A Moldable Online Scheduling Algorithm and Its Application to Parallel Short Sequence Mapping

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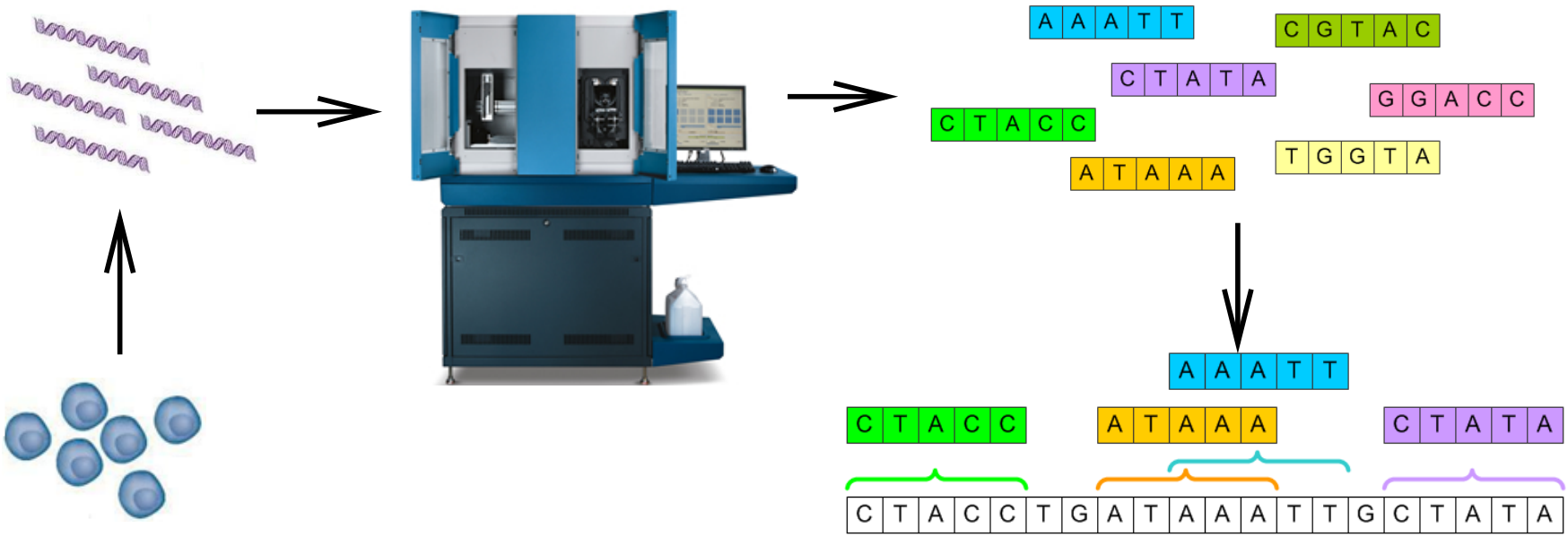
Motivation



Sequencing

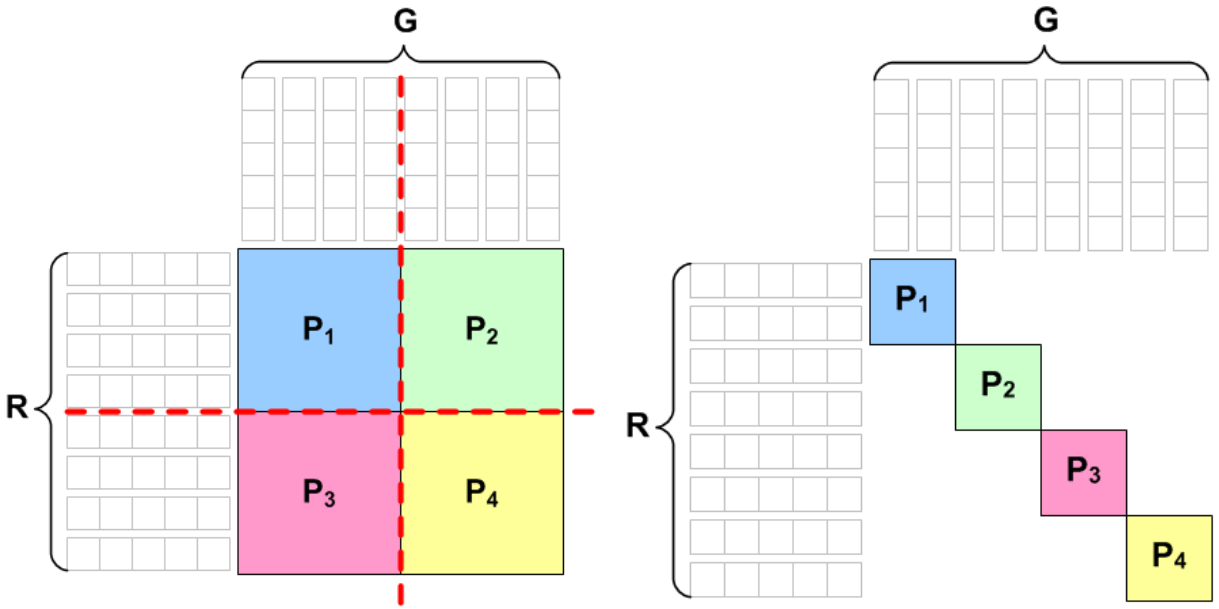
- Next generation sequencing instruments (SOLiD, Solexa, 454) can sequence up to 1 billion bases a day
  - Hundreds of millions of 35-50 base reads

Mapping

- Map reads to a reference genome efficiently (Human genome: 3Gb)
- Sequential mapping takes about a day
- Need fast, parallel algorithms that can handle mismatches

Parallel Short Sequence Mapping[Bozdag *et al.*, IPDPS 09]

Three partitioning dimensions:



$$P(m_g, m_r, m_s) = c_{gs}\frac{G}{m_g} + c_g\frac{G}{m_g m_s} + c_{rs}\frac{R}{m_r} + (c_r + c_c\frac{G}{m_g m_s})\frac{R}{m_r m_s}$$

Partitioning on m processors is finding minimum $P(m_g, m_r, m_s)$ such that $m_g m_r m_s \leq m$

This talk

A cost efficient approach

To reduce cost, Ohio SuperComputing Center is building a bioscience dedicated cluster. It will host a Short Sequence Mapping service.

- Laboratories submits mapping request over the network.
- The service computes the mapping using the parallel algorithm.
- And sends the result back.

This talk

How to schedule the mapping request ?

This talk

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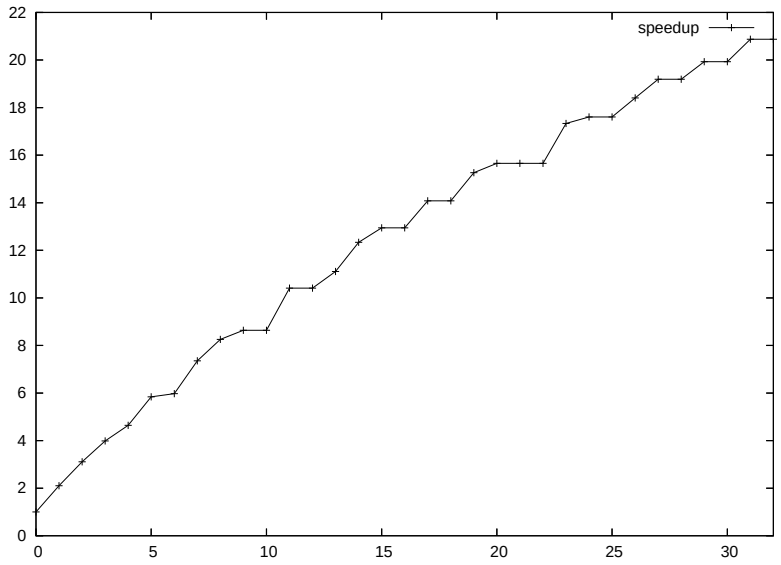
How to schedule the mapping request ?

Outline of the Talk

Parallel Short Sequence Mapping

The important facts:

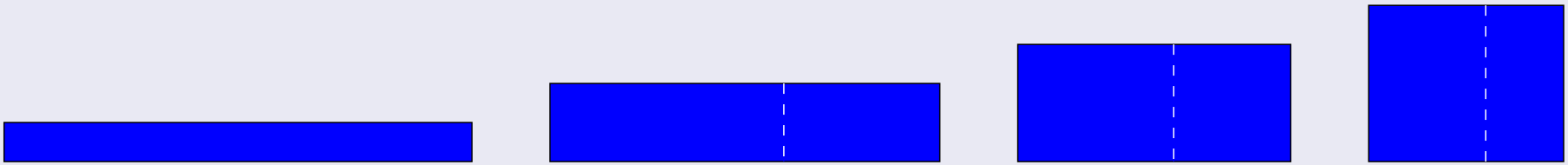
- can adapt to different number of processor
- good runtime prediction function
- no super linear speed up
- non convex speedup function (steps)
- no preemption



Moldable Scheduling

Instance

- m processors
- n tasks
- Task i arrives at r_i
- The execution of i on j processors takes $p_{i,j}$ time units



Solution

- Task i is executed on π_i processors
- Task i starts at σ_i
- Task i finishes at $C_i = \sigma_i + p_{i,\pi_i}$

Objective Function

Flow time

The flow time is the time spent in the system per a task $F_i = C_i - r_i$.

- Does not take task size into account.
- Optimizing the maximum flow time is unfair to small tasks.
- Optimizing the average flow time should starve large tasks.

Stretch [Bender *et al.* SoDA 98]

The stretch is the flow time normalized by the processing time of the task $s_i = \frac{C_i - r_i}{p_{i,1}}$.

- It provides a better fairness between tasks.
- Optimizing maximum stretch avoids starvation.

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Online maximum stretch can not be approximated

Adversary technique on one processor

A large task enters in the system

On several processors

There are similar techniques on several processors but there are more complicated and thus less prone to appear in practice.
The key point: if all processors are busy, a small task entering the system will have a large stretch.

