Genetic Algorithms for Automatic Registration of Laser Scans with Imperfect and Subdivided Features (GAReg-ISF)

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Summary: The easy on-site application and the possibility of high quality post processing of terrestrial laser scans make their use highly attractive for architectural, archaeological and sculptural documentation. In this paper we present a strategy for handling the fully automatic registration of point clouds characterized by significant noise level, imperfect geometry and occlusions.

To handle these datasets we propose to work with both imperfect and subdivided features and to divide the pair-wise matching process into three subsequent stages. First rough feature registration finds auspicious regions in search space, next Genetic Algorithms are used to exploit those areas and form approximate solutions which are then refined in a third step.

By combining imperfect and subdivided features with Genetic Algorithms in general feature detection, pair-wise scan matching and multi-view registration, we are able to show globally consistent registrations of real world scenes.

Zusammenfassung: *Vollautomatische Registrierung von Laserscans mit Genetischen Algorithmen sowie genäherten und unterteilten Merkmalen.* Die einfache Vor-Ort-Anwendung und die Möglichkeit einer hochwertigen Weiterverarbeitung terrestrischer Laserscans machen deren Einsatz bei architektonischen, archäologischen und skulpturalen Dokumentationen überaus interessant. In diesem Artikel präsentieren wir eine Methode zur vollautomatischen Registrierung von Punktwolken, welche durch einen signifikanten Rauschpegel, unvollendete Geometrie sowie Verdeckungen gekennzeichnet sind.

Um diese Datensätze zu verarbeiten, verwenden wir genäherte und unterteilte Merkmalen und führen die paarweise Registrierung der Scans in drei aufeinander folgenden Schritten durch. Zuerst erfolgt eine Grobregistrierung mittels Merkmalen um erfolgversprechende Bereiche im Suchraum ausfindig zu machen. Im nächsten Schritt werden Genetische Algorithmen verwendet, um diese Bereiche zu erforschen und Näherungslösungen für die im dritten Schritt durchgeführte, abschließende Verfeinerung zu bilden.

Durch die Kombination genäherter und unterteilter Merkmale mit Genetischen Algorithmen in der Merkmals-Erkennung, der paarweisen Scan-Zuordnung und der Multiview-Registrierung können global richtige Registrierungen von realen Scans erstellt werden.

1 Introduction

Terrestrial laser scanners have become very popular for fast scene acquisition in the last decade. The need of having several stations when scanning complex objects, in order to avoid hidden or missing parts, leads to the task of registering the single scans. Setting up artificial spherical, cylindrical or plain targets into the scene is a common (and robust geodetic) way to connect the scans (Hanke et al. 2006). In many applications, however, this is not possible or useful for different reasons and the registration of point clouds using only object's features comes in as a popular approach. To enable this non linear spatial transformation, an (often manual) selection of at least 3

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common points has to precede the final registration process to provide approximation values for shift and rotation. This selection, however, is time consuming and error-prone and should, thus, be avoided by using a robust and automated algorithm. One of the possible solutions is proposed in the following.

1.1 *Genetic Algorithms*

In the present paper the principles of biological processes are used to create a computer-based simulation of natural evolution, the so-called Genetic Algorithm (GA). GAs became popular through the work of (Holland 1975) and can be characterized as heuristic search strategies. They are suitable for problems where search space is large or poorly understood and no simple mathematical analysis of the solution is available. Due to their simple and clear structure, GAs can easily be adapted to arbitrary kinds of constraints and objectives. In this paper we are working with a GA by (Reed et al. 2005) originally developed for tunnel design optimisation. With only a few modifications we are able to use the same algorithm for laser scan registration; a proof of the great flexibility of GAs.

Natural evolution can be seen as optimisation process and, according to Charles Darwin, is mainly characterised by one keyword: *natural selection*. Natural selection, also known as "survival of the fittest", means that individuals with higher quality – called *fitness* – have a higher probability of surviving and reproduction than those with lower fitness. The so-called *fitness function* evaluates all individuals of a population and calculates their fitness. The specific characteristics of each individual are stored in chromosomes, or more precisely in its subparts named genes. Genes are essentially for reproduction characterised by both *mutation* (substitution of single gene parts) and *cross-over* (merging of two or more genes). By translating these processes into mathematical algorithms we are able to create a simple but effective tool for optimisation. Hereby a single *individual* is equal to a mathematical solution, while a *population* refers to a group of possible solutions. Equally to natural evolution, GAs too have an iterative structure, performed in single steps known as *generations.*

The initialisation of a GA is done by creating a start population either out of a pool of randomly generated solutions or a given set of rough solutions. Afterwards an iterative process as shown in Fig. 1 is initiated, based on reproducing new individuals by mutation and cross-over, evaluating their fitness and implementing natural selection; this is done until either a certain number of generations or a pre-defined termination condition is reached.

