



DEVELOPMENT TOOLS ON FERMI



Introduction to the FERMI Blue Gene/Q, for users and developers

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PROFILING & DEBUGGING ON FERMI

This talk will show the most important tools installed on FERMI for development purposes, i.e. debugging & profiling tools

FERMI isn't the proper cluster for development, since its particular architecture, so profiling and debugging on this machine may not be easy at all. However, something can still be done!



DISCLAIMER: This is NOT a lecture about how to use the tools presented, but about how to use them ON FERMI (compiling, running, etc.). For more informations about the tools general functionalities, please consult the documentation linked on the last slide.







PART I

PROFILING ON FERMI





FERMI PROFILING TOOLS





HPC toolkit



Scalasca







GPROF





GNU Profiler – Gprof : The GNU profiler can be used to determine which parts of a program are taking most of the execution time.

Gprof can produce the following output styles:

- Flat Profile: The flat profile shows how much time was spent executing directly in each function.
- Call Graph: The call graph shows which functions called which others, and how much time each function spent when its subroutine calls are included.





GPROF – FLAT PROFILE



The **flat profile** shows the total amount of time your program spent executing each function.

Note that if a function was not compiled for profiling, and didn't run long enough to show up on the program counter histogram, it will be indistinguishable from a function that was never called.

Flat profile:

Each sa	ample counts	as 0.01	seco	nds.			
२ ०	cumulative	self			self	total	
time	seconds	seconds	ca	lls	ms/call	ms/call	name
33.34	0.02	0.02	7	208	0.00	0.00	open
16.67	0.03	0.01		244	0.04	0.12	offtime
16.67	0.04	0.01		8	1.25	1.25	memccpy
16.67	0.05	0.01	12	7	1.43	1.43	write
16.67	0.06	0.01					mcount
0.00	0.06	0.00		236	0.00	0.00	tzset
0.00	0.06	0.00		192	0.00	0.00	tolower
0.00	0.06	0.00		47	0.00	0.00	strlen
0.00	0.06	0.00		45	0.00	0.00	strchr
0.00	0.06	0.00		1	0.00	50.00	main
0.00	0.06	0.00		1	0.00	0.00	memcpy
0.00	0.06	0.00		1	0.00	10.11	print
0.00	0.06	0.00		1	0.00	0.00	profil
0.00	0.06	0.00		1	0.00	50.00	report





GPROF – CALL GRAPH



The **call graph** shows how much time was spent in each function and its children. With this you may spot functions that may not have used much time by themselves, but called other functions that did use unusual amounts of time

index	% time	self	children	called	name
[1]	100.0	0.00	0.05	1/1	<pre><spontaneous> start [1] main [2]</spontaneous></pre>
		0.00	0.00	1/2 1/1	on_exit [28] exit [59]
[2]	100 0	0.00	0.05	1/1	start [1]
	100.0	0.00	0.05	1/1	report [3]
1.21	100.0	0.00	0.05	1/1	main [2]
[3]	100.0	0.00	0.03	8/8	timelocal [6]
		0.00	0.01	9/9	print [9] fgets [12]
		0.00	0.00	12/34 8/8	strncmp <cycle 1=""> [40] lookup [20]</cycle>
		0.00	0.00	1/1 8/8	fopen [21] chewtime [24]
		0.00	0.00	8/16	skipspace [44]
[4]	59.8	0.01 0.01 0.00	0.02 0.02 0.00	8+472 244+260 236+1	<cycle 2="" a="" as="" whole=""> [4] offtime <cycle 2=""> [7] tzset <cycle 2=""> [26]</cycle></cycle></cycle>

granularity: each sample hit covers 2 byte(s) for 20.00% of 0.05 seconds





COMPILE, RUN & ANALYZE



Compile and link the program with options: -g -pg -qfullpath
 -g is for activating debugging specifics, -pg is for profiling ones
 -qfullpath is for displaying the fullpath of the source code files in gprof output

2. Run the executable with a jobscript as usual

3. Several files will be generated, named gmon.out.<*MPI rank*>. Those are binary files and therefore can't be read with normal text editors.

