

## Steps to Download and Use BACI

1. Type in the url of the **BACI** home page in your favorite browser:  
[www.mines.edu/fs\\_home/tcamp/baci](http://www.mines.edu/fs_home/tcamp/baci)
2. Download and unzip the **BACI DOS** executables. You should put the folder called **badosex** directly on the C drive so it's easy to find. You should do all your BACI work inside this directory.
3. Say if your **badosex** folder in C:\badosex, then in your command prompt (cmd) your path should be **C:\badosex> bacc <file\_name>**

## Compiling and Running using BACI

1. Make sure that **prog1.cm** is in the **badosex** folder. Note the .cm extension. This is the extension that identifies BACI source files to the BACI compiler.
2. Invoke the compile command **bacc prog1** This creates an object file called **prog1.pco** and also a listing file called **prog1.lst**.
3. Invoke the interpreter through the command **bainterp prog1** to execute your code. **bainterp** has an option **-t** that will display the order in which processes terminate within the program.

A BACI source file using the C-- compiler should use a .cm suffix. To execute a program in BACI, there are two steps:

1. Compile a ".cm" file to obtain a PCODE file (.pco)  
Usage: **bacc** [optional\_flags] source\_filename  
Optional\_flags:
  - h show this help
  - c make a .pob object file for subsequent linking
2. Interpret a PCODE file (.pco) to execute the program  
Usage **bainterp** [optional\_flags] pcode\_filename  
Optional\_flags:
  - d enter the debugger, single step, set breakpoints
  - e show the activation record (AR) on entry to each process
  - x show the AR on exit from each process
  - t announce process termination
  - h show this help
  - p show PCODE instructions as they are executed