The use of GAs is often "computationally expensive" and, as in nature, also simulated evolution usually can't provide neither perfect nor exact results, but good approximations. It can however be said that GAs are a good choice for complex or unknown problems where other approaches may fail.

Genetic Algorithms were already used for the registration of close-up objects for example by (Brunnström & Stoddard 1996), (Cordón et al. 2003), (Silva et al. 2005) or (Lomonosov et al. 2006). We propose to implement an adapted version of these approaches in the classical registration process. This helps

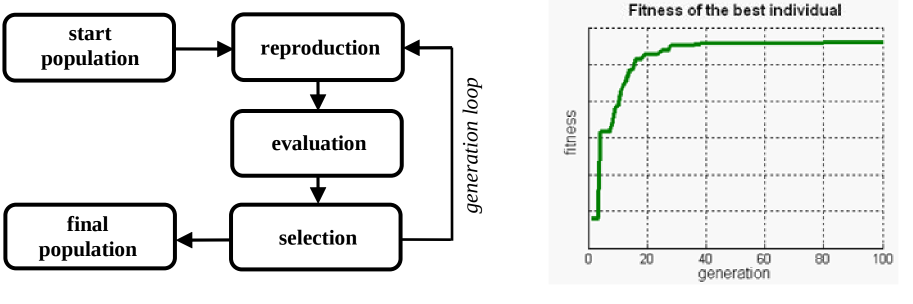

Fig. 1: Left: Structure of a Genetic Algorithm (GA); Right: Fitness progress of a typical GA.

to maintain robustness and computational performance also when registering scans of bigger sized objects characterised by a notably increased number of points, a significant noise level and occlusions.

1.2 *Imperfect Features*

Laser scanners are able to capture thousands of points a second, which allows a detailed representation of scenes in a fairly short amount of time. For registration purposes datasets have often to be reduced to a more usable form. This can either be done by finding characteristic features inside the scans or by simplifying the point cloud as seen, e. g., in (MOENNING & DOGSON 2003).

Features have the advantage that they can often be robustly detected and contain useful information such as barycentres or normal directions and radii. This can be used to ensure a robust pair-wise alignment of two scans.

It might however be the case that we receive datasets where point density is too low or noisy for exact feature detection; a typical example for noisy data is grassland. While scanning such landscape, the laser ray hits partially blades of grass and partially the ground. An approach to smooth noisy point clouds while recovering the edges of the original surface can be found in (LANGE & POLTHIER 2005).

Further problems that may be encountered when acquiring real-life scenes are shown in a simplified way in Fig. 2. While on one hand the number of scanning stations has often to be reduced to safe precious time, on the other hand occlusions - produced either by the object itself or obstacles between the laser scanner and the object - arise in an increased quantity. Hereby edges and borders may emerge differently when scanning from different stations due to their often round, bevelled or simply their rough shape. The fact that the overlapping parts are lying on parallel planes makes processing just more difficult. Moreover, data may be partially missing or too fragmentary for further processing. Different feature types, however, react with different sensibility to the above mentioned effects. Borders and edges, for example, are more likely to be influenced than other features such as planes. In this paper these datasets are referred to as "imperfect" which means that we can work with it, but we have to keep in mind that they might be noisy or even misrepresent the original scenery.

1.3 *Subdivided Features*

Generally a high number of features can be detected in typical scenes; it does however happen, e. g., with larger features such as planes, that due to unfavourable occlusions, noise or lack of information, the needed correspondences get rather poor. To overcome this problem we propose to subdivide features into smaller subparts; those subdivided features which are not influenced by occlusion anymore can then be successfully matched.

