Robust Feature Matching for Endoscopic Reconstruction

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Xiang Xiang, PhD student in Computer Science, JHU (xxiang3@jhu.edu)
under the auspices of Prof. Gregory Hager, Dr. Daniel Mirota and Prof. Russell Taylor

Introduction

- >200,000 functional endoscopic (sinus) surgeries per year.
- Needs to visualize critical structures.
- Structures must not be disturbed during surgery.
- Structures can be smaller than a millimeter.
- A qualitative sense of location in need.
- This work mainly prototypes the image matching and motion estimation, which are essential to the reconstruction pipeline.

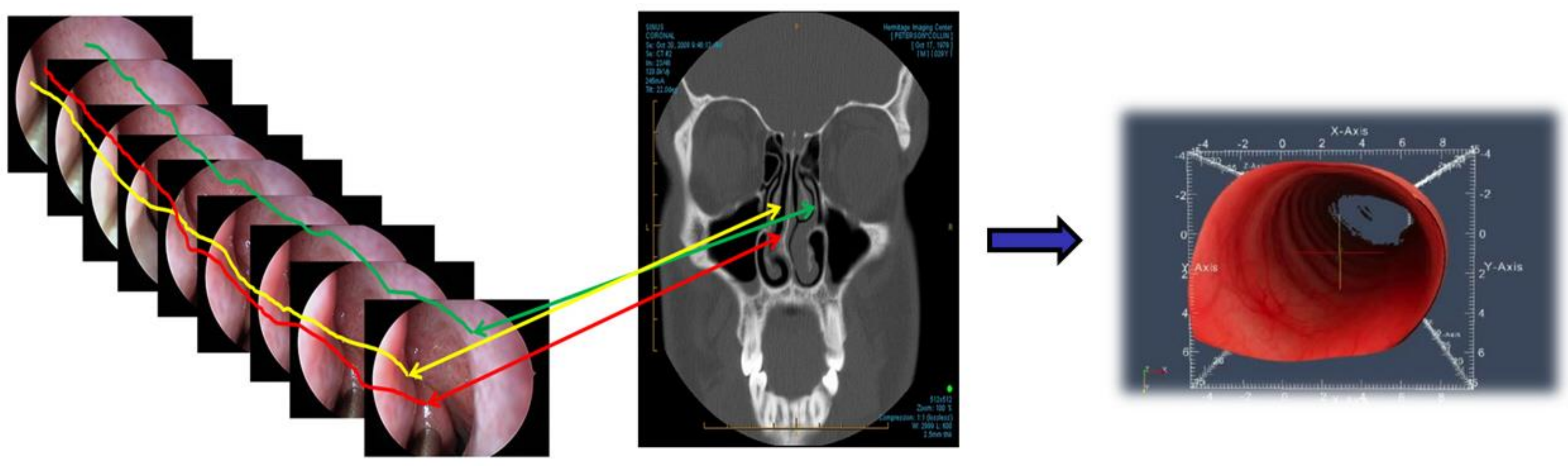

Figure 1. Basic idea of Endoscopic Reconstruction.

The Problem

- Since camera is moving and surfaces are non-planar and deformable, feature matching is not satisfactory.

