





Extending a scientific workflow engine with streaming I/O capabilities: DAGonStar and CAPIO





<u>Simone Perrotta</u>, Ciro Giuseppe De Vita, Gennaro Mellone, Marco Edoardo Santimaria, Giuseppe Salvi, Marco Lapegna, Massimo Torquati, Angelo Ciaramella



Introduction

1.1 Introducing data-intensive workflows

Data-intensive workflows:

- Involves complex sequences of computational tasks;
- Requires **resilient** systems for effective data flow and processing.

Challenges with Traditional Workflow Engines:

- Significant limitations with real-time data streams;
- Struggles with **in-memory** data management;
- Increasing data complexity and scale exacerbate these issues.



Introducing WFEs and DAGonStar

Workflow Engines (WFEs):

- Designed to manage complex scientific workflows;
- Example: **DAGonStar**.

Functionality:

- Use directed acyclic graphs (**DAGs**) to ensure correct data flow;
- Enable parallel **task execution**.

Limitations:

• Performance can be limited by reliance on traditional disk-based storage.





Introducing CAPIO

CAPIO:

• Innovative **in-memory file storage system**.

Purpose:

• Overcomes limitations of **disk-based storage** in high-performance computing.

Benefits:

- Faster data access;
- Reduced latency crucial for real-time processing.

Architecture:

- Supports **concurrent access**;
- Facilitates parallel processing;
- Ideal for managing high-speed **data streams** in modern scientific workflows.







Why integrate DAGonStar with CAPIO?

• Workflow Description: DAGonStar uses the workflow://schema to describe workflows as dataflows. This means that by analyzing the data flow processed and managed by the various tasks, we can perform I/O overlap to save a significant percentage of the total execution time.



Timeline of integration

- **Current State**: DAGonStar with workflow://schema, no I/O overlap.
- **Integration Goal**: Combine DAGonStar's robust workflow description with CAPIO's efficient streaming I/O.
- **Expected Outcome**: Achieve simultaneous computation and I/O for improved performance and efficiency.



Without CAPIO (i.e., batch execution of S and Q)

Our objective

Integration of CAPIO with DAGonStar:

• Creates a **hybrid system**.

Combination:

- Efficient task orchestration (**DAGonStar**);
- High-speed, low-latency data handling (CAPIO).

Paper Details:

- Design and implementation;
- Highlighting how CAPIO's streaming I/O capabilities enhance **DAGonStar's performance**.

Primary Objective:

- Demonstrate significant **performance improvement**;
- Particularly for real-time data processing in scientific workflows.





Design and architecture

DAGonStar's architecture

Principal components:

- Runtime;
- Service;
- Workflow:// Schema;
- Garbage collector;
- Stager;



CAPIO's architecture



- The CAPIO **server**, which will run on each node belonging to the cluster. A **JSON** configuration file must be passed to this during execution, which indicates how and where the **streaming** must be carried out, and will generally be produced by users or software;
- The CAPIO **system call intercept library**, a library that allows the CAPIO server to stream by intercepting essential posix calls regarding file management.

Our architecture



- DAGonStar batch tasks generate the JSON file based on the dependencies between tasks, identified thanks to the workflow:// Schema;
- This JSON file is used by the CAPIO server for configuration;
- Tasks A and B make up a pipeline in which A produces files and B reads them;
- Posix calls made on these output files will be **intercepted** by the CAPIO server, allowing it to process this data in RAM.

Case studies

Introducing the pipeline

The presented case studies all focus on the use of a **pipeline**, which includes:

- **Producer** A: which **generates** numbers by inserting them into files;
- **Consumer** B: which **reads** these files, **sums** all the numbers within each file, calculates the **average**, and saves it in another file.
- In our scenario, there is also another component of the pipeline, **C**: which **opens** all the files produced by B, and computes the **average of all the individual averages**.



Pipeline implementation

The implementation of the pipeline was carried out following these **steps**:

- Implementation of the **pipeline** composed of two C programs, namely **A** and **B** in **CAPIO**;
- Identify the points in DAGonStar to modify for integration purposes and apply these improvements;
- Create two tasks that make up the pipeline in **DAGonStar** plus another task that saves the results **permanently**;
- Run the pipeline workflow and collect **timing results** for comparison.



Experimented pipelines

There were various types of pipelines tested, but they all have in common the type of numbers within the files, as they are all between **0** and **1** with a decimal precision of **6** digits. The specific types of pipelines experimented with are as follows:

- 10 files with 1 million numbers per file;
- 10 files with 2 million numbers per file;
- 20 files with 1 million numbers per file;
- 20 files with 2 million numbers per file;
- 30 files with 1 million numbers per file;
- 30 files with 2 million numbers per file;
- 40 files with 1 million numbers per file;
- 40 files with 2 million numbers per file.



Evaluation and results

We tested the pipeline in two scenarios:

- DAGonStar running bash scripts sequentially;
- DAGonStar with **CAPIO integration**.

Execution times were recorded from the start of Program A to the end of Program C to compare performance gains.





2 Million Random Numbers

Conclusions

This work was carried out according to the following points:

- **Exploration**: Examined workflows, WMS, and DAGonStar;
- Study: Analyzed CAPIO middleware;
- Integration: Integrated CAPIO into DAGonStar.

The results of this work have shown that:



- Execution times were reduced by **20%** to **32%**;
- There are **significant benefits** of using **RAM-based file systems** in **Workflow Management Systems.**