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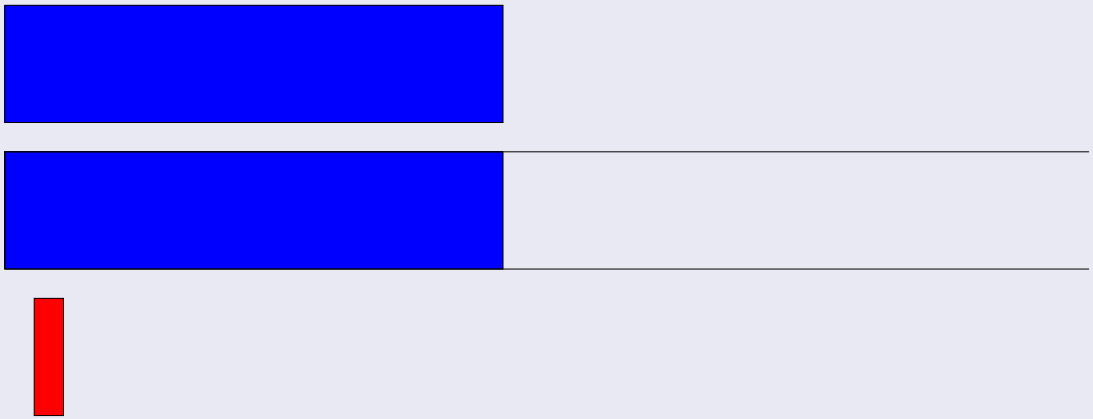

If it is scheduled immediately, a small task is sent

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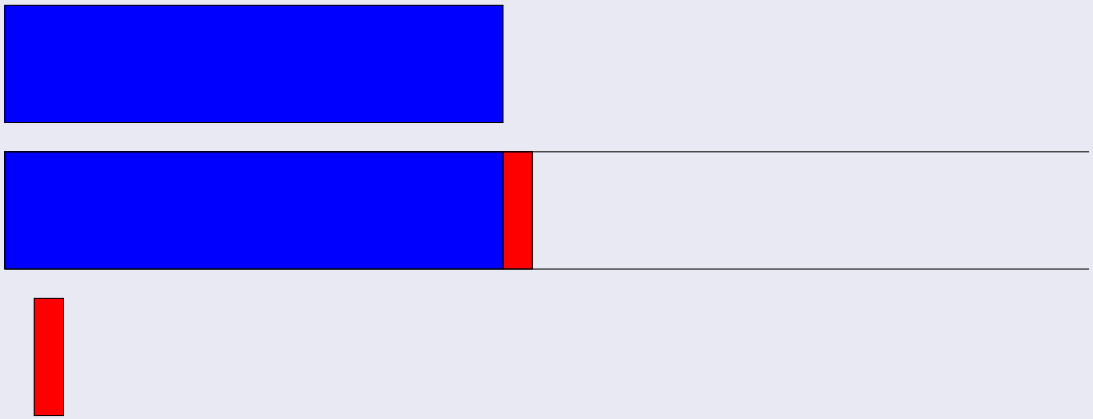

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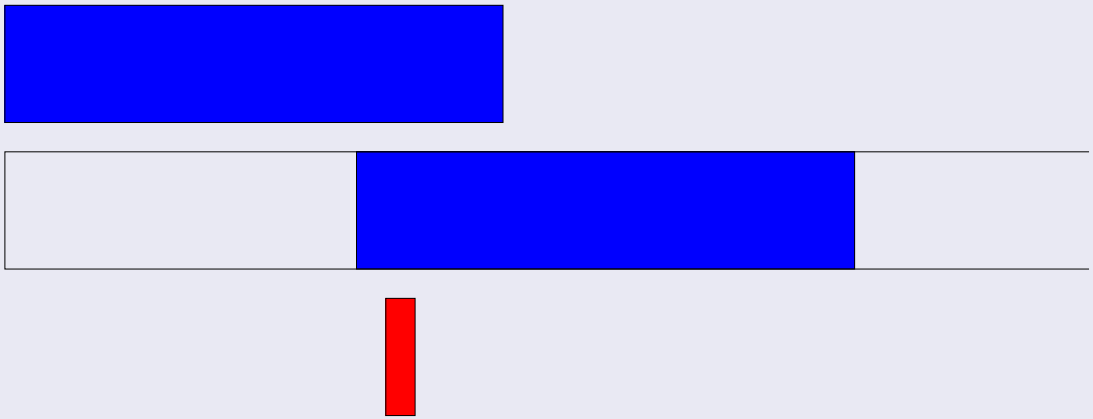

If the large task is scheduled later, a small task is sent accordingly

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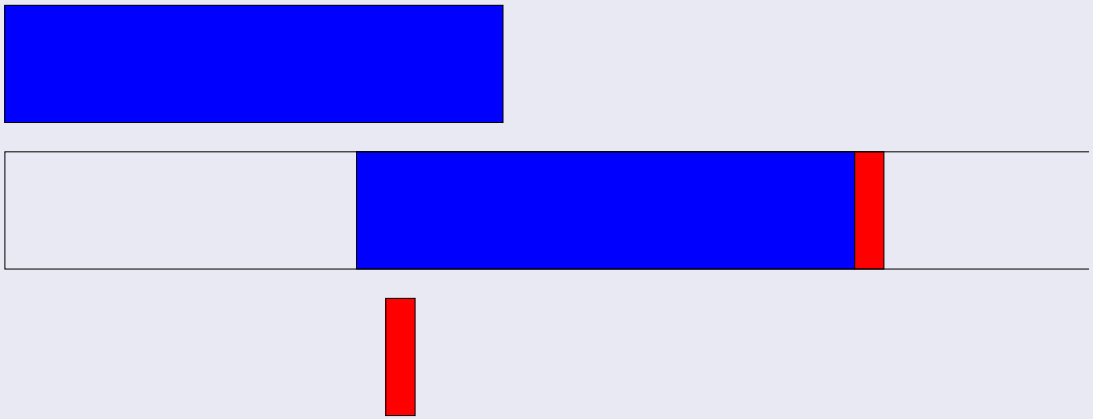

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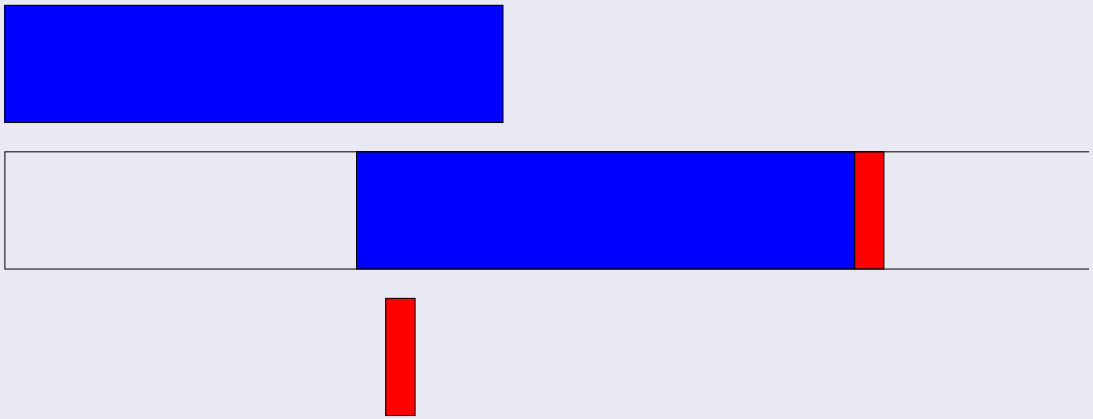

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Outline of the Talk

Principle of the Deadline Based Online Scheduler (DBOS)

- All tasks running concurrently should get the same stretch to maximize efficiency
- Using the optimal maximum stretch as an instant measure of the load
- Aim at a more efficient schedule than the optimal instant maximum stretch one to deal with still-to-arrive tasks

The DBOS Algorithm

Targeting a maximum stretch S

Task i must complete before the deadline $D_i = r_i + p_{i,1}S$.

Moldable Earliest Deadline First (MEDF)

- Considers task in deadline order.
- Allocates the minimum number of processors to each task to completes before the deadline.
- Schedules the task as soon as possible without moving any other task.

DBOS(ρ)

- Estimate the optimal maximum stretch S^* using a binary search.
- The deadline problem is solved by MEDF.
- Build a schedule of good efficiency of stretch ρS^*.
  - ρ is the online parameter