Convert them to text files with the command: gprof test_gprof.exe gmon.out.0 > gprof.0.txt





SCAI DEALING WITH TASKS AND THREADS



By default, gmon.out files are generated only for ranks 0 - 31. You can customize the number of profiled ranks by setting the environment variable **BG_GMON_RANK_SUBSET**:

> **BG_GMON_RANK_SUBSET = N** -- Generates the gmon.out file for rank N only

- **BG_GMON_RANK_SUBSET = N:M** -- Generates gmon.out files for from rank N to M
- **BG_GMON_RANK_SUBSET = N:M:S** -- Generates gmon.out files from rank from N to M, skipping S. For example, 0:16:8 generates gmon.out.0, gmon.out.8 and gmon.out.16

By default, thread profiling is not enabled. To enable it, set this environmental variable: **BG_GMON_START_THREAD_TIMERS = all** -- enables the SIGPROF timer on all threads

> **BG_GMON_START_THREAD_TIMERS = nocomm** -- enables the SIGPROF timer on all threads, except for the ones created to support MPI

- Add a call to the gmon_start_all_thread_timers() function to the program, from the main thread

- Add a call to the gmon_thread_timer(int start) function on the thread to be profiled: 1 to start, 0 to stop



IBM® HPC TOOLKIT





HPC toolkit is a collection of tools created for analyzing performance of parallel applications written in C or Fortran on BG/Q systems.

The tools provided by the toolkit provide profile analysis that can be categorized in four groups of interest:

Hardware Performance Monitor (HPM): measurement of cache misses, number of floating point instructions executed, branch prediction counts, ...

MPI profiling: tracing of MPI calls, communication patterns observation, measurement of the time spent in each MPI function and the size of the MPI messages

OpenMP profiling: informations about the time spent in OpenMP constructs, overhead in OpenMP constructs, balancing of the workload across OpenMP threads

I/O profiling: informations about I/O calls made in the application, understanding of the I/O performance of the application and to identifying possible I/O performance problems in the application (not treated in this presentation)



HPM LIBRARIES



To profile with HPM libraries, you have to add to the source code the proper functions/routines in charge of event countering. It is possible to choose from a list of sets of hardware counter events to focus on a specific performance area.

The main functions are:

- **hpmInit()** for initializing the instrumentation library.
- **hpmTerminate()** for generating the reports and performance data files and shutting down the HPM environment.
- **hpmStart()** for identifying the start of a section of code in which hardware performance counter events will be counted.
- hpmStop() for identifying the end of the instrumented section.
- hpmStart and hpmStop can be inserted as desidered, but they must be executed in pairs.
- The section identifier label is passed as the parameter to the **hpmStart** and the matching **hpmStop** function.





HPM LIBRARIES EXAMPLE



#include <hpm.h> int main(int argc, char *argv[]){ float x; hpmlnit(); x=10.0; hpmStart("Instrumented section 1"); for(int i=0; i<100000; i++){ x=x/1.001; hpmStop("Instrumented section 1"); hpmStart("Instrumented section 2"); /* other computation */ hpmStop("Instrumented section 2"); hpmTerminate();

#include "f_hpm.h"
integer i
real*4 x
call f_hpminit();
x=10.0
 call f_hpmstart('Instrumented section 1', 22)
 do i=1,00000
 x=x/1.001
 enddo
 call f_hpmstop('Instrumented section 1', 22)
...
call f_hpmstart('Instrumented section 2', 22)
! other computation

```
call f_hpmstop('Instrumented section 2', 22)
call f_hpmterminate()
end program
```





COMPILE & RUN

- Set environment variables: run the setup script cd /bgsys/ibmhpc/ppedev.hpct ./env_sh (for sh, bash,ksh shell) source snv_csh (for csh shell)
- 2. Compile with **-g** and statically link HPM libraries. non-threaded application:
 - mpixlc myprog.c -o myprog -l/bgsys/ibmhpc/ppedev.hpct/include/ \
 - -L/bgsys/drivers/ppcflor/bgpm/lib/ \
 - -L/bgsys/ibmhpc/ppedev.hpct/lib64 -lhpc -lbgpm

threaded application:

mpixlc_r myprog.c -o myprog_r -l/bgsys/ibmhpc/ppedev.hpct/include/ \

- -L/bgsys/drivers/ppcflor/bgpm/lib/ \
- -L/bgsys/ibmhpc/ppedev.hpct/lib64 -lhpc_r -lbgpm -qsmp=omp
- 3. Run the application as usual.

WARNING:

HPM libraries collect information and compute summaries during run time. Because of this, there may be **overhead** if instrumentation sections are inserted inside inner loops which are executed many times.





PERFORMANCE DATA FILES



HPM will generate a performance data file for each rank, named *hpmCounts_<rank>.txt* There is also a .viz file for visualization with Peekperf (more on this later).

