

# Robust Feature Matching for Endoscopic Reconstruction

Checkpoint presentation for CIS II Project

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*May 2, 2013*

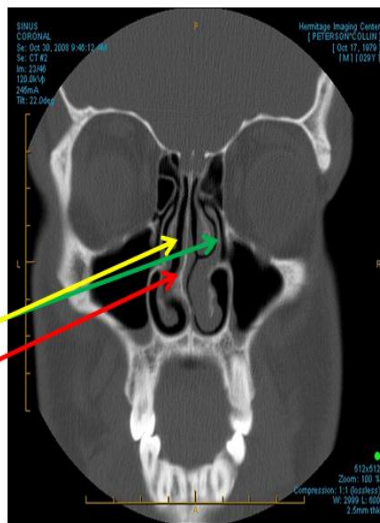
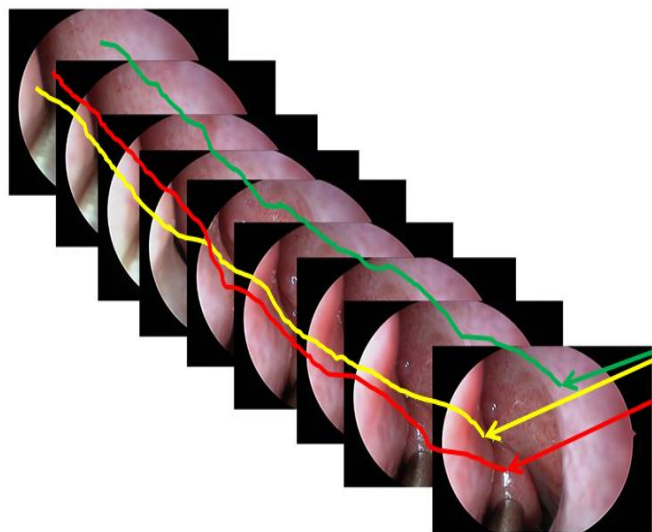
Claim: Do not disclose due to confidential patient data and unpublished work.

# Outline

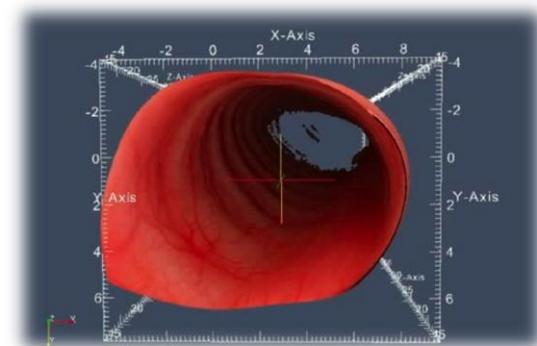
- Project Review
  - Progress on feature matching and motion estimation: HMA vs. SIFT
  - Deliverables, Milestones and Dependencies

# Endoscopic reconstruction

- > 200,000 functional endoscopic (sinus) surgeries per year in US.
- Needs surgical navigation systems to visualize critical structures.
- Structures must not be disturbed during surgery.
- Structures can be smaller than a millimeter in size.
- A qualitative sense of location in need.



Exemplar CT image from [www.newyorkentspecialist.com](http://www.newyorkentspecialist.com)



A full 3D reconstruction of a pediatric airway from video imagery acquired with a tracked endoscope. [Image from a NIH-funded project proposal with permission.]

# Feature matching

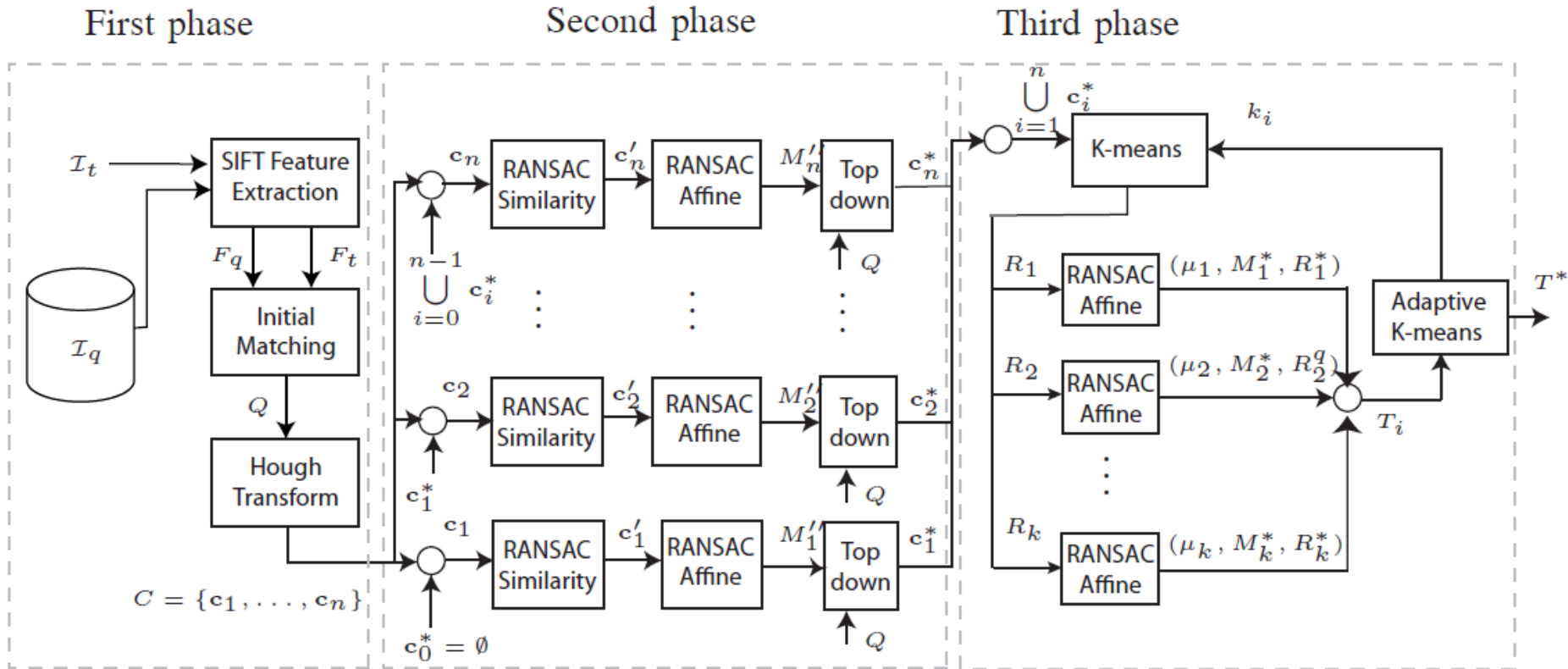
- Feature matching is key to 3D reconstruction, stereo, tracking and recognition.
- Features are expected to be
  - invariant to image scaling and rotation,
  - (partially) invariant to changes in illumination and 3D camera viewpoint,
  - highly discriminative,
  - Efficiently extracted.

➡ Scale Invariant Feature Transform (SIFT): key point detection and description  
SIFT provides a feature pool.
- Matching is expected to be
  - robust to outliers and deformation (e.g., non-planar object)
  - ➡ Multiple affine components vs. SIFT matching's global affine
  - Efficient
  - ➡ Hierarchical clustering



Figure from [Puerto-Souza *et al* 2011]

# Estimating multiple affine components



Remarks.

Hough Transform: to cluster SIFT keypoints according to a similarity transformation

RANSAC: first to estimate a similarity model and then to estimate an affine model to provide a refined list of matches.

Top-down: to recover lost matches

Figure from [Puerto-Souza *etal* 2011]

# Hierarchical Multi-Affine (HMA)

- quantizes matches according to their spatial position on the object's surface
- Hierarchical K-means
  - **Binary (tree) search** vs. Exhaustive search

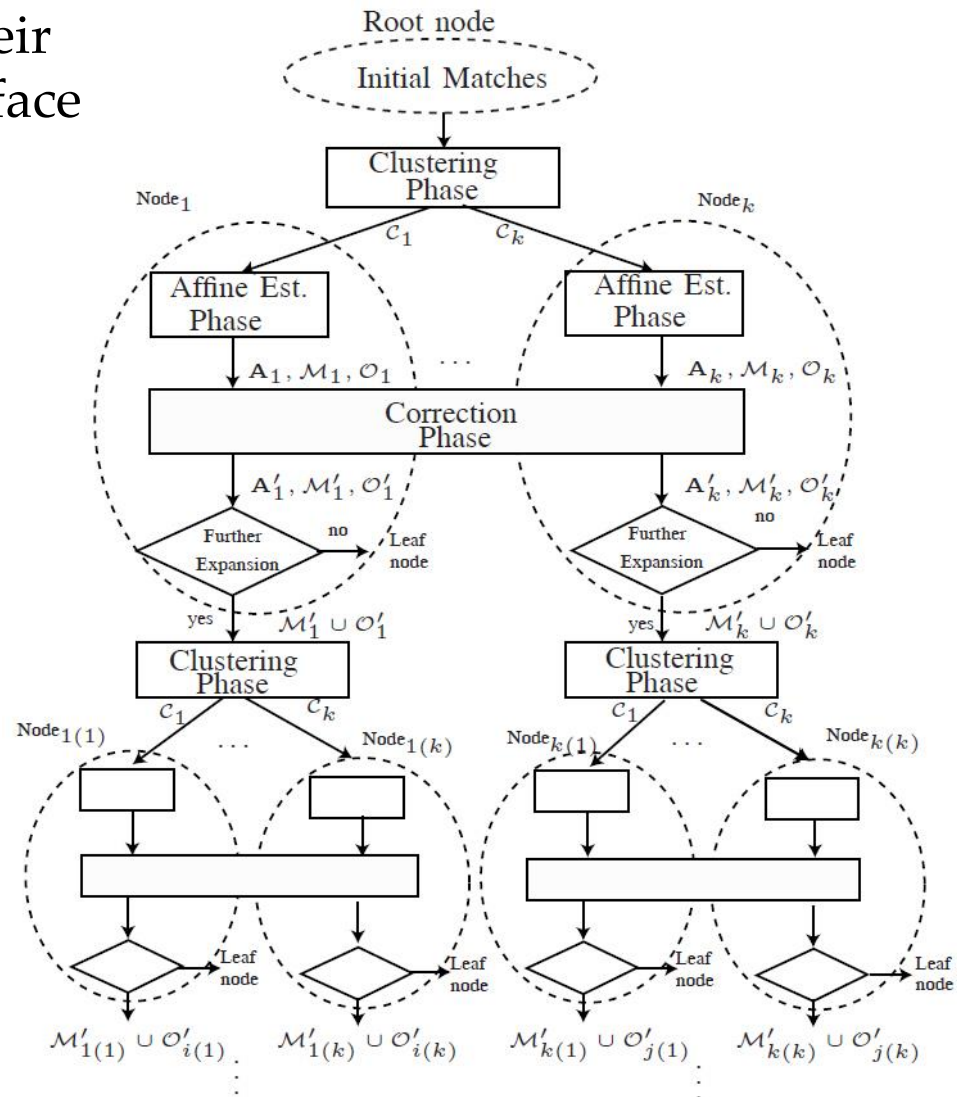
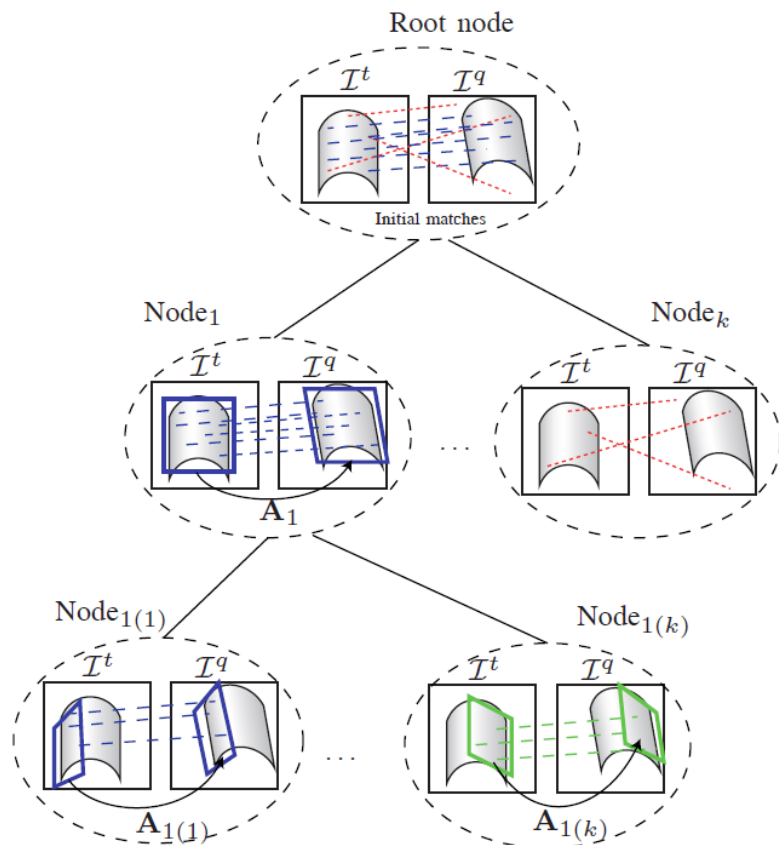


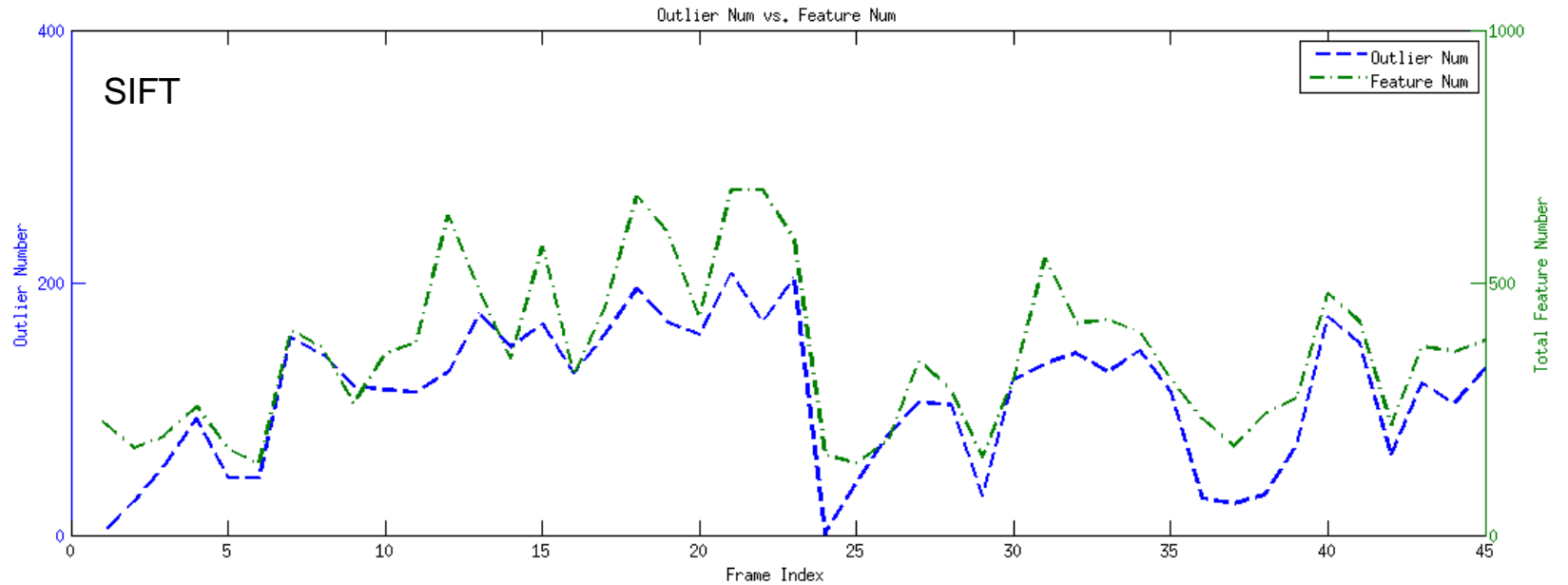
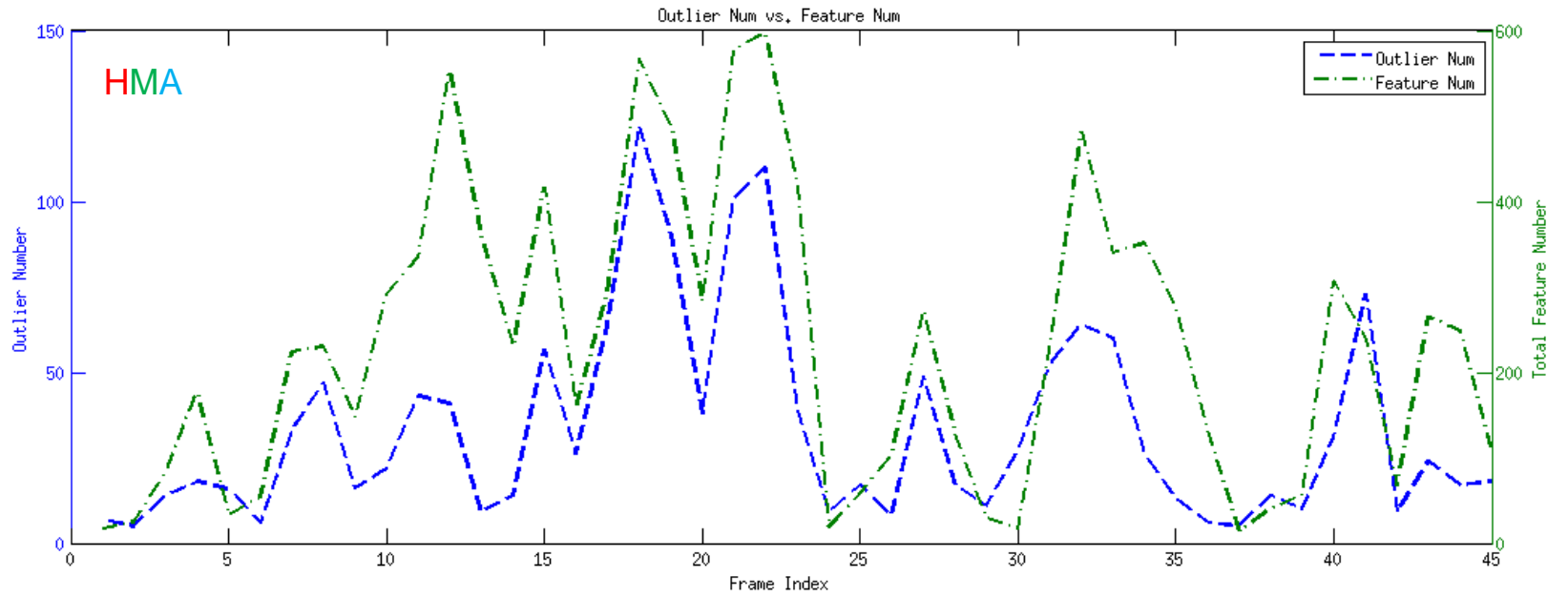
Figure from [Puerto-Souza *et al* 2012]

# Outline

- Project Review
- Progress on feature matching and motion estimation: **HMA** vs. SIFT
- Deliverables, Milestones and Dependencies

