

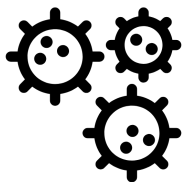
Adaptive Tool Selection in a Scalable Genomics Pipeline

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CICF 2025, Globus Labs

Mentors: Alok Kamatar, Greg Pauloski, and Kyle Chard

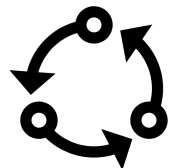
My Project



Created FMT viral detection pipeline as part of my undergraduate research

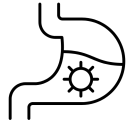


Use Parsl make my original pipeline more efficient and scalable



Apply adaptive tool selection with Academy

FMT Viral Detection



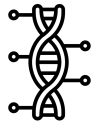
FMT for *C. diff*



Tracking viruses



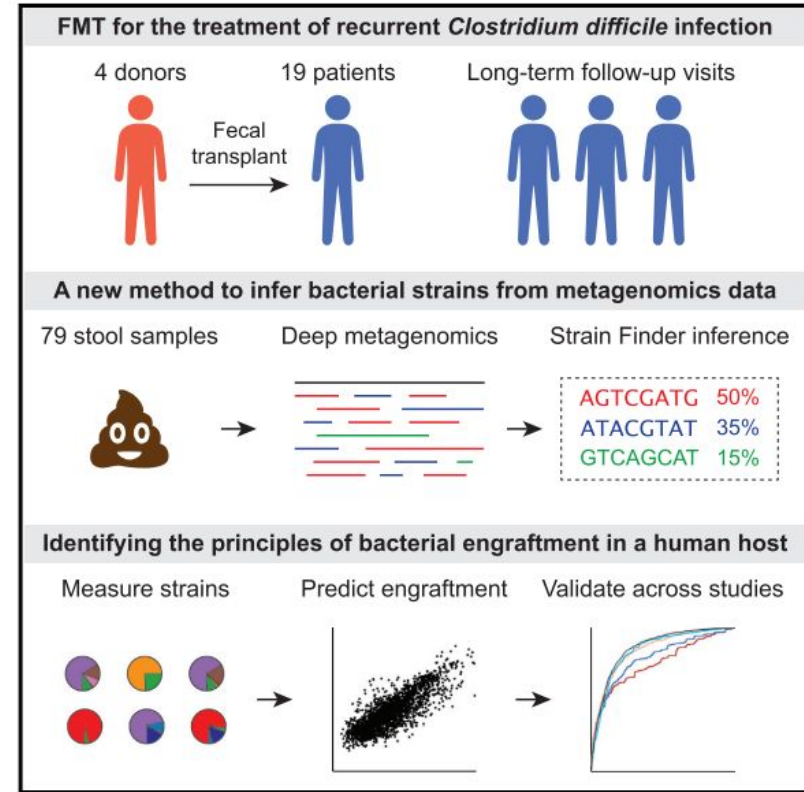
From donor to patient, and over time



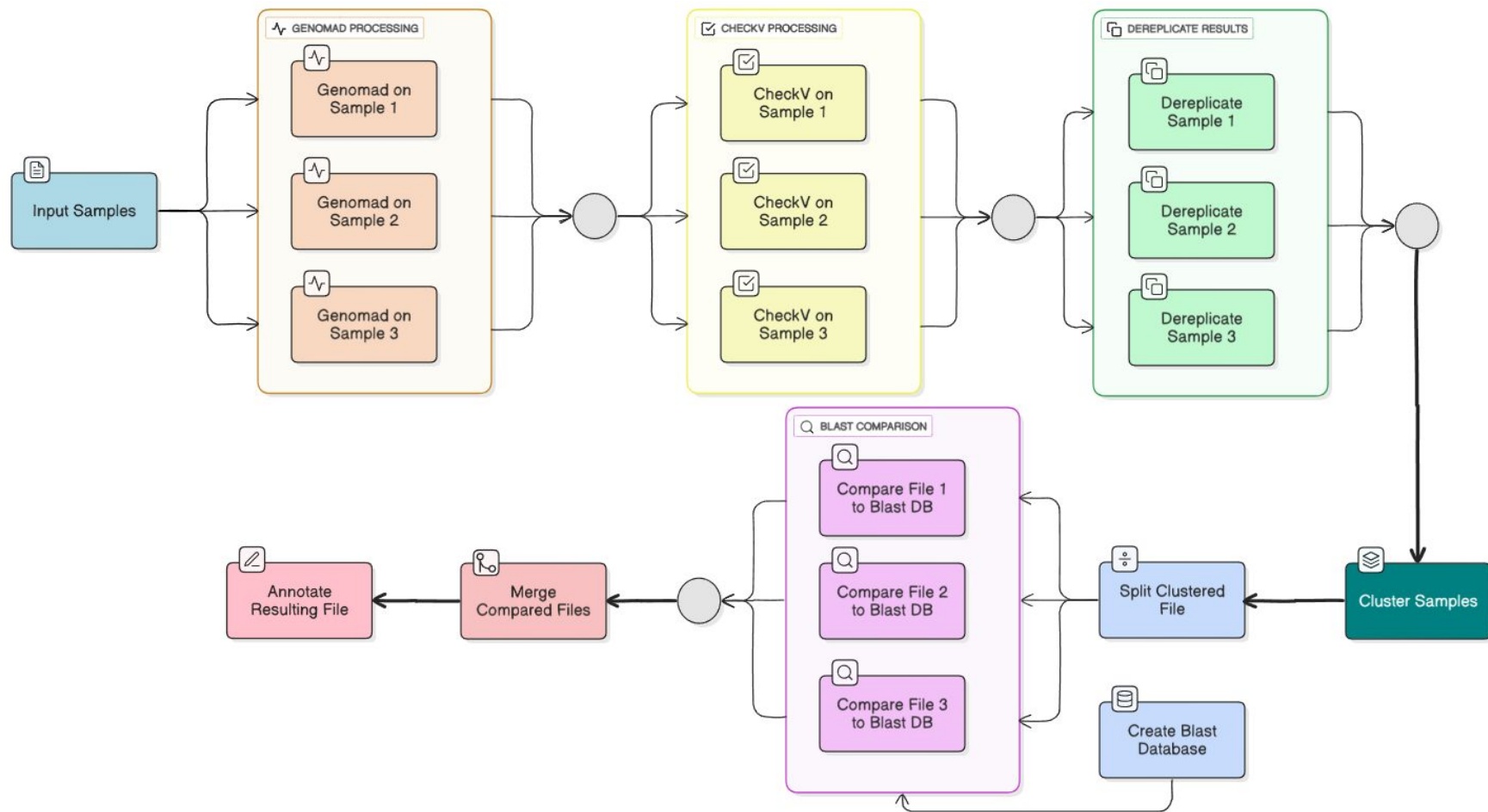
Metagenomic approach



Assembled contigs → annotated viruses

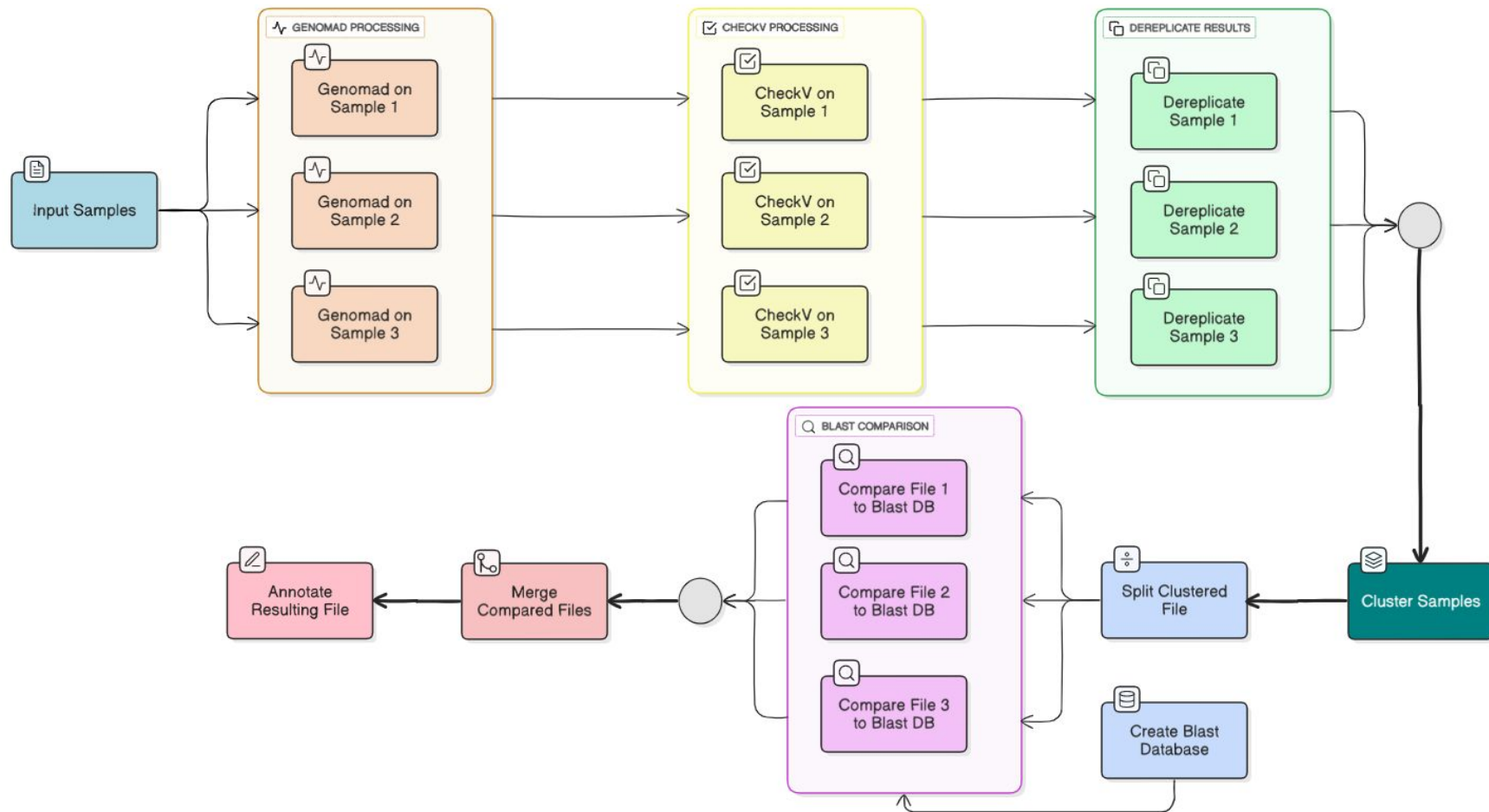


From: Smillie et al., *Cell Host Microbe* 2018;23(2):229–240.
DOI: 10.1016/j.chom.2018.01.003.