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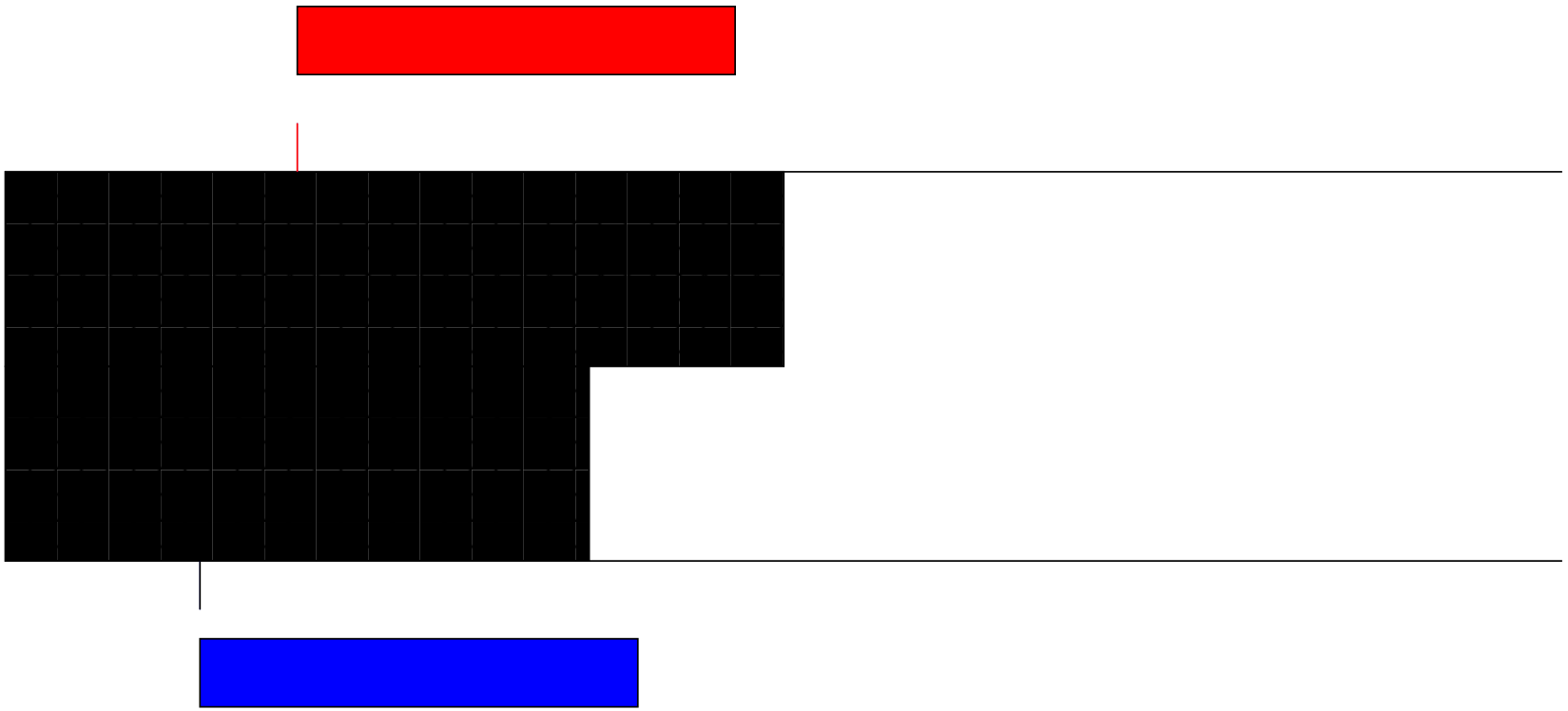
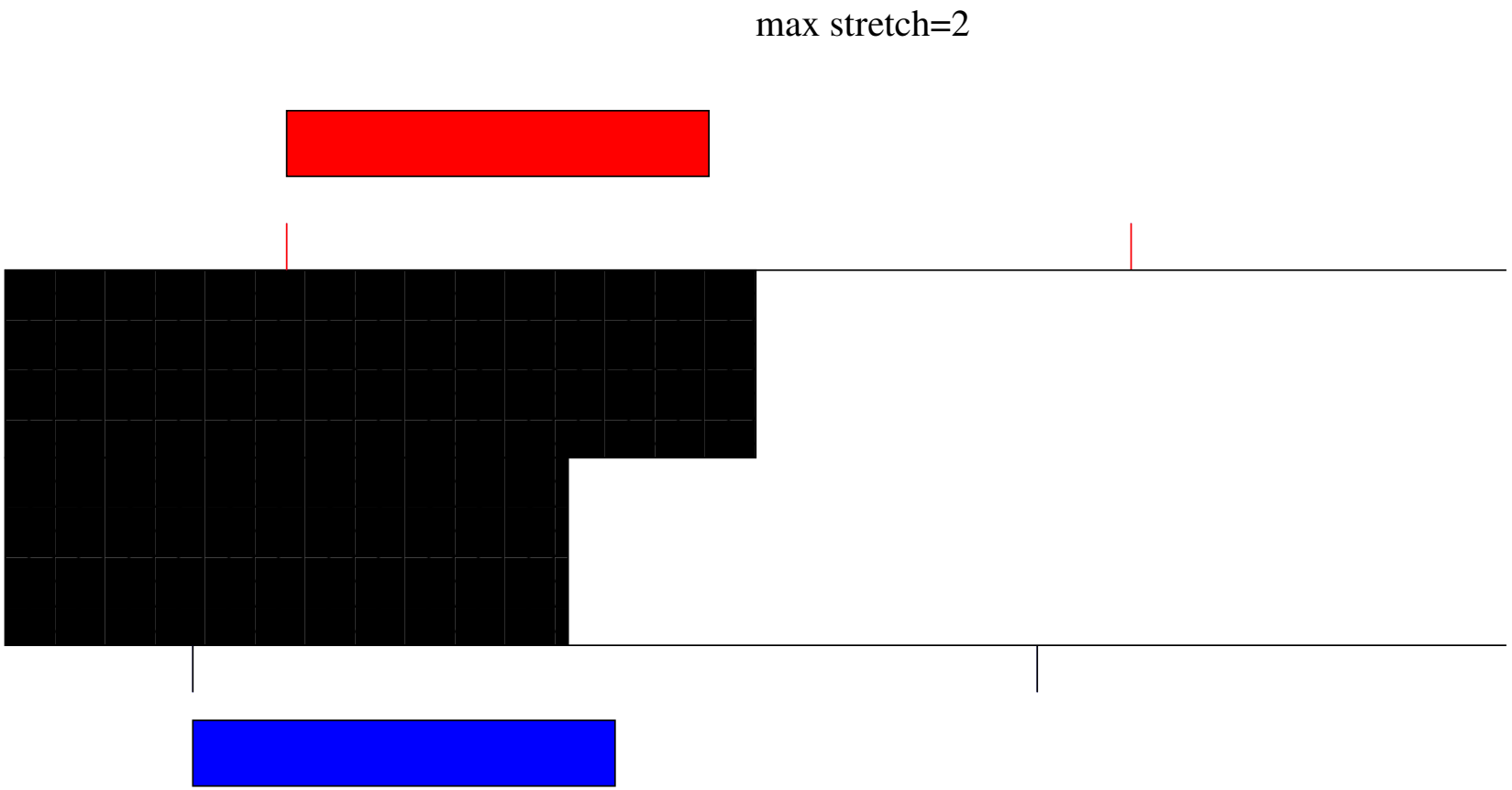
An example