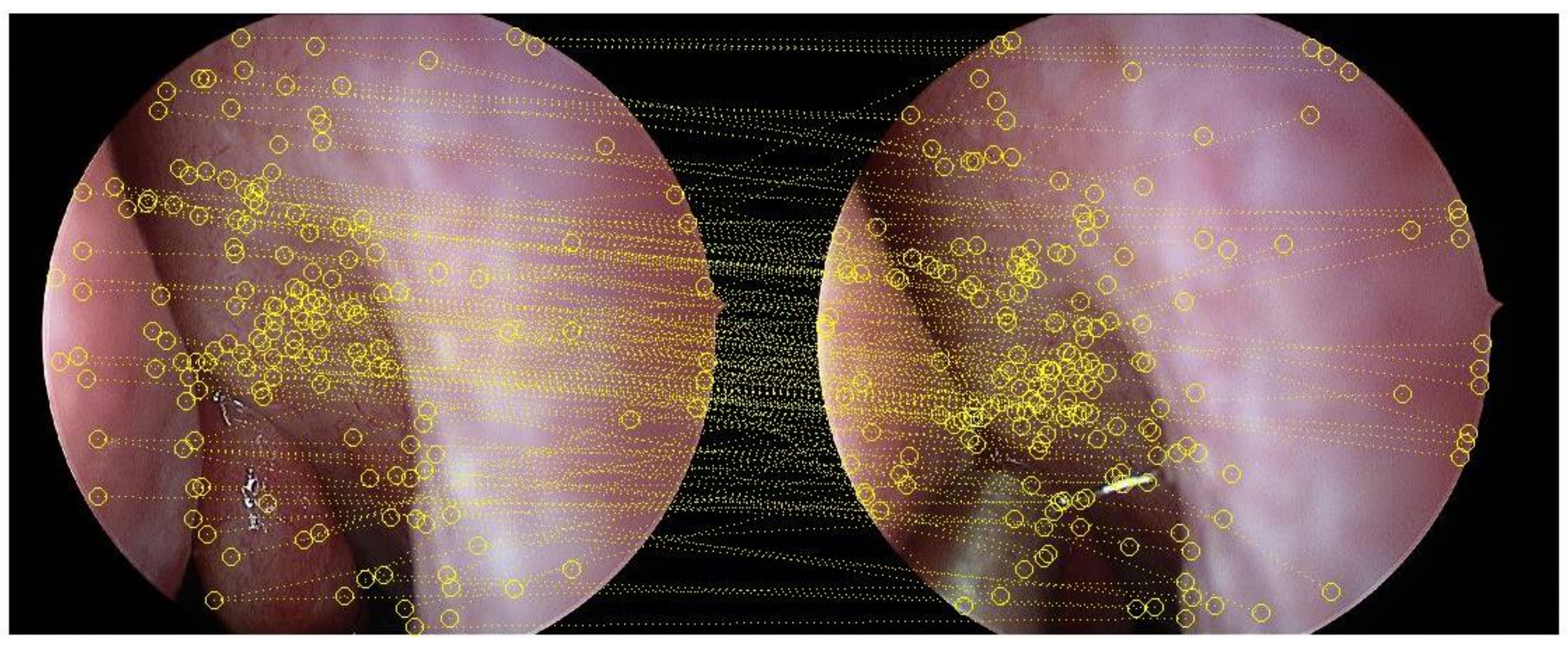

Figure 2. Results of SIFT features with SIFT matching [2]. Shown for adjacent frames.

The Solution

- Multiple affine components [1] vs. SIFT's global affine [2].
- Empirical covariance analysis and motion estimation evaluation by leaving-one-out cross validation (LOOCV).

