

gputools: an R package for GPU computing

GETTING UP AND RUNNING WITH gputools

- gputools is already installed on impact1.stat.iastate.edu, ready to load with `library(gputools)` in R.
- For other GPU systems, download gputools from CRAN with a simple `install.packages("gputools")` in R.
- Documentation:
 - <http://brainarray.mbni.med.umich.edu/Brainarray/Rgpgpu/>
 - <http://cran.r-project.org/web/packages/gputools/index.html>
 - <http://cran.r-project.org/web/packages/gputools/gputools.pdf>
- Requirements:
 - R (\geq version 2.8.0)
 - Nvidia's CUDA toolkit (\geq version 2.3)

CONTENTS OF gputools

A handful of selected R functions implemented with CUDA C for use on a GPU:

- Choose your device:

gputools function	CPU analog	Same usage?
chooseGpu()	none	NA
getGpuId()	none	NA

- Linear algebra:

gputools function	CPU analog	Same usage?
gpuDist()	dist()	no
gpuMatMult()	%*% operator	no
gpuCrossprod()	crossprod()	yes
gpuTcrossprod()	tcrossprod()	yes
gpuQr()	qr()	almost
gpuSolve()	solve()	no
gpuSvd()	svd()	almost

- Simple model fitting:

gputools function	CPU analog	Same exact usage?
gpuLm()	lm()	yes
gpuLsfrit()	lsfit()	yes
gpuGlm()	glm()	yes
gpuGlm.fit()	glm.fit()	yes

- Hypothesis testing:

gputools function	CPU analog	Same exact usage?
gpuTtest()	t.test()	no

- Other useful algorithms:

gputools function	CPU analog	Same exact usage?
gpuHclust()	hclust()	no
gpuDistClust()	hclust(dist())	no
gpuFastICA()	fastICA() (fastICA package)	yes
gpuGranger()	grangertest() (lmtest package)	no
gpuMi()	???	???
gpuSvmPredict()	See www.jstatsoft.org/v15/i09/paper	no
gpuSvmTrain()	See www.jstatsoft.org/v15/i09/paper	no

MANAGING YOUR DEVICES: chooseGpu() AND getGpuId()

Background: Impact1 has four GPUs, each with a unique index from 0 to 3. To see this for yourself, log into impact1 and run the following:

```
[landau@impact1 ~]$ cd /usr/local/NVIDIA_GPU_Computing_SDK/C/bin/linux/release  
[landau@impact1 release]$ ./deviceQuery
```

Here are some pieces of the (quite verbose) output of `./deviceQuery`:

```
[deviceQuery] starting...
```

```
./deviceQuery Starting...
```

```
  CUDA Device Query (Runtime API) version (CUDA static linking)
```

```
Found 4 CUDA Capable device(s)
```

```
Device 0: "Tesla M2070"
```

CUDA Driver Version / Runtime Version	4.1 / 4.1
CUDA Capability Major/Minor version number:	2.0
Total amount of global memory:	5375 MBytes (5636554752 bytes)
(14) Multiprocessors x (32) CUDA Cores/MP:	448 CUDA Cores
GPU Clock Speed:	1.15 GHz
Memory Clock rate:	1566.00 Mhz
Memory Bus Width:	384-bit
L2 Cache Size:	786432 bytes

Device 1: "Tesla M2070"

CUDA Driver Version / Runtime Version	4.1 / 4.1
CUDA Capability Major/Minor version number:	2.0
Total amount of global memory:	5375 MBytes (5636554752 bytes)
(14) Multiprocessors x (32) CUDA Cores/MP:	448 CUDA Cores
GPU Clock Speed:	1.15 GHz
Memory Clock rate:	1566.00 Mhz
Memory Bus Width:	384-bit
L2 Cache Size:	786432 bytes

Device 2: "Tesla M2070"

CUDA Driver Version / Runtime Version	4.1 / 4.1
CUDA Capability Major/Minor version number:	2.0
Total amount of global memory:	5375 MBytes (5636554752 bytes)
(14) Multiprocessors x (32) CUDA Cores/MP:	448 CUDA Cores
GPU Clock Speed:	1.15 GHz
Memory Clock rate:	1566.00 Mhz
Memory Bus Width:	384-bit
L2 Cache Size:	786432 bytes

Device 3: "Tesla M2070"

CUDA Driver Version / Runtime Version	4.1 / 4.1
CUDA Capability Major/Minor version number:	2.0
Total amount of global memory:	5375 MBytes (5636554752 bytes)
(14) Multiprocessors x (32) CUDA Cores/MP:	448 CUDA Cores
GPU Clock Speed:	1.15 GHz
Memory Clock rate:	1566.00 Mhz
Memory Bus Width:	384-bit
L2 Cache Size:	786432 bytes

Things to note:

- Device 3 is a GPU
- "Tesla M2070" is the name of the model of the GPU.
- Device 3 contains multiple cores, or "sub-processors".
From the output, it has 448 CUDA-capable cores.