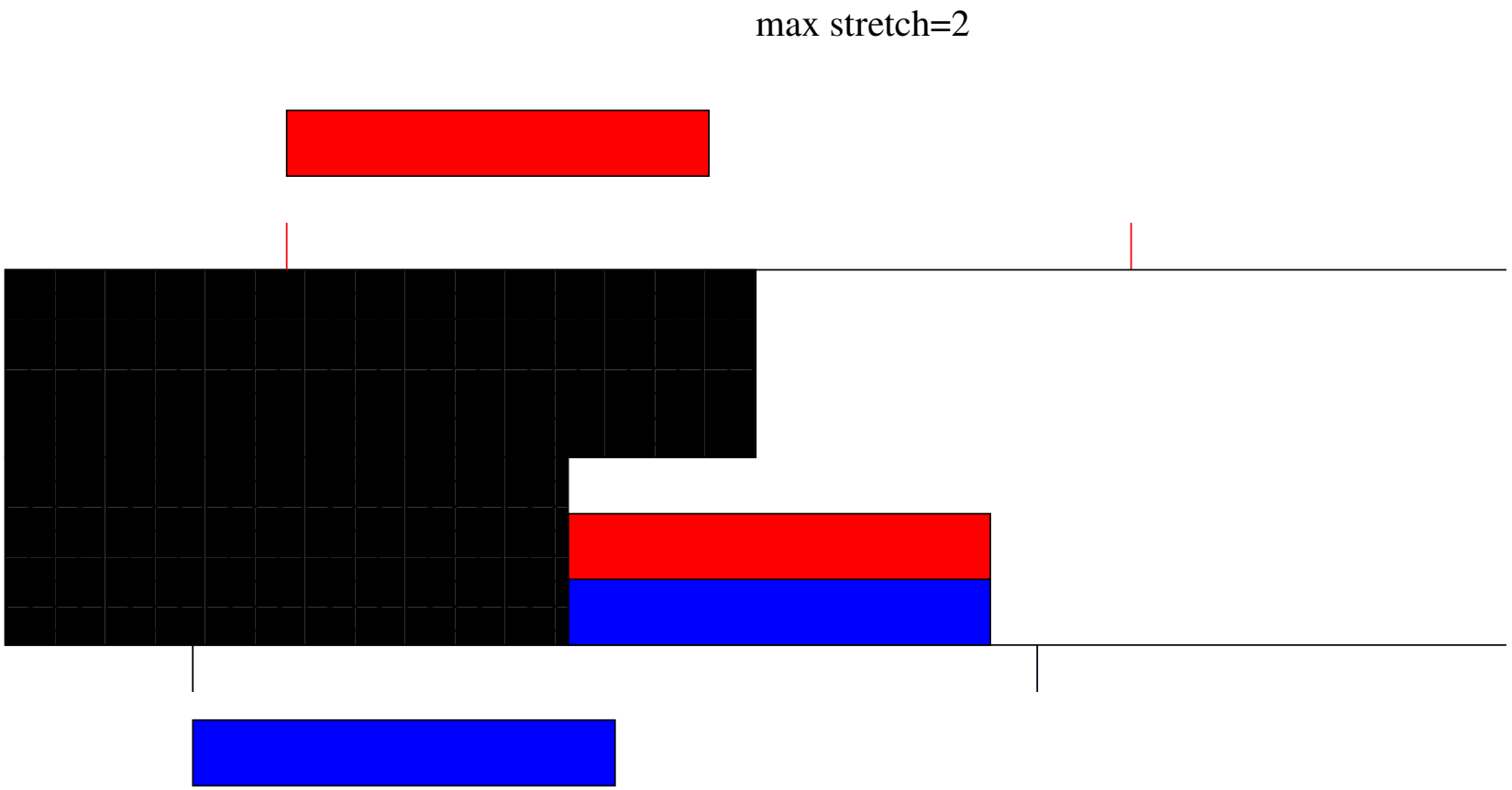
A system with two pending tasks

An example



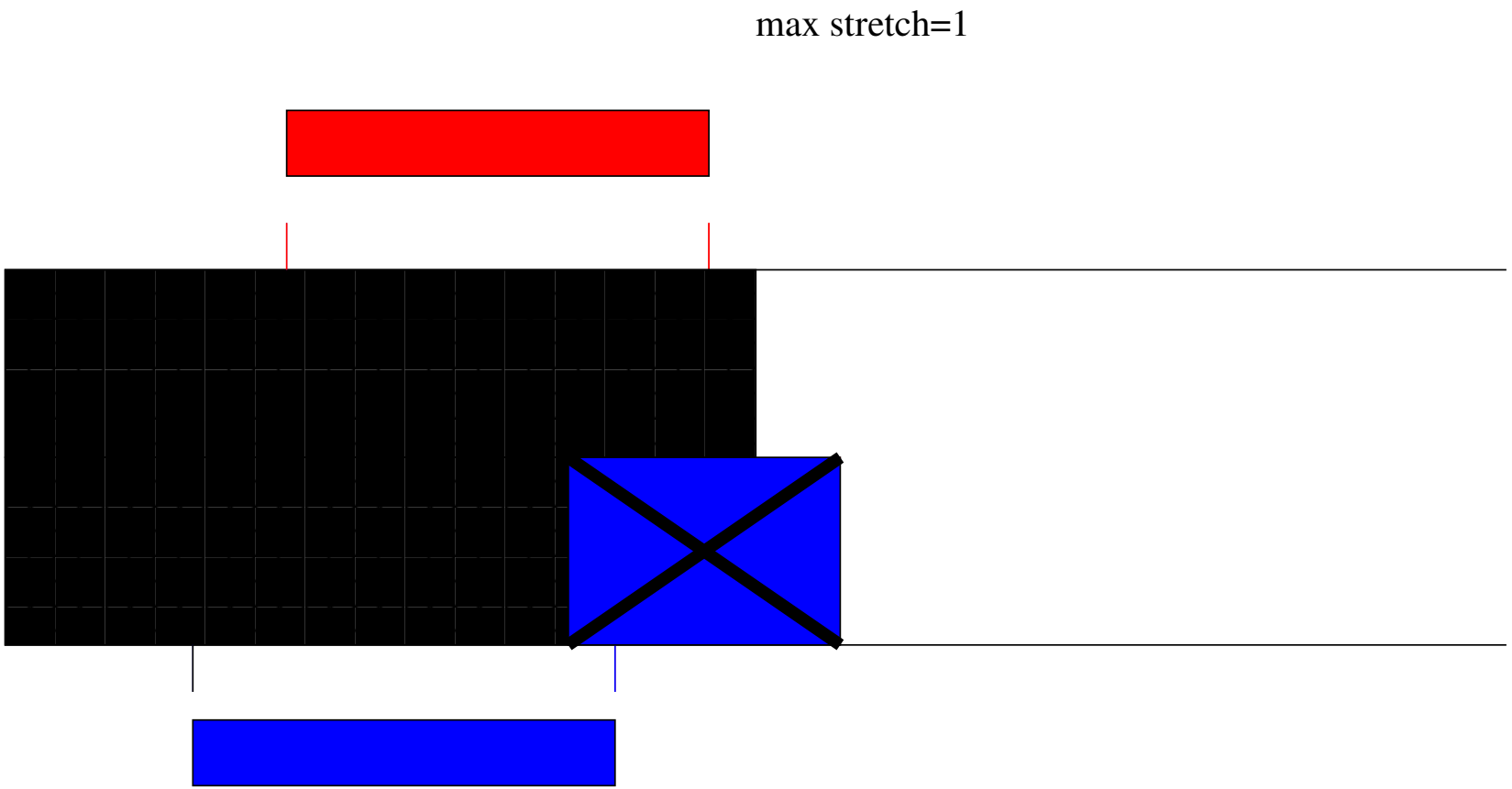
Deadlines induced by a stretch of 2

An example



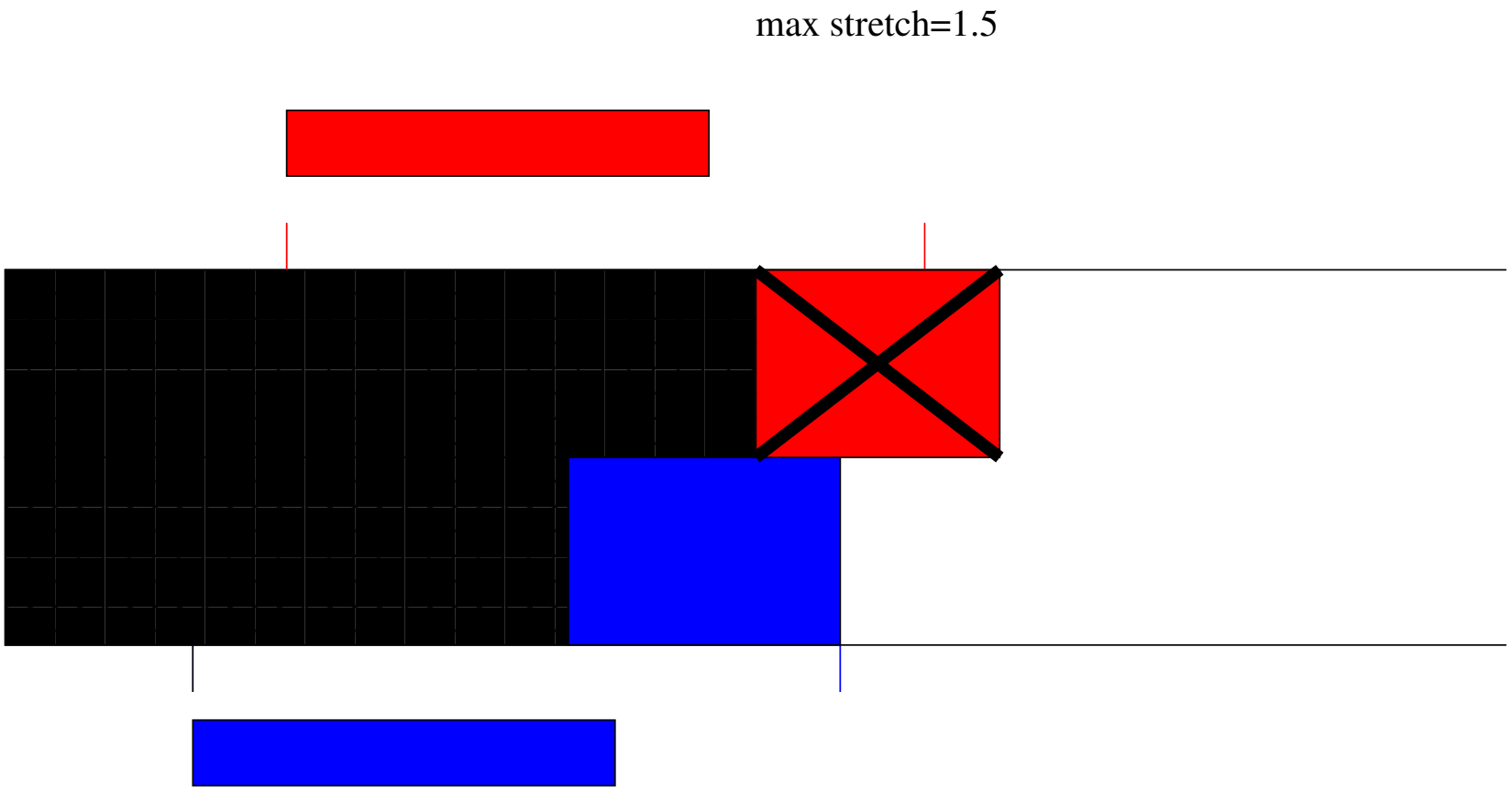
A maximum stretch of 2 is reachable

An example



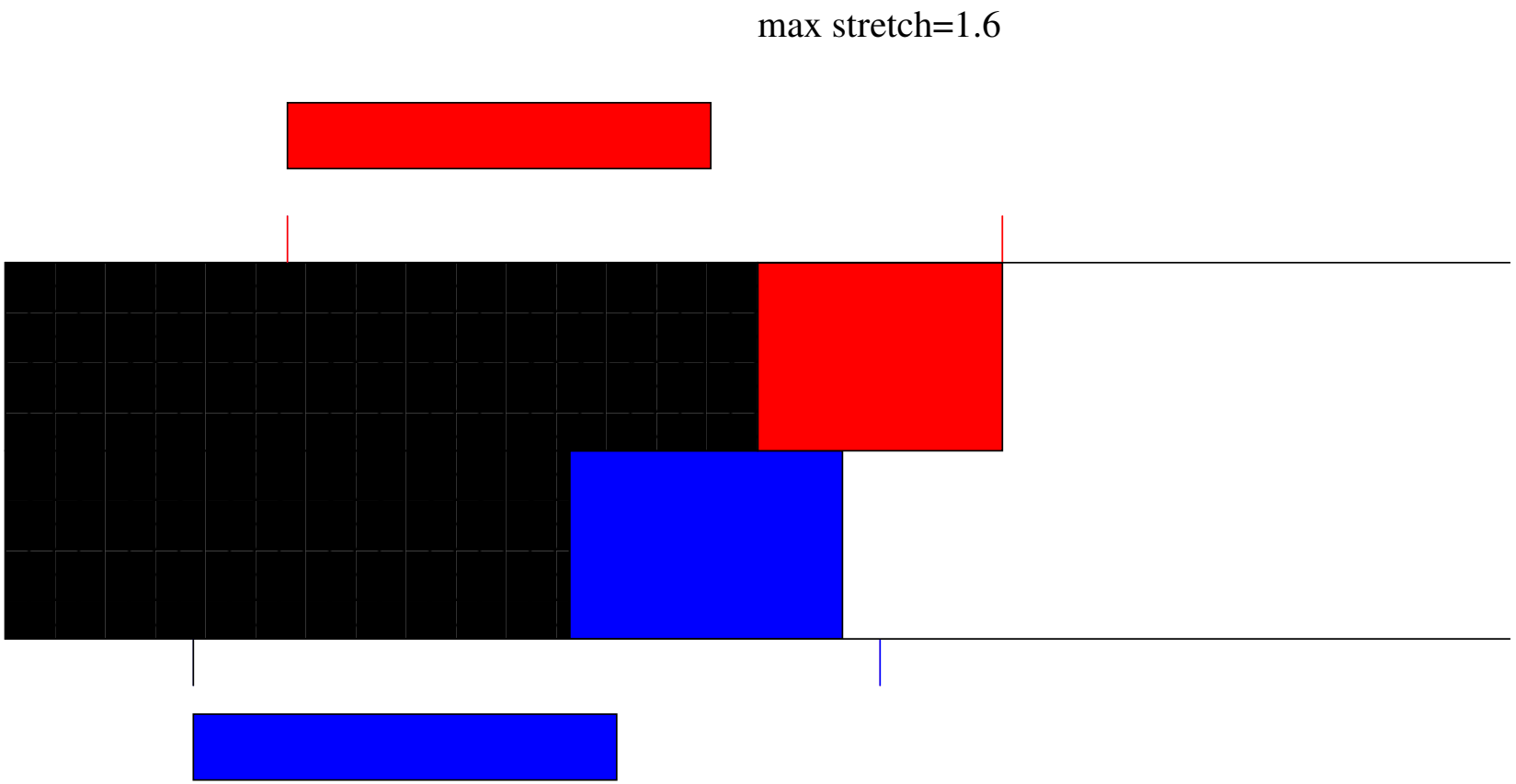
But 1 is not

An example



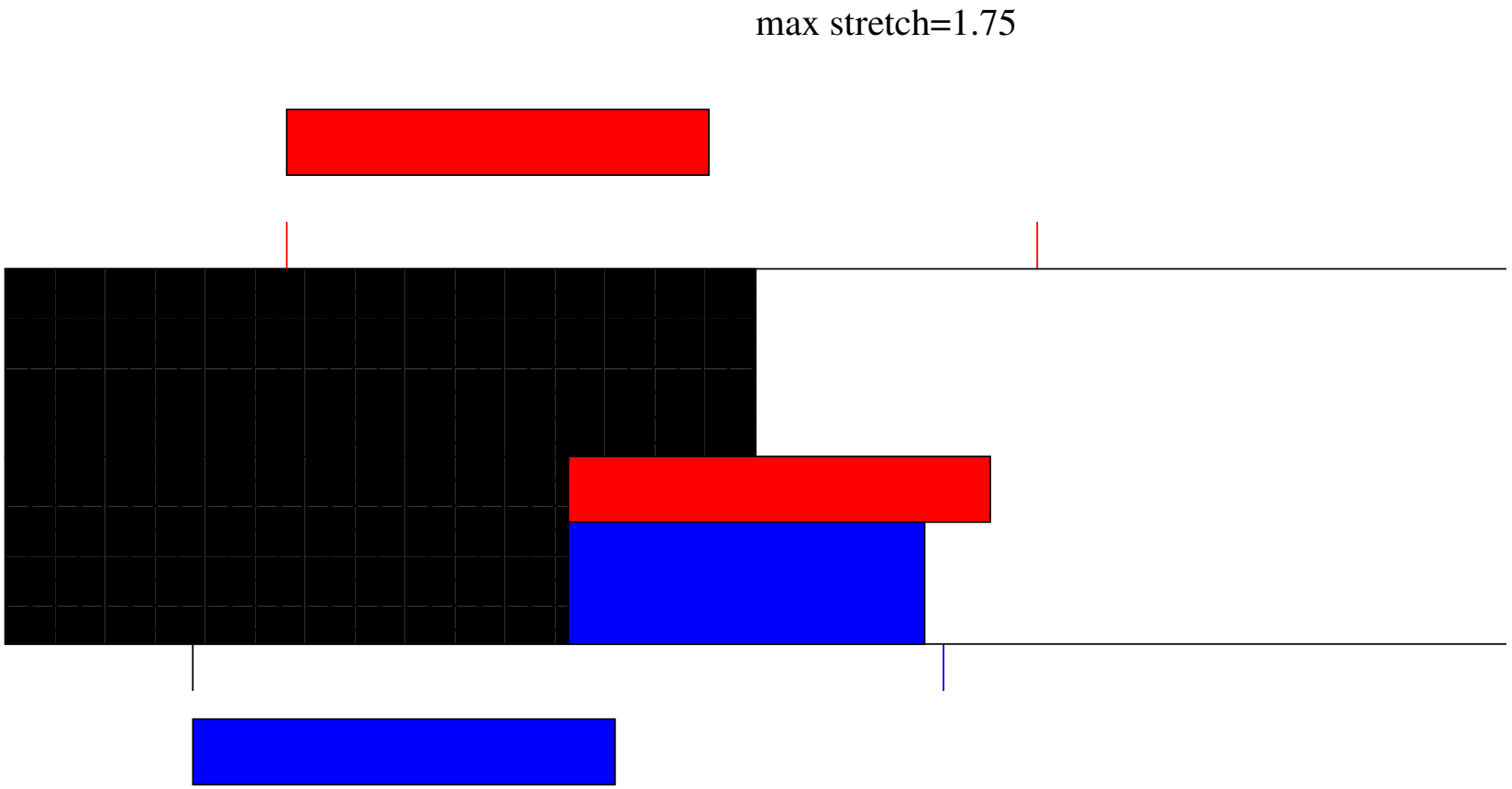
Neither 1.5

An example



The optimal stretch is 1.6

An example



The online parameter $\rho = 1.1$ leaves much more space (thanks to MEDF).

Outline of the Talk

An Iterative Process [Sabin et al, JSSPP 06]

The algorithm

- $\forall i, \pi_i \leftarrow 1, mark[i] \leftarrow false$
- $\sigma \leftarrow schedule(\pi)$
- while $\exists i \mid mark[i] = false$
  - Get unmarked i such that $p_{i,\pi_i} - p_{i,\pi_i+1}$ is maximal and positive
  - $\pi_i \leftarrow \pi_i + 1$
  - $\sigma' \leftarrow schedule(\pi)$
  - if $avgflow(\sigma') < avgflow(\sigma)$