Algorithm. Motion estimation and covariance analysis by LOOCV

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Algorithm 1. Motion estimation and covariance analysis by LOOCV.
for $k = 1...FrmNum$
  Compute SIFT feature keypoints to form a candidate feature pool.
  Perform HMA matching to select keypoints, which are grouped into affine components.
  Perform image rectification considering radial distortion.
  Convert image coordinates to World's coordinates using camera's intrinsic parameters.
  if $MatchFeaNum > 4$
    for $trial = 1...MatchFeaNum$
      Leave the $trial$-th keypoint out as a query point.
      Perform RANSAC on the left keypoints to generate an inlier set.
      Perform 5-point algorithm to estimate the essential matrix $E$ using the inlier set.
      Decompose $E$ into a rotation matrix $R$ and a translation vector $t$.
      Convert $R$ to a quaternion.
      Compute projection error for the hold-out query point:
        $residual = (R * X_{left}^{query} + t) - X_{right}^{query}$
        $sqErr = L2norm(residual)$
    end for
    Compute the mean and standard deviation of a sequence of $sqErr$.
    Compose a $R_{mean}$ from $mean(quaternion)$.
    for $trial = 1...MatchFeaNum$
      $R_{mean} * R^{-1}$ is approximately a skew-symmetric matrix $skew(\alpha, \beta, \gamma)$,
        where $\alpha, \beta, \gamma$ are the rotation angle (scalar) in X, Y, Z axis, respectively.
    end for
    Compute the covariance matrix of a sequence of vector $< \alpha, \beta, \gamma >$.
  end if
end for
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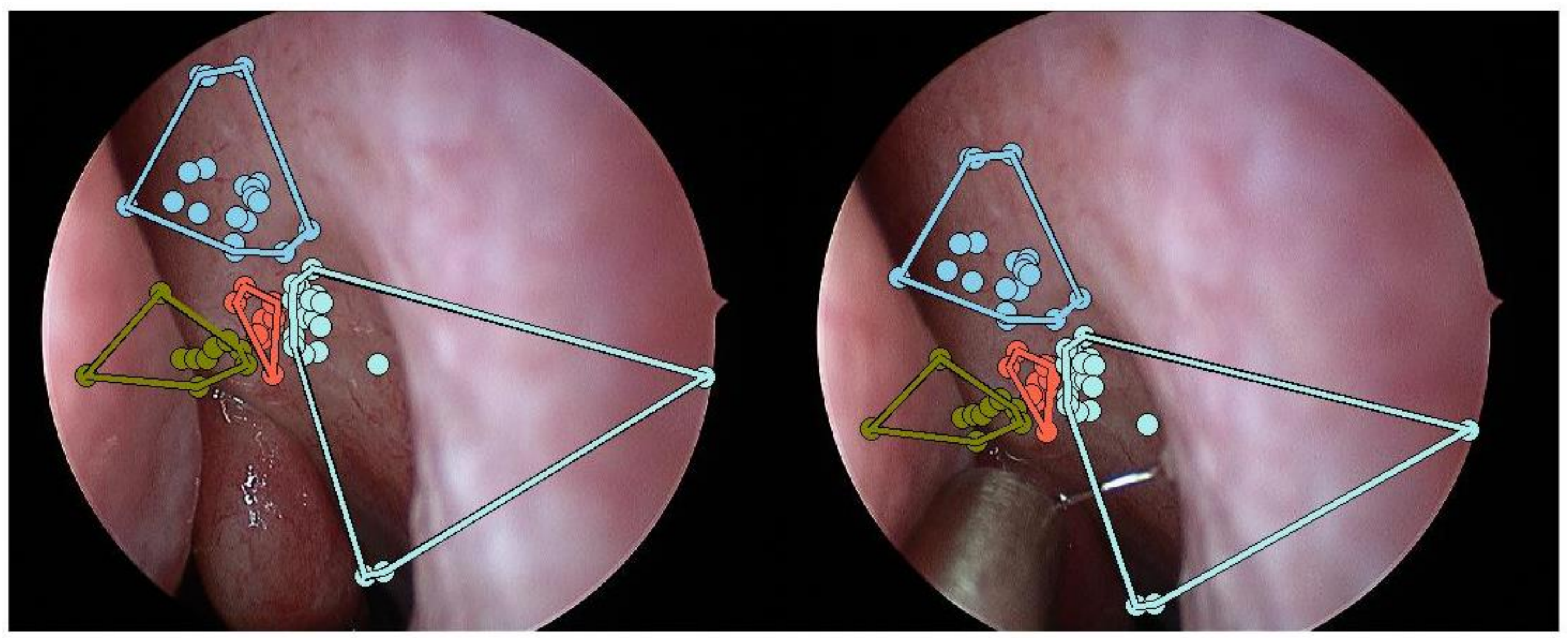

Figure 3. Results of SIFT features with Hierarchical Multi-Affine (HMA) matching [1].

Results and Comparison

- Testing data: a sample video sequence collected on Dec. 12, 2012 at Johns Hopkins Hospital.

