A fusion framework for automatic neuron reconstruction

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Abstract. Neuron reconstruction is an important step to study the relationship between brain neuron morphology and function. Existing neuron reconstruction algorithms have achieved relatively good results under certain conditions. In the context of whole brain research, the conditions are more demanding, so the previous methods cannot guarantee high-quality results in any brain image data. This paper proposes a fusion framework for automatic reconstruction, which is dedicated to improving the applicability of traditional reconstruction algorithms and obtaining high-quality neuron morphological data. Experiments show that this framework is more flexible than traditional reconstruction methods and has broad application prospects in the current research background.

1. Introduction
Neuron morphology data is closely related to the information processing process of the brain [1, 2]. In order to obtain neuron morphology data, manual or automatic reconstruction methods are generally used [3, 4, 5]. The neuron reconstruction process is to extract neuron morphological data from images and save them in a format that can be recognized by the computer. A common general format is the SWC format, which is proposed by Cannon in 1998 [6]. It describes neurons as a tree-like structure composed of a large number of nodes with a radius. Manual reconstruction is often time-consuming and labor-intensive, and a full neuron tracing process requires at least two experts to spend several hours. The automated reconstruction algorithm solves the problem of high requirements in the experimental environment of the manual tracing process and accelerates the speed of data acquisition. However, the current automatic reconstruction algorithm cannot achieve the accuracy of manual reconstruction [7, 8].

Most automated reconstruction algorithms start tracing from the soma and gradually obtain complete neuron reconstruction results [9, 10, 11]. However, there are always strong noises or branches of other neurons near the soma of neuron images, which greatly affects the tracing quality of these automatic reconstruction algorithms, resulting in completely different reconstruction results in the same experimental environment. In addition, the result of the automatic reconstruction algorithm highly depends on the configuration of related parameters, and the optimal parameter configuration under different reconstruction experimental data is often different.

In order to make the automatic reconstruction algorithm more universal and suitable for different neuron images, we propose a fusion strategy. Based on the feature distribution of neural dendrites, we first filter out candidate data from the reconstruction results under multiple different parameter configurations, and then consensus these results to obtain more accurate neuron morphological data. This framework uses different parameter settings of the tracing method, so it has a wider applicability...
than the previous reconstruction method. In addition, the screening process takes into account the prior knowledge of neural dendrites, which can remove erroneous structures that do not conform to the morphological rules, and to a large extent ensure the biological correctness of the reconstruction results.

2. Method
In the application of this framework, we chose APP2 [11], a graph-based reconstruction algorithm for 3D neuron morphological data. APP2 is implemented based on the Fast matching framework, which has the characteristics of low computational cost and fast processing speed. The process of the APP2 algorithm is shown in Table 1.

**Table 1.** The process of the APP2 algorithm.

| Step | Description |
|------|-------------|
| 1    | Use $\varepsilon$ as the background signal intensity threshold for the gray image, and perform the gray-weight image distance transform (GWDT) to enhance the image intensity at the center of the signal and reduce the image intensity near the edge. |
| 2    | Use the fast matching FM method for initial reconstruction, covering as much signal as possible. |
| 3    | The initial reconstruction result is decomposed into segments, and then sorted according to the length of the segments; then the coverage between the segments is calculated. If the coverage between the two segments is greater than the threshold, the covered segments and sub-segments are deleted. Iterate this step until no segments are removed. |

Fig. 1 shows the 3D neuron morphological reconstruction results obtained from neuron image using APP2. It uses Vaa3d [12] software to display. Vaa3d means 3D visualization-assisted analysis. It is a fast and versatile 3D/4D/5D image visualization and analysis for biological images and surface objects [12]. It is also equipped with plugin development tools, allowing you to freely develop what you need plugin.

![Origin neuron image](image1.png)  ![Reconstruction results](image2.png)

**Figure 1.** APP2 reconstruction results.

In practical applications, the choice of algorithm can be more flexible, and other efficient reconstruction algorithms such as Rivulet [13], TReMAP [14], MOST [15], etc. can also be used for...
neuron reconstruction under the framework of this article. By comparing the results of the above-mentioned reconstruction algorithms on experimental data, we find that the APP2 algorithm is more suitable for our experimental data, as shown in Fig.2, so this article chooses the APP2 algorithm as the test algorithm.

