



Using the Batch Farm



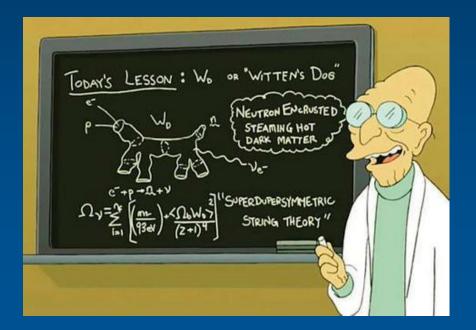
All information + scripts from this talk also available in

A) transfer.ktas.ph.tum.deB) /home/www/papers/computing

Overview

ПШ

- Infrastructure
- Parallel vs single job computing
- Basic commands
- How to ...
 - ... arrange a job... send a job... monitor my stuff
- Please don't...

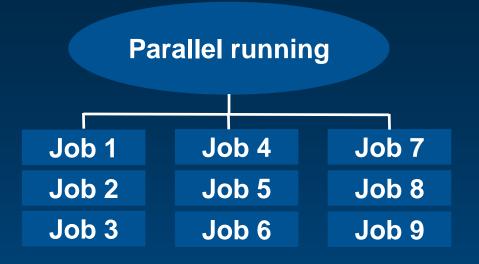




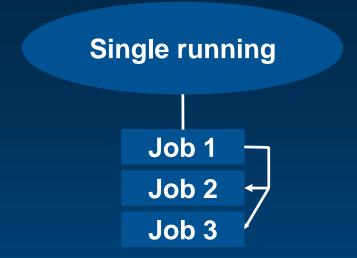
- 21 compute nodes \rightarrow 570 cores
- ~ 2 Gb RAM / cores
- 20 GPU job slots
- Standard queue: 2,5h / job
- Long queue: 12h / job
- Local storage ~100 Gb per node
- 1/10 Gbit/s network connection / node

SLURM job scheduler https://www.schedmd.com

Parallel vs single job



- Independent jobs
- Parameter scans
- MC production
- Data analysis (runwise)
- Creating of independent output files



- Code development
- Compiling
- Create Plots / Graphs
- Small nTuple analysis
- Merging of several files

Example: Parallel job

Detector Summary Tape File Analysis (DSTs)

Problem

• 1000 files with 250 events/file

Solution

- Create code locally
- Analyse 1 file per job
- Create 1 output file per job (Plots, Ntuples...)
- Send 1000 jobs to farm
- Merge plots/ntuples afterwards

Example: Single job

Fitting of a peak in plot

Problem

• Fit peaks in 1 or 2 plots

Solution

- Create a macro / program to fit
- Do it locally and check the output

Don't make life more complicated than it is!

ТІП

- sview
- sshare
- sbatch
- scancel
- squeue
- sinfo
- Monitoring software
 - Graphical
 - Text based

Here you will get some information about the basic commands. Most of them provide more information, see "command –help"



ПШ

- sview
- sshare
- sbatch
- scancel
- squeue
- sinfo
- Monitoring software
 - Graphical
 - Text based

SLURM overview. Job, partition and node information in an graphical overview

Just enter "sview" in a terminal

Job	Jobs 📮 Partitions 🚍 Nodes 🏺 Visible Tabs 🛊													
	Name 🗸 :	State	CPU Count	Used CPU Count	Error CPU Count	Sockets	CoresPerSocket	ThreadsPerCore	Real Memory	Tmp Disk				
		allocated	8	8	0	2	4	1	48000M	500000M				
	- bert	mixed	80	58	0	2	40	1	125G	500000M				
	- bigbird	allocated	24	24	0	2	12	1	250G	500000M				
	- bishop	allocated	16	16	0	4	4	1	32000M	500000M				
	- brett	allocated	16	16	0	4	4	1	32000M	9000M				
	- cronos	idle	1	0	0	1	1	1	2000M	5000M				
	- dallas	allocated	16	16	0	4	4	1	32000M	100000M				
	- ernie	mixed	80	58	0	2	40	1	125G	500000M				
	- kane	allocated	16	16	0	4	4	1	32000M	500000M				
	- kermit	allocated	6	6	0	1	6	1	30000M	300000M				
	- lambert	allocated	16	16	0	2	8	1	48000M	500000M				
	- monk	allocated	16	16	0	4	4	1	32000M	500000M				
	- morse	allocated	16	16	0	2	8	1	32000M	500000M				
	- nx1	allocated	8	8	0	2	4	1	32000M	50000M				
	- nx2	allocated	8	8	0	2	4	1	32000M	50000M				
	- nx3	allocated	8	8	0	2	4	1	32000M	50000M				
	- parker	allocated	16	16	0	4	4	1	32000M	500000M				
	- ripley	allocated	16	16	0	4	4	1	32000M	500000M				
	- slimfast	allocated	6	6	0	2	3	1	60000M	100000M				
	- transfer	idle	1	0	0	1	1	1	2000M	5000M				
	vasquez	allocated	8	8	0	2	4	1	40000M	500000M				

