Robustness in Motion Averaging

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Abstract. The averaging of multiple pairwise relative motions in a sequence provides a fast and accurate method of camera motion estimation with a wide range of applications, including view registration, robotic path estimation, super-resolution. Since this approach involves averaging in the Lie-algebra of the underlying motion representation, it is non-robust and susceptible to contamination due to outliers in the individual relative motions. In this paper, we introduce a graph-based sampling scheme that efficiently remove such motion outliers. The resulting global motion solution is robust and also provides an empirical estimate of the inherent statistical uncertainty. Example results are provided to demonstrate the efficacy of our approach to incorporating robustness in motion averaging.

1 Introduction

Estimation of the camera motion from an image sequence is a well-studied problem [1]. Most conventional approaches can be classified either as *algebraic* methods involving a few frames or *optimisation* methods that solve for the global motion of the entire sequence. Examples of the former approach include epipolar and trilinear geometry representations whereas motion estimation using bundle-adjustment is an example of the later approach. While the algebraic approaches are fast, they are inherently inaccurate as they use information from only a few frames. In contrast, bundle-adjustment results in accurate solutions but is computationally expensive and also requires an accurate initial guess.

To overcome both these limitations, averaging of relative motions between image pairs was introduced in [2] and further developed in [3]. In this approach the efficiency of the algebraic approach was exploited to provide multiple relative motion estimates between image pairs that were subsequently averaged resulting in a fast, flexible and accurate estimate of the global motion. This method uses the Lie group structure of the motion representation to give a principled algorithm for averaging of relative motions. The averaging scheme has a wide range of applications including camera motion estimation, robotic path reconstruction, multi-view registration, and super-resolution. However since the method involves averaging of multiple relative motions in their corresponding Lie-algebra, it is inherently susceptible to error due to contamination by outliers. This is the property of any scheme that involves averaging of multiple observations, for example the arithmetic average of a scalar $\hat{\mathbf{x}} = \frac{1}{N}\sum \mathbf{x}_i$. A single outlier

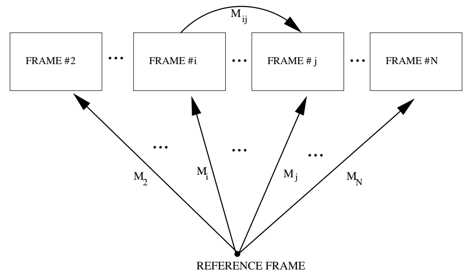


Fig. 1. The relative motions are estimated from the data. The global motion with respect to the first frame is estimated by averaging the over-determined set of relative motion constraints.

element $\mathbf{x}_i$ will cause the estimate $\hat{\mathbf{x}}$ to be grossly incorrect. In the case of relative motions, the outliers may arise due to incorrect feature correspondences. In this paper we introduce a randomised sampling scheme that can detect such outliers in the set of relative motions estimated from a sequence. While we will elaborate the approach in subsequent sections, we briefly describe our approach here. In the spirit of the RANSAC [4, 5] approach to robustness we derive global motion estimates that involve the minimal number of pairwise observations. As we shall show in Sec. 3 this is equivalent to selecting minimum spanning trees (MST) of a graph. The relative motions that survive the sampling process are data *inliers* that can be averaged resulting in accurate and robust estimates. The sampling scheme can be further applied to the inliers themselves to provide covariance estimates which is equivalent to the bootstrap approach to empirical estimation of uncertainty [6].

The rest of the paper is organised as follows. In Sec. 2 we describe the motion averaging scheme presented. Sec. 3 motivates and develops the graph-sampling based approach to outlier detection in relative motions. The result of applying this approach to a real image sequence is shown in Sec. 4. Finally, Sec. 5 presents some conclusions and directions for further work.

2 Averaging of Relative Motions

In this section we summarise previous results on motion averaging. The following analysis applies equally to both rotation and Euclidean motion estimation and a linear solution for this formulation was described earlier in [2] and developed into a Lie group representation in [3]. For N images, the globally motion can be described by $N-1$ motions, if we pick any image as the reference frame. Without loss of generality, we can assume that the reference frame is attached to the first image frame. We denote the motion between frame i and the reference frame as $\mathbf{M}_i$, and the relative motion between two frames i and j as $\mathbf{M}_{ij}$, where $\mathbf{M}_{ij} = \mathbf{M}_j\mathbf{M}_i{}^{-1}$. This relationship captures the notion of "consistency", i.e. the composition of any series of transformations starting from frame i and ending in frame j should be identical to $\mathbf{M}_{ij}$ (See Fig. 1). Due to the presence of noise in our observations the various transformation estimates would not be consistent with each other. Hence $\mathbf{M}_{ij} \neq \mathbf{M}_j {\mathbf{M}_i}^{-1}$, where $\mathbf{M}_{ij}$ is the estimated transformation between frames i and j. However we can rewrite the given relationship as a constraint on the global motion model $\{\mathbf{M}_2, \cdots, \mathbf{M}_N\}$ which completely describes the motion. The first image being the reference frame, $\mathbf{M}_1$ is an identity transformation. Since in general we have upto $\frac{N(N-1)}{2}$ such constraints, we have an over-determined system of equations.

