FAST HYPOTHESIS FILTERING FOR MULTI-STRUCTURE GEOMETRIC MODEL FITTING

LOKENDER TIWARI, SAKET ANAND

IIIT-Delhi, India

{lokendert, anands}@iiitd.ac.in



MOTIVATION

- Performance of clustering based robust multi-model fitting algorithms depends on quality of hypotheses generated.
- Sampling based hypothesis generation leads to a significant proportion of irrelevant hypotheses.

CONTRIBUTIONS

- We propose a novel fast and efficient two-stage hypothesis filtering technique that can improve performance of clustering based robust multi-model fitting algorithms.
- Our approach leverages the asymmetry in the distributions of points around the inlier/outlier boundary via the sample skewness computed in the residual space.
- The output is a set of promising hypotheses which aid multi-model fitting algorithms in improving accuracy as well as running time.

ILLUSTRATIVE EXAMPLE- MULTIPLE LINE FITTING

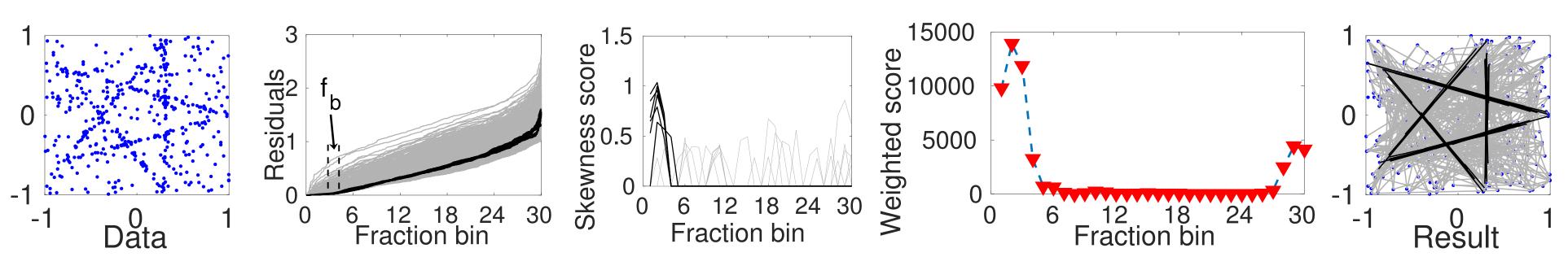


Figure 1: FHF pipeline: Grey:- Bad hypotheses, Black:- Good hypotheses

RESULTS- QUANTITATIVE

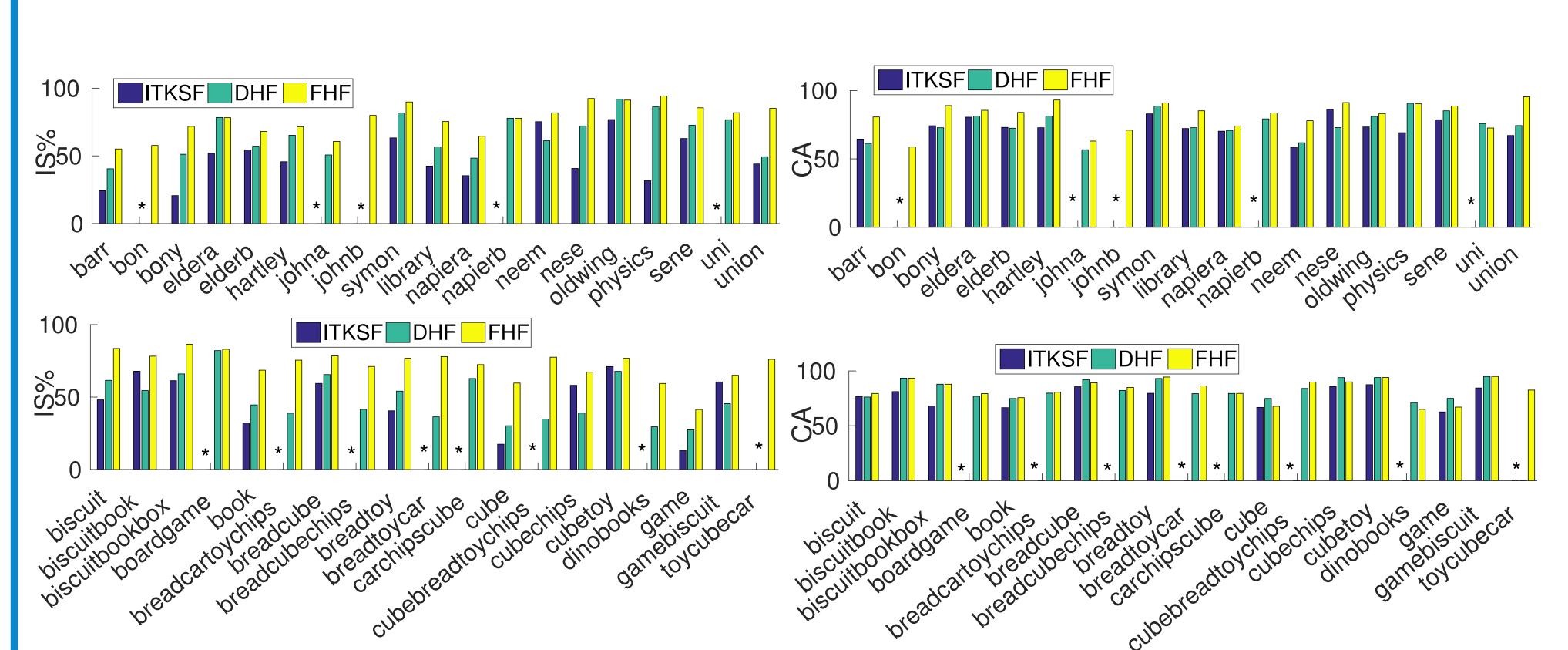


Figure 2: Comparison with ITKSF[1] and DHF[1]. **Row-1:** Homography fitting, **Row-2:** Fundamental matrix fitting. Clustering Accuracy(CA in %) of T-Linkage[3] when the input was the set of hypotheses retained by FHF. (AdelaideRMF[2] dataset).

