Big graphs for big data: parallel matching and clustering on billion-vertex graphs

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Graph Matching

- Introduction
- Greedy algorithm
- Parallelisable 1/2-approximation algorithm
- BSP algorithm
- GPU algorithm
- Results

Clustering

- Introduction
- Sequential algorithm
- GPU algorithm
- Results

2D sparse matrix partitioning

2D (edge-based) matching

Conclusion

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Matchmaker, Matchmaker, Make me a match

From the film *Fiddler on the roof*

- Hodel: Well, somebody has to arrange the matches. Young people can't decide these things themselves.
- Hodel: For Papa, make him a scholar.
- Chava: For Mama, make him rich as a king.

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Matching can win you a Nobel prize

Marriage as an Economic Problem

Lloyd Shapley and Alvin Roth win the Nobel Prize for showing the best way to match people with what they really want.

By Matthew Yglesias | Posted Monday, Oct. 15, 2012, at 1:51 PM ET

The Nobel Prize in economics went to Alvin E. Roth and Lloyd S. Shapley "for the theory of stable allocations and the practice of market design"

Source: Slate magazine October 15, 2012

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Motivation of graph matching

- Graph matching is a pairing of neighbouring vertices.
- It has applications in
  - medicine: finding suitable donors for organs
  - social networks: finding partners
  - scientific computing: finding pivot elements in matrix computations
  - graph coarsening: making the graph smaller by merging similar vertices before partitioning it for parallel computations
  - bioinformatics: finding similarity in Protein-Protein Interaction networks

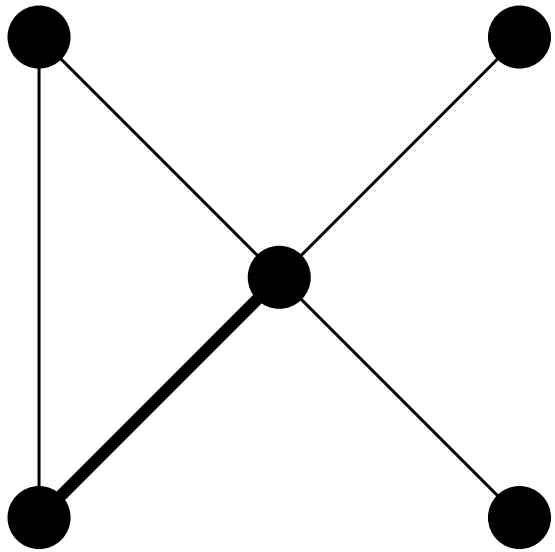
Motivation of greedy/approximation graph matching

- Optimal solution is possible in polynomial time.
- Time for weighted matching in graph $G = (V, E)$ is $\mathcal{O}(mn + n^2 \log n)$ with $n = |V|$ the number of vertices, and $m = |E|$ the number of edges (Gabow 1990).
- The aim is a billion vertices, $n = 10^9$, with 100 edges per vertex, i.e. $m = 10^{11}$.
- Thus, a time of $\mathcal{O}(10^{20}) = 100,000$ Petaflop units is far too long. Fastest supercomputer today, the Tianhe-2, performs 33.8 Petaflop/s.
- We need linear-time greedy or approximation algorithms.

Formal definition of graph matching

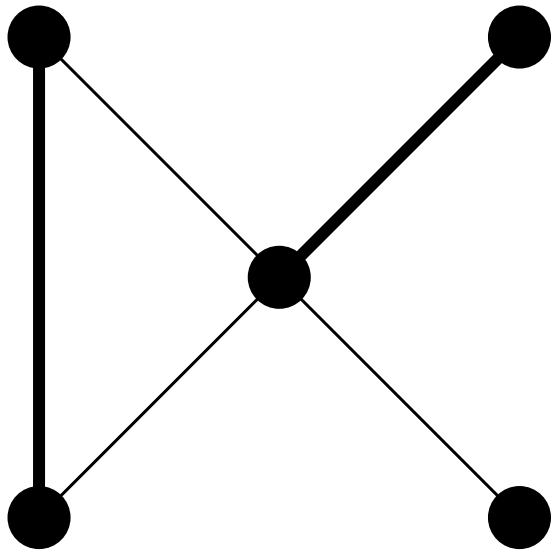
- A graph is a pair $G = (V, E)$ with vertices V and edges E.
- All edges $e \in E$ are of the form $e = (v, w)$ for vertices $v, w \in V$.
- A matching is a collection $M \subseteq E$ of disjoint edges.
- Here, the graph is undirected, so $(v, w) = (w, v)$.

Maximal matching



- A matching is maximal if we cannot enlarge it further by adding another edge to it.

Maximum matching



- A matching is maximum if it possesses the largest possible number of edges, compared to all other matchings.

Edge-weighted matching

- If the edges are provided with weights $\omega : E \to \mathbb{R}_{>0}$, finding a matching M which maximises

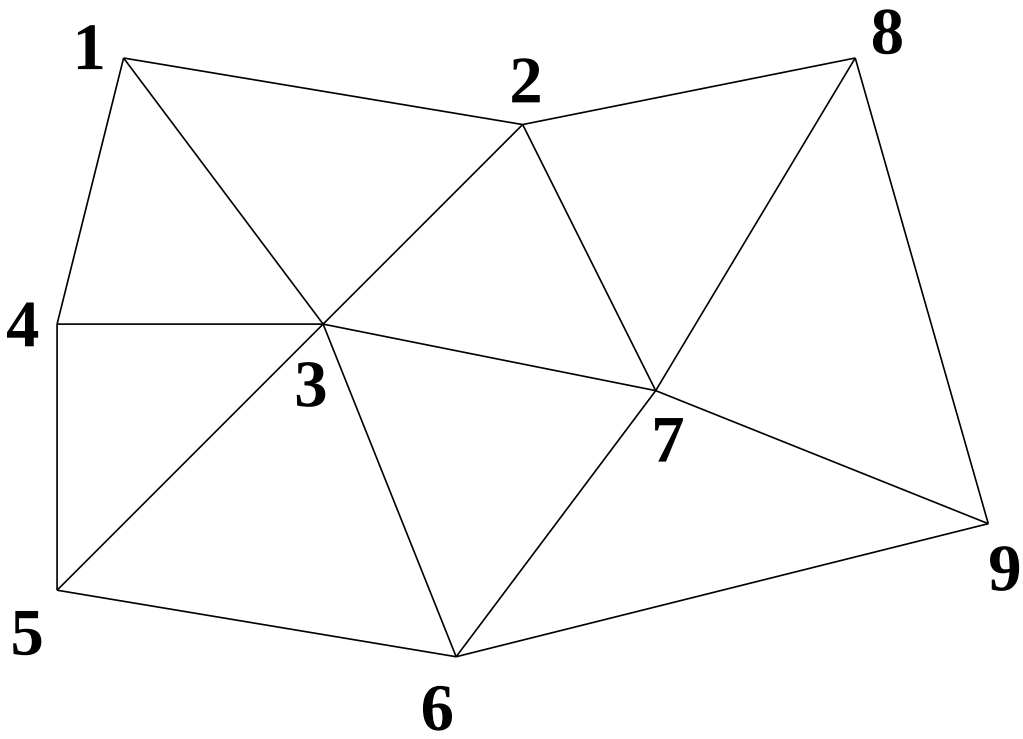
$$\omega(M) = \sum_{e \in M} \omega(e),$$

  is called edge-weighted matching.
- Greedy matching provides us with maximal matchings, but not necessarily with maximum possible weight.

Sequential greedy matching

- In random order, vertices $v \in V$ select and match neighbours one-by-one.
- Here, we can pick
  - the first available neighbour w of v, greedy random matching
  - the neighbour w with maximum $\omega(v, w)$, greedy weighted matching
- Or: we sort all the edges by weight, and successively match the vertices v and w of the heaviest available edge (v, w). This is commonly called greedy matching.

Sequential greedy random matching



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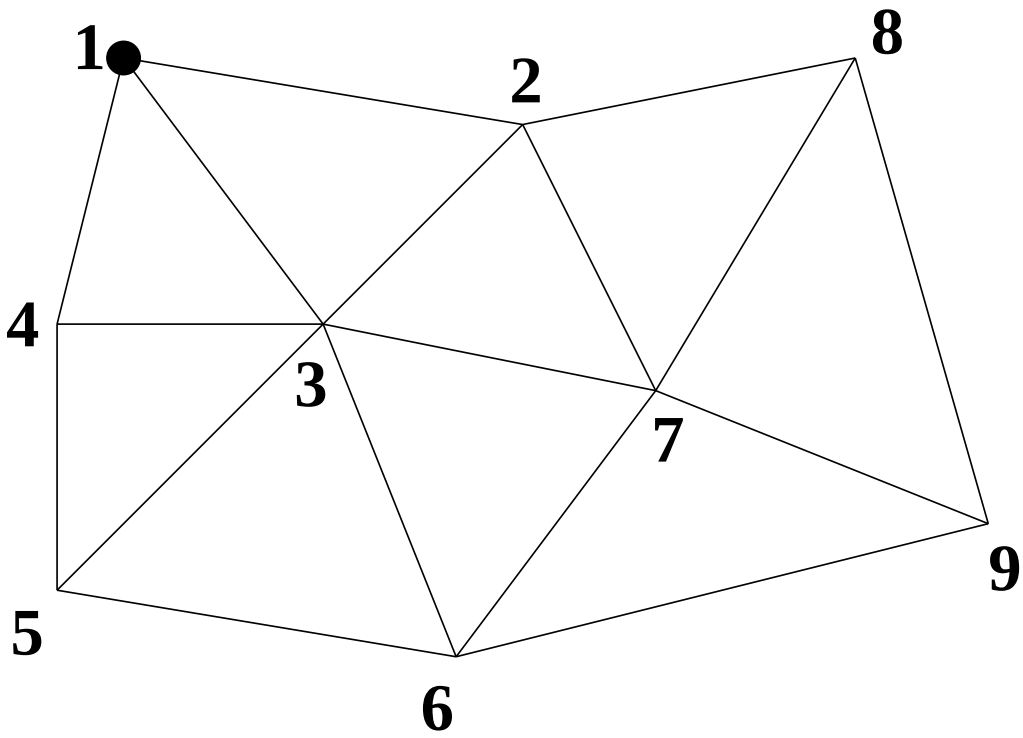
Sequential greedy random matching



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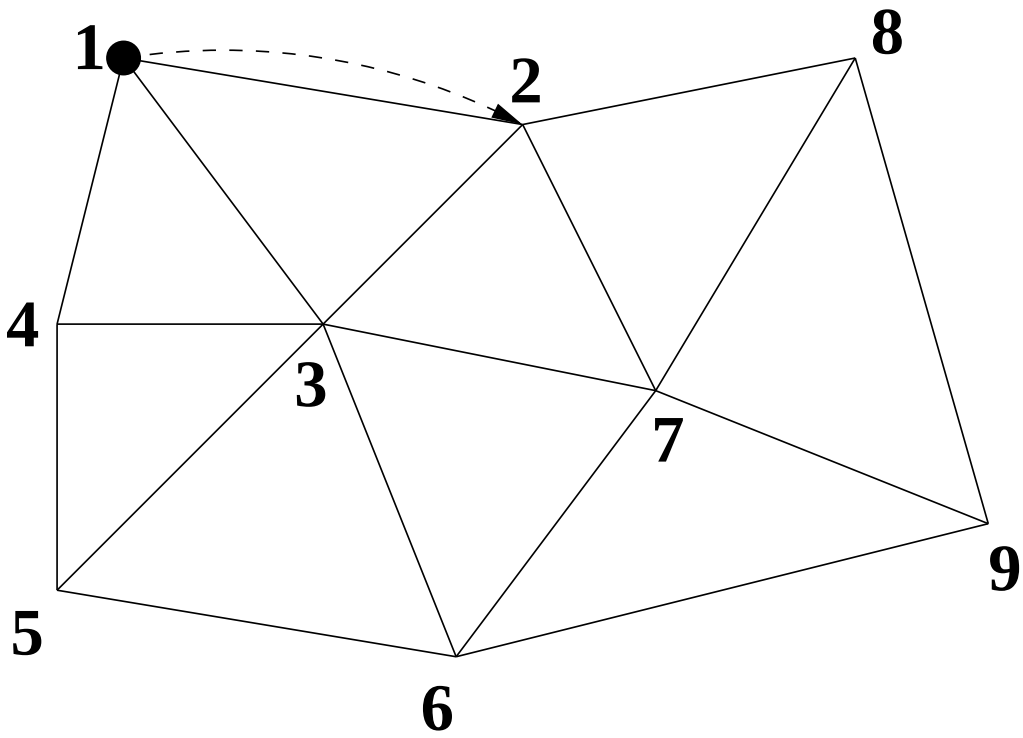
Sequential greedy random matching



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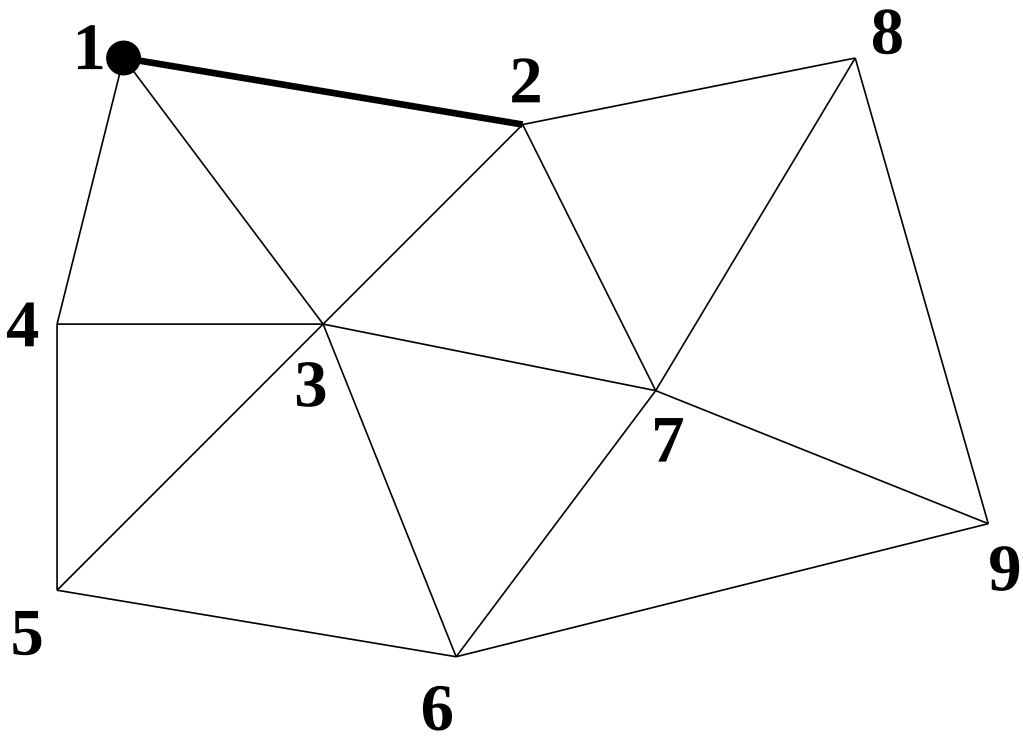

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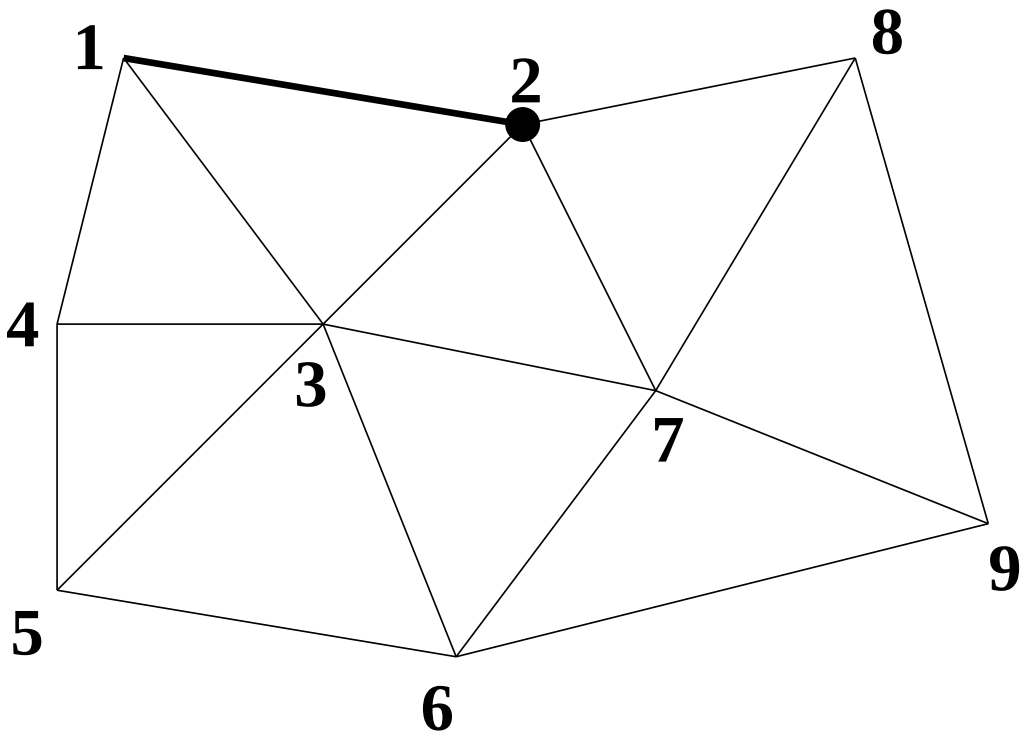