EXAMPLE: MATRIX MULTIPLICATION

Now, suppose I want to do a giant matrix multiplication on Device 3. I'm automatically set to Device 0:

```
> getGpuId()
[1] 0
```

So I change to Device 3:

```
> chooseGpu(3)
[[1]]
[1] 3
```

and then if I want, I can verify the change:

```
> getGpuId()  
[1] 3
```

Now, I define the matrices that I want to multiply on Device 3:

```
> A <- matrix(runif(1e+7), nrow = 1e+4)  
> B <- matrix(runif(1e+7), ncol = 1e+4)
```

Then, I tell the device to multiply **A** and **B** using the GPU hardware:

```
> ptm <- proc.time(); C <- gpuMatMult(A, B); proc.time() - ptm
  user  system elapsed
 2.959   2.190   5.159
```

Compare the run time to that of the analogous CPU run on impact1:

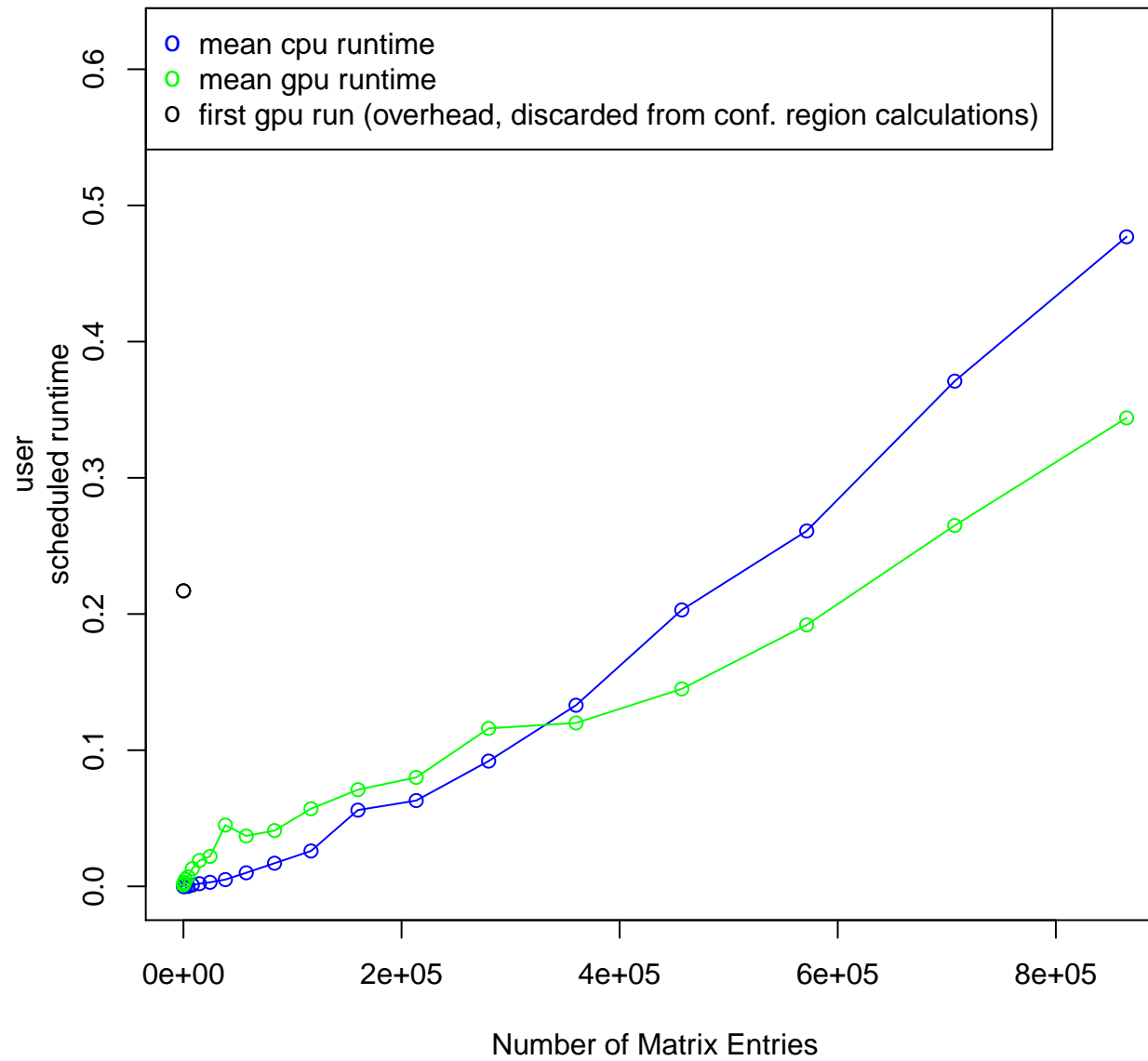
```
> ptm <- proc.time(); D <- A %*% B; proc.time() - ptm
  user  system elapsed
116.389   0.166  116.503
```

