**[Informatics Core](http://informatics.fas.harvard.edu/)**

**URL:** <http://informatics.fas.harvard.edu/>

**Director:** Tim Sackton (Bioinformatics); Aaron Kitzmiller (Software Operations)

**Please Note:** Faculty are strongly encouraged to contact Tim Sackton ([tsackton@g.harvard.edu](mailto:tsackton@g.harvard.edu)) directly for projects that may need significant bioinformatics support to tailor support document language to reflect project needs.

**Description:**

The Informatics Core integrates expertise in compute systems, software, data management and analysis, with background in genetics and genomics research to provide a full spectrum of scientific and software support for Core facilities and FAS scientists. The group aims to work alongside researchers with the intention of spreading knowledge and enabling people to run analyses themselves. We provide consultations on experimental design and analysis best practices for a variety of sequencing-based approaches, and support for shared bioinformatics software infrastructure.

**Services:**

We offer consultation, workshops, or web-based best practices tutorials for the following topics, among others:

* Training and assistance with common scientific programming environments (R, Python, Perl, etc.)
* Parallel and cluster computing assistance
* General operational support for Core facilities including LIMS, billing and scheduling systems
* Scientific application deployment and trouble shooting
* Custom analysis tool development
* RNA-seq expression analysis, including de novo transcriptome assembly, bulk RNA-seq differential expression, and single cell RNA-seq workflows
* Support for long read sequencing with Nanopore or PacBio technology
* Read mapping and variant calling for a variety of resequencing experiments, including RAD-seq, pooled sequencing, and WGS
* Comparative genomics, including whole genome alignment
* ChIP-Seq/ATAC-Seq/FAIRE-Seq analysis using MACS and other tools, including single cell methods
* Genome assembly and annotation
* Phylogenetic reconstruction and phylogenetic analysis / comparative methods in R
* Methods for metagenomic sequencing and taxonomic classification