A method for global non-rigid registration of multiple thin structures

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***Abstract*—We present a global algorithm for drift-free alignment of multiple range scans of "thin" data into a single point cloud that is suitable for further processing, such as triangular meshing and volume calculation. We consider two sets of non-rigid data: synthetic vascular data and real Arabidopsis plant data. Our method builds on the coherent point drift algorithm, and aligns multiple point clouds into a single 3D point cloud. The plant data was acquired in a growth chamber, where the fan caused jittering in both the branch and leaf data. For each scan, we construct a target scan from the centroids of its Mutual Nearest Neighbours (MNN) in all other scans and iteratively register to this, as opposed to registering pairwise scans sequentially. We have have adapted MNN for use in non-rigid scenarios, producing a method that will will not degrade as more scans are registered, and produces better results than sequential pairwise registration.**

***Keywords*-Multiview Reconstruction; 3D Plant Growth; Thin Structures; Coherent Point Drift; Mutual Nearest Neighbour;**

I. Introduction

Building a 3D model is extremely useful for many practical applications where inferring measurements about the shape or size of an object is a requirement. With the rapid acceleration of hardware capability in terms of CPU power, storage and 3D scanners, we can now capture huge amounts of data and the fidelity of the resultant models is constrained by the quality of merging/reconstruction algorithms. Due to recent advancements of robotic technologies and low cost laser scanners, building real time automated systems is becoming possible for plant science and agricultural applications, where a major task is to build a 3D model of the plant to analyze different biological properties. However, the complex structure of a plant makes the problem of aligning multiple views extremely hard, unlike building a 3D model of a rigid object like Stanford bunny. In medical robotics, automatic analysis of medical images is a crucial step: a common application is to build a 3D model of thin artery data from multiple tomographic or CT images. This involves pairwise registration and alignment of different scans. However, registration of vascular data is a challenging problem and despite several years of research ([23], [7]), still it remains an open problem in medical imaging community. One motivation of this paper is to address the problem of aligning multiple views of thin, complex structures like plant or artery data.

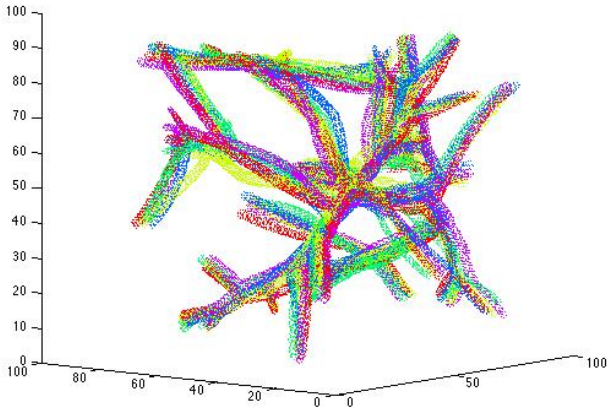

Figure 1. A subset of the views of the synthetic vascular data. We take one scan and then apply a set of random, non-rigid deformations to obtain our dataset.

We introduce a drift-free algorithm for merging non-rigid scans, where *drift* is the build-up of alignment error caused by sequential pairwise registration. Sequential pairwise registration entails the alignment of each scan to its neighbour, followed by the alignment of another neighbouring scan to the resultant scan, and so on. The error between any two scans accumulates the error from the previously merged scans used in the current merging.

Inspired by Toldo *et. al.*'s work [25] in rigid registration, we solve this problem by constructing an "average" scan to which we register. For a scan X, we find the set of points that are Mutual Nearest Neighbors (MNN) for each point in the scan from every other scan. That is, we compute the MNNs for each point in X for each scan individually, and we then combine them into a single scan that is composed of the calculated centroids from each point. We describe this in Section III. To overcome the limitations of 2D image-based plant analysis (lack of accurate spatial and volumetric information [17]), 3D imaging is essential for measuring various plant parameters that indicate plant growth. A significant body of literature has been reported on plant growth analysis. For example, Clark *et. al.* [6] proposed a high throughput software system for analyzing

978-1-4799-1986-4/15 $31.00 © 2015 Crown Copyright
DOI 10.1109/CRV.2015.35

the root structure of a plant. Paproki *et. al.* [17] demonstrated a 3D approach for measuring plant growth in vegetative stage. They captured data as high resolution 2D images and generated 3D mesh data from these images. Recently, Paulus *et. al.* [18] used 3D laser scanning technology to perform organ classification of plants. Li *et. al.* [13] proposed a technique to track budding and bifurcation of plants from raw point cloud data.