    - $\sigma \leftarrow \sigma'$
  - else
    - $\pi_i \leftarrow \pi_i + 1; mark[i] \leftarrow true$

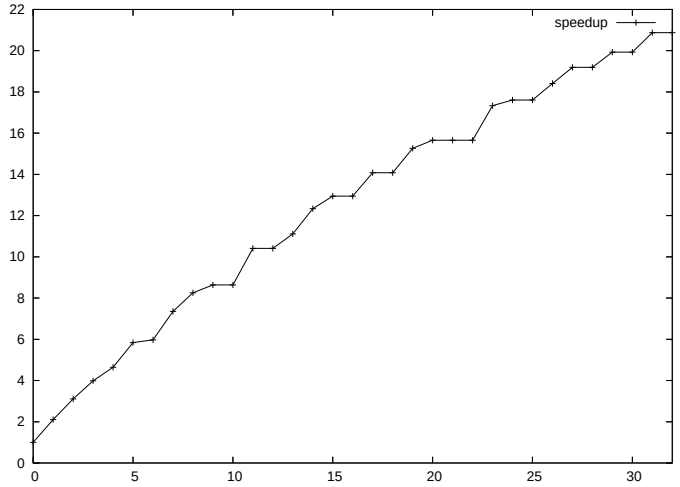
schedule

schedule is a conservative backfilling algorithm. Unspecified, we used FCFS.

An Iterative Process [Sabin et al, JSSPP 06]

Properties

- Optimizing flow time
- Claimed to outperform fair share
- Parameter-less



Improvement

If the speedup function is non convex or has steps. The algorithm gets stuck. (It was originally tested with a model where the speedup is convex)
Modification:

- Get unmarked i and k such that $(p_{i,\pi_i} - p_{i,\pi_i+k})/k$ is maximal and positive
- $\pi_i \leftarrow \pi_i + k$

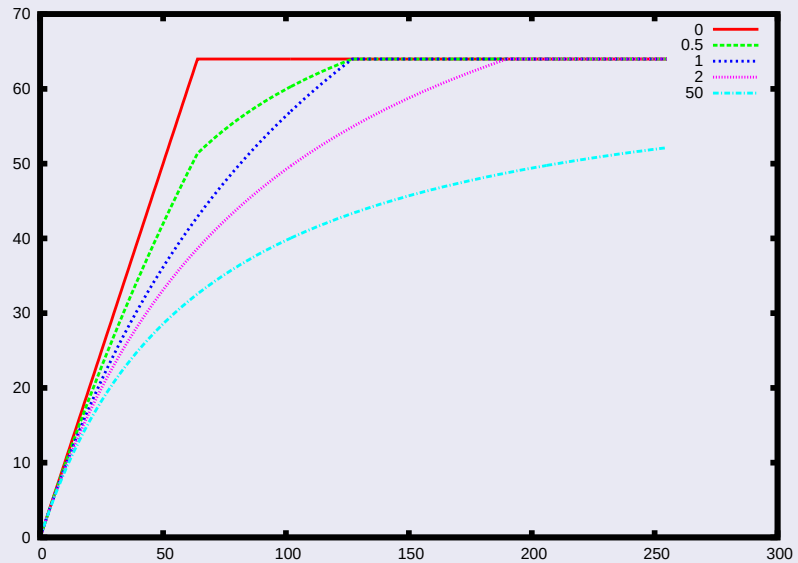
First Experimental Setting

Goal: assess performance on a well known setting

Downey model

Two parameters:

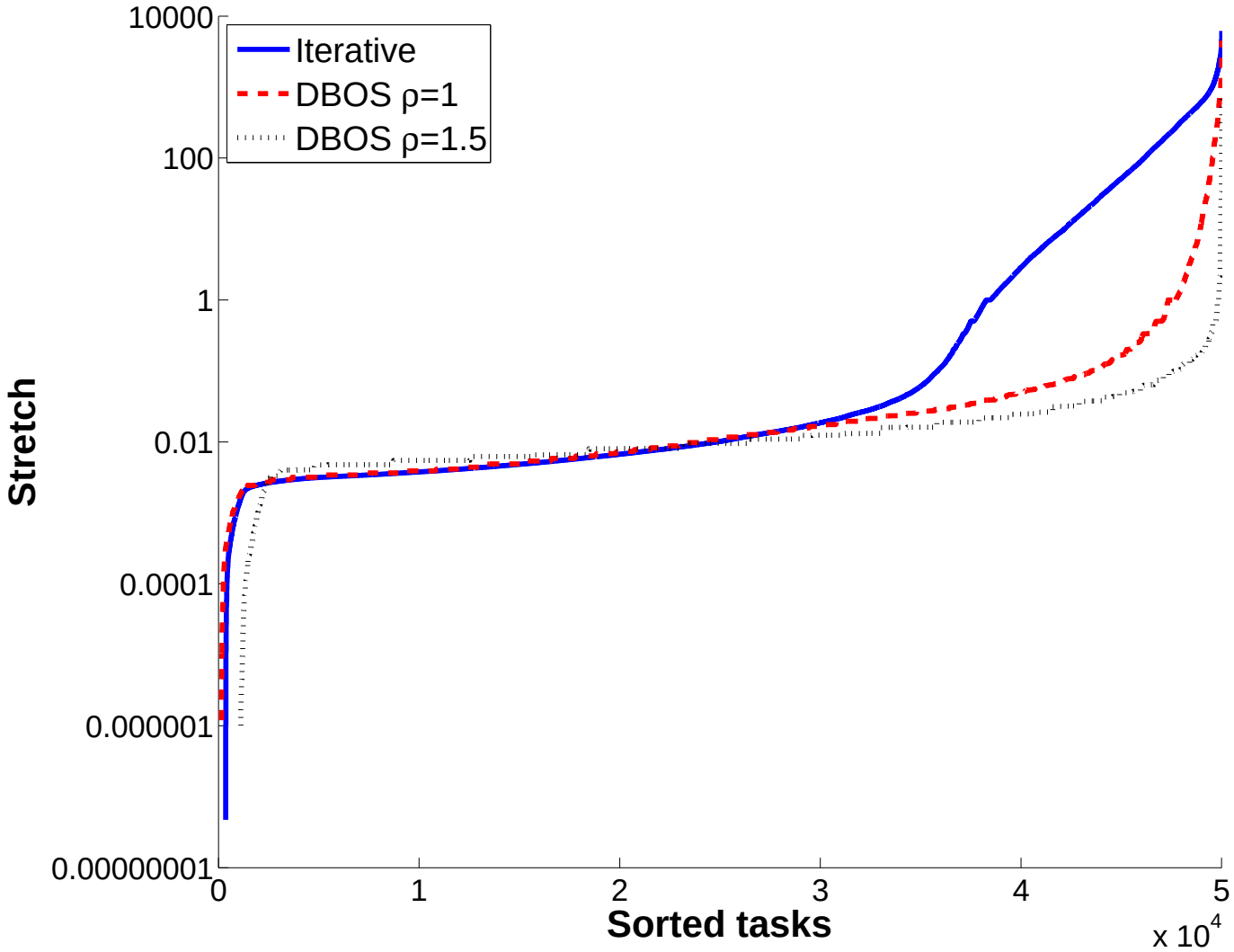
- Average parallelism (64)
- Distance to linear speedup



