

Minimum Spanning Tree

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DPHPC

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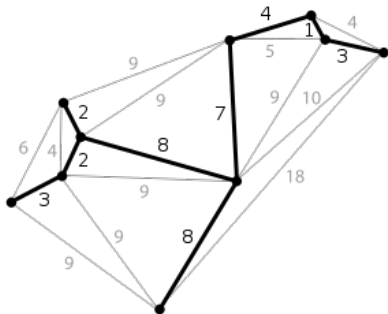


Problem definition - reminder



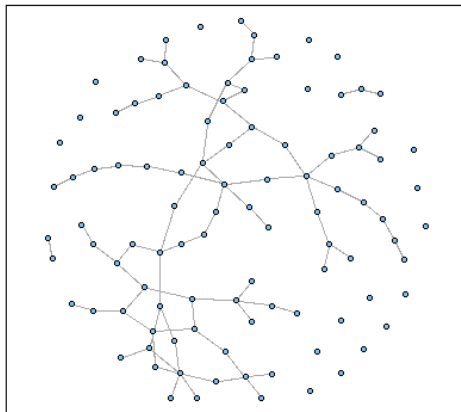
The MST problem

A minimum spanning tree (MST) or minimum weight spanning tree is a subset of the edges of a connected, edge-weighted (un)directed graph that connects all the vertices together, without any cycles and with the minimum possible total edge weight.



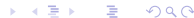
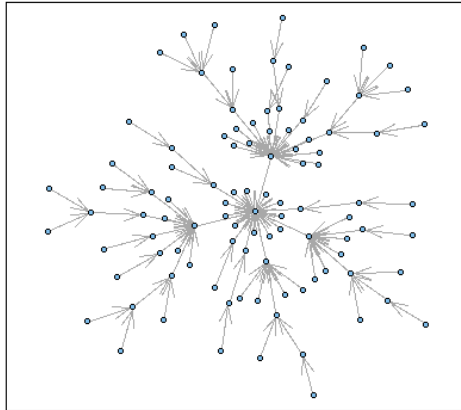
Input sets: $G(n, p)$

$G(100, 0.02)$



Input sets: $PA(n)$

$PA(100)$



USA Roads

Name	Description	# nodes	# arcs
USA	Full USA	23,947,347	58,333,344
CTR	Central USA	14,081,816	34,292,496
W	Western USA	6,262,104	15,248,146
E	Eastern USA	3,598,623	8,778,114
LKS	Great Lakes	2,758,119	6,885,658
CAL	California and Nevada	1,890,815	4,657,742
NE	Northeast USA	1,524,453	3,897,636
NW	Northwest USA	1,207,945	2,840,208
FLA	Florida	1,070,376	2,712,798
COL	Colorado	435,666	1,057,066
BAY	San Francisco Bay Area	321,270	800,172
NY	New York City	264,346	733,846



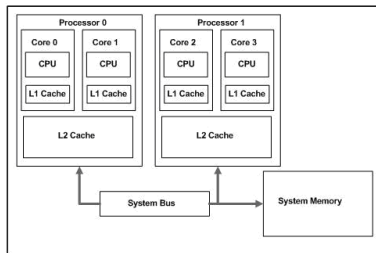
Setup



- OMP
- Intel Threading Building Blocks (TBB)
- Parallel Streaming Transformation Loader Service (PSTL)



- 1 node limitation (OMP)
- 2 sockets filled with 18 cores - up to 3.7Ghz
- Inter-sockets bus speed: 10.4 GT/s



Algorithms and parallel implementations



- 1 For each connected component, find adjacent edge with minimum weight
- 2 Add edge to mst (each edge add at most twice)
- 3 Merge connected components



```
1:  $A = \emptyset$ 
2: for all  $v \in G.V$  do
3:   MAKE-SET( $v$ )
4: end for
5: Sort (asc.)  $(weight(u, v))_{(u,v) \in G.E}$ 
6: for all  $(u, v)$  in  $G.E$  ordered by weight do
7:   if FIND-SET( $u$ )  $\neq$  FIND-SET( $v$ ) then
8:      $A = A \cup (u, v)$ 
9:     UNION( $u, v$ )
10:  end if
11: end for
12: return  $A$ 
```



- Boost-Kruskal used as a reference



Parallel sorting on Kruskal





S_p is the speedup with p cores, f is the part of the program that is sequential.

$$S_p = \frac{1}{\frac{1-f}{p} + f}$$
$$f = \frac{\frac{p}{S_p} - 1}{p - 1}$$



Graph: Erdos-Renyi (100,000 nodes, $p = 0.0005$)

Cores	Median speed-up	Standard deviation	f
1	1	0.0129805395	-
2	1.1881513396	0.0400305172	0.6832872491
4	1.3340592415	0.0130798641	0.6661225318
8	1.3134515984	0.01048841	0.7272602975
16	1.4399618642	0.0088220116	0.6740936918
32	1.3877640643	0.0442081933	0.7115701488



Graph: Preferential attachment (10,000 nodes, 1,000 edges per vertex)

Cores	Median speed-up	Standard deviation	f
1	1	0.174182691	-
2	1.6268639022	0.2472258016	0.2293591353
4	2.669168898	0.5213238241	0.1661979381
8	5.3584384444	0.9757941767	0.0704246098
16	5.7447285937	1.108109986	0.1190108026
32	5.6322979489	1.497976882	0.1510166972



Same complexity, but Sollin computing steps are more fine-grained
Sollin is entirely paralelizable
Filter Kruskal can be adapted to Filter Sollin





Results overview







