Multi-model fitting based on Minimum Spanning Tree

Radwa Fathalla
http://www.aast.edu/cv.php?ser=36825
College of Computing and Information Technology,
Arab Academy for Science and Technology
George Vogiatzis
http://www.george-vogiatzis.org
School of Engineering and Applied Science,
Aston University

Simultaneous parametric estimation of multiple primitive geometric models plays a key role in the overall interpretation of complex 3d scenes. This is characterized in the literature as a problem of irregular sites with discrete labels, on which techniques of unsupervised classification and optimization can be applied. This paper presents a novel approach to the computation of primitive geometrical structures, where no prior knowledge about the visual scene is available and a high level of noise is expected. We based our work on the grouping principles of proximity and similarity, of points and preliminary models. The former was realized using Minimum Spanning Trees (MST), on which we apply a *stable alignment* and a *goodness of fit criteria*. As for the latter, we used *spectral clustering* of preliminary models. The algorithm can be generalized to various model fitting settings in which the spatial coherence constraint applies, without fine tuning of run parameters.

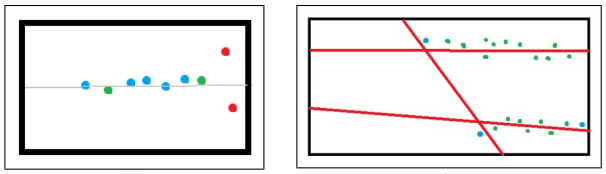
Stating our problem formally, let $\mathbf{X} = \{\mathbf{x}_i\}_{i=1}^{n}$ be a set of n data points. It is required to find $L = \{L_i\}_{i=1}^{M}$, such that L is a set of models that best describe$\mathbf{X}$. L_i is the parameter vector of model i which, together with the variable M are unknown a priori. In addition, the data points are contaminated by varying levels of outliers.

The literature of model fitting can be broadly categorized into the following subdivisions.

Energy-based formulation. Early attempts include the work in the RANSAC-adaptations to the multi-model case [5]. The initial randomly populated models compete according to some poor greedy heuristics which results in enhancing each model locally. Generally, the oversimplified single objective formulation overlooks cues that are inherent to the human visual system. These include, the compactness of points in areas that belong to the same model and the intuitive merging of adequately similar models. This gave rise to the need for regularized functions, as in PEARL [2]. It is inspired by the energy function of the incapacitated facility location problem (FLP) [4]. Mapped to our application, it incorporates a data cost and a cost for establishing a new label. They added a smoothness prior that ensures the spatial coherence in the search. The random initial set of hypotheses are verified using the α -expansion graph cut optimization. The main shortcomings of this paradigm are the determination of the trade off between the various energy terms and settling for approximate solutions to preserve computational feasibility causing it be susceptible to local minima. In addition, it is not difficult to find a counter example, as in figure 1 (a), for relying on absolute proximity to enforce spatial coherence (implying that possible inliers are closer to each other than to outliers).

Similarity-based formulation. This category exploits the fact that a structure can be detected by the presence of several entities sharing a certain property, defined upon a parameter, residual or conceptual space. The entities can be the given points, as the system proposed in [6]. An agglomerative algorithm clusters points based on the Jaccard distance and the final models are the best fits of these clusters. The points are expressed by their set of preferred models based on residuals. This can be very misleading in case of random generation of models that may result in cross structures (figure 1 (b)). Their assumption "Residuals for each data point have peaks corresponding to the true models" struggles in case of initial random sampling in high levels of outliers, because points can be equidistant to completely different models.

Our proposed algorithm provides a solution to the problems presented in figure 1 by relying on analysis of models layout in space, focusing on point arrangements rather than optimizing on residual values. It belongs to the category of model-based similarity formulation of the model fitting problem. To ensure the correct detection of clusters, the sampling of the hypothesized models should guarantee the repeated presence of optimal/sub-optimal models, in order to form agglomerated dense regions in some space. For this reason and because random sampling fails in this respect, we have resolved to the guided sampling paradigm. At each point we initiate a sample set. Gradually, this set is expanded by incorporating



(a) (b)

Figure 1: Snapshots of point arrangements, (a) showing 3 randomly formed models (lines) and some points scattered around them. The points in blue share very similar preference based on the cross structure despite the discrepancy in their true belonging; (b) showing 2 inliers in green with an in-between distance larger than the distances between one of them and the gross outliers in red.

more points that belong to the minimum spanning tree (MST) and we find the best fitting model. Due to the presence of geodesic paths between inliers of a model on its surface, we argue that MST-based sampling is more robust to varying noise levels than propagation-based ones. We introduce a novel *stable alignment* criterion to select the best size of the sample set that generates the model at the investigated point. It relies on the fact that at a certain phase, the model alignment is not drastically altered by the inclusion of gross outliers. Because, the growing size of the subtree enhances the spread of inlier points and the adherence of the generated model to the underlying structure. The subtree selection is further enhanced by the incorporation of the *margin of error* criterion, which geometrically indicates how well aligned and dense the points are in the consensus zone. For measuring the alteration in the model alignment, we introduce an arbitrary dissimilarity measure: *model deviation*. We have shown its superiority to the commonly utilized measure of Jaccard distance, with respect to being more linear and sensitive to small perturbations.

We construct a similarity matrix between populated models and then pass it to spectral clustering algorithm [3] to produce subsets. We handled the issue of the unknown number of models and subsequently clusters with the *Repeated 2-clustering method* in a top-down approach. The regularization function is the *Daives Bouldin* (DB) index [1]. Each cluster promotes its centroid model to the final set, defined as the model that is least dissimilar to the rest of models in the same cluster. Our algorithm was shown to outperform the state-of-the-art techniques, in some aspects.

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