Some environmental variables can control the generation of the HPM files:

HPM_IO_BATCH = set it to **yes** to reduce the number of output simultaneously opened by HPM in order to reduce file system impact

HPM_OUTPUT_PROCESS = set it to **all** if you want that all the MPI task write the performance data files; set it to **root** if you want that only root processor writes the performance data file.

HPM_SCOPE (non-threaded version) = set it to **node** to aggregate at node level the sum of the data file produced; set it to **process** if you want the each task produces a performance data file.

Default:

HPM_ASC_OUTPUT = no HPM_VIZ_OUTPUT = yes HPM_IO_BATCH = no HPM_OUTPUT_PROCESS = all HPM_SCOPE = process





MPI PROFILING LIBRARIES



The **libmpitrace** library is used for profiling the MPI function calls, by creating a trace of them;

when an application is linked with such library, it intercepts the MPI calls in the application, using the Profiled MPI (PMPI) interface defined by the MPI standard, and obtains the needed profiling and trace informations.

The library also provides a set of functions that can be used to control how profiling and trace data is collected can be used to customize the trace data (see the manual linked at the documentation slide)





COMPILE & RUN



 Set environment variables: run the setup script cd /bgsys/ibmhpc/ppedev.hpct ./env_sh (for sh, bash,ksh shell) source snv_csh (for csh shell)

2. Compile with -g and statically link libmpitrace library. mpixlc myprog.c -o myprog \ -l/bgsys/ibmhpc/ppedev.hpct/include/ \ -L/bgsys/ibmhpc/ppedev.hpct/lib64 -Impitrace

3. Run the application as usual.





PERFORMANCE DATA FILES



A data file for each rank will be generated: *mpi_profile_<world_id>_<world_rank>.txt* There is also a .viz file for visualization with Peekperf (more on this later). *world_id* is the MPI world id; world_rank is the MPI task rank of the task that generated

the file. The file *single_trace_<world_id>* contains trace data, and can be visualized with Peekperf.

Default settings:

- number of trace event collected per task = 30000.
 - (MAX_TRACE_EVENTS)
- only 4 output files will be generated: for task 0, and for tasks having maximum, minimum and median total MPI communication time. (OUTPUT_ALL_RANKS)
- all the MPI calls after MPI_Init() are traced. (TRACE_ALL_EVENTS)
- max 256 MPI tasks are traced (MAX_TRACE_RANK, TRACE_ALL_TASKS)



OPENMP PROFILING LIBRARIES



- The openMP profiling libraries are used for analyzing performance problems in an OpenMP application.
 - They help in determining if the OpenMP application properly structures its processing for achieving the best performance.
 - They obtain informations about:
 - time spent in OpenMP constructs in the application
 - overhead in OpenMP constructs
 - how is the workload balanced across OpenMP threads in the application





COMPILE & RUN



- Set environment variables: run the setup script cd /bgsys/ibmhpc/ppedev.hpct ./env_sh (for sh, bash,ksh shell) source snv_csh (for csh shell)
- Compile with -g and statically link openMP profiling libraries. mpixlc myprog.c -o myprog -qsmp=omp \
 -L/bgsys/ibm_compilers/prod/opt/ibmcmp/xlsmp/bg/3.1/bglib64/ \
 -lxlsmp_pomp -L/bgsys/ibmhpc/ppedev.hpct/lib64 -lpompprof_probe \
 -lm -g
- 3. Run the application as usual.

A data file for each MPI rank will be generated: popenmp_prof_<*rank>* There is also a .viz file for visualization with Peekperf





PEEKPERF



Peekperf provides a GUI interface to view application performance data.

It allows to visualize and analyze the collected performance data, collected in the in the visualization (.viz) files from the various instrumentation libraries.

If more than one visualization file is specified, peekperf combines the data from them and displays the result.

It also provides filtering and sorting capabilities to help you analyze the data.

GI DAT	A VISUALIZ	ATION WINDOW	8	SOURCE CODE WINDOW	- 0 8
hpmdata			worker.c	.c time.c	
Label rusage time.c worker.c calc_load	User time 2.588	X_L2_RQSTS_PREFETCH_HIT 92771 66383	231 232 233 234 235 236 237	neighbour_send(prv, my_id, CALC1b, u, jstart); neighbour_send(prv, my_id, CALC1c, v, jstart); neighbour_receive(nxt, my_id, CALC1a, p, (jend+1) % n); neighbour_receive(nxt, my_id, CALC1b, u, (jend+1) % n); neighbour_receive(nxt, my_id, CALC1c, v, (jend+1) % n);	
I			238 239 240 241 242 243	/* this procedure does all the message passing after the call to _calcuvzh_ */ calc_unload(prv,nxt,my_id,jstart,jend,cv,z) int prv; int nxt;	

/bgsys/ibmhpc/ppedev.hpct/bin/peekperf

Figure 14: Peekperf viewing hardware performance counter data



SCALASCA





SCALASCA (SCalable performance Analysis of LArge SCale Applications) is a software tool that supports the performance optimization of parallel programs by measuring and analyzing their runtime behavior. The analysis identifies potential performance bottlenecks – in particular those concerning communication and synchronization – and offers guidance in exploring their causes.