A COMPARISON OF `gpuQr()` AND `qr()`

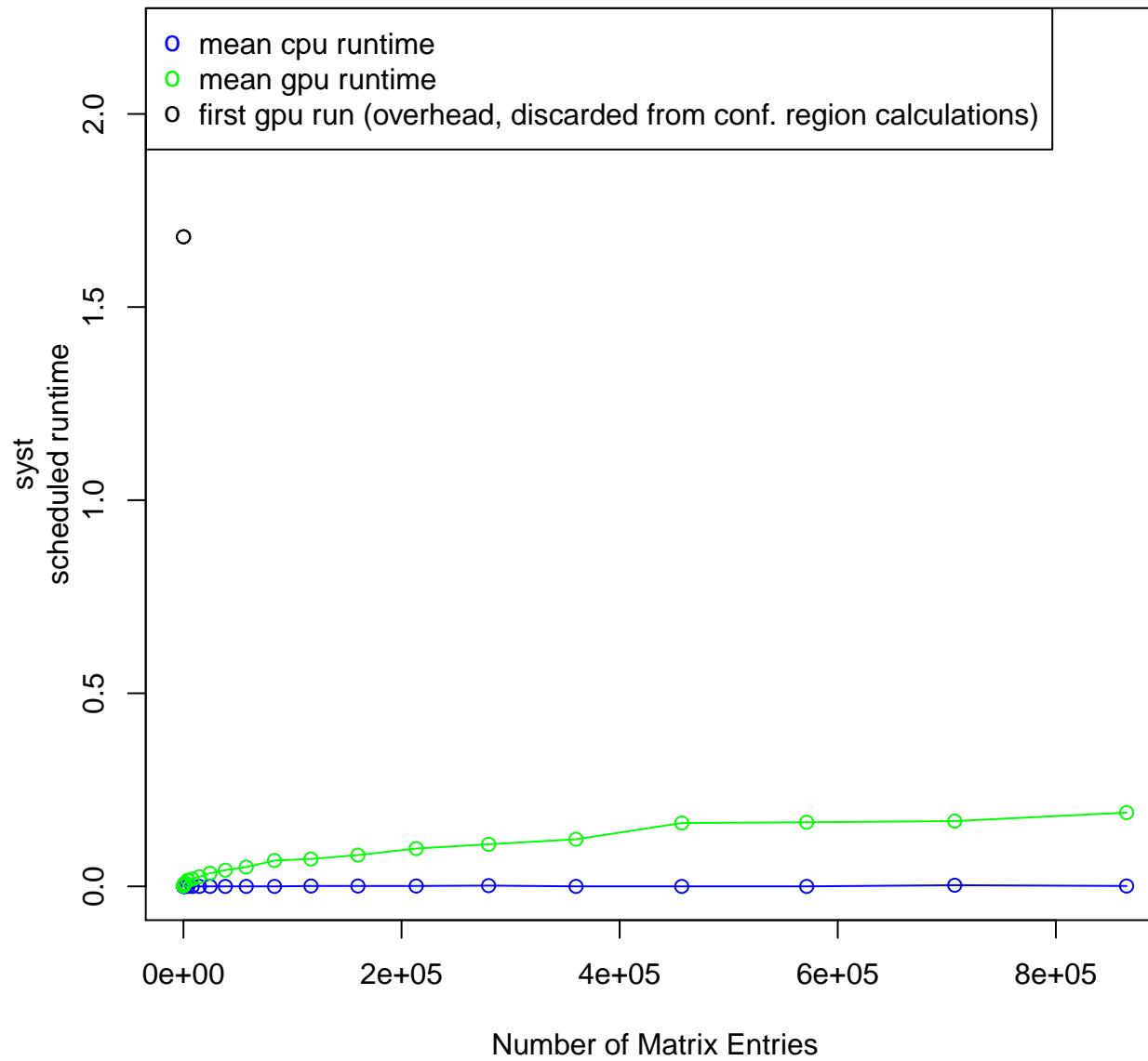
The R script, `perf_gpuQr.r`, compares the performance of `gpuQr(x)` and `qr(x)` for matrices `x` of varying sizes. See the results on the next few slides.

NOTE: ALL TIMES ARE IN SECONDS.

