# Experimental results on Cartesius

## Section 5.10 of Parallel Scientific Computation, 2nd edition

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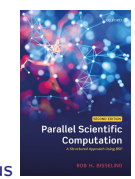
# Test set of graphs from SuiteSparse Matrix Collection

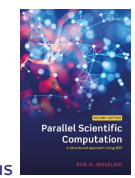
| Name | $n$ | $m$ | $d$ | $\Delta$ | Origin |
|---|---|---|---|---|---|
| `tx2010` | 914 231 | 2 228 136 | 4.9 | 121 | redistricting Texas |
| `mouse_gene` | 45 101 | 14 461 095 | 641.3 | 8 031 | gene regulatory network |
| `cage15` | 5 154 859 | 47 022 346 | 18.2 | 46 | DNA electrophoresis |
| `kmer_P1a` | 139 353 211 | 148 914 992 | 2.1 | 40 | protein $k$-mer |

- Parameters: $n$ = number of vertices, $m$ = number of edges, $d$ = average degree, $\Delta$ = maximum degree.
- `tx2010`: $V$ = Texas land areas from the 2010 US Census; $E$ = connections to neighbouring areas; $\omega$ = length of the shared border.
- `mouse_gene`: $V$ = probes from a DNA microarray; $E$ = regulatory interactions; $\omega$ = mutual information value.
- `cage15`: $V$ = states of a polymer of length 15; $E$ = possible state transitions; $\omega$ = probability.
- `kmer_P1a`: $V$ = segments of length $k$ of amino acids; $E$ = overlapping segment pairs; $\omega = 1$.



# Partitioning time vs. matching time

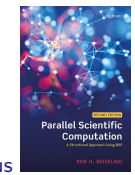
- The vertices of the test graphs were partitioned by a run of the Mondriaan partitioner in 1D row mode for the purpose of a parallel SpMV with $p = 1, 2, 4, \ldots, 1024$.
- Here, the input graph was translated to a matrix by creating the sparse symmetric adjacency matrix $A$ and adding a diagonal $I$.
- Partitioning a test graph takes much longer than running a matching algorithm on a partitioned test graph. Still, this resembles a likely use case, where the graph is available in a sensible distributed form as part of a larger application.
- In contrast, randomly distributing the vertices would be cheap, but would cut most edges and make the algorithm communication-bound.



# Measured execution time (in ms) for graph matching

| $p$ | tx2010 | mouse_gene | cage15 | kmer_P1a |
|---|---|---|---|---|
| 1 | 208.5 | 671 | 2 358 | 59 057 |
| 2 | 107.0 | 356 | 1 237 | 32 473 |
| 4 | 52.4 | 322 | 646 | 17 618 |
| 8 | 28.1 | 305 | 424 | 9 054 |
| 16 | 15.1 | 251 | 194 | 4 454 |
| 32 | 9.1 | 317 | 178 | 2 756 |
| 64 | 7.5 | 538 | 88 | 911 |
| 128 | 7.9 | 836 | 76 | 561 |
| 256 | 8.3 | 2 005 | 77 | 299 |
| 512 | 15.1 | 2 526 | 129 | 204 |
| 1 024 | 29.3 | 6 295 | 218 | 302 |

- Experiments performed on $p$ processor cores of the Broadwell subsystem of Cartesius running BSPonMPI.
- The largest speedup achieved, compared to the parallel program with $p = 1$, is $S_{512} = 289$ for kmer_P1a. The smallest speedup is $S_{16} = 2.7$ for mouse_gene.

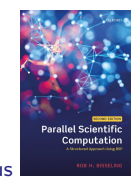


# Upper bound on the number of matches

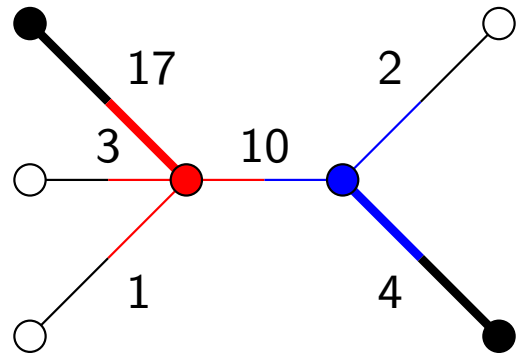
- A trivial upper bound on the number of matches is

$$|\mathcal{M}| \leq \left\lfloor \frac{|\mathcal{V}|}{2} \right\rfloor,$$

because every match involves 2 vertices.



