Graph-based analysis of biochemical networks

Concepts of graph theory

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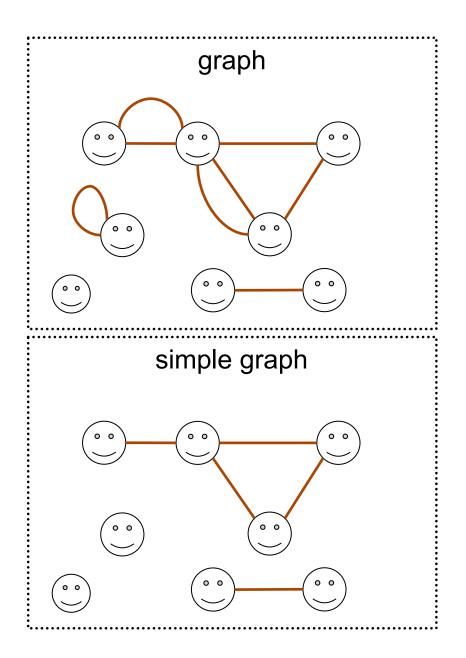
- Basic concepts of graph theory
 - Definitions
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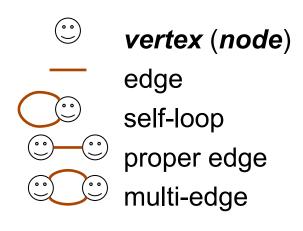
DEA in Bioinformatics 2001

Basic concepts of graph theory

Basic concepts of graph theory

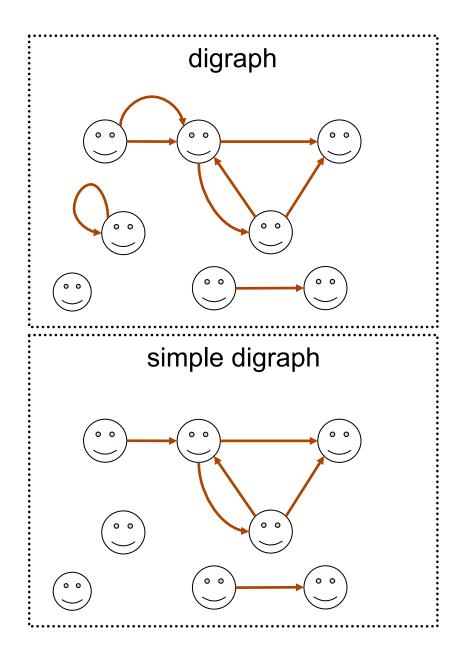
Graph definitions

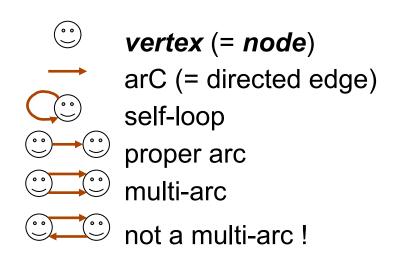




- A grapH (G) contains a set of vertices (V) and a set of edges (E)
- A simple graph contains no self-loop and no multi-edge

Directed GrapH (= Digraph)





- A directed edgD (or arc) is characterized by a head and a tail
- A digraph is a graph whose edges are directed
- A partially directed graph is a graph combining directed and non-directed edges

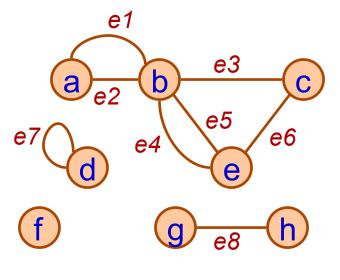
Basic concepts of graph theory

Graph descriptions

Graph descriptions : incidence matrix

- one row per edge
- one colum per vertex
- value = 1 if edge and vertex are incident
- Problems
 - only valid for undirected graphs
 - inefficient storagD (many empty cells)