Like with HPC toolkit libraries, Scalasca takes advantage of a process of **event tracing**: for each thread/task is defined a buffer that measures the number of calls to functions, the time spent on each routine and so on. Final results are collected at the end.





PROFILING WITH SCALASCA



In order to profile an application with Scalasca, you have to compile and execute your application with the proper setting. Follow these instructions:

1. *module load autoload scalasca* (autoload the bgq-xl compiler)

2. Compile with *scalasca -instrument* (or its alias "skin"): *skin mpixlf90 -openmp -o bar bar.f90* Notice that there are no other specific flags that have to be added

3. Execute in a job script with *scalasca -analyze* (before the runjob command)



SCALASCA JOB SCRIPT EXAMPLE



#!/bin/bash

- # @ job_name = myjob.\$(jobid)
- # @ output = \$(job_name).out
- # @ error = \$(job_name).err
- # @ environment = COPY_ALL
- # @ job_type = bluegene
- # @ wall_clock_limit = 1:00:00
- # @ bg_size = 128
- # @ account_no = <Account number>
- # @ notification = always
- # @ notify_user = <valid email address>

@ queue

export OMP_NUM_THREADS=4 module load autoload scalasca/1.4.2

scalasca -analyze runjob --np 256 --ranks-per-node 4 --env-all --exe <my_exe>





EPIK ARCHIVE



After the execution, a folder named **epik_<myexe>_<resources>_sum** will be created. It contains the following files:

- epik.conf Measurement configuration of the execution
- epik.log Output of the instrumented program and measurement system
- epik.path Callpath-tree recorded by the measurement system
- epitome.cube Intermediate analysis report of the runtime summarization system
- summary.cube[.gz] Post-processed analysis report of runtime summarization





EXAMINE RESULTS



The content of the epik folder can be examinated via the *scalasca -examine* command:

scalasca -examine epik_<myexe>_<resources>_sum
to examinate the report by GUI

scalasca -examine -s epik_<myexe>_<resources>_sum
to examinate the report by textual score output
 (the file epik.score will be added in the epik directory)

Results are displayed using three coupled tree browser showing:

- Metrics (i.e. Performance properties/problems)
- Call-tree or flat region profile
- System location





EXAMINATION BY GUI









METRICS



Time	Total CPU allocation time
Visits	Number of times a routine/region was executed
Synchronizations	Total number of MPI synchronization operations that were executed
Communications	The total number of MPI communication operations, excluding calls transferring no data (which are considered Synchronizations)
Bytes transferred	The total number of bytes that were sent and received in MPI communication operations. It depends on the MPI internal implementation.
MPI file operations	Number of MPI file operations of any type.
MPI file bytes transferred	Number of bytes read or written in MPI file operations of any type.
Computational imbalance	This simple heuristic allows to identify computational load imbalances and is calculated for each (call-path, process/thread) pair.



MANUAL SOURCE CODE INSTRUMENTATION



Region or phase annotations manually inserted in source file can augment or substitute automatic instrumentation, and can improve the structure of the analysis reports to make them more comprehensible to read

These annotations can be used to mark any sequence or block of statements, such as functions, phases, loop nests, etc., and can be nested, provided that every enter has matching exit

If automatic compiler instrumentation is not used, it is typically desiderable to manually instrument at least the **main** function/program and perhaps its major phases (e.g. initialization, core/body, finalization).



SCA MANUAL INSTRUMENTATION EXAMPLE

#include "epik_user.h"

```
void foo(){
   ......// local declarations
   .....// more declarations
   EPIK_FUNC_START();
   if(...){
      EPIK_FUNC_END();
      return;
   } else {
      EPIK_USER_REG (r_name,
        "region");
      EPIK_USER_START (r_name);
      EPIK_USER_END (r_name);
   }
   EPIK FUNC END();
   return;
```

#include "epik_user.inc"



```
subroutine bar()
   EPIK_FUNC_REG("bar")
   EPIK_USER_REG (r_name,
      "region")
   ....! local declarations
   EPIK_FUNC_START();
   ....! executable statements
   if(...) then
       EPIK_FUNC_END()
       return
   else
       EPIK_USER_START (r_name)
       EPIK_USER_END (r_name)
   endif
   ....! executable statements
   EPIK FUNC END()
   return
```





PART II

DEBUGGING ON FERMI





DEBUGGING ON FERMI...