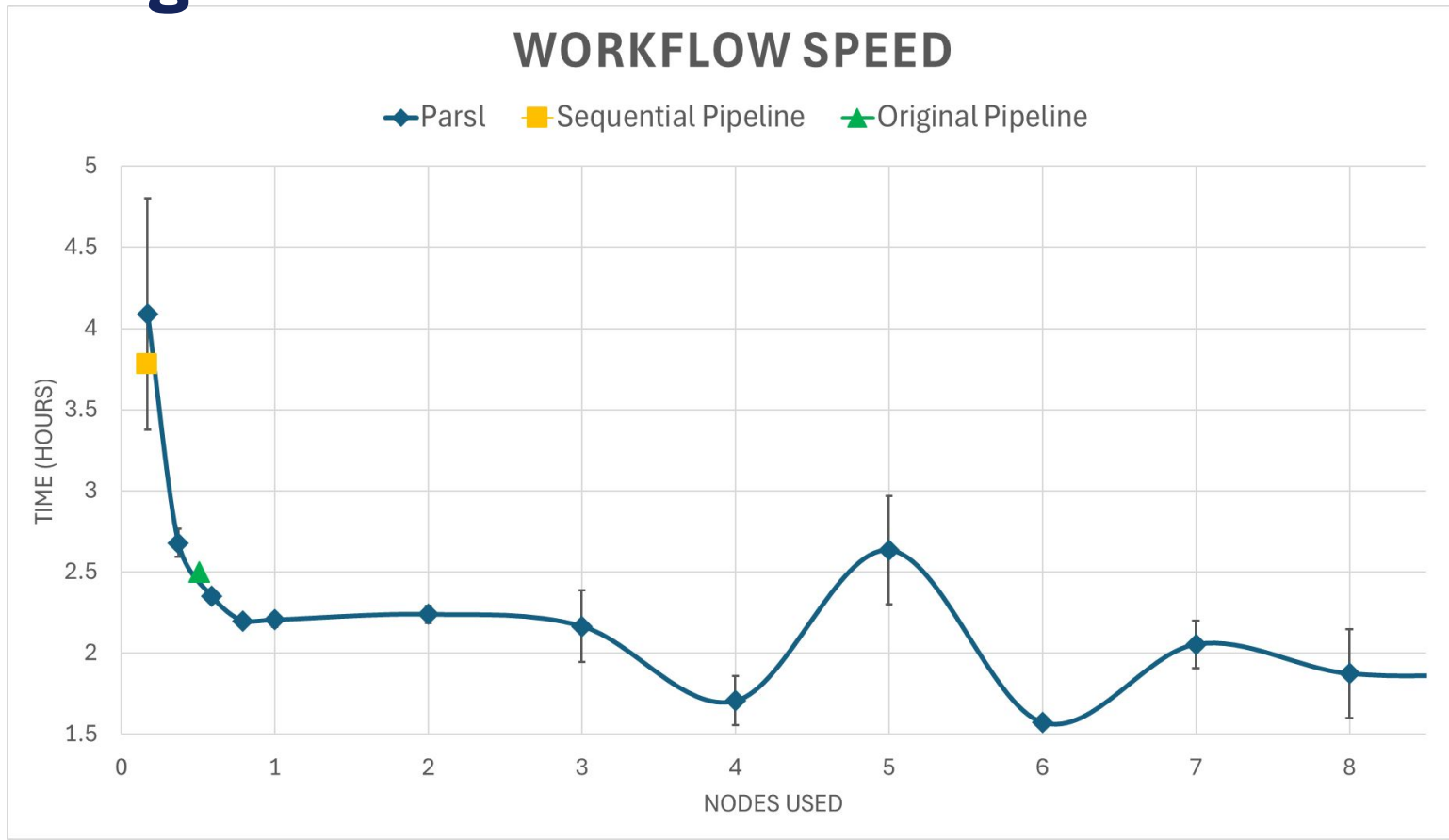


Parsl

- Apps run concurrently
- Parsl creates a dynamic graph of tasks and their dependencies
- Tasks executed when their dependencies are met
- “Natural parallel programming!”