In order to obtain the 3D structure of an object, a range scanner is used to capture point cloud data from multiple viewpoints. These datasets are merged together and then triangulated to build a polygonal mesh of the object. However, most of the current methods for doing this concentrate on the optimization involved in reconstructing standard 3D models, with the constraint that the calculation be computationally inexpensive. Here, we are interested mainly in modelling complex plant objects and, as well, have to consider the non-rigidity of the plant caused by the inter-scan movement of the object due to weak and uncontrollable wind currents in the growth chamber. We are investigating how well a plant's volume is a function of its growth as a long term goal.

Registration is a fundamental task in 3D reconstruction, where the aim is to find a coordinate transformation to align source and target views (referred to as *pairwise registration*). The basic Iterative Closest Point (ICP) [2] algorithm finds a rigid transformation that registers two views using local optimization. Several variants and applications of the classical ICP and were reported in the literature, including [27], [29], [14], [19], [20], [9], [3]. Registration of the set of plant range scans, using the existing methods whose implementations are available, were poor because of the inter-scan movements between different parts of the plant range images (the plant is not rigid). Recently, Gaussian Mixture Models (GMM) have been used for non-rigid registration. Our plant data (Arabidopsis plant) is extremely sparse in the flowering stage (with long stems, a few leaves and flowers), so it is necessary to use a large area of support to construct the GMMs to smooth the solution space, and as a result, the registrations are not sufficiently good to pass a visual inspection. We have concluded from our experimental work, that Myronenko *et. al.*'s Coherent Point Drift (CPD) [16], [15] method works best for aligning two point clouds of the plant data. However, Myronenko *et. al.* didn't consider aligning more than two views. We propose an algorithm based on CPD which can align many views with minimal error. Our data (of the Arabidopsis plant) consists of 12 views of the plant, uniformly sampled at 30° increments, thus allowing a complete 3D reconstruction of the plant. We roughly align adjacent point clouds from adjacent range scans by performing sequential pairwise registration and then use our global method to create the final point cloud.

II. Previous Work

Among several robust methods for registration, some notable work can be found in [5], [26], [28], [24]. These algorithms belong to a similar class of approaches. We found that various non-rigid registration methods are reasonably effective in registering adjacent scans, but any attempt to merge multiple registrations into a single point cloud was problematic.

Fitzgibbon [8] modified ICP by deriving an error function between the model and target data which is minimized by the Levenberg-Marquardt algorithm (LMICP). The energy is formulated in terms of the L_2 distance of the closest point in the data to each point in the model, but he instead computed distances to each point in a discrete volume, thus allowing to compute the spatial derivatives needed for energy minimization. This approach makes the registration process more general than ICP. The method requires rigid data and works well on the standard Stanford Bunny dataset (which satisfies this constraint). Applying the algorithm to our plant data yielded poor results.

The Point Cloud Library (PCL) [1] provides a method for point cloud alignment that is based on Rusu *et. al.*'s method [22], [21] for Fast Point Feature Histograms (FPFH). Rusu *et. al.*'s contribution is in finding efficient matching of features between two sets of point clouds. Each point in a dataset is assigned multiple informative labels as features and these are then used to establish correspondence, thus resulting in a good initial alignment for registration. The geometrical information (16 dimensional) for the neighbourhood of each point is extracted and stored in histograms. The method has also been shown to be robust to pose invariance. Unfortunately, this method still does not overcome the difficulties associated with iterative algorithms like ICP. We have implemented Rusu *et. al.*'s algorithm using PCL. The results are shown later in this section.

Some robust rigid registration methods have used GMM: Jian and Vemuri [11] (GMMReg) proposed an approach to minimize the discrepancy between two Gaussian mixtures by minimizing the L_2 distance between two mixtures. However, they can't handle large datasets. Their experimental results are for the downsampled Bunny dataset. The algorithm does not work for our plant dataset (over 2 million points). In fact, for complex plant structures, it is impossible to retain the geometry of the model by downsampling the over 2 million points (to about 5000 points, which the algorithm can process).[1] The plant under consideration has lot of branches and has a canopy of leaves at its base, which makes the geometry more complicated. The Stanford Bunny can be approximated by a few hundred points, but for plant structures using such a small number of points is not possible. Hence, we could not apply this algorithm in our

[1]Correspondence between the authors and ourselves revealed that this downsampling could not be avoided.

plant data.