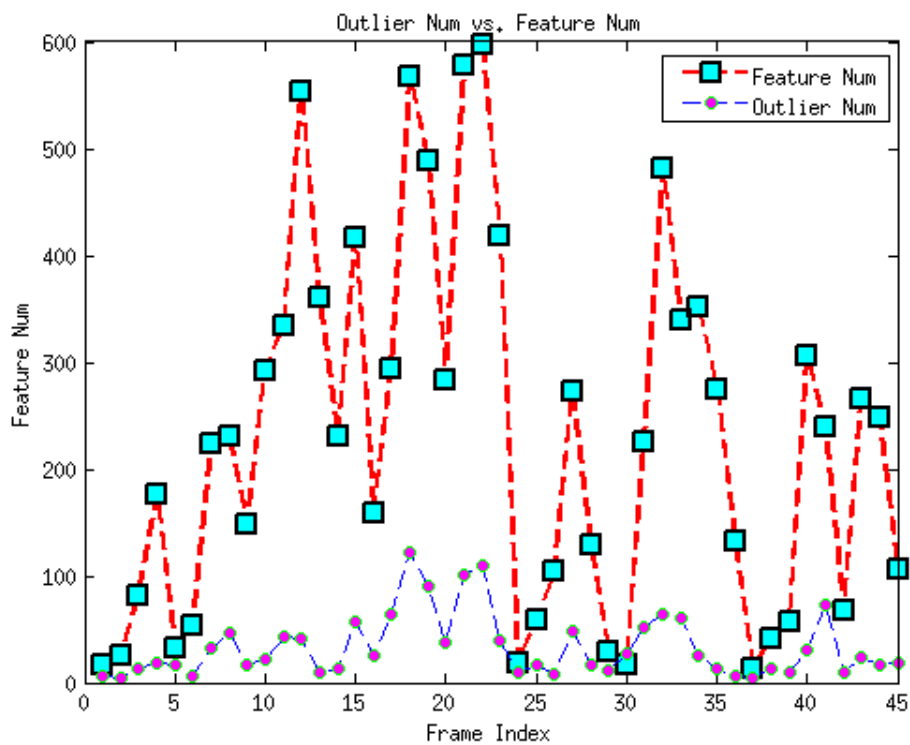
**SIFT keypoints  
with **HMA** matching vs. SIFT matching**

# RANSAC detected outlier number vs. Total 'matched' feature number

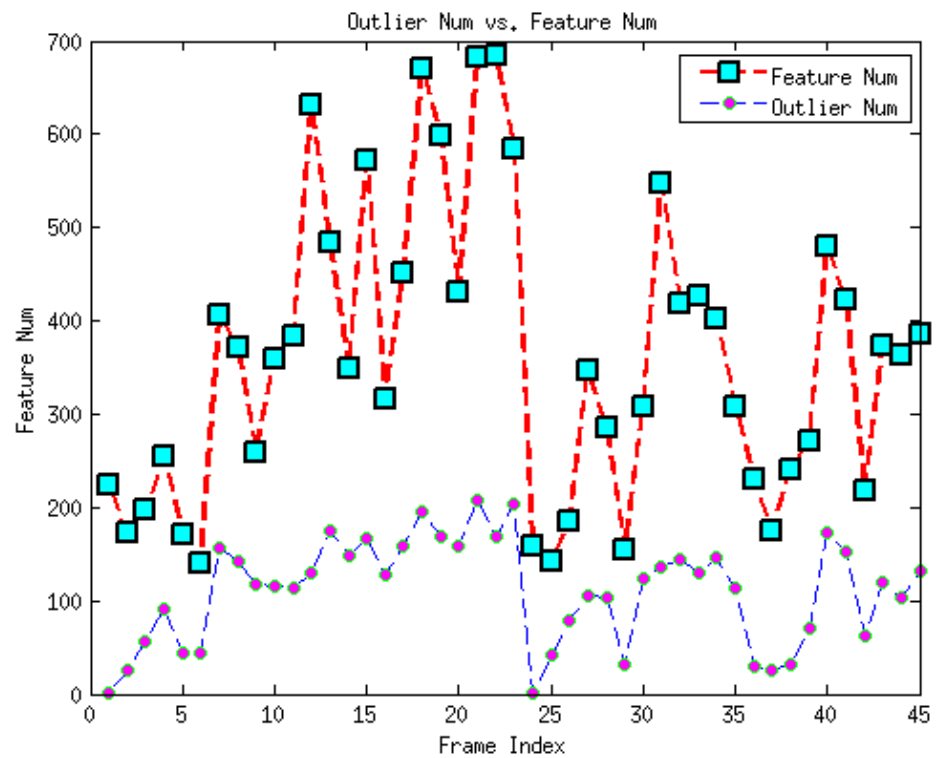




HMA



SIFT



# Empirical Covariance Analysis and Motion Estimation Evaluation by Leaving-One-Out Cross Validation

for  $k = 1 \dots FrmNum$

Compute SIFT feature keypoints to form a candidate feature pool.

Perform HMA matching to select keypoints, which are grouped into affine components.

Convert image coordinates to World's coordinates using camera's intrinsic parameters.

if  $MatchFeaNum > 4$

for  $trial = 1 \dots MatchFeaNum$

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  $trial = 1 \dots MatchFeaNum$

$R_{mean} * R^{-1}$  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  $\langle \alpha, \beta, \gamma \rangle$ .

end if

end for

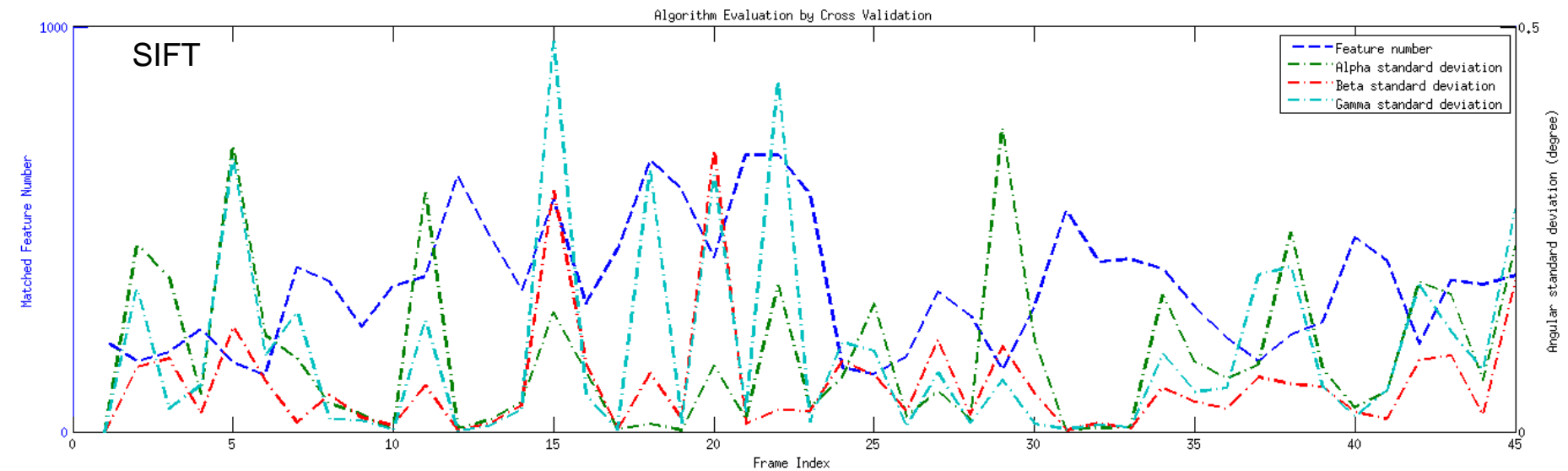
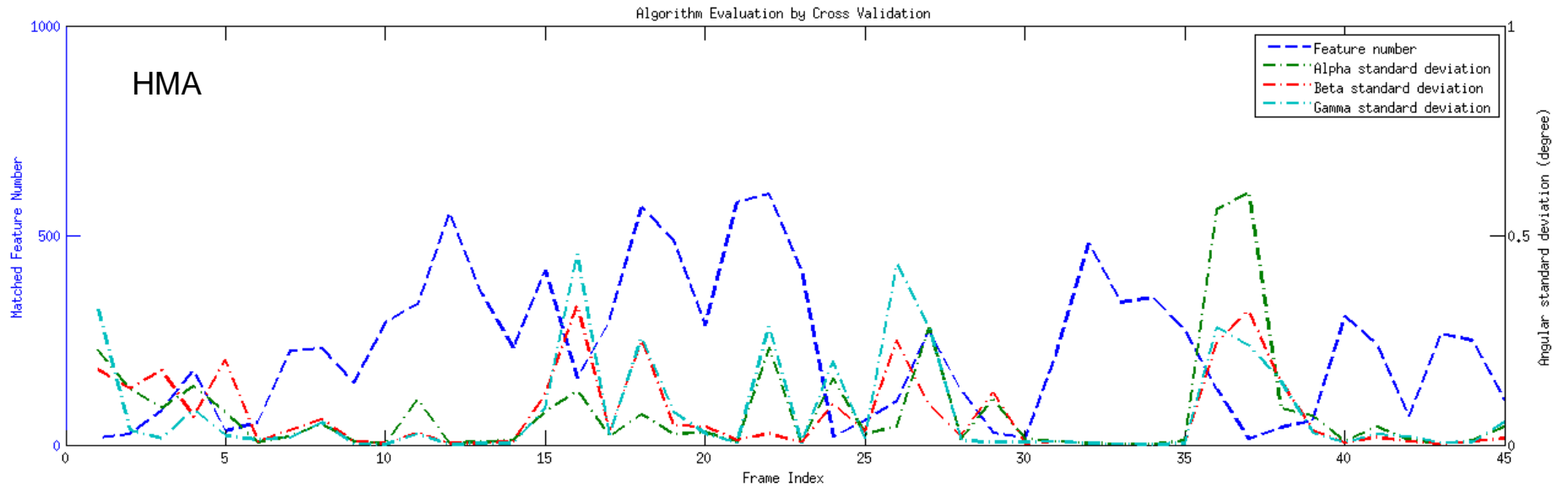
$$\begin{bmatrix} 1 & -\gamma & \beta \\ \gamma & 1 & -\alpha \\ -\beta & \alpha & 1 \end{bmatrix}$$

Remark.

Skew parameters via Cayley's formula.

# Overall evaluation

Alpha, beta, gamma with feature number



# Covariance matrix

original cov

```

val(:,1) =
  0.0507  0.0096 -0.0253
  0.0096  0.0320 -0.0390
 -0.0253 -0.0390  0.1042

val(:,2) =
  0.0180 -0.0173 -0.0039
 -0.0173  0.0181  0.0042
 -0.0039  0.0042  0.0012

val(:,3) =
  0.0077  0.0092  0.0002
  0.0092  0.0314  0.0019
  0.0002  0.0019  0.0002

val(:,4) =
  0.0196  0.0016 -0.0113
  0.0016  0.0044 -0.0026
 -0.0113 -0.0026  0.0072

val(:,5) =
  0.0059  0.0155 -0.0014
  0.0155  0.0410 -0.0035
 -0.0014 -0.0035  0.0005
    
```

sqrt(cov-diag) and  
convert to degree

```

val(:,1) =
  12.9002
  10.2554
  18.4927

val(:,2) =
  7.6863
  7.7102
  2.0129

val(:,3) =
  5.0384
  10.1588
  0.8634

val(:,4) =
  8.0279
  3.8214
  4.8564

val(:,5) =
  4.4111
  11.6050
  1.2478
    
```

original cov

```

val(:,1) =
  0  0  0
  0  0  0
  0  0  0

val(:,2) =
  0.0535 -0.0031  0.0117
 -0.0031  0.0064  0.0020
  0.0117  0.0020  0.0310

val(:,3) =
  0.0365  0.0068 -0.0019
  0.0068  0.0081  0.0011
 -0.0019  0.0011  0.0008

val(:,4) =
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  0.0008  0.0005 -0.0011
 -0.0026 -0.0011  0.0033

val(:,5) =
  0.1248 -0.0313 -0.0843
 -0.0313  0.0168  0.0279
 -0.0843  0.0279  0.1144
    
```

sqrt(cov-diag) and  
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```

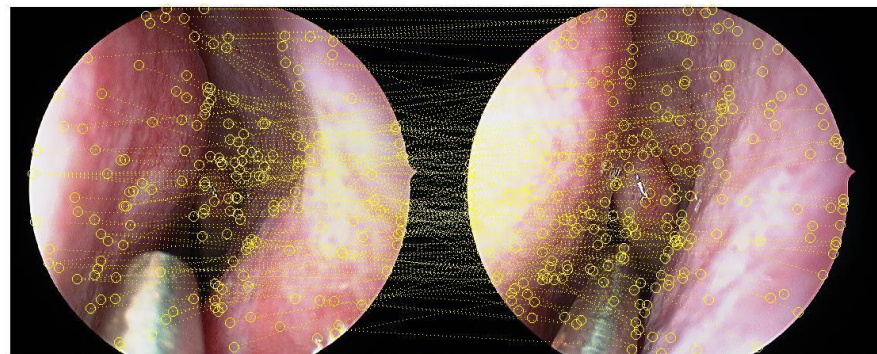
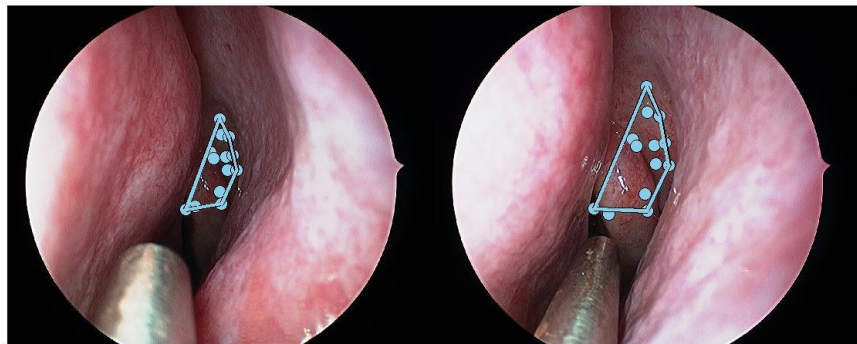
val(:,1) =
  0  0  0
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val(:,2) =
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  4.5710
  10.0842

val(:,3) =
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  5.1710
  1.6188

val(:,4) =
  2.6581
  1.2876
  3.3025

val(:,5) =
  20.2427
  7.4315
  19.3781
    
```



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val(:,4) =
  8.0279
  3.8214
  4.8564
val(:,5) =
  4.4111
  11.6050
  1.2478
  
```

original cov

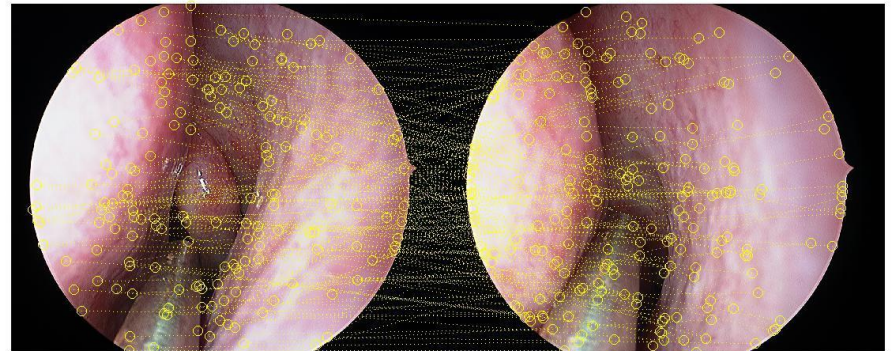
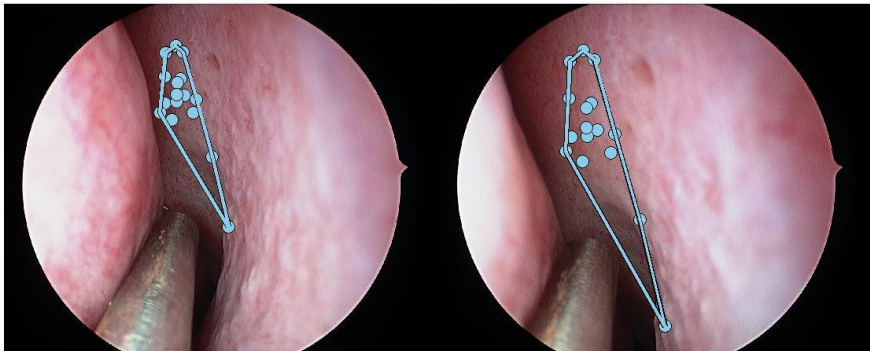
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sqrt(cov-diag) and convert to degree

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  1.6188
val(:,4) =
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val(:,5) =
  20.2427
  7.4315
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val(:,5) =
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 -0.0313  0.0168  0.0279
 -0.0843  0.0279  0.1144
    
```

sqrt(cov-diag) and convert to degree

```

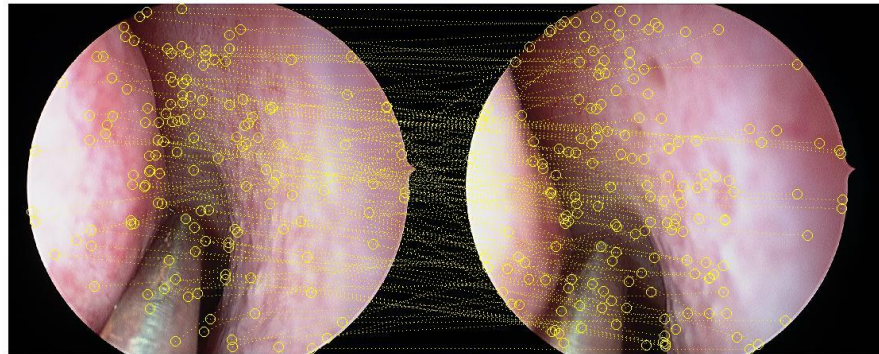
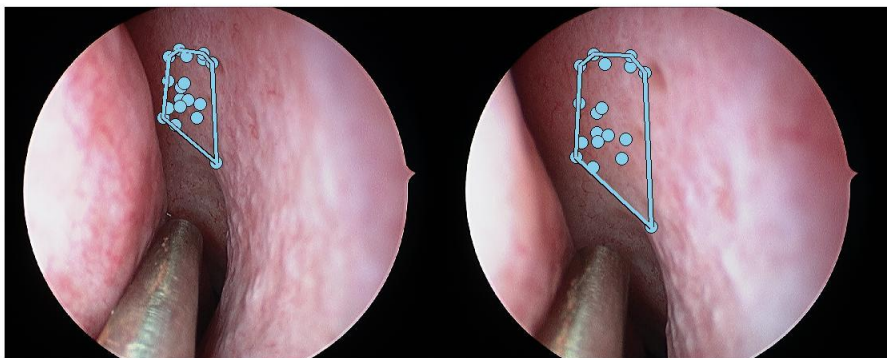
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sqrt(cov-diag) and convert to degree

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sqrt(cov-diag) and convert to degree