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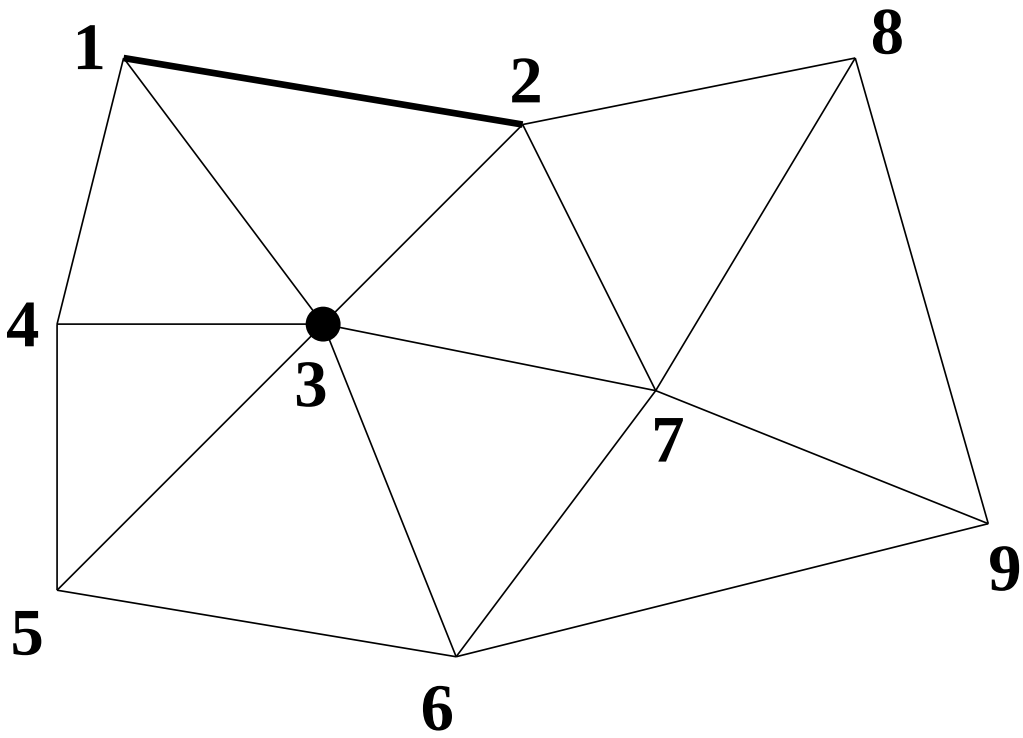

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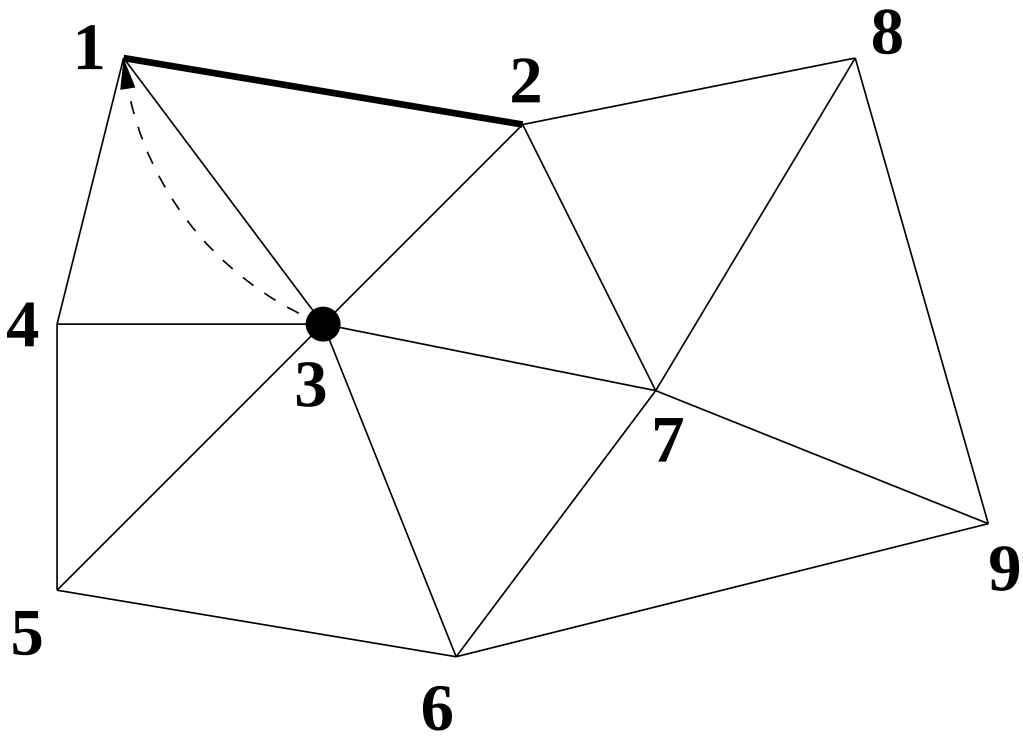

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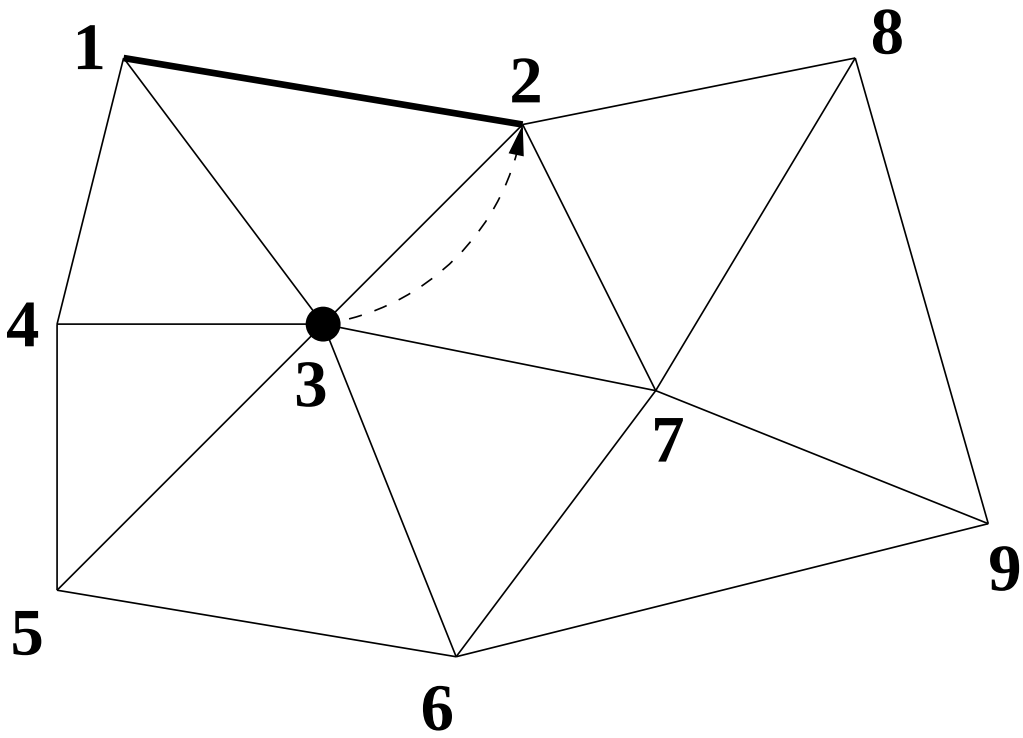

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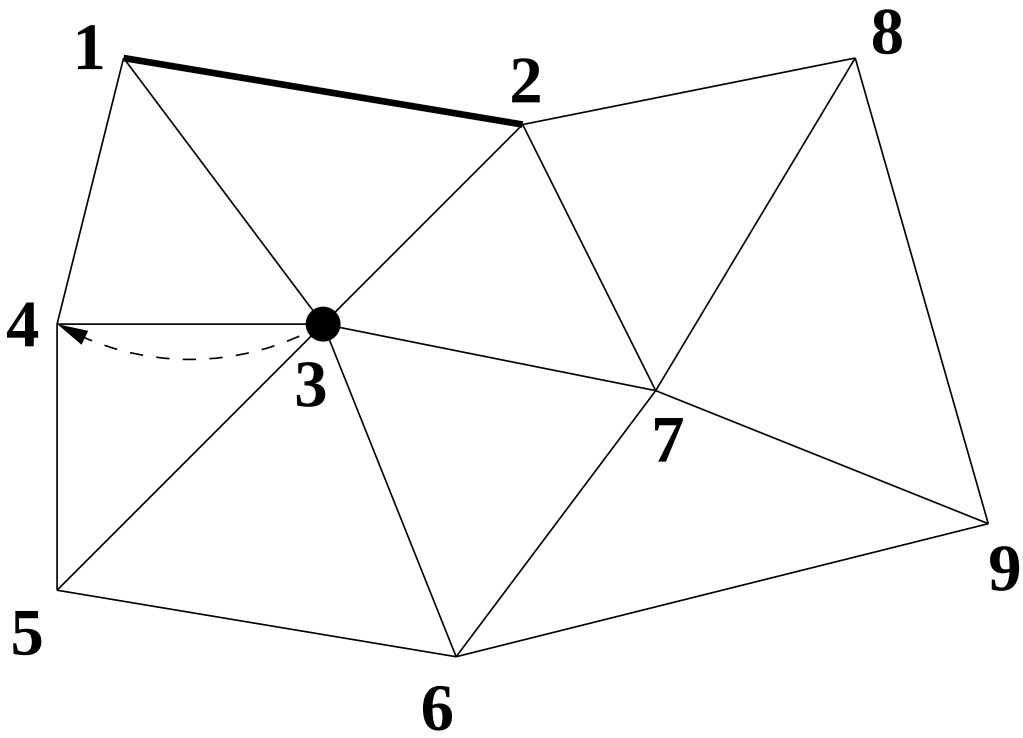

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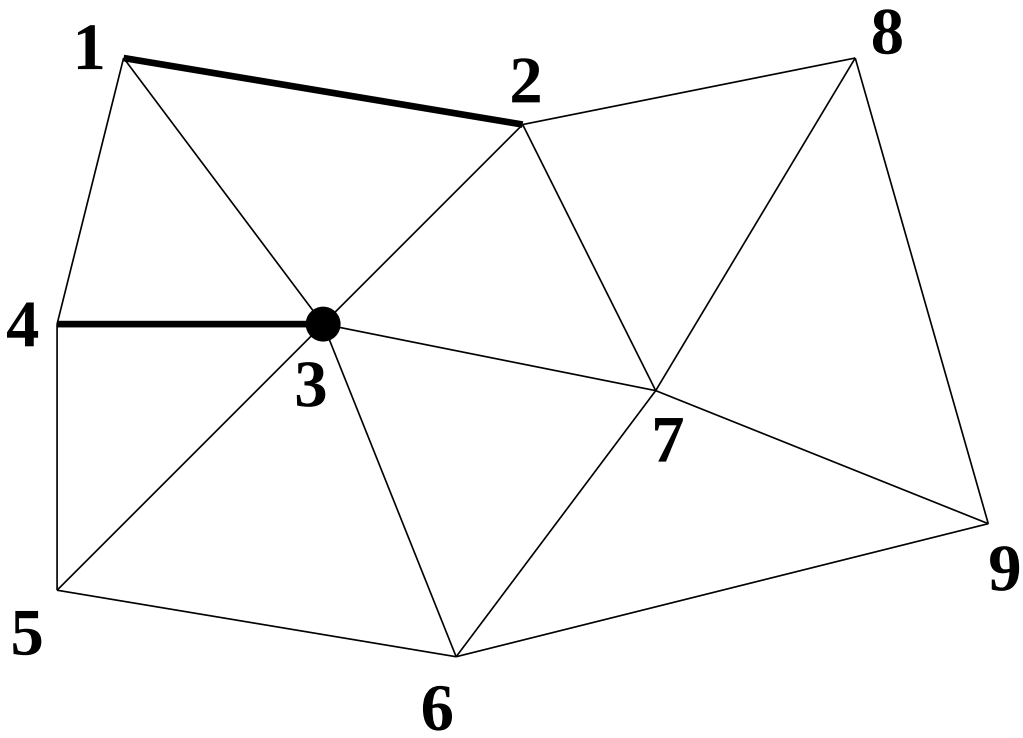

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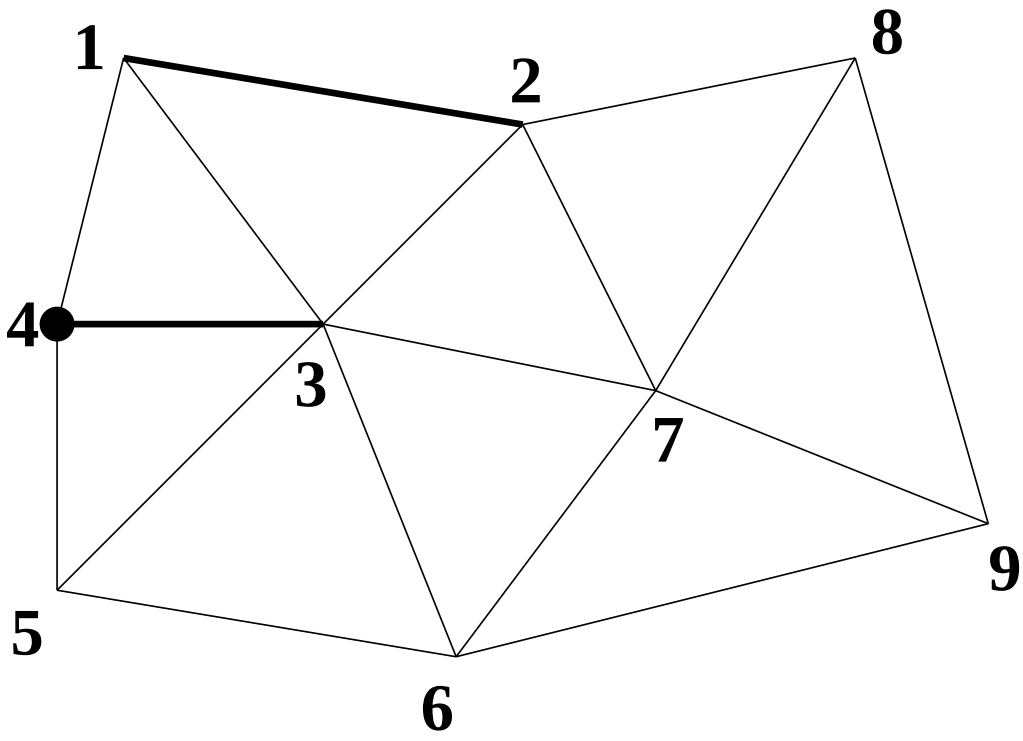

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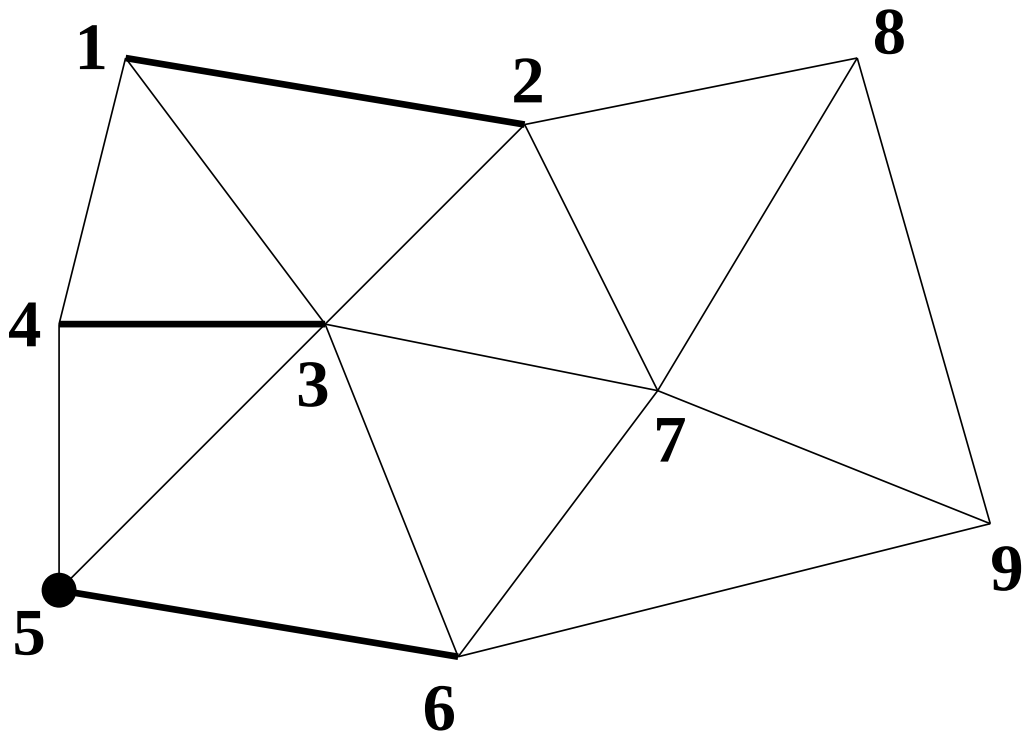

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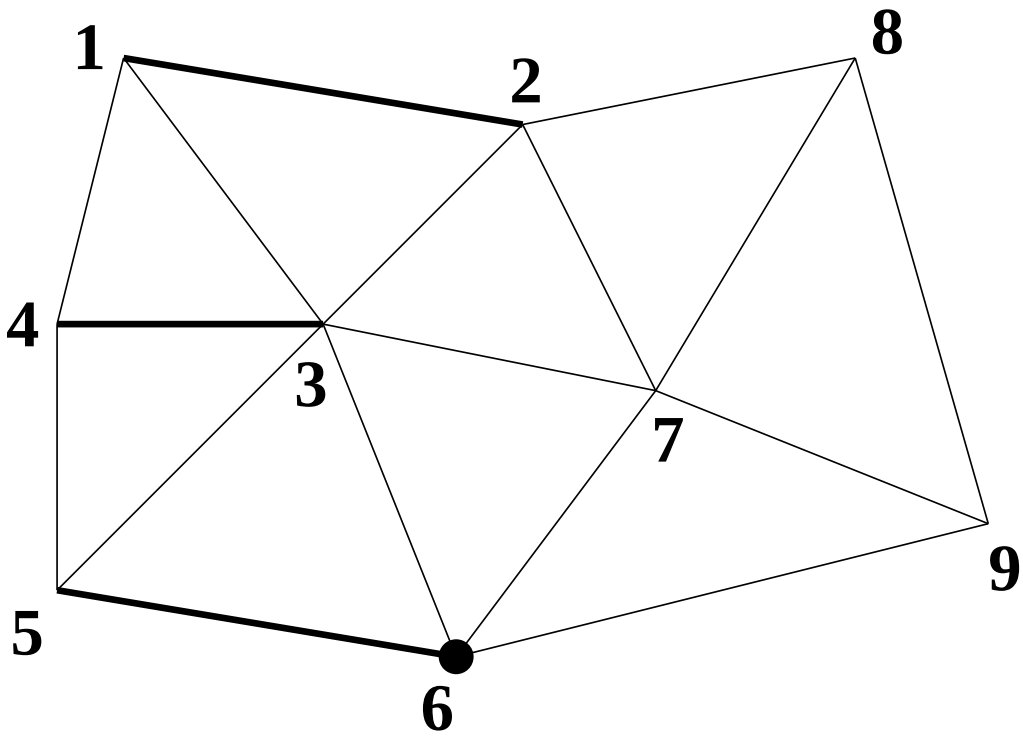

