

## **pcj-blast - highly parallel similarity search implementation**

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- Sequence alignment is essential for NGS
- There is a number of software packages for sequence alignment based on various a similarity search methods
- BLAST Basic Local Alignment Search Tool (1991)
  - The heuristic algorithm it uses is much faster than other approaches
  - The search time can be long (days or weeks) for large datasets
- NCBI blast is the most widely used implementation
  
- There is strong interest in using large computer systems to run blast
  - Blast running on cloud or grid
  - Parallel versions of blast running on HPC systems

>C1093377\_2.0

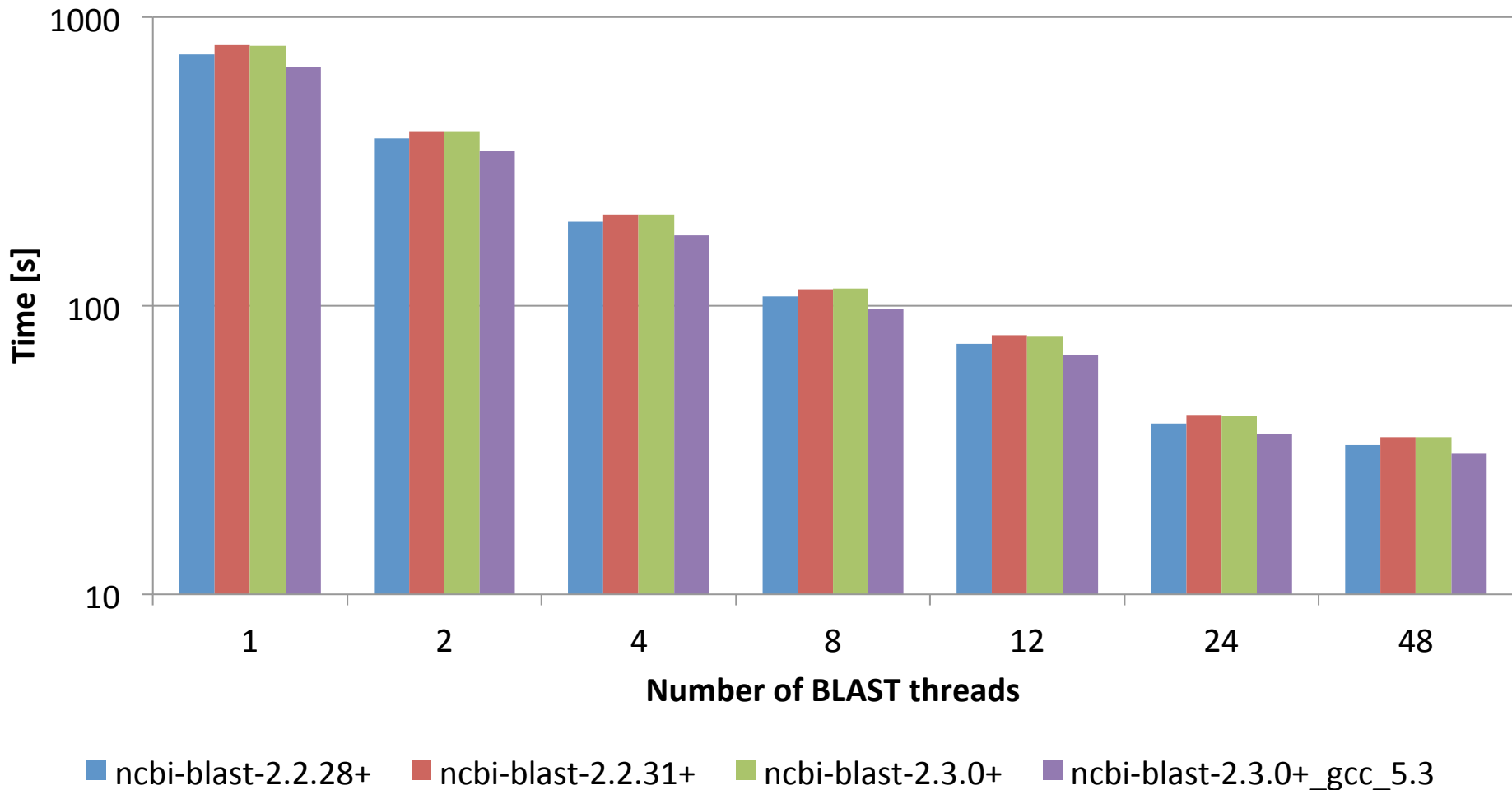
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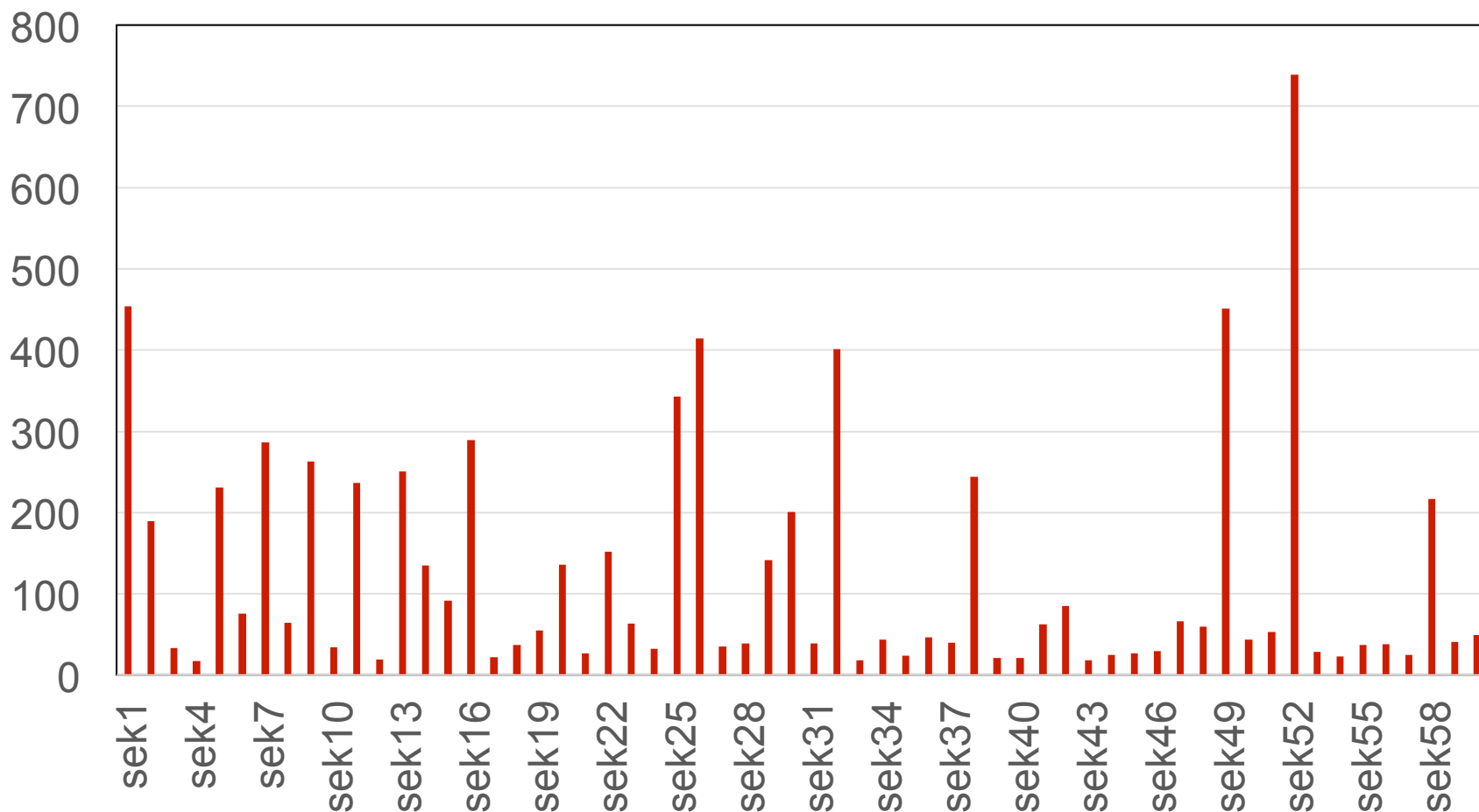
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GACTGGAGTGCAAGTGGTGCAATCATAGCT
```

...

Time of processing 48 sequences at once using 1 instance of different version of NCBI BLAST with different number of BLAST threads



Processing time [s]

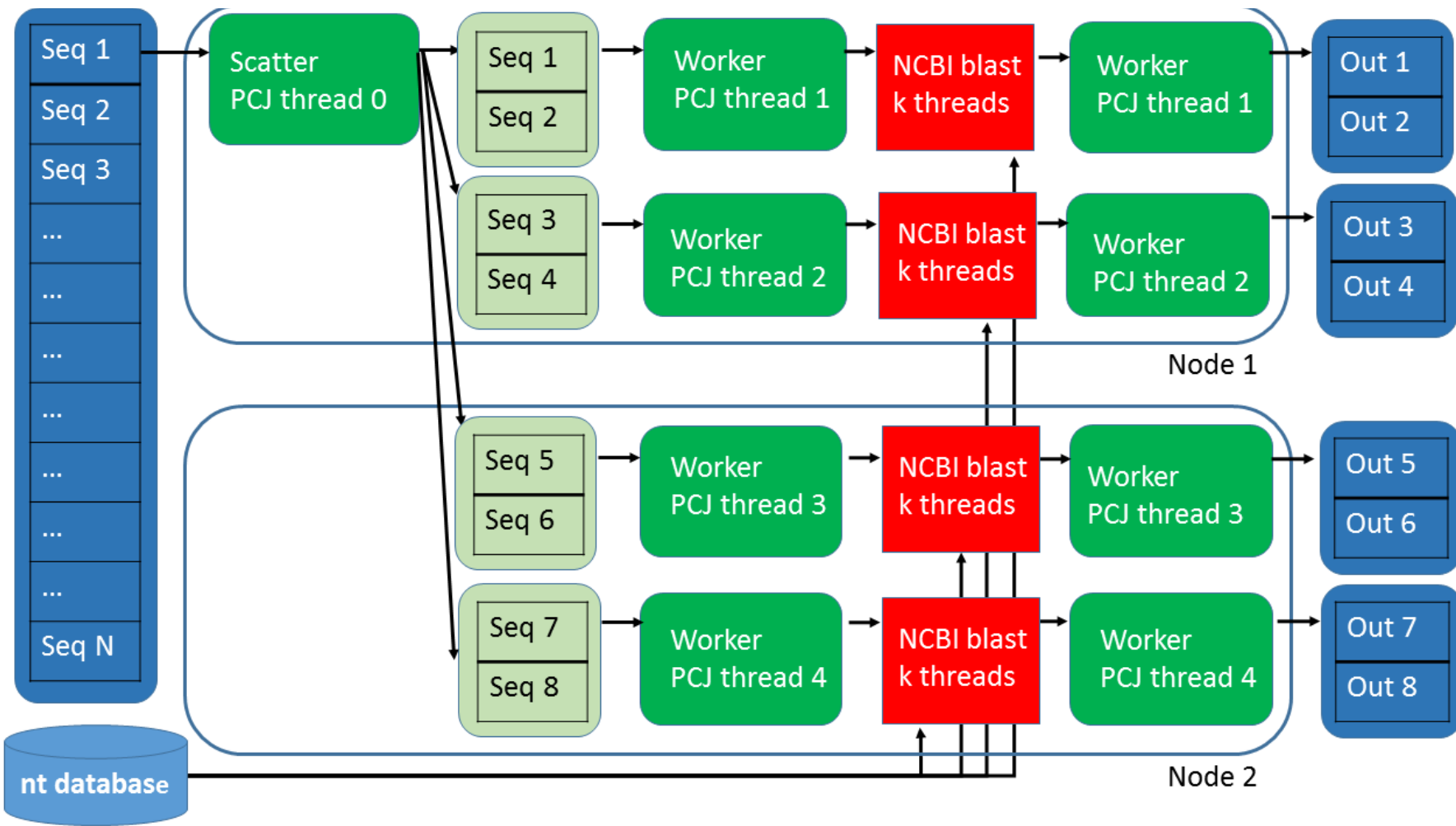


- mpiBLAST – uses old version (2012) of blast
- parallel\_blast.py – limited to single node, regular split of input
- Paracel BLAST (based on NCBI blast 2.2.26) – costly!