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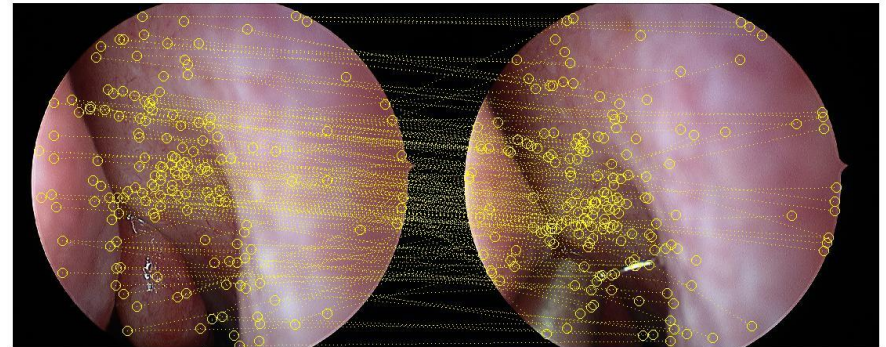
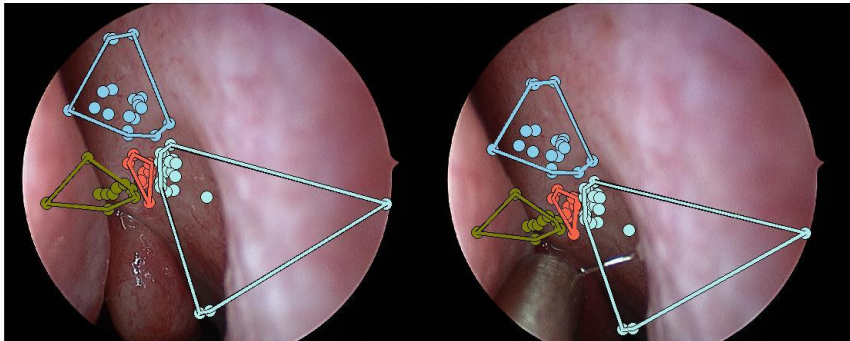
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  10.0842

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sqrt(cov-diag) and  
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val(:,4) =
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val(:,5) =
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```

original cov

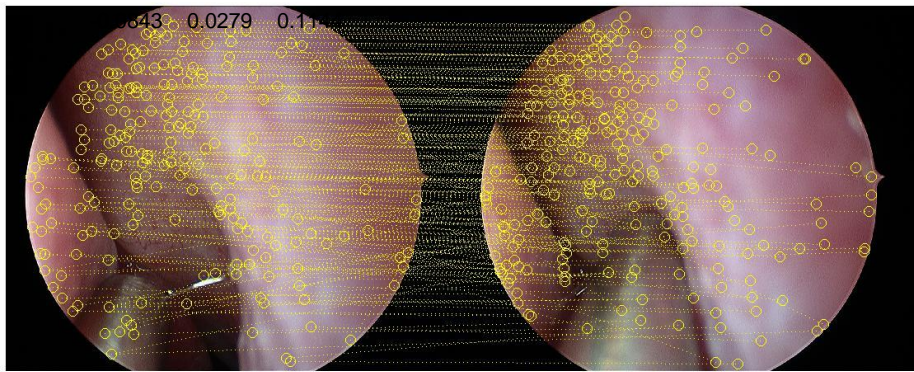
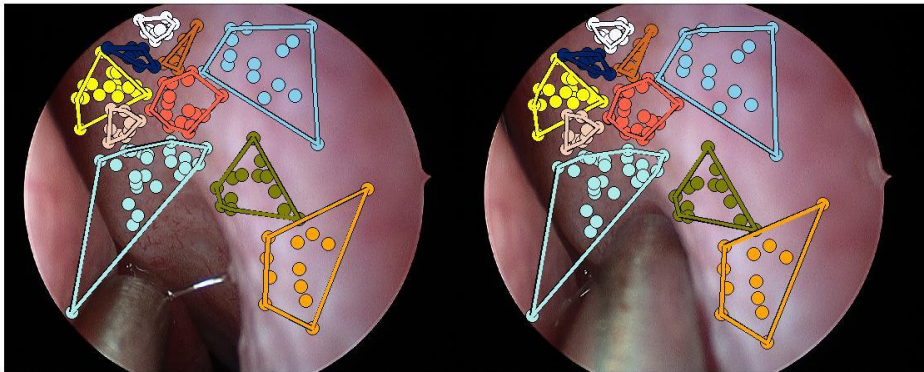
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val(:,5) =
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sqrt(cov-diag) and  
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```

val(:,1) =
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  1.6188
val(:,4) =
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  1.2876
  3.3025
val(:,5) =
  20.2427
  7.4315
  19.3781
  
```





original cov

```

val(:, :, 1) =
  0.0507  0.0096 -0.0253
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val(:, :, 2) =
  0.0180 -0.0173 -0.0039
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 -0.0039  0.0042  0.0012

val(:, :, 3) =
  0.0077  0.0092  0.0002
  0.0092  0.0314  0.0019
  0.0002  0.0019  0.0002

val(:, :, 4) =
  0.0196  0.0016 -0.0113
  0.0016  0.0044 -0.0026
 -0.0113 -0.0026  0.0072

val(:, :, 5) =
  0.0059  0.0155 -0.0014
  0.0155  0.0410 -0.0035
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  0.1248 -0.0313 -0.0843
 -0.0313  0.0168  0.0279
 -0.0843  0.0279  0.1144
    
```

sqrt(cov-diag) and  
convert to degree

```

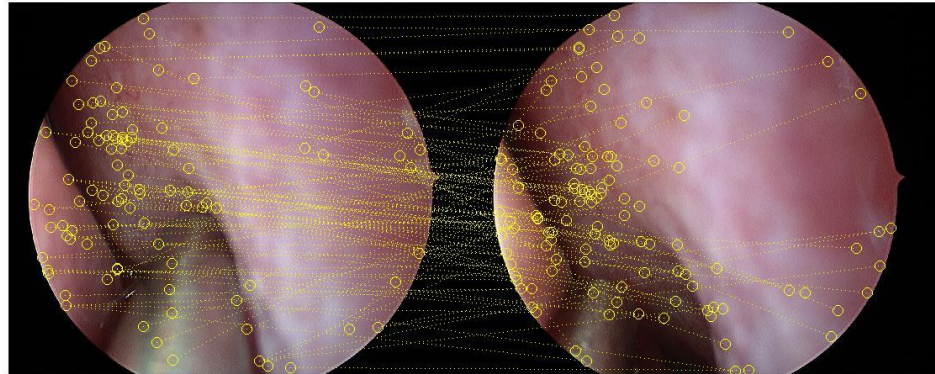
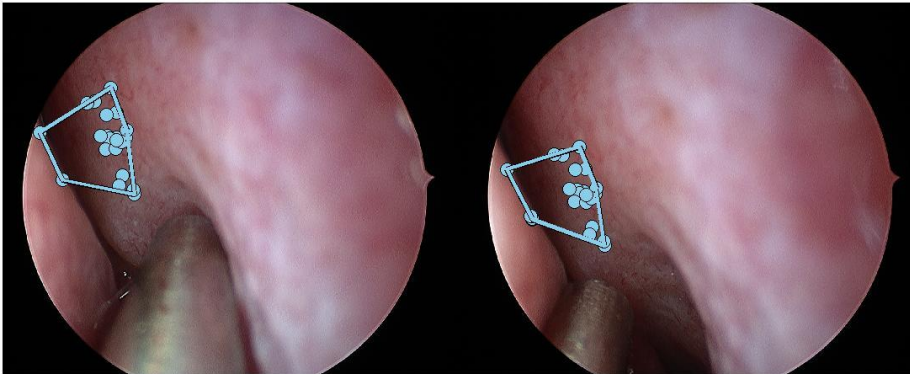
val(:, :, 1) =
  0  0  0
  0  0  0
  0  0  0

val(:, :, 2) =
  13.2501
  4.5710
  10.0842

val(:, :, 3) =
  10.9486
  5.1710
  1.6188

val(:, :, 4) =
  2.6581
  1.2876
  3.3025

val(:, :, 5) =
  20.2427
  7.4315
  19.3781
    
```



HMA

sqrt(cov-diag) and convert to degree

original cov

```

val(:,6) =
  1.0e-03 *
  0.0347  0.0259 -0.0625
  0.0259  0.0732 -0.0755
 -0.0625 -0.0755  0.1588
val(:,7) =
  0.0004 -0.0001 -0.0002
 -0.0001  0.0012 -0.0002
 -0.0002 -0.0002  0.0003
val(:,8) =
  0.0024 -0.0006 -0.0012
 -0.0006  0.0036 -0.0002
 -0.0012 -0.0002  0.0029
val(:,9) =
  1.0e-04 *
  0.7090 -0.2440 -0.0874
 -0.2440  0.5469 -0.0552
 -0.0874 -0.0552  0.0384
val(:,10) =
  1.0e-04 *
  0.1001  0.0929  0.0045
  0.0929  0.1485  0.0131
  0.0045  0.0131  0.0072

```

```

val(:,6) =
  0.3377
  0.4903
  0.7221
  1.0910
  1.9899
  0.9586
  2.7816
  3.4329
  3.0840
  0.4825
  0.4237
  0.1122
  0.2208
  0.0487

```

SIFT

sqrt(cov-diag) and convert to degree

original cov

```

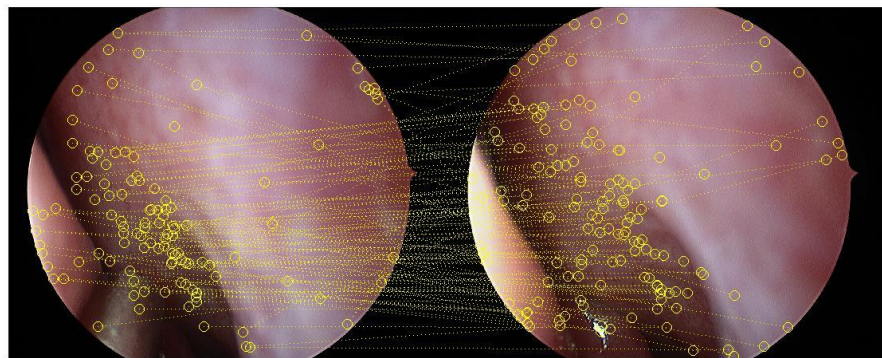
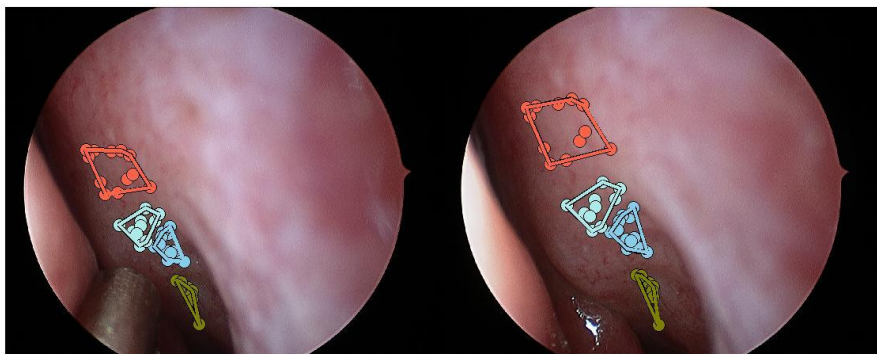
val(:,6) =
  0.0141  0.0027 -0.0050
  0.0027  0.0039  0.0036
 -0.0050  0.0036  0.0085
val(:,7) =
  0.0081  0.0009 -0.0132
  0.0009  0.0001 -0.0015
 -0.0132 -0.0015  0.0217
val(:,8) =
  0.0012 -0.0016 -0.0005
 -0.0016  0.0020  0.0007
 -0.0005  0.0007  0.0002
val(:,9) =
  1.0e-03 *
  0.4813 -0.3411 -0.2652
 -0.3411  0.3088  0.1746
 -0.2652  0.1746  0.1868
val(:,10) =
  1.0e-04 *
  0.0334 -0.0028  0.0222
 -0.0028  0.5534 -0.1232
  0.0222 -0.1232  0.0550

```

```

val(:,6) =
  6.8132
  3.5875
  5.2930
  5.1675
  6.281
  8.4446
  1.9925
  2.5732
  0.8993
  1.2570
  1.0068
  0.7831
  0.1047
  0.4262
  0.1344

```



# HMA

## original cov

```

val(:, :, 6) =
1.0e-03 *
0.0347 0.0259 -0.0625
0.0259 0.0732 -0.0755
-0.0625 -0.0755 0.1588
val(:, :, 7) =
0.0004 -0.0001 -0.0002
-0.0001 0.0012 -0.0002
-0.0002 -0.0002 0.0003
val(:, :, 8) =
0.0024 -0.0006 -0.0012
-0.0006 0.0036 -0.0002
-0.0012 -0.0002 0.0029
val(:, :, 9) =
1.0e-04 *
0.7090 -0.2440 -0.0874
-0.2440 0.5469 -0.0552
-0.0874 -0.0552 0.0384
val(:, :, 10) =
1.0e-04 *
0.1001 0.0929 0.0045
0.0929 0.1485 0.0131
0.0045 0.0131 0.0072
    
```

## sqrt(cov-diag) and convert to degree

```

val(:, :, 6) =
0.3377
0.4903
0.7221
val(:, :, 7) =
1.0910
1.9899
0.9586
val(:, :, 8) =
2.7816
3.4329
3.0840
val(:, :, 9) =
0.4825
0.4237
0.1122
val(:, :, 10) =
0.1812
0.2208
0.0487
    
```

# SIFT

## original cov

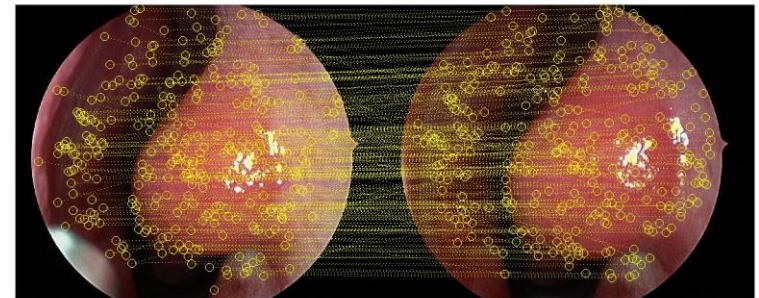
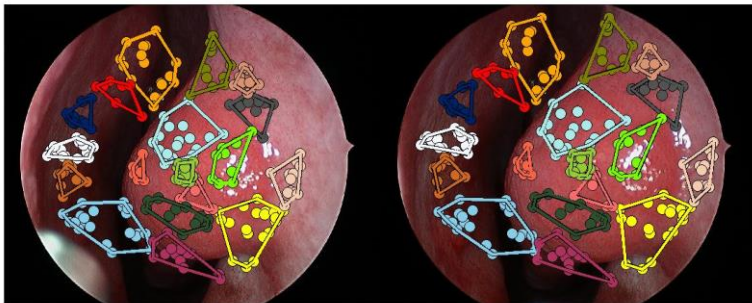
```

val(:, :, 6) =
0.0141 0.0027 -0.0050
0.0027 0.0039 0.0036
-0.0050 0.0036 0.0085
val(:, :, 7) =
0.0081 0.0009 -0.0132
0.0009 0.0001 -0.0015
-0.0132 -0.0015 0.0217
val(:, :, 8) =
0.0012 -0.0016 -0.0005
-0.0016 0.0020 0.0007
-0.0005 0.0007 0.0002
val(:, :, 9) =
1.0e-03 *
0.4813 -0.3411 -0.2652
-0.3411 0.3088 0.1746
-0.2652 0.1746 0.1868
val(:, :, 10) =
1.0e-04 *
0.0334 -0.0028 0.0222
-0.0028 0.5534 -0.1232
0.0222 -0.1232 0.0550
    
```

## sqrt(cov-diag) and convert to degree

```

val(:, :, 6) =
6.8132
3.5875
5.2930
val(:, :, 7) =
5.1675
6.6281
8.4446
val(:, :, 8) =
1.9925
2.5732
0.8993
val(:, :, 9) =
1.2570
1.0068
0.7831
val(:, :, 10) =
0.1047
0.4262
0.1344
    
```



# HMA

original cov

```

val(:, :, 11) =
    0.0118 -0.0033 -0.0025
   -0.0033  0.0009  0.0007
   -0.0025  0.0007  0.0007

val(:, :, 12) =
    1.0e-04 *
    0.1464 -0.0920 -0.0310
   -0.0920  0.0990  0.0329
   -0.0310  0.0329  0.0126

val(:, :, 13) =
    1.0e-04 *
    0.4442 -0.0785 -0.1743
   -0.0785  0.0929 -0.0061
   -0.1743 -0.0061  0.1624

val(:, :, 14) =
    1.0e-03 *
    0.1337 -0.0766 -0.0387
   -0.0766  0.0770  0.0258
   -0.0387  0.0258  0.0145

val(:, :, 15) =
    0.0060  0.0091  0.0018
    0.0091  0.0142  0.0016
    0.0018  0.0016  0.0075
    
```

sqrt(cov-diag) and  
convert to degree

```

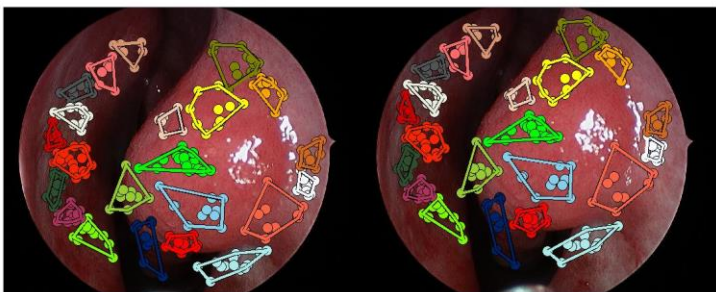
val(:, :, 11) =
    6.2301
    1.7545
    1.4977

val(:, :, 12) =
    0.2192
    0.1803
    0.0643

val(:, :, 13) =
    0.3819
    0.1746
    0.2309

val(:, :, 14) =
    0.6625
    0.5028
    0.2182

val(:, :, 15) =
    4.4278
    6.8243
    4.9622
    
```



# SIFT

original cov

```

val(:, :, 11) =
    0.0870 -0.0161 -0.0088
   -0.0161  0.0032  0.0020
   -0.0088  0.0020  0.0189

val(:, :, 12) =
    1.0e-04 *
    0.1544 -0.1018 -0.0222
   -0.1018  0.0760  0.0120
   -0.0222  0.0120  0.0070

val(:, :, 13) =
    1.0e-03 *
    0.2057 -0.0942  0.0326
   -0.0942  0.0987 -0.0473
    0.0326 -0.0473  0.0427

val(:, :, 14) =
    0.0014 -0.0009 -0.0010
   -0.0009  0.0010  0.0006
   -0.0010  0.0006  0.0007

val(:, :, 15) =
    0.0217  0.0433  0.0050
    0.0433  0.0891 -0.0115
    0.0050 -0.0115  0.2319
    