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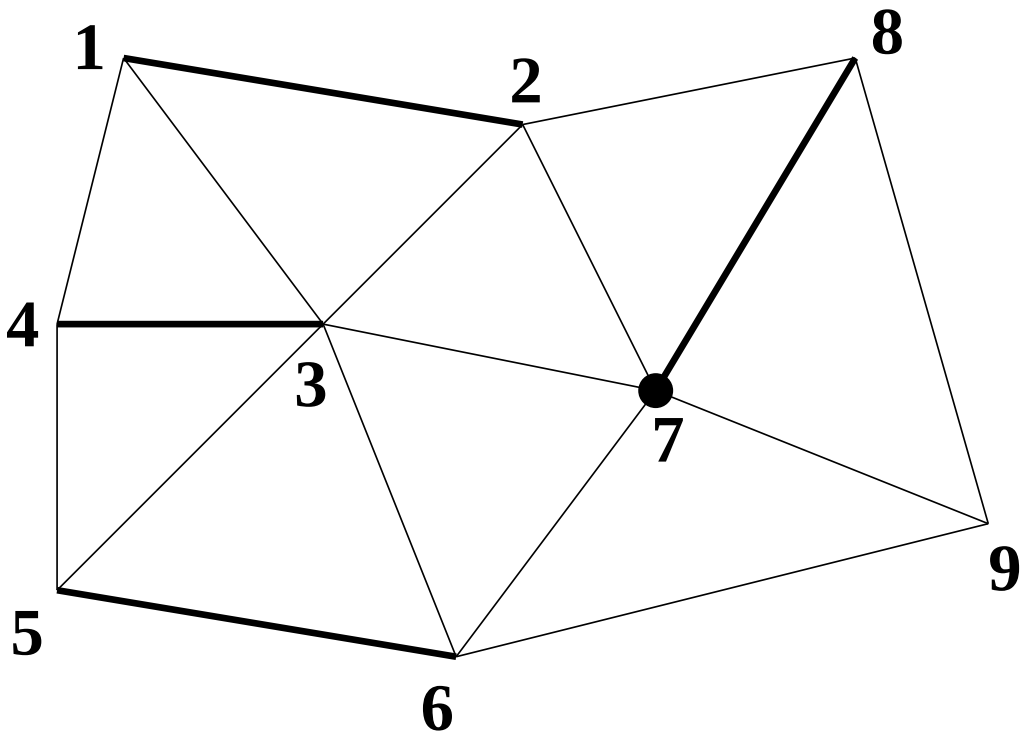

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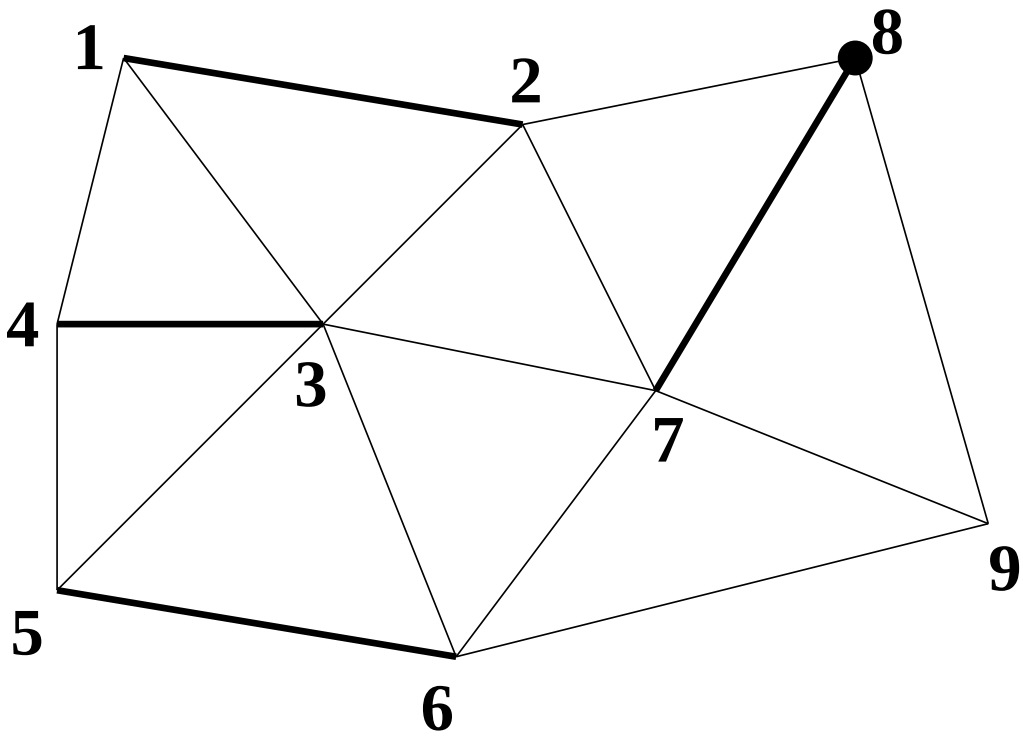
Sequential greedy random matching



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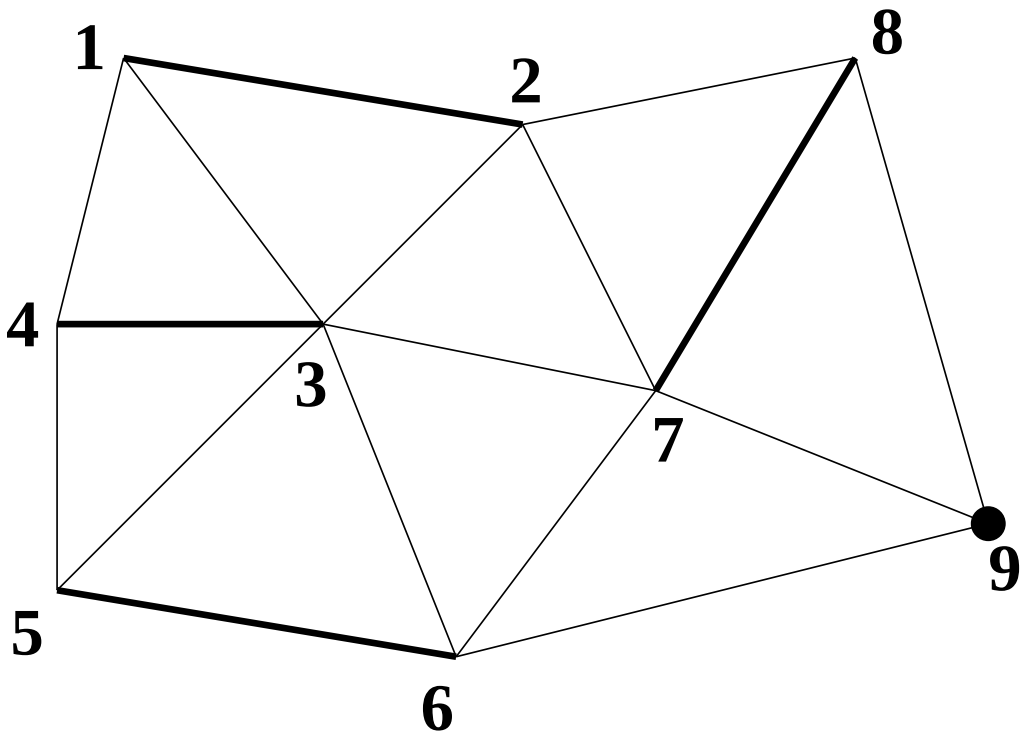
Sequential greedy random matching



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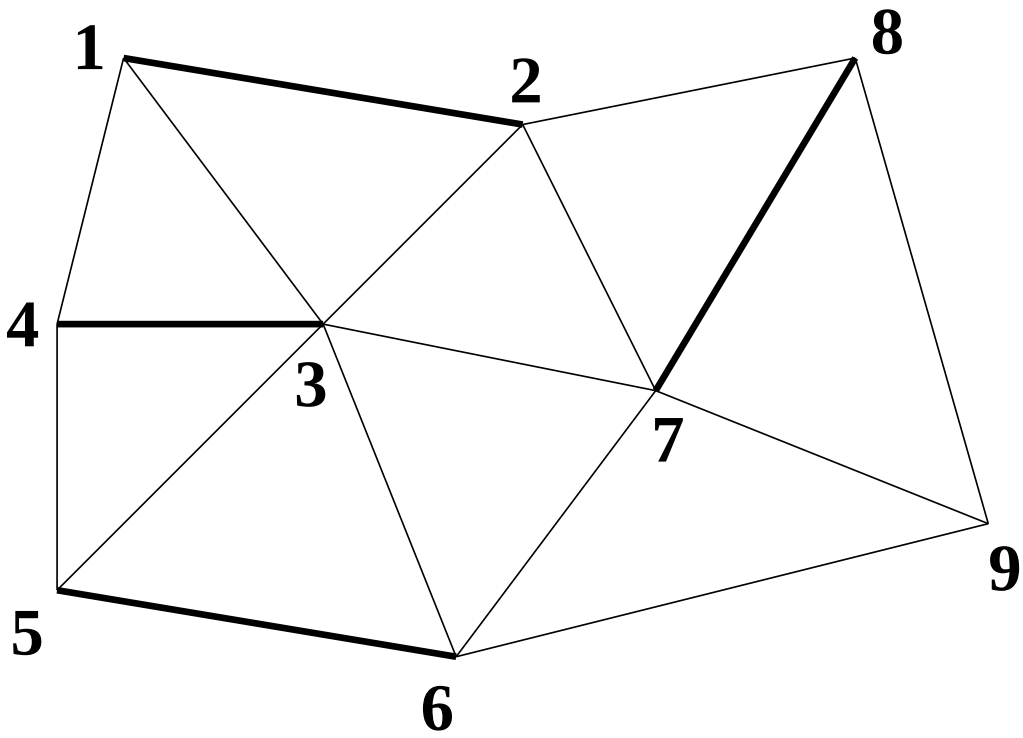
Sequential greedy random matching



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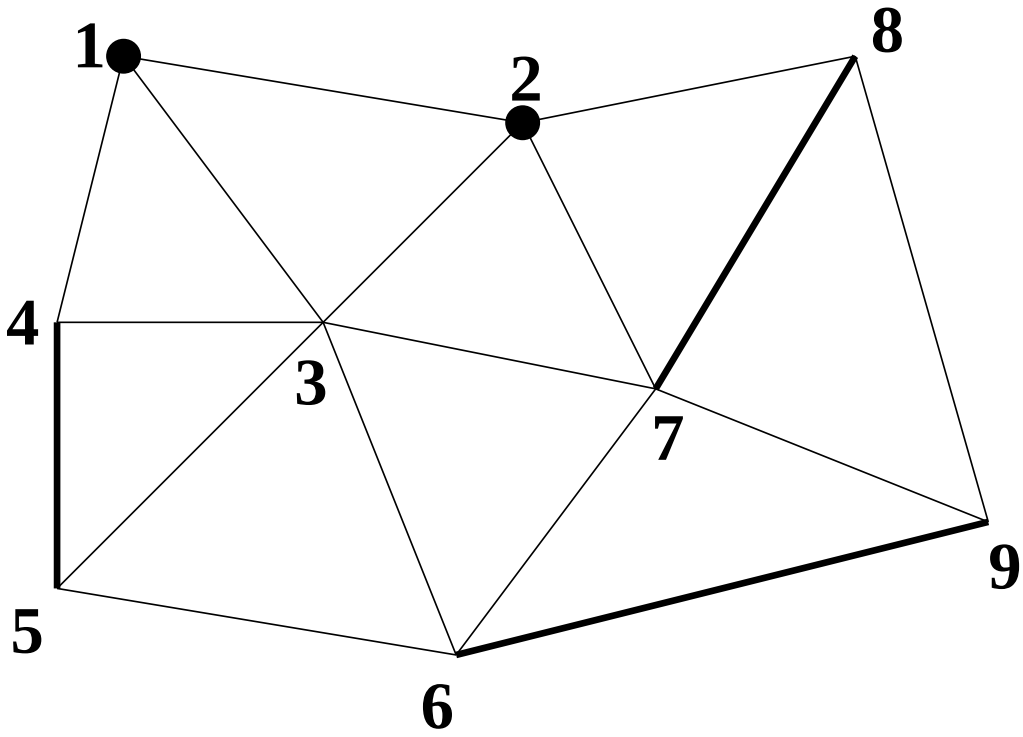
Greedy matching is a 1/2-approximation algorithm

- Weight $\omega(M) \geq \omega_{\text{optimal}}/2$
- Cardinality $|M| \geq |M_{\text{card}-\max}|/2$, because M is maximal.
- Time complexity is $\mathcal{O}(m \log m)$, because all edges must be sorted.

Parallel greedy matching: trouble



Suppose we match vertices simultaneously.

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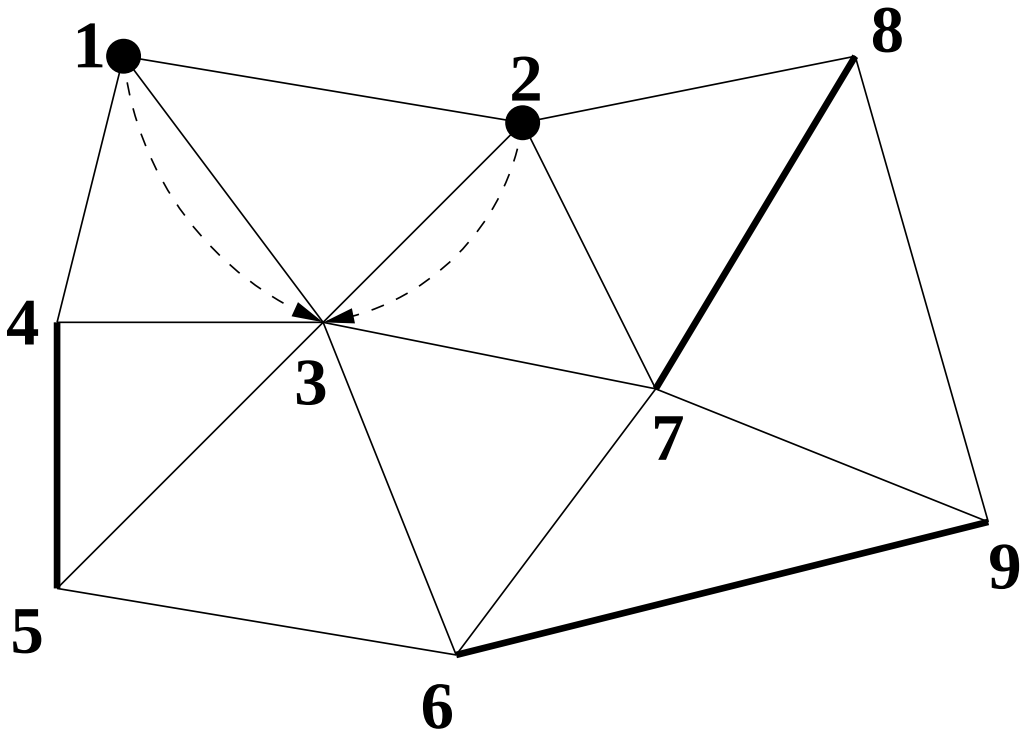
Parallel greedy matching: trouble



Two vertices each find an unmatched neighbour. . .

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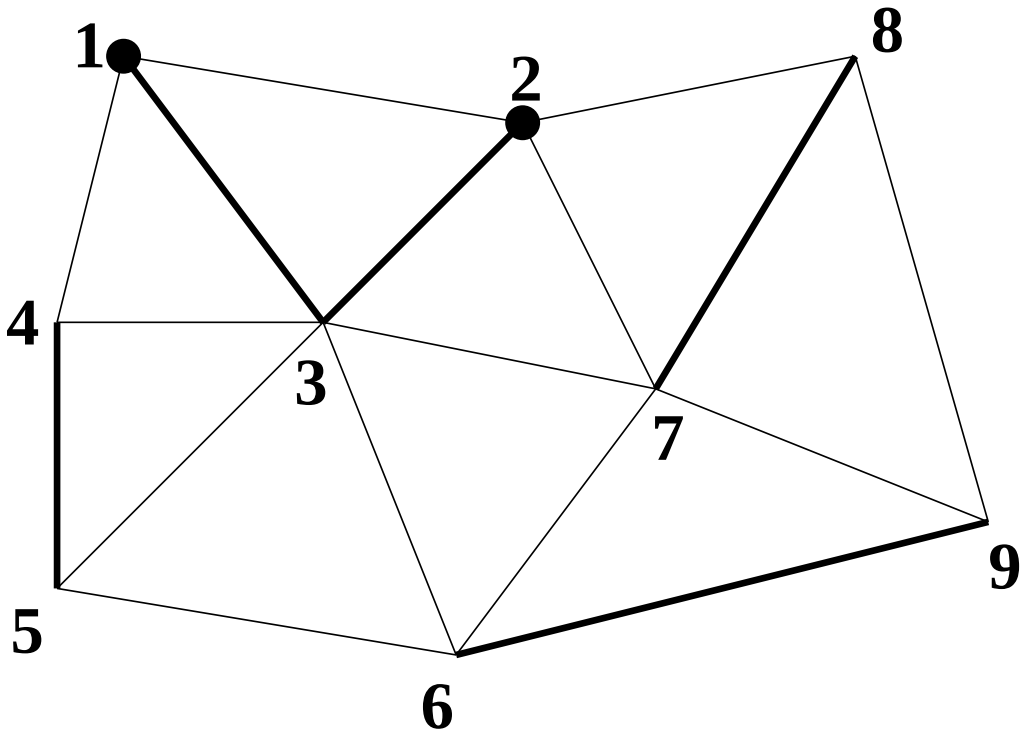
Parallel greedy matching: trouble



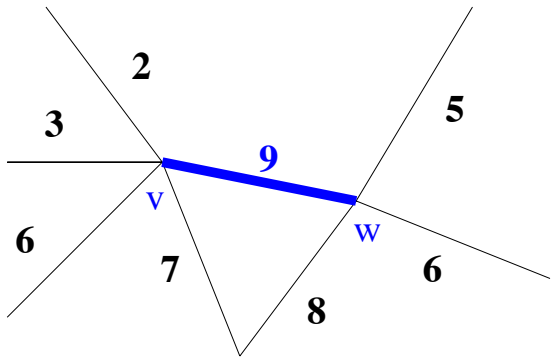
. . . but generate an invalid matching.