- The BlueGene implementation – limited to IBM BGQ systems
- pioBLAST parallel version which uses MPIIO – memory problems while reference database is large
- ...

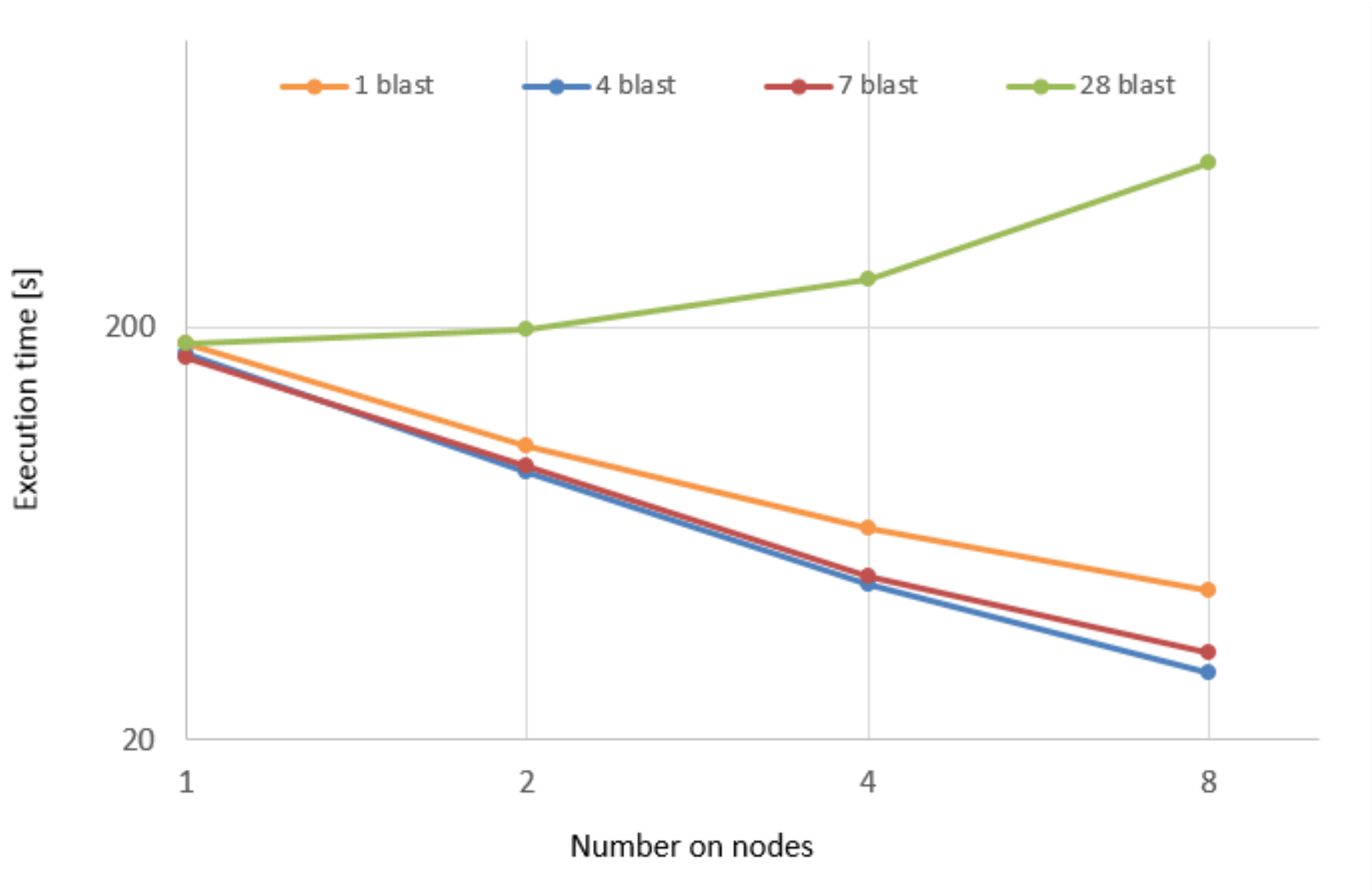
- Parallel version developed using PCJ (Parallel Computing in Java library developed at ICM)
- Java code is responsible for reading fasta input and execute NCBI-blast on set of sequences (reads)
- The NCBI blast (currently 2.2.28) is executed with the `-num_threads` option
  - For 28 core nodes: 4 PCJ threads with `-num_threads=7`
- The solution can be executed on any multinode system with Java 8 installed