SAMPLE RESULTS- QUALITATIVE

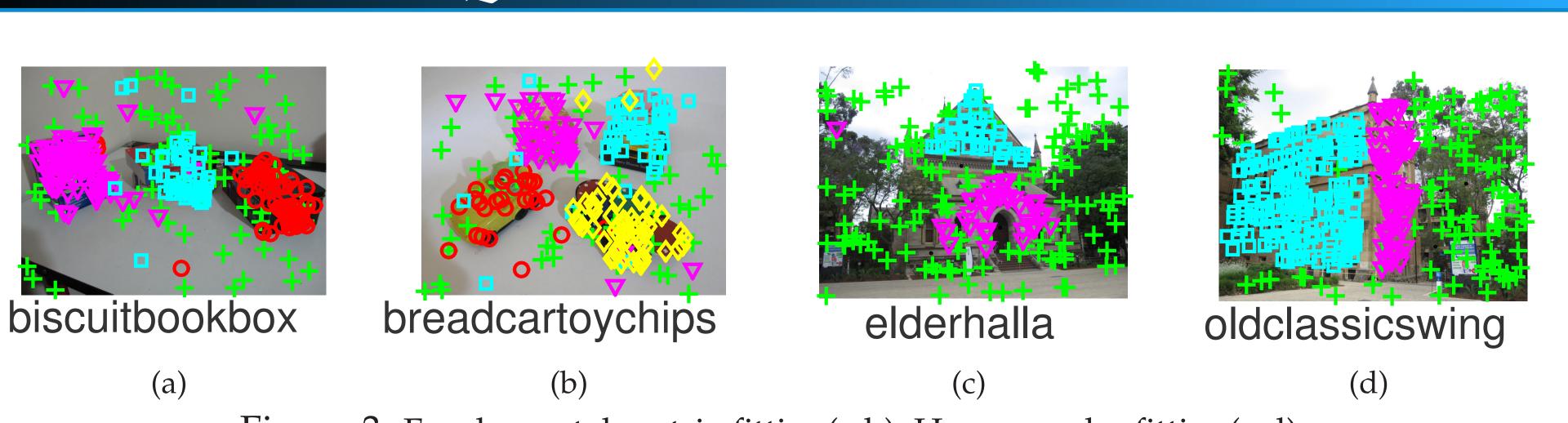


Figure 3: Fundamental matrix fitting(a,b), Homography fitting(c,d)

REFERENCES

- [1] H. S. Wong, T. T. Chin, J. Yu, D. Suter. A simultaneous sample-and-filter strategy for robust multi-structure model fitting In CVIU'13
- [2] H. S. Wong, T. T. Chin, J. Yu, D. Suter. Dynamic and hierarchical multi-structure geometric model fitting. In *ICCV'11*
- [3] L. Magri, A. Fusiello. T-linkage: A continuous relaxation of j-linkage for multi-model fitting In CVPR'14

PROPOSED APPROACH

Data: $\mathcal{X} = \{x_j\}_{j=1}^{N}$

Initial hypotheses: $\vartheta = \{\theta_i\}_{i=1}^M$ Absolute residuals: $r_i^j = \phi(\theta_i, x_i)$

Stage-1 Skewness Based Filtering

- compute skewness score \mathbf{S}_{iq} at each q^{th} fraction bin, $q=1,\ldots,Q$.
- $\mathbf{S}_{iq} = \frac{1}{\lceil wN \rceil} \sum_{j \in f_i^q} \left(\frac{\phi(\theta_i, x_j) \mu}{\sigma} \right)^3$
- for each hypothesis retain only top three skewness scores \overline{S} .
- skewness threshold $\tau = \min_q \max_i \overline{\mathbf{S}}_{iq}$
- \mathcal{H}_q be the index set of hypotheses at the q^{th} fraction bin that yield a skewness value at least τ .
- weighted score $\mathbf{c}_q = |\mathcal{H}_q| \sum_{i \in \mathcal{H}_q} \overline{\mathbf{S}}_{iq}$
- largest fraction bin $\hat{q} = \arg \max_{q} \mathbf{c}_{q}$
- $\vartheta_{\mathrm{I}} = \{\theta_i | \overline{\mathbf{S}}_{iq} \geq \tau, \ \theta_i \in \vartheta, q = 1, \dots, \widehat{q}\}$

Stage-2 Preference Based Pruning

- $\mathcal{X}^{\vartheta_I} \subset \mathcal{X}$, comprising all minimal subsets corresponding to hypotheses in ϑ_I .
- $\mathcal{I}_k^{\theta_j^i}$ be the index set of points in $\mathcal{X}^{\theta_{\mathrm{I}}}$ with the smallest k residuals with respect to $\theta_j^{\mathrm{I}} \in \theta_{\mathrm{I}}$.
- β is the overlap threshold.
- α is the minimum similar hypotheses.

SOURCE CODE

The source code is available at author's webpage



https://www.iiitd.edu.in/~lokendert/