Parallelisable dominant-edge algorithm

while $E \neq \emptyset$ **do**
  pick a dominant edge $(v, w) \in E$
  $M := M \cup \{(v, w)\}$
  $E := E \setminus \{(x, y) \in E : x = v \vee x = w\}$
  $V := V \setminus \{v, w\}$
return M

- An edge $(v, w) \in E$ is dominant if

$$\omega(v, w) = \max\{\omega(x, y) : (x, y) \in E \wedge (x = v \vee x = w)\}$$



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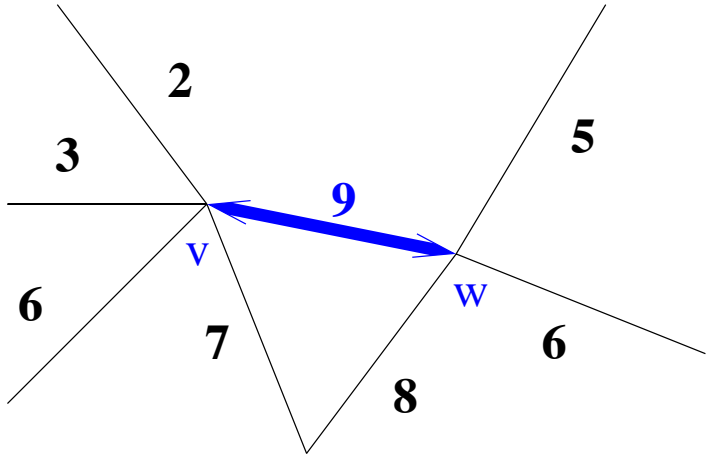
Sequential approximation algorithm: initialisation

function SeqMatching(V, E)
  for all $v \in V$ **do**
    $pref(v) = null$
  $D := \emptyset$
  $M := \emptyset$

  { Find dominant edges }
  for all $v \in V$ **do**
    $Adj_v := \{w \in V : (v, w) \in E\}$
    $pref(v) := \text{argmax}\{\omega(v, w) \ : \ w \in Adj_v\}$
    if $pref(pref(v)) = v$ **then**
      $D := D \cup \{v, pref(v)\}$
      $M := M \cup \{(v, pref(v))\}$

Mutual preferences



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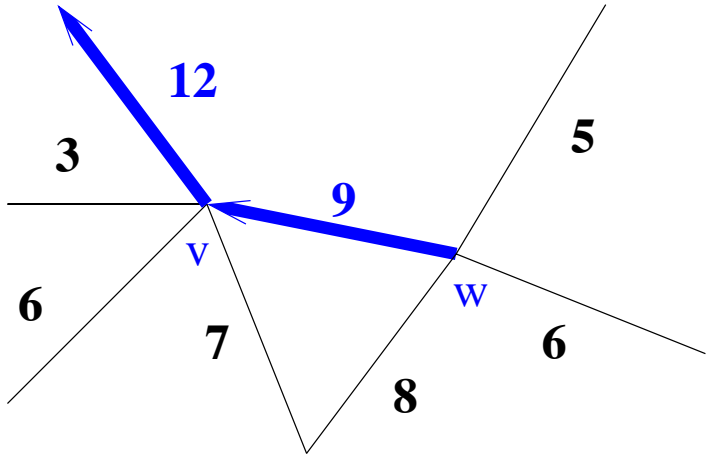
Non-mutual preferences



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Sequential approximation algorithm: main loop

while $D \neq \emptyset$ **do**
  pick $v \in D$
  $D := D \setminus \{v\}$
  for all $x \in Adj_v \setminus \{pref(v)\} \ : \ (x, pref(x)) \notin M$ **do**
    $Adj_x := Adj_x \setminus \{v\}$

    { Set new preference }
    $pref(x) := \mathrm{argmax}\{\omega(x, w) \ : \ w \in Adj_x\}$
    if $pref(pref(x)) = x$ **then**
      $D := D \cup \{x, pref(x)\}$
      $M := M \cup \{(x, pref(x))\}$
return M

Properties of the dominant-edge algorithm

- Dominant-edge algorithm is a 1/2-approximation:

$$\omega(M) \geq \omega_{\text{optimal}}/2$$

- Dominant edge means mutual preference:

$$v = \mathit{pref}(w) \text{ and } w = \mathit{pref}(v).$$

- Dominance is a local property: easy to parallelise.
- Algorithm keeps going until set of dominant vertices D is empty and matching M is maximal.
- Assumption without loss of generality: weights are unique. Otherwise, use vertex numbering to break ties.

Time complexity

- Linear time complexity $\mathcal{O}(|E|)$ if edges of each vertex are sorted by weight.
- Sorting costs are

$$\sum_v deg(v) \log deg(v) \leq \sum_v deg(v) \log \Delta = 2|E| \log \Delta,$$

  where Δ is the maximum vertex degree.
- This algorithm is based on a dominant-edge algorithm by Preis (1999), called LAM, which is linear-time $\mathcal{O}(|E|)$, does not need sorting, and also is a $1/2$-approximation, but is hard to parallelise.

Parallel algorithm (Manne & Bisseling, 2007)

- Processor $P(s)$ has vertex set V_s, with

$$\bigcup_{s=0}^{p-1} V_s = V$$

  and $V_s \cap V_t = \emptyset$ if $s \neq t$.
- This is a *p*-way partitioning of the vertex set.

Halo vertices

- The adjacency set Adj_v of a vertex v may contain vertices w from another processor.
- We define the set of halo vertices

$$H_s = \bigcup_{v \in V_s} Adj_v \setminus V_s$$

- The weights $\omega(v, w)$ are stored with the edges, for all $v \in V_s$ and $w \in V_s \cup H_s$.
- $E_s = \{(v, w) \in E : v \in V_s\}$
  is the subset of all the edges connected to V_s.

Parallel algorithm for $P(s)$: initialisation

function ParMatching(V_s, H_s, E_s, distribution ϕ)
    for all $v \in V_s$ **do**
        $pref(v) = null$
    $D_s := \emptyset$
    $M_s := \emptyset$

    { Find dominant edges }
    for all $v \in V_s$ **do**
        $Adj_v := \{w \in V_s \cup H_s : (v, w) \in E_s\}$
        $SetNewPreference(v, Adj_v, pref, V_s, D_s, M_s, \phi)$
    Sync

Setting a vertex preference

function SetNewPreference(v, Adj, V, D, M, ϕ)
  $pref(v) := \text{argmax}\{\omega(v, w) \ : \ w \in Adj\}$
  if $pref(v) \in V$ **then**
    if $pref(pref(v)) = v$ **then**
      $D := D \cup \{v, pref(v)\}$
      $M := M \cup \{(v, pref(v))\}$
  else
    put $proposal(v, pref(v))$ in $P(\phi(pref(v)))$

How to propose

Source: www.theguardian.com

proposal(v, w): v proposes to w

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Parallel algorithm for $P(s)$: main loop

while $D_s \neq \emptyset$ **do**
  pick $v \in D_s$
  $D_s := D_s \setminus \{v\}$
  for all $x \in Adj_v \setminus \{pref(v)\} \ : \ (x, pref(x)) \notin M_s$ **do**
    if $x \in V_s$ **then**
      $Adj_x := Adj_x \setminus \{v\}$
      $SetNewPreference(x, Adj_x, pref, V_s, D_s, M_s, \phi)$
    else $\{x \in H_s\}$
      put $unavailable(v, x)$ in $P(\phi(x))$
Sync

Parallel algorithm for $P(s)$: communication

for all messages m received **do**
  if $m = proposal(x, y)$ **then**
    if $pref(y) = x$ **then**
      $D_s := D_s \cup \{y\}$
      $M_s := M_s \cup \{(x, y)\}$
      put $accepted(x, y)$ in $P(\phi(x))$
  if $m = accepted(x, y)$ **then**
    $D_s := D_s \cup \{x\}$
    $M_s := M_s \cup \{(x, y)\}$
  if $m = unavailable(v, x)$ **then**
    if $(x, pref(x)) \notin M_s$ **then**
      $Adj_x := Adj_x \setminus \{v\}$
      $SetNewPreference(x, Adj_x, pref, V_s, D_s, M_s, \phi)$

Termination

- The algorithm alternates supersteps of computation running the main loop and communication handling the received messages.
- The whole algorithm terminates when no messages have been received by processor $P(s)$ and the local set D_s is empty, for all s.
- This can be checked at every synchronisation point.

Load balance

- Processors can have different amounts of work, even if they have the same number of vertices or edges.
- Use can be made of a global clock based on ticks, the unit of time needed to 'handle' a vertex x (in $\mathcal{O}(1)$).
- Here, 'handling' could mean setting a new preference.
- After every k ticks, everybody synchronises.

Synchronisation frequency

- Guidance for the choice of k is provided by the BSP parameter l, the cost of a global synchronisation.
- Choosing $k \geq l$ guarantees that at most 50% of the total time is spent in synchronisation.
- Choosing k sufficiently small will cause all processors to be busy during most supersteps.
- Good choice: $k = 2l$?

Sending messages

- The BSP system takes care that messages are sent automatically, in bulk. A useful BSPlib primitive for doing this is `bsp_send`.
- In the next superstep, all received messages are read (using `bsp_move`) and processed.
- Google's Pregel system (Malewicz 2010) follows this BSP style.

MulticoreBSP enables shared-memory BSP

KU Leuven | Flanders ExaScience Lab | Utrecht University

MulticoreBSP *efficient, easy & correct parallelisation*

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- Introduction
- BSP model
- BSP library

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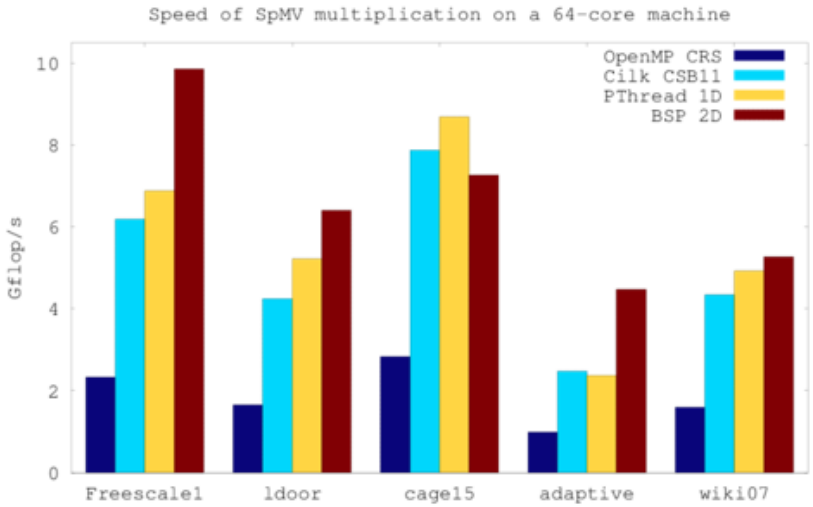
RECENT NEWS

- Version 1.2, and a roadmap for future releases.
- MulticoreBSP for C, version 1.1 released.

see all news items

Introduction

MulticoreBSP brings **Bulk Synchronous Parallel (BSP)** programming to modern multicore processors. BSP programming leads to high-performance codes:



Albert-Jan Yzelman 2014, www.multicorebsp.org

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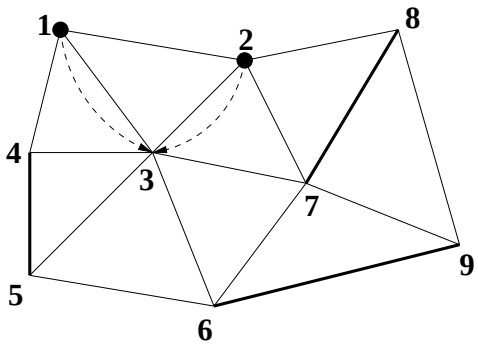
Matching with MulticoreBSP

- BSP program can remain the same, giving portability.
- To exploit the ease of reading data in shared memory, the `bsp_direct_get` is available in MulticoreBSP.
- This performs the communication immediately and blocks until the communication has been carried out.
- Possible use: replace the set M_s of matched edges by a boolean array $matched_s$ marking the local matched vertices.
- This array can be read by all processors using `bsp_direct_get`, to replace the check $(x, pref(x)) \notin M_s$.

GPU matching



- A different approach, tightly coupled to the GPU architecture.
- To prevent matching conflicts, we create two groups of vertices:
  - **Blue** vertices propose.
  - **Red** vertices respond.
- Proposals that were responded to, are matched.

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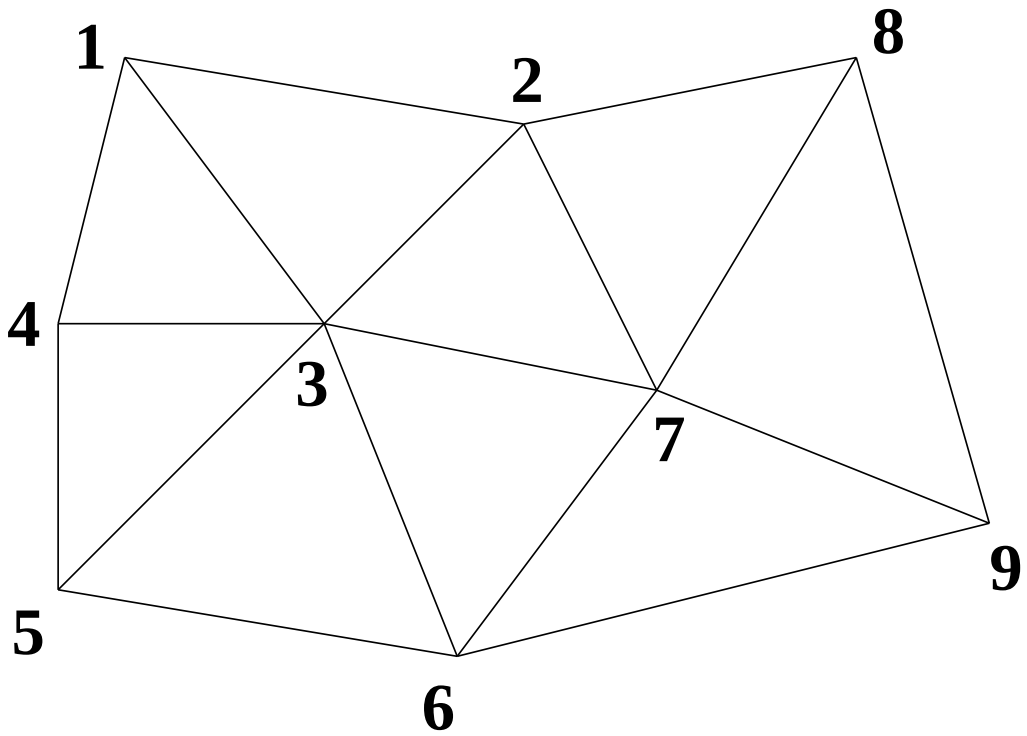
GPU implementation

- The graph (neighbour ranges, indices, and weights) is stored as a triplet of 1D textures (read-only arrays).
- We create one thread for each vertex in V.
- Each vertex $v \in V$ only updates
  - its colour/matching value $\pi(v)$;
  - and its proposal/response value $\sigma(v)$.
- $\pi(v) = \pi(w)$ means $(v, w) \in M$.
- Both π and σ are stored in 1D arrays in global memory. and hence are visible to all threads.

GPU matching

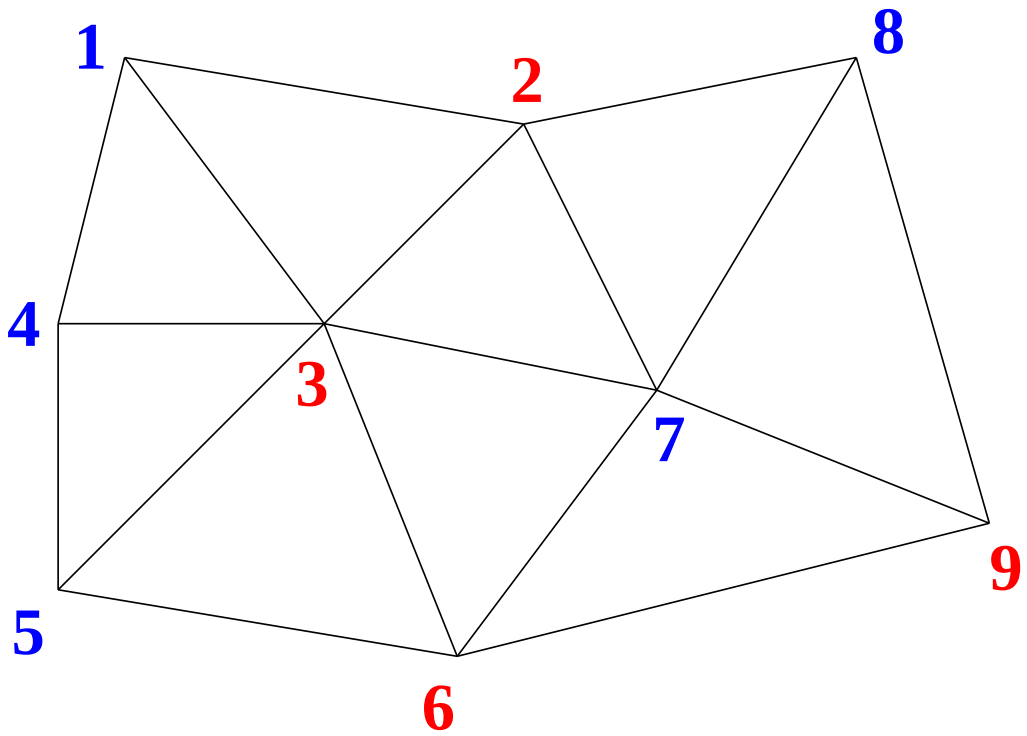
Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	-	-	-	-	-	-	-	-	-
σ	-	-	-	-	-	-	-	-	-

GPU matching

Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	b	r	r	b	b	r	b	b	r
σ	-	-	-	-	-	-	-	-	-