The Coherent Point Drift (CPD) registration method was proposed by Myronenko et al. [16], [15]. Their method is based on GMM, where the centroids are moved together. Given two point clouds, $\mathcal{M} = (x_1, x_2, ..., x_m)^T$ and $\mathcal{S} = (y_1, y_2, ..., y_n)^T$, in general for a point x, the GMM probability density function will be $p(x) = \sum_{i=1}^{M+1} P(i)p(x|i)$, where:

$$p(x|i) = \frac{1}{(2\pi\sigma^2)^{D/2}} \; exp[-\frac{||x - y_i||^2}{2\sigma^2}]. \tag{1}$$

Instead of maximizing the GMM posterior probability, the negative log-likelihood function can be minimized to obtain the optimal alignment:

$$E(\theta, \sigma^2) = -\sum_{j=1}^{N} log \sum_{i=1}^{M+1} P(i)p(x|i). \tag{2}$$

They iteratively use the Expectation Maximization algorithm to optimize the cost function. The algorithm is also robust to noise. We have used this algorithm and have run the same 2 adjacent point clouds of our plant data as for the other algorithms we tested. The results indicate that CPD works best among all other tested algorithms for registering plant data.

We present a comparative framework to perform a quantitative comparison in registering two point clouds. First, we show our experimental results on the Bunny data (downsampled to 376 points). We show our results on real Arabidopsis plant data. The results are shown in Figure 2 for the Stanford Bunny dataset and Figure 3 for the real Arabidopsis plant.

To perform quantitative analysis of results we manually chose a small number of 3D points in the 2 scans that we believe are correct correspondences. For the Bunny and Arabidopsis plant data, we acquired 18 and 44 correspondences respectively. Using that ground truth, we computed the average error rate as the L_2 distances (in mm) between source and target points, where the correspondence was manually measured for the different algorithms. These are listed in Table I. We can observe that for Bunny datasets, almost

	Algorithms			
Datasets	FPFH	LMICP	GMMReg	CPD
Bunny	0.149	0.046	0.012	0.014
Arabidopsis Plant	9.661	4.114	N/A	2.312

Table I
QUANTITATIVE RESULTS FOR DIFFERENT ALGORITHMS AND DATASETS.

all the algorithms work well. However, for real Arabidopsis data, the error measures are considerably higher. We note that while collecting the ground truth correspondence points, there may have been some errors. Although it is difficult to capture the exact error, we expect the error to be in the range 2-5 mm for each point. As we can see, CPD works best among all other methods in processing plant data.

III. PROPOSED METHOD

We first approximately align the scans sequentially, and then we use a global method to refine our result. The global method involves registering each scan X_i to an "average" shape, which we construct using the centroids of the *mutual nearest neighbours* (MNN) of each point. For X_i, we use scans X_j where $j \neq i$ to obtain the average shape Y_{cent} from the centroids, and X_i is then registered to this average shape. This is repeated for every scan until the result converges.

We modify Equation (1) to perform global registration

$$p(x|i) = \frac{1}{(2\pi\sigma^2)^{D/2}} \exp[-\frac{||x - \hat{y}_i||^2}{2\sigma^2}]. \tag{3}$$

where $\hat{y}_i \in Y_{cent}$ are the points in the target scan Y_{cent}, which is constructed from all scans other than itself.

For a pair of scans X and Y, we say that a point $x_i \in X$ and $y_j \in Y$ are MNN if $x_i = x_{i_n}$ and $y_{j_n} = y_j$, where

$$x_{i_n} = \min(|x_p - y_j|), \forall x_p \in X, \tag{4}$$

and

$$y_{j_n} = \min(|y_q - x_i|), \forall y_q \in Y. \tag{5}$$

For each point x_j in scan X_i, we find the set of points $\mathbf{x_k}$ from all scans other than X_i that are mutual nearest neighbours of x_j. For each of these sets of points $\mathbf{x_k}$, we find the centroid

$$y_{cent} = \sum_{i}^{n} \frac{\mathbf{x_{k}}_i}{n}. \tag{6}$$

We register Y_{cent}, the set of centroids calculated for each x_j, to scan X_i.

