

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
2. Download and unzip the **BACI DOS** executables. You should put the folder called **badosxe** 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 **badosxe** folder in C:\badosxe, then in your command prompt (cmd) your path should be **C:\badosxe> bacc <file_name>**

Compiling and Running using BACI

1. Make sure that **prog1.cm** is in the **badosxe** 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