$$\mathbf{M}_j {\mathbf{M}_i}^{-1} = \mathbf{M}_{ij}, \forall i \neq j \tag{1}$$

where the variables on the left-side are unknowns to be estimated ("fitted") in terms of the observed data $\mathbf{M}_{ij}$ on the right. Intuitively, we want to estimate a global motion model $\{\mathbf{M}_i\}$ that is most consistent with the measurements $\{\mathbf{M}_{ij}\}$ derived from the data. Thus the errors in individual estimates of $\mathbf{M}_{ij}$ are "averaged" out resulting in reduced error. It may be noted that in Eqn. 1, we are not required to use every pairwise constraint. For extended sequences, there is seldom any overlap between frames well separated in time, therefore their relative two-frame motions cannot be estimated. However we can still get a consistent solution as long as we have at least $N-1$ relative motions. In fact, the sampling procedure to be outlined in Sec. 3 exploits this property to incorporate robustness into the estimation procedure.

2.1 Averages on the Lie Group

The idea of averaging on the Lie group is at the heart of the motion averaging approach used in this paper. In this subsection we shall provide an extremely elementary summary of the properties of Lie groups and the related approach to averaging. For further details, the reader should consult [3]. A group G is a set whose elements satisfy the relationships of *associativity*, *identity* and the existence of an *inverse*. A Lie group is a group which also behaves like a smooth, differentiable manifold. Intuitively, Lie groups can be locally viewed as topologically equivalent to the vector space, $\mathbb{R}^n$ and can be locally described by its tangent-space whose elements form a Lie algebra $\mathfrak{g}$. The Lie algebra $\mathfrak{g}$ is equipped with a bilinear operation $[.,.] : \mathfrak{g} \times \mathfrak{g} \rightarrow \mathfrak{g}$ known as the Lie bracket which satisfies the property of *anti-symmetry* and the *Jacobi identity*. All finite-dimensional Lie groups have matrix representations and the bracket in this case is the commutator operation $[\mathbf{x}, \mathbf{y}] = \mathbf{xy} - \mathbf{yx}$. The Lie algebra and the associated Lie group are related by the exponential mapping. This exponential mapping and its inverse (i.e. logarithm) enable us to freely operate in either the Lie group or its associated algebra according to convenience. The motion models that we are interested in, namely three-dimensional rotations and three-dimensional Euclidean motion are elements of the Special Orthogonal $\mathbf{SO(3)}$ and Special Euclidean $\mathbf{SE(3)}$ groups respectively. For non-commutative Lie groups, the usual exponential relation $e^{\mathbf{x}} e^{\mathbf{y}} = e^{\mathbf{x}+\mathbf{y}}$ does not hold. The equivalent mapping is defined by $d : \mathfrak{g} \times \mathfrak{g} \mapsto \mathfrak{g}$, i.e. $e^{\mathbf{x}} e^{\mathbf{y}} = e^{d(\mathbf{x},\mathbf{y})}$, where $d(.,.)$ is given by the Baker-Campbell-Hausdorff (BCH) formula [7] and is the intrinsic (Riemannian) distance on the manifold representing the group. For example, for rotations $\boldsymbol{\omega_1}$ and $\boldsymbol{\omega_2}$,

$d(\boldsymbol{\omega_2}, -\boldsymbol{\omega_1})$ represents the rotation ("distance") that will take us from $\boldsymbol{\omega_1}$ to $\boldsymbol{\omega_2}$. Using this *intrinsic* distance between points on a Riemannian manifold the 'intrinsic' average can be defined as

$$\mu = \arg \min_{\mathbf{X} \in G} \sum_{k=1}^{N} d^2(\mathbf{X}_k, \mathbf{X})$$

In general this intrinsic average is preferable to other approximations as the estimation process always confirms to the underlying group structure involved. The reader can refer to [8] for further details including an algorithm for averaging elements on the group manifold. For matrix groups, the Riemannian distance is defined by the matrix logarithm operation. By using the BCH formula this distance can be approximated as $d(\mathbf{X}, \mathbf{Y}) = ||\log(\mathbf{Y}\mathbf{X}^{-1})|| \approx ||\log(\mathbf{Y}) - \log(\mathbf{X})|| = ||\mathbf{y} - \mathbf{x}||$ where $\mathbf{x}$ and $\mathbf{y}$ are logarithms of matrices $\mathbf{X}$ and $\mathbf{Y}$ respectively.