As (BRENNER & DOLD 2007) and (BRENNER et al. 2008) show, planar structures can successfully be used for registration. (VON HANSEN 2007) uses a similar approach: After the scenery has been segmented according to a regular

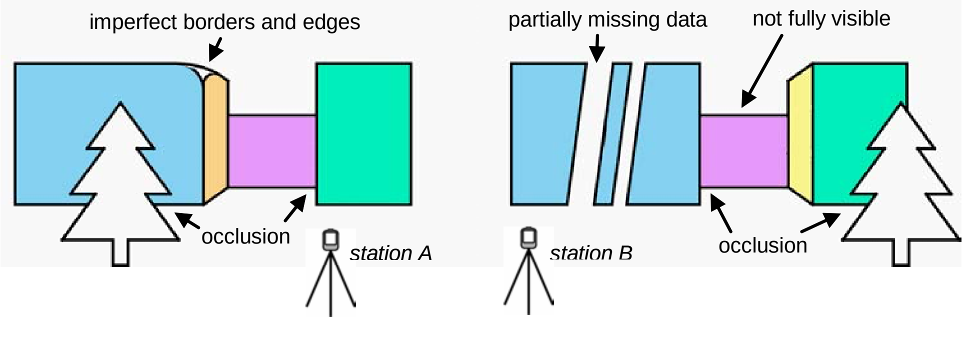

Fig. 2: Typical problems in data acquisition.

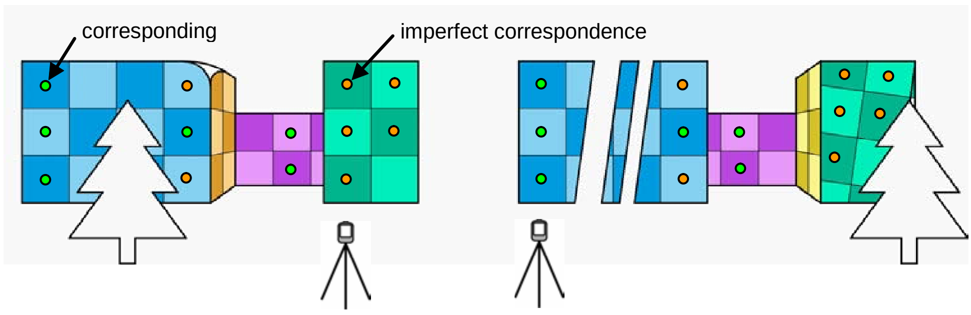

Fig. 3: Subdividing and matching the acquired features.

3D raster, RANSAC plane detection is applied to all raster cells which are then grouped to larger planes using neighbourhood and co-planarity checks.

We suggest evolving the idea of raster cells during coarse registration and using the additional information of the larger planes for their subdivision: The principal directions of the planes can be calculated; they are used to create a local coordinate system for each plane which is then employed for dividing the planes into smaller subparts as shown for example in Fig. 3.

One of the main advantages of our approach is that whenever a plane is fully visible and detectable equally in two scans, by using the principal directions as local coordinate system for subdivision the resulting subplanes will have corresponding values and barycentres.

If a plane is, however, not fully visible and also in cases where the principal directions are ambiguous, subdivision can result in a differing grid; in this case the barycentres of the subplanes might contain in the worst case a maximal distance error of half the raster cell diagonal and can be handled the same way as imperfect features ("imperfect correspondence").

2 Registration Strategy

The proposed automatic registration of laser scans without artificial targets consists of three parts. As illustrated in Fig. 4, in the first step all scans are analysed, and the detection and subdivision of features (planes) is used to describe characteristic areas in each scan.

Afterwards pair-wise scan registration is initiated, whereby the subdivided and imperfect features detected in the first step are combined to create a start population for a Genetic Algorithm, which then reduces and refines the possible registration solutions. Since a typical

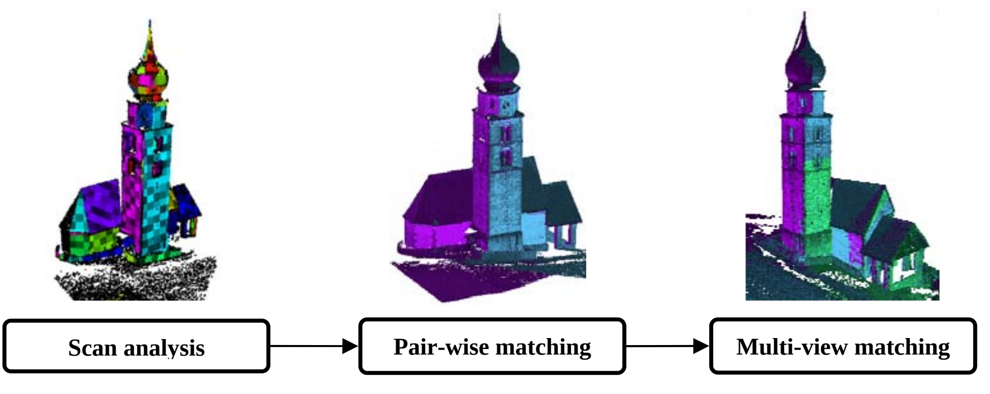

Fig. 4: Automatic registration strategy.

