These days, structural connectomes from diffusion-weighted tractography have been applied to the clinical, anatomical, and cognitive studies. To obtain informative and accurate structural connectomes, many tracking algorithms and post-processed optimization methods were developed. In the pipelines of structural connectome analyses, probabilistic tractography is used more than other tracking methods such as global tractography and deterministic tractography because the structural connectomes are based on the end-to-end networks. The nodes of the connectome are determined by the macroscopic brain atlas since brain atlases such as the AAL atlas and the Desikan-Killiany atlas are conventionally used in these studies. Probabilistic tractography generates more fibers than other tracking algorithms and can terminate the tracking of certain voxels, but it has some weak points because of the nature of its algorithm. (1) The density of reconstructed connections between two regions by a probabilistic tractography is not originally reflected in the density of underlying axon connections. (2) Probabilistic tractography generates many spurious outlier fibers that are inappropriate from the viewpoint of the brain's white matter anatomy.

The problem of (1) was addressed by some optimization algorithms. Former studies could reduce tracking biases, and the structural connectome comparison based on the number of fibers of the end-to-end network has been practical. Some validation of these methods by comparing whole-brain fiber reconstructions with and without these methods to evaluate the measures of white matter estimated from post-mortem brain dissection studies.

However, the problem of (2) has not been addressed sufficiently. The most conventional and simple outlier removing method is a length based outlier filtering. But, the length-based outlier filtering often fails to remove outlier fibers because the length of outlier fibers is not always too long or too short within the fiber population.

To overcome this problem, we propose a novel method for outlier removing that the fibers are characterized by the three-dimensional feature vector (length, mean-density, mean-curvature) and based on a robust statistic. This proposed method enables us to remove outlier fibers within whole-brain connectome by one objective threshold.

In this paper, we first introduce an algorithm of a novel method for outlier removing. Next, we will apply this method for the open access data from the Human Connectome Project (HCP) and compared the length-based outlier filtering method results. We generate the eleven subjects of whole brain tractograms by using the Anatomy Constraint Tractography (ACT) and applied the proposed method to these 11 connectomes. We show the reproducibility and the effects for connectomes in the result section and discuss the effectiveness of this method in the analysis of the structural connectome.