



CBSR-Research Technologies Seminar Series



Bioinformatic Workflows with Nextflow and NF-core

Presenter: **Dr. Ramiro Barrantes-Reynolds, UVM Bioinformatics Shared Resources**

Wednesday, Feb. 12, 2025 – HSRF 200 – 12-1pm. Join us!

Attend in-person: Lunch will be served

Attend via Zoom: <https://uvmcom.zoom.us/j/91418328196?from=addon>

Bioinformatics projects usually require pipelines to go from data to an output of interest. Each pipeline consists of many steps, each one processing the output of the previous step with a different tool. Nextflow is a powerful language for creating pipelines, taking advantage of containers, parallelization using HPCs, and version control, allowing for pipelines to be easily reproducible, portable and extensible. The CBSR Bioinformatics core uses Nextflow and NF-core extensively and will show examples of how this can be of benefit to your research.