real-life scene does not consist of features such as planes only, the gathered solutions are supplied to another GA performing free-form matching with a reduced point cloud. By applying these steps in a clearly targeted way, speed and robustness of the registration process can be significantly increased. In the last step the so-called multi-view matching is used to reassemble the single scans to a globally consistent solution. As seen in Fig. 4 our algorithm is able to successfully register the scans of the church of Seis, Italy (Burger & Thaler 2008), captured with a Trimble GX laser scanner.

2.1 *Scan Analysis*

Our input datasets consist of single points and if available also intensities or colour information. All steps are executed directly on the point clouds and no additional structure such as a triangulated mesh is necessary. Since the algorithm should work almost independently of the object size we adopt the idea stated in (Gelfand et al. 2003). We scale the point clouds uniformly so that the average distance of the points from the mass centre is 1; hereby the global scaling factor is set accordingly to the first analysed scan. This helps to make sure that registration thresholds are within similar dimensions. To keep computing low the original point clouds – consisting of up to millions of points – are reduced by random sampling and a data-pyramid is constructed; this enables to access different levels of resolution in a very efficient way. Further we use a kd-tree structure to gather the neighbours of each point on the surface and use them for principal component analysis (PCA) to find the tangent plane and the normal vector in each point (Hoppe et al. 1992).

As (Pauly et al. 2003) show, this approach can further be evolved by using the resulting eigenvalues for the estimation of the change in geometric curvature named *surface variation*. Multi-scale surface variation however has not improved significantly our registration process.

According to (Vieira & Shimada 2005) we use the surface variation to identify seed points for surface extraction through region growing. They show that the proposed method is even able to extract non-rational bicubic Bézier surfaces; for now however we use the approach for plane detection only.

2.2 *Pair-wise Matching*

The registration of laser scans – an overview of popular registration methods is found in (Salvi et al. 2007) – can be seen as search problem in six-dimensional space. This can be solved either by feature matching – which means omitting all additional geometric information that can not be assigned to one of the used features – or by free-form matching typically done on reduced point clouds as they are generally not restricted to any geometric shape.

To achieve both robustness and flexibility we propose – as shown in Fig. 5 – to extend classical coarse and fine registration by implementing a third step as a combination of feature matching and free-form matching.

First feature matching with an extension for imperfect and subdivided features is employed for coarse registration. Generally three pairs of corresponding features with linearly inde-

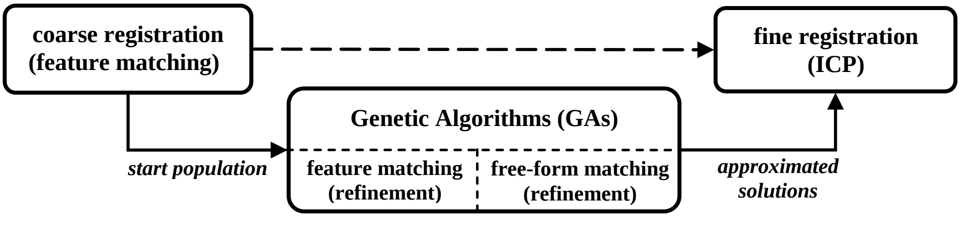

Fig. 5: Pair-wise matching strategy using Genetic Algorithms (GAs) – ICP: iterative closest point algorithm.

