.59	99.64	98.56

SC$_2$-PCR++ show significant improvements in registration recall without the generalization problem. This further demonstrates the effectiveness of our method.

Generalization and Robustness

Robustness to Noises



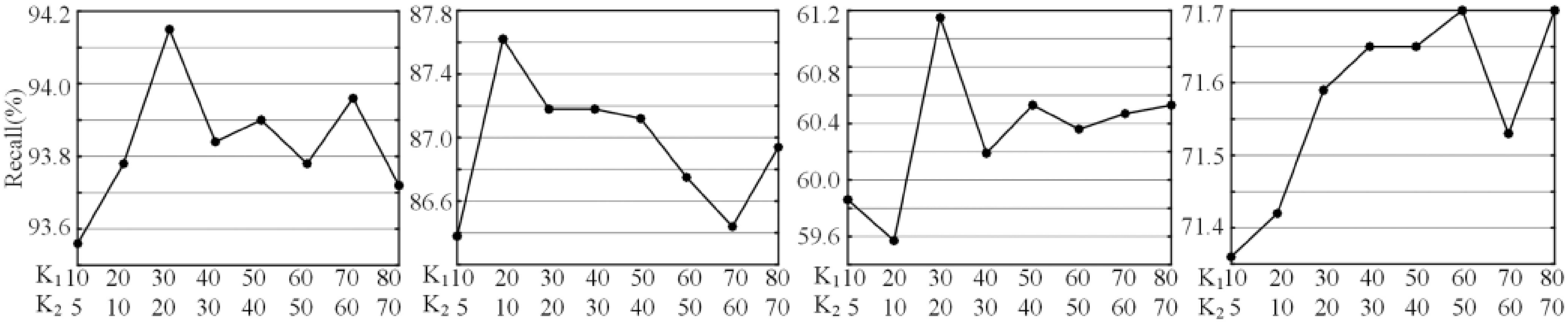
(a) 3DMatch (b) 3DLoMatch

Fig. 8. The registration recall under the different inlier ratio of the putative correspondences.

When the inlier rate is less than 2%, SC2-PCR++ is significantly better than other baselines. When the inlier rate is 0.5% - 1%, the success rate of most methods is extremely low, while SC2-PCR++ significantly improves the success rate.

Robustness to Parameters

The SC2-PCR adopts a two-stage sampling strategy. It finds *K*1 instances for each seed in the first stage, and remains *K*2(*K*2 < *K*1) samples for model estimation in the second stage.



(a) 3DMatch with FCGF (b) 3DMatch with FPFH (c) 3DLoMatch with FCGF (d) 3DLoMatch with Predator

10. Experiments results for the analysis of the sampling parameters.

On the whole, the results with (*K*1, *K*2) being (30, 20) are the best,
Changing parameters does not have a great impact on registration recall, which can also demonstrate the robustness of SC2-PCR++.