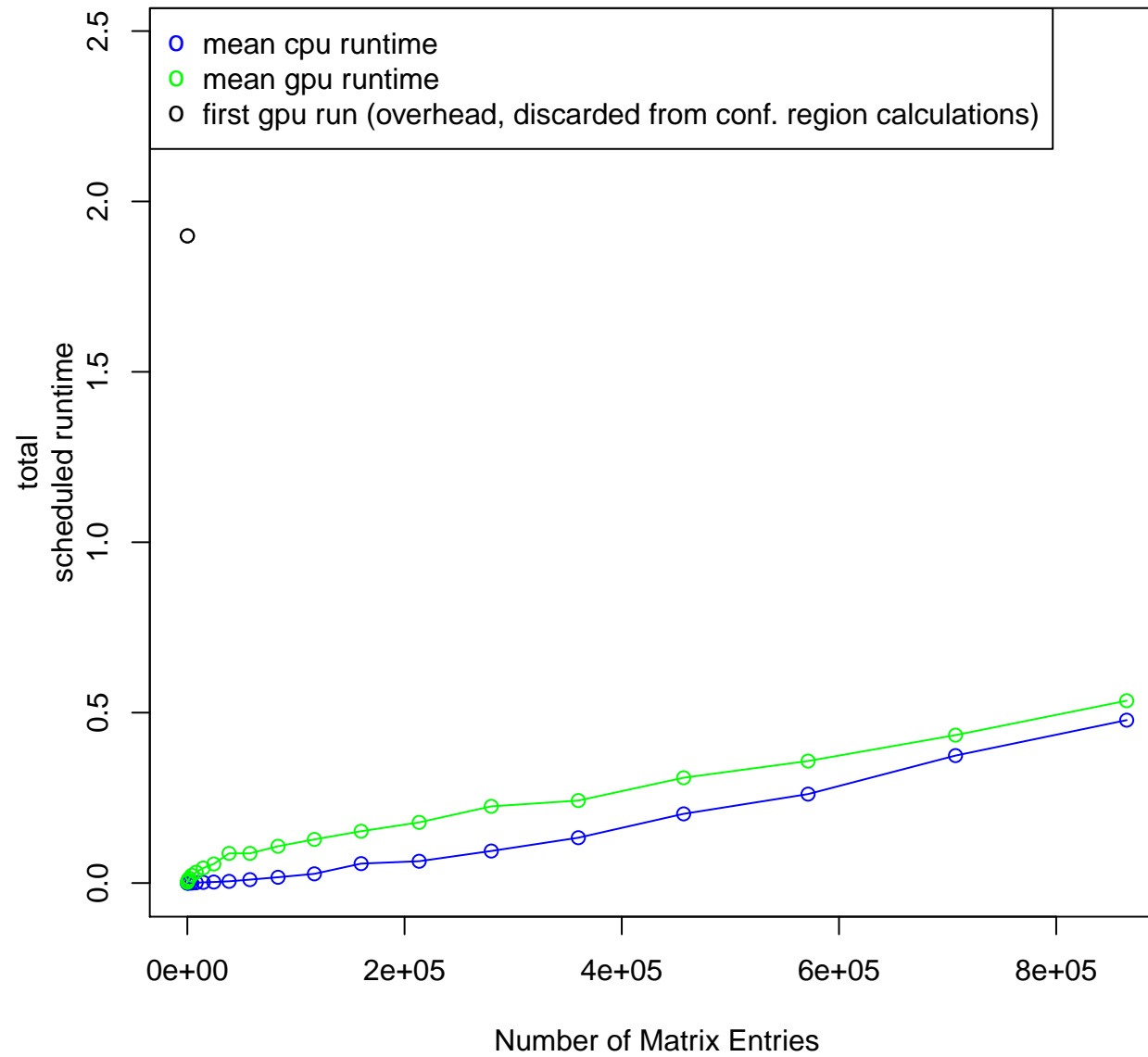
**user
scheduled runtime:
qr() vs gpuQr()**



