Comparative Analysis of Model Fitting Techniques in Computer Vision

Aryan Kaul
2021136

Ganeev Singh
2021389

Param Gupta
2021175

Abstract

In computer vision, estimating homographies across multiple views is essential for tasks such as image stitching, 3D reconstruction, and augmented reality. Traditional algorithms like RANSAC struggle with complex scenes involving multiple planes due to their sequential, single-instance fitting approach. The Progressive-X (Prog-X) algorithm addresses these challenges by employing a robust multi-model fitting technique that iteratively proposes and optimizes multiple homographies, allowing for simultaneous detection and fitting of multiple planes in a scene. This paper analyzes Prog-X, reproduces its code, and evaluates its performance against the Multi-X algorithm, a state-of-the-art multi-class model fitting method.

Homography estimation refers to the process of determining the transformation that relates points in one image to corresponding points in another image. This transformation is typically represented by a 3x3 matrix known as the homography matrix. Homography estimation is commonly used in computer vision for various tasks such as image registration, panorama stitching, augmented reality, and object recognition.

In this project, we aim to explore homography estimation algorithms by reproducing the results from two recent papers authored by Daniel Barath and Jiri Matas: "Progressive-X: Efficient, Anytime, Multi-Model Fitting Algorithm" and "Multi-Class Model Fitting by Energy Minimization and Mode-Seeking." Our objective is to evaluate and compare the performance of these algorithms in homography estimation.

1 Problem Statement

In computer vision, estimating homographies across multiple views is essential for tasks such as image stitching, 3D reconstruction, and augmented reality. Traditional algorithms like RANSAC struggle with complex scenes involving multiple planes due to their sequential, single-instance fitting approach. The Progressive-X (Prog-X) algorithm addresses these challenges by employing a robust multi-model fitting technique that iteratively proposes and optimizes multiple homographies, allowing for simultaneous detection and fitting of multiple planes in a scene. This paper analyzes Prog-X, reproduces its code, and evaluates its performance against the Multi-X algorithm, a state-of-the-art multi-class model fitting method.

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2 Description of the Approaches Used

2.1 Progressive-X (Prog-X) Algorithm

- **Hypothesis Generation**: Uses Graph-Cut RANSAC to propose new homography hypotheses by sampling minimal subsets of points.

- **Validation and Integration**: Validates new hypotheses against existing models using a modified MSAC function and Jaccard similarity to ensure distinctness.

- **Optimization**: Optimizes the set of homographies using energy minimization techniques, specifically PEARL (Pairwise Energy and Relaxation Labeling), to refine model parameters and point assignments.

- **Termination**: Employs an adaptive criterion to terminate when further significant models are unlikely to be found.

2.2 Multi-X Algorithm

- **Energy Minimization and Mode-Seeking**: Extends the PEARL algorithm with a new move in the label space, replacing labels with density modes in the model parameter domain to achieve fast and robust optimization.

- **Automatic Parameter Setting**: Sets key optimization parameters automatically, making the algorithm applicable as a black box across various problems.

- **Cross-Validation**: Removes statistically insignificant instances post-optimization to enhance robustness.

3 Results of the Analysis Experiments

3.1 Dataset 1: AdelaideRMF Homography Dataset

- **Prog-X**:
    - Demonstrated high accuracy in fitting multiple homographies with low misclassification error. The iterative refinement process ensured robust handling of noise and outliers.
    - Average Misclassification Error (ME): 0.070
    - Average Run-Time: 0.199 seconds

- **Multi-X**:
    - Showed strong performance but required careful tuning of parameters for optimal results. Its mode-seeking approach contributed to efficient model fitting.

3.2 Evaluation Metrics

3.2.1 Misclassification Error

Explanation: Misclassification Error (ME) is a metric that measures the proportion of data points incorrectly labeled or assigned to the wrong model. In the context of homography estimation, it quantifies how well the algorithm assigns points to the correct homographies.

    Findings:

- **Prog-X**: Achieved an average ME of 0.070 on the AdelaideRMF Homography Dataset, demonstrating high accuracy in fitting multiple homographies.

- **RANSAC (Expected)**: Likely to have a higher ME, estimated around 0.150, due to its sequential and greedy approach to fitting models.

3.2.2 Processing Time

Explanation: Processing Time is the total time taken from the input to the output of the model fitting process. It includes the time required for hypothesis generation, model validation, optimization, and final fitting.

    Findings:

- **Prog-X**: Recorded an average run-time of 0.199 seconds on the AdelaideRMF Homography Dataset, indicating efficient processing and quick convergence.

- **RANSAC (Expected)**: Estimated to have a longer run-time, around 0.400 seconds, due to its iterative re-estimation and sequential fitting process.

Figure 1: Original Image

Figure 2: RANSAC Warping

3.2.3 Parametric Study

Explanation: Parametric Study involves examining how the performance of the algorithm varies with different parameters and settings. It assesses the sensitivity and robustness of the algorithm to changes in its parameters.

    Findings:

- **Prog-X**: Demonstrated robustness to parameter changes, with adaptive termination criteria and iterative refinement ensuring stable performance across different settings.

- **RANSAC (Expected)**: More sensitive to parameter settings, potentially requiring careful tuning to achieve optimal results, which can increase processing time and misclassification error.

3.2.4 Qualitative Analysis

Explanation: Qualitative Analysis involves a visual and interpretative assessment of the algorithm's performance. It includes examining the visual output of the homography estimation to ensure that the fitted models accurately represent the underlying structures in the data.

Aryan Kaul's Commentary: *[In our study comparing the results of the models on the AdelaideRMF dataset, we focused on evaluating misclassification errors and processing times. Progressive-X had lower misclassification errors, likely because its method of continuously adjusting to new data helps it fit models more accurately. On the other hand, Multi-X processed data faster, thanks to its effective energy minimization and mode-seeking approach, which quickly identifies and focuses on promising solutions, cutting down unnecessary computations. Both algorithms performed better than traditional*

Figure 3: PROG-X Warping

models in these areas. Progressive-X's accuracy benefits from its ability to intelligently stop when further adjustments won't improve the model much. Meanwhile, Multi-X's speed advantage comes from its automated settings and efficient approach to simplifying the problem, making it a strong choice for tasks where time is a critical factor.]

Ganeev Singh's Commentary: *[During the project, I observed that multi-model fitting techniques, particularly the Progressive-X and Multi-X algorithms, greatly improved the accuracy of homography estimation. Homography estimation, which involves finding the transformation matrix relating points between images, is essential for tasks like image stitching and 3D reconstruction.]*

Param Gupta's Commentary: *[Working with these advanced algorithms allowed me to appreciate the complexity of model fitting challenges and the innovative solutions that Prog-X and Multi-X offer. The project was an excellent opportunity to apply theoretical knowledge in a practical setting, enhancing my understanding of computational geometry and optimization]*