From: Adam Byrd <adam1.byrd@gmail.com>
Subject: **Re: job ran perfectly on 32 processors**
Date: September 9, 2011 3:15:07 PM EDT
To: Mark Jack <mark.a.jack@gmail.com>
1 Attachment, 2.0 KB

Dr. Jack,

I managed to get a factor of 5-10 speed up on the code. We're seeing 1 second energy steps on the Macs and about 1.5 second steps on Pegasus. It was a simple matter of reconfiguring PETSc and it performed perfectly. I submitted jobs for 1, 2, 4, 8 ,16, 32, 64, 128 processors and I'll check all of them tomorrow to compare the times. I'll plot them all and see what kind of scaling we're really seeing. If they complete successfully, I'll be completely convinced there are no bugs left. I'm attaching the scripts I used to configure PETSc. Just note that you need to be in the PETSc folder you want set as PETSC_DIR for it to work, else you'll have to change the script to set PETSC_DIR manually. Also, you'll have to set your PETSC_ARCH after it's finished installing (export PETSC_ARCH=whatever was used in the script). It will also need to be changed in .profile (Mac) or .bashrc (clusters) to make it permanent. You can change between PETSc installations at any time just by changing the environment variable for PETSC_ARCH.

I'll run the same 8 jobs again when these finish with -log_summary to see any sources of delay for higher processor counts as well. That should gives us an idea of why it takes a little longer to set up sometimes.

If you have any questions, shoot me an email.

Respectfully,
Adam Byrd

On Thu, Sep 8, 2011 at 6:58 PM, Mark Jack <mark.a.jack@gmail.com> wrote:

> It's submitted for 256 processors specified as 'large' in the queue. It might take a while until it starts in the job queue.
>
> Check with Xerox and their job postings. You might be able to get something in coding part-time there. One of my Sunday jogging partners is a former Xerox employee there. He hasn't worked there in more than 15 years but he might still have some contacts there if you're interested.
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> I'll be in 419 after 9:30 a.m. I'm taking that one box to MAC Business Systems in the afternoon to get it fixed, should be still under warranty. I could use a hand carrying the thing to my car.
>
> MJ
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> On Sep 8, 2011, at 6:46 PM, Adam Byrd wrote:
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> > Great news! I'm glad it's finally working. I should be in tomorrow morning to get some benchmarking done. I'm still hoping for 1 second steps. I also plan to see what causes the initial delay if I have time.
> >
> > I checked into tutoring at TCC, but they only pay $9 an hour. They mentioned being able to make more if you're there long enough and go through certain training courses. I thought it would be useful info to know in case anyone else considers it in the future.
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> > On Thu, Sep 8, 2011 at 4:22 PM, Mark Jack <mark.a.jack@gmail.com> wrote:
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> > i forgot to attach the output of the run.
> > mj
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> > On Sep 8, 2011, at 3:52 PM, Mark Jack wrote:
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> > > >
> > > > Yesterday's job ran perfectly on 32 processors in about 58 minutes on U Miami Pegasus using Intel compilers and Intel MPICH2.
> > > >
> > > > We now have a working code! I'll rerun it on 64 processors. Indications were that it'll literally be done in 15 minutes. That means we'll be able to create magnetoresistance plots I vs. B easily in a day. Now we can start doing some physics. First task for the next week:
> > > > Benchmarking runs, optimizations in compilation etc. from 32 to 512 processors with some plots on code performance.
> > > >

> > Attached is that latest version you sent me for Dr. Encinosa and Leon.
> >
> > I'll contact Dr. Leamy that we can now run his data.
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> > Hopefully, over the weekend I'll find time to get correct numbers also for zigzag.
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> > MJ
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> > <PETScCntor.rar>
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> > P.S.: Simply unzip with 'unzip PETSc....rar'. Compile (if you have PETSc library installed with C++ and Fortran compilers) with 'make cntor'. And then run on one or multiple processors with MPI.
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> > On Sep 8, 2011, at 2:23 PM, Adam Byrd wrote:
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> >> Any luck with the latest version of the code? I ran 3 full runs, 2 ran perfect and 1 failed, but I'm almost 100% positive the failure was a fluke on one of the nodes. It looked like one of them went down. I've also run half a dozen runs over random energy values, I can't get any more failures to occur.
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