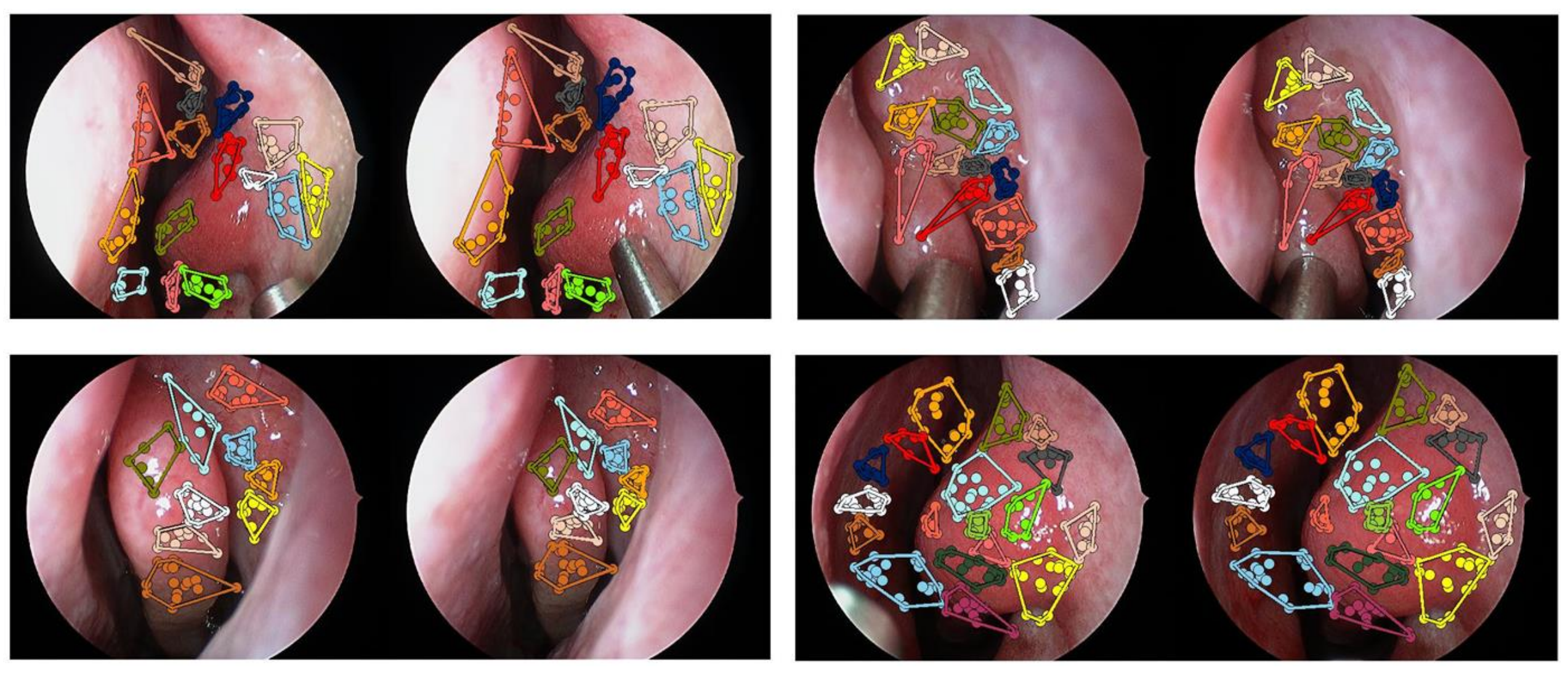

Figure 5. Examples of HMA matching results.