Combined With Learning Network

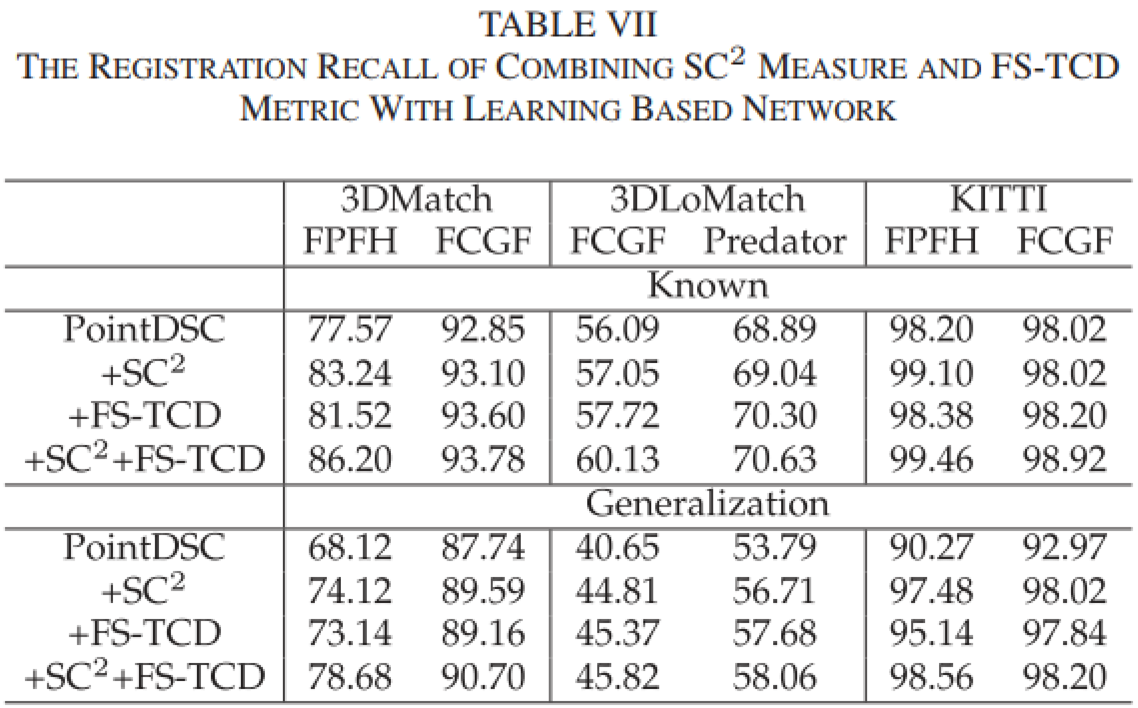


TABLE VII

THE REGISTRATION RECALL OF COMBINING SC^2 MEASURE AND FS-TCD METRIC WITH LEARNING BASED NETWORK

	3DMatch		3DLoMatch		KITTI	
	FPFH	FCGF	FCGF	Predator	FPFH	FCGF
	Known					
PointDSC	77.57	92.85	56.09	68.89	98.20	98.02
+SC^2	83.24	93.10	57.05	69.04	99.10	98.02
+FS-TCD	81.52	93.60	57.72	70.30	98.38	98.20
+SC^2+FS-TCD	86.20	93.78	60.13	70.63	99.46	98.92
	Generalization					
PointDSC	68.12	87.74	40.65	53.79	90.27	92.97
+SC^2	74.12	89.59	44.81	56.71	97.48	98.02
+FS-TCD	73.14	89.16	45.37	57.68	95.14	97.84
+SC^2+FS-TCD	78.68	90.70	45.82	58.06	98.56	98.20

It can be seen that adding SC2-PCR++ can significantly boost the performance of the network, especially for the generalization performance of the network.