```

sqrt(cov-diag) and  
convert to degree

```

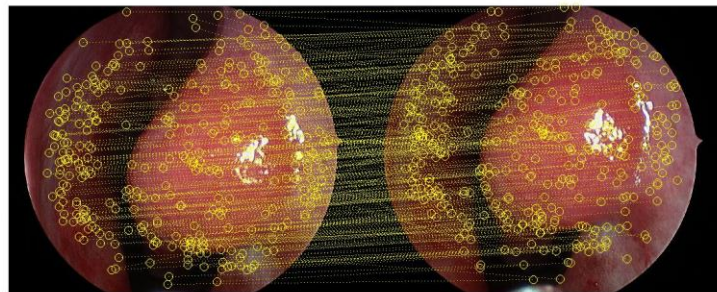
val(:, :, 11) =
    16.8958
    3.2474
    7.8724

val(:, :, 12) =
    0.2251
    0.1580
    0.0481

val(:, :, 13) =
    0.8217
    0.5691
    0.3744

val(:, :, 14) =
    2.1287
    1.8484
    1.5288

val(:, :, 15) =
    8.4441
    17.1055
    27.5938
    
```



# HMA

## original cov

```

val(:, :, 11) =
    0.0118 -0.0033 -0.0025
   -0.0033  0.0009  0.0007
   -0.0025  0.0007  0.0007

val(:, :, 12) =
    1.0e-04 *
    0.1464 -0.0920 -0.0310
   -0.0920  0.0990  0.0329
   -0.0310  0.0329  0.0126

val(:, :, 13) =
    1.0e-04 *
    0.4442 -0.0785 -0.1743
   -0.0785  0.0929 -0.0061
   -0.1743 -0.0061  0.1624

val(:, :, 14) =
    1.0e-03 *
    0.1337 -0.0766 -0.0387
   -0.0766  0.0770  0.0258
   -0.0387  0.0258  0.0145

val(:, :, 15) =
    0.0060  0.0091  0.0018
    0.0091  0.0142  0.0016
    0.0018  0.0016  0.0075
  
```

## sqrt(cov-diag) and convert to degree

```

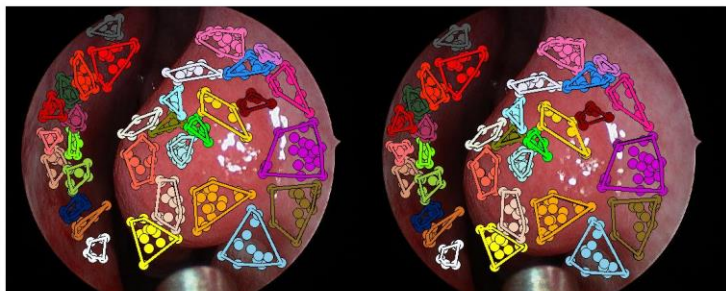
val(:, :, 11) =
    6.2301
    1.7545
    1.4977

val(:, :, 12) =
    0.2192
    0.1803
    0.0643

val(:, :, 13) =
    0.3819
    0.1746
    0.2309

val(:, :, 14) =
    0.6625
    0.5028
    0.2182

val(:, :, 15) =
    4.4278
    6.8243
    4.9622
  
```



# SIFT

## original cov

```

val(:, :, 11) =
    0.0870 -0.0161 -0.0088
   -0.0161  0.0032  0.0020
   -0.0088  0.0020  0.0189

val(:, :, 12) =
    1.0e-04 *
    0.1544 -0.1018 -0.0222
   -0.1018  0.0760  0.0120
   -0.0222  0.0120  0.0070

val(:, :, 13) =
    1.0e-03 *
    0.2057 -0.0942  0.0326
   -0.0942  0.0987 -0.0473
    0.0326 -0.0473  0.0427

val(:, :, 14) =
    0.0014 -0.0009 -0.0010
   -0.0009  0.0010  0.0006
   -0.0010  0.0006  0.0007

val(:, :, 15) =
    0.0217  0.0433  0.0050
    0.0433  0.0891 -0.0115
    0.0050 -0.0115  0.2319
  
```

## sqrt(cov-diag) and convert to degree

```

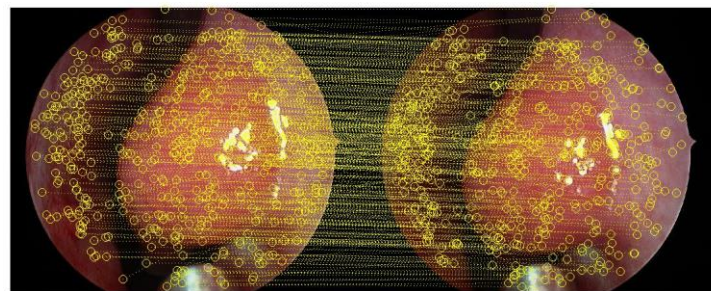
val(:, :, 11) =
    16.8958
    3.2474
    7.8724