# Upper bound on the total matching weight

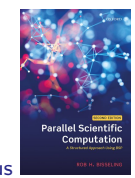



$$\omega(\mathcal{M}) = 17 + 4 = 21 \leq \tfrac{1}{2}(17 + 3 + 1 + 17 + 10 + 2 + 4) = 27$$

- An upper bound on the total matching weight is

$$\omega(\mathcal{M}) \leq \frac{1}{2} \sum_{v \in \mathcal{V}} \max \ \{\omega(u, v) \ : \ (u, v) \in \mathcal{E}\},$$

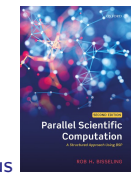
because every vertex $v$ contributes at most the weight of one half-edge to the total matching weight, and this weight is at most half the weight of its heaviest edge.



# Number of matches and total matching weight

| | tx2010 | mouse_gene | cage15 | kmer_P1a |
|---|---|---|---|---|
| Matches | 375 342 | 18 273 | 2 575 446 | 59 735 594 |
| Matches upper bound | 457 115 | 22 550 | 2 577 429 | 69 676 605 |
| | | | | |
| Weight | 28 933 021 703 | 1 287.998 | 76 890.186 | 59 735 594 |
| Weight upper bound | 39 547 303 682 | 1 553.424 | 77 709.076 | 69 676 605 |

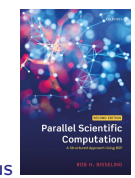
- Given are the total number of matches $|\mathcal{M}|$ and the total matching weight $\omega(\mathcal{M})$, together with their upper bounds, for $p = 1$.
- The preference for a local match in tie-breaking causes a variation of $\leq 0.1\%$ for varying $p$.
- The matching weight is between 73.2% of the upper bound (tx2010) and 98.9% (cage15), so that the 50% guarantee of the 1/2-approximation is more than satisfied.
- Compared to the (unknown) maximum matching weight, the percentages will even be better.



# Number of operations performed

| | $p$ | tx2010 | mouse_gene | cage15 | kmer_P1a |
|---|---|---|---|---|---|
| Operations lower bound | | 8.9 | 58 | 188 | 596 |
| Operations | 1 | 9.5 | 59 | 193 | 873 |
| | 32 | 9.5 | 148 | 206 | 872 |
| | 1 024 | 9.8 | 168 | 225 | 872 |

- The number of operations (in millions) performed was obtained by summing the sizes of the ranges encountered.
- The lower bound given is $4m$, the cost of partially sorting only the upper parts of adjacency lists.
- The operation counts for $p = 1$ fit well with their lower bound, meaning that in practice the partial sort leads to a linear-time sequential algorithm.
- The number of operations grows a bit with $p$, because operations are performed on the basis of increasingly incomplete information, e.g., about a new suitor for a halo vertex.

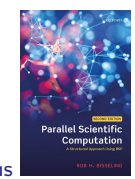


# Number of supersteps

| | $p$ | tx2010 | mouse_gene | cage15 | kmer_P1a |
|---|---|---|---|---|---|
| Supersteps | 2 | 8 | 957 | 55 | 26 |
| | 32 | 10 | 1 613 | 69 | 67 |
| | 1 024 | 13 | 2 099 | 82 | 72 |
| Parallel depth | | 146 | 309 | 141 | 145 |

- The number of supersteps needed for parallel matching grows with $p$, again because of increasingly incomplete information.
- The parallel depth of an algorithm is the length of its critical path.
- An theorem by Ferdous *et al.* states that the parallel depth for matching on a graph with uniformly random edge weights is $\mathcal{O}((\log_2 m) \log_2 \Delta)$. Note: our test graphs are not random.
- The parallel depth given is $(\log_2 m) \log_2 \Delta$, which we take as an asymptotic lower bound on the number of supersteps for $p = \infty$ in the random case.

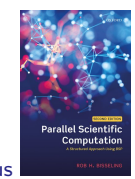
S. M. Ferdous, A. Khan, and A. Pothen, In: Proceedings IPDPS 2018, IEEE, pp. 22–33.