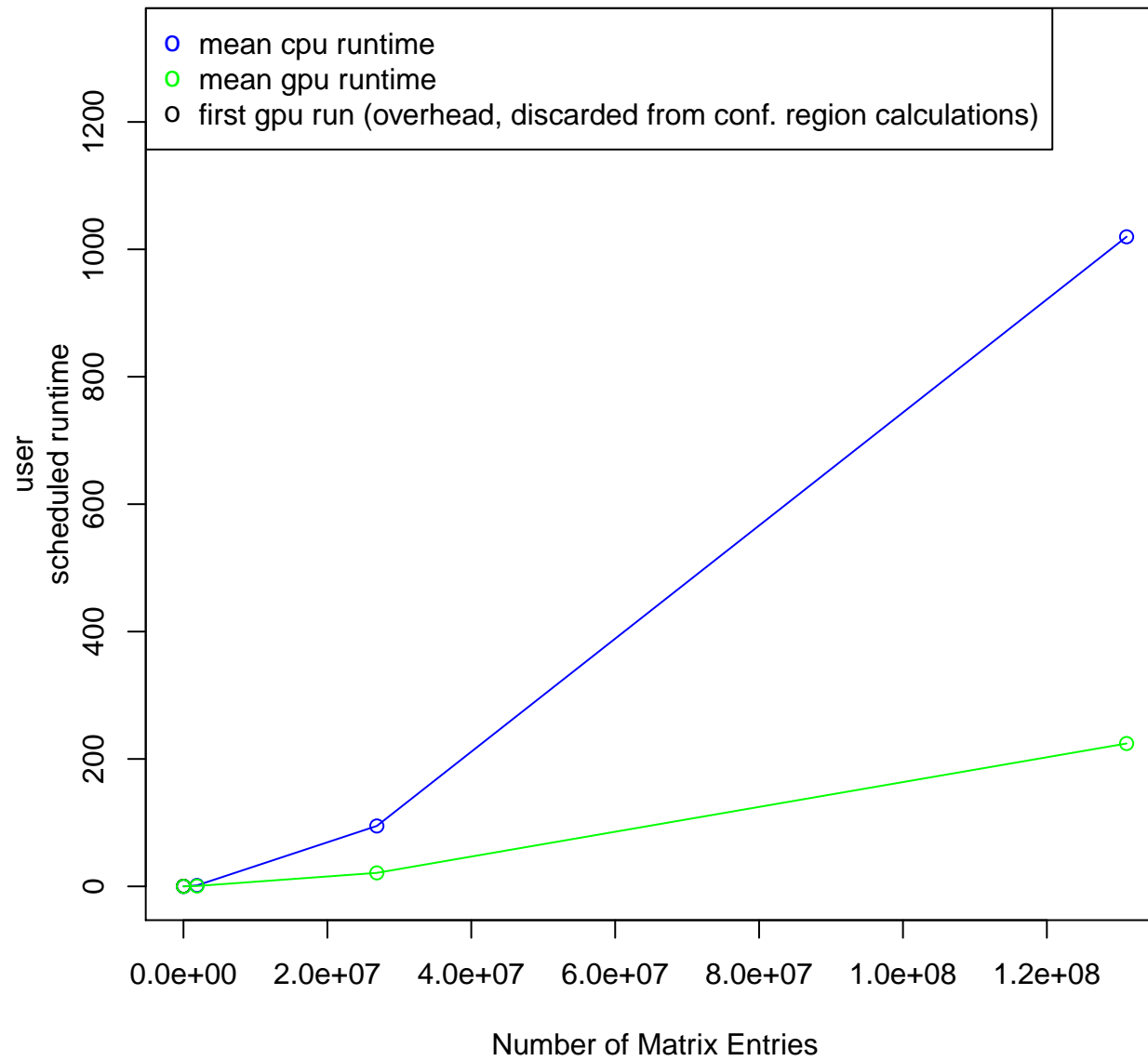
**syst
scheduled runtime:
qr() vs gpuQr()**



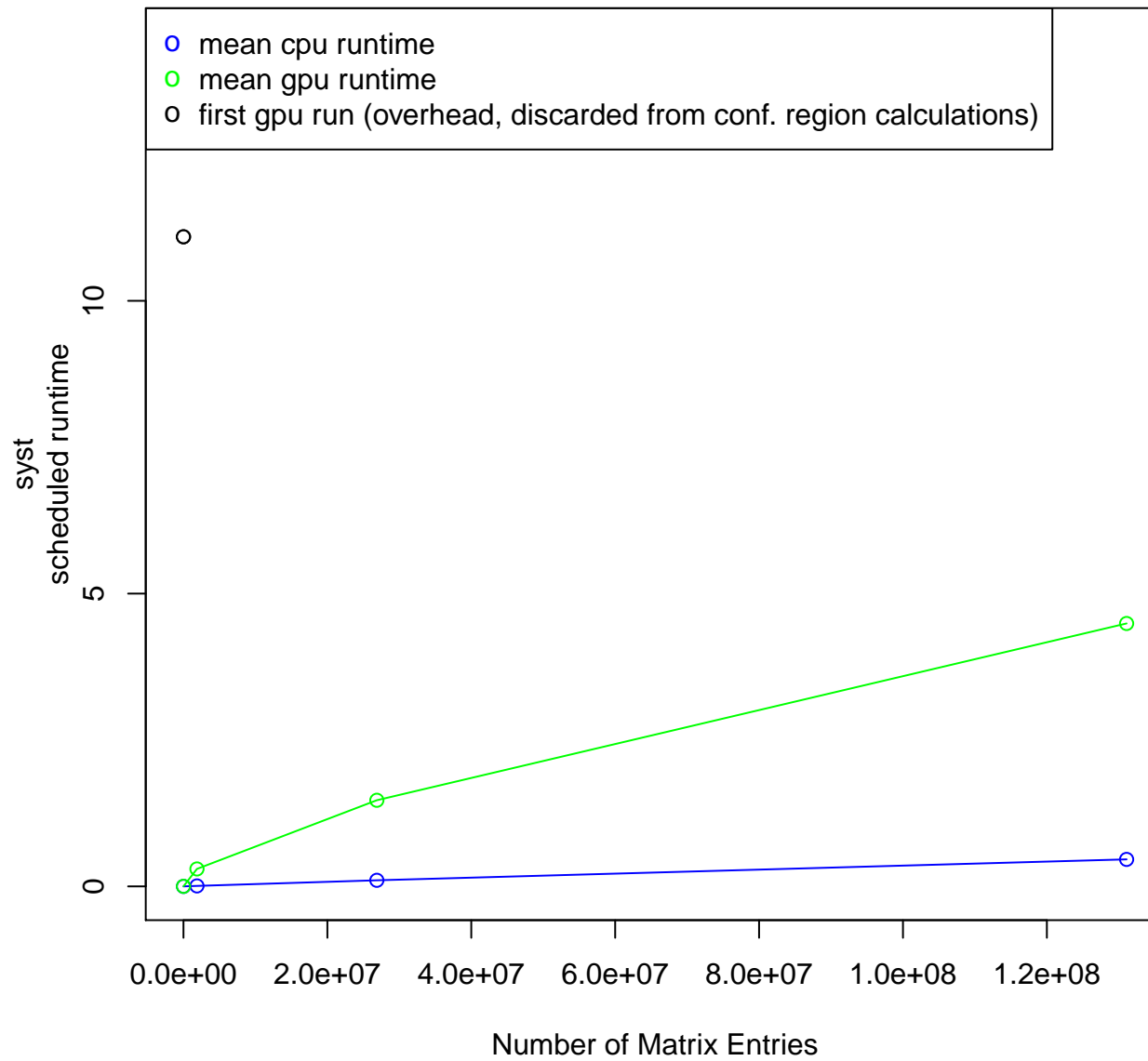
**total
scheduled runtime:
qr() vs gpuQr()**



