

HPC conda3 software environments

In order to minimize costs associated with installation of Bioinformatics & related software to RedHat Enterprise Linux, most software will only be available as a **conda** environment.

To obtain an up-to-date list of conda environments available, use:

```
module load anaconda3
conda-env list
```

Generally speaking, HPC staff are not familiar with using software installed on the HPC cluster. However, we may be able to provide general assistance with running software when requested.

Example (bamtools):

If a user of this software would like to provide something to replace "<INSERT BAMTOOLS COMMAND(S) HERE>" below, please contact HPC staff.

```
module load anaconda3
source $CONDA_PROF/conda.sh
conda activate bamtools
<INSERT BAMTOOLS COMMAND(S) HERE>
conda deactivate
```

Conda software environments installed (21-Apr-2021)

A	abyss , admixtools , admixture , angsd , assembly-scan , assembly-stats , astral , augustus ,
B	bamm , bamtools , bayescan , bazel , bcftools , beast , beast2 , bedtools , biopython , bismark , blast , boost , bowtie2 , busco , bwa ,
C	cairoffi , canu , cap3 , cdhit , checkm-genome , cloog , corset , coverm , cufflinks , cutadapt ,
D	dadi , das_tool , diamond , dlcpair , dmd , drep ,
E	emboss , enrichm , exonerate ,
F	fasta3 , fastai , fastme , fastp , fastqc , faststructure , fastx , ffmpeg-431 , flye , freebayes , freexl ,
G	gatk , gatk4 , gblocks , gdal , gdc , glpk , gmap , gmsh , gnuplot , google-sparsehash , googlesparsehash , gradle , graftm , graftm_genome , graphbin , gtdbtk ,
H	hdf4 , hdf5 , hisat2 , hmmer , hmmer2 ,
I	iqtree , iqtree1 , itsx ,
J	jags , jellyfish , julia ,
K	kraken , kraken2 , krona ,
L	lastz , libnetcdf ,
M	mafft , mapdamage2 , maxbin2 , mcl , medaka , megahit , metabat2 , metawrap-mg , metis , mfqe , migrate , minimap2 , mirdeep2 , mrbayes , multiqc , muscle ,
N	netcdf-fortran , netcdf4 , nettle , newick_utils , nlopt ,
O	orfm , orthofinder ,
P	pal2nal , paml , pandoc , parallel , pcre , pcre2 , pear , petsc , phyluce-1.7.0 , picard , pipits , plink , pplacer , prodigal , proj4 , proteinortho , purge_haplotigs , pyfastx , pyproj ,
Q	qgis , qualimap , quast ,
R	R-36 , R-403 , r-rstan , raxml , rcorrector , rdpclassifier , repeatmodeller , rsem , ruby ,
S	salmon , samtools , scalpel , seqtk , sga , shannon , shovill , slim , sortmerna , spades , sparsehash , sratools , stacks , star , stringtie , structure ,
T	tophat , tpp , transdecoder , transrate , treemix , treeshrink , trimal , trimalore , trimmomatic , trinity , trinotate ,

v

vcflib , vcftools , velvet , vsearch ,