Although CPD alone is effective in registering pairs with a fair amount of overlap, when registering multiple scans, especially scans that have not been pre-aligned, our method achieves a much better fit both visually and quantitatively than CPD by itself, utilizing sequential pairwise registration. Our method is a two step process, beginning with aligning the scans approximately. We then register a single scan to "average" shape, constructed from all other scans, and update the set to include the newly registered result, performing the same process with all other sets of scans. In this way, we avoid accumulation of merging error.

A. Approximate Alignment

We capture a set of scans around the plant at 30° increments. After acquiring them, we first solve for the rigid transformation $T_0 = (R_0, \vec{t_0})$ (where R is a rotation angle and $\vec{t}$ is a translation vector) between the the first scan (X_0) and the second scan (X_1) using the rigid version of

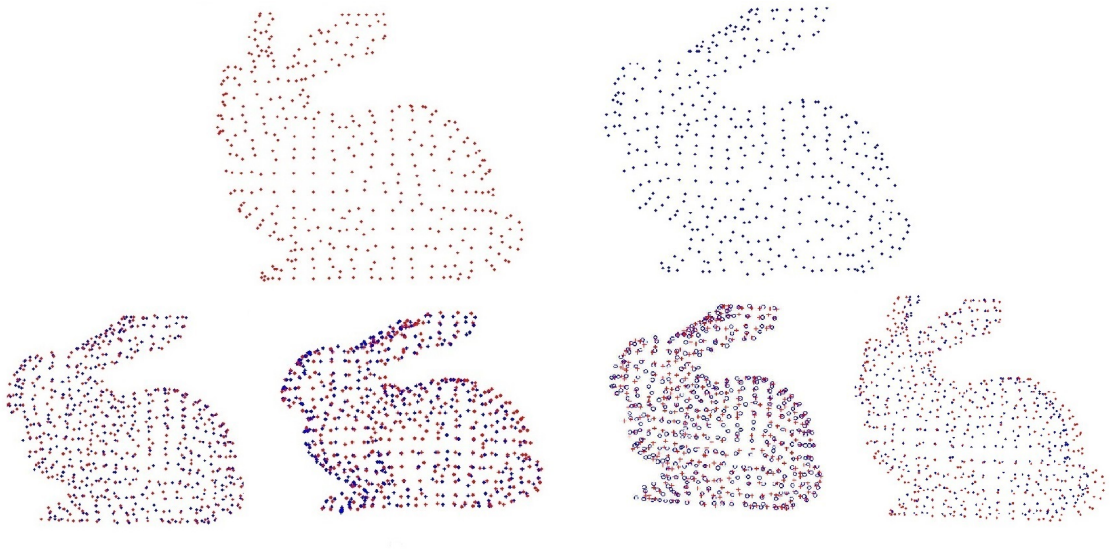

Figure 2. Pairwise registration results for two scans of the Stanford Bunny. Top row: original two views, Bottom row: results obtained using Rusu et al. (FPFH) [22], Fitzgibbon (LMICP) [8], Jian and Vemuri (GMMReg) [11] and Myronenko and Song (CPD) [15].

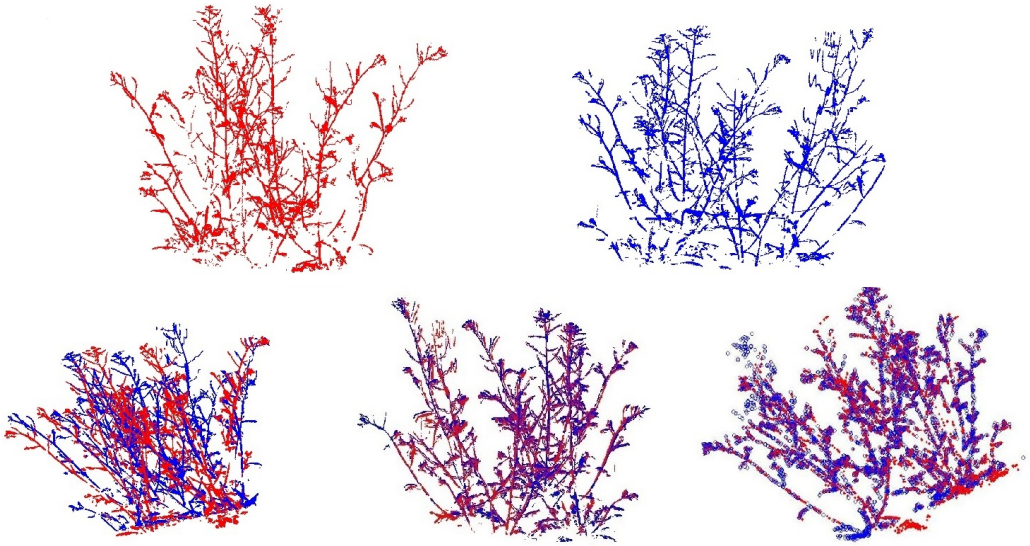

Figure 3. Pairwise registration results two scans of the real Arabidopsis plant data. Top row: the original two views. Bottom row: results obtained using Rusu et al. (FPFH) [22], Fitzgibbon (LMICP) [8] and Myronenko and Song (CPD) [15].