ПП

- sview
- sshare
- sbatch
- scancel
- squeue
- sinfo
- Monitoring software
 - Graphical
 - Text based

"Fair share" ranking. (How fast do I get the slot for the next job?)

Just enter "sshare --all" in a terminal

8 🗖 🗖	ga93yut@nx1:# Sear						
[ga93yut	t@nx1 ~]\$ sshare -	-all					
	Account	User	RawShares	NormShares	RawUsage	EffectvUsage	FairShare
root				1.000000	9839673	0.000000	1.000000
all			1	1.000000	9839673	1.000000	0.500000
all	ecp)-admin	1	0.035714	336269	0.068674	0.263730
all	g	a45mof	1	0.035714	6582981	0.688579	0.000002
all	g	a49zaf	1	0.035714	0	0.035714	0.500000
all	g	a54bow	1	0.035714	0	0.035714	0.500000
all	g	a54mof	1	0.035714	0	0.035714	0.500000
all	ģ	a54puv	1	0.035714	0	0.035714	0.500000
all	ģ	a56got	1	0.035714	0	0.035714	0.500000
all	g	a65xaz	1	0.035714	0	0.035714	0.500000
all	g	a67taj	1	0.035714	0	0.035714	0.500000
all	g	a69buq	1	0.035714	2864436	0.316343	0.002156
all	g	ja74yub	1	0.035714	0	0.035714	0.500000
all	g	a92luw	1	0.035714	0	0.035714	0.500000
all	g	a93tok	1	0.035714	0	0.035714	0.500000
all	g	a93yut	1	0.035714	0	0.035714	0.500000
all	g	a95zik	1	0.035714	0	0.035714	0.500000
all	g	a96hih	1	0.035714	0	0.035714	0.500000
all	-	i27guy	1	0.035714	0	0.035714	0.500000



- sview
- sshare
- sbatch
- scancel
- squeue
- sinfo
- Monitoring software
 - Graphical
 - Text based

Submit a job to the farm

Enter "sbatch --help" for info about the parameters (will be described later)

🔋 🗇 💷 ga93yut@nx1:/home/software/administration/testbatch

[ga93yut@nx1 testbatch]\$ sbatch testBatch.sh Submitted batch job 1999320 [ga93yut@nx1 testbatch]\$ ■

ТШ

- sview
- sshare
- sbatch
- scancel
- squeue
- sinfo
- Monitoring software
 - Graphical
 - Text based

Kill your jobs by id or all of your jobs using "scancel –u [ADS]"

😣 🖨 💷 ga93yut@nx1:/home/software/administration/testbatch

[ga93yut@nx1 testbatch]\$ sbatch testBatch.sh Submitted batch job [999320 [ga93yut@nx1 testbatch]\$ scancel -i 1999320 scancel: error: Kill job error on job id 1999320: Invalid job id specified [ga93yut@nx1 testbatch]\$ scancel -u ga93yut [ga93yut@nx1 testbatch]\$ ■

ПШ

- sview
- sshare
- sbatch
- scancel
- squeue
- sinfo
- Monitoring software
 - Graphical
 - Text based

Gives information about the status of the running jobs and the queue.

Just enter "squeue" in a terminal

😣 🗏 🗉 🛛 ga93yut@nx	1:/home/softv	vare/admin	istration/te	stba	tch		
[ga93yut@nx1 testb	oatch]\$ sque	eue -u ecp	o-admin				
JOBIC	PARTITION	NAME	USER	ST	TIME	NODES	NODELIST(REASON)
1991145	5 gpu	glidein	ecp-admi	R	16:59:00	1	ernie
1990527	7 gpu	glidein	ecp-admi	R	19:02:29	1	bigbird
1990261	L gpu	glidein	ecp-admi	R	20:03:36	1	bigbird
1991851	L gpu	glidein	ecp-admi	R	15:01:14	1	bert
1989996	5 gpu		ecp-admi	R	20:50:41	1	ernie
1999317	7 gpu		ecp-admi	R	1:02:50	-	bert
1999318	3 gpu	glidein	ecp-admi	R	3:52	1	bigbird
1999008	3 gpu	glidein	ecp-admi	R	1:45:34	1	bert
1999007	7 gpu		ecp-admi	R	1:47:40	1	ernie
1999006	5 gpu	glidein	ecp-admi	R	1:58:16	1	ernie
1999005	5 gpu	glidein	ecp-admi	R	2:42:09	1	bigbird
1995020) <u>g</u> pu	glidein	ecp-admi	R	5:02:22	1	bert
[ga93yut@nx1 testb	patch]\$						