val(:, :, 12) =
    0.2251
    0.1580
    0.0481

val(:, :, 13) =
    0.8217
    0.5691
    0.3744

val(:, :, 14) =
    2.1287
    1.8484
    1.5288

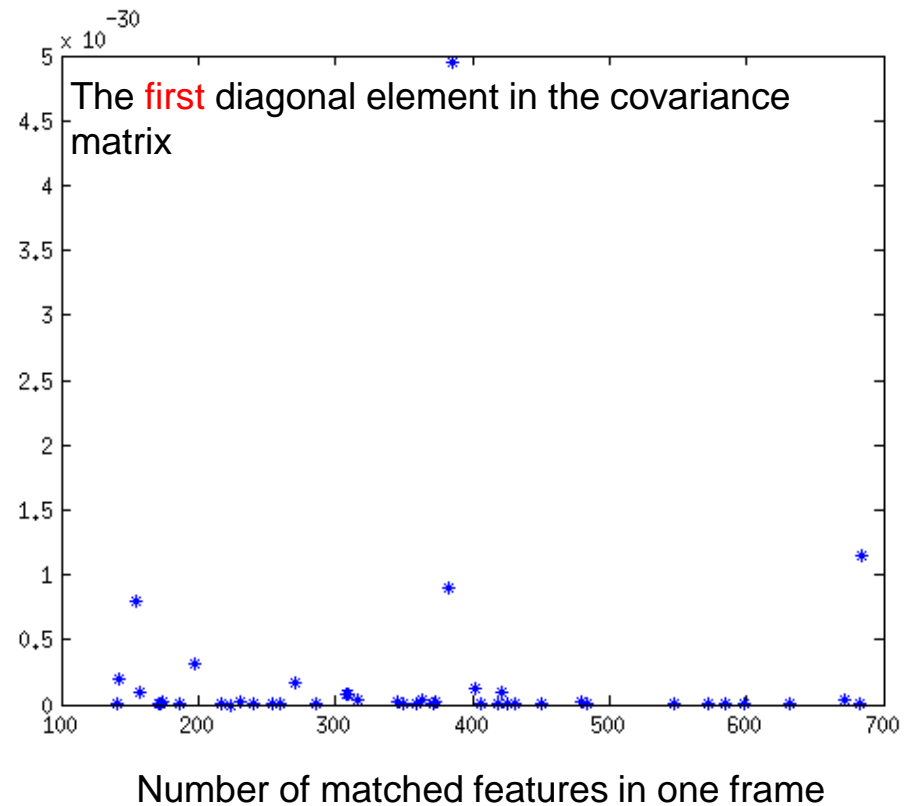
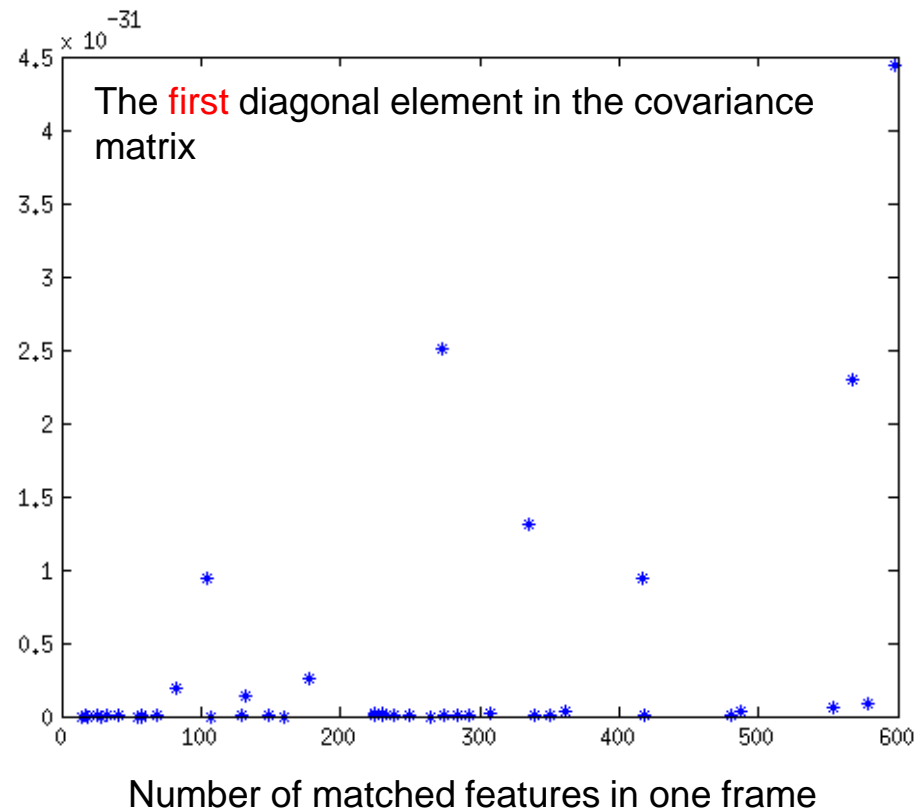
val(:, :, 15) =
    8.4441
    17.1055
    27.5938
  
```



# Analysis of diagonal elements in covariance matrix (1/3)

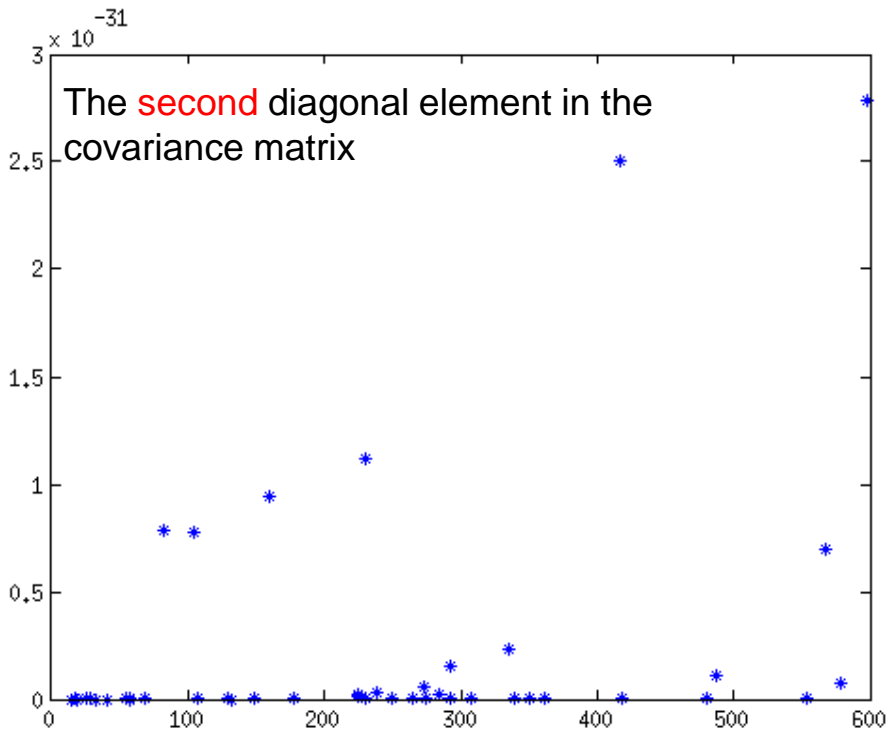
HMA

SIFT



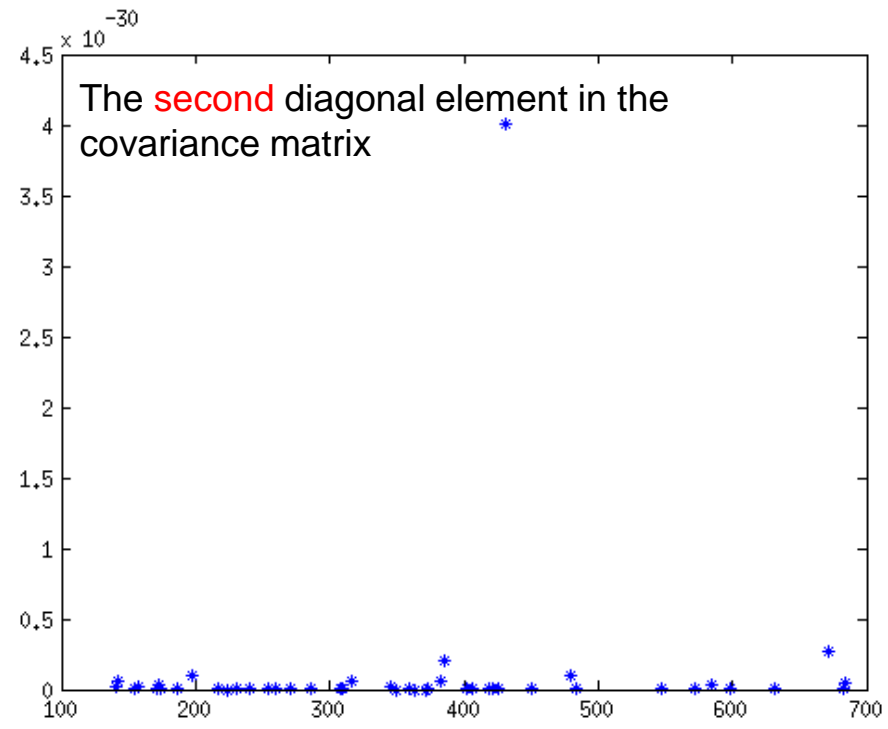
# Analysis of diagonal elements in covariance matrix (2/3)

HMA



Number of matched features in one frame

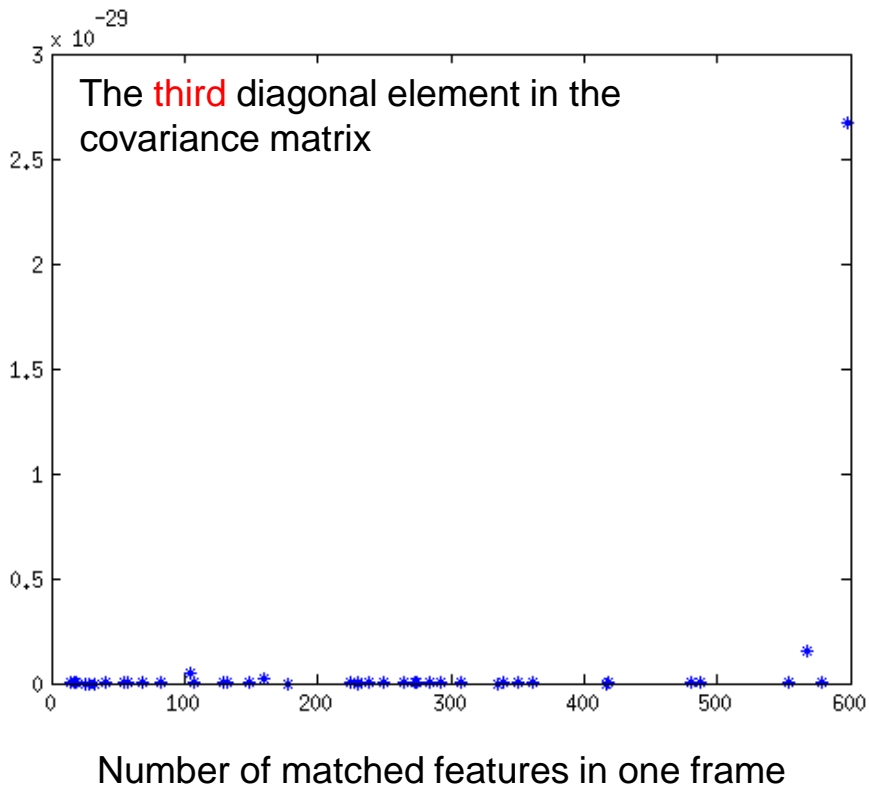
SIFT



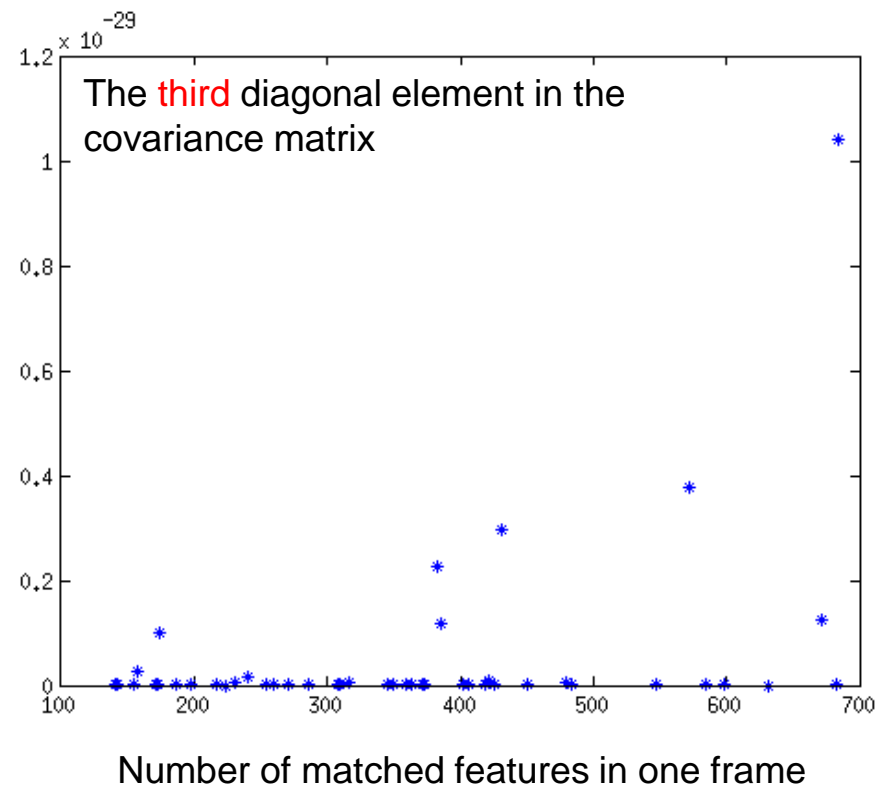
Number of matched features in one frame

# Analysis of diagonal elements in covariance matrix (3/3)

HMA



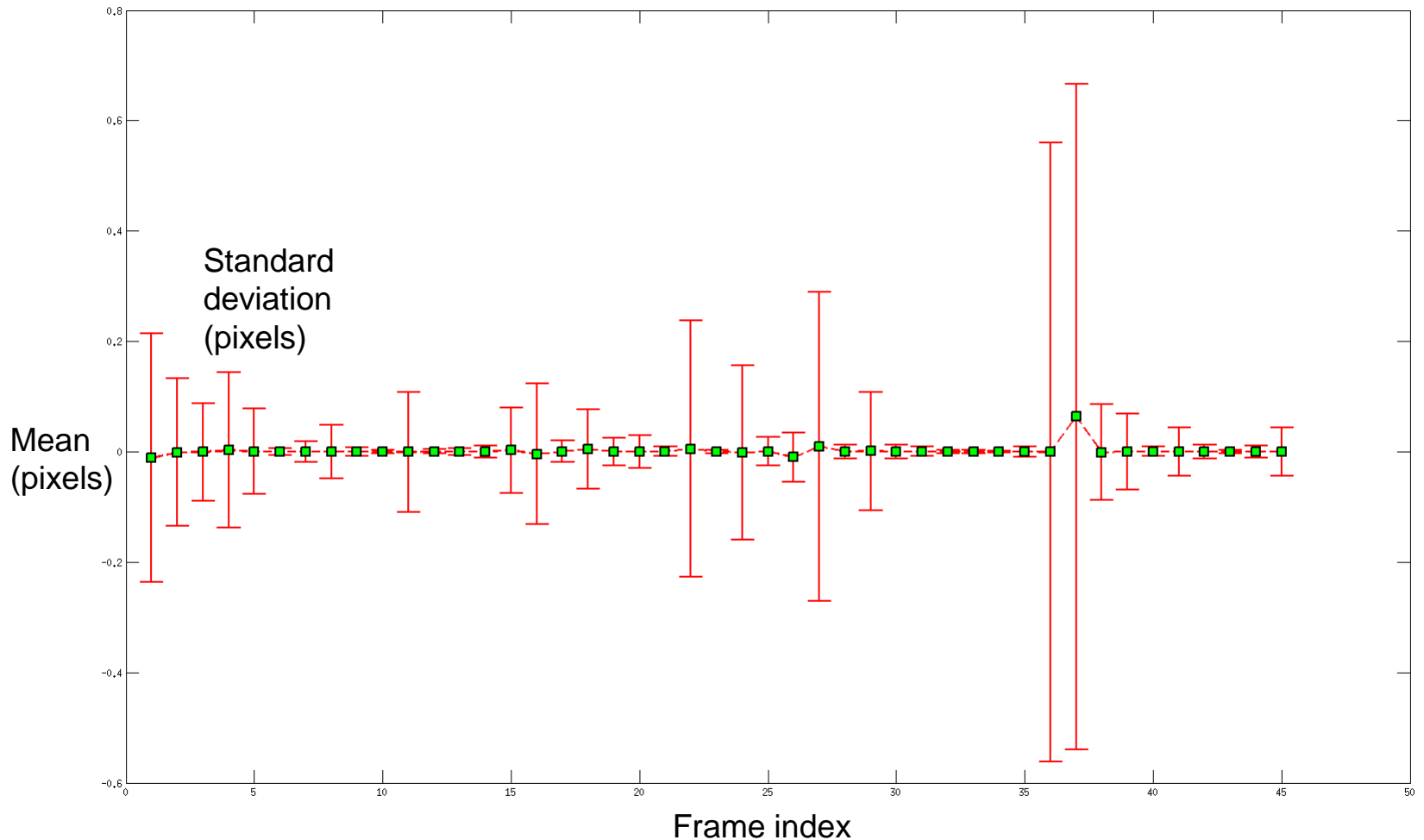
SIFT





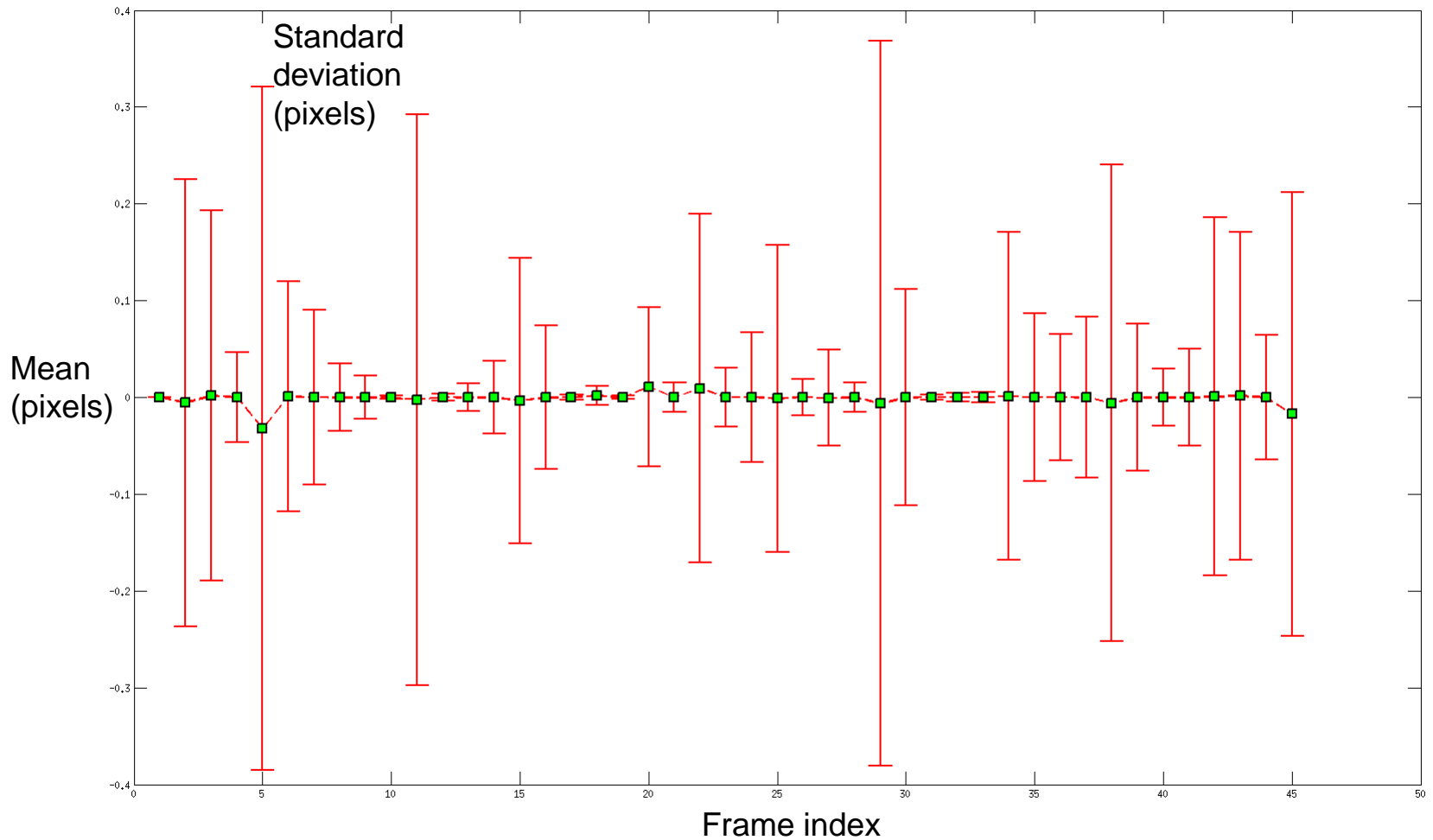
# Analysis of rotation angles: Alpha (1/5)

HMA



# Analysis of rotation angles: Alpha (2/5)

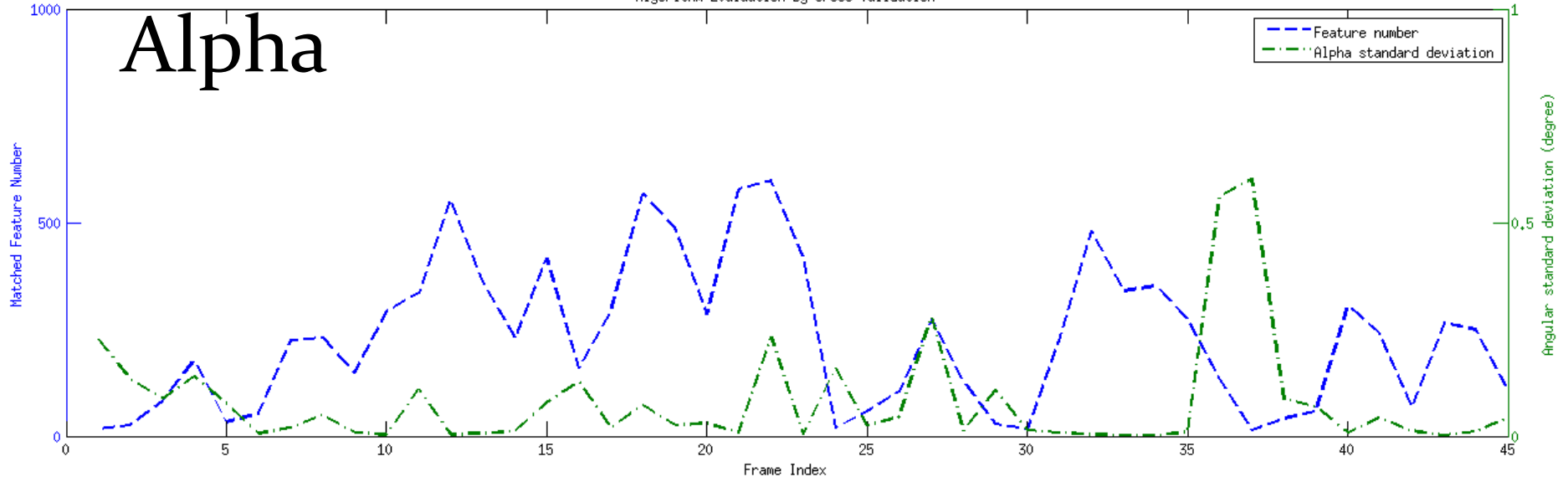
## SIFT



# HMA

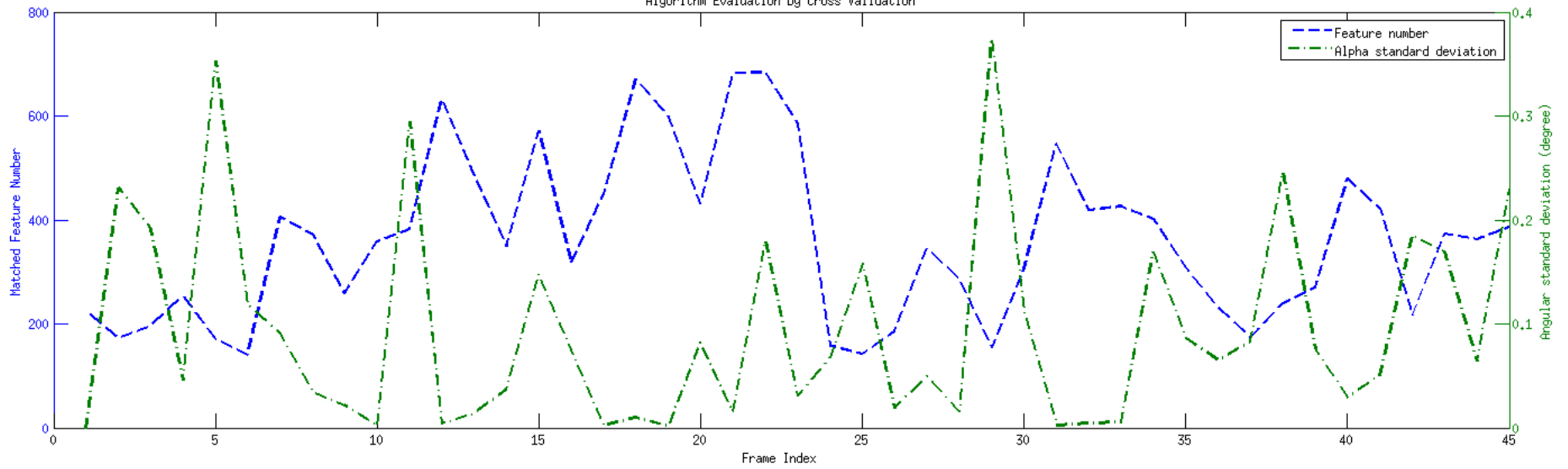
Algorithm Evaluation by Cross Validation

## Alpha



## SIFT

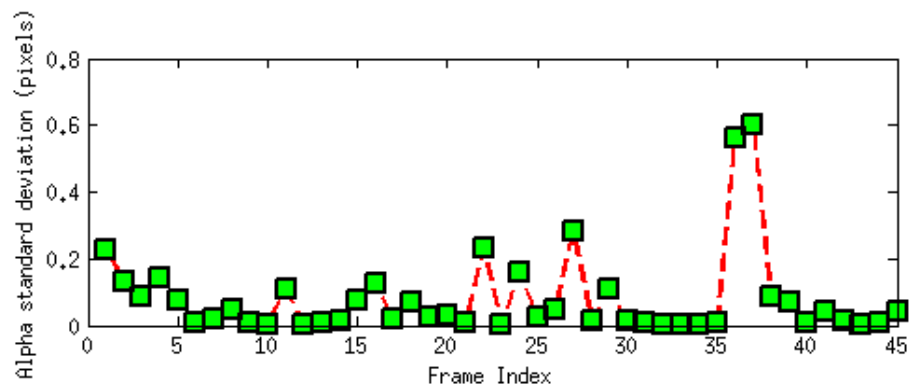
Algorithm Evaluation by Cross Validation



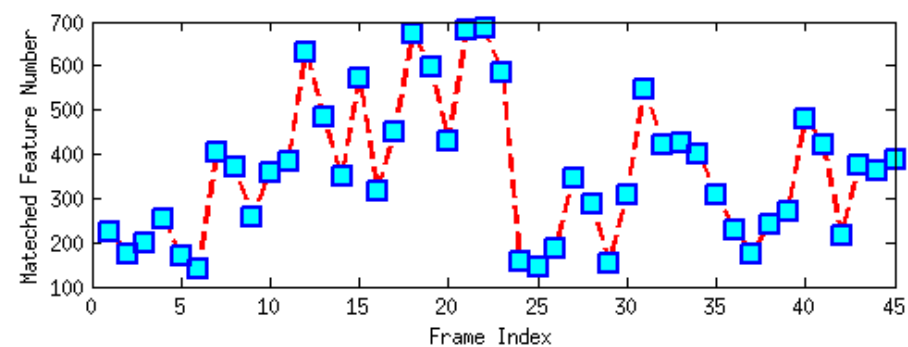
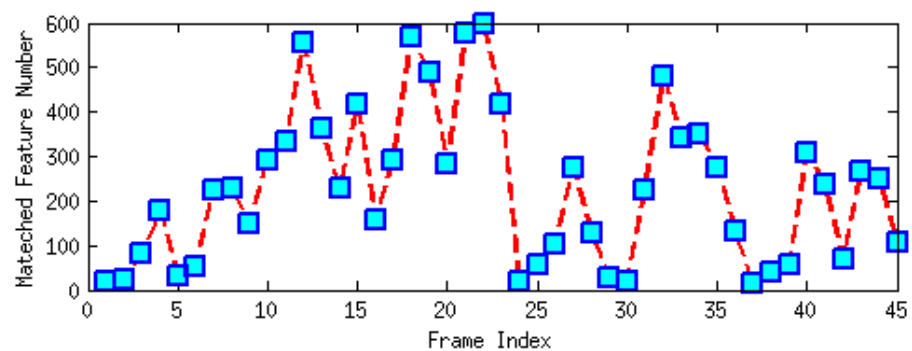
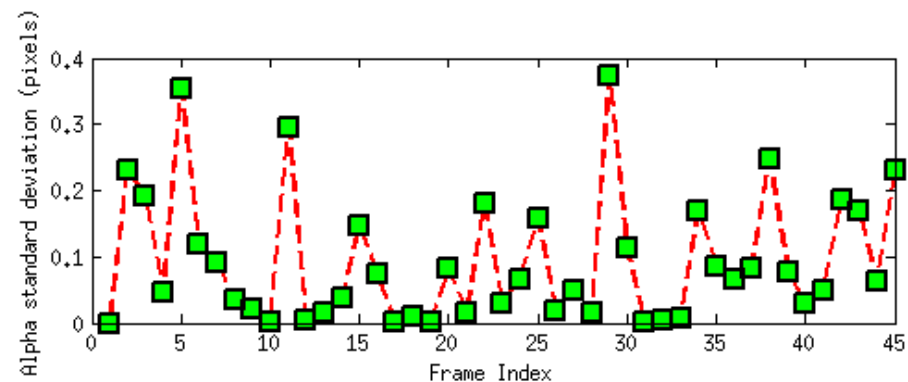
# Analysis of rotation angles: Alpha (4/5)

Alpha standard deviation with feature number

HMA

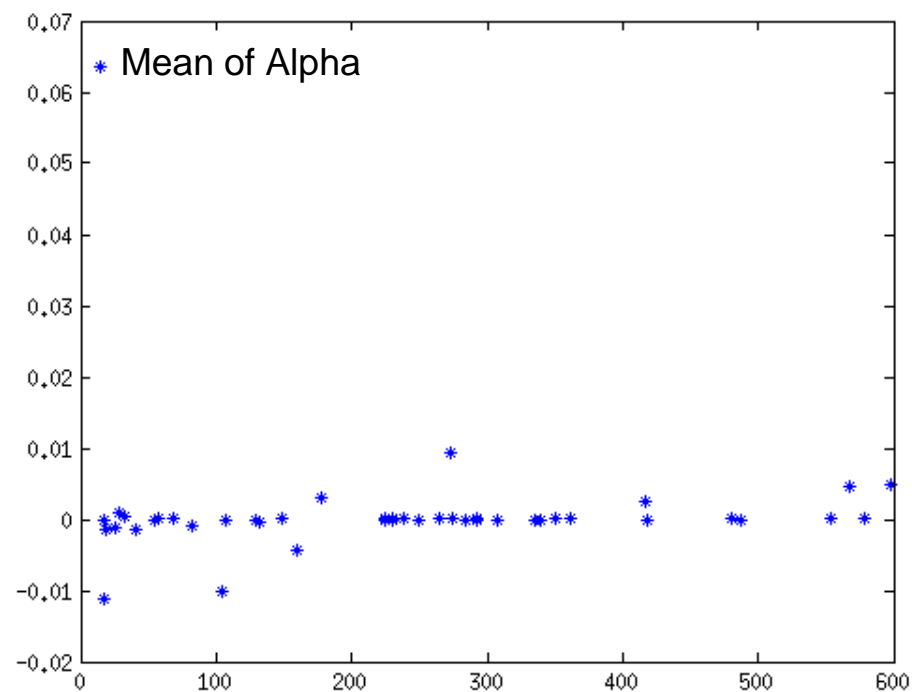


