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RESEARCH GOAL

SCIENTIA

We present a novel framework for *finding kinematic structure correspondences* between two videos of heterogeneous objects via hypergraph matching

Kinematic Structure Represent kinematic properties between rigid body parts

> Skeleton Generally a framework of bones



APPLICATIONS

- Robot learning by imitation
- Viewpoint invariant human action recognition by 3D skeleton
- Affordance based articulated object/tool categorisation & manipulation
- > Motion retargeting to robots

CONTRIBUTIONS

Casting the kinematic structure correspondence problem into the *hypergraph matching framework,* incorporating *multi-order similarities* with *normalisation weights*

- 1st order Structural topology similarity by a new topology constrained

subgraph isomorphism aggregation

- 2nd order Kinematic correlation similarity between pairwise nodes
- 3rd order Combinatorial local motion similarity using geodesic distance on the
- **Riemannian manifold**

OVERALL FRAMEWORK

st order: Topology 2nd order: Kinematic correlation Kinematic structure Feature extraction generation & Motion segmentation 3rd order: Combinatorial motion

PREVIOUS CORRESPONDENCE MATCHING APPROACHES

- Local shape feature matching [10,20,26,43]
- Skeleton corresponding points matching
- Graph alignment methods [25,37]

CONTACT



- Video result, source code, and the new dataset are available: www.imperial.ac.uk/PersonalRobotics • Dr. Hyung Jin Chang (hj.chang@imperial.ac.uk) and Prof. Yiannis Demiris (y.demiris@imperial.ac.uk)
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Hypergraph Matching



Kinematic Structure Correspondences via Hypergraph Matching

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EXPERIMENTAL RESULTS 1st order **Structure Topology** And And And And Synthetic Dataset Validations on 2nd order roposed 2nd term only Proposed 3rd term only **Kinematic Correlation** 3 4 Symmetry order 0.3 0.4 0.5 0.6 0.7 1 2 3 4 5 6 - Topology changes ematic deformation test in 2D (N = 1(c) Symmetry test in 2D - Kinematic deformation $\sum \mathcal{F}^3_{(i,i')(j,j')(k,k')} X_i X_j X_k$ 3rd order **Combinatorial Motion** - Structure symmetricity Proposed 2nd term only Proposed 3rd term only Algorithm 1: Generating the first order similarity fu 1 2 3 4 5 6 7 0.3 0.4 0.5 0.6 3 Symmetry order (d) Outlier test in 3D (N = 10) (e) Kinematic deformation test in 3D (N = 10(f) Symmetry test in 3D tion using structural topology Real Kinematic Structure Dataset $\mathcal{M} \leftarrow \text{calculate by Eq.}(3) \text{ based on } \mathbb{I}$ **Comparison with Other Matching Methods** for $j \in [1:N']$ do $\leftarrow \mathsf{VF2}(G, \{G' \setminus v_j\})$ $\mathcal{M}'_i \leftarrow \text{calculate by Eq.(3) based on } \mathbb{I}$ Appearance feature matching: ACC Appearance feature match Appearance feature matching: ACC Appearance feature mat **Kinematic Correspondence Chain Ger** [3] H. J. Chang and Y. Demiris. Unsupervised Learning of Complex Articulated Kinematic Structures combining Motion and Skeleton Information. In CVPR, 2015 [10] O. Duchenne, F. Bach, I.-S. Kweon, and J. Ponce. A Tensor-Based Algorithm for High-Order Graph Matching. In TPAMI, 2011 [20] J. Lee, M. Cho, and K. M. Lee. Hyper-graph Matching via Reweighted Random Walks. In CVPR, 2011 [25] B. Neyshabur, A. Khadem, S. Hashemifar, and S. S. Arab. NETAL: A new graph-based method for global alignment of protein-protein interaction networks. Bioinformatics, 2013 [26] Q. Nguyen, A. Gautier, and M. Hein. A Flexible Tensor Block Coordinate Ascent Scheme for Hypergraph Matching. In CVPR, 2015 [37] V. Vijayan, V. Saraph, and T. Milenkovic. MAGNA++: Maximizing Accuracy in Global Network Alignment via both node and edge conservation. Bioinformatics, 2015 [43] R. Zass and A. Shashua. Probabilistic Graph and Hypergraph Matching. In CVPR, 2008

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	Metho	ods	Accuracy (%)
	Proposed $\mathcal{F}(X)$	to HGM [43]	35.06 (±30.73)
TAL Graph alignment: MAGNA++	Proposed $\mathcal{F}(X)$	to TM [10]	29.76 (±21.65)
	Proposed F to B [26]	3CAGM+MP	69.09 (±20.65)
	NETAL [25]		67.72 (±39.59)
M Proposed <i>F</i> to BCAGM+MP	MAGNA++ [37]		63.42 (±33.66)
ng: RRWM Appearance feature matching: PGM	Proposed $\mathcal{F}(X)$ [20] without we normalisation	to RRWHM eight	88.23 (±13.07)
	Proposed $\mathcal{F}(X)$ [20] with weigh normalisation	to RRWHM າt	92.99 (±10.41)
AL Graph alignment: MAGNA++ Image: Alignment: MAGNA++ Image: Alignment: MAGNA++ Image: Alignment: Alignment: MAGNA++ Image: Alignment: Alignmen	Additional of the second se	btw Diffe	erent Domains
eration	Robot :	self left arm	to right arm
	Robot self	f left arm to	human arm