Installed Software

HPCC has an extensive list of software installed. To use a piece of software, an appropriate module must be loaded. This page reviews how to use modules before providing a list of installed software.

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Modules

A module manages environment variables needed to load a particular piece of software. The login process loads a few modules by default for HPCC users. The default loaded modules include the GNU compilers, the OpenMPI communication library, MATLAB and R.

- To see a list of modules that are currently loaded, type "module list"

```
$ module list
Currently Loaded Modulefiles:
1) GNU/4.4.5(default)       5) Boost/1.47.0(default)      9) R/2.13.2(default)
2) OpenMPI/1.4.3(default)   6) CMake/2.8.5(default)       10) Stata/12.0(default)
3) TBB/4.1.0(default)       7) Python/2.7.2(default)       8) MATLAB/R2011b(default)
4) MKL/10.3(default)
```

- To see a list of modules that are available to be loaded, type "module avail"

- To see what environment variables would be set/changed if you load a specific module, type "module show <module_name>"

- To load a module, type "module load <module_name>"

- To unload a module, type "module unload <module_name>"

A video tutorial of how to use the modules can be found here: Video Tutorial - Modules

List of installed software

The following is a list of installed software, sorted by application area. If you require a software title that is not installed, you may install it locally to your home directory. Alternatively, if the software will benefit other users at HPCC, a request can be submitted to http://www.hpcc.msu.edu/contact to request a more global installation by HPCC staff.
Bioinformatics Software

<table>
<thead>
<tr>
<th>Module Name</th>
<th>Version</th>
<th>Brief Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>SEEDS</td>
<td>1.0.0, 1.0.1, 1.0.2, 1.0.3, 1.0.4, 1.0.5, 1.0.6, 1.0.7, 1.0.8, 1.0.9, 1.0.10, 1.0.11, 1.0.12, 1.0.13</td>
<td>Stochastic Cellular Artificial Life Simulator</td>
</tr>
<tr>
<td>avida</td>
<td>2011.09.05</td>
<td>Program for studying biological evolution.</td>
</tr>
<tr>
<td>NetworkX</td>
<td>1.1, 1.6, 1.9</td>
<td>Python package for the creation, manipulation, and study of the structure, dynamics, and functions of complex networks.</td>
</tr>
</tbody>
</table>

Biology Software

Chemistry Software

Engineering Software

Geography Software

Mathematics Software and Libraries

Molecular Dynamics Software

Profiling and Debugging Tools
Software Specific Tutorials

Various software specific tutorials are available.