SIFT



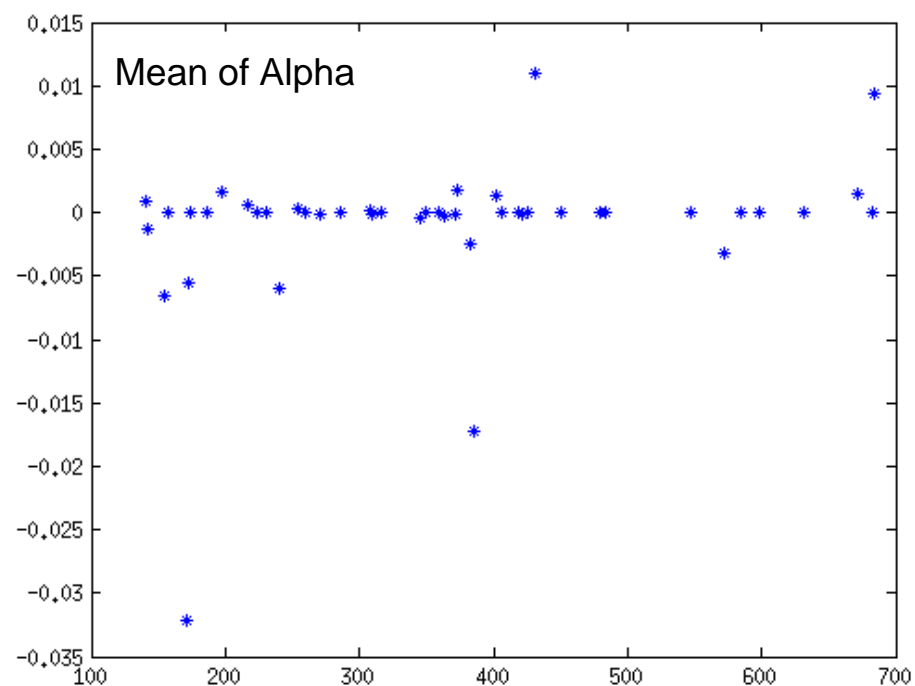
# Analysis of rotation angles: Alpha (5/5)

HMA



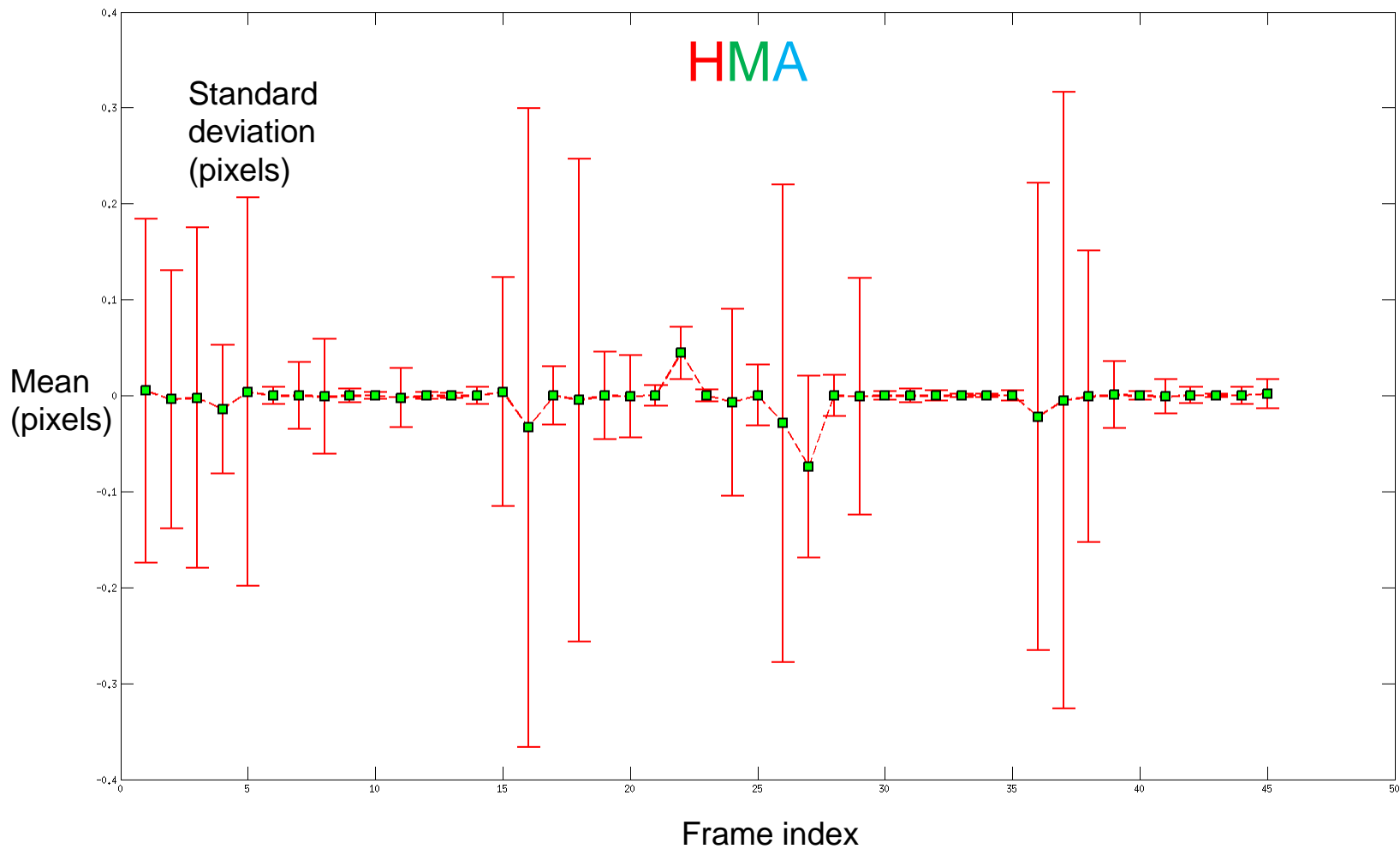
Matched feature number in one frame

SIFT

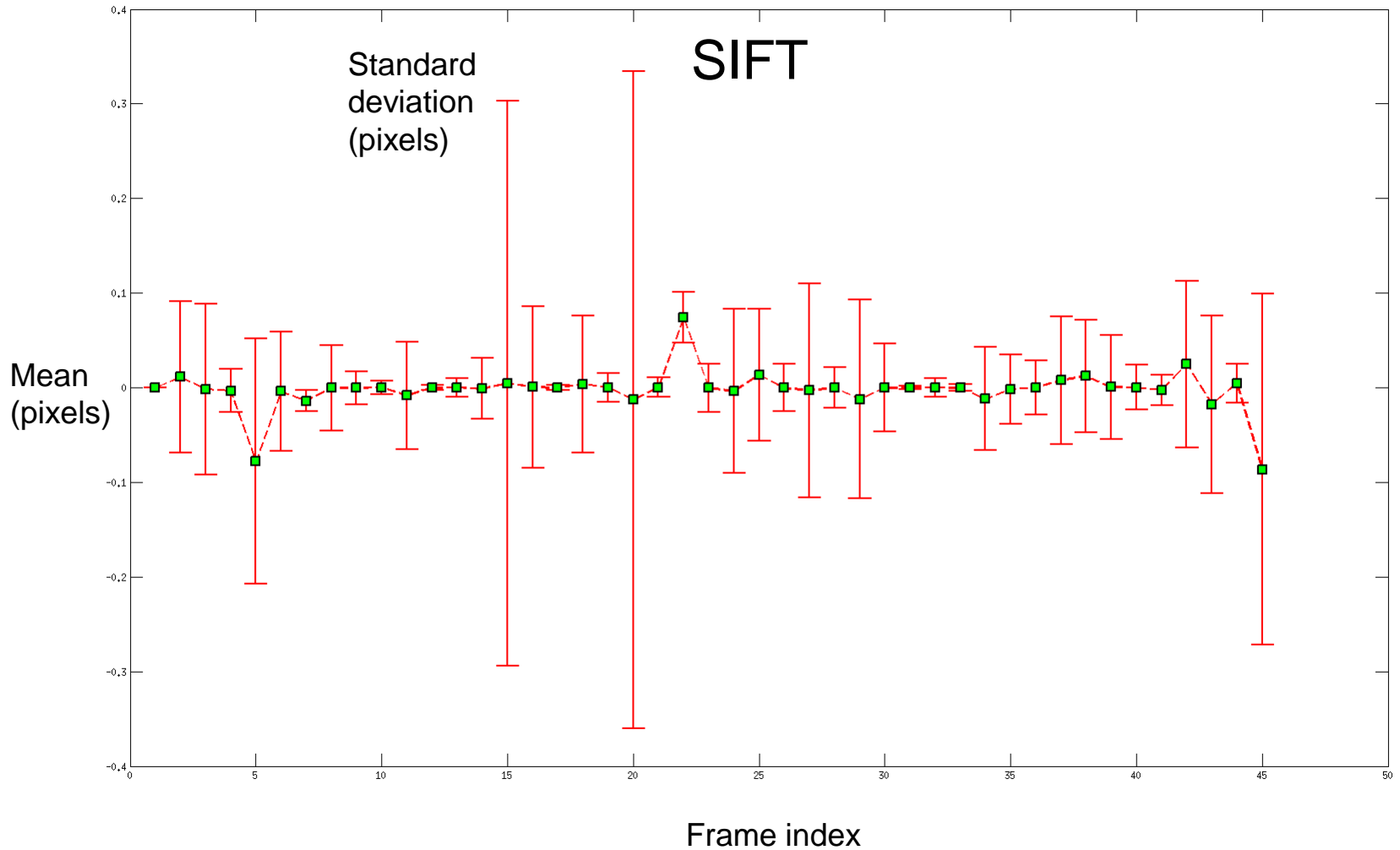


Matched feature number in one frame

# Analysis of rotation angles: Beta (1/5)

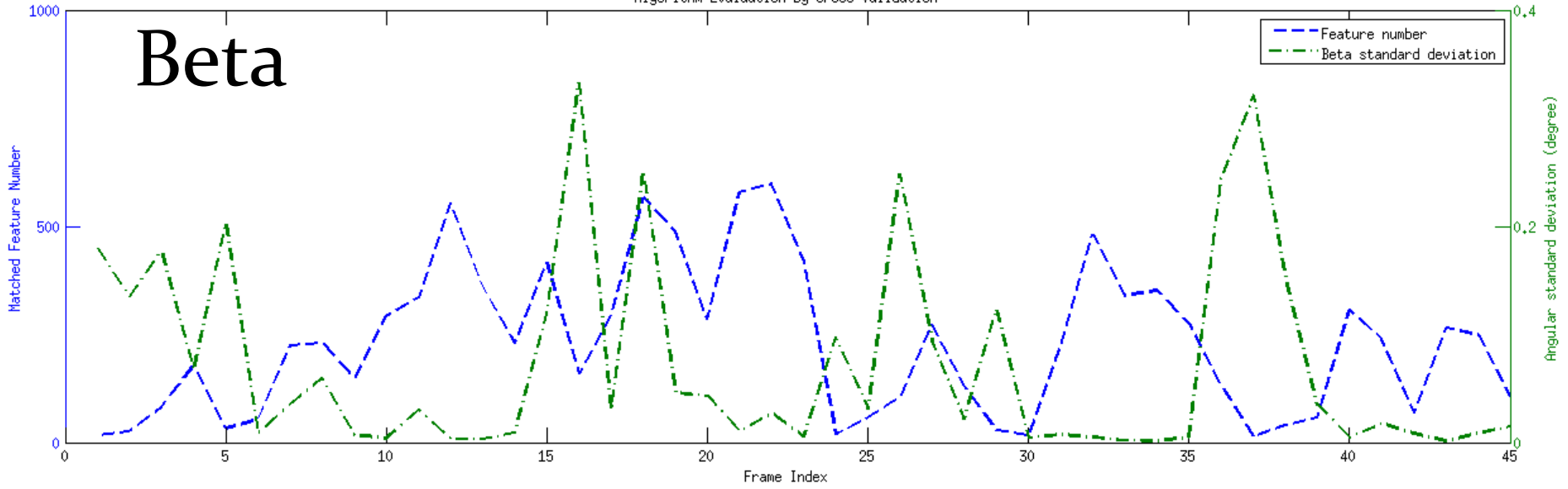


# Analysis of rotation angles: Beta (2/5)



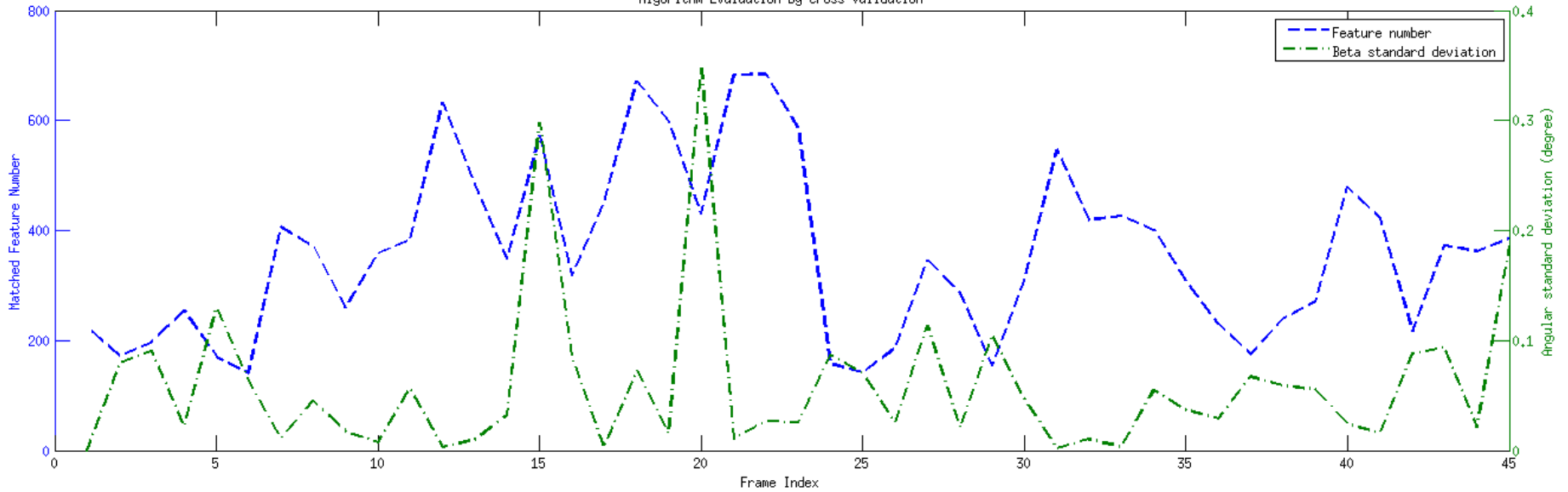
# HMA

Algorithm Evaluation by Cross Validation



# SIFT

Algorithm Evaluation by Cross Validation



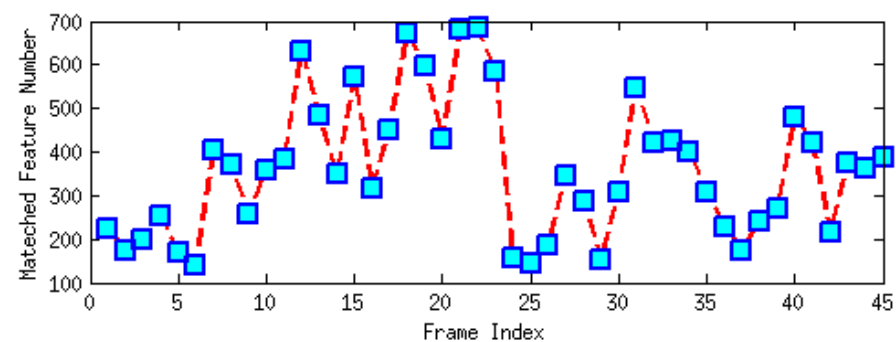
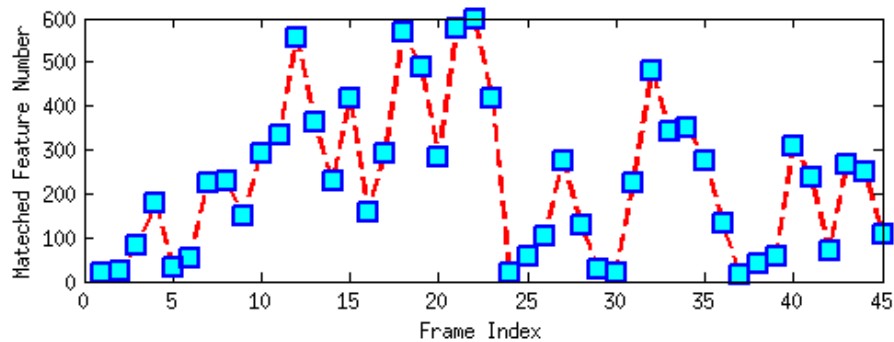
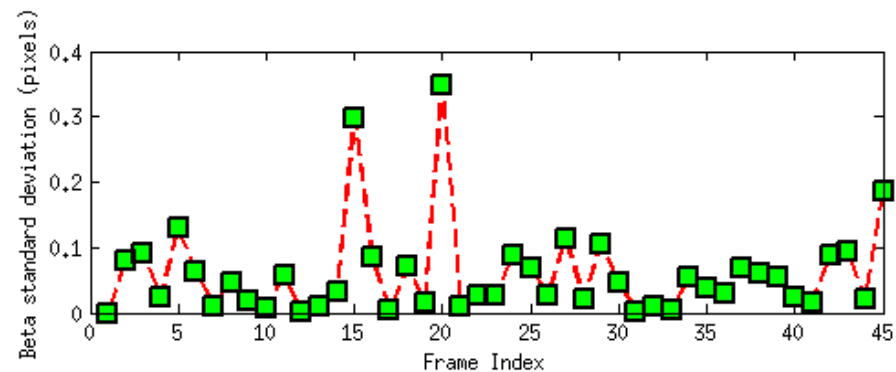
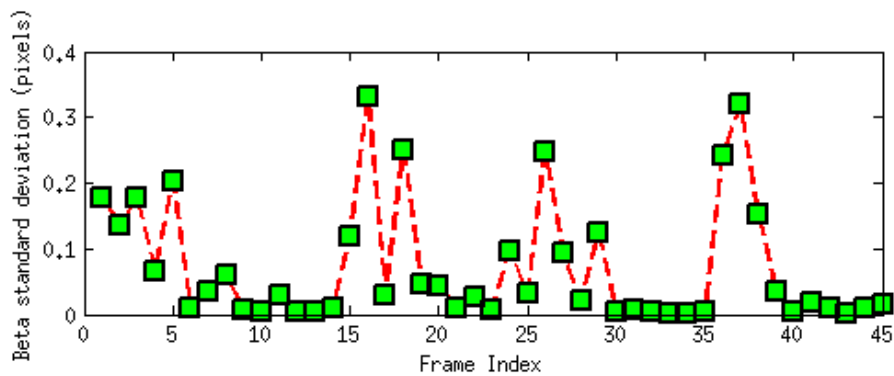


# Analysis of rotation angles: Beta (4/5)

Beta standard deviation with feature number

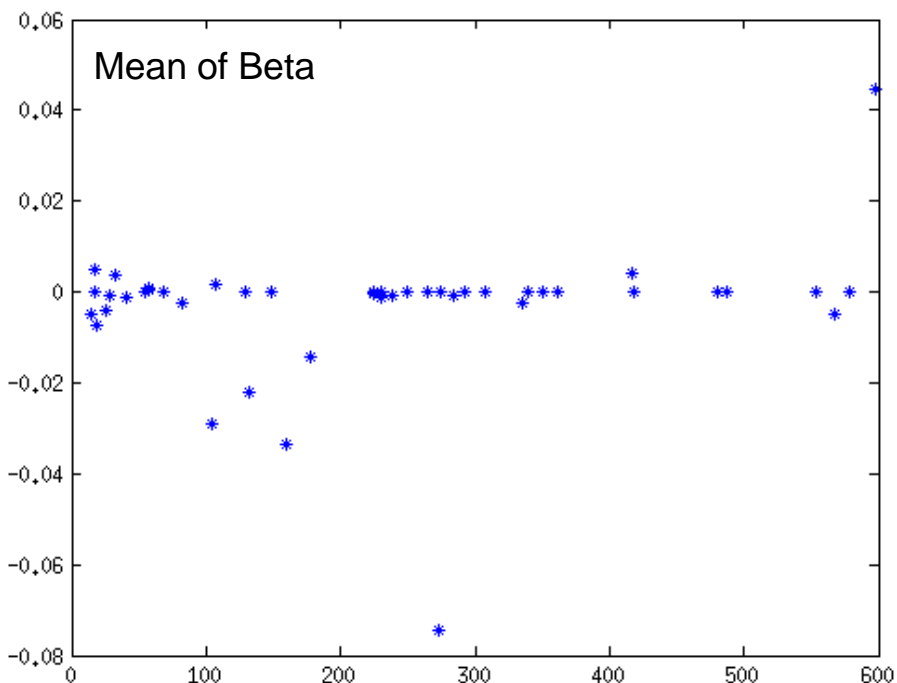
HMA

SIFT



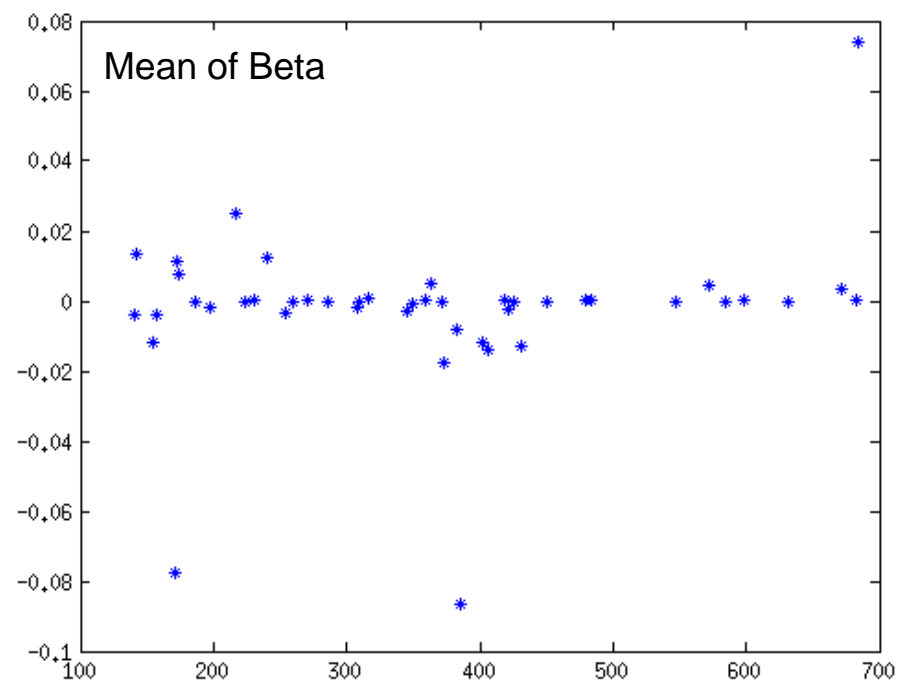
# Analysis of rotation angles: Beta (5/5)

HMA



Matched feature number in one frame

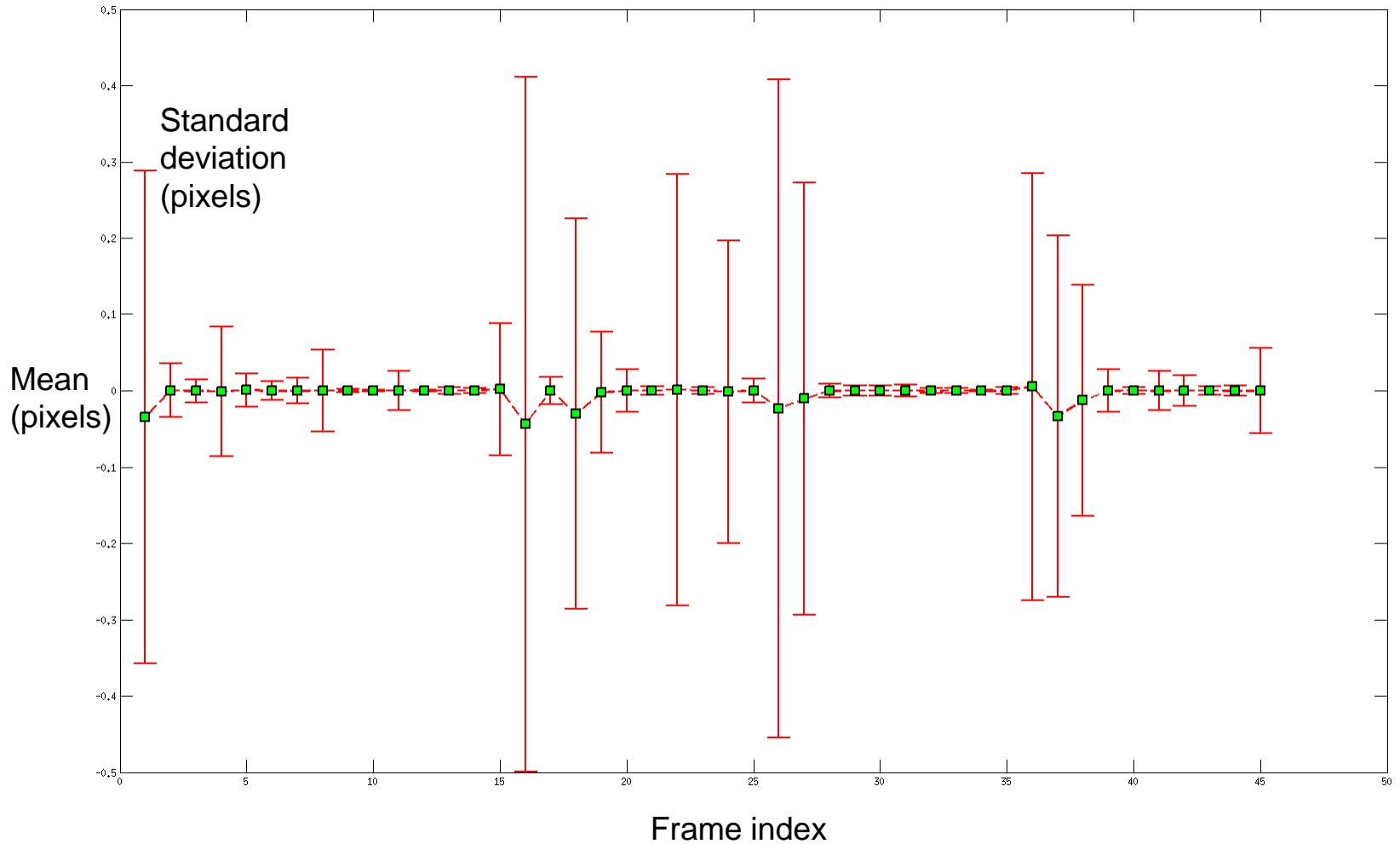
SIFT



Matched feature number in one frame

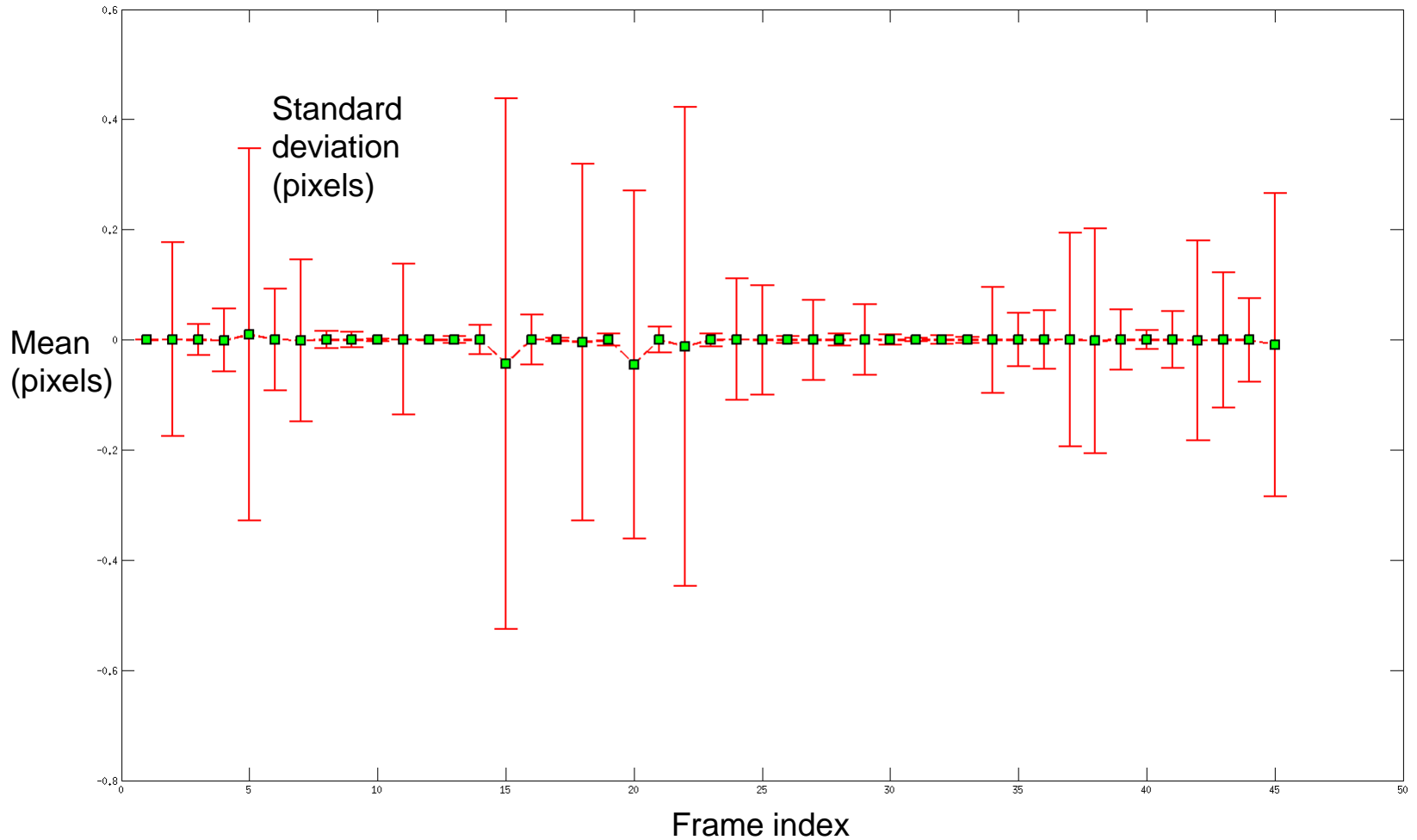
# Analysis of rotation angles: Gamma (1/5)

HMA



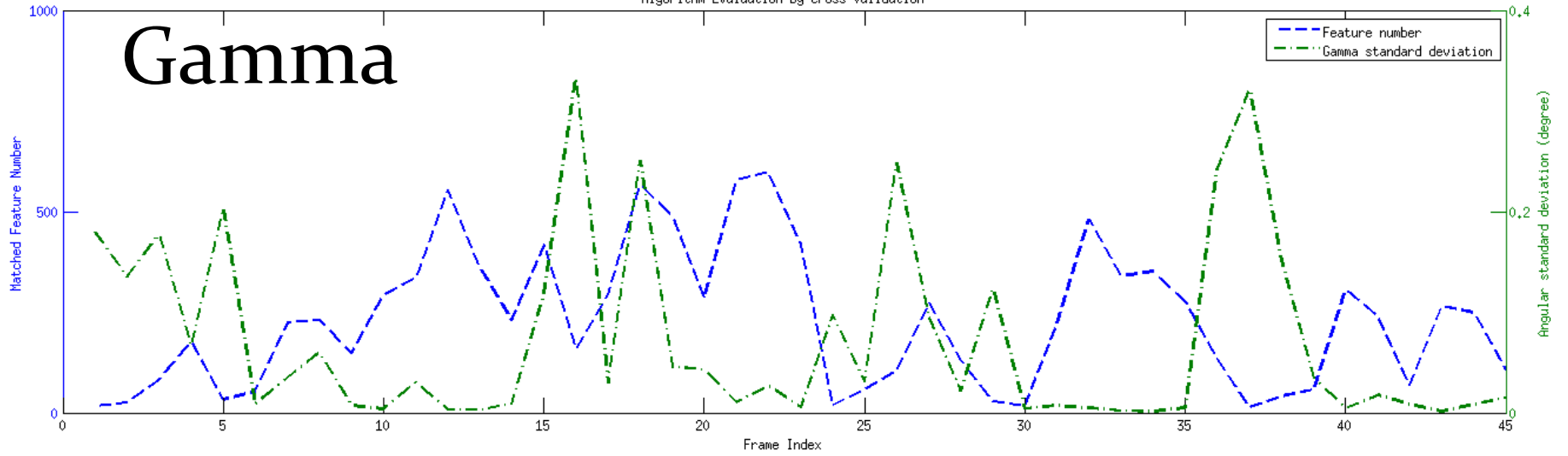
# Analysis of rotation angles: Gamma (2/5)

SIFT



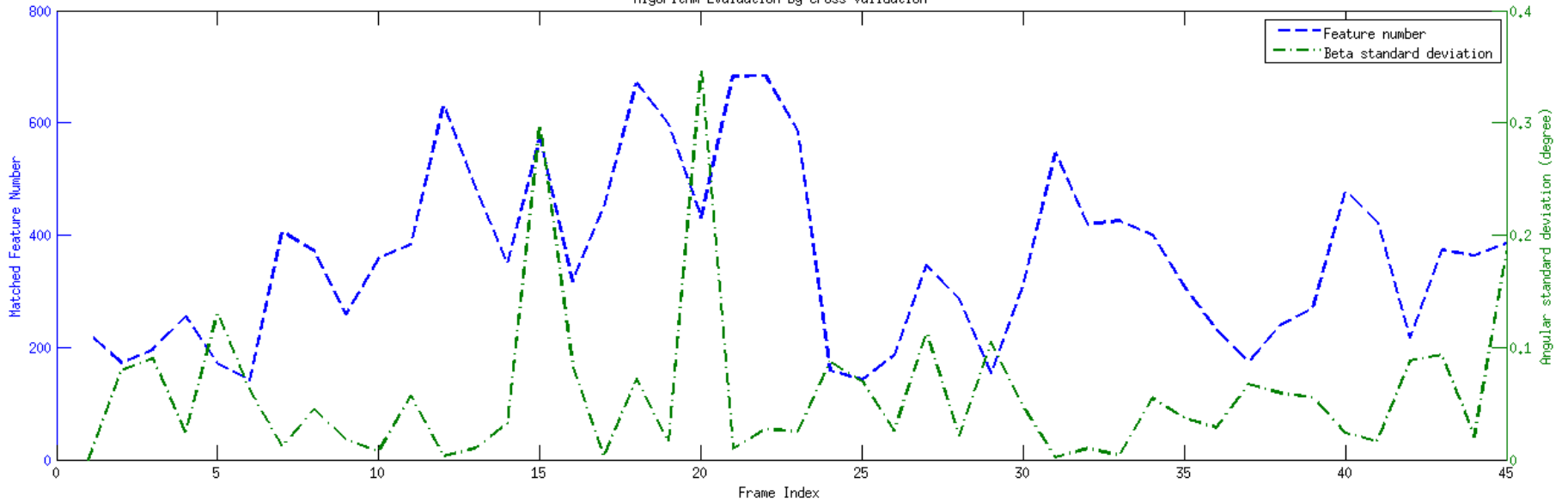
# HMA

Algorithm Evaluation by Cross Validation



# SIFT

Algorithm Evaluation by Cross Validation

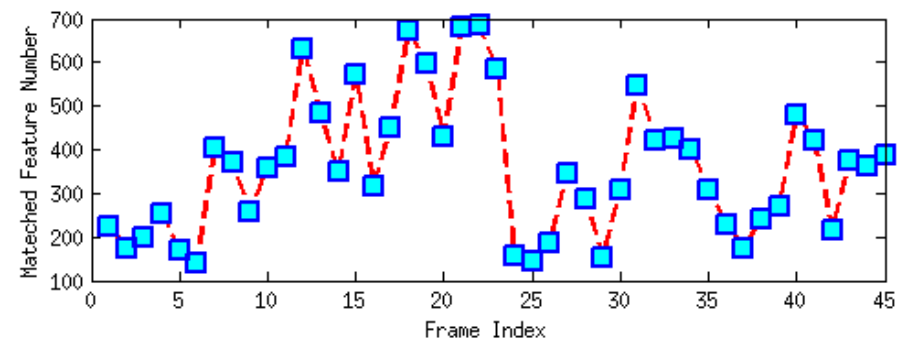
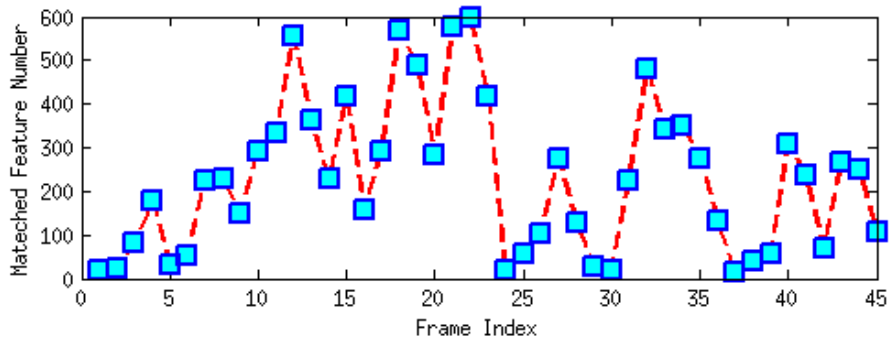