CPD. After we solve for $\vec{t_0}$, for each scan X_i, we apply the transformation i times as follows:

$$\hat{X}_i = R_i X_i + \vec{t_i}, \tag{7}$$

where $R_i = \prod_{k=0}^{i} R_0$ and $\vec{t_i} = \sum_0^i \vec{t_0}$. Our new set of transformed scans $\hat{X}$ should now be roughly aligned. We use this method to obtain a rigid registration. The initial registration is important when the pair of scans to be registered has minimal overlap.

The approximately aligned scans can be seen in Figure 4.

B. Global Non-Rigid Registration via MNN

Once the initial registration is complete, we use CPD in conjunction with MNN to recover the non-rigid deformation field that the plant undergoes between the capture of each scan. At this point, the scans should be approximately aligned to one another. We now construct the centroid/average scan and then register to it.

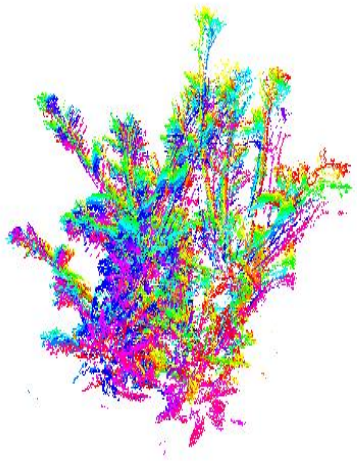

Figure 4. 12 scans of the Arabidopsis plant, prior to registration, but with rotation and and translation pre-applied.

1) Global Registration: We use Algorithm 1 to merge all scans, where MNN(·) computes the mutual nearest neighbour for each point in scans X_i and X_j and the centroids function likewise takes the centroids computed for each point in each scan and combines them into one average scan using Equation (6). For each point in scan X_i, we find the single nearest neighbour from all other scans and use the set of distances to compute the L_2-norm.

Algorithm 1 MNN Registration

Require: $\mathbf{X} = [X_1, \cdots, X_n]$, where each X_i is a range scan that has been approximately adjusted. A predefined tolerance tol_{max}.
$tol = \sum_{i=1}^{N}$ error_$L_2(X_i)/N$
while $tol < tol_{max}$ **do**
  for $i = 1$ **to** N **do**
    for $j = 1$ **to** N **do**
      if $j \neq i$ **then**
        $Y_{i_{cent}}$ = MNN(X_j, X_i)
      end if
    end for
    Y_{cent} = centroids($Y_{1_{cent}}, \cdots, Y_{N_{cent}}$)
    X_i =register_cpd(Y_{cent}, X_i)
  end for
end while

IV. Results

A. Plant Data

Figure 5 shows all 12 scans, merged into a single point cloud after subsampling each scan. Each color in the point cloud represent a different scan. Despite the noisiness of the range scans from jitter, our method successfully performed the 12 view registration, resulting in a single point cloud that accurately captures the shape of the Arabidopsis plant. By ensuring that the scans are all approximately registered before proceeding (for both methods), we minimize the likelihood that erroneous parts of the point cloud datasets will bias the motion of a scan that is being registered. Figure IV-A displays the resultant error between the first scan in the set and all subsequent scans. First, we see that the error is lower for scans that have more overlap (the first scan shares a fair deal of overlap with the last, for example) for both sequential pairwise and our proposed methods. We see that our method always outperforms its pairwise counterpart. Sequential registration still rendered a useful result, though as the number of scans grows, the drift would theoretically increase.

Figure 6. MNN versus sequential pairwise registration.