# Load balancing for cage15 and $p = 8$

| Max operations ($\times 10^3$) | Time (in ms) | Supersteps |
|---:|---:|---:|
| 4 | 845 | 6 618 |
| 8 | 657 | 3 340 |
| 16 | 555 | 1 694 |
| 32 | 500 | 875 |
| 64 | 465 | 465 |
| 128 | 445 | 261 |
| 256 | 429 | 159 |
| 512 | 417 | 108 |
| 1 024 | 400 | 83 |
| 2 048 | 377 | 71 |
| 4 096 | 352 | 65 |
| 8 192 | 346 | 62 |
| 16 384 | 341 | 60 |
| $\infty$ | 341 | 60 |

- We can try to balance the computational work load by imposing a maximum number of operations carried out by a processor in a superstep.



# Load balancing for cage15 and $p = 8$

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| ... | ... | ... |
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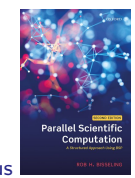
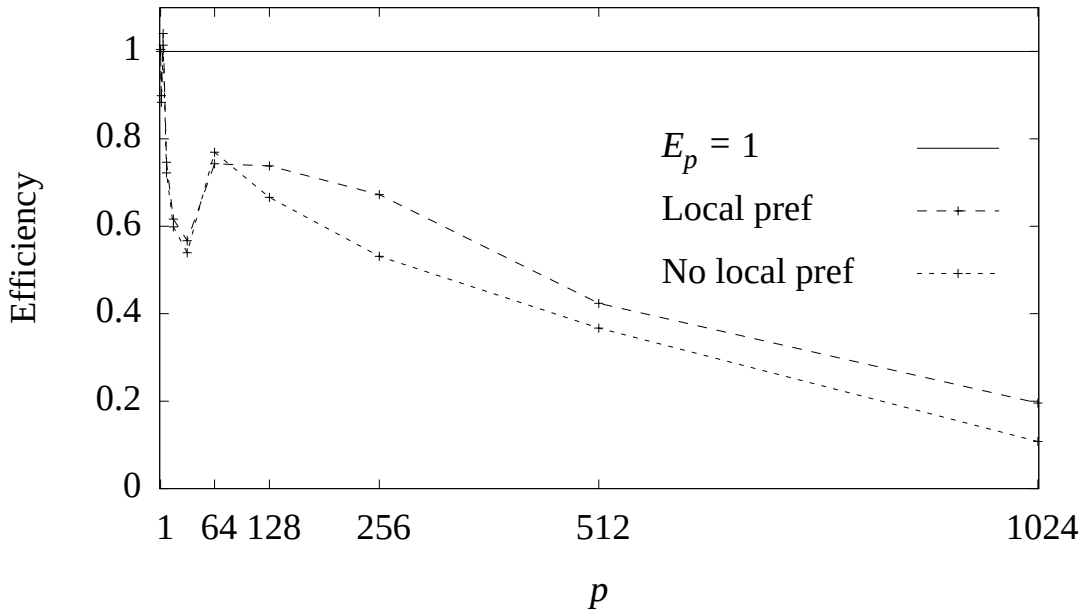
| 4 096 | 352 | 65 |
| 8 192 | 346 | 62 |
| 16 384 | 341 | 60 |
| $\infty$ | 341 | 60 |

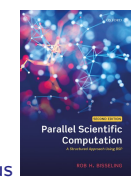
- The total synchronization time for 60 supersteps based on the benchmark value of $l$ is only 2.2 ms, so that the cost of the synchronizations themselves is insignificant.
- Still, we do not observe any gain from the load balancing procedure, which indicates that our work counters are not accurate enough: communication operations were not taken into account, and, how sobering a thought, perhaps not all $\mathcal{O}(1)$-operations are created equal.



# Local preferences are beneficial




- Shown is the eficiency (relative to $p = 1$) for the graph `kmer_P1a`, with and without tie-breaking by preferring local matches.
- This graph has unit weights, so that all weight comparisons are ties.
- For $p = 1\,024$, the efficiency is 19.6% with local preferences, and 10.7% without.



# Summary

- Partitioning a test graph takes much longer than running a matching algorithm. Still, parallel matching is useful as part of a larger application.
- An upper bound on the total matching weight is

$$\omega(\mathcal{M}) \leq \frac{1}{2} \sum_{v \in \mathcal{V}} \max \ \{\omega(u,v) \ : \ (u,v) \in \mathcal{E}\}.$$

- In practice, the matching weight achieved by the parallel 1/2-approximation algorithm is much higher than the guarantee of 50% and the total operation count is linear in the number of edges.
- The load balancing procedure based on imposing a maximum number of operations should be improved.
- There is always further work to do. Fortunately!