Running Amber GPU jobs

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To request one GPU card, use SBATCH directives in job script:

```bash
#SBATCH --gres=gpu:1
```

To request a specific card type, use e.g. `--gres=gpu:k80:1`. The card types currently available are k80, p1080, p40, p100 and v100. As an example, let's submit an Amber job. Amber is a molecular dynamics software package. The recipe is:

```bash
$ mkdir -p /scratch/$USER/myambertest
$ cd /scratch/$USER/myambertest
$ cp /share/apps/Tutorials/slurm/example/amberGPU/* .
$ sbatch run-amber.s
Submitted batch job 14257
```

From the tutorial example directory we copy over Amber input data files "inpcrd", "prmtop" and "mdin", and the job script file "run-amber.s". The content of the job script "run-amber.s" is:

```bash
#!/bin/bash
#
#SBATCH --job-name=myAmberJobGPU
#SBATCH --nodes=1
#SBATCH --cpus-per-task=1
#SBATCH --time=00:30:00
#SBATCH --mem=3GB
#SBATCH --gres=gpu:1
module purge
module load amber/openmpi/intel/16.06

cd /scratch/$USER/myambertest
pmemd.cuda -O
```

The demo Amber job should take ~2 minutes to finish once it starts running. When the job is done, several output files are generated. Check the one named "mdout", which has a section most relevant here:

```
--------- INFORMATION 16.00 02/25/2016
GPU (CUDA) Version of PMEMD in use: NVIDIA GPU IN USE.
  Version 16.0.0

--------- GPU DEVICE INFO

  CUDA_VISIBLE_DEVICES: 0
  CUDA Capable Devices Detected: 1
  CUDA Device ID in use: 0
    CUDA Device Name: Tesla K80
  CUDA Device Global Mem Size: 11439 MB
  CUDA Device Num Multiprocessors: 13
    CUDA Device Core Freq: 0.82 GHz
```