

Launcher: A simple tool for executing high throughput computing workloads

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Software Repository: <https://github.com/TACC/launcher>

Software Archive: <http://dx.doi.org/10.5281/zenodo.841337>

Summary

Launcher (Wilson and Fonner 2014, Wilson (2016), Wilson (2017)) is a utility for performing simple, data parallel, high throughput computing (HTC) workflows on clusters, massively parallel processor (MPP) systems, workgroups of computers, and personal machines. It can be easily run from userspace or installed for system-wide use on shared resources. Launcher will perform automatic process binding on multi-/many-core architectures where hwloc (“Portable Hardware Locality (Hwloc)” 2017) is installed.

Use Cases

Launcher is commonly used in situations where search or analysis of a large data space on independent points is required. Launcher is frequently used for: * Sequence alignment scoring for many hundreds or thousands of DNA/RNA sequence pairs * Docking/scoring (protien/ligand dock scoring, drug/immunotherapy development, etc.) * Immune repetoire analysis * Statistical analysis on unknown variables

Workflow

Launcher uses a tree-based parallel startup mechanism (similar to MPI) to scatter jobs to multiple nodes/processors. The filesystem is used to gather data from separate tasks (typically into individual output files). Multiple launcher invocations can be chained together to perform pipelined analysis or to perform chained simulation/analysis workflows.

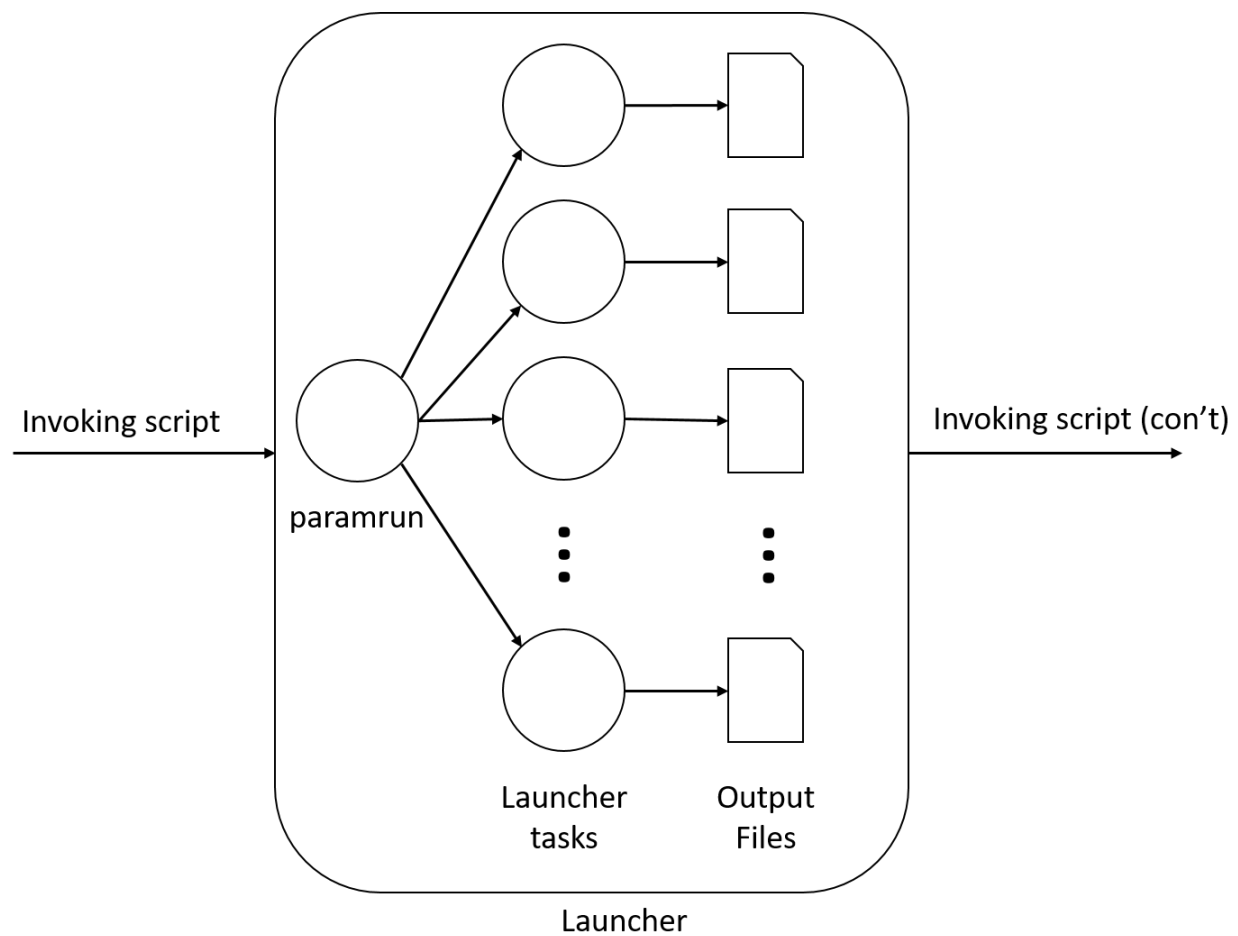


Figure 1: launcher workflow

References

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