B. Synthetic Vascular Data

We further demonstrate the efficacy of our method on synthetic vascular data. We take a 3D point cloud of synthetic veins, as generated by VascuSynth [10] and apply a non-rigid deformation to the point cloud to create a total of 20 scans. This was performed using the deformation method provided with the CPD software. We use the parameters $\mathbf{sampling} = 0.1$, $\mathbf{power} = 3$ and $\lambda = 4$. Initially, $\sigma = 5$ and we increase its value by 0.5 for each successive deformation. This gives us a new set of point clouds, as seen in Figure 7. The magnitude of this transformation is

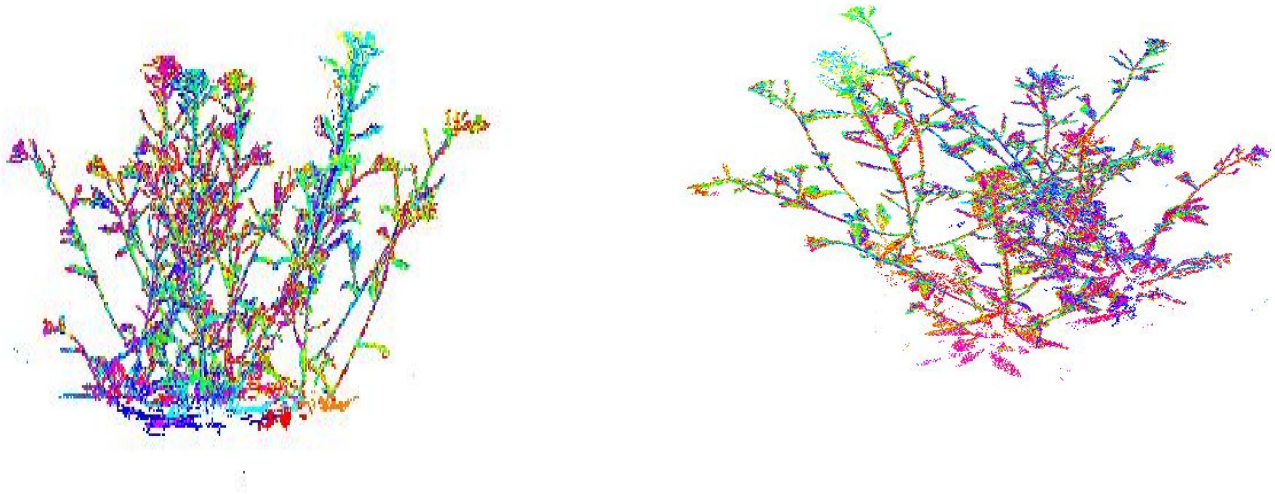

Figure 5. 12 scans captured in 30° increments about the plant and then merged into a single point cloud using MNN. Shown from two viewpoints, front facing on the left and from above on the right.

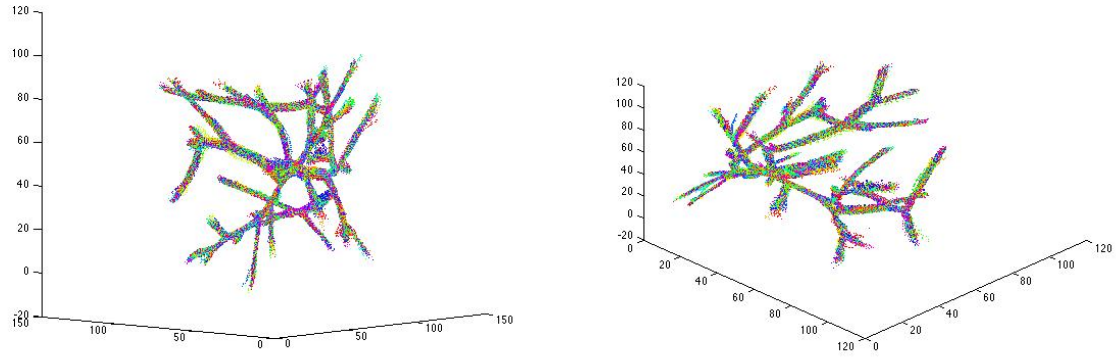

Figure 7. 20 synthetic scans of vascular data merged into a single point cloud using MNN, as seen from two viewpoints, front and back.

substantially larger than those created by the wind in the Arabidopsis set. We utilized more scans than we did with the Arabidopsis in hopes of verifying our hypothesis that pairwise registration gets progressively worse as we add more scans, though the effect of drift is partially obscured by the fact that the deformation increases between the first and each successive scan.