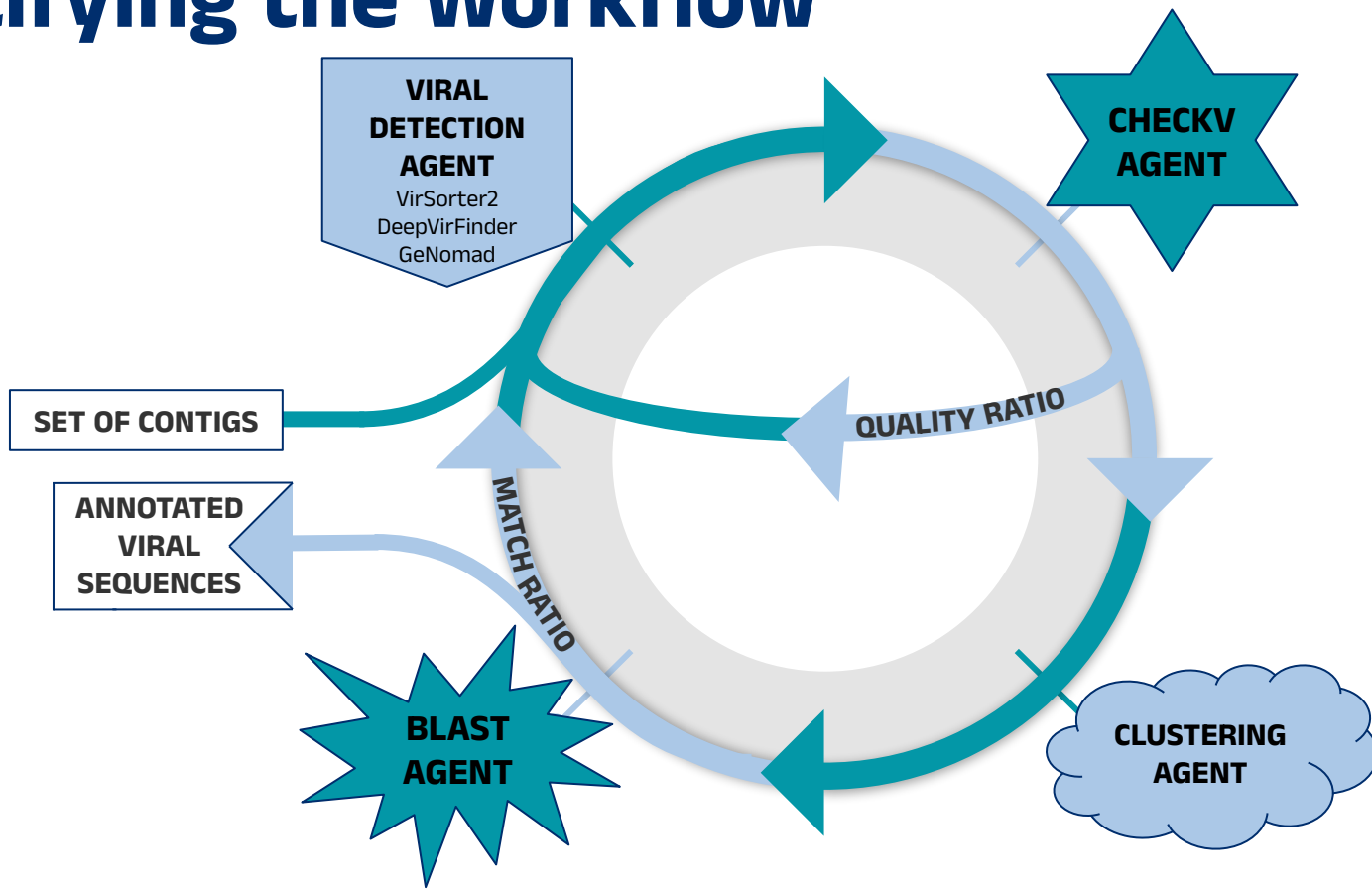
Scaling the Workflow



Academy

- Modular middleware for building autonomous agents
- Manage inter-agent communication
- “Deploy agents across distributed, federated, and heterogeneous resources”

Agentifying the Workflow



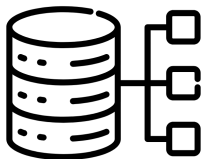
Skills Learned and Takeaways

1. Understanding of HPC and resource management
2. Understanding of workflow management (Parsl, Academy, etc)
3. Learned about autonomous agents and how to agentify a workflow
4. Data collection and documentation
5. Creativity in a workflow

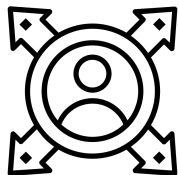
Future of the Project



Submitting poster to the ACM Student Research Competition at SC25



Expanding to other datasets to understand and explore tool selection process



Exploring possibilities of agents (annotation, clustering, etc.)

Acknowledgments

Thank you to my mentors Alok Kamatar, Greg Pauloski,
and Kyle Chard!

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the U.S. National Science Foundation, Grant #2127548 for
supporting me and making this opportunity possible!

Check out my code!

<https://github.com/globus-labs/academy-fmt-viral-workflow>