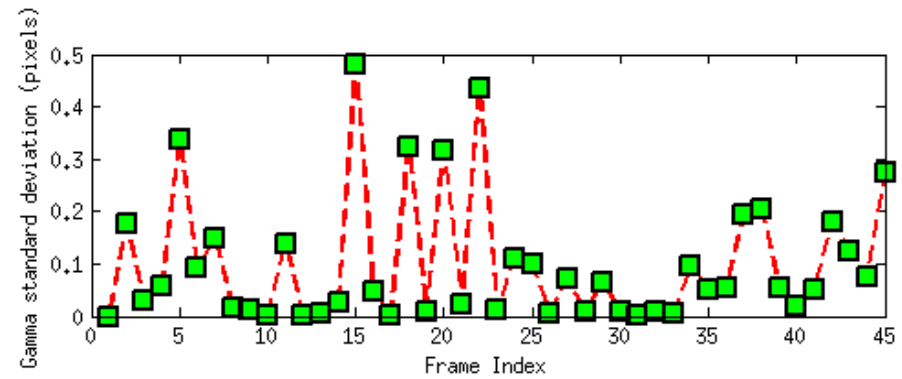
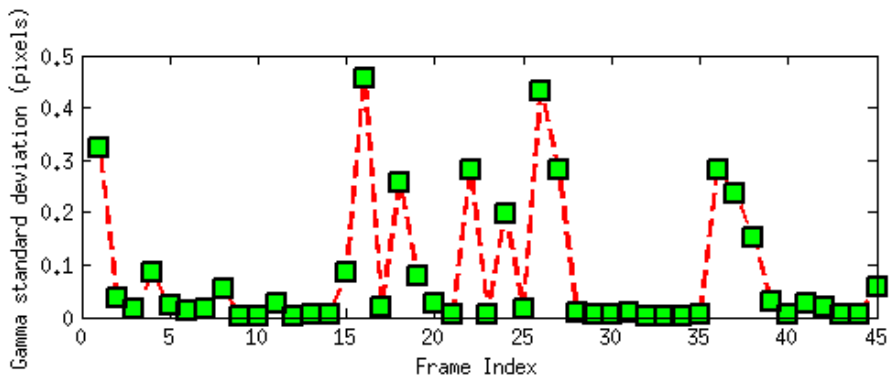


# Analysis of rotation angles: Gamma (4/5)

Gamma standard deviation with feature number

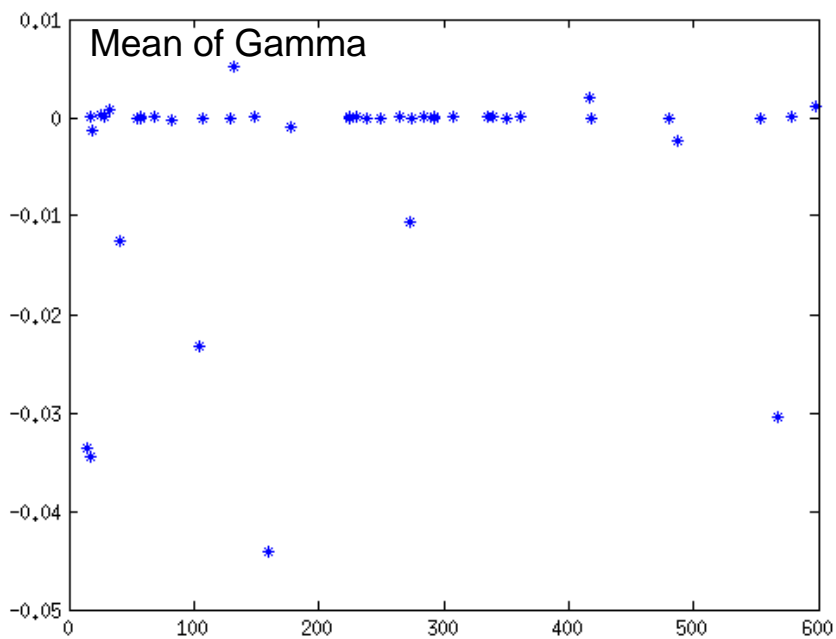
HMA

SIFT



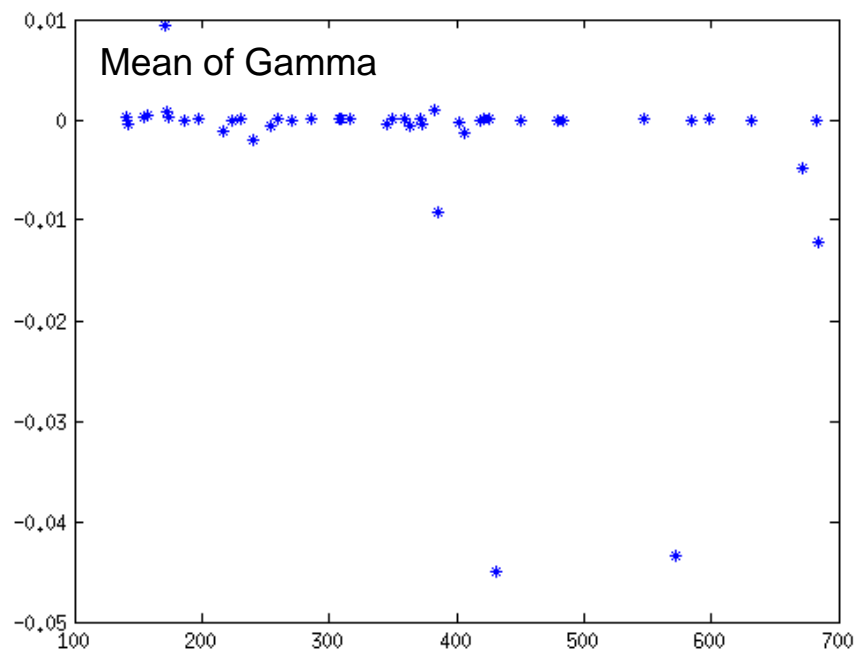
# Analysis of rotation angles: Gamma (5/5)

HMA



Matched feature number in one frame

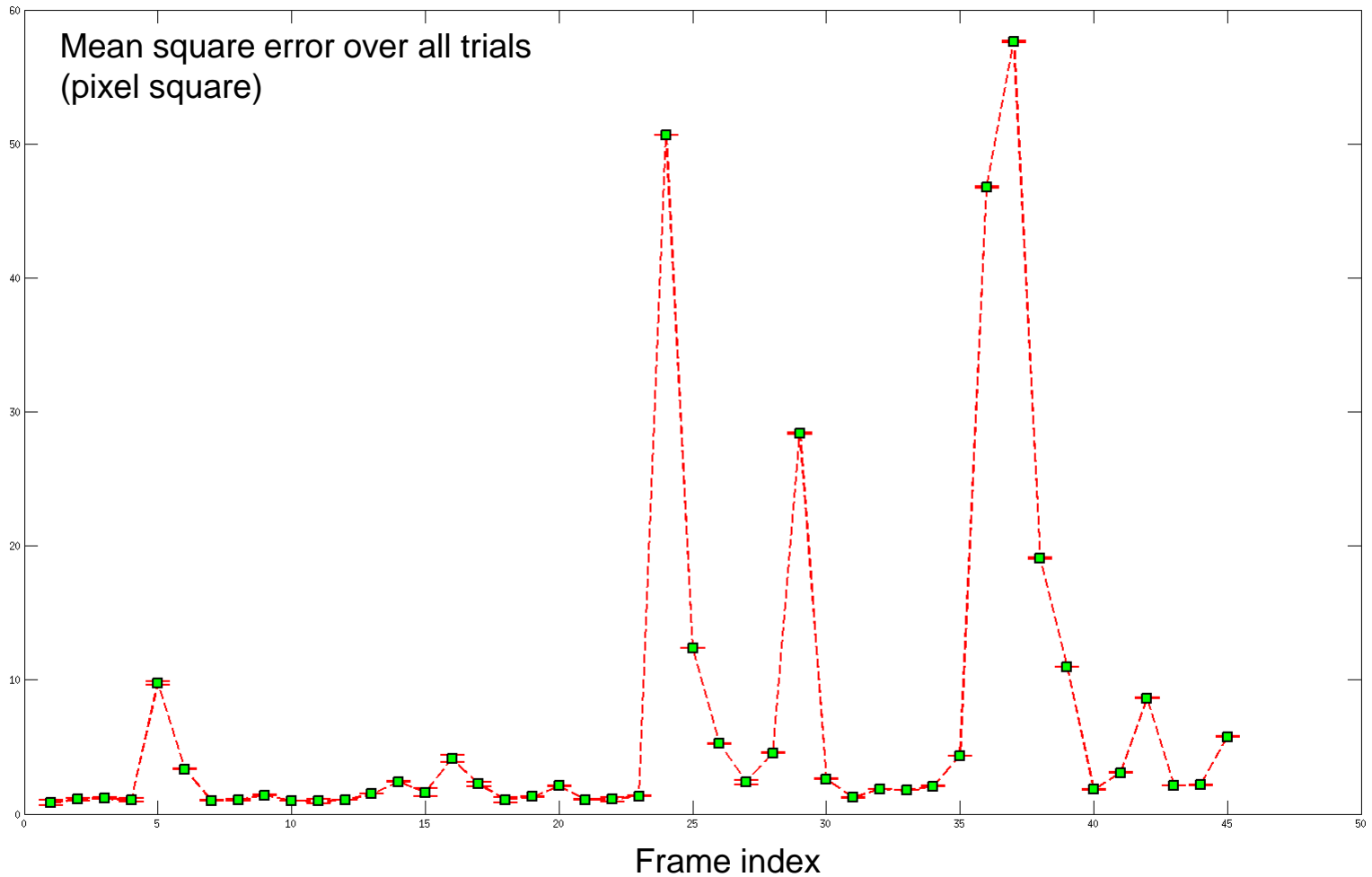
SIFT



Matched feature number in one frame

# Projection error of the hold-out testing point

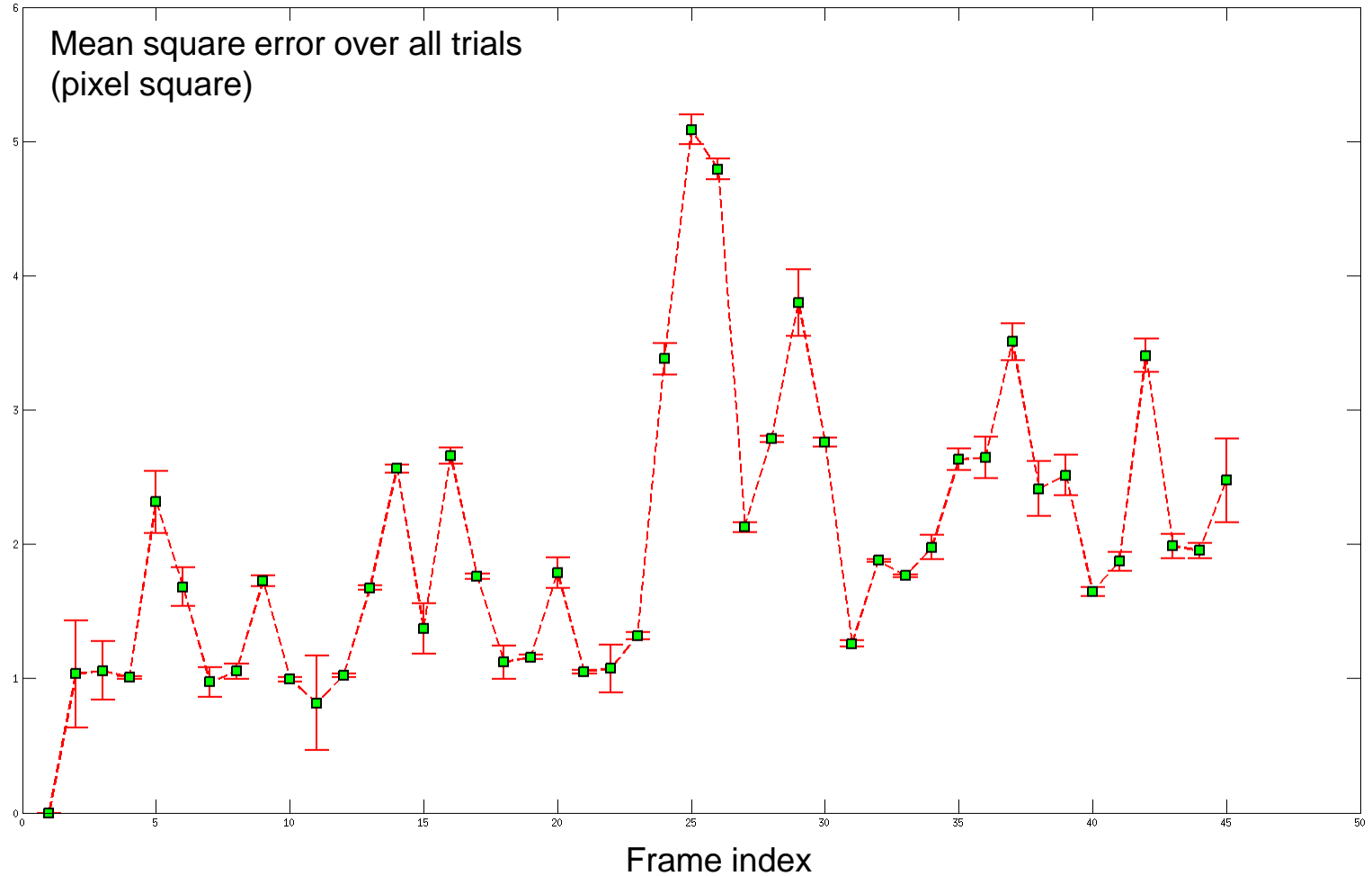
HMA



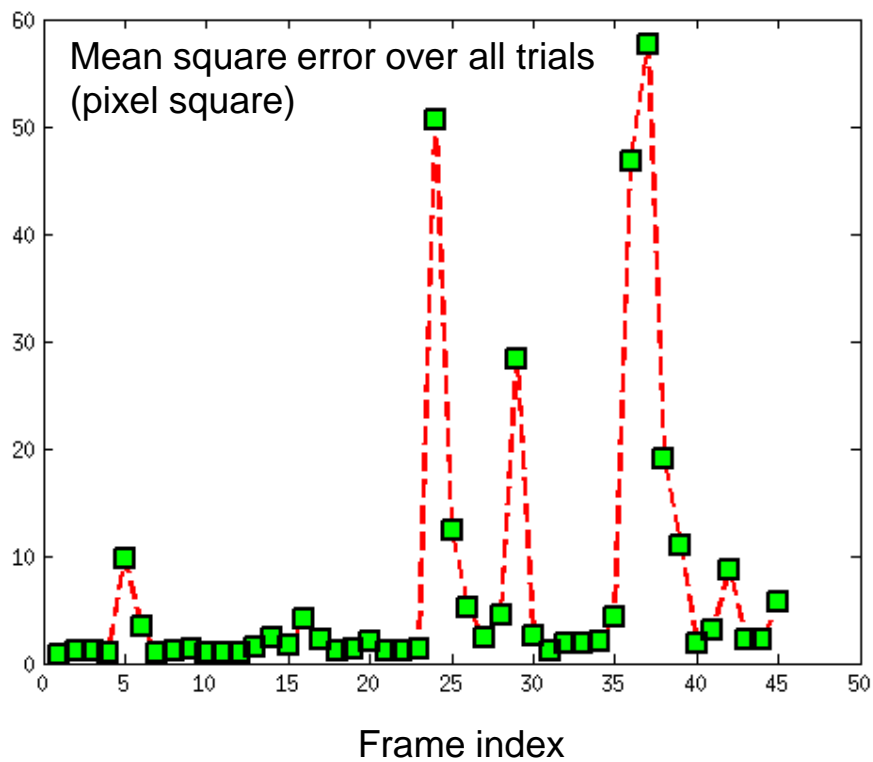


# Projection error of the hold-out testing point

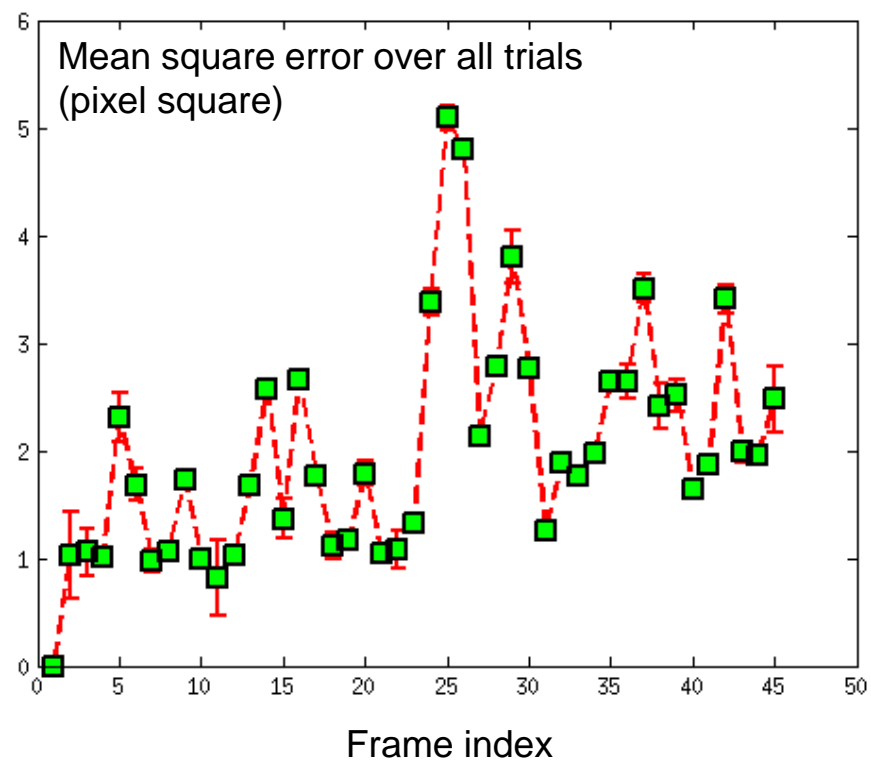
## SIFT



HMA



SIFT



# Deliverables

- **Minimum:** (Expected by 7th April - 14th April)
  1. Matlab program for robust feature matching by HMA algorithm.
  2. Feature matching validation experiments, analysis and documentation.
  3. C++ Program for motion estimation by RANSAC and 5 point algorithm.
  4. Motion estimation validation experiments, analysis and documentation.
  5. Empirical quantitative comparison of HMA and SIFT algorithms.
  
- **Expected:** (Expected by 21st April - 28th April)
  1. C++ program for image registration by Trimmed ICP algorithm.
  
- **Maximum:** (Expected by 9th May)
  1. Video-CT registration validation experiments, analysis and documentation.

# Milestones

1. Milestone 1: Program for robust feature matching by HMA algorithm.
