FastTENET: an accelerated TENET algorithm based on manycore computing in Python

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Single-cell RNA sequencing (scRNAseq) has significantly advanced our understanding of cellular dynamics. As a large amount of scRNAseq data has accumulated, requiring the development of various algorithms and software for scRNAseq data analysis. Reconstruction or inference of a gene regulatory network (GRN) is one of the most important approaches to understand biological mechanisms by analyzing the regulatory relationships between genes at the system level. TENET, designed for the reconstruction of gene regulatory network (GRN), employs the concept of transfer entropy (TE) from information theory to quantify the strength of causal relationships between genes in scRNAseq expression data. TENET has been successfully employed to reconstruct gene regulatory networks and the identification of key regulators in a variety of datasets, including mouse embryonic stem cells, cardiomyocyte reprogramming, and mouse embryonic fibroblasts during autophagy. However, TENET has the limitation that it requires long computation times for large datasets. To improve the performance of TENET, we have developed **FastTENET**, an accelerated implementation of TENET based on parallel processing on manycore processors such as GPUs. We have designed array structures specialized for parallel computing, and FastTENET utilizes parallel algorithms to compute TE based on these structures. Compared to the original TENET, FastTENET has achieved up to 973 times better performance.