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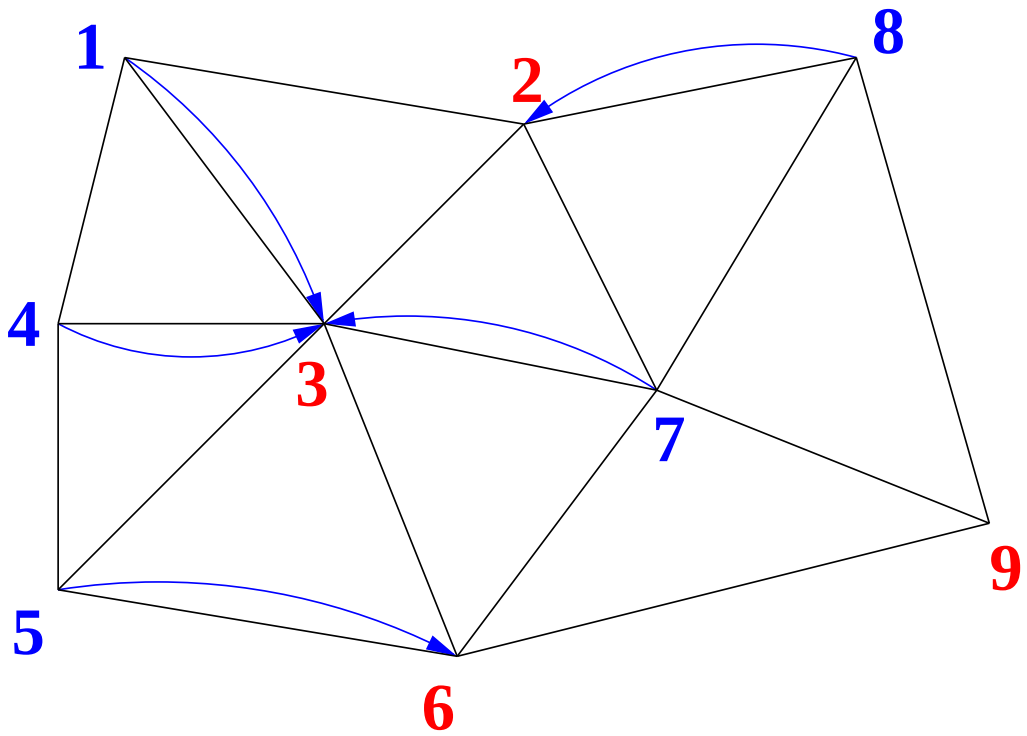
GPU matching

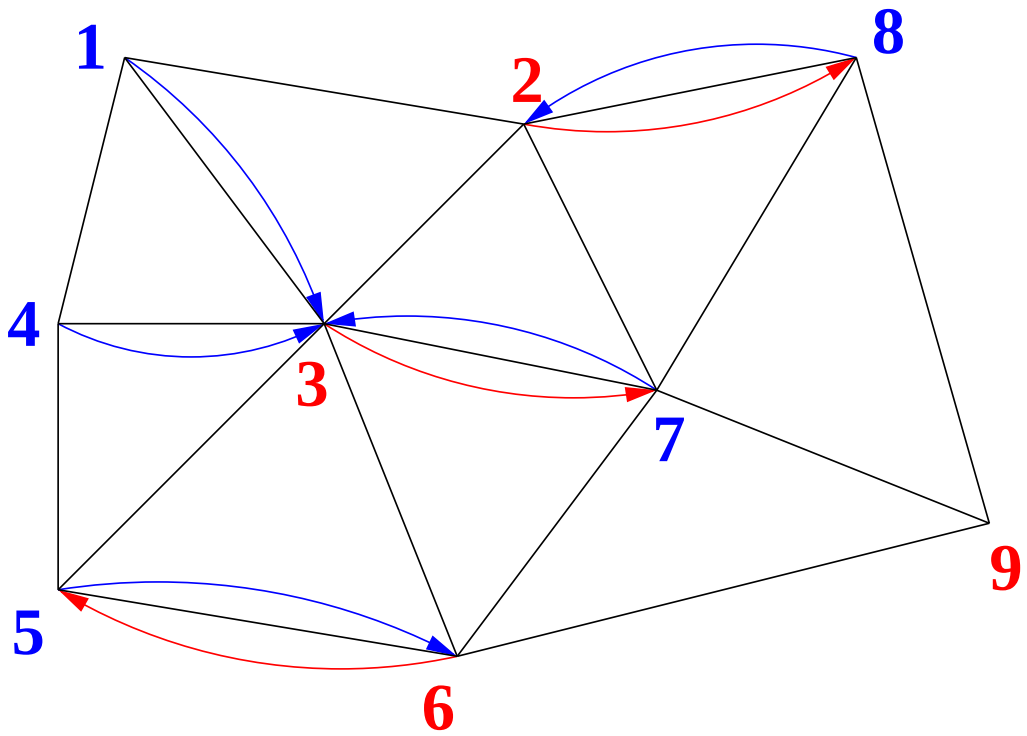
Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	b	r	r	b	b	r	b	b	r
σ	3	-	-	3	6	-	3	2	-

GPU matching

Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	**b**	**r**	**r**	**b**	**b**	**r**	**b**	**b**	**r**
σ	3	8	7	3	6	5	3	2	-

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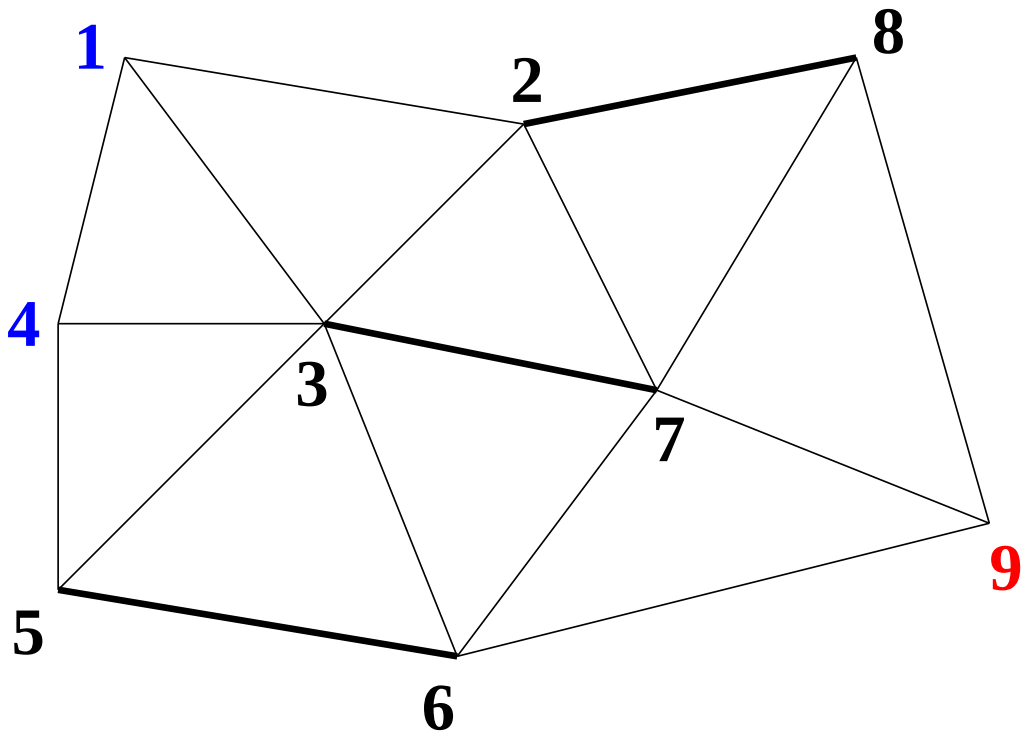
GPU matching

Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	**b**	2	3	**b**	5	5	3	2	**r**
σ	3	8	7	3	6	5	3	2	-

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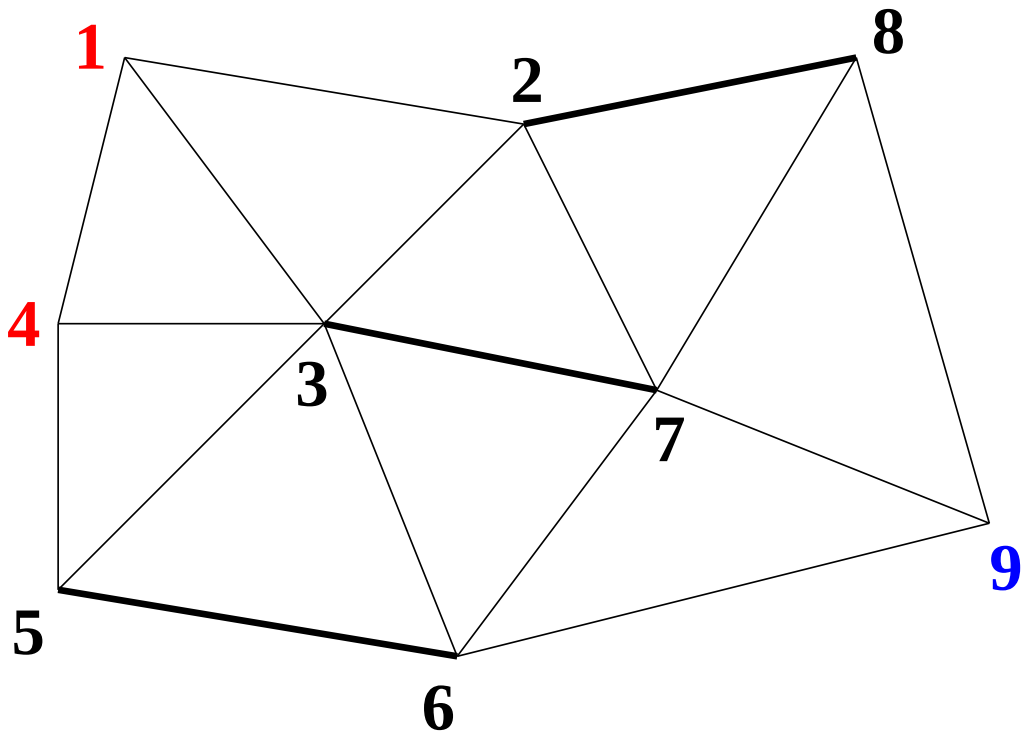
GPU matching

Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	r	2	3	r	5	5	3	2	b
σ	3	8	7	3	6	5	3	2	-

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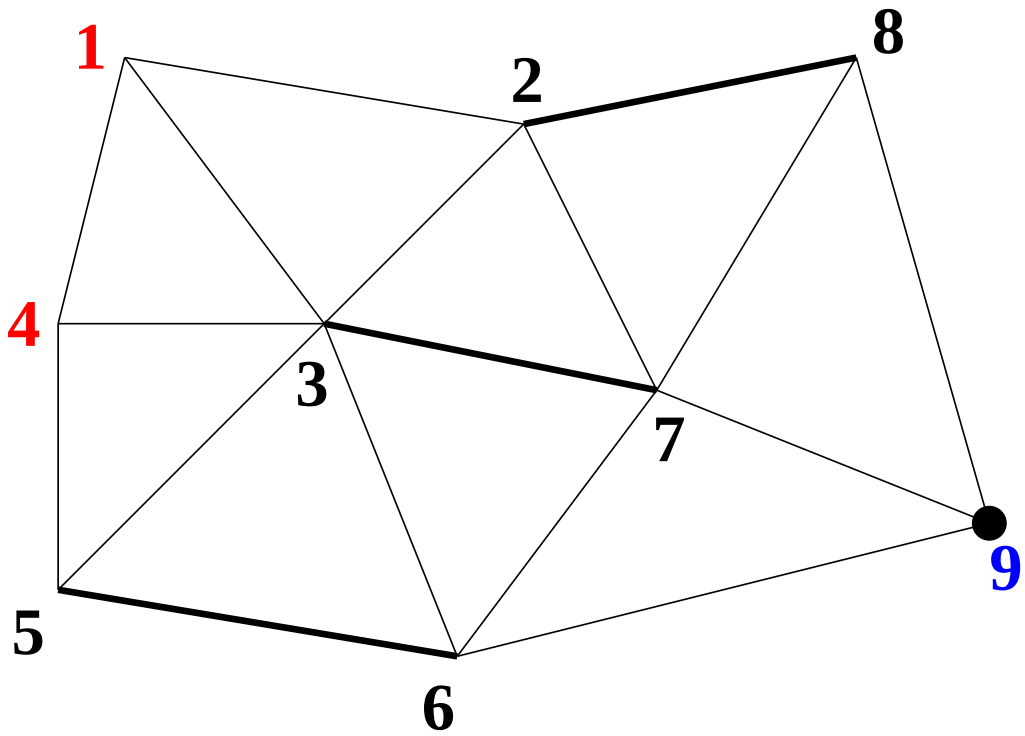
GPU matching

Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	**r**	2	3	**r**	5	5	3	2	**b**
σ	-	-	-	-	-	-	-	-	**d**

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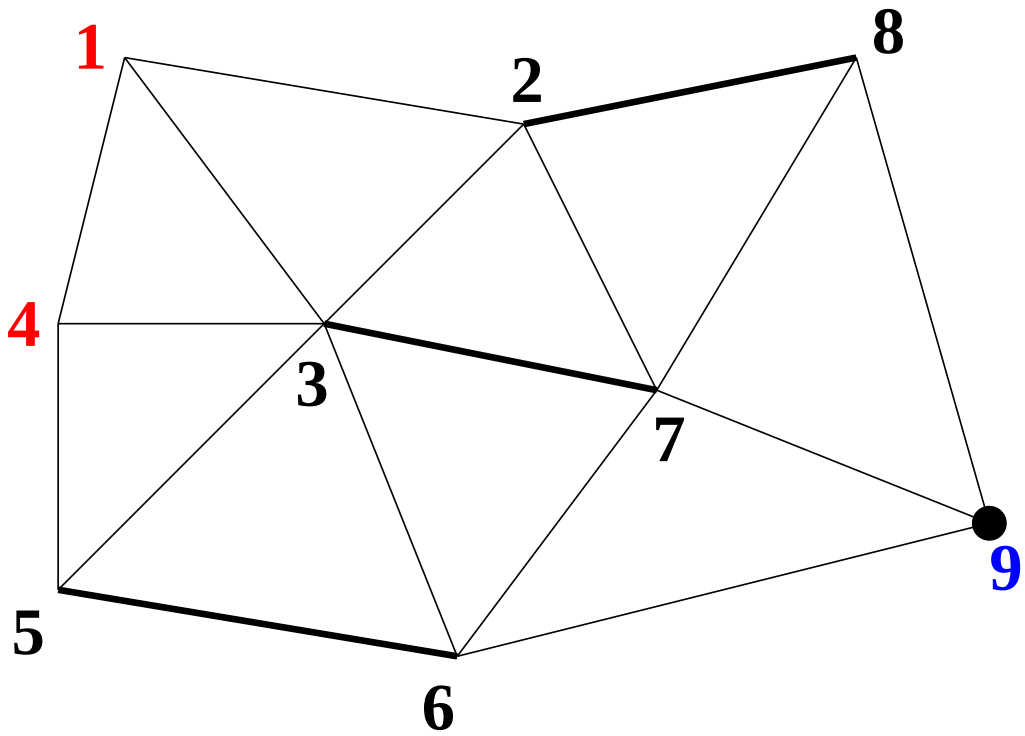
GPU matching

Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	**r**	2	3	**r**	5	5	3	2	**b**
σ	-	-	-	-	-	-	-	-	**d**

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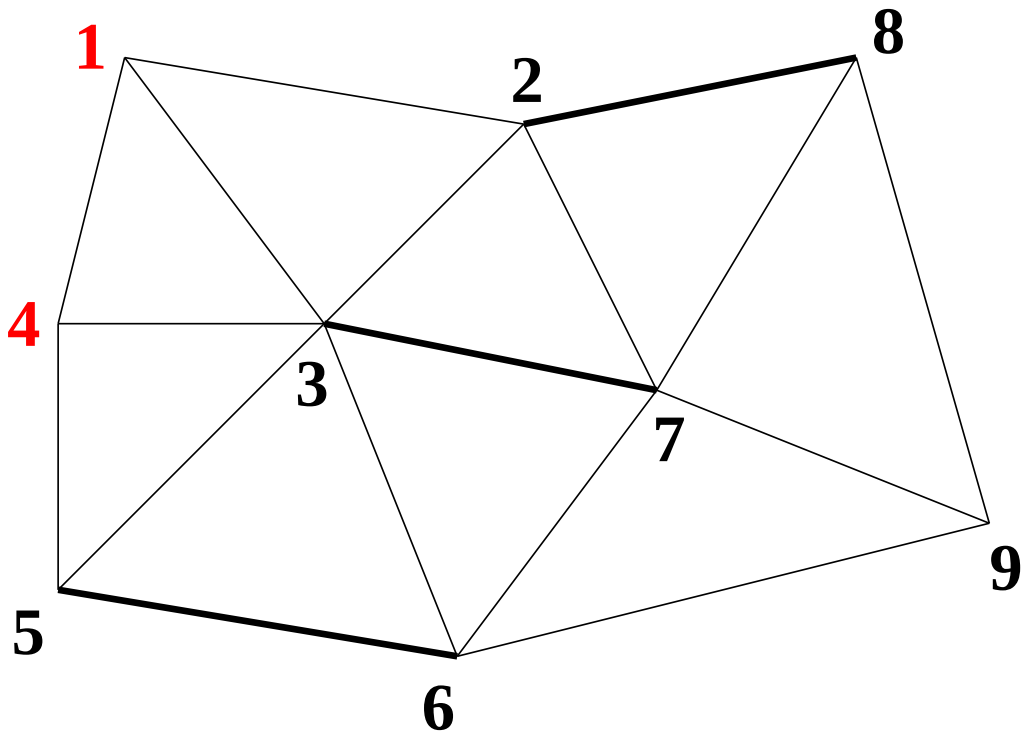
GPU matching

Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	**r**	2	3	**r**	5	5	3	2	**d**
σ	-	-	-	-	-	-	-	-	**d**