Generation

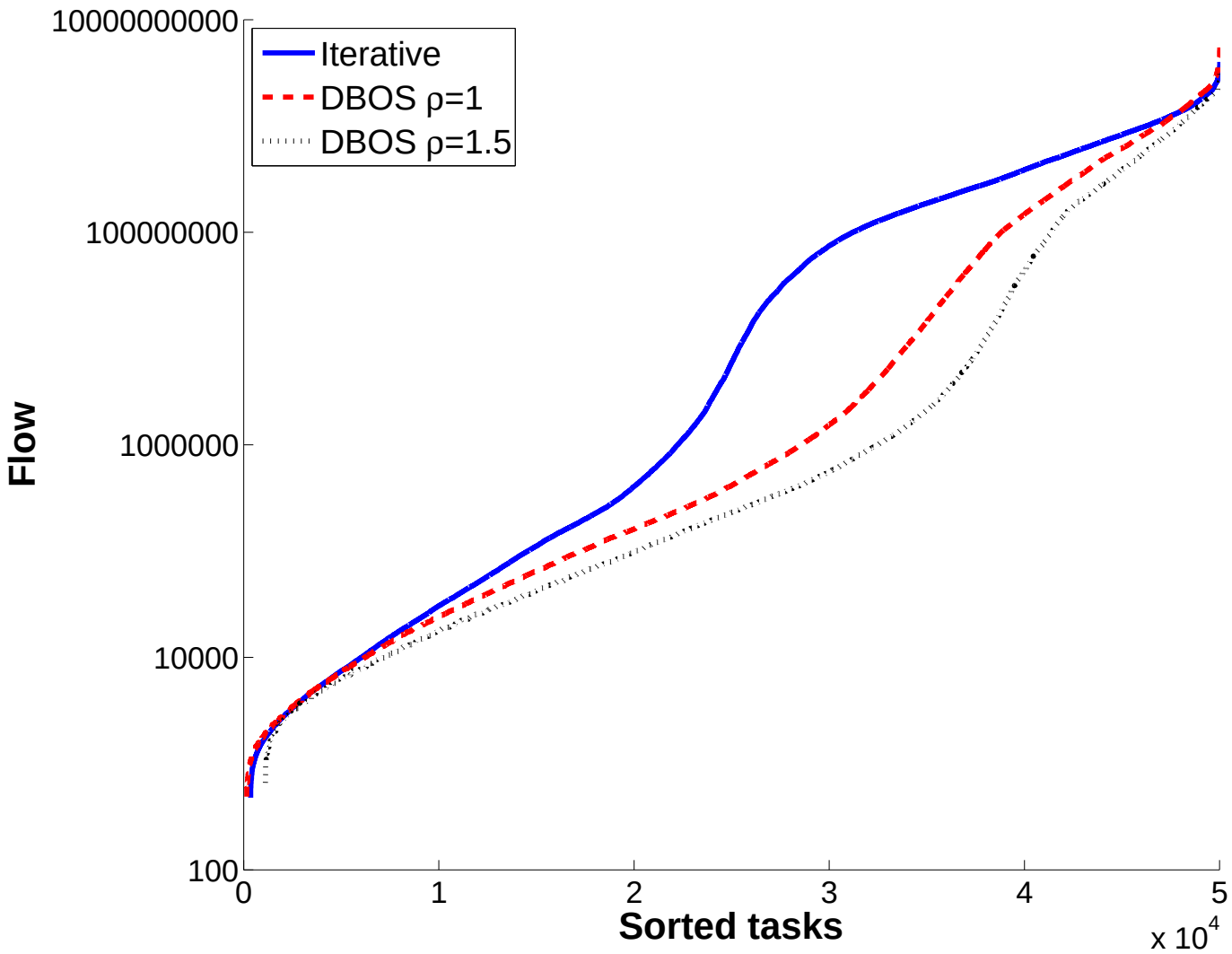
- 512 processors
- First 5000 tasks of SDSC Par 96 (From the Feitelson archive)
- Sequential time : total execution time
- Average parallelism : between number of used processor and 512
- Distance to linear speedup : between 0 and 2

Downey model results



DBOS generates less tasks with high stretch.

Downey model results



DBOS leads to better flow time. Iterative could be improved.

Second Experimental Setting

Goal: test case reflecting the cluster usage

Generation

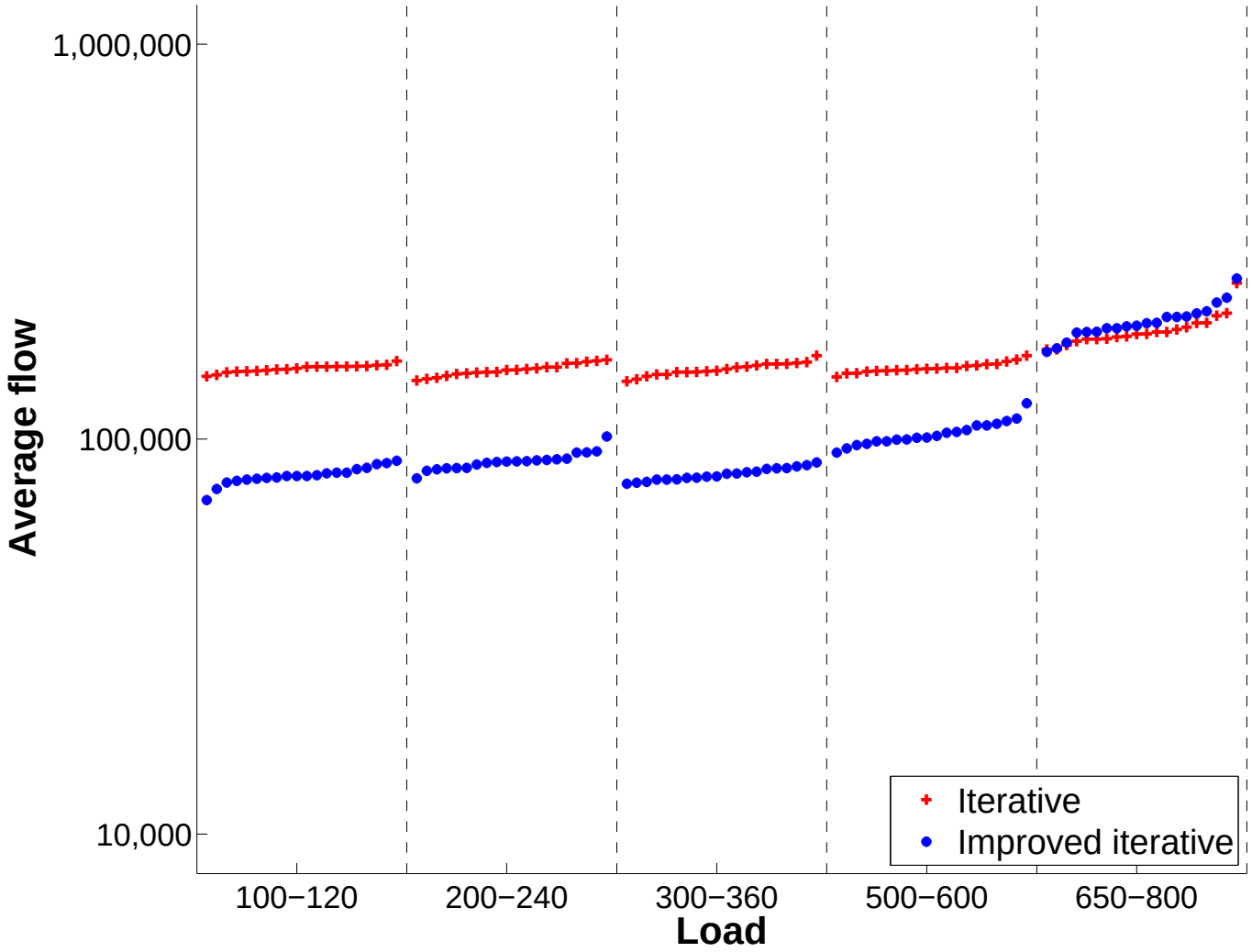
- 512 processors
- Each task corresponds to one lab studying one genome
- Speedup according to the runtime prediction function
- 2000 tasks are uniformly distributed in an time interval
- Changing the span of the interval to control the load

Real data

Sequencing machine	Reads
454 GS FLX Genome Analyzer	1 million
Solexa IG sequencer	200 million
SOLiD system	400 million

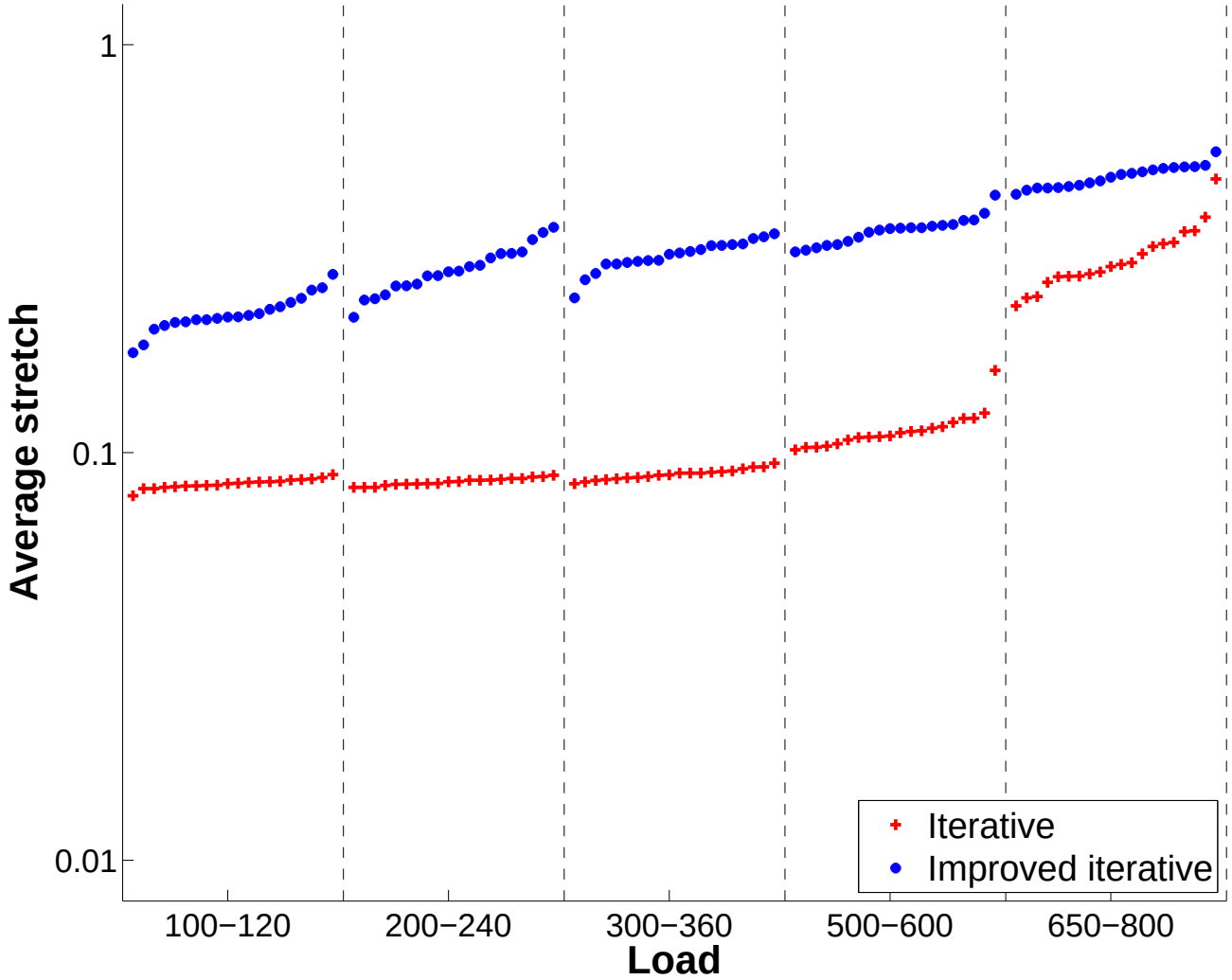
Genome	Size
E. Coli	4.6 million
Yeast	15 million
A. Thaliana	100 million
Mosquito	280 million
Rice	465 million
Chicken	1.2 billion
Human	3.4 billion