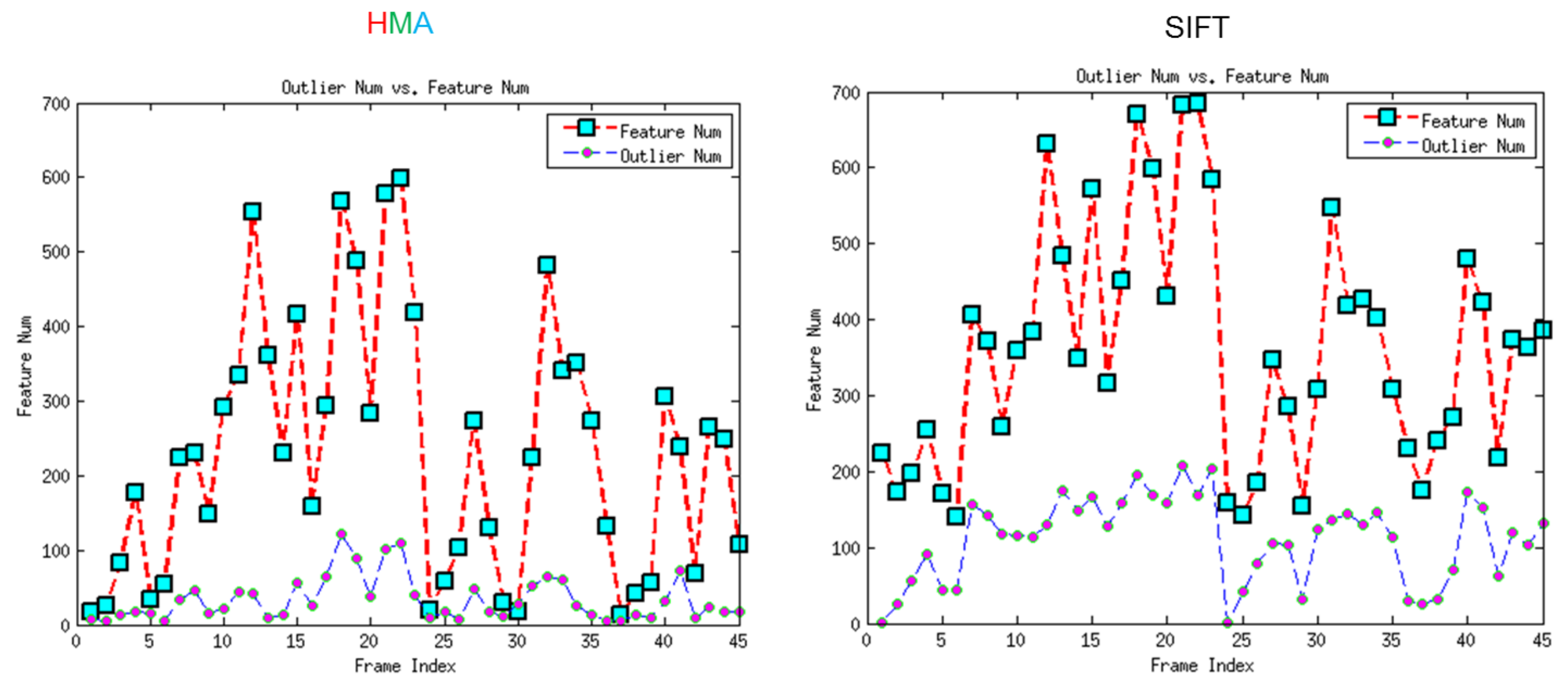

Figure 6. RANSAC detected outlier number vs. 'matched' feature number

- From $R_{mean} \bullet R^{-1}$, rotation angles α, β, γ can be extracted. Each angle's standard deviation is expected to be generally consistent with the feature number.