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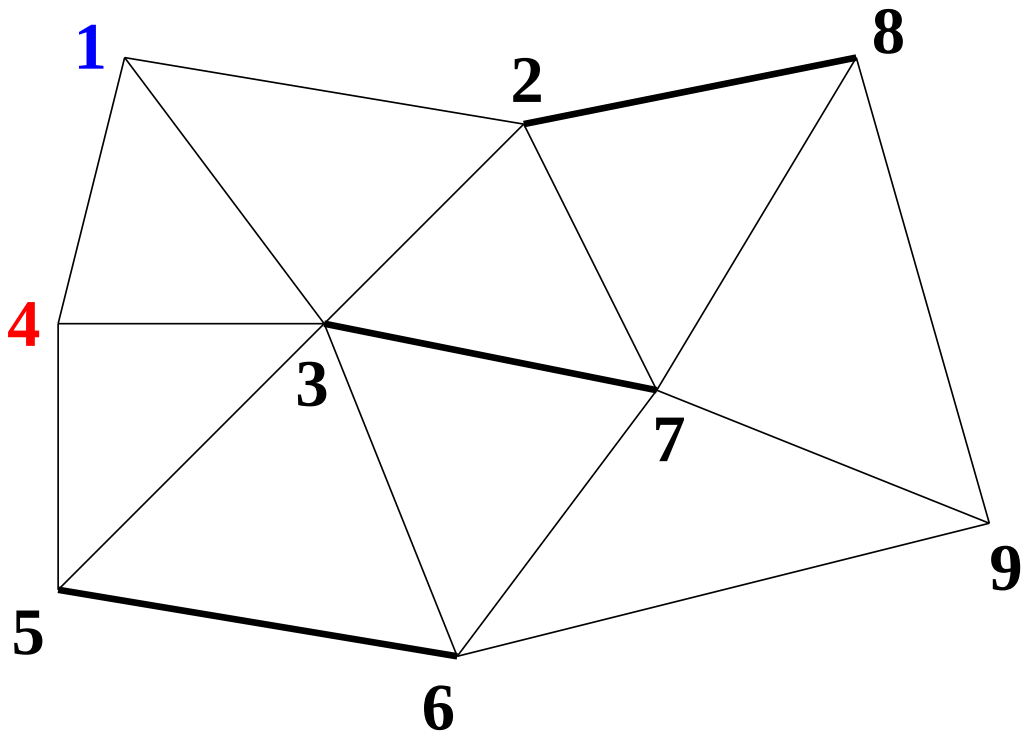
GPU matching

Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	**b**	2	3	**r**	5	5	3	2	**d**
σ	-	-	-	-	-	-	-	-	**d**

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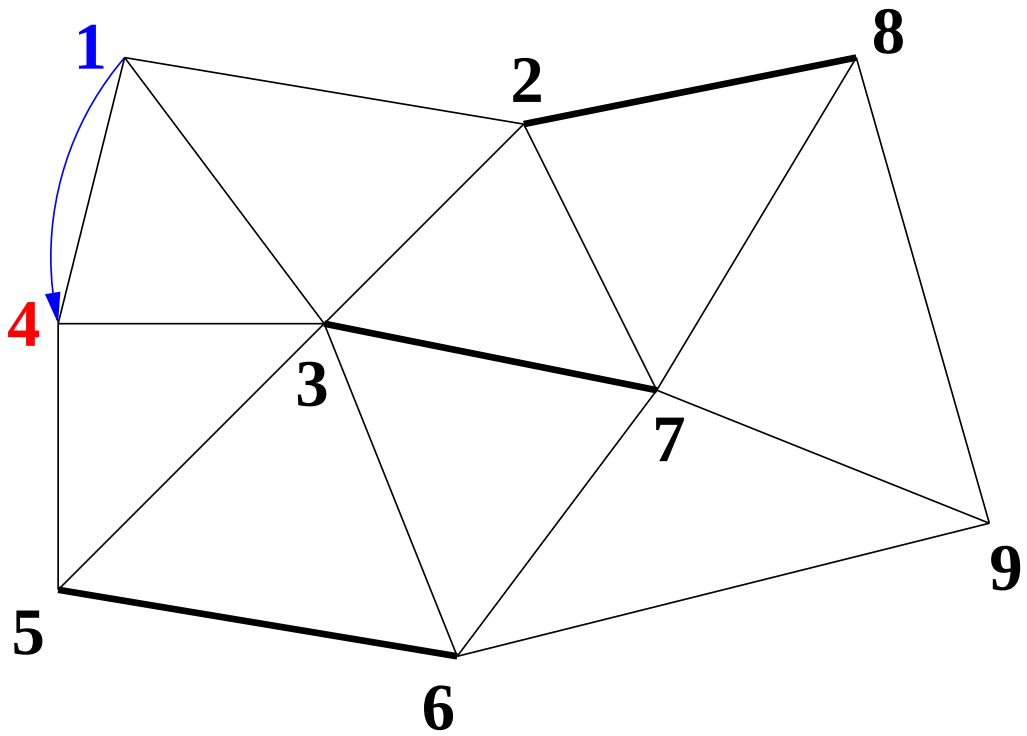
GPU matching

Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	**b**	2	3	**r**	5	5	3	2	**d**
σ	4	-	-	-	-	-	-	-	-

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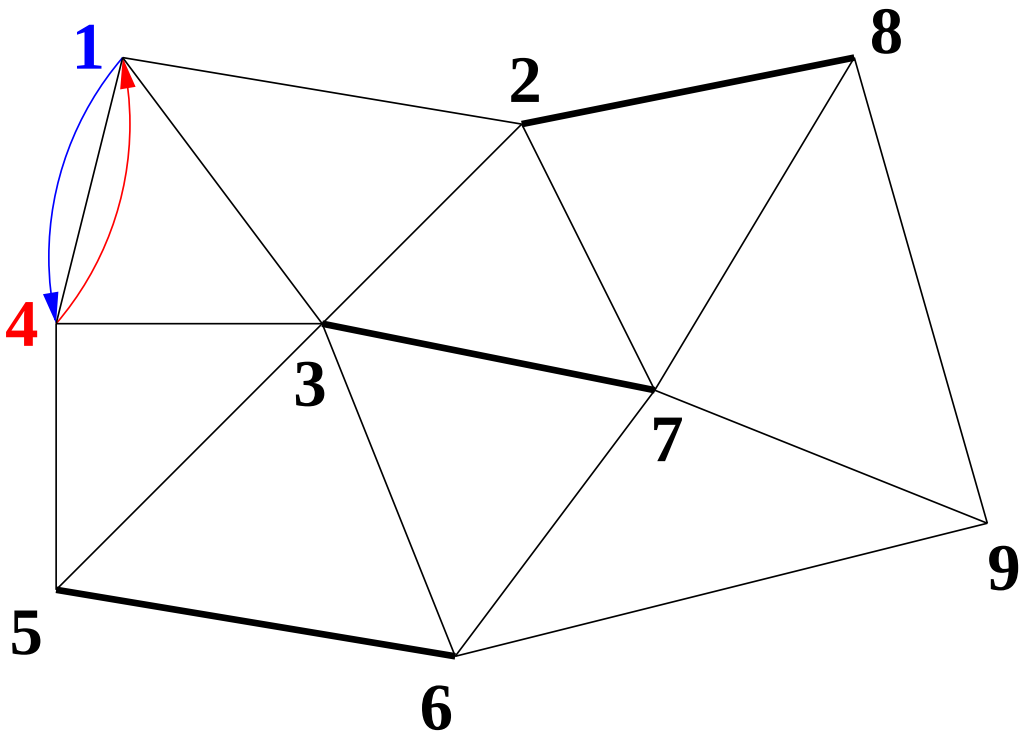
GPU matching

Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	**b**	2	3	**r**	5	5	3	2	**d**
σ	4	-	-	1	-	-	-	-	-

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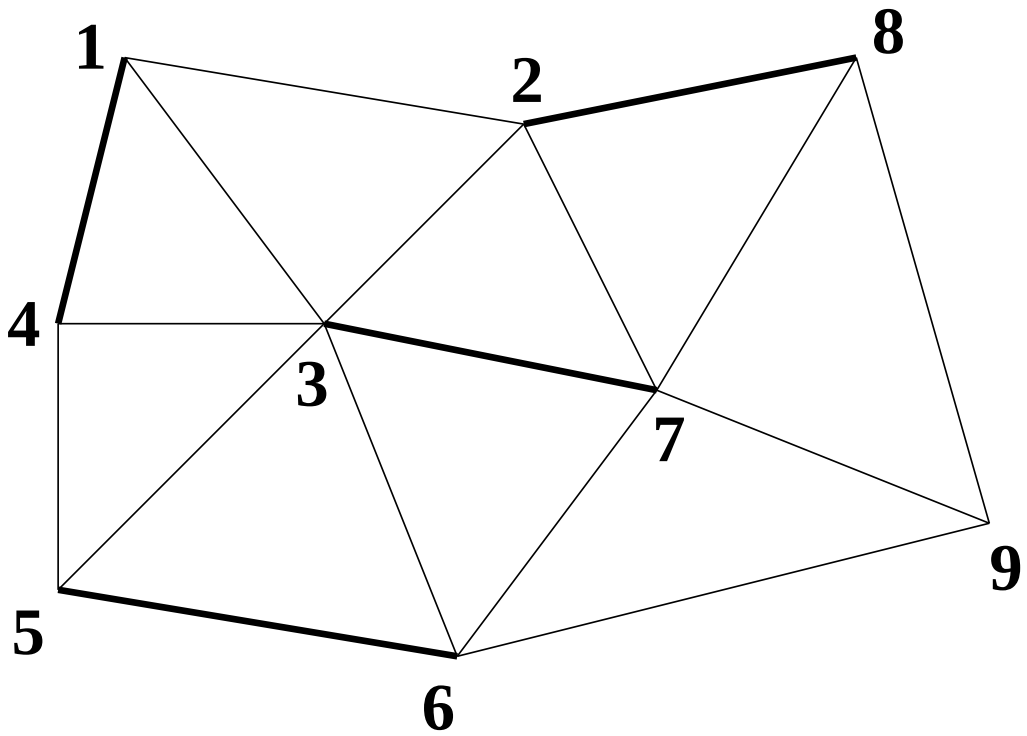
GPU matching

Colour
Propose
Respond
Match



	1	2	3	4	5	6	7	8	9
π	1	2	3	1	5	5	3	2	**d**
σ	4	-	-	1	-	-	-	-	-

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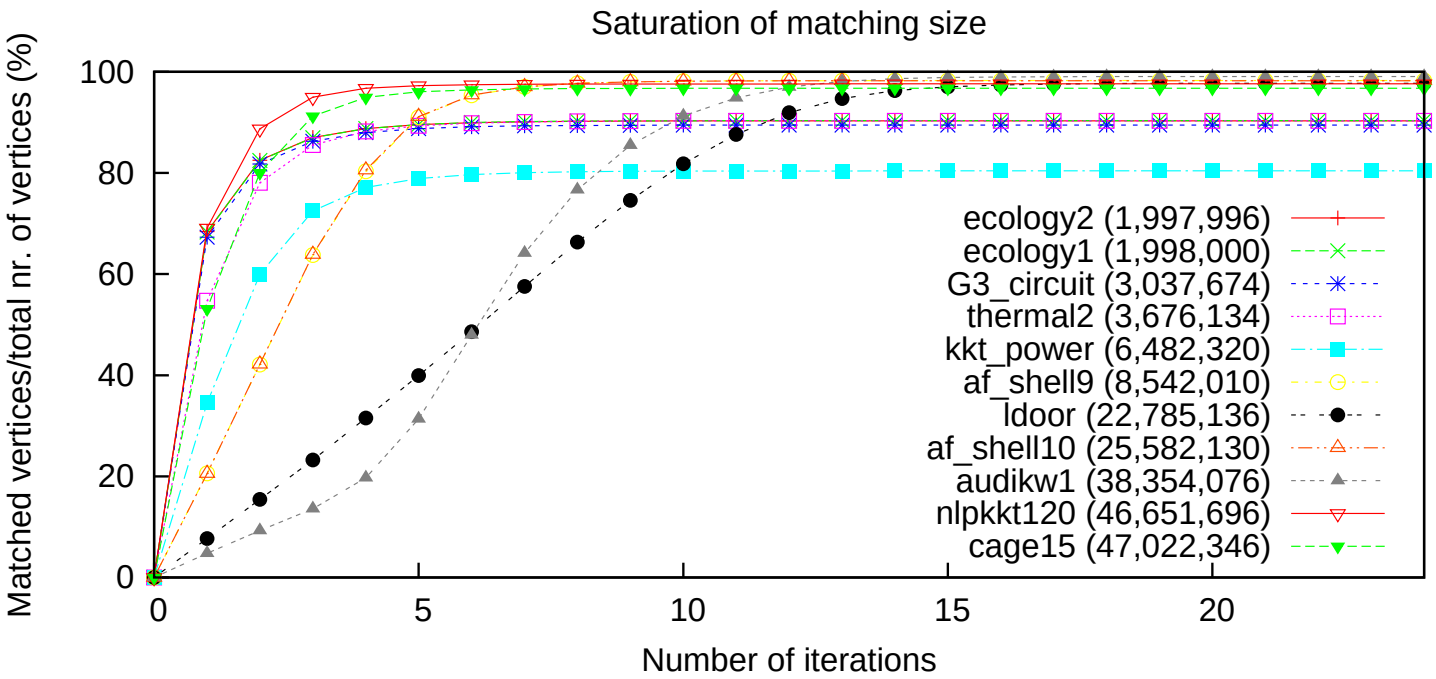
Quality of the matching



Fraction of matched vertices as a function of the number of iterations. Number of edges between 2 and 47 million.

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Random colouring of the vertices

- At each iteration, we colour the vertices $v \in V$ differently.
- For a fixed $p \in [0, 1]$

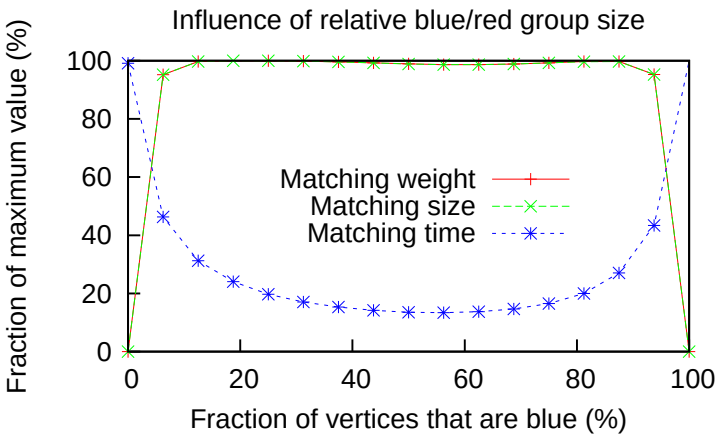
$$\textbf{colour}(v) = \begin{cases} \textbf{blue} & \text{with probability } p, \\ \textbf{red} & \text{with probability } 1 - p. \end{cases}$$

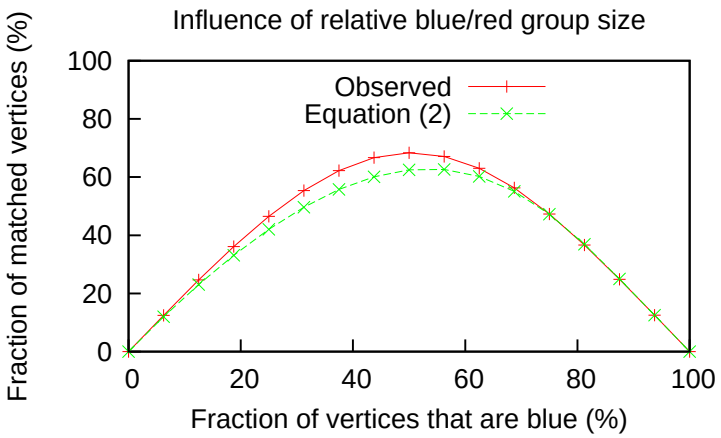
- How to choose p? Maximise the number of matched vertices.
- For large random graphs, the expected fraction of matched vertices can be approximated by

$$2\,(1-p)\left(1 - e^{-\frac{p}{1-p}}\right).$$

This is independent of the edge density.

Choosing the probability p





Following the expectation formula, we should choose $p \approx 0.53406$.

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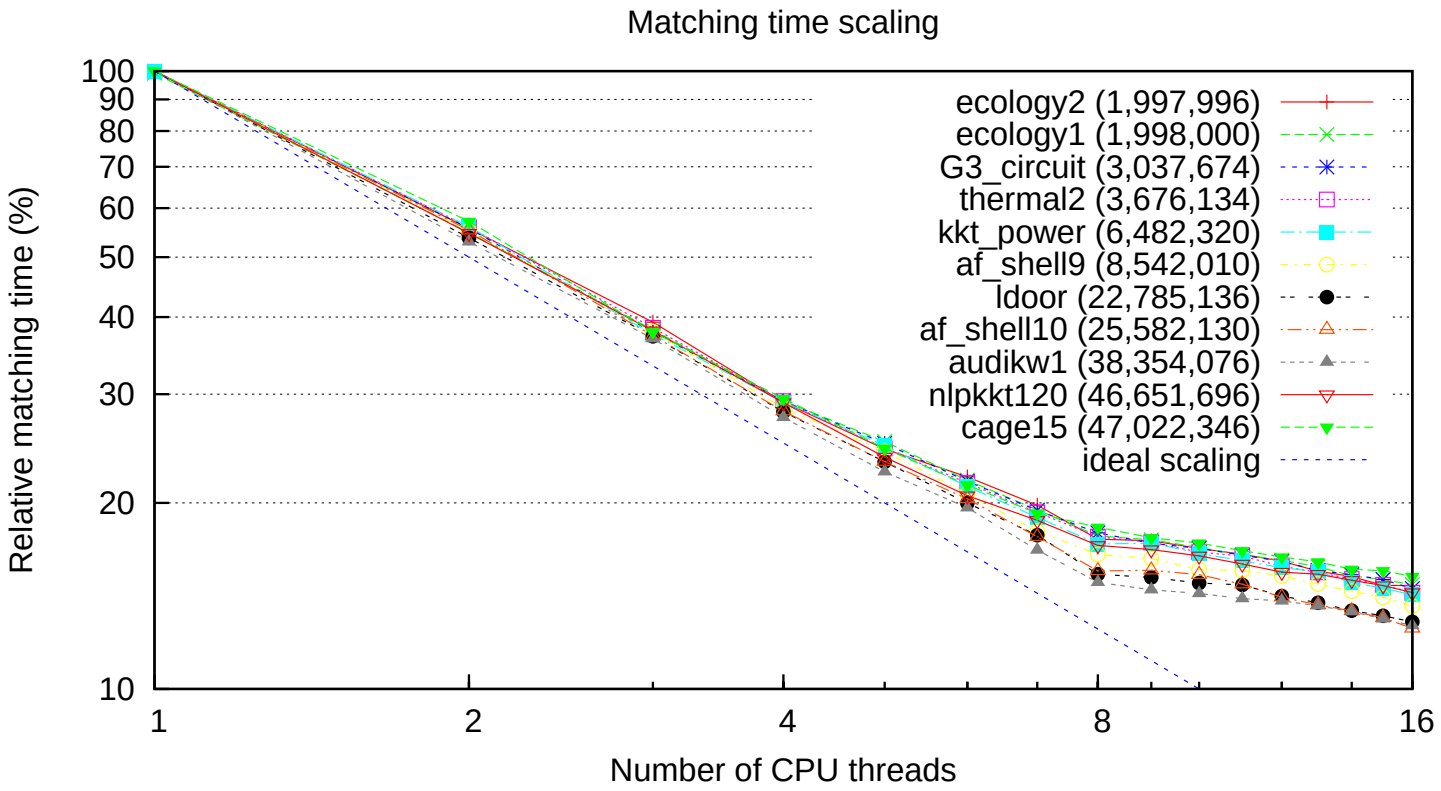
Experimental results (Fagginger Auer & Bisseling 2012)

- Implementation on the GPU using CUDA, on the CPU using Intel Threading Building Blocks (TBB).
- We consider both greedy random and greedy weighted matching.
- Test set: 10th DIMACS challenge on graph partitioning and University of Florida Sparse Matrix Collection.
- Test hardware: dual quad-core Xeon E5620 and an NVIDIA Tesla C2050 (the Little Green Machine).