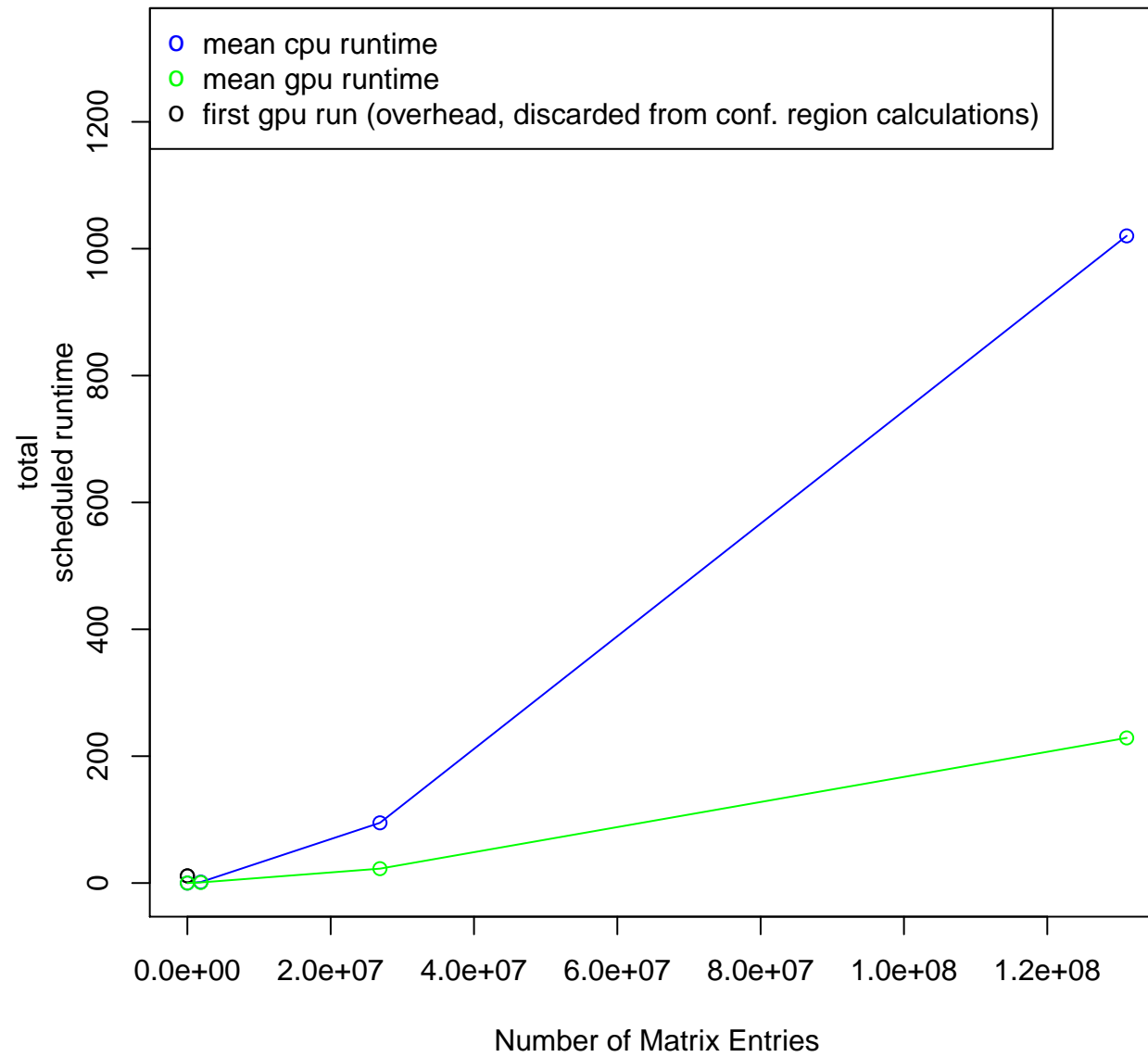
**user
scheduled runtime:
qr() vs gpuQr()**