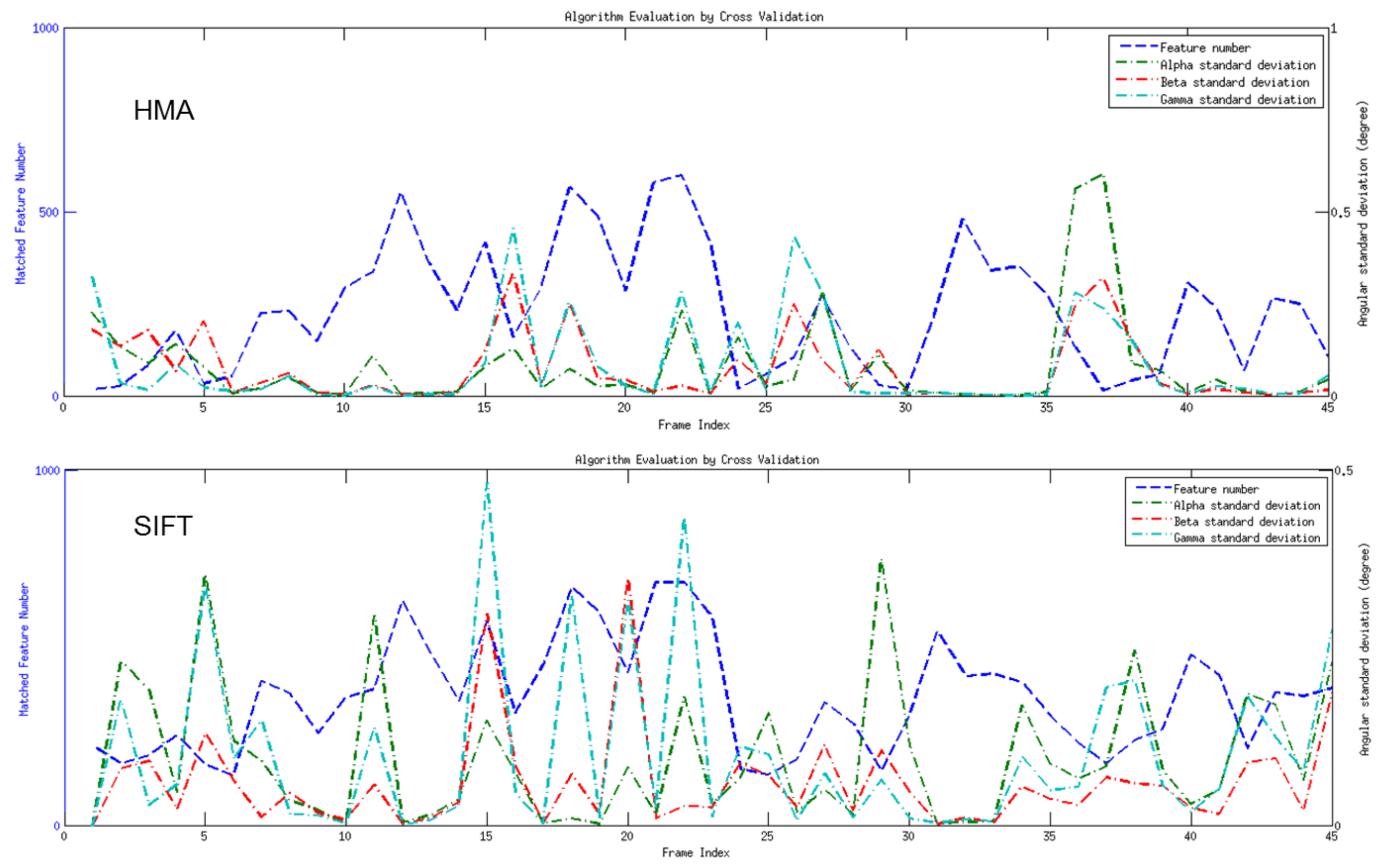

Figure 7. Rotation angle's standard deviation vs. feature number.

