Yeo Meng Han A0251772A EE3801 Lab 8A

# Lab 8 part A Step 8

freq-slurm.sh

```
...6-104:/data/src/PyHipp — ssh -i ./MyKeyPair.pem ec2-user@13.213.30.174
 GNU nano 2.9.8
                                                                          freq-slurm.sh
#!/bin/bash
# Submit this script with: sbatch <this-filename>
#SBATCH --time=24:00:00 # walltime
#SBATCH --ntasks=1 # number of processor cores (i.e. tasks)
#SBATCH --cpus-per-task=1 # number of CPUs for this task
#SBATCH -J "freq" # job name
## /SBATCH -p general # partition (queue)
#SBATCH -o freq-slurm.%N.%j.out # STDOUT
#SBATCH -e freq-slurm.%N.%j.err # STDERR
# LOAD MODULES, INSERT CODE, AND RUN YOUR PROGRAMS HERE
python →u →c "import PyHipp as pyh; \
import time; \
pyh.FreqSpectrum(saveLevel=1); \
pyh.FreqSpectrum(loadHighPass=True, pointsPerWindow=3000, saveLevel=1);
print(time.localtime());"
```

## Step 9 fsall-slurm.sh

#### Step 11

```
...6-104:/data/src/PyHipp — ssh -i ./MyKeyPair.pem ec2-user@13.213.30.174

GNU nano 2.9.8 consol_fsjobs.sh

#!/bin/sh

temp1=($(squeue))

cmd1="sbatch — dependency=afterary:"

counter1=0
    for i in "${temp1[@]}"; do
        if [["$i" == "queue1"]]; then
        idd=${temp1[$counter1-1]}
        cmd1="${cmd1}${id1}:"
    fi
    counter1=$((counter1+1))

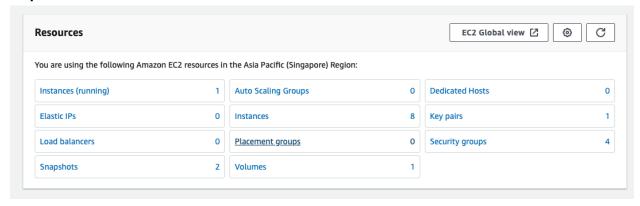
done

cmd1=${cmd1::-1}
    cmd1="${cmd1} / data/src/PyHipp/fsall-slurm.sh"

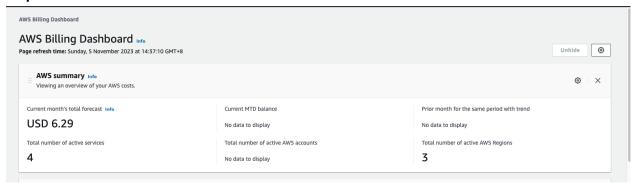
echo $cmd1
eval $cmd1
```

## Repeat these steps from Lab 5:

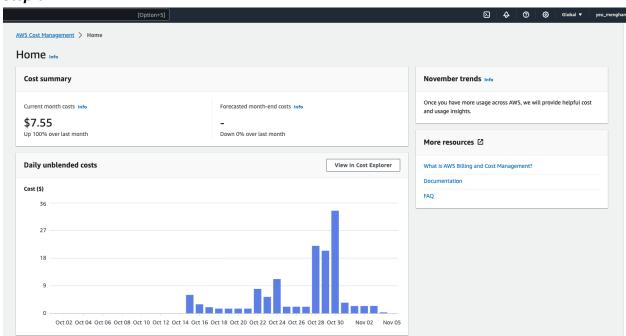
#### Step 34



#### Step 36



## Step 37



## Step 75

