In recent years, the probabilistic tractography has been widely applied to connectome-based diffusion tractography studies, and high-quality fiber tracking plays a critical role in this study. Unfortunately, because of the nature of probabilistic tractography, many spurious outlier fibers that traverse looped pathways or pathways that are too long are generated. In this study, we demonstrate how the outlier fibers generated by the probabilistic tractography could not be removed with the conventional length-based removal method. Then, we propose a novel method to remove the outlier fibers without heuristic adjustments in each network. In this method, fibers are characterized by the three-dimensional feature vectors (length, mean density, and mean curvature) to obtain more effective features than the fiber length. The features are statistically tested by robust Mahalanobis distances with a certain threshold. This proposed algorithm could remove most of the outlier fibers without any heuristic manual procedures. We applied this filter to healthy subjects from the Human Connectome Project (n=11). We compared the non-filtered connectome matrices and the connectomes with this outlier removal, and we found that the number of fibers in each subject fell by an average of 9%.

We addressed the effectiveness of this result in structural connectome studies.