![Image data](image1.png)

**Figure 2.** Comparison of tracing results of different reconstruction algorithms.

The overall framework is divided into the following parts:

1. Image segmentation: Because the file size of whole-brain-level image data can reach the terabyte level, it is difficult for a computer to process the entire image data at one time. Therefore, this framework first takes the soma as the center to obtain an image block of 512*512*256 (voxel) size for tracing.

2. Multi-parameter configuration reconstruction: For the image block obtained in the first step, use the automatic reconstruction algorithm to obtain the reconstruction results under various threshold settings as the candidate set C:

   \[ C = \{ t_1, t_2, ..., t_n \} \]  

   In Eq. 1, \( t_i \) is the reconstruction result obtained under the i-th parameter configuration.

3. Screening based on dendrite morphological features: We use the L_Measure \[16\] to extract dendritic features, and then obtain the guiding knowledge of neuron dendritic morphology in a set of prior data, which is used to screen candidate results. In the implementation of this framework, screening is mainly based on the number of stems and location distribution: first, the soma is optimized to the centroid position \( S \). Subsequently, according to the optimized soma position \( S \) and the estimated soma radius \( R \), the position distribution \( D \) of the stem and the number of the stem \( N \) can be obtained. Secondly, according to the BFS, the neuron tree height \( H \) and the number of branches \( B \) can be obtained. Finally, the eligible reconstruction results can be filtered out based on the above calculation parameters:

   \[ C_s = \{ t_i | t_i \in C \ and \ Select(t_i) = 1 \} \]  

   Select () is execution function of the screening process. When the above features meet the real data distribution, it outputs 1; otherwise, it outputs 0.

4. Consensus strategy: First, resample the reconstruction results under various parameter settings to obtain a normalized data set, which ensures that all data points in the reconstruction results can be matched and compared. Subsequently, each sampling point in the normalized data is judged separately. When the matching result of this point exceeds 1/3 of the total number of reconstruction results, the matching point can be retained. Finally, perform the minimum spanning tree algorithm to connect all the retained matching points, and the final neuron morphological data can be obtained.
3. Results
The experiments are all running on windows 10, computer configuration: CPU Intel i7-7820, 2.9GHz, memory 32G. Datasets: 436 neurons are a semi-automatically reconstructed mouse full neuron morphology datasets produced by the American Brain Science Project.

First, we calculate the feature distribution on the datasets to obtain prior knowledge. Then, we set the APP2 parameter threshold to 10, 20, 40, 80 for neuron tracing. Secondly, Use the prior knowledge obtained before to filter the reconstruction results, and then use the consensus strategy to obtain the final result.

We select the tracing results of three different image samples for display. As shown in Fig. 3, the first column is neuron images, the middle column is the best reconstruction result of APP2 under a single parameter setting, and the last column is the result of our method. It can be seen from the figure that the APP2 algorithm can obtain the correct reconstruction result when the image quality is good (the first row in the figure), but when there is more interference in the image, a large number of error branches are prone to appear (the second row in the figure). The reconstruction framework based on the Consensus strategy maintains a high reconstruction accuracy in various environments, which proves the applicability of this framework.

![Image 3](image.png)

**Figure 3.** Neuron reconstruction results in different image environments.
4. Conclusions
This paper proposes an automatic reconstruction algorithm fusion framework based on a consensus strategy. The framework is guided by the general regularity of artificial annotation neuron data and solves the problem that the general automatic reconstruction algorithms are highly dependent on parameter configuration, and can obtain accurate reconstruction results in a variety of different experimental environments. In recent years, with continuous breakthroughs in related technologies, terabytes of brain image data can be generated, pushing neuron morphology research to the whole-brain scale. As brain science research gradually focuses on whole-brain data, the types of data will become more and more abundant, and the limited neuron reconstruction algorithm can’t be applied to all image data. This framework brings new ideas to solve the precise tracing of neuron structure in messy scenes. It can combine the advantages of a single reconstruction algorithm or multiple reconstruction algorithms to meet the needs of different images and achieve precise neuron tracing. Experiments have also proved that our method is practical and will have a wide range of application prospects in the future.

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