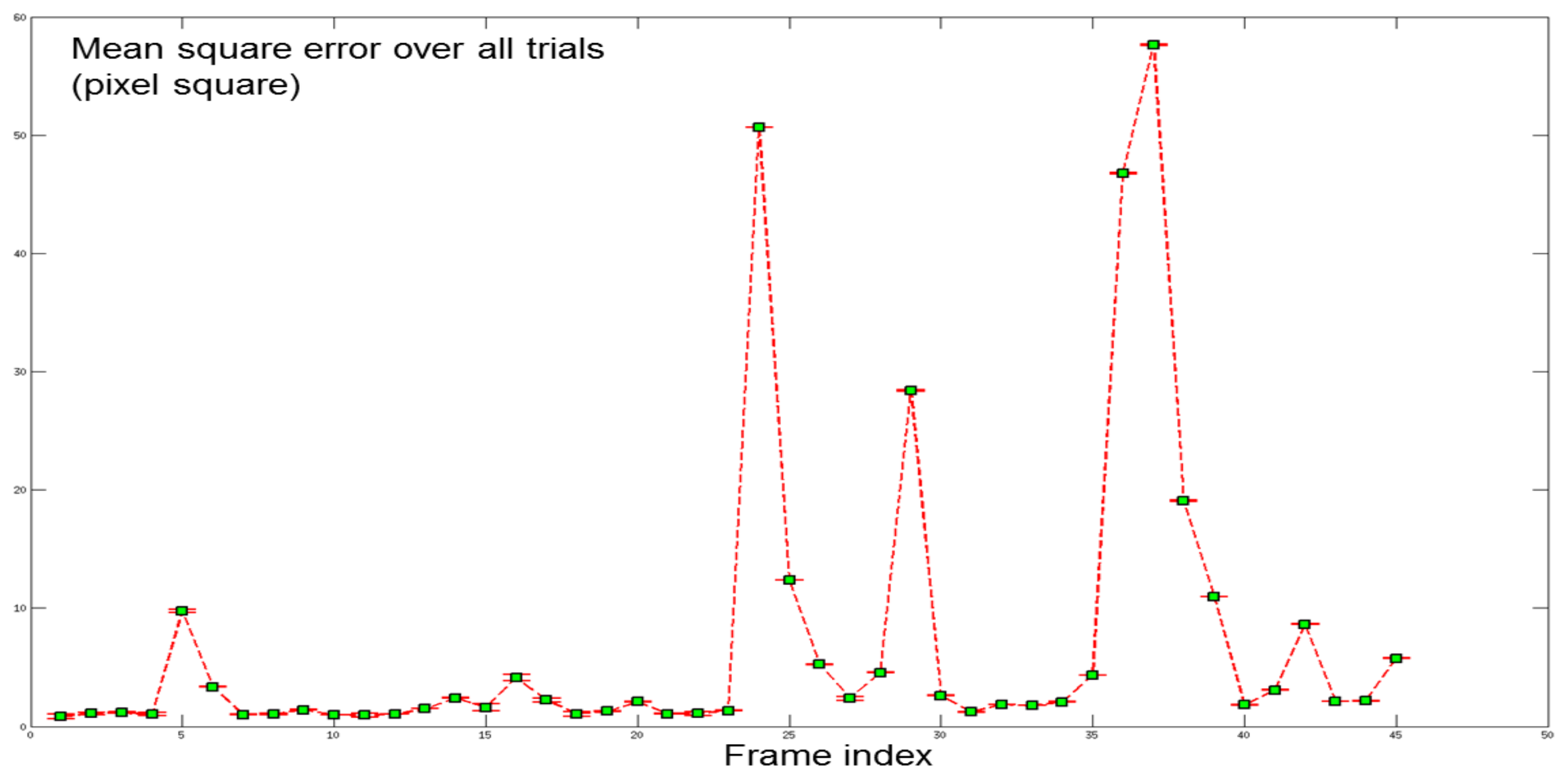

Figure 8. Projection error of the hold-out query point with HMA matching.

Future Work

- To test the reconstruction pipeline's performance with HMA feature matching.

Reference

- [1] G.A. Puerto and G.L. Mariottini. A Fast and Accurate Feature-Matching Algorithm for Minimally Invasive Endoscopic Images. IEEE Trans. Med. Imaging (T-MI), Jan. 14, 2013 .
- [2] D. Lowe. Distinctive Image Features from Scale-Invariant Keypoints. IJCV, 60(2), 2004.

Publication and Acknowledgements

- Potentially submitted to IEEE T-MI with analytics and the pipeline.
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