Hyper-graph Matching using Reweighted Random Walk

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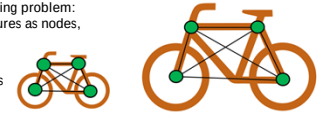
INTRODUCTION

Feature Matching by Hyper-graph Matching

- Establishing feature correspondence is essential task for vision problem
- Well formulated as graph matching problem: Represent object or image features as nodes, features' relations as edges
- Why hyper-graph? Exploiting higher-order relations Ex. Distances are varying Angles are not varying



- Find the solution which best preserves graph attributes

Challenges & Motivations

Outlier Noise → Challenging NP-hard Problem ← Deformation Noise

- Due to background clutters Imperfect feature detector
- Object motion View-point change Class variation

Previous Works & Limitations

- **Pair-wise** methods: Leordeanu & Hebert, ICCV05; Cour et al, NIPS06; Gold & Rangarajan, PAMI96; Wyk & Wyk, PAMI04
- **Higher-order** methods: Zass & Shashua, CVPR08; Duchenne et al, CVPR09; Chertok & Keller, PAMI10

Not able to consider **higher order relations**

Mapping constraints are not effectively incorporated

Our Approach

Random walks on the association hyper-graph

- A novel view for solving hyper-graph matching problem

Personalized Jumps **with a reweighting scheme**

- **The mapping constraints are effectively reflected during random walk process**

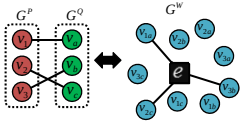
Our Contribution

- Generalization the hyper-graph matching formulation to mixed orders
- A state-of-the-art hyper-graph matching method robust to deformation & outliers
- Extensive comparison with recent hyper-graph matching methods

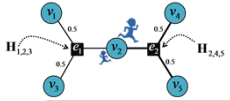
PROPOSED METHOD

Association Hyper-graph

- Nodes represent candidate correspondences
- Hyper-edge weights are higher-order similarity of connected correspondences
- Random walker travels along correspondences in association hyper-graph
- Matching problem can be solved using a node ranking method



Random Walks on Hyper-graph

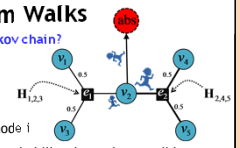


- A random walker select along the hyper-edge e_1 or e_2 with the probabilities proportional to hyper-edge weights
- Then, uniformly moves to one of selected hyper-edge's enclosed nodes

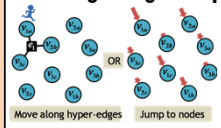
Problematic: Conventional stochastic normalization can strengthen the adverse effect of outliers and weak correspondences

Affinity-preserving Random Walks

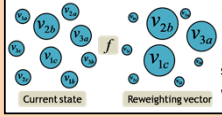
- How to preserve original affinities in the Markov chain?
- **Solution**: A new **Absorbing** node is augmented
- Degree d_i: Total outgoing hyper-edge weights of node i
- Absorbing node soaks affinity d_{max}-d_i from the node i
- A candidate match with more degree has more probability than other candidates



Reweighting Jumps



- How to incorporated the matching constraints (1-to-1) in affinity-preserving random walks?
- **Solution**: **Personalized Jump** Haveliwala, Topic-sensitive pagerank, *WWW02*
- Reweighting function guides the current solution to move toward a solution that satisfies the mapping constraints at each step



- **Inflation**: Strong candidates are amplified while weak candidates are attenuated
- **Bistocastic-Norm**: Make inflated distribution satisfy constraints. Sinkhorn, Ann. Math. Statistics 64'

What f does: Inflation & Bistochastic Normalization

EXPERIMENTS

Project Site Open

http://cv.snu.ac.kr/research/~RRWHM

- Full experimental results and source code are available

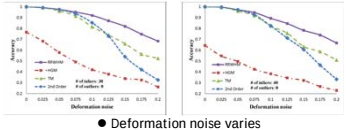
Comparing with standard methods

- HGM: Zass & Shashua, CVPR2008
- TM: Duchenne et al, CVPR2009
- 2nd Order: Cho et al, ECCV2010 (state-of-the-art 2nd order method)

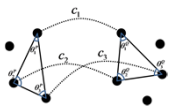
Synthetic Point-set Matching

- Generate two point-sets which share a common pattern
- Triplet distance: differences of angles of two triangles

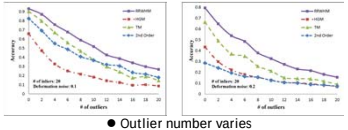
- Generation example



- Deformation noise varies



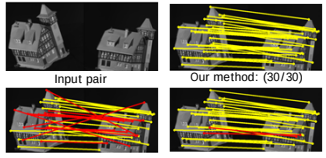
- Tensor calculation



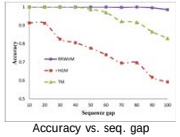
- Outlier number varies

Feature Point Matching across Image Sequences

- CMU house sequence
- 30 pts are manually tracked
- Triplet distance: differences of angles of two triangles



Input pair; Our method: (30/30); HGM: (10/15); TM: (27/30)



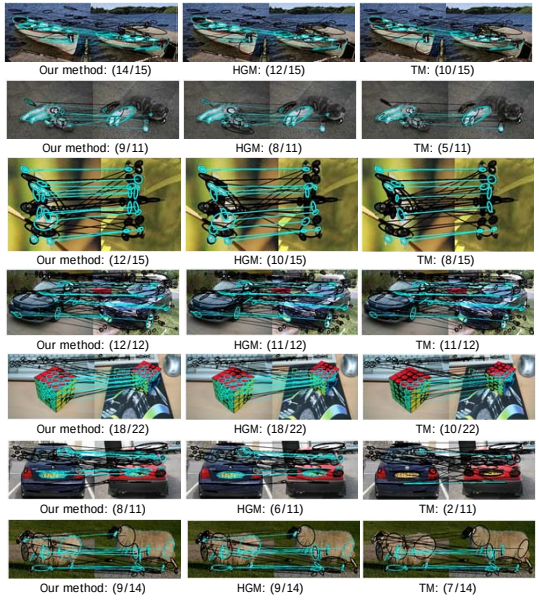
Accuracy vs. seq. gap

Real Image Matching

- Caltech-101 & MSRC dataset
- MSER detector & SIFT descriptor
- Triplet distance: differences of angles of two triangles
- Matching performance on the real image dataset (30 pairs)

Methods	RRWHM	HGM	TM
Avg. of accuracy (%)	**45.03**	41.36	41.12
Avg. of relative score (%)	**98.38**	81.50	81.57

- Matching examples



Our method: (14/15); HGM: (12/15); TM: (10/15)
Our method: (9/11); HGM: (8/11); TM: (5/11)
Our method: (12/15); HGM: (10/15); TM: (8/15)
Our method: (12/12); HGM: (11/12); TM: (11/12)
Our method: (18/22); HGM: (18/22); TM: (10/22)
Our method: (8/11); HGM: (6/11); TM: (2/11)
Our method: (9/14); HGM: (9/14); TM: (7/14)