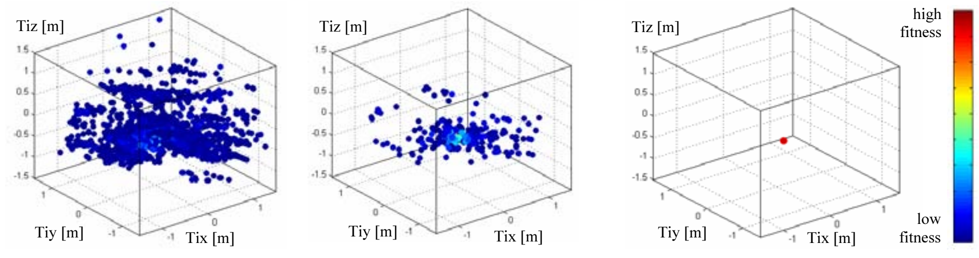

Fig. 6: Convergence of a Genetic Algorithm (GA): From left to right: Displacement components (T_{ix}, T_{iy}, T_{iz}) of the population in generation 1, 10 and 50.

pendent normal vectors are necessary to form a solution when working with planar surfaces. According to (He et al. 2005) the barycentres of a pair of matching planes can be used to compute the registration so that only two feature pairs are necessary. As stated in (Brunnström & Stoddard 1996) using four invariants – the barycentres' distances, pairwise relative orientations of two normals and an additional twist angle – can further reduce the number of possible combinations. By implementing imperfect and subdivided features, in the worst case one plane – which can be partly occluded – is enough to create rough solutions. These solutions are then supplied as start population to a GA which refines the feature matching results and uses a reduced point cloud for free-form matching to include as much geometric information as possible in the early registration process.

At the moment only the best solution of each pair-wise matching – determined by the GA's fitness function – is used for the final multi-piece matching; we are however working on implementing niching techniques so that the population itself is able to adapt the search process dynamically to the specific requirements and to exploit different solutions simultaneously.

Our GAs use a real-coded representation of the possible solutions comparable to (Cordón et al. 2003). We use a single individual X_i in the form of $X_i = (Q_i, T_{ix}, T_{iy}, T_{iz})$, whereby Q_i represents the quaternion of the rotation and T_{ix}, T_{iy}, T_{iz} are the components of the displacement vector.

In each generation new individuals are formed either by creating a *mutant* (with a 10% probability) or through a *cross-over* (90% probability). Additional *mutation* is applied on all new individuals with a 5% probability. These values were selected according to (Silva et al. 2005) and according to our own test results. While mutants and mutation force the population to spread out and explore the search space, cross-over is mainly used to concentrate the population in auspicious regions and improve existing solutions.

A typical convergence process is illustrated by the populations' displacement components (T_{ix}, T_{iy}, T_{iz}) in Fig. 6 where, after initially shifting the centres of mass to the origin, the point sets are scaled so that the average distance of points from the origin is 1.

The mutant operation selects an already existing parent individual X_1 by roulette-wheel-selection; hereby individuals with higher fitness are chosen more probably by assigning them a larger space on the roulette-wheel. Next randomly selected genes of the parent X_1 are partly altered, and the result is stored in a new individual X_{new}. Cross-over is done by merging the genes of two selected parent individuals X_1 and X_2 and creating two new individuals $X_{new,A}$ and $X_{new,B}$ which are formed by spreading the parents genes randomly over the new individuals.

We propose to run the GA twice: at first it runs for 50 generations using feature matching to refine the possible combinations; in the second run the same GA works with the remaining solutions for another 50 generations doing free-form matching directly on the original but reduced point cloud. Although generally one run would be enough to identify and refine the good solutions, two consecutive algorithms are used in order to raise robustness.

Our fitness function – similar to (LOMONOSOV et al. 2006) – forces the GA to increase the amount of overlapping parts and, at the same time, to reduce their distance error. After evaluating all individuals with the fitness function we use a binary tournament, where repeatedly two individuals are randomly selected from the population and – according to their fitness – the better one is selected for the next generation.

In the last stage we refine the gathered solutions with the well-known iterative closest point algorithm (ICP) proposed by (BESL & MCKAY 1992). To improve robustness and stability of the algorithm we use the geometrically more stable version of (GELFAND et al. 2003). An overview of other efficient variants of the ICP algorithm can be found in (RUSINKIEWICZ & LEVOY 2001).

2.3 *Multi-view Matching*

A lot of investigation has already been done in multi-view matching, also known as multi-piece matching (HUANG et. al 2006). Similar to (PULLI 1999), we take the pair-wise matching results and order them according to their quality. The best matching pair is fixed and iteratively another view is added to the fixed set. In order to ensure a globally consistent reconstruction of all views, additional checks are used after every step to see if penetration effects are encountered when adding the next view. If they reach a certain threshold, the view is skipped and the next views are handled. Moreover, an inner loop ensures that the fixed set is realigned in every iteration step.

3 Experimental Results

To prove the potential of our registration strategy we processed a number of real-life scenes. All scans were neither pre-processed nor ordered accordingly to their neighbourhood relationship. The results are shown in the following.

