

# HPC for Bioinformatics

Hosted by Tufts TTS Research Technology



Join us for a comprehensive **virtual** workshop series designed to equip you with the essential skills needed for bioinformatics using Tufts High-Performance Computing (HPC). This hands-on series will cover everything from basic to advanced HPC workflows, software installation, and environment management, tailored for life science researchers.

**October 9th, 10th, 17th, & 24th, 1:00 PM - 3:00 PM. This is an online event. Register for individual workshops using links below.**

## Lecture Series Schedule

### 1 Introduction to Tufts High-Performance Computing (HPC)

Wednesday, October 9th 1:00 PM - 3:00 PM

In this workshop, you will gain a solid foundation in HPC, learning about login and computing nodes, partitions, and the use of modules. We will explore the differences between interactive and batch modes, and cover essential job assessment techniques.

<https://tufts.libcal.com/event/13096040>

### 2 Getting Started with Bioinformatics on HPC

Thursday, October 10th 1:00 PM - 3:00 PM

This session introduces you to Linux and bioinformatics basics within the HPC environment. You will navigate available resources, write SLURM job scripts for both CPU and GPU tasks and work with essential bioinformatics file formats such as FASTA, FASTQ, GenBank, GTF, GFF3, SAM, and BAM. You will explore tools such as bowtie2 and STAR through live demos.

<https://tufts.libcal.com/event/13096234>

### 3 Software Installation and Environment Management in HPC

Thursday, October 17th 1:00 PM - 3:00 PM

In this workshop, you'll gain skills in software installation and Conda environment management on HPC systems. We'll also cover the installation of R and Python packages and the creation of Jupyter kernels for personalized and shared use. By the end, you'll be equipped to efficiently manage your computational tools on HPC, enhancing both individual and collaborative research efforts.

<https://tufts.libcal.com/event/13096170>

### 4 Advanced HPC Workflows and Job Management

Thursday, October 24th 1:00 PM - 3:00 PM

Take your HPC skills to the next level by learning how to run a large number of jobs simultaneously on HPC systems. We will introduce you to Nextflow and the community-led project "nf-core", showing you how to use these tools for reproducible bioinformatics analysis on Tufts HPC through both the command line interface and Open OnDemand (OOD). We will use the nfcore-rnaseq pipeline as a hands-on example.

This session is designed to enable you to scale and speed up your analysis to reach your research goals.

<https://tufts.libcal.com/event/13096253>

Register today by scanning the QR code, or by clicking the link [here](#).

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