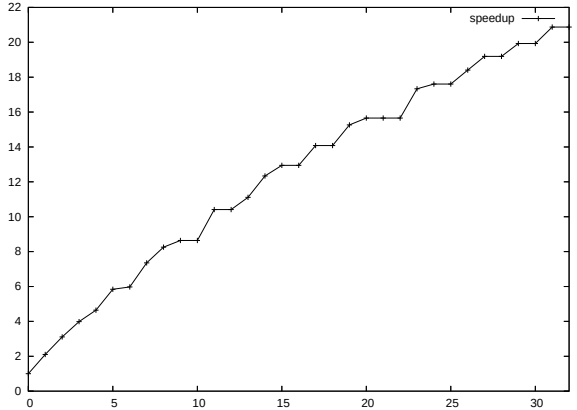
Mapping : Improvement on Iterative (flow)



The improvement really improves. The iterative got stuck.

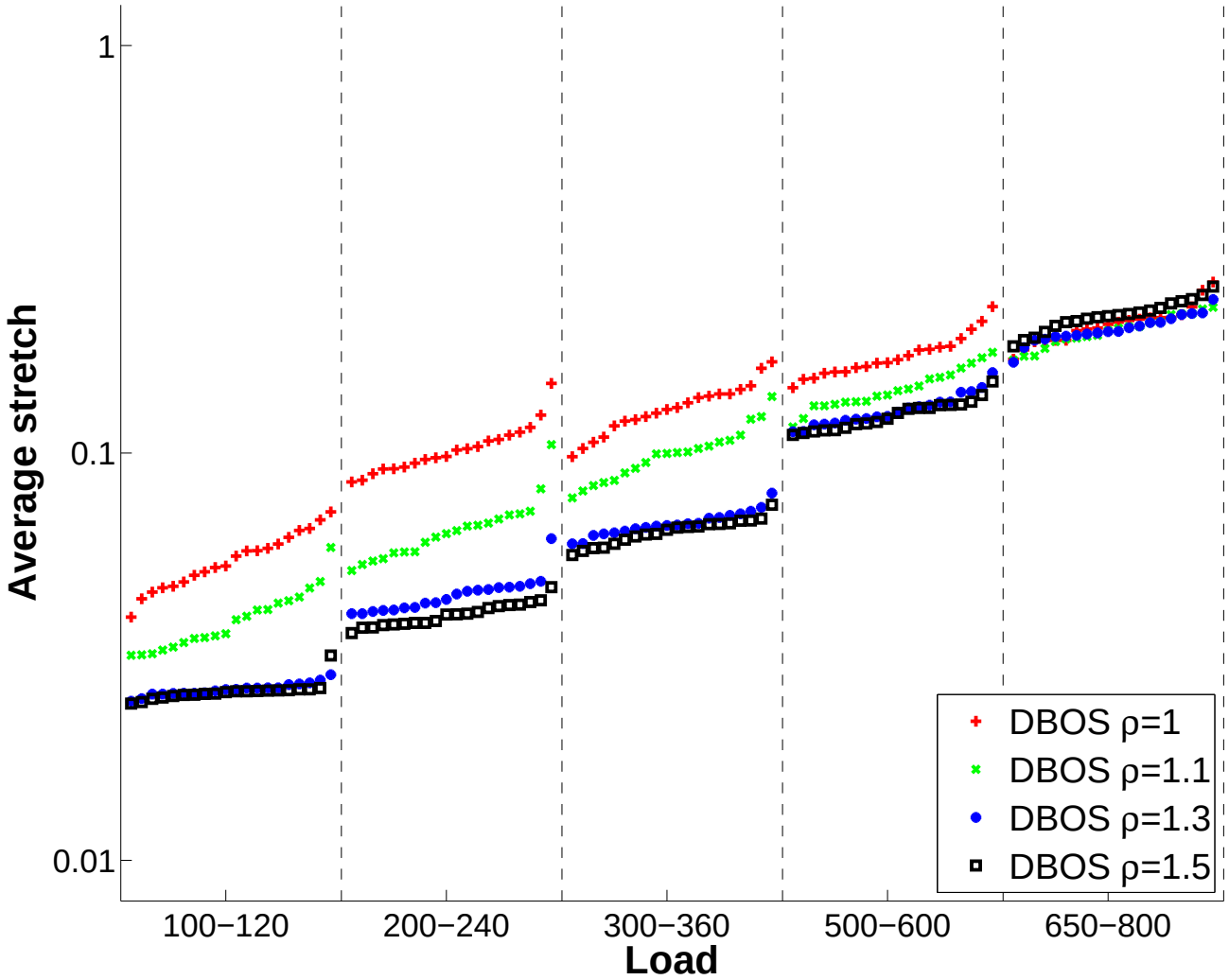
Mapping: Improvement on Iterative (stretch)





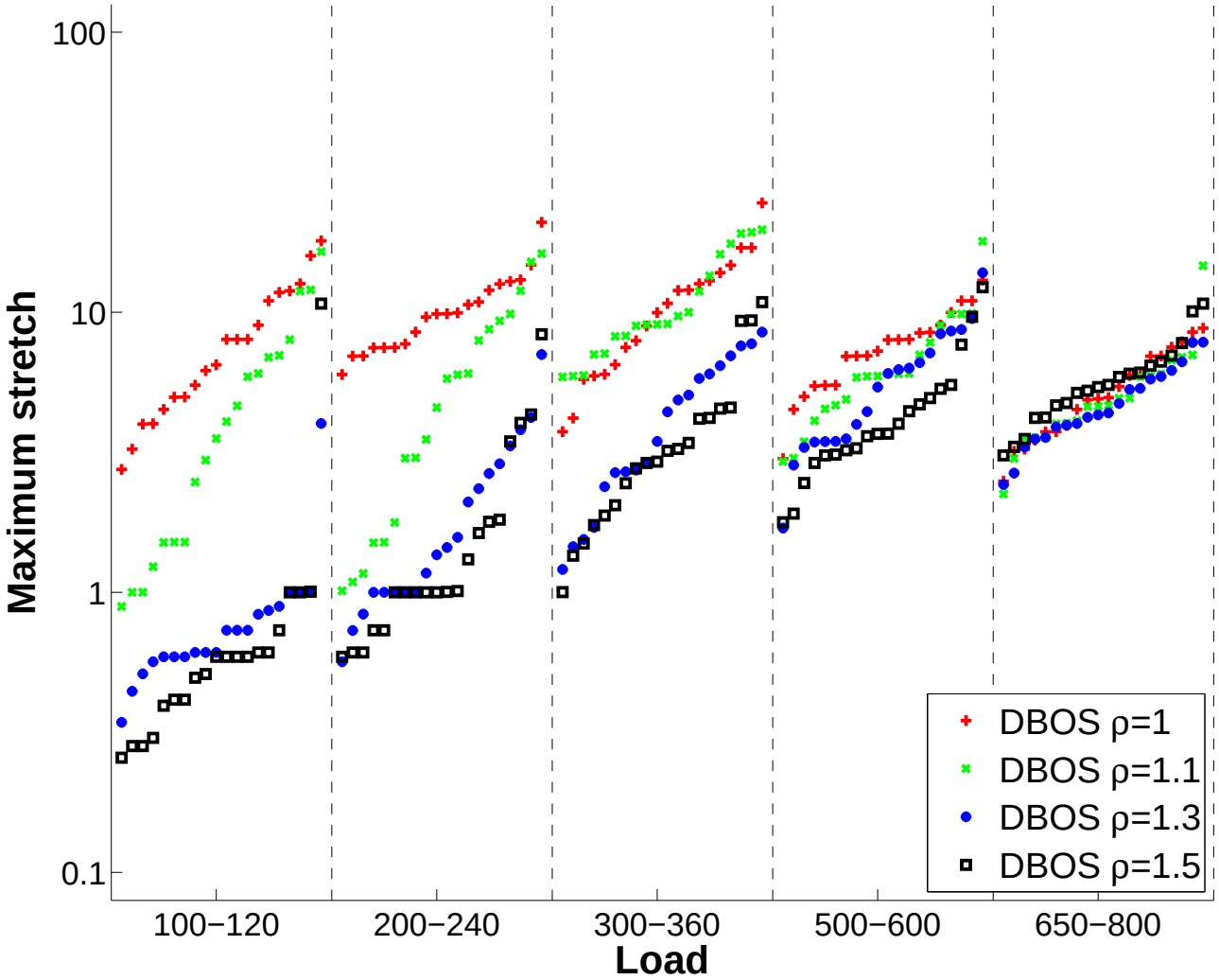
Getting stuck is good for stretch since it avoids interrupting tasks. They are just lucky.