3.1 *Agia Sanmarina, Greece*

One dataset we tested our registration strategy on is the dataset of the Agia Sanmarina church in Greece, scanned with a Cyra Cyrax 2500 laser scanner. The eight point clouds were provided by the ISPRS working group V/3 on terrestrial laser scanning (www.commission5.isprs.org/wg3/), whereas the reference values for the comparison were taken from (BAE 2006).

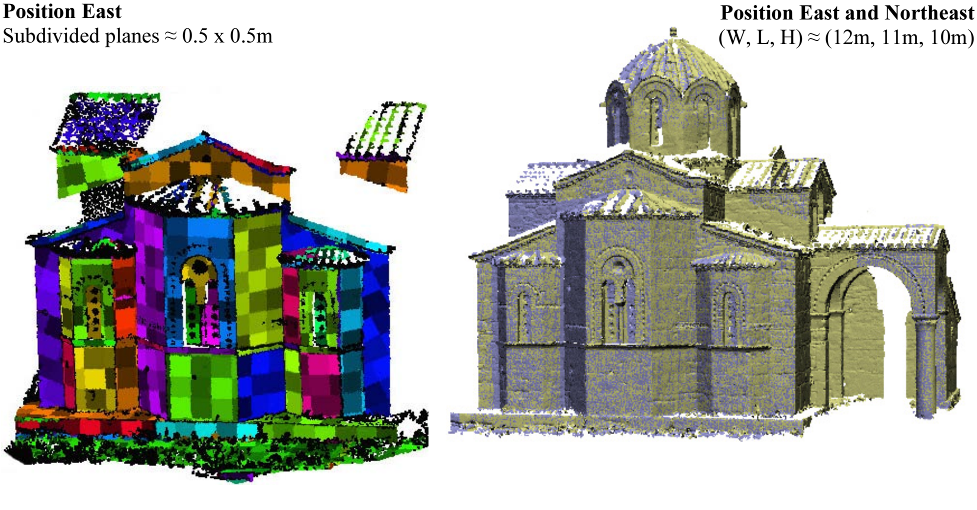

Fig. 7: Registration of position East and position Northeast: Left: Subdivided features of position East; Right: Pair-wise matching result (smoothed and shaded view).

Tab. 1: Registration results of position East (identity transformation) and Northeast: Left: Pair-wise matching results of direct georeferencing method, Leica Cyclone, GP-ICPR (Bae 2006) and GAReg-ISF; Right: Differences to direct georeferencing method.

	Estimated transformation parameters			
	Direct georef.	**Leica Cyclone**	**GP-ICPR**	**GAReg-ISF**
ω [°]	**5.2348**	5.2084	5.2353	5.2272
φ [°]	**42.5217**	42.5260	42.5466	42.5457
κ [°]	**−9.2648**	−9.1781	−9.1497	−9.1493
x [m]	**15.6092**	15.6110	15.6140	15.6146
y [m]	**−0.3940**	−0.3800	−0.4004	−0.3910
z [m]	**−2.1943**	−2.1950	−2.1971	−2.1990

	Direct georeferencing method vs.		
	Leica Cyclone	**GP-ICPR**	**GAReg-ISF**
dω [°]	−0.0264	0.0005	−0.0076
dφ [°]	0.0043	0.0249	0.0240
dκ [°]	0.0867	0.1151	0.1155
dx [m]	0.0018	0.0048	0.0054
dy [m]	0.0140	−0.0064	0.0030
dz [m]	−0.0007	−0.0028	−0.0047

In the following we show the pair-wise alignment of position East (515.308 points) and Northeast (491.384 points) and compare our results with those of a registration using a total station (direct geo-referencing method), a registration using the commercial software Cyclone (Leica, 2006, 5.0) and a registration using the GP-ICPR algorithm – a method based on geometric primitives such as the surface normal vectors – all stated in (Bae 2006).

To increase the effect of "imperfectness" our algorithm selects a random subset of 100.000 points (about 1/5 of the original point cloud) from each scan for feature detection and the final ICP; 3.000 points are used in the second Genetic Algorithm for free-form matching. These start conditions have to be considered when comparing the results of our registration strategy, based on Genetic Algorithms and imperfect and subdivided features (GAReg-ISF), with other methods.

