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Resource Optimization in Diffusion MRI Image Analysis

Motivation

- Diffusion MRI involves modeling techniques and complex diffusion models, imposing a high computational burden;
- Parallelization can enhance both computational efficiency and storage capabilities, leading to faster data access and processing speeds.

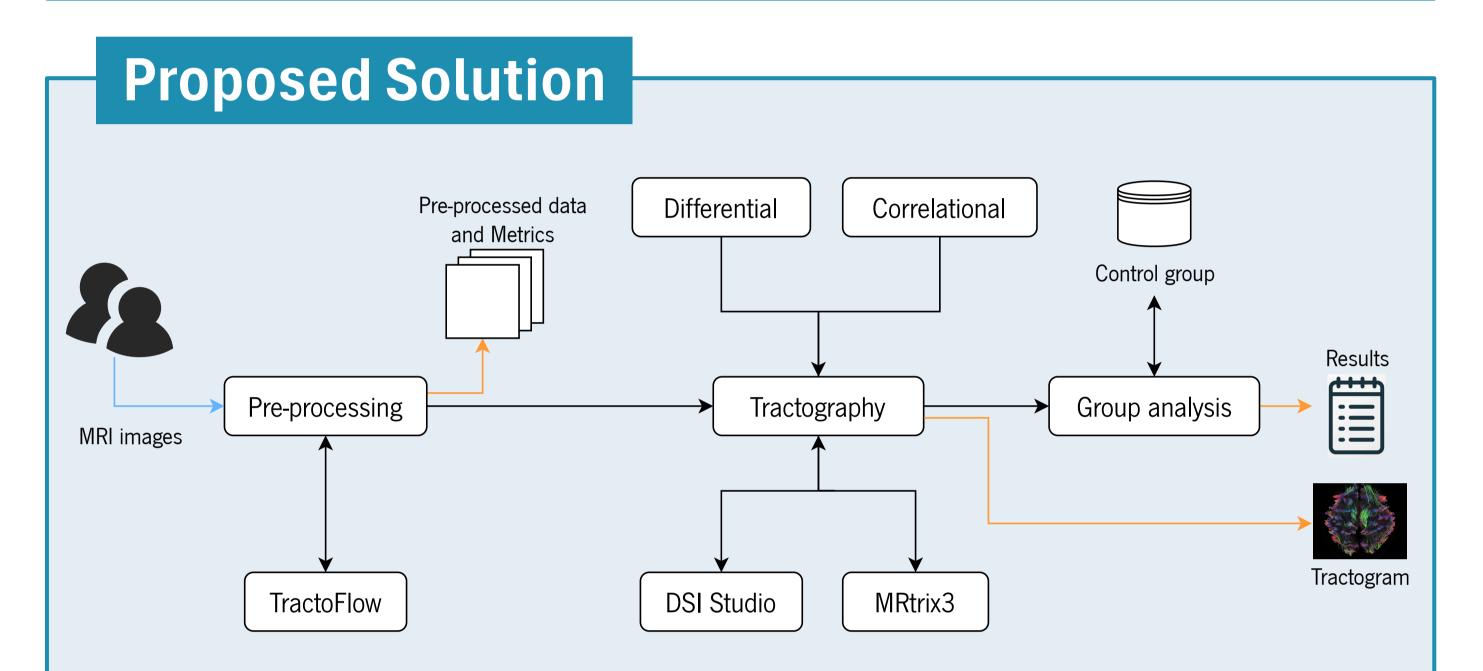


Figure 1: Architecture of the proposed solution. The input and outputs of the pipeline are represented in blue and orange, respectively.

Goals

- Optimize task execution to take advantage of the computational resources available;
- Implement the workflow in a distributed setting and distribute the workload across multiple nodes.

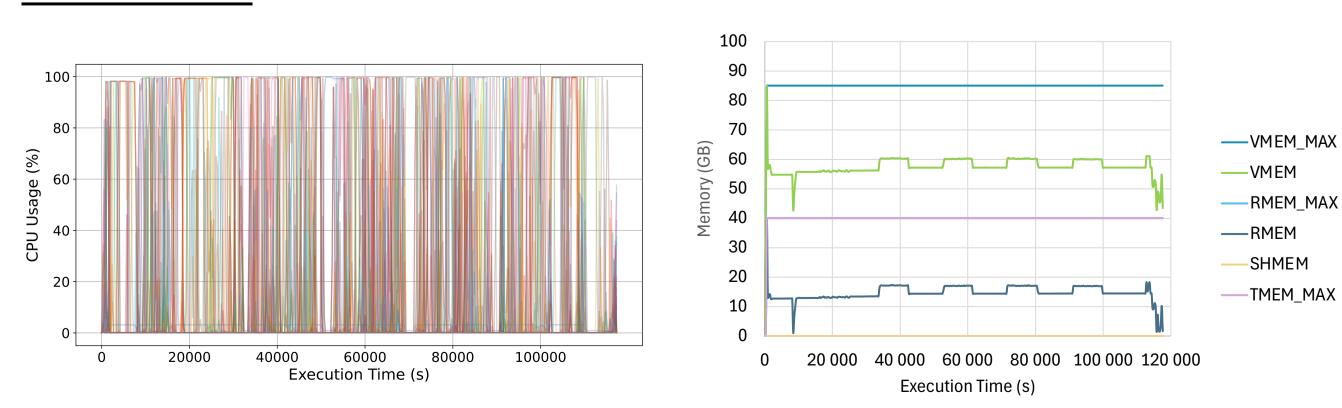
Preliminary Results — Profiling the Tools

Monitoring the execution in single-node configuration on the Deucalion supercomputer (2 AMD EPYC 7742 64-core 2.25 GHz CPUs with 256 GB of memory) with the REMORA tool.

Table 1: Execution times for each tool with two MRI images of different sizes.

Image Size	Pre-processing (TractoFlow)	Tractography	
		MRtrix3	DSI Studio
27 MB	1h 17min 18s	33min 14s	39s
3.5 GB	1d 8h 41min	37min 13s	39s

TractoFlow



MRtrix3 RMEM MAX ----RMEM ---TMEM_MAX Execution Time (s) Execution time (s) DSI Studio —RMEM_MAX -TMEM MAX Execution Time (s) Execution Time (s)

Key Takeaways

- Pre-processing execution time is higher than that of the tractography;
- Image size has a great influence in the pre-processing, but not in the tractography;
- All tools perform multi-threading, but some do not use all the available resources;
- CPU usage is not uniform over time, which can indicate concurrency problems;
- None of the tools is able to run in a multi-node configuration.

Future Work

- Optimize the tools by implementing multi-node execution;
- Ensure fault tolerance in case of node failure;
- Ensure data privacy is maintained throughout the multi-node execution.

References

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