Problem Definition and Contribution

**Goal:** Establish correct feature correspondences between two images of the similar or same scene.

**Motivations:**
- Existing parametric matching methods require a predefined transformation model and may fail in nonrigid situations, such as RANSAC and its varieties.
- Existing non-parametric matching methods require high computational cost and are easily affected by the noise, outlier and unknown image transformation.

**Key Contributions:**
- A simple but efficient method for feature matching.
- The convolution operation in our method may provide a guide to address the feature matching problem with deep learning techniques in future.
- The gridding strategy enables our method to achieve linear time complexity, which only requires dozens of milliseconds for thousands of matches.

**Schematic Illustration**

PFFM comprises three parts: putative matches gridding, convolution operation and consistency checking, and it is implemented based on coarse-to-fine theory with an iterative manner. (Red:mismatches, Blue: correct matches)

**Problem Formulation**

**Main idea:** By assuming that the motion field of correct matches is smooth-and-slow, and considering the false matches as the outliers or noise, we formulate feature matching as a progressive filtering problem.

- Convert the putative match space into motion space and gridding:
  \[ S = \{(x_i, y_i)\}^N_{i=1} \rightarrow S' = \{(x_i, m_i)\}^N_{i=1}, \]
  where \( S \) is putative match set, and the matched feature points \( x_i \) and \( y_i \) are the pixel coordinates of the image pair. \( m_i = y_i - x_i \) denotes the motion vector.
- Calculate the average motion vector in each cell:
  \[ \overline{m}_{j,k} = \frac{1}{|C_{j,k}|} \sum_{i \in C_{j,k}} m_i, \quad \text{if } |C_{j,k}| > 0, \]
  \[ 0 \quad \text{if } |C_{j,k}| = 0, \]
  where \( C_{j,k} \) is the putative set in \((j, k)\)th-cell.
- Density estimation to deal with the isolated situation:
  \[ S(n) = \frac{S(n) - F(1-n)}{\sqrt{F(1-n) + 1}}, \]
  where \( S(n) \) measures the density degree of cell \( n \).
- Kernel convolutional filtering operation:
  \[ f(\lambda) : M = W_f \overline{m}_{j,k}, \]
  where \( M_{j,k} = \overline{m}_{j,k} \) denotes the typical motion vector of cell \((j, k)\), \( W_f \) is a count matrix with \( W_f_{j,k} = |C_{j,k}| \), and \( \kappa \) is a Gaussian kernel distance matrix.
- Check motion consistency and identify inlier set \( T^* \):
  \[ d_i = 1 - \exp \left( -\frac{|m_i - \overline{m}_{j,k}|^2}{\beta} \right), \quad \forall i \in C_{j,k}, \]
  \[ T^* = \{ i : d_i \leq \lambda \}. \]

**Experiments & Results**

**Dataset:**

**Qualitative results on real image pairs:**

**Quantitative results of Precision (P) and Recall (R) on real data:**

**Quantitative results of F-score \( F \) and Run-time \( T \) on real data:**

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**Progressive Filtering for Feature Matching**

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