2.2 Lie Averaging of Relative Motions

The scheme for averaging relative motions is similar in spirit to the intrinsic averaging approach of [8]. Starting from the constraint $\mathbf{M}_{ij} = \mathbf{M}_j {\mathbf{M}_i}^{-1}$, by applying the first-order approximation to the Riemannian distance, we have $\mathfrak{m}_{ij} = \mathfrak{m}_j - \mathfrak{m}_i$ since $\mathfrak{m} = \log(\mathbf{M})$. Arranging in the form of a column vector, we have $\mathfrak{v} = vec(\mathfrak{m})$ implying $\mathfrak{v}_{ij} = \mathfrak{v}_j - \mathfrak{v}_i$. If we stack all the column vectors for the global motion model into one big vector $\mathfrak{V}$ we have $\mathfrak{V} = [\mathfrak{v}_2; \cdots; \mathfrak{v}_N]$. Given this unified vector representation for the global motion model, we have

$$\begin{aligned} \mathbf{M}_{ij} = \mathbf{M}_j {\mathbf{M}_i}^{-1} &\Rightarrow \mathfrak{m}_{ij} = \mathfrak{m}_j - \mathfrak{m}_i \\ \Rightarrow \mathfrak{v}_{ij} = \mathfrak{v}_j - \mathfrak{v}_i &= \underbrace{\left[\cdots - \mathbf{I} \cdots \mathbf{I} \cdots\right]}_{=\mathbf{D}_{ij}} \mathfrak{V} \end{aligned} \tag{2}$$

where $\mathbf{I}$ denotes an identity matrix. While Eqn. 2 denotes a single relative motion in terms of the global motion model, we can stack all the relative motion vectors $\mathfrak{v}_{ij}$ into one big vector $\mathbb{V}_{ij} = [\mathfrak{v}_{ij1}; \mathfrak{v}_{ij2}; \cdots]$ where $ij1, ij2$ etc. denote different relative motion indices. Similarly we can stacked $\mathbf{D} = [\mathbf{D}_{ij1}; \mathbf{D}_{ij2}; \cdots]$ leading to

$$\begin{aligned} &\mathbf{M}_j {\mathbf{M}_i}^{-1} = \mathbf{M}_{ij} \\ &\quad \rightsquigarrow \mathbf{D}\mathfrak{V} = \mathbb{V}_{ij} \Rightarrow \mathfrak{V} = \mathbf{D}^{\dagger}\mathbb{V}_{ij} \end{aligned} \tag{3}$$

where $\mathbf{D}^{\dagger}$ is the pseudo-inverse. This results in the following iterative scheme :

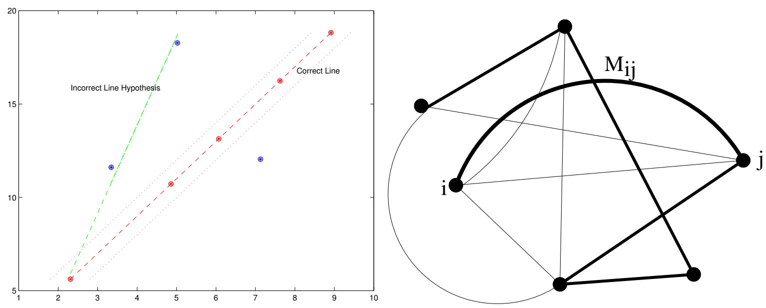
A1 : Algorithm for Relative Motion Averaging
Input : $\{\mathbf{M}_{ij1}, \mathbf{M}_{ij2} \cdots, \mathbf{M}_{ijn}\}$ (n relative motions)
Output : $\mathbf{M}_g : \{\mathbf{M}_2, \cdots, \mathbf{M}_N\}$ (N image global motion)
Set $\mathbf{M}_g$ to an initial guess (Linear solution in [2])
Do
$\Delta\mathbf{M}_{ij} = \mathbf{M}_j{}^{-1}\mathbf{M}_{ij}\mathbf{M}_i$
$\Delta\mathfrak{m}_{ij} = log(\Delta\mathbf{M}_{ij})$
$\Delta\mathfrak{v}_{ij} = vec(\mathfrak{m}_{ij})$
$\Delta\mathfrak{V} = \mathbf{D}^{\dagger}\Delta\mathbb{V}_{ij}$
$\forall k \in [2, N], \mathbf{M}_k = \mathbf{M}_k exp(\Delta\mathfrak{v}_k)$
$Repeat\ till\ ||\Delta\mathfrak{V}|| < \epsilon$

