add warning that separate PME ranks are never used with GPUs

With GPUs separate PME ranks are never used. This is partly because resource splitting between PP and PME ranks is too complex in GPU accelerated tuns to manage in an automated fashion. Secondly, as the CPU does PME and bondeds overlapping with the GPU, offloading PME to separate ranks leaves very little computation on the CPU to overlap with the GPU. Additionally, the number of PME ranks is closely linked to the number of GPUs and therefore the user would anyway have to make sure that enough ranks are launched to accomodate PP ranks for all GPUs as well as separate PME ranks.

However, in practice, partly due to multi-threaded scaling, using separate PME ranks (which implicitly leads to less threads being used in both PP and PME) does improve performance. Most notably, on the Cray XK7 this is true already at moderate node counts.

Some related discussion can be found here: [https://gerrit.gromacs.org/#/c/2694](https://gerrit.gromacs.org/#/c/2694) (comments on patch set 15-17).

Related issues:
Related to Gromacs - Bug #1148: switching to separate PME nodes with hybrid p... Closed

Associated revisions
Revision 094302b3 - 06/17/2014 08:48 PM - Berk Hess

Updated mdrun -npme documentation

The number of nodes at which PME nodes are used has increased.
Added note on PME nodes not being selected automatically with GPUs.

Fixes #1374.

Change-id: le1de87abd3d1204d99af8b4f8e6809e7806f5c08

Revision 31cc5ae9 - 06/05/2015 07:46 PM - Berk Hess

Don't use PME ranks with GPUs and -npme=-1

The code disabling the automated PME rank choice with GPUs was accidentally moved after init_domain_decomposition. This caused PME ranks to be set up, but later a fatal_error occured for inconsistent PP rank and GPU counts.
Refs #1374.

Change-id: 5f6bccc90fecac7f63b332b8f1acca7368b5f71bc
So there seem to be two regimes where PME nodes can help with GPUs:
1) Many physical nodes/ MPI ranks. Here the user start MPI with a number of ranks and we have the number of GPUs given, so we can't really freely choose PME ranks, since \#MPI-ranks==\#GPUs.
2) A single node. But here we won't reach our current MPI rank limit, since we won't have more than 4 GPUs in a single node. So although PME ranks might help, we can't automate for 1) and case 2) is very different from the current switching.

I agree. Note that i ma not suggesting to automate the switching, but to warn the user that separate PME ranks may help, but he/she has to set it up manually. Some criteria on when to trigger the warning would be nice (based on the total number of cores/hardware threads used?) to avoid issuing spurious notes. However, as noted in the gerrit discussion, to be able to do this we'd need to solve \#1148 first.

I don't think this requires a warning. I updated mdrun -h with a note on PME nodes not being selected automatically with GPUs. Since now mdrun does what it says, a warning is not necessary.
#8 - 06/17/2014 10:45 PM - Berk Hess
- Status changed from Fix uploaded to Resolved
- % Done changed from 0 to 100

Applied in changeset 094302b350cf0e4e5ec755a9b06972ac652a724e.

#9 - 06/18/2014 01:10 PM - Mark Abraham
- Status changed from Resolved to Closed

#10 - 06/19/2014 09:30 PM - Szilárd Páll
I missed the part that the recently merged change "fixes" this.

Most users expect that mdrun or mpiun -np N mdrun mpi just works optimally. Don't you think that the user should be explicitly warned, if nothing else, at the rank count where the switching would automatically happen in CPU-only runs (unless #1148 gets fixed) that he/she should really consider separate PME ranks. On all machines where I ran so far, using separate PME ranks was always faster above 4-8 sockets.

#11 - 05/18/2015 03:05 AM - Szilárd Páll
Actually, this is not true, the fixing commit added an incorrect statement to the docs:

```
$ $mdrun -version 2>&1 | grep ' VERSION'
Gromacs version: VERSION 4.6.6-dev-20140522-d77dddb

$mdrun -ntmpi 32 -ntomp 1 -gpu_id $(strrep 0 16)$($(strrep 1 16) -s ../topol.tpr
[...]
Will use 24 particle-particle and 8 PME only nodes
This is a guess, check the performance at the end of the log file
Using 32 MPI threads
Using 1 OpenMP thread per tMPI thread
Compiled acceleration: AVX_256 (Gromacs could use AVX_128_FMA on this machine, which is better)

2 GPUs detected:
#0: NVIDIA GeForce GTX TITAN, compute cap.: 3.5, ECC: no, stat: compatible
#1: NVIDIA GeForce GTX TITAN, compute cap.: 3.5, ECC: no, stat: compatible

2 GPUs user-selected for this run.
Mapping of GPUs to the 24 PP ranks in this node: #0, #0, #0, #0, #0, #0, #0, #0, #0, #0, #0, #0, #0, #0, #0, #0, #1, #1, #1, #1, #1, #1, #1, #1, #1, #1, #1, #1, #1, #1, #1, #1

-------------------------------------------------------
Program mdrun, VERSION 4.6.8-dev-20150212-c060264
Source code file: /nethome/pszilard/projects/gromacs/gromacs-4.6/src/gmxlib/gmx_detect_hardware.c, line: 380

Fatal error:
Incorrect launch configuration: mismatching number of PP thread-MPI threads and GPUs.
mdrun was started with 24 PP thread-MPI threads, but you provided 32 GPUs.
For more information and tips for troubleshooting, please check the GROMACS website at http://www.gromacs.org/Documentation/Errors

```

11/25/2015 3/4
Gerrit received a related patchset '1' for Issue #1374.
Uploader: Berk Hess (hess@kth.se)
Change-Id: i5f6bcc90fecac7f63b332b8f1acca7368b5f71bc
Gerrit URL: https://gerrit.gromacs.org/4619