  - Planned Date: 28th February
  - Expected Date: 7nd March
  - Status: Done
2. Milestone 2: Program for motion estimation by RANSAC and 5 point algorithm.
  - Planned Date: 14th March
  - Expected Date: 14th March
  - Status: Done
3. Milestone 3: Empirical quantitative comparison of HAM and SIFT algorithms
  - Planned Date: 2nd May
  - Expected Date: 9th May
  - Status: Done
4. Milestone 4: Program for video-CT registration by Trimmed ICP algorithm
  - Planned Date: 9th May
  - Expected Date: 12nd May
  - Status: pending

# Dependency

- Sample CT data: still not available.

# Reference

- D. Mirota, H. Wang, R. H. Taylor, M. Ishii, G. L. Gallia and G. D. Hager. A System for Video-Based Navigation for Endoscopic Endonasal Skull Base Surgery. IEEE Trans. Med. Imaging, 31(4), 963-976, 2012.
- G. Puerto, M. Adibi, J. Cadeddu<sup>1</sup> and G. L. Mariottini, Adaptive Multi-Affine (AMA) Feature-Matching Algorithm and its Application to Minimally-Invasive Surgery Images. IEEE/RSJ International Conference on Intelligent Robots and Systems (IROS), pp. 2371 - 2376, Sept. 25-30, San Francisco, California, 2011.
- G. A. Puerto-Souza and G. L. Mariottini. Hierarchical Multi-Affine (HMA) algorithm for fast and accurate feature matching in minimally-invasive surgical images. 2012 IEEE/RSJ International Conference on Intelligent Robots and Systems October 7-12, 2012. Vilamoura, Algarve, Portugal.

*Thank you! Comments!*