The L_2 error of the merged scans using sequential pairwise was higher than MNN and the resultant shape no longer looked like the initial one when we used the default CPD parameters ($\lambda = 1, \beta = 1$), where λ controls the "stiffness" and β controls the point "spread". In order to maintain the shape of the veins, we couldn't use a value of $\lambda < 70$. The quantitative results for the pairwise sequential method in Figure 8 were calculated using $\lambda = 90$, which still ends up rendering a badly warped result. In addition, as we increased the value of λ, the drift increased quickly.

By contrast, MNN performs very well on this data, as seen in Figure 7. Quantitatively, we have shown that it easily outperforms sequential pairwise registration, and that our method limits drift.

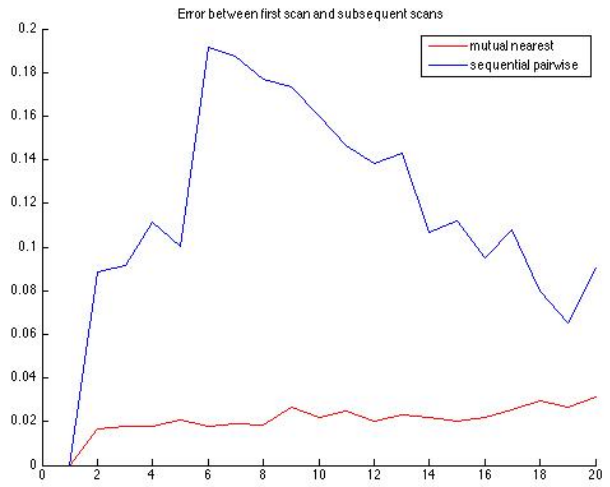

Figure 8. MNN versus sequential pairwise registration on vascular data, registering the first scan to each of the subsequent scans.

V. Conclusion

We have presented an approach to merge multiple scans into a single point cloud. Our plan is to triangulate this cloud into a triangular mesh and measure the volume of the plant. We hope that the quantitative volumes of the plant over time comprise a growth metric for the plant that is both non-invasive and non-contact. We have chosen, from our experience, the best existing algorithm to work on sparse plant data and built our model on top of it: it can handle non-rigid objects with noise. One possible future research direction may be computing a quantitative analysis of how many scans should be sufficient to reconstruct the plant within tolerable range (for example, using 8, 6 or 4 scans instead of 12 scans), and we are also working on even faster methods for registration, using approximations of CPD. We also intend to use the junction points proposed by Chaudhury *et. al.* [4] to obtain an initial alignment more efficiently.

Acknowledgment

This research was partly funded through a NSERC Discovery grant.

References

[1] "Point cloud library," http://pointclouds.org/.

[2] P. Besl and N. McKay, "A method for registration of 3d shapes," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. 14, no. 2, Feb. 1992.

[3] S. Bouaziz, A. Tagliasacchi, and M. Pauly, "Sparce iterative closest point," *Computer Graphics Forum (Symposium on Geometry Processing)*, vol. 32, no. 5, pp. 1–11, 2013.

[4] A. Chaudhury, M. Brophy, and J. Barron, "Junction based correspondence estimation of plant point cloud data using subgraph matching," in *submitted*, 2015.

[5] H. Chui and A. Rangarajan, "A feature registration framework using mixture models," in *Proceedings of the IEEE Workshop on Mathematical Methods in Biomedical Image Analysis*, ser. MMBIA, 2000.

[6] R. Clark, R. MacCurdy, J. Jung, J. Shaff, S. McCouch, D. Aneshansley, and L. Kochian, "Three-dimensional root phenotyping with a novel imaging and software platform," *Plant Physiology*, vol. 156, no. 2, pp. 455–465, 2011.

[7] K. Deng, J. Tian, J. Zheng, X. Zhang, X. Dai, and M. M. Xu, "Retinal fundus image registration via vascular structure graph matching," *Journal of Biomedical Imaging*, vol. 2010, pp. 14:1–14:13, 2010.

[8] A. Fitzgibbon, "Robust registration of 2d and 3d point sets," in *Proceedings of the British Machine Vision Conference*, ser. BMVC, 2001, pp. 43.1–43.10.

[9] D. Huber and M. Hebert, "Fully automatic registration of multiple 3d data sets," *Image and Vision Computing*, vol. 21, no. 7, pp. 637–650, 2003.

[10] P. Jassi and G. Hamarneh, "VascuSynth: Vascular Tree Synthesis Software," *Insight Journal*, vol. January-June, pp. 1–12, 2011.