Results: strong scaling



Scaling of Intel TBB implementation (8 physical cores + hyperthreading).

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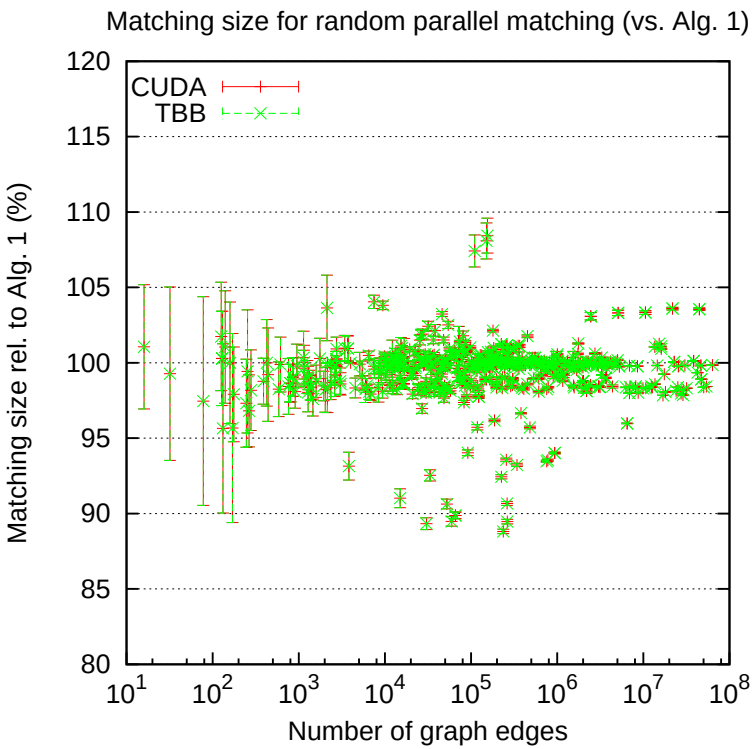
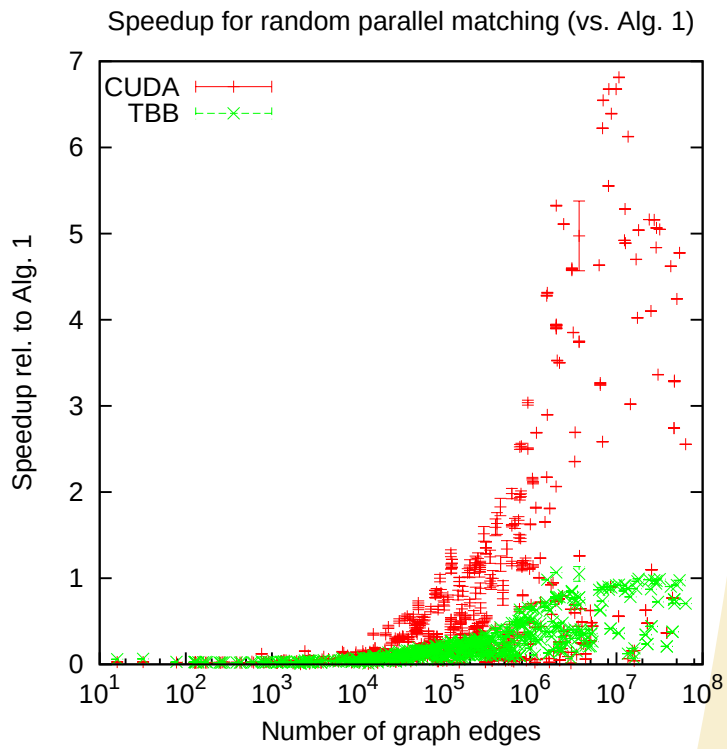
Parallel vs. sequential greedy random matching





Matching size and speedup.

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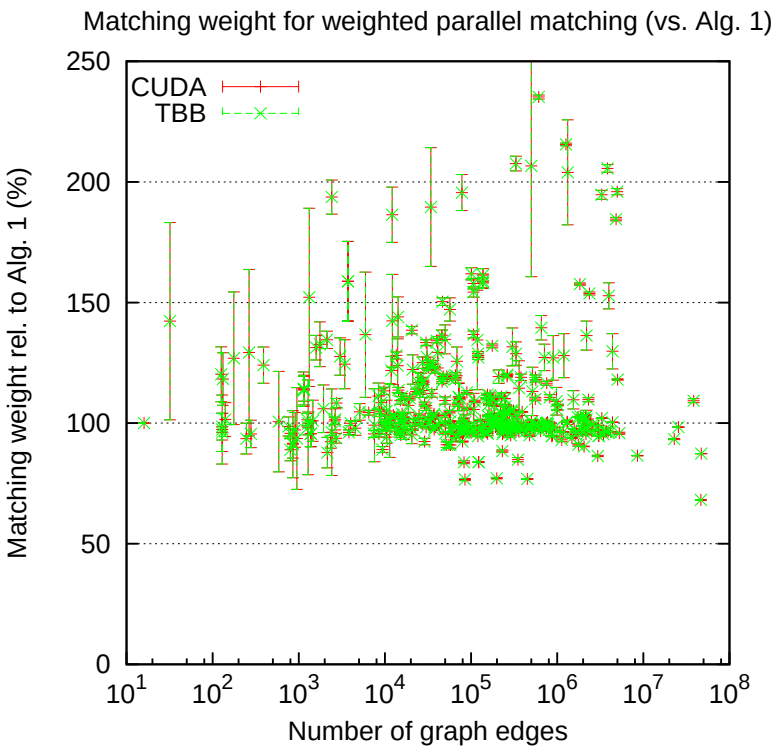
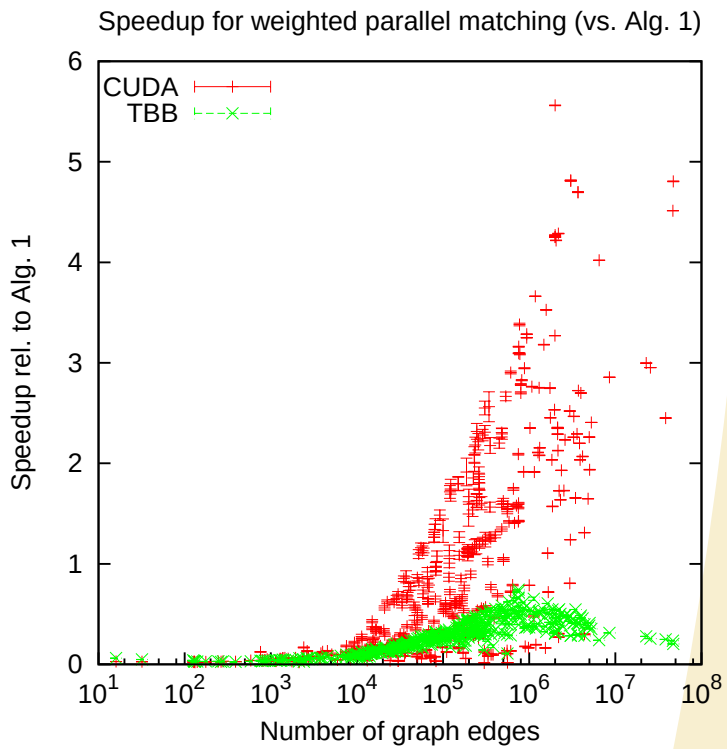
Parallel vs. sequential greedy weighted matching





Matching weight and speedup.

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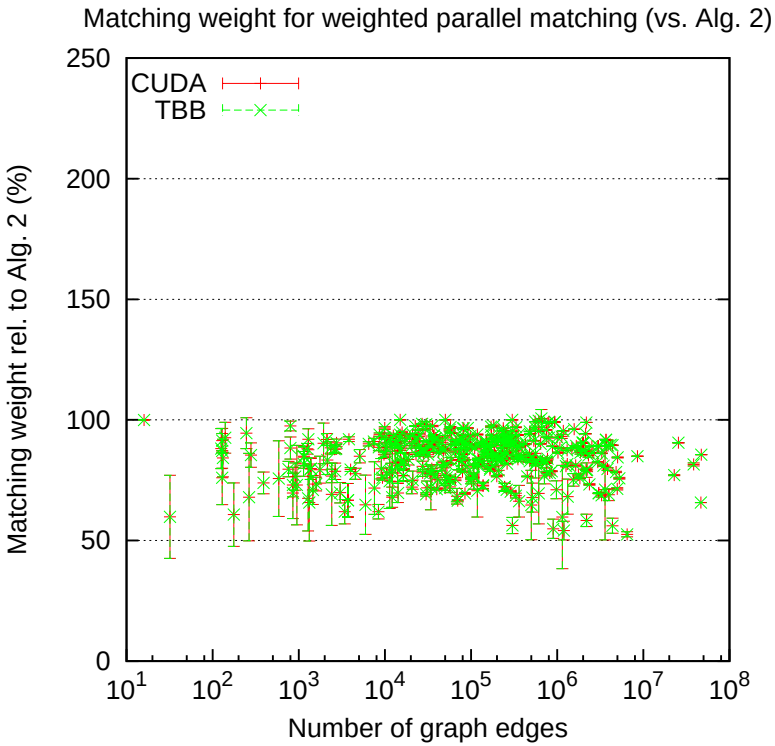
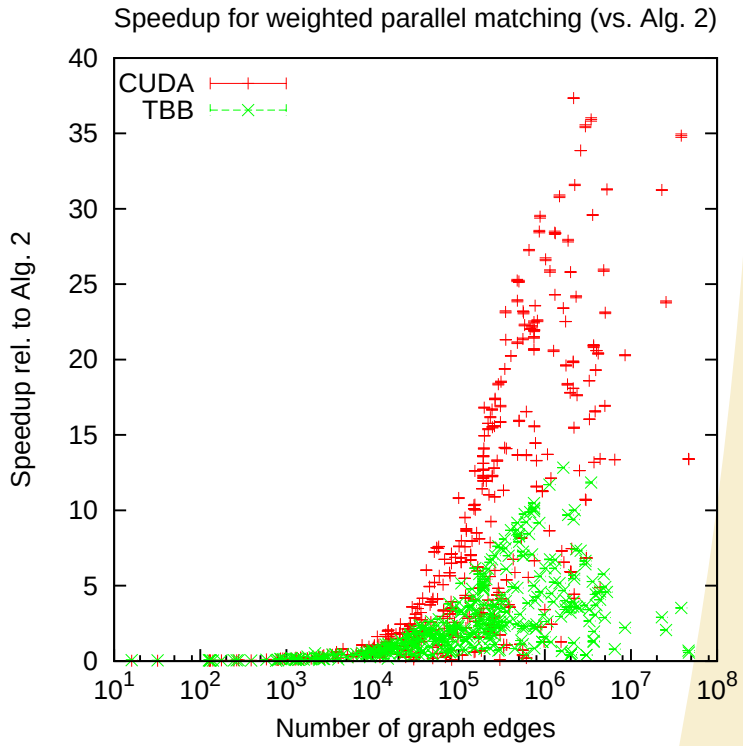
Parallel weighted vs. sequential greedy matching





Matching weight and speedup.
Sequential greedy matching is 1/2-approximation.

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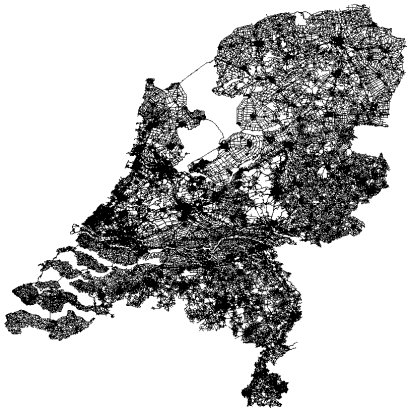
Clustering of road network of the Netherlands

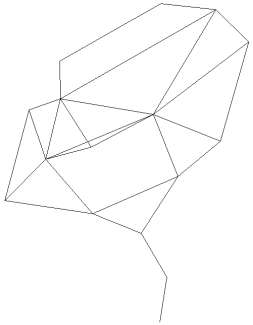


(a) G^0

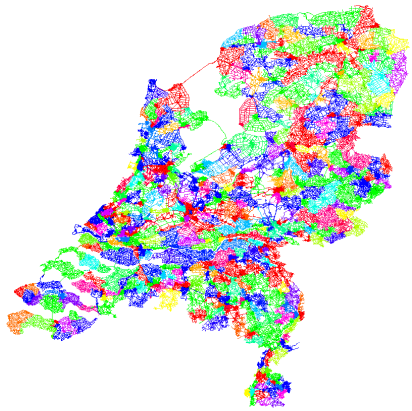
(b) G^{11}

(c) G^{21}

(d) G^{26}



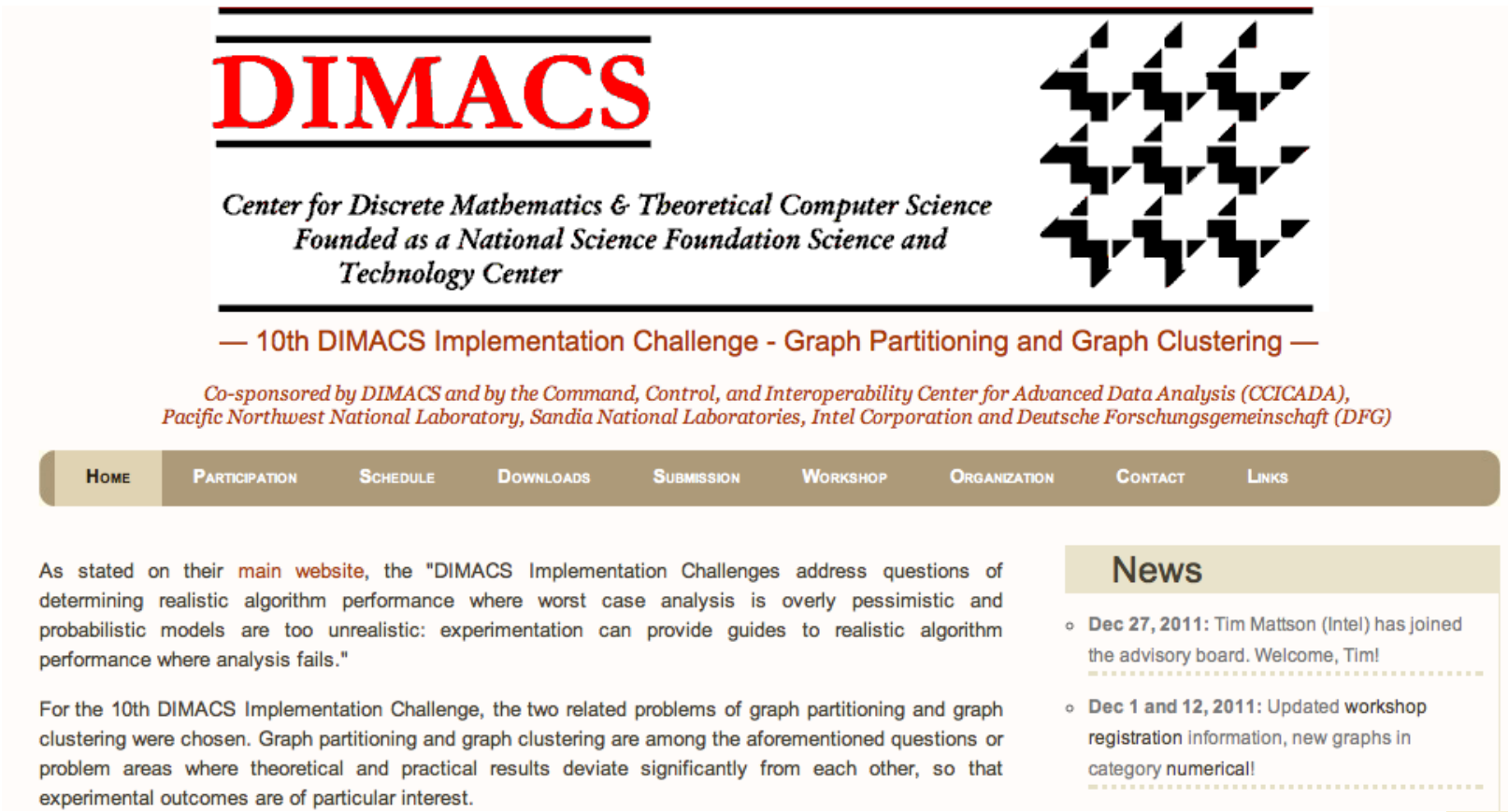
(e) G^{33}



(f) Best clustering (G^{21})

Graph with 2,216,688 vertices and 2,441,238 edges yields 506 clusters with modularity 0.995.

DIMACS challenge February 2012



DIMACS

Center for Discrete Mathematics & Theoretical Computer Science
Founded as a National Science Foundation Science and Technology Center

— 10th DIMACS Implementation Challenge - Graph Partitioning and Graph Clustering —

Co-sponsored by DIMACS and by the Command, Control, and Interoperability Center for Advanced Data Analysis (CCICADA), Pacific Northwest National Laboratory, Sandia National Laboratories, Intel Corporation and Deutsche Forschungsgemeinschaft (DFG)

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As stated on their main website, the "DIMACS Implementation Challenges address questions of determining realistic algorithm performance where worst case analysis is overly pessimistic and probabilistic models are too unrealistic: experimentation can provide guides to realistic algorithm performance where analysis fails."

For the 10th DIMACS Implementation Challenge, the two related problems of graph partitioning and graph clustering were chosen. Graph partitioning and graph clustering are among the aforementioned questions or problem areas where theoretical and practical results deviate significantly from each other, so that experimental outcomes are of particular interest.