- The I/O performance is important
  - thousands of blast instances reads blast database (52GB) concurrently
  - lustra filesystem performs worse than nfs

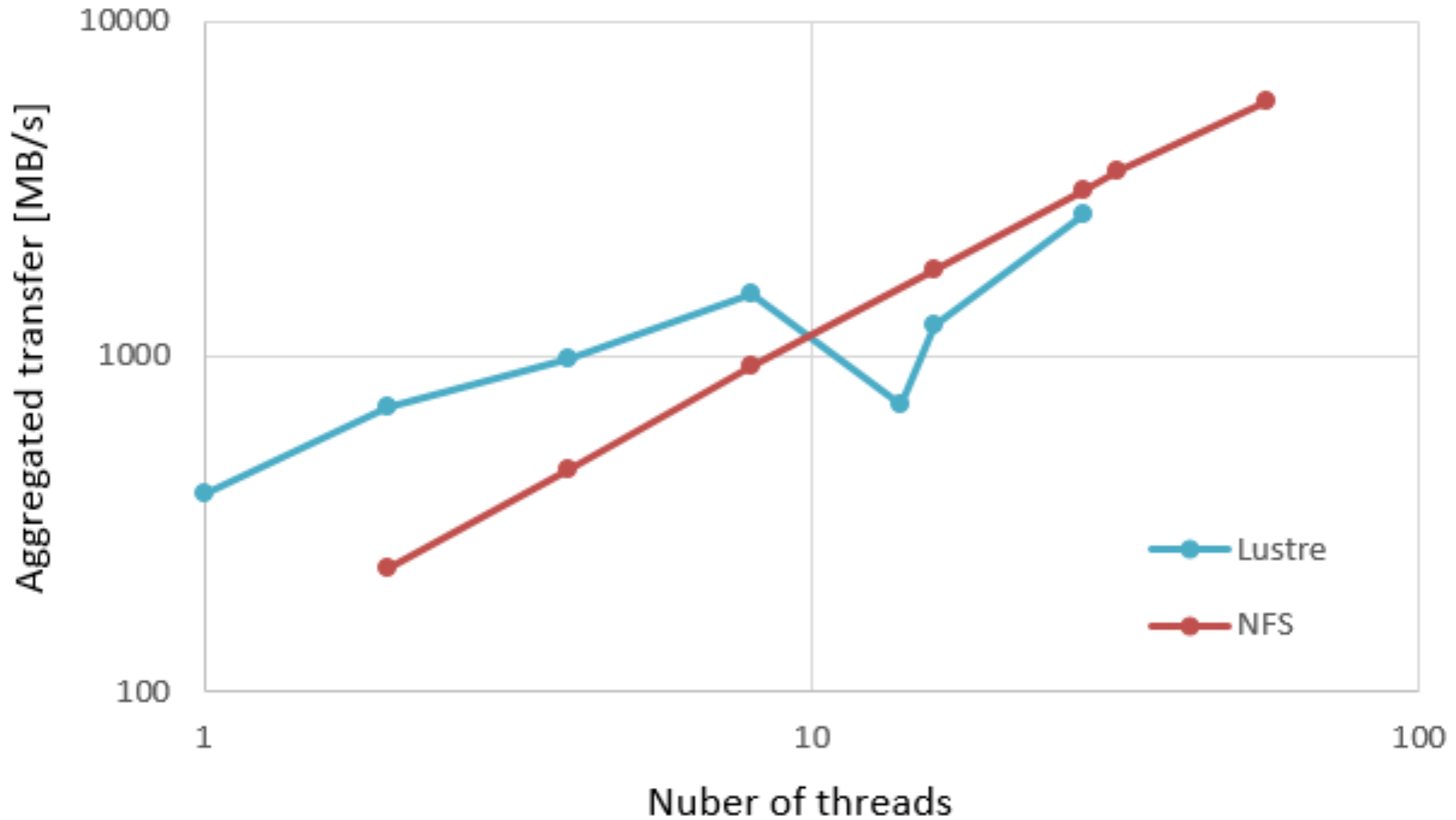
- Reads input sequence (fasta) line by line
- Blocks of lines (reads) are used as input for blast query
- Pcj-blast can start hundreds of blast instances
- NCBI blast is used
  - pcj-blast not bounded to particular version
- One or more NCBI blast instances are run on the hardware node
- Output from each node (text or XML) is gathered
- Output is postprocessed and is stored in a single file
  - Postprocessing is parallelized
