Efficient implementation and acceleration of DIP-NMF-MM algorithm for high-precision 4D PET image reconstruction

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Introduction.

Positron emission tomography(PET) is a technique to observe biomolecular mechanisms such as metabolic processes by measuring the distribution of radioactive tracers in a human body. PET images are reconstructed from observed data called sinograms, and there are high expectations for the use of GPUs to handle large data and computationally intensive algorithms. In this study, we evaluate the performance of this 4D PET image reconstruction code implementing the DIP-NMF-MM algorithm by increasing the size of

the input data and optimizing the execution time.

4D PET image reconstruction.

PET images are obtained by repeating the following four processes using the observed data as input.

- 1. Adding noise to input data
- 2. Update U-Net parameters
- 3. Normalize each spatial basis
- 4. Update time basis using MM algorithm

Implementation.

UVM

UVM is used to address the GPU memory shortage



problem. This feature is a memory management system that simplifies GPU development by providing a single memory space that can be accessed by all CPUs and GPUs in the system.



4 Accelerated implementations

For the optimization of execution time, we implemented and evaluated the performance of the following four acceleration methods.

- 1. Optimization of noise additive processing
- 2. Computational graphing of the entire process
- 3. Embedding input data into computed graphs
- 4. Distributed execution of U-Net

with twice higher resolution by using UVM with respect to the 4D PET image reconstruction code using the DIP-NFM-MM algorithm. In addition, a maximum speed-up of 10x was achieved by applying four speed-up methods.

References

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