News

- **Dec 27, 2011:** Tim Mattson (Intel) has joined the advisory board. Welcome, Tim!
- **Dec 1 and 12, 2011:** Updated workshop registration information, new graphs in category numerical!

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Formal definition of a clustering

- A clustering of an undirected graph $G = (V, E)$ is a collection $\mathcal{C}$ of disjoint subsets of V satisfying

$$V = \bigcup_{C \in \mathcal{C}} C.$$

- Elements $C \in \mathcal{C}$ are called clusters.
- The number of clusters is not fixed beforehand.
- Extreme cases: a single large cluster, $|V|$ single-vertex clusters.

Quality measure for clustering: modularity

- The quality measure modularity was introduced by Newman and Girvan in 2004 for finding communities.
- Let $G = (V, E, \omega)$ be a weighted undirected graph without self-edges. We define

$$\zeta(v) = \sum_{(u,v)\in E} \omega(u,v), \qquad \Omega = \sum_{e\in E} \omega(e).$$

- Then, the modularity of a clustering $\mathcal{C}$ of G is defined by

$$\mathrm{mod}(\mathcal{C}) = \frac{\sum_{C\in\mathcal{C}} \sum_{\substack{(u,v)\in E \\ u,v\in C}} \omega(u,v)}{\Omega} - \frac{\sum_{C\in\mathcal{C}} \left(\sum_{v\in C} \zeta(v) \right)^2}{4\Omega^2}.$$

- $-\frac{1}{2} \leq \mathrm{mod}(\mathcal{C}) \leq 1$.

Merging clusters: change in modularity

- The weight of a cluster is

$$\zeta(C) = \sum_{v \in C} \zeta(v).$$

- The set of all cut edges between clusters C and C' is

$$\text{cut}(C, C') = \{\{u, v\} \in E \mid u \in C, v \in C'\}$$

- If we merge clusters C and C' from $\mathcal{C}$ into one cluster $C \cup C'$, then the modularity of the new clustering $\mathcal{C}'$ is

$$\text{mod}(\mathcal{C}') = \text{mod}(\mathcal{C}) + \frac{1}{4\,\Omega^2}\left(4\,\Omega\,\omega(\text{cut}(C, C')) - 2\,\zeta(C)\,\zeta(C')\right),$$

and $\zeta(C \cup C') = \zeta(C) + \zeta(C')$.

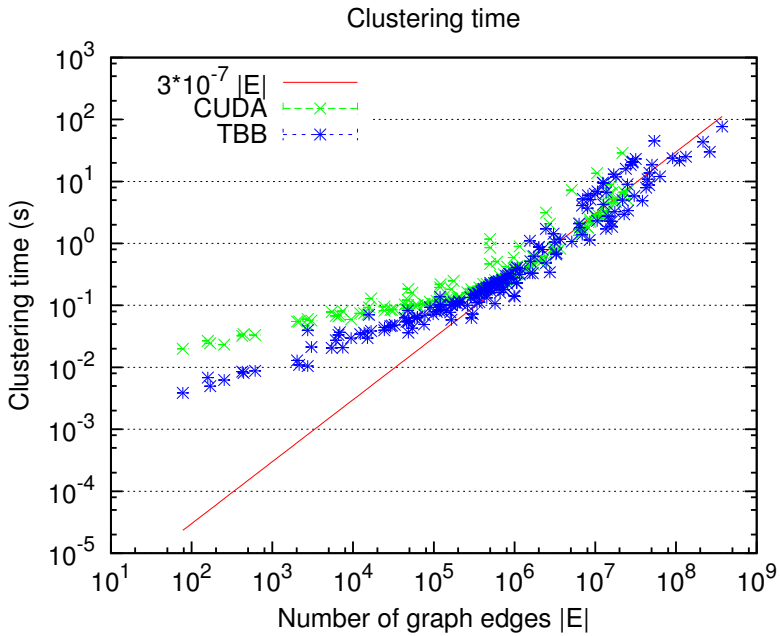
Agglomerative greedy clustering heuristic

$\max \leftarrow -\infty$
$G^0 = (V^0, E^0, \omega^0, \zeta^0)$
$i \leftarrow 0$
$\mathcal{C}^0 \leftarrow \{\{v\} \mid v \in V\}$
while $|V^i| > 1$ **do**
  if $\mathrm{mod}(G, \mathcal{C}^i) \geq \max$ **then**
    $\max \leftarrow \mathrm{mod}(G, \mathcal{C}^i)$
    $\mathcal{C}^{\text{best}} \leftarrow \mathcal{C}^i$
  $\mu \leftarrow$ **weighted_match_clusters**(G^i)
  $(\pi^i, G^{i+1}) \leftarrow$ **coarsen**(G^i, μ)
  $\mathcal{C}^{i+1} \leftarrow \{\{v \in V \mid (\pi^i \circ \cdots \circ \pi^0)(v) = u\} \mid u \in V^{i+1}\}$
  $i \leftarrow i + 1$
return $\mathcal{C}^{\text{best}}$

Parallelisation

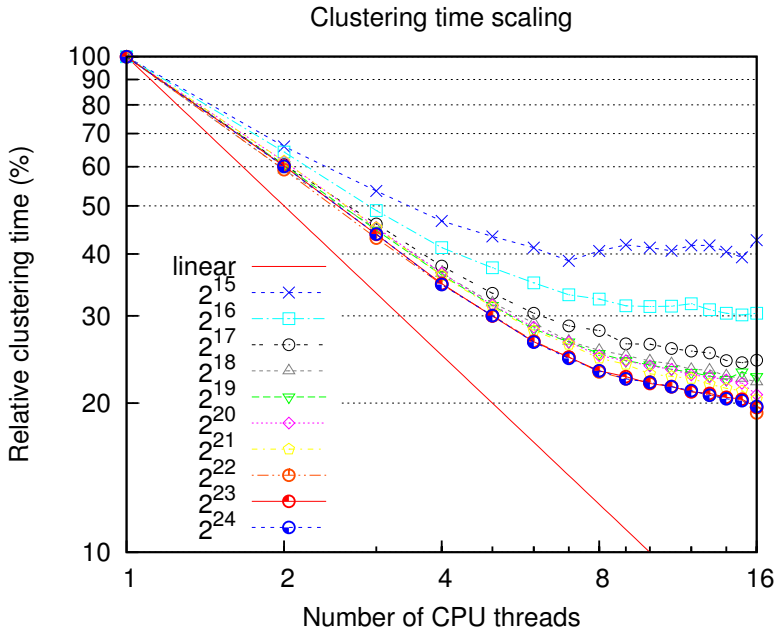
- Based on slight adaptations of functions from Thrust, an open-source template library for developing CUDA applications (modelled after C++ STL).
- Also, **for. . . parallel do** constructs indicating a for-loop where each iteration can be executed in parallel.

Results: clustering time for DIMACS graphs



- DIMACS categories: `clustering/`, `coauthor/`, `streets/`, `random/`, `delaunay/`, `matrix/`, `walshaw/`, `dyn-frames/`, and `redistrict/`.
- CUDA implementation with the Thrust template library and Intel TBB implementation.
- Web link graph `uk-2002` with 0.26 billion vertices clustered in 30 s using Intel TBB.

Results: strong scaling



- The clustering time as a function of the number of threads.
- Graphs from the category `random/` with 2^{15}–2^{24} vertices.
- Intel TBB implementation on 2 quad-core 2.4 GHz Intel Xeon E5620 processors with up to 16 threads by hyperthreading.

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DIMACS road networks and coauthor graphs

G	$\|V\|$	$\|E\|$	mod CU	t CU	mod TBB	t TBB
luxembourg	114,599	119,666	0.99	0.13	0.99	0.14
belgium	1,441,295	1,549,970	0.99	0.44	0.99	1.11
netherlands	2,216,688	2,441,238	0.99	0.62	0.99	1.72
italy	6,686,493	7,013,978	1.00	1.54	1.00	5.26
great-britain	7,733,822	8,156,517	1.00	1.79	1.00	6.00
germany	11,548,845	12,369,181	1.00	2.82	1.00	9.57
asia	11,950,757	12,711,603	1.00	2.69	1.00	9.33
europe	50,912,018	54,054,660	-	-.-	1.00	45.21
coAuthorsCite	227,320	814,134	0.84	0.42	0.85	0.23
coAuthorsDBLP	299,067	977,676	0.75	0.59	0.76	0.28
citationCite	268,495	1,156,647	0.64	0.89	0.68	0.32
coPapersDBLP	540,486	15,245,729	0.64	6.43	0.67	2.28
coPapersCite	434,102	16,036,720	0.75	6.49	0.77	2.27

mod = modularity, t = time in s, CU = CUDA

Sparse matrix partitioning and graph partitioning

- A sparse matrix is the adjacency matrix of a sparse graph:

$$a_{ij} \neq 0 \Leftrightarrow (i,j) \in E$$

- Partitioning the nonzeros of a matrix is the same as partioning the edges of a graph.
- 2D partitioning splits both rows and columns.
- Partitioning for parallel sparse matrix-vector multiplication (SpMV) can be used in Google PageRank computation.
- Partitioning for SpMV also gives a good partitioning for many graph computations.

Advantage of 2D partitioning

- We can use both dimensions of the matrix to reduce SpMV communication.
- For a $\sqrt{p} \times \sqrt{p}$ block distribution, each matrix row or column is distributed over at most $\sqrt{p}$ processors, instead of p processors for a 1D distribution.
- Relatively dense rows and columns can be split and do not cause load imbalance or memory overflow.

Methods for 2D partitioning

- Existing 2D methods: coarse-grain, fine-grain, Mondriaan.
- New medium-grain method (Pelt & Bisseling 2014) based on splitting the $m \times n$ matrix

$$A = A^r + A^c,$$

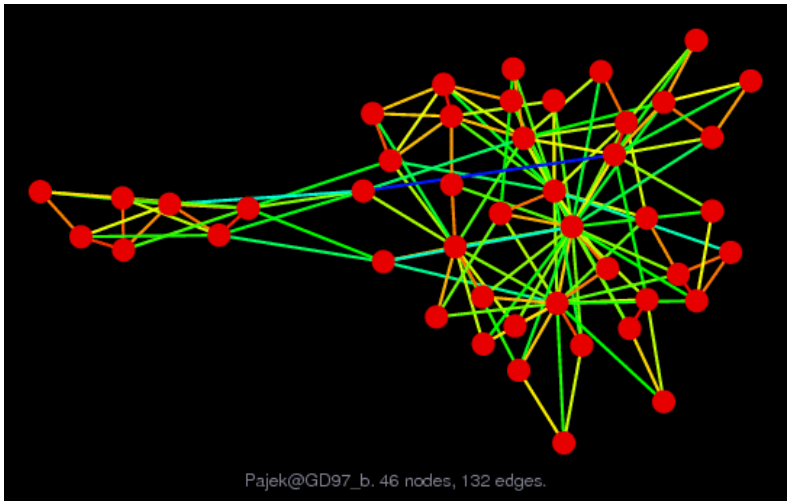
putting a nonzero a_{ij} into A^r if row i has less nonzeros than column j, and in A^c otherwise.

- Then partition the $(m+n) \times (m+n)$ matrix B by a 1D column partitioning:

$$B = \begin{bmatrix} I_n & (A^r)^T \\ A^c & I_m \end{bmatrix},$$

where I_m is the identity matrix of size $m \times m$.

Pajek Graph Drawing contest 1997



- 46 nodes, 132 edges
- Source: University of Florida Sparse Matrix Collection

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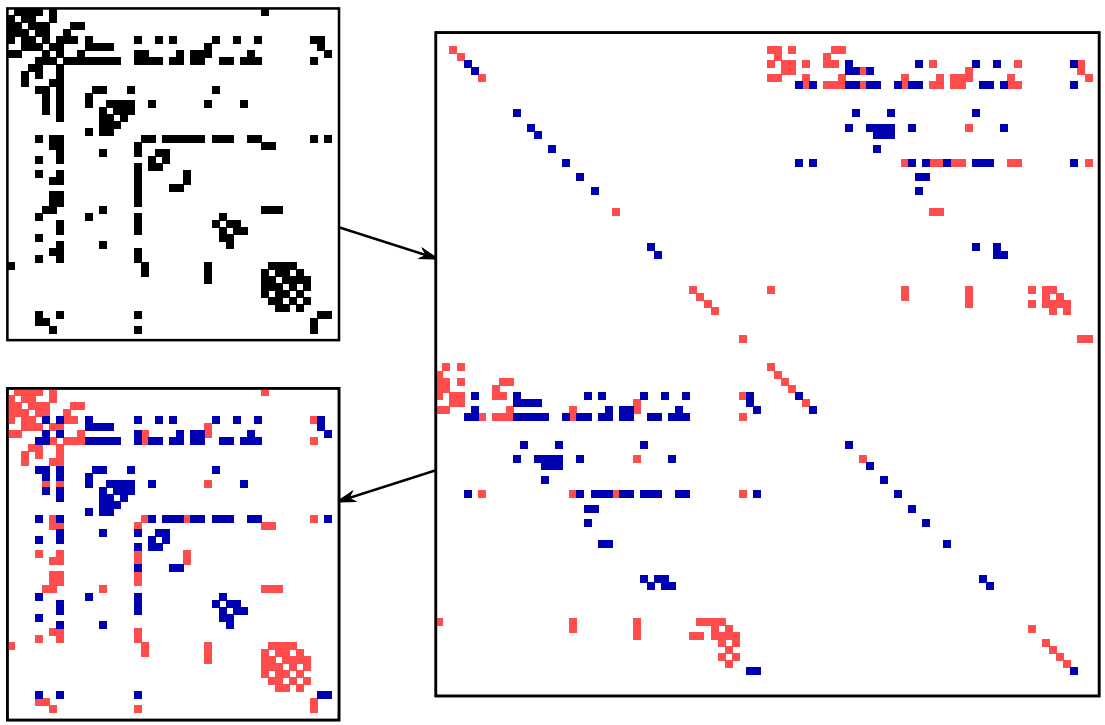
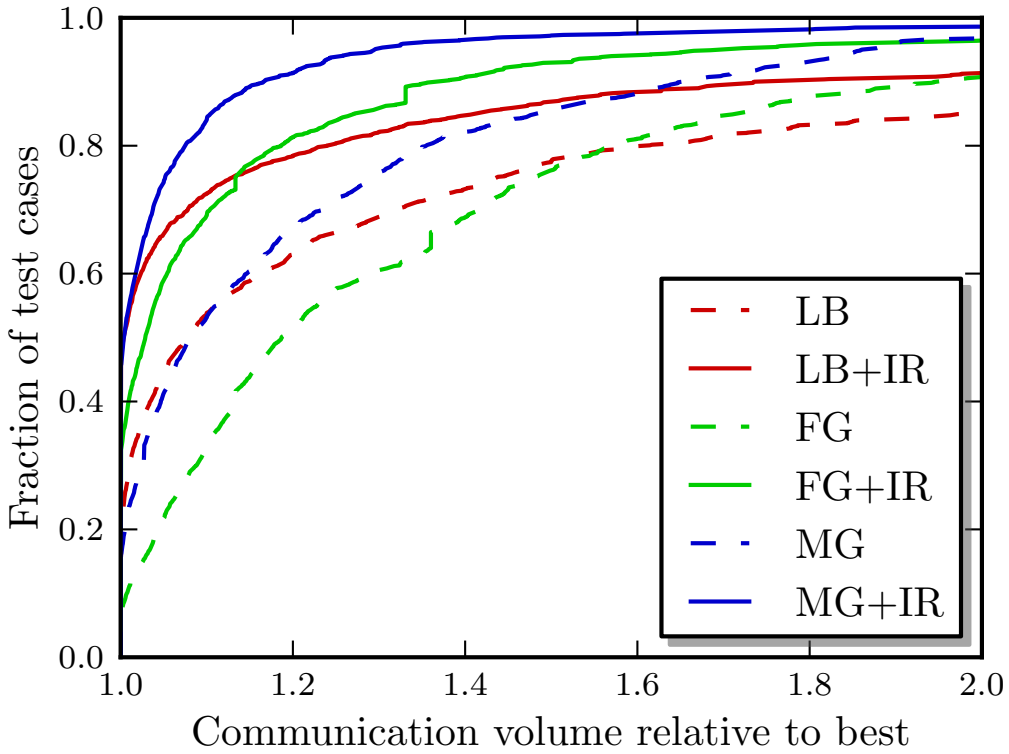
Medium-grain method for partitioning



- 47×47 matrix gd97_b with 264 nonzeros
- Partitioning for 2 processors
- Communication volume $= 11$, which is optimal

Communication volume for 2 processors



- Test set: 2264 Florida matrices, $500 \leq nz \leq 5,000,000$
- LB = localbest (original Mondriaan) = best of 1D row and 1D column partitioning
- FG = fine-grain
- MG = medium-grain
- IR = iterative refinement, to improve the partitioning

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2D (edge-based) parallel matching

Name	SpMV		Matching	
	1D	2D	1D	2D
rw9 (af_shell10)	113	105	169	150
rw10 (boneS10)	150	145	228	189
rw11 (Stanford)	340	141	479	234
rw12 (gupta3)	710	44	1,305	61
rw13 (St_Berk.)	716	448	1,152	812
rw14 (F1)	139	130	148	139
sw1 (small world)	1,007	417	2,111	303
sw2	1,957	829	3,999	563
sw3	2,017	832	4,255	528
er1 (random)	1,856	1,133	1,788	1,157
er2	3,451	1,841	3,721	1,635
er3	5,476	2,569	6,350	1,990

Communication volume in sparse matrix–vector multiplication and Karp–Sipser matching.
Source: Patwary, Bisseling, Manne (2010).

Conclusions

- BSP is extremely suitable for parallel graph computations:
  - no worries about communication because we buffer messages until the next synchronisation;
  - no send-receive pairs;
  - BSP cost model gives synchronisation frequency;
  - correctness proof of algorithm becomes simpler;
  - no deadlock possible.
- Matching can be the basis for clustering, as demonstrated for GPUs and multicore CPUs.
- We clustered Europe's road network with 51M vertices and 54M edges in 45 seconds on an 8-core CPU.
- Partitioning for sparse matrix-vector multiplication reduces communication volume for Karp–Sipser matching as well:

$$\frac{1}{2}\mathit{Vol}(\mathrm{SpMV}) \leq \mathit{Vol}(\mathrm{Matching}) \leq \frac{3}{2}\mathit{Vol}(\mathrm{SpMV}).$$

- Parallel graph algorithms will benefit from partitioning the edges instead of the vertices.

It's all about the connections...

Merci beaucoup!

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