Debugging on FERMI is **no** easy task!

Error messages are often vague, and core files may be rather incomprehensible...

However, there are some useful tools that can help on the task!

Before that, let's see some general advice for the setting of a debug session





COMPILING FOR A DEBUG SESSION



3 flags are required for compiling a program that can be analyzed by debugging tools:

- -g : integrates debugging symbols on your code, making them "human readable" when analyzed from debuggers
- -O0 : avoids any optimization on your code, making it execute the instructions in the exact order they're implemented
- -qfullpath : Causes the full name of all source files to be added to the debug informations





OTHER USEFUL FLAGS



- -qcheck Helps detecting some array-bound violations, aborting with SIGTRAP at runtime
- -qflttrap Helps detecting some floating-point exceptions, aborting with SIGTRAP at runtime
- -qhalt=<sev> Stops compilation if encountering an error of the specified lever of severity
- -qformat Warns of possible problems with I/O format specification (C/C++) (printf,scanf...)
- -qkeepparm ensures that function parameters are stored on the stack even if the application is optimized.





FERMI DEBUGGING TOOLS



GDB





addr2line

Totalview







GDB



On FERMI, GDB is available both for front-end and back-end applications



Front-end: *gdb* <*exe*> **Debugger** Back-end: */bgsys/drivers/ppcfloor/gnu-linux/bin/powerpc64-bgq-linux-gdb* <*exe*> Back-end shortcut: *module load gdb be-gdb* <*exe*>

It is possible to make a post-mortem analysis of the **binary** core files generated by the job: *module load gdb be-gdb <exe> <corefile>*

To generate binary core files, add the following envs to runjob: --envs BG_COREDUMPONEXIT=1

--envs BG_COREDUMPBINARY=*

"" means "all the processes". It is possible to indicate which ranks generate their core by specifying their number





GDB – REMOTE ACCESS



The Blue Gene/Q system includes support for using GDB real-time with applications running on compute nodes.

IBM provides a simple debug server called gdbserver. Each running instance of GDB is associated with one process or rank (also called GDB client).

Each instance of a GDB client can connect to and debug one process. To debug multiple processes at the same time, run multiple GDB tools at the same time. A maximum of four GDB tools can be run on one job.



...so, how to do that?





USING GDB ON RUNNING APPLICATIONS



1) First of all, submit your job as usual; *llsubmit <jobscript>*

2) Then, get your job ID; *llq -u \$USER*

3) Load the GDB module; it contains the shortcut for the backend GDB and the script for the environment setting *module load gdb*

4) Launch the "gdb-setup" script. It will print the instructions for the next steps gdb-setup -j <jobid> -r <rank #>



USING GDB ON RUNNING APPLICATIONS



5) Launch GDB! (back-end version); be-gdb ./myexe

6) Connect remotely to your job process (the value of *<IP* address> was printed on the screen after step 4); (gdb) target remote *<IP* address>:10000

7) Start debugging!!!

(Although you aren't completely free...for example, command 'run' does not work)





ADDR2LINE



If nothing is specified, an unsuccesful job generates a text core file for the processes that caused the crash...

...however, those core files are all but easily readable!



addr2line is an utility that allows to get from this file informations about where the job crashed





CORE FILES



Blue Gene core files are lightweight text files

Hexadecimal addresses in section STACK describe function call chain until program exception. It's the section delimited by tags: +++STACK / ---STACK

+++STACK

Frame	Address	Saved	Link	Reg
000000	1fffff5ac0	0000	00000	000001c
000000	1ffff5bc0	0000	00000	18b2678
000000	1ffff5c60	0000	00000	15046d0
000000	1ffff5d00	0000	00000	15738a8
000000	1ffff5e00	0000	00000	15734ec
000000	1ffff5f00	0000	00000	151a4d4
000000	1ffff6000	0000	00000	15001c8
STA	CK			

In particular, "Saved Link Reg" column is the one we need!