While further details cannot be provided here due to space constraints, for our purposes it is sufficient to note that we can use the above approach to accurately average the relative motions on the appropriate Lie group representation.

3 Sampling on the view-graph of relative motions

While the algorithm described in Sec. 2 is an effective scheme for estimating the global camera motion from multiple estimates of relative motions, it suffers from the limitation of being non-robust. Consider a scenario where an individual relative motion is corrupted, say, due to incorrect correspondences used in the estimation of epipolar geometry. This would result in an incorrect estimate for $\mathbf{M}_{ij}$. When this incorrect measurement is incorporated into the averaging scheme of Algorithm **A1**, the entire result would be corrupted. Therefore, we require a procedure that would identify outliers in the set of relative motions and discard them prior to the averaging of these measurements using the Lie-algebraic averaging scheme.

A well-known approach for incorporating robustness in computer vision is the Randomised Sampling Consensus (RANSAC) method [4, 5]. This randomised scheme has been shown to have desired statistical properties in that it can effectively identify data outliers that do not satisfy a given geometric model. The idea behind RANSAC is illustrated in Fig. 3(a) where we have points that lie on a straight line along with some outlier points. If we were to seek the least squares fit for the full set of data points the resulting line solution would be grossly incorrect as it would average over the correct points and the outliers. The RANSAC approach to detecting outliers works by generating solutions that use the *minimal* number of data points. Since a line can be defined by two non-identical points, we randomly select a pair of points and use the line passing through them as our *hypothesis*. All points that fall within a pre-specified distance (say D) from this hypothesis line are declared to fit the line. In Fig. 3(a) this range is indicated by the two dotted lines around the true line. For each trial, we count the number of points that fall within this bounding region. For a given number of trials, the hypothesis with the maximum number of points within the bounding region is selected and all points within the bounding region are declared as *inliers* and those outside this region



(a) RANSAC Example (b) Viewgraph of relative motions

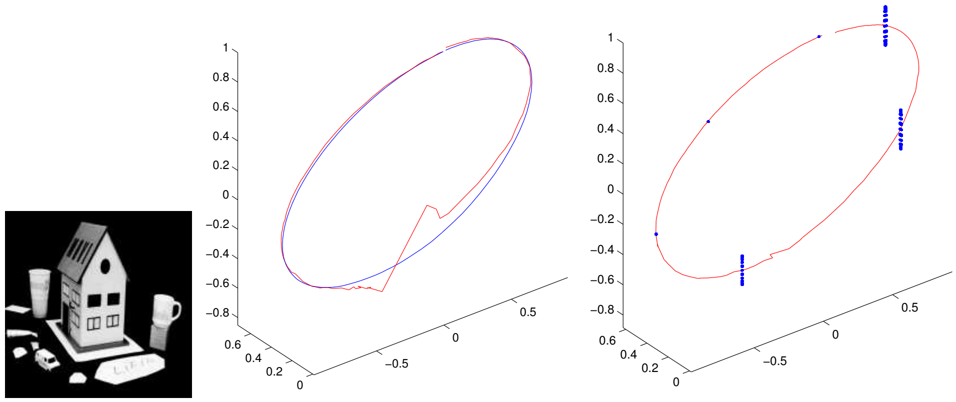
Fig. 2. (a) illustrates the RANSAC approach. Some points fall on a line whereas others are outliers. (b) shows a view graph representing relative motions identified by the vertices. Each edge represents an estimated relative motion between the two vertices. The bold edges represent a minimum spanning tree (MST).

are classified as outliers. The line estimate is now obtained by least-squares fitting of all inliers. The green line in Fig. 3(a) indicates a line hypothesis that includes outliers, but the score for this line will always be less than that for a true hypothesis, implying robustness to as many as 50% of data outliers.