Mapping : the online parameter (average stretch)



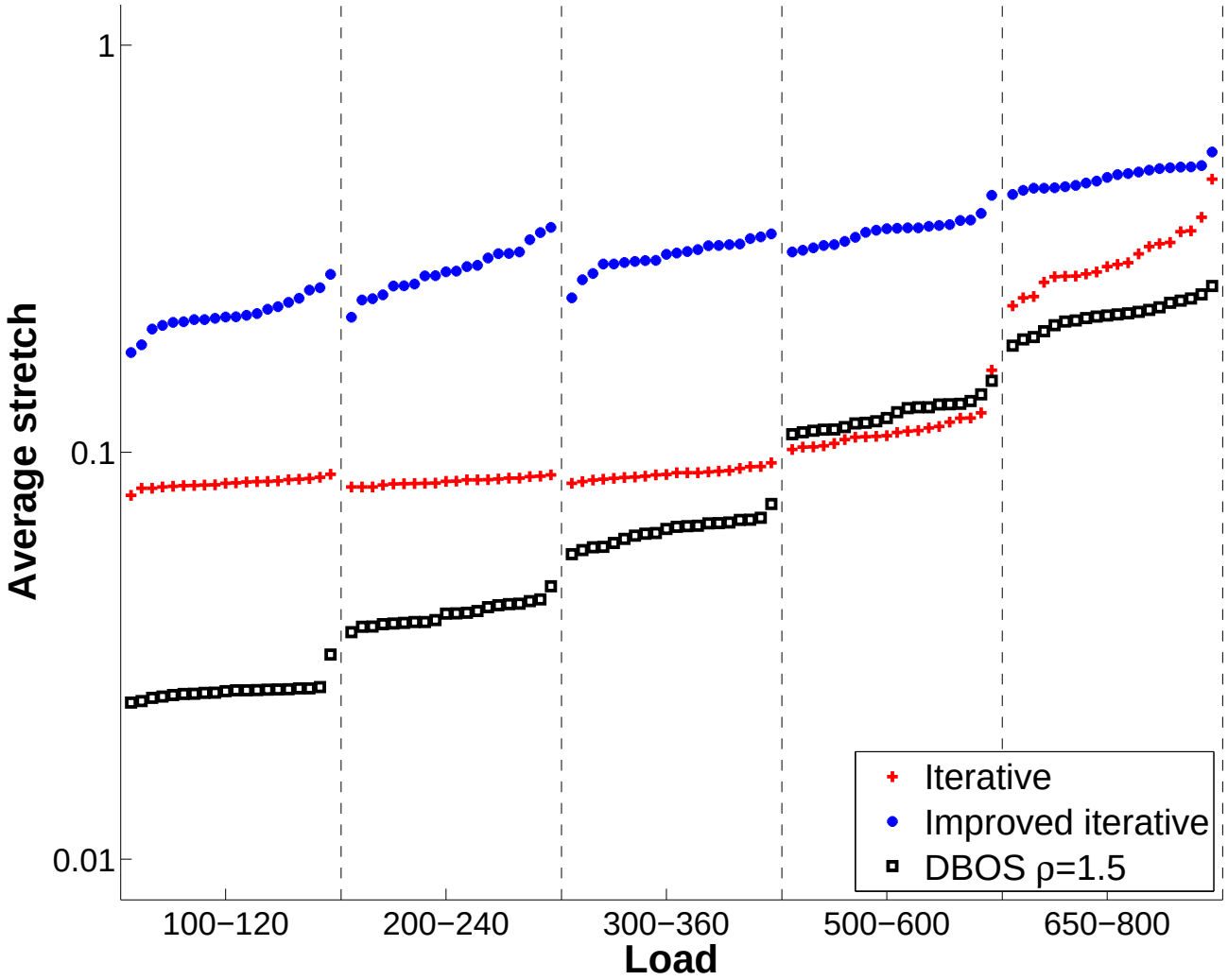
Quickly drops with ρ. Step at $\rho = 1.3$.

Mapping : the online parameter (maximum stretch)



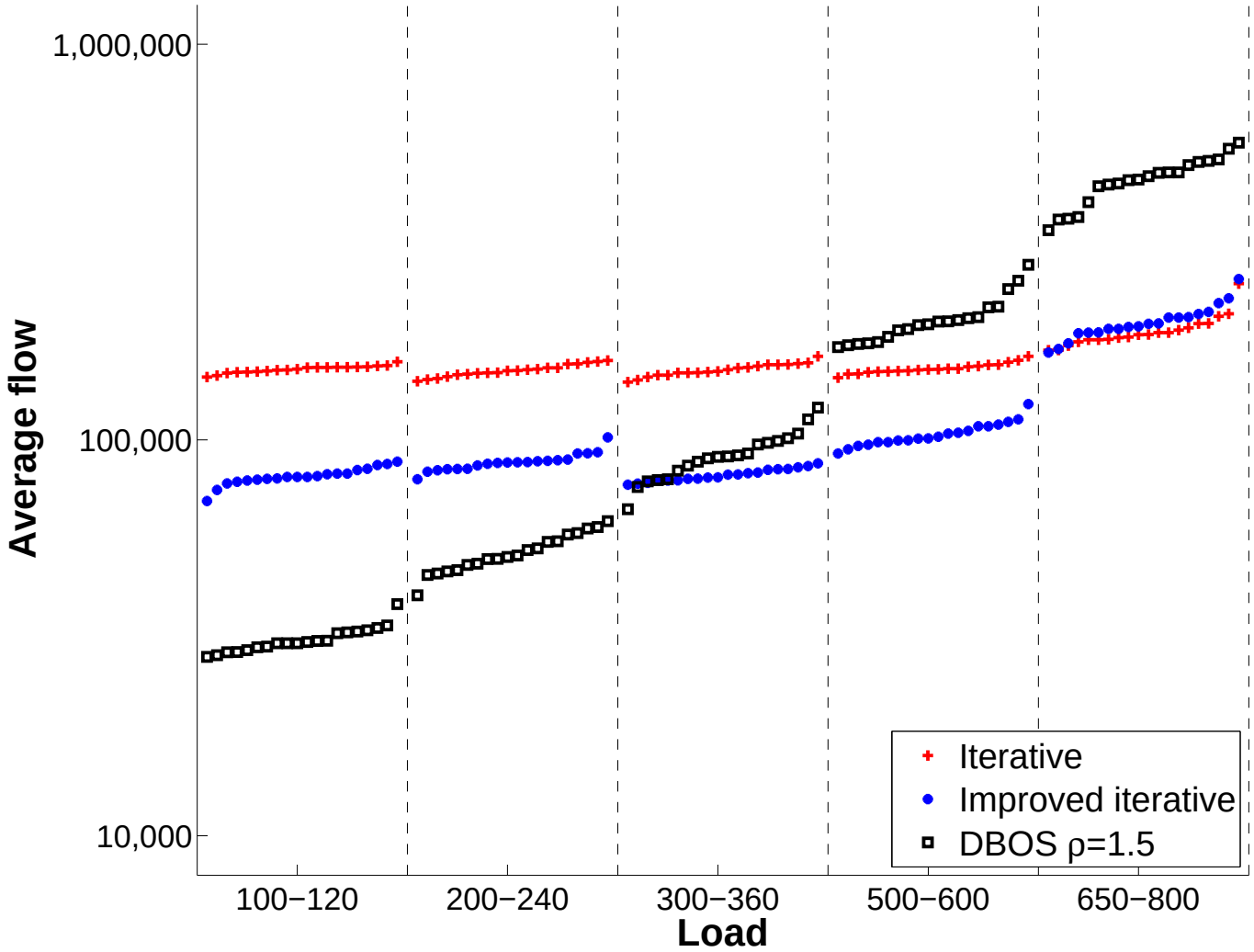
Max stretch is kept at a reasonable level. The online parameter ρ is very helpful here.

Mapping : DBOS vs Iterative (average stretch)



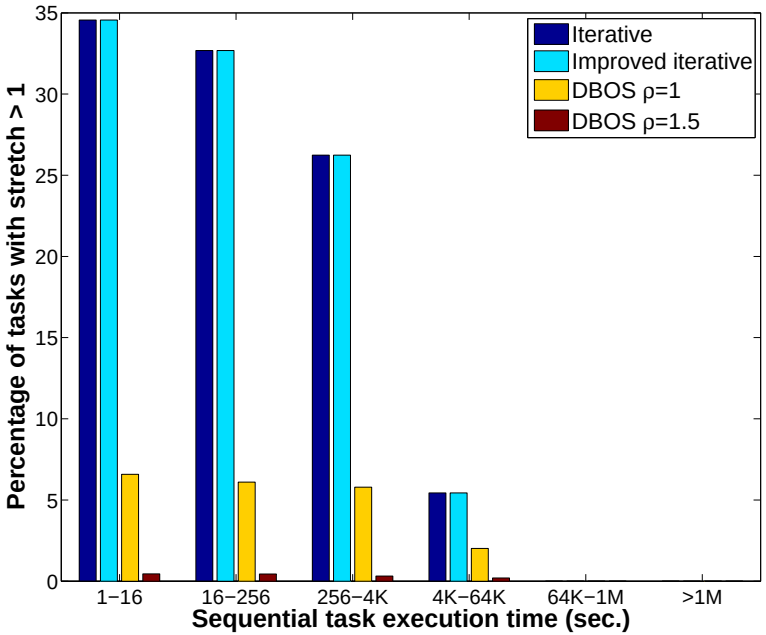
DBOS leads to much better stretch (even when iterative got stuck).

Mapping : DBOS vs Iterative (average flow)

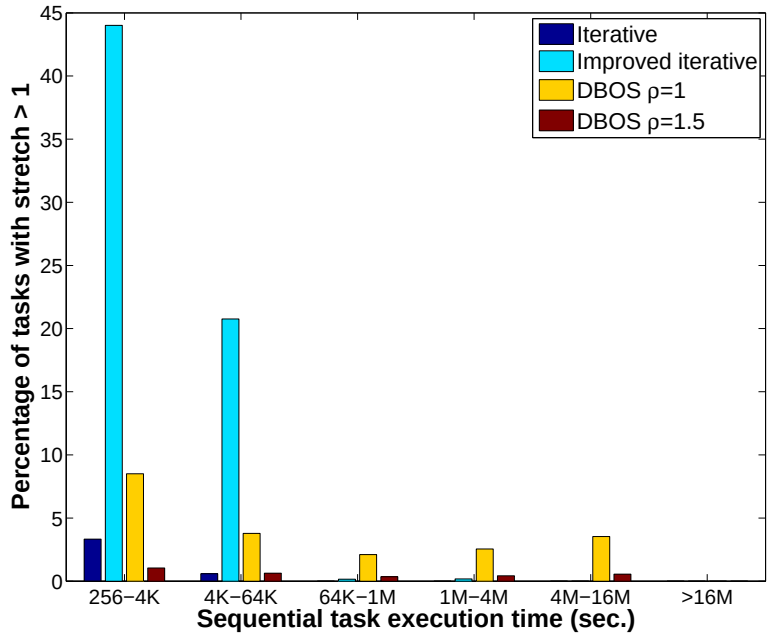


Confirm there is room for improvement for Iterative. DBOS is not bad.

Mapping : DBOS vs Iterative (Fairness Issues)



Downey model



Short Sequence Mapping

The Iterative algorithm leads to high stretch for a lot of the smaller tasks. DBOS has better performance and less fairness issues thanks to stretch optimization.

Outline of the Talk

The end

Conclusion

- A cluster dedicated to bioscience will be built.
- To provide fairness stretch should be considered instead of flow time.
- An scheduling algorithm is proposed to optimize stretch and avoid worst case online scenario.
- Which performs well on Short Sequence Mapping application.

Perspective

- Investigate other way to avoid worst case scenarios.
- Study more simple algorithm to get reference points.
- Build the service !

The end

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