**syst
scheduled runtime:
qr() vs gpuQr()**



**total
scheduled runtime:
qr() vs gpuQr()**



CLAIMS FROM THE AUTHORS OF gputools

(All of the following is from
[http://brainarray.mbni.med.umich.edu/Brainarray/Rgpgpu/.](http://brainarray.mbni.med.umich.edu/Brainarray/Rgpgpu/))

“Tested on a subset of GSE6306, non-GPU enabled
fastICA took over four hours while gpuFastICA took
just 80 seconds!”

Fig. 1: Speedup (R GPU vs. CPU)

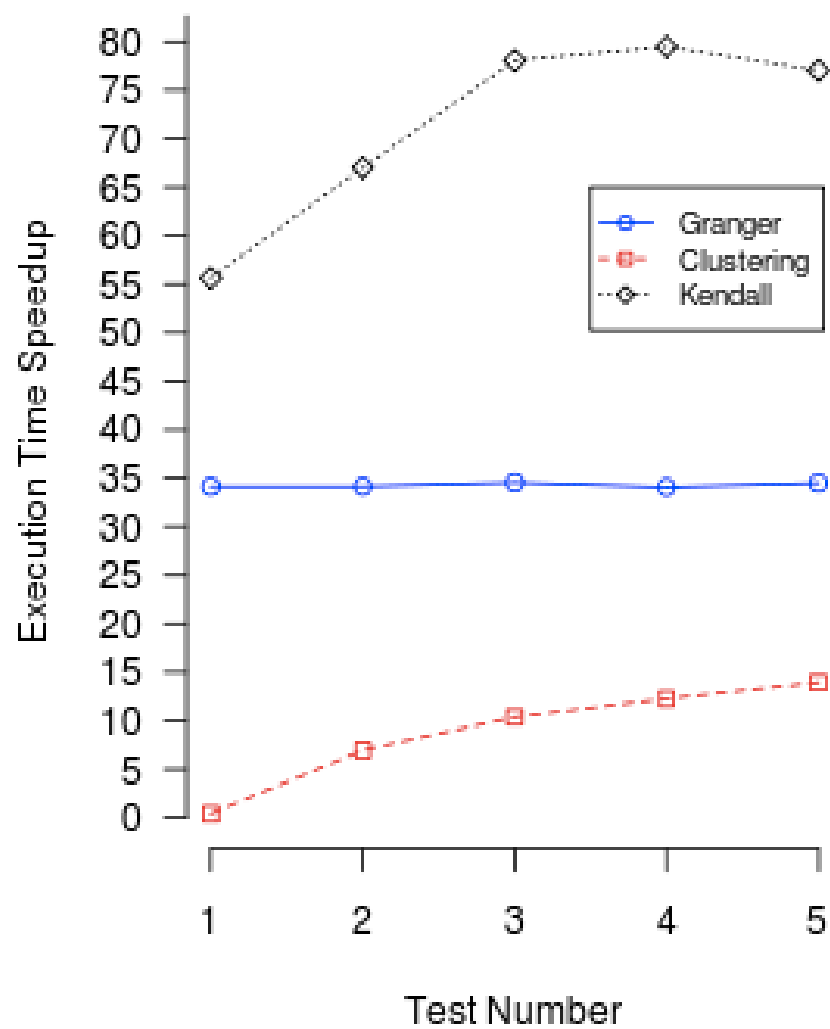


Fig. 2: Granger Times

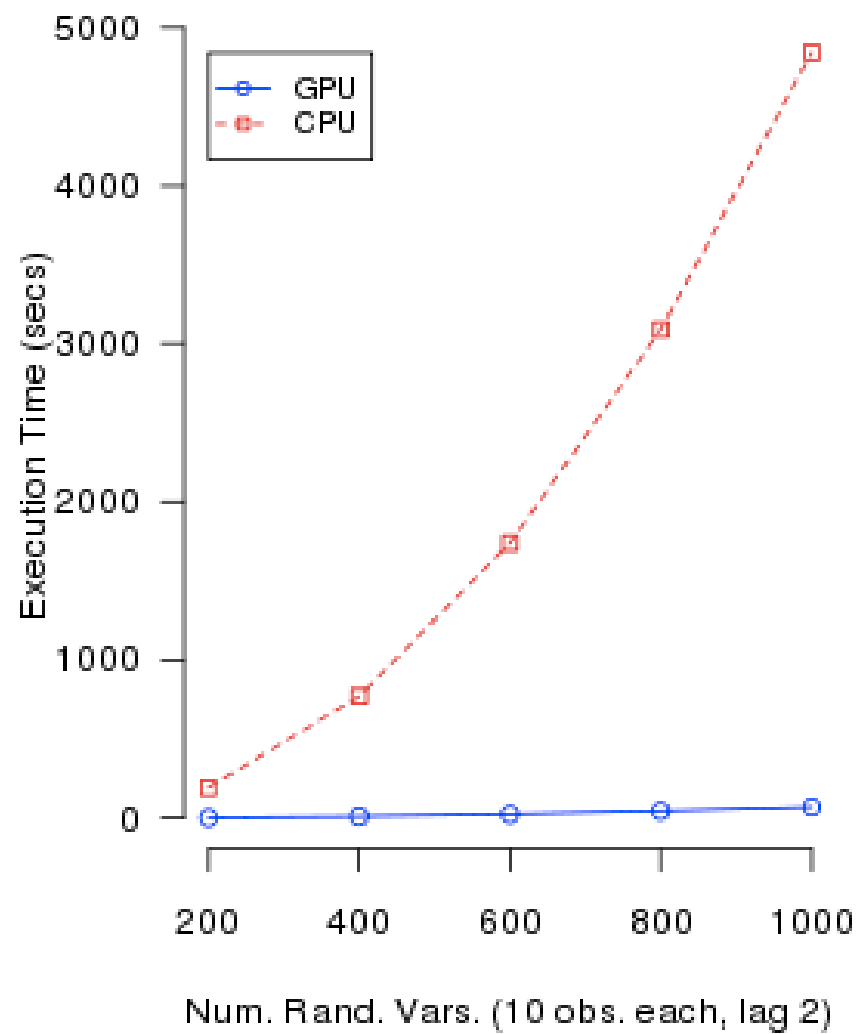


Fig. 3: Cluster Times

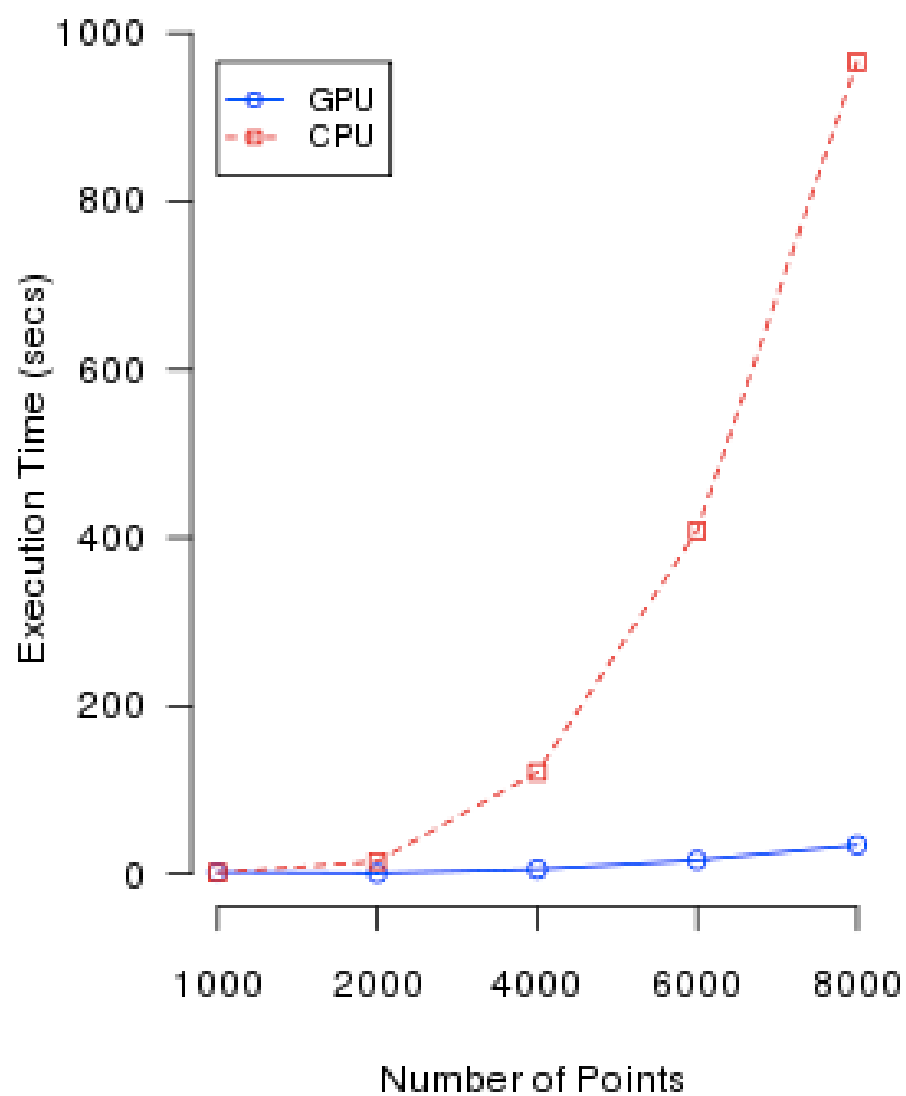


Fig. 4: Kendall Times