3.1 A Robust Algorithm for Motion Averaging

In the case of motion models that describe the global motion we can develop a sampling method similar in spirit to RANSAC. We can describe the information of all the relative motions estimated in a sequence in a graph. Consider a graph $G = (V, E)$ where V is the set of vertices and E the set of edges. Each vertex of the graph denotes an individual image, resulting in N vertices. If we are able to estimate the relative motion between a pair of images i and j we add an edge E_{ij} between the said vertices. Such a representation of relative motions is called a view-graph and capture all the information available and has also been used to solve other problems, for instance see [10]. We show an example of such a view-graph in Fig. 3(b). The absence of an edge connecting two vertices implies that the relative motion between those two vertices in not available. To keep our analysis simple, we assume that we are given a set of relative motions $\{\mathbf{M}_{ij}\}$ and no more information to indicate their reliability. Therefore no weight information is used for the edges, i.e. all edges have the same weight. Moreover the resulting graph is bidirectional.

Since the RANSAC approach requires a *minimal* solution we need such a solution that can capture the global motion for the image sequence. Since the relative motions between images are represented by edges on the view graph it will be immediate obvious that the minimal solution for our problem is given by the *minimum spanning tree* (MST) of the graph G. When the graph G has a single connected component, the minimum



(a) MOVI data (b) Non-robust Averaging (c) Robust Averaging

Fig. 3. (a) shows one image from the MOVI sequence; (b) shows the results from [9] and the incorrect estimate due to outliers; (c) shows our estimate after automatic removal of the outliers. The covariance is shown in an exaggerated form for visualisation. See text for details.

spanning tree is a set of edges such that every vertex in V is reachable from every other vertex in V and the total weight of all edges in the tree is minimum. For a graph with N vertices, the minimum spanning tree always has $N-1$ edges [11]. In Fig. 3(b) we have a graph representing the relative motions available and an MST is shown in bold edges. Since in an MST every vertex is reachable from any vertex, given an MST and the corresponding relative motions we can solve for the global motion model [1]. Now given an MST on the view-graph G, we can solve for the global motion model $\{\mathbf{M}_i\}$ and consequently every relative motion can be compared to this solution. For example, if the global motion model for an MST is $\mathbf{M} = \{\mathbf{M}_2, \cdots, \mathbf{M}_N\}$ and the relative motion between vertices i and j is given by $\mathbf{M}_{ij}$, then the "distance" of this edge from the global motion model is given by $d(\mathbf{M}_{ij}, \mathbf{M}_j{\mathbf{M}_i}^{-1})$.

Each MST of the view-graph represents a model hypothesis, i.e. a solution for the global motion. Given a pre-specified distance threshold, we can count the number of relative motions (i.e. edges) that fall within this distance from the global motion. Thus for each MST, we count the number of *inliers* in the original set of relative motions. This is repeated for a given number of trials and the MST with the maximum number of inliers declared the winner. Subsequently we use Algorithm **A1** to solve for the global motion using all inliers, resulting in an accurate solution that is also robust to the presence of outliers. Since each edge has the same weight and every MST has $N-1$ edges, the

[1] Consider a case where an MST has edges between vertices $\{1, 2\}$ and $\{2, 3\}$ but not between $\{1, 3\}$. In such a case we can reach vertex 3 from vertex 1 via vertex 2. Thus the relative motion $\mathbf{M}_{13}$ is given by $\mathbf{M}_{13} = \mathbf{M}_{23}\mathbf{M}_{12}$.

total weight for all spanning trees is the same. Therefore for our problem we need to generate many spanning trees for the view-graph. This can be achieved by randomising a *depth first search* (DFS) on the graph G. The DFS is a standard algorithm for systematically creating a tree given a starting vertex of a graph. In our modification, in each instance we start at a random vertex and at every parent vertex, we randomly pick the next adjacent vertex to be visited in the search process. For each run of this procedure we generate a spanning tree that is used in the RANSAC procedure as described above.