- Pcj-blast can be run on HPC systems, clusters
  - Requires Java 8 and NCBI blast installed

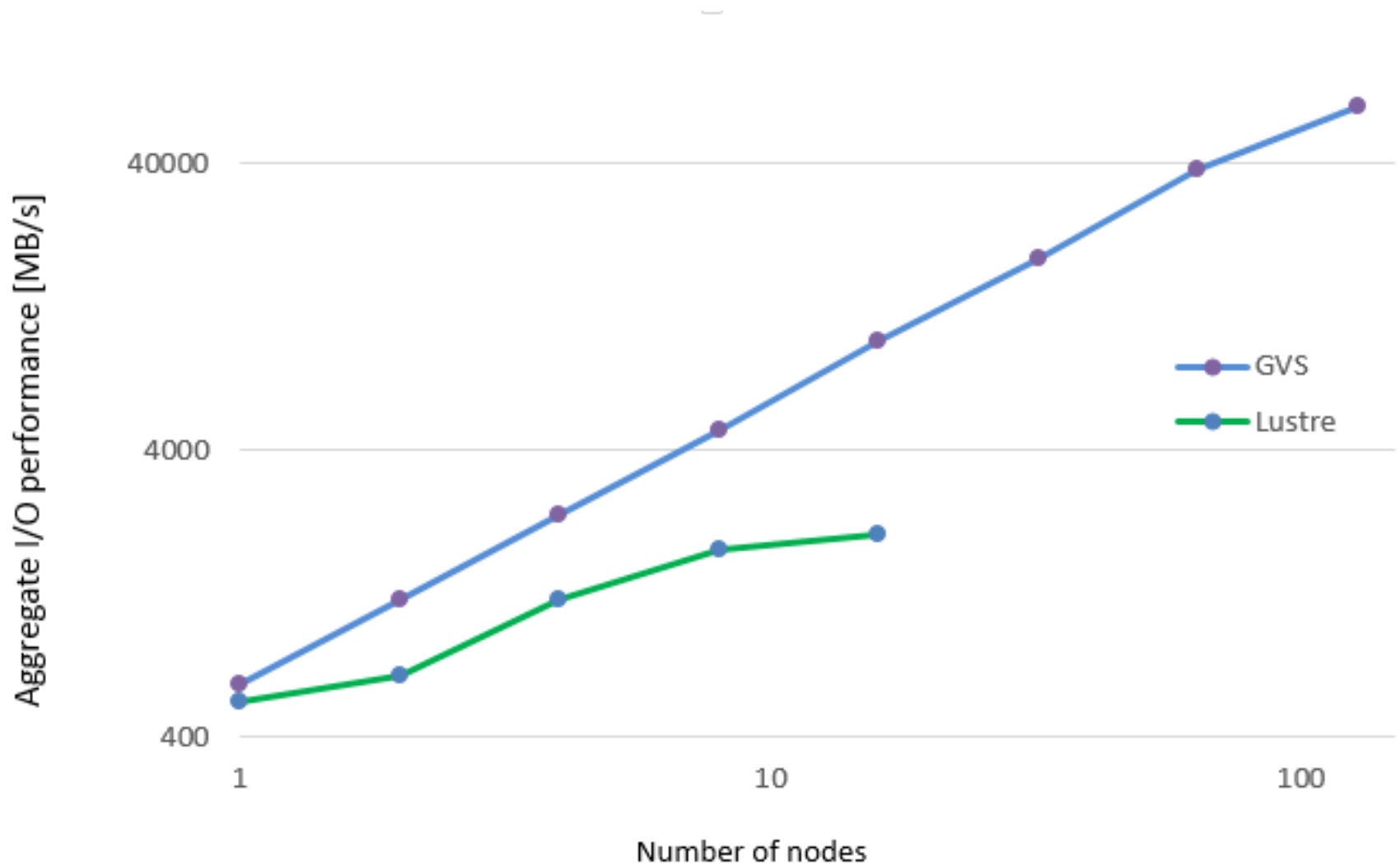




# Multiple NCBI blast running on single node (X86 cluster)

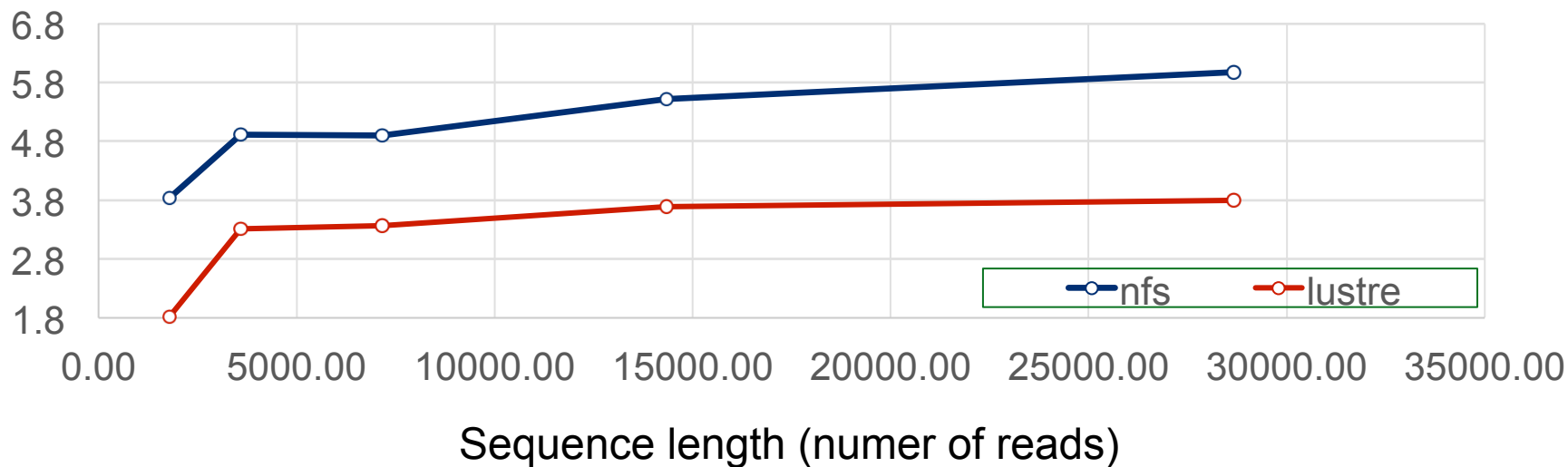


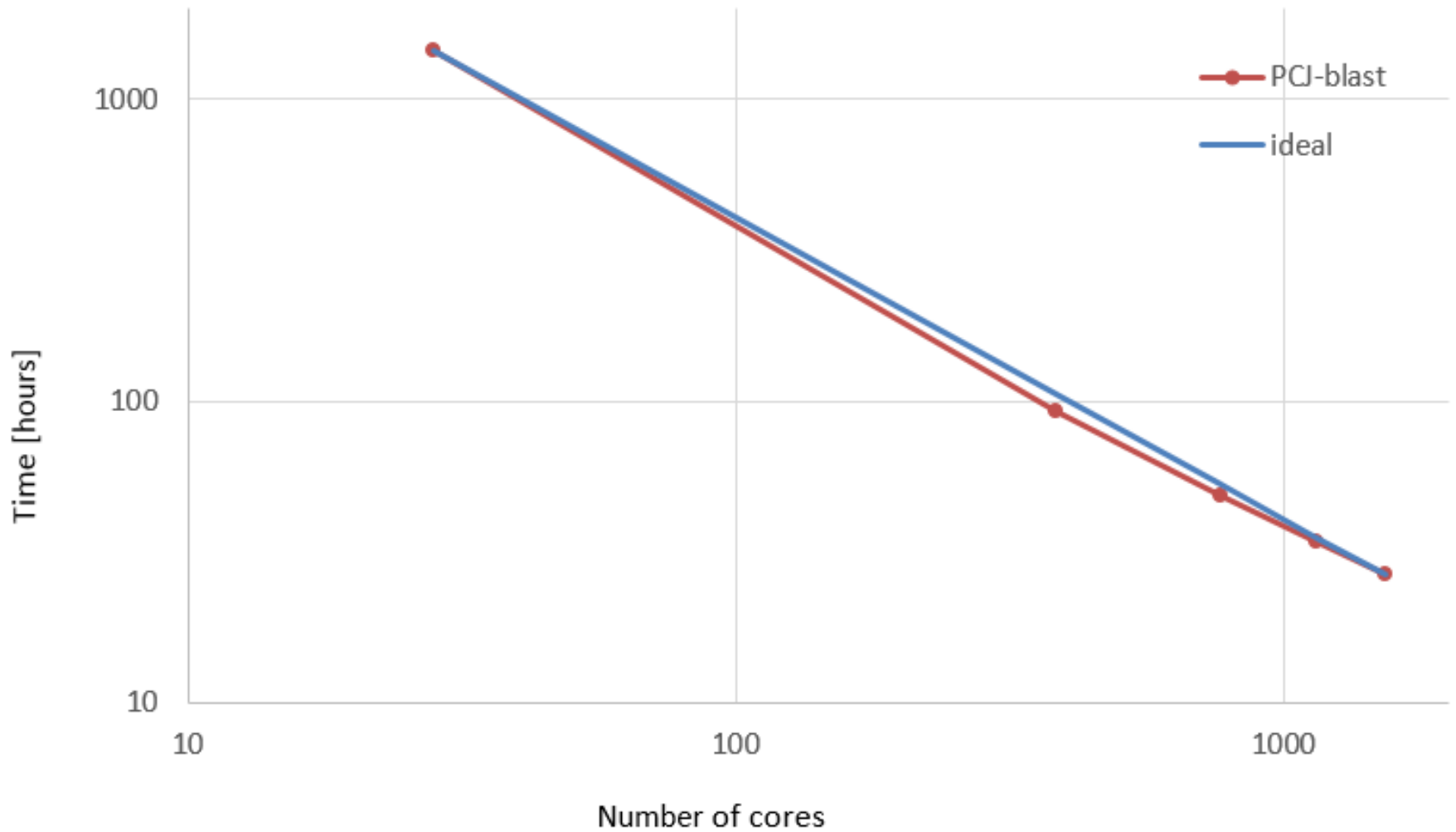


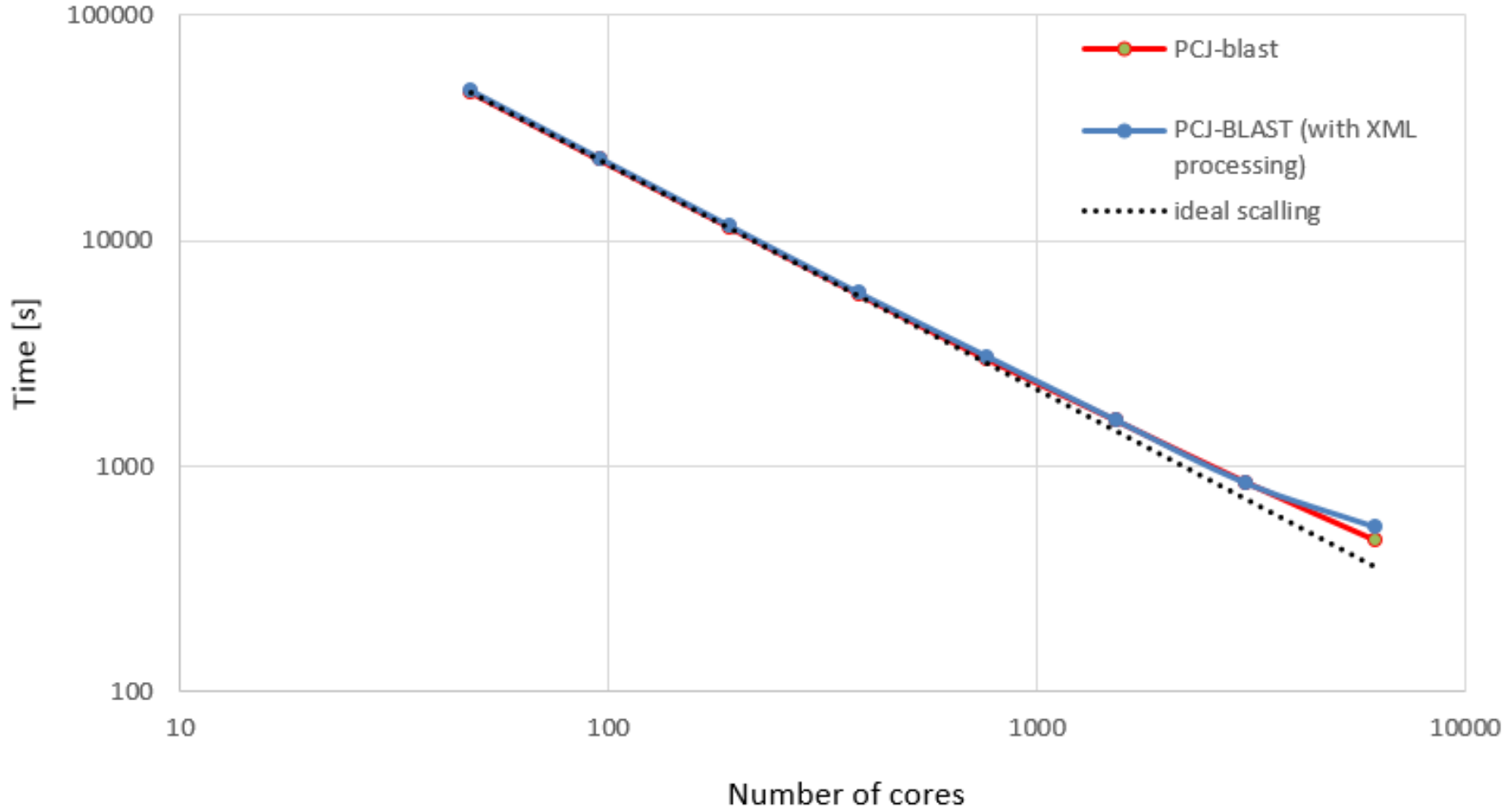


nodes	cores	Time [hours]	Time [days]	1 mln reads
1	28	1600.0	67.0	estimated
32	768	49.9	2.0	
48	1152	34.1	1.4	
64	1536	26.5	1.1	

Performance [reads/s] @32 nodes







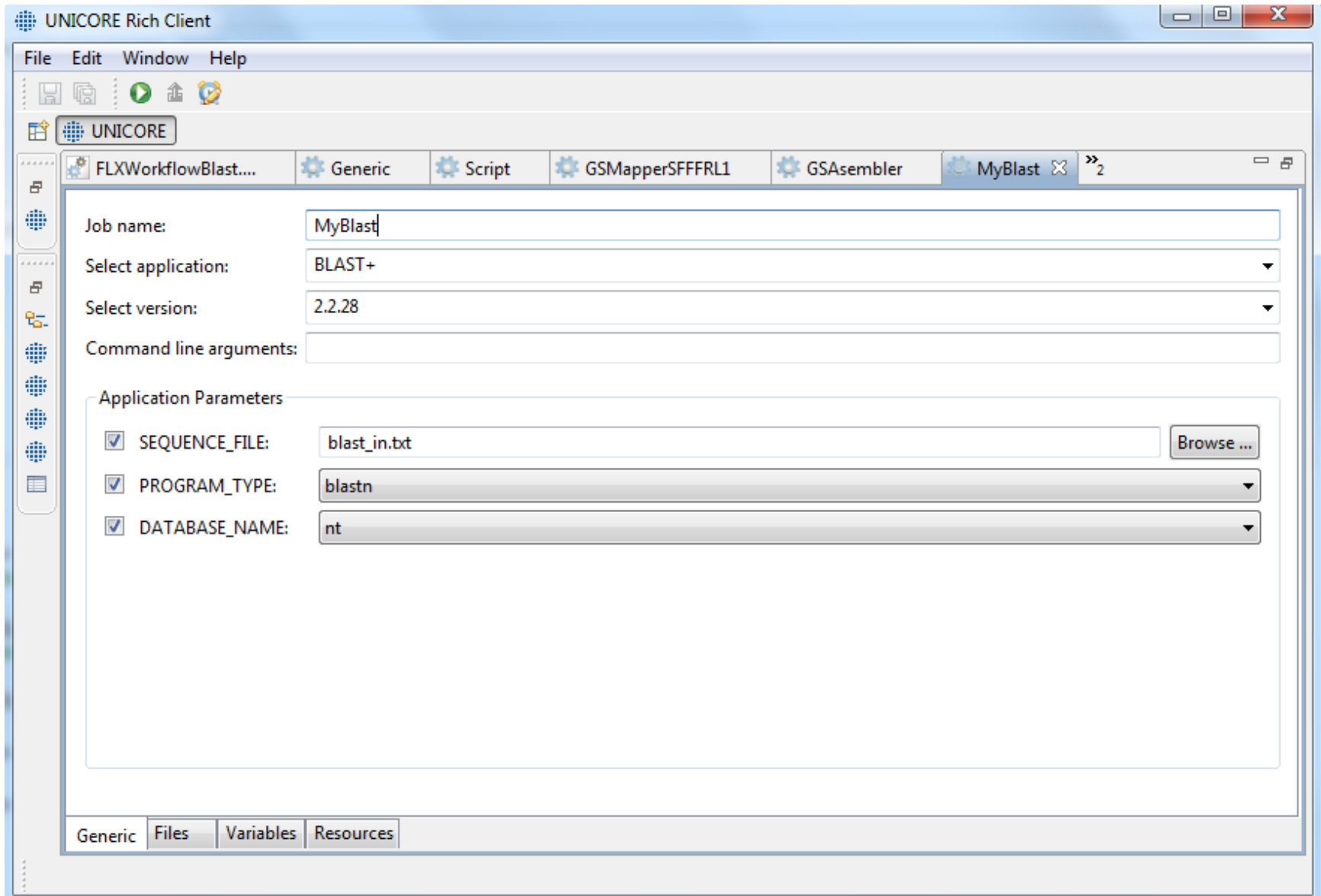
# Workflow development

- Complicated workflow has been developed by Davit
- The bottleneck is sequence alignment with blast