ПП

- sview
- sshare
- sbatch
- scancel
- squeue
- sinfo
- Monitoring software
 - Graphical
 - Text based

Gives information about the nodes, queues and user of the farm.

Just enter "sinfo" in a terminal

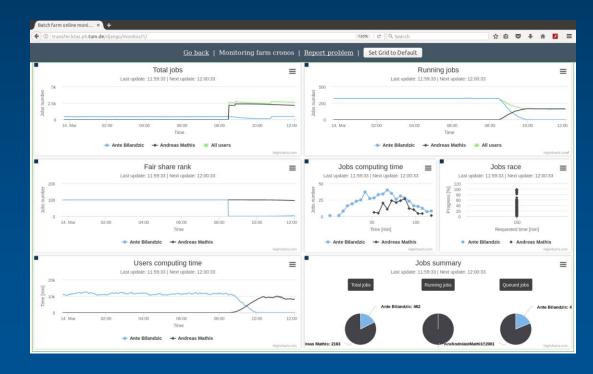
😣 🖨 🗊 gaiþa yūdi@nkitex/hoteaar/stofteranier/aldminitijstration/testbatch							
[ga93yut@nx1 testbatch]\$ sinfo							
PARTITION AV	/AIL	TIMELIMIT	NODES	STATE NODELIST			
gpu	up	1-00:00:00	2	mix bert,ernie			
gpu	up	1-00:00:00					
long	up	12:00:00	4	alloc bishop,brett,dallas,ripley			
kta*	up	2:30:00	2	mix bert,ernie			
kta*	up	2:30:00		alloc ash, bigbird, bishop, brett, dallas, kane, kermit, lambert, mon			
k,morse,nx[1-3],parker,ripley,slimfast,vasquez							
[ga93yut@nx1 testbatch]\$							



- sview
- sshare
- sbatch
- scancel
- squeue
- sinfo
- Monitoring software
 - Graphical
 - Text based

A short graphical overview over the users currently running jobs on the farm.

https://transfer.ktas.ph.tum.de/django/monitor/1/





- sview
- sshare
- sbatch
- scancel
- squeue
- sinfo
- Monitoring software
 - Graphical
 - Text based

A short text based overview over the users currently running jobs on the farm.

https://transfer.ktas.ph.tum.de/webpage/monitori ng_batchfarm.html

Batchfarm Info × +	<u>B</u> ookmarks <u>T</u> ools <u>H</u> elp						
(Itransfer.ktas.ph.tum.de/w	ebpage/r 120% C Q Search	☆ 自		Ŧ	⋒	£	≡
Status: Tue 14 Mar 11:58:01 CET 2017							
Queues:							
Total Jobs:	173 / 2637						
 kta	162 / 2626						
long	0 / 0						
extralong	0 / 0						
extrating							

Ante Bilandzic	0 / 462
Andreas Mathis	162 / 2164

How to... arrange a job

- Input:
 - File to analyse? (Filelist?)
 - Parameters?
- Output:
 - Different names/ directories
- Compile before sending to farm
- How much CPUtime / RAM
- Do I need temporary space?
- Do I need access to /scratch
- Check before farm