[11] B. Jian and B. Vemuri, "Robust point set registration using gaussian mixture models," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. 33, no. 8, pp. 1633–1645, Aug. 2011.

[12] N. Kumar, P. Belhumeur, A. Biswas, D. Jacobs, W. Kress, I. Lopez, and J. B. Soares, "Leafsnap: A computer vision system for automatic plant species identification," in *In proc. of 12th European Conference on Computer Vision (ECCV)*, October 2012.

[13] Y. Li, X. Fan, N. J. Mitra, D. Chamovitz, D. Cohen-Or, and B. Chen, "Analyzing growing plants from 4d point cloud data," *ACM Transactions on Graphics (Proceedings of SIGGRAPH Asia 2013)*, vol. 32, 2013.

[14] T. Masuda and N. Yokoya, "A robust method for registration and segmentation of multiple range images," *Computer Vision and Image Understanding*, vol. 61, no. 3, pp. 295–307, May 1995.

[15] A. Myronenko and X. Song, "Point set registration: Coherent point drift," *IEEE Transactions on Pattern Analysis and Machine Intelligence*, vol. 32, no. 12, pp. 2262–2275, Dec. 2010.

[16] A. Myronenko, X. Song, and M. Carreira-Perpinan, "Non-rigid point set registration: Coherent point drift," in *Advances in Neural Information Processing Systems*, ser. NIPS, 2006, pp. 1009–1016.

[17] A. Paproki, X. Sirault, S. Berry, R. Furbank, and J. Fripp, "A novel mesh processing based technique for 3d plant analysis," *BMC Plant Biology*, vol. 12, no. 1, p. 63, 2012.

[18] S. Paulus, J. Dupuis, A. Mahlein, and H. Kuhlmann, "Surface feature based classification of plant organs from 3d laser-scanned point clouds for plant phenotyping," *BMC Bioinformatics*, vol. 14, no. 238, 2013.

[19] K. Pulli, "Multiview registration for large data sets," in *Proc. Second International Conference on 3-D Digital Imaging and Modeling*, October 1999, pp. 160–168.

[20] S. Rusinkiewicz and M. Levoy, "Efficient variants of the ICP algorithm," in *Third International Conference on 3D Digital Imaging and Modeling (3DIM)*, June 2001.

[21] R. Rusu, N. Blodow, and M. Beetz, "Fast point feature histograms (fpfh) for 3d registration," in *Proceedings of the 2009 IEEE International Conference on Robotics and Automation*, ser. ICRA'09. Piscataway, NJ, USA: IEEE Press, 2009, pp. 1848–1853. [Online]. Available: http://dl.acm.org/citation.cfm?id=1703435.1703733

[22] R. Rusu, N. Blodow, Z. Marton, and M. Beetz, "Aligning point cloud views using persistent feature histograms," in *Proceedings of the 21st IEEE/RSJ International Conference on Intelligent Robots and Systems*, ser. IROS, 2008.

[23] D. Smeets, P. Bruyninckx, J. Keustermans, D. Vandermeulen, and P. Suetens, "Robust matching of 3D lung vessel trees," in *MICCAI workshop on pulmonary image analysis*, 2010.

[24] S. Somayajula, A. Joshi, and R. Leahy, "Non-rigid image registration using gaussian mixture models," in *Proceedings of the 5th international conference on Biomedical Image Registration*, ser. WBIR, 2012, pp. 286–295.

[25] R. Toldo, A. Beinat, and F. Crosilla, "Global registration of multiple point clouds embedding the generalized procrustes analysis into an ICP framework," in *In Proceedings of 3DPVT'10 Conference*, May 2010.

[26] Y. Tsin and T. Kanade, "A correlation-based approach to robust point set registration," in *In proc. of 8th European Conference on Computer Vision (ECCV)*, 2004, pp. 558–569.

[27] G. Turk and M. Levoy, "Zippered polygon meshes from range images," in *Proc. of SIGGRAPH*, July 1994.

[28] J. Zhang, Z. Huan, and W. Xiong, "An adaptive gaussian mixture model for non-rigid image registration," *Journal of Mathematical Imaging and Vision*, vol. 44, no. 3, pp. 282–294, Nov. 2012.

[29] Z. Zhang, "Iterative point matching for registration of free-form curves and surfaces," *International Journal of Computer Vision*, vol. 13, no. 2, pp. 119–152, Oct. 1994.