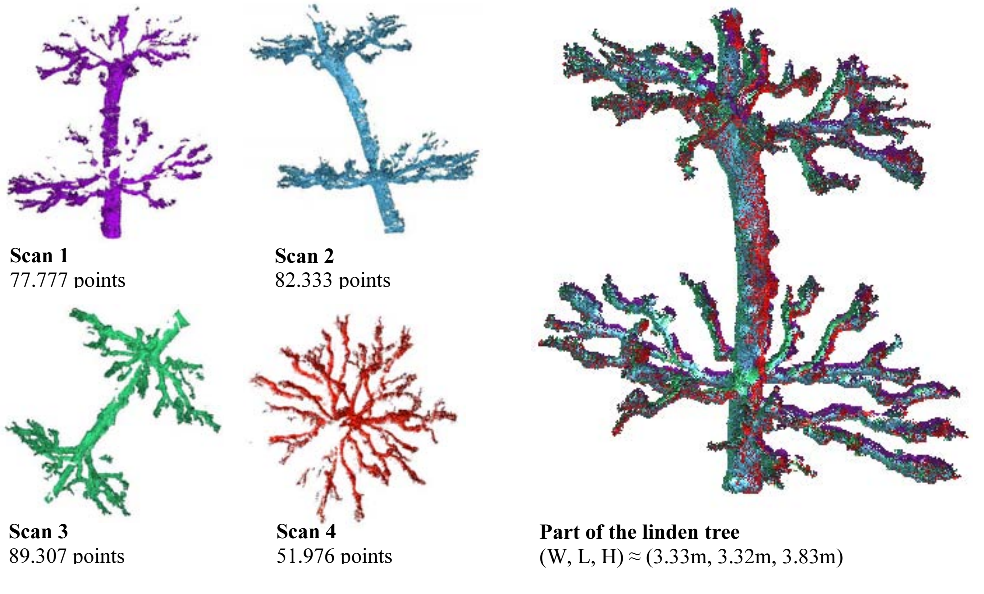

Fig. 8: Left: Four single scans of the linden tree; Right: Multi-view matching result.

Fig. 7 shows on the left side the subdivided features of position East which were used for the pair-wise matching (right side) with position Northeast. The six transformation parameters (rotation and translation) of the two scans from Agia Sanmarina church as well as the difference to the direct geo-referencing method can bee seen in Tab. 1.

By using imperfect and subdivided features we successfully performed the registration with a similar quality as in (Bae 2006).

3.2 *Linden Tree, Grettstadt, Germany*

Although our approach is mainly thought for architectonical objects featuring geometrical shapes such as planes we tried to apply our algorithm to a part of a linden tree scanned from four sides using a Trimble GX scanner. The data used is part of a project for the documentation of a so-called "Tanzlinde". This is a kind of dancing floor build into a tree, a local architectural specialty in some parts of Southern Germany.

The linden tree is interesting insofar as it does not contain "perfect" features such as planes or straight borders. In this case neither cylinders are well suited because of the curved and rough surface of the tree. However, due to the use of imperfect and subdivided features (planes) and by allowing more tolerance during feature detection, the algorithm could gather enough information for a rough pair-wise alignment; the results of the pair-wise alignment were afterwards refined by the two Genetic Algorithms. Using the point-to-plane error metric we observed a RMSE of 1.58 to 1.79 mm from the pair-wise matching of the single scans after applying the ICP algorithm. Fig. 8 shows the four scans of the dataset linden tree and the multi-view matching result.

4 Conclusions and Future Work

In this paper we proposed an improvement to the state of the art for handling the fully automatic registration of arbitrary orientated and partially occluded point clouds characterized by a significant noise level and imperfect geometry.

One of the main ideas is to strictly accept a certain amount of inaccuracies (imperfectness) in our datasets and features and to create a registration framework able to handle them. Furthermore we subdivide features into smaller sub-features to overcome occlusion and implement Genetic Algorithms (GAs) as clearly targeted steps in between classical coarse and fine registration. This way we are able to maintain both robustness and computational performance also when registering objects of bigger size.

Currently we are implementing more kinds of features such as lines, cylinders and spheres in our algorithm and are, moreover, extending the Genetic Algorithms with niching techniques to handle cases in pair-wise matching where more than just one optimum can lead to correct solutions.

At the moment our algorithm – able to combine the positive aspects of different registration techniques and use them in a both appropriate and efficient way – is still under development; nevertheless already now it shows a great potential in all our tested datasets.

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