While in this paper we have chosen to ascribe equal weights to all edges, in the presence of appropriate measures of reliability for each individual relative motion estimate, we can easily incorporate that information as a weight on the view-graph G. For example, if $\mathbf{e}_{ij}$ is the root mean squares error for the estimation procedure for relative motion $\mathbf{M}_{ij}$ we can choose the weight for the edge connecting vertices i and j as $\mathbf{w}_{ij} = {\mathbf{e}_{ij}}^2$. In such a scenario the minimum spanning tree procedure will seek to minimise the sum of the edge weights, which is equivalent to a minimal solution for the global motion model with the least squared error for all the measurements used. However since now the edge weights are not identical the procedure for generating a randomised MST has to utilise the weight information. The algorithm in [12] is a randomised linear time algorithm for generating MST's and can be used as the MST-generator for the RANSAC procedure. While this approach will be considered in subsequent work, in this paper we shall use an unweighted graph so as to focus on the basic idea of our approach. Thus our method can be summarised as :

A2 : RANSAC Algorithm for Robust Motion Averaging
Input : $\{\mathbf{M}_{ij1}, \mathbf{M}_{ij2} \cdots, \mathbf{M}_{ijn}\}$ (n relative motions)
Distance threshold $\mathbf{D}_0$ and number of trials $\mathbf{T}$
Output : $\mathbf{M}_g : \{\mathbf{M}_2, \cdots, \mathbf{M}_N\}$ (N image global motion)

- Set G : view-graph of relative motions
- Generate MST $\mathbf{e} = MST(G)$
- Solve for global motion $\mathbf{M}_{mst}$ using MST $\mathbf{e}$
- Count number of relative motions within distance $\mathbf{D}_0$ of $\mathbf{M}_{mst}$
- Repeat for $\mathbf{T}$ trials and select MST with maximal count
- Discard relative motions that are outliers for this MST
- Using the inliers solve for $\mathbf{M}_g$ using Algorithm **A1**

4 Examples

To demonstrate the efficacy of robust motion estimation we present an experiment on the well-known MOVI house sequence[2]. This sequence consists of 118 images of a house model and other objects rotated on a turn-table. Fig. 3(a) shows one image from the sequence. As a baseline for comparison, we use the point correspondences of this

[2] We are unable to present an analysis of the method's performance on synthetic data due to space constraints.

sequence used in [9].[3] For every possible image pair with more than 20 correspondences we estimated the epipolar geometry using the Eight Point Algorithm of [13]. The camera calibration was estimated using the method outlined in [14] and subsequently the epipolar geometries were decomposed into rotations and translation directions. Instead of applying our approach to the entire set of relative rotations we used a sliding window of 10 images with a shift of 5 images. In other words, we applied the outlier detection algorithm to images 1 to 10, 6 to 15, etc. The RANSAC threshold was set to $0.25°$ and 10000 trials were used. Out of an original set of 2209 relative geometries, only 1130 were selected as inliers. The results of using our method are shown in Fig. 3(b) and (c). In all cases we represent the result as the location of the camera's viewing direction. In Fig. 3(b) the viewing directions of the result of [9] are shown in solid line and the results of an average of all 2209 relative motions is shown as a dashed line. As can be seen there are gross errors in the averaging result due to the presence of outliers. In comparison the motion shown in Fig. 3(c) is the result of our averaging scheme applied to the 1130 inliers detected. Here the correct nature of the sequence is captured implying that outliers were correctly identified and removed, thus demonstrating the effectiveness of our approach to robust motion averaging [4]. In addition to using graph-sampling to identify outliers we can also apply the same MST-based sampling approach on a graph representing all the inliers. This results in a different solution for each MST generated and these solutions represent an empirical estimate of the covariance in our estimation process. This is a principled approach in statistics known as *bootstrap*, further details can be found in [6]. In our case we generate 100 such estimates and the covariance of viewing directions were computed. In Fig. 3(c) we show the covariance of the viewing direction for 6 images in the entire sequence. The covariances were exaggerated 25 times to enable easy visualisation. As can be observed, for some images there is larger variance of the viewing direction in a direction orthogonal to the viewing direction of the camera. This implies that for these frames the uncertainty of the rotation estimate is higher in a direction orthogonal to the viewing direction. The ability to estimate the covariance in this manner can be used in further analysis and improvement of the estimates.

5 Conclusions

In this paper we have presented a RANSAC style sampling approach to incorporate robustness into motion averaging algorithms which accurately identifies statistical outliers in a set of relative motions. The effectiveness of the method was demonstrated on a motion estimation problem. Future work will include effective utilisation of confidence information for the relative motions which can be used in the randomised MST approach of [12] and the development of this robust motion averaging approach for image

[3] Thanks to Bogdan Georgescu for providing us with his correspondences and motion estimates for this sequence.

[4] While we do not have any ground truth for this sequence, our results for rotation estimation are on an average within 2 degrees from the estimate of [9]. This is a very good fit given that the estimation of the eight-point algorithm is intrinsically error prone.

registration and super-resolution, and robotic path planning approaches like *Simultaneous Localisation and Mapping* (SLAM).

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