USING ADDR2LINE



From the core file output, save only the addresses in the Saved Link Reg column:

000000000000001c 00000000018b2678 00000000015046d0 00000000015738a8 00000000015734ec 00000000151a4d4

Replace the first eight 0s with 0x:

 $0000000018b2678 => 0 \times 018b2678$ If you load the module "superc", a simple script called "a2I-translate" is capable of doing the replacement for you: module load superc a2I-translate corefile

Lauch addr2line: addr2line -e ./myexe 0x018b2678 addr2line -e ./myexe < addresses.txt





TOTALVIEW

TotalView is a GUI-based source code defect analysis tool that gives you control over processes and thread execution and visibility into program state and variables.



It allows you to debug one or many processes and/or threads with complete control over program execution.

It is by far the most versatile and user-friendly debugger on our clusters!!



REMOTE CONNECTION MANAGER (RCM)



Launching Totalview on FERMI is complicated, since it involves working with a GUI during a working execution. Thus you need to see what's inside the computing nodes, that aren't very "graphicalfriendly"

There are some workarounds for this issue, one of them involves estabilishing a VNC connection and use it for SSH tunneling to your local workstation

The easiest, however, is to use the Remote Connection Manager devolped by CINECA!!





USING TOTALVIEW: PREPARATION



1) Download the version of RCM that suits your Operative System: <u>http://www.hpc.cineca.it/services/remote-visualisation</u>

	74 RCM Login:					
ng						
	REMO	TE CONNECTION MANAGER				
		version: 1.1.405				
	Sessions:	amarani0@login.fermi.cineca.it 💻				
	Host:	login.fermi.cineca.it				
	User:	youruser				
	Password:	****				
		LOGIN				

 For Windows users, an X server like Xmin may be needed: <u>http://sourceforge.net/projects/xming/</u>.
 Download and launch it.

3) Launch RCM and fill the boxes as in the picture (type the credentials you use for accessing FERMI)

4) Select "new display". A job (budget-free) in the special "visual" queue will create a remote display for 12 hours



USING TOTALVIEW: JOB SCRIPT SETTING

5) Inside your job script, you have to load the proper module and export the DISPLAY environment variable:

module load totalview

export DISPLAY=fen<no>:xx

where xx and <no> are as you can see in the name of the remote display window (as in the picture)

TurboVNC: fen02:9 (amarani0) [Tight + JPEG 1X Q95]

6) Totalview execution line (inside your LoadLeveler script) will be as follows: totalview runjob -a <runjob arguments: --np, --exe, --args...>

7) Launch the job. When it will start running, you will find a Totalview window opened on your remote display! Closing Totalview will also kill the job.





Using Totalview: start debugging

••	Startup Parameters - runjob (on fen03)	×			
Debugging Options	Arguments Standard I/0 Parallel				
Please Note: If y Use the Arguments	your parallel settings were entered as arguments, do not enter : tab to modify them.	them here.			
Parallel system:	None	Y			
Tasks:	n 🔺 Nodes:				
Additional starte	r arguments:				
Ĭ					
📕 Show Startup Parameters when TotalView starts					
Changes take effect at process startup.					
OK	Cancel	Help			

Select "BlueGene" as a parallel system, and a number of tasks and nodes according to the arguments you gave to runjob during submission phase.

Click "Go" (the green arrow) on the next screen and your application will start running.

WARNING: due to license issues, you are NOT allowed to run Totalview sessions with more than 1024 tasks simultaneously!!!

WARNING: The BG/Q version of Totalview doesn't implement Replay Engine yet.





DOCUMENTATION



PROFILING:

GPROF

http://www.cs.utah.edu/dept/old/texinfo/as/gprof_toc.html

HPC TOOLKIT (ON BG\Q)

http://community.hartree.stfc.ac.uk/access/content/group/admin/HPC%20Training/BG_Q %20training%20course%20February%202013/Reference/hpct_guide_bgq_V1.1.1.0.pdf SCALASCA

http://apps.fz-juelich.de/scalasca/releases/scalasca/1.4/docs/UserGuide.pdf

DEBUGGING: <u>http://www.hpc.cineca.it/sites/default/files/Debug%20guide_0.pdf</u>

GDB

https://sourceware.org/gdb/current/onlinedocs/gdb/

TOTALVIEW

http://www.roguewave.com/portals/0/products/totalview-

family/totalview/docs/8.13/html/index.html#page/User_Guides/totalviewug-title.html

The course "Introduction to HPC Scientific Programming: tools and techniques" may also prove useful! <u>http://www.hpc.cineca.it/content/hpc-scientific-programming</u>