Ablation Study

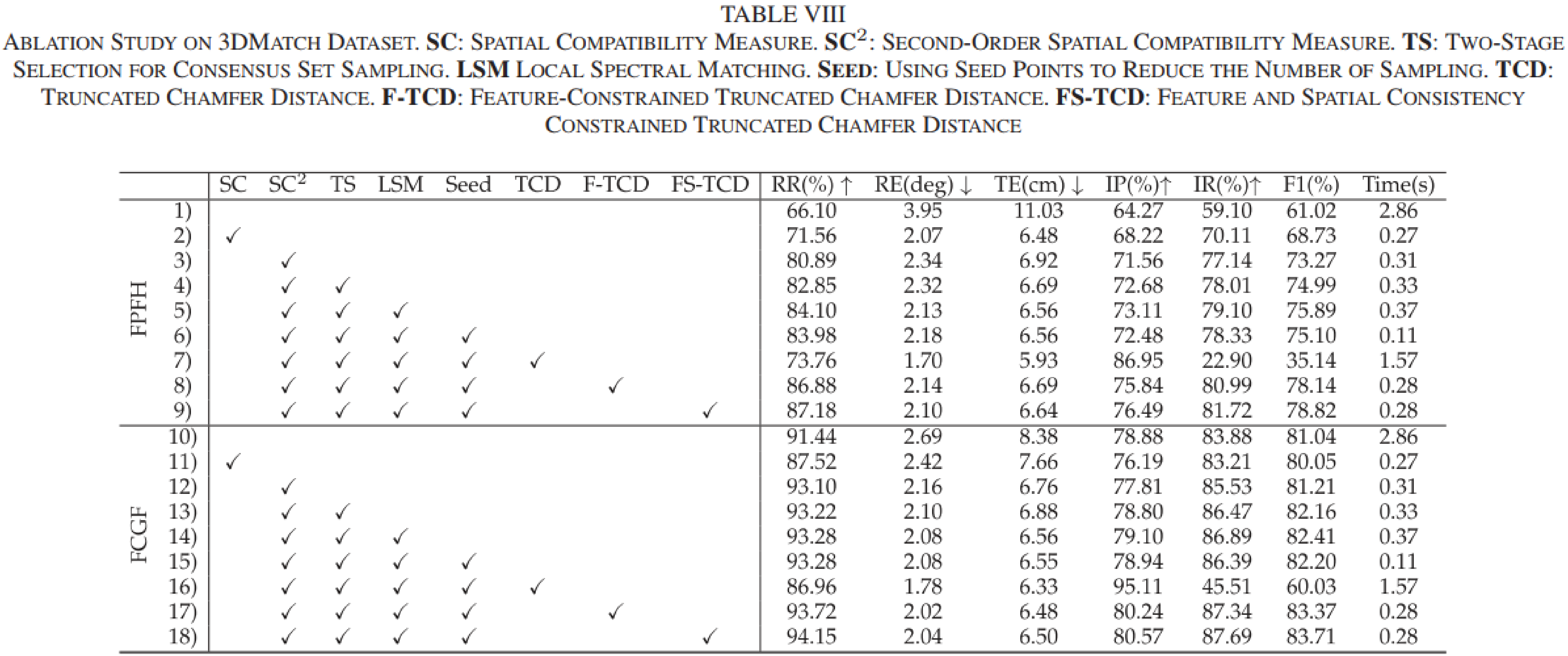


TABLE VIII

ABLATION STUDY ON 3DMATCH DATASET. **SC**: SPATIAL COMPATIBILITY MEASURE. **SC^2**: SECOND-ORDER SPATIAL COMPATIBILITY MEASURE. **TS**: TWO-STAGE SELECTION FOR CONSENSUS SET SAMPLING. **LSM** LOCAL SPECTRAL MATCHING. **SEED**: USING SEED POINTS TO REDUCE THE NUMBER OF SAMPLING. **TCD**: TRUNCATED CHAMFER DISTANCE. **F-TCD**: FEATURE-CONSTRAINED TRUNCATED CHAMFER DISTANCE. **FS-TCD**: FEATURE AND SPATIAL CONSISTENCY CONSTRAINED TRUNCATED CHAMFER DISTANCE

		SC	SC^2	TS	LSM	Seed	TCD	F-TCD	FS-TCD	RR(%) ↑	RE(deg) ↓	TE(cm) ↓	IP(%)↑	IR(%)↑	F1(%)	Time(s)
FPFH	1)									66.10	3.95	11.03	64.27	59.10	61.02	2.86
	2)	✓								71.56	2.07	6.48	68.22	70.11	68.73	0.27
	3)		✓							80.89	2.34	6.92	71.56	77.14	73.27	0.31
	4)		✓	✓						82.85	2.32	6.69	72.68	78.01	74.99	0.33
	5)		✓	✓	✓					84.10	2.13	6.56	73.11	79.10	75.89	0.37
	6)		✓	✓	✓	✓				83.98	2.18	6.56	72.48	78.33	75.10	0.11
	7)		✓	✓	✓	✓	✓			73.76	1.70	5.93	86.95	22.90	35.14	1.57
	8)		✓	✓	✓	✓		✓		86.88	2.14	6.69	75.84	80.99	78.14	0.28
	9)		✓	✓	✓	✓			✓	87.18	2.10	6.64	76.49	81.72	78.82	0.28
FCGF	10)									91.44	2.69	8.38	78.88	83.88	81.04	2.86
	11)	✓								87.52	2.42	7.66	76.19	83.21	80.05	0.27
	12)		✓							93.10	2.16	6.76	77.81	85.53	81.21	0.31
	13)		✓	✓						93.22	2.10	6.88	78.80	86.47	82.16	0.33
	14)		✓	✓	✓					93.28	2.08	6.56	79.10	86.89	82.41	0.37
	15)		✓	✓	✓	✓				93.28	2.08	6.55	78.94	86.39	82.20	0.11
	16)		✓	✓	✓	✓	✓			86.96	1.78	6.33	95.11	45.51	60.03	1.57
	17)		✓	✓	✓	✓		✓		93.72	2.02	6.48	80.24	87.34	83.37	0.28
	18)		✓	✓	✓	✓			✓	94.15	2.04	6.50	80.57	87.69	83.71	0.28

Ablation Study

Second-Order Spatial Compatibility: As shown in Row 1, 3, and 10, 12 of Table VIII, the registration recall obtained by using SC2 measure as guidance is 14.79% higher than RANSAC when combined with FPFH, and 1.66% higher when combined with FCGF.

Two-Stage Selection: Comparing Row 3, 4, and 12, 13 in Table VIII, using two-stage selection achieves a recall improvement of 1.96% when combined with FPFH, and 0.12% improvement when combined with FCGF.

Local Spectral Matching: Comparing Row 4, 5, and 13, 14 in Table VIII, using local spectral matching can boost the performance, especially for the mean rotation and translation error.

Seed Selection: Row 5, 6, and 14, 15 of Table VIII shows that Seed Selection can reduce registration time by more than half without much performance degradation .

Hypothesis Selection Strategies: Comparing Row 6, 8 and 15, 17, we can find that F-TCD achieves 2.90% and 0.44% improvement of RR when combined with FPFH and FCGF descriptors respectively.

Conclusion

(1) Extensive experiments demonstrate that SC2-PCR++ achieves state-of-the-art performance and high efficiency.

(2) The proposed SC2 and FS-TCD are flexible measures, which can be combined with learning networks to further boost their performance.

Thank You!

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