  - typical data to process consists of ca. 1 mln reads
  - Input size ca. 300MB, output size (XML file) ca. 1TB
  - Blast outputs is than processed by python scripts and R



- Applications

Application	ACK	ICM	PCSS	TASK	WCSS
AutoDock	X	X		X	X
AutoDock Vina	X	X			
Blast	X	X			
Blast+	X	X			
BWA	X	X			
ClustalW2		X			X
Custal Omega	X	X		X	X
GATK		X			
MrBayes		X			
PicardTools	X	X			
R	X	X	X	X	X
GS Data Analysis Software		X			
Rosetta	X	X			X



- Home
- Create Job
- My Jobs
- My Sites
- Angio Merge
- Sinus MED

## Job Computation



Alignment ×

Application  Input Files  Output Files  Resources

Job name:  \*

Tag:  ▼

Select application:  ▼

Select version:  ▼

Command line arguments:

### Input parameters

PROGRAM\_TYPE:  ▼

DATABASE\_NAME:  ▼

BLAST\_PLUS\_ARGUMENTS:

SEQUENCE\_FILE:  \*






## Alignment workspace

Select/Unselect all      

Path:    Show hidden files

Name	Ext
file.fasta	fasta
stderr	
stdout	
TSI_script_file_32625	
UNICORE_SCRIPT_EXIT_CODE	

https://unicore-...y/14/stdout.txt X +

←  https://unicore-portal.gric   Szukaj

```

BLASTN 2.2.28+

Reference: Zheng Zhang, Scott Schwartz, Lukas W
Miller (2000), "A greedy algorithm for aligning
Comput Biol 2000; 7(1-2):203-14.

Database: nt
          20,485,291 sequences; 51,580,221,569

Query= C1093377_2.0

Length=200

Score      E
Sequences producing significant alignments:
(Bit)  Value

    gi|2578066|emb|Z98036.1| Human DNA sequence f
333      3e-88
    gi|195963538|gb|AC217054.3| MACACA MULATTA BA
110      6e-21
    gi|29366933|gb|AC009054.8| Homo sapiens chrom
106      8e-20
    gi|15145261|gb|AC073413.6| Homo sapiens BAC c
99.0     1e-17
    gi|148727464|gb|AC198790.3| Pongo abelii BAC
95.3     2e-16
                
```

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**PCJ: [pcj.icm.edu.pl](http://pcj.icm.edu.pl)**

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