Example: Random Numbers

ТЛТ

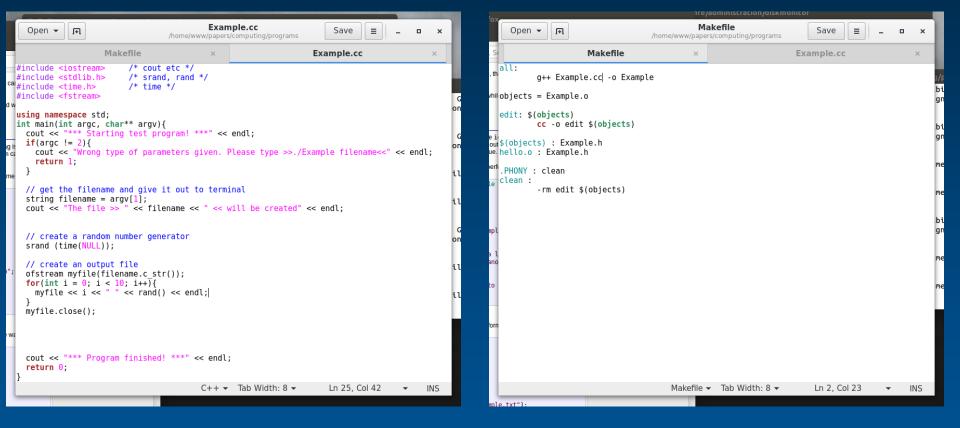
Problem

- Create file with 10 different lines and random numbers
- Must be scalable to farm

Solution

- Input: the name of the output file has to be given
- Compile
- "Full program"
 - Example.cc
 - Makefile
 - \rightarrow This generates a executable program

Example: Random Numbers



Example: Random Numbers

• Run it locally to check if it works

röibt @blish ope/lb opea/www.papeds/detpputing/programs [root@bishop programs]# ./Example /var/tmp/TestDatei-Tobias.txt *** Starting test program! *** The file >> /var/tmp/TestDatei-Tobias.txt << will be created *** Program finished! *** [root@bishop programs]# cat /var/tmp/TestDatei-Tobias.txt 0 676633619 1 2060896067 2 1262601684 3 1419026663 4 87771625 5 1378388270 6 549609861 7 348456336 8 1024578901 9 14367215 [root@bishop programs]#

How to... send a job

ТШП

- Select your parameters:
 - CPU
 - RAM
 - Partition
- SLURM can only submit scripts
- Loop over all the jobs you want to submit
- Create a bash/ python script
- Example:
 - Create a script with a submit loop (submit.sh)
 - Inside, create a temporary script with your job inside
 - Run your script

Example: Send 10 jobs

#!/bin/sh

cpu=5	# time limit in minutes for your job,
	# will be killed after that time!
mem=100	# ram limit in Mb for your job,
	# it will be killed if it exceeds this
nJobs=10	# number of jobs to be performed

the program is defined here program=/home/www/papers/computing/programs/Example name=Example

the output parameters are defined here
output_path=/home/www/papers/computing/testoutput
output_name=Event
output_end=txt

Example: Send 10 jobs

generate a random number to identify the jobs stuff exactly randomID=\$RANDOM

for i in `seq 1 \$nJobs`; do tmp_scriptname=/var/tmp/sub_\${randomID}_\$i.sh

set your default environment
echo "#!/bin/sh" > \$tmp_scriptname
echo ". ~/.bashrc" >> \$tmp_scriptname

execute your program to the local disk
echo "\${program} /var/tmp/local_\${randomID}_\$i.txt" >> \$tmp_scriptname

```
# copy the completed output to your location
echo "cp /var/tmp/local_${randomID}_$i.txt ${output_path}/${output_name}-$i.${output_end}" >>
$tmp_scriptname
# clean up your stuff
echo "rm /var/tmp/local_${randomID}_$i.txt " >> $tmp_scriptname
```

submit your temporary script to the farm
sbatch --mem-per-cpu=\${mem} --time=\${cpu} --job-name=\$name-\${counter} \${tmp_scriptname}

delete your temporary script rm -rf \${tmp_scriptname}

Example: Send 10 jobs

```
ПП
```

```
# submit your temporary script to the farm
sbatch --mem-per-cpu=${mem} --time=${cpu} --job-name=$name-${counter}
${tmp_scriptname}
```

delete your temporary script
rm -rf \${tmp_scriptname}

done

How to... monitor my stuff

- Check your jobs frequently (squeue...)
 - Do they disappear suddenly?
 - Do they go down too fast?
- Check the log files in case of problems
 - What is written there?
 - Is it depending on one machine?
- Try to run a job locally



Error handling

- Have you checked the logfile?
- Are your scripts and code valid?
- Is your data available?
- Is the fileserver present or under heavy usage?
- Do your jobs last unusually long?





Some important notes:

- Don't use /tmp. Use /var/tmp
- Don't write directly to /scratch, copy at the end of the job
- Clean up after your job
- Try to stay under 50k jobs at one time
- Adjust your CPU and RAM usage reasonable
- Always check your work

Be friendly to the others I



ПΠ

Questions?