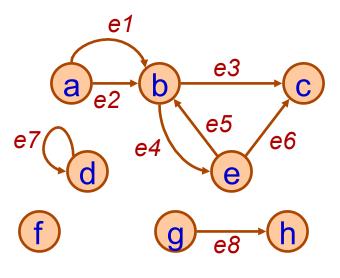
edge\vertex	a	b	С	d	е	f	g	h
e1	1	1	0	0	0	0	0	0
e2	1	1	0	0	0	0	0	0
e3	0	1	1	0	0	0	0	0
e4	0	1	0	0	1	0	0	0
e5	0	1	0	0	1	0	0	0
e6	0	0	1	0	1	0	0	0
e7	0	0	0	0	1	0	0	0
e8	0	0	0	0	0	0	1	1



Graph descriptions : adjacency matrix

- one row per vertex
- one colum per vertex
- value = 1 if vertices are adjacent
- diagonal = self-loops
- Problems
 - no possibility to represent multi-arcs
 - inefficient storagD (many empty cells)

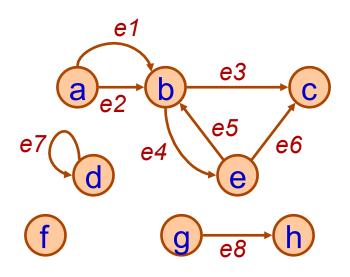
from\to	a	b	С	d	е	f	g	h
a	0	1	0	0	0	0	0	0
b	0	0	1	0	1	0	0	0
C	0	0	0	0	0	0	0	0
d	0	0	0	1	0	0	0	0
е	0	1	1	0	0	0	0	0
f	0	0	0	0	0	0	0	0
g	0	0	0	0	0	0	0	1
h	0	0	0	0	0	0	0	0



Graph descriptions : adjacency list

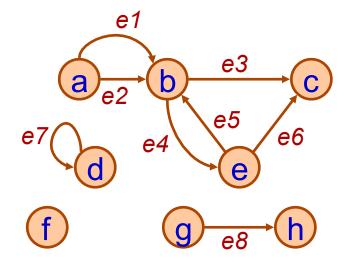
- A list of out-going vertices is associated to each vertex
- Compact representation
- Optionally, a list of in-going vertices can be added to allow reverse-traversal of the graph

Vertex	out	in
а	(b,b)	()
b	(c,e)	(a,e)
C	()	(b,e)
d	(d)	(d)
е	(b,c)	(b)
f	()	()
g	(h)	()
h	()	(h)



Graph descriptions : formal description

- one row per edge
- one column for heads
- one column for tails
- optional columns for edge attributes (label, weight, color, ...)



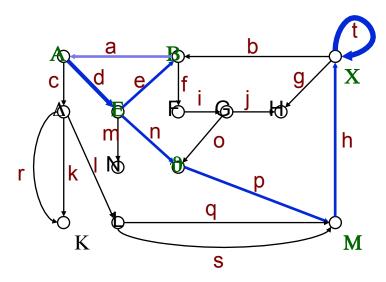
head	tail	label
а	b	e1
а	b	e2
b	С	e3
b	е	e4
е	b	e5
е	С	e6
d	d	e7
g	h	e8

Basic concepts of graph theory

Walks, trails and paths

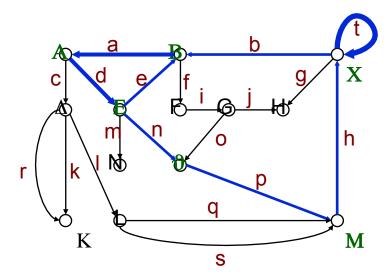
Walk

- A walk from vertex A to vertex B is an alternating sequence of vertices and edges, representing a continuous traversal from A to B
- Remarks
 - □ A walk can be described unequivocally by the sequence of edges (e.g.: d, e, a, d, n,p,h,t,t,t)
 - In a non-simple grapH (i.e. with multi-edges), a walk is not described unequivocally by a sequence of vertices
 - An edge or a vertex can appear repeatedly in the same walk
 (e.g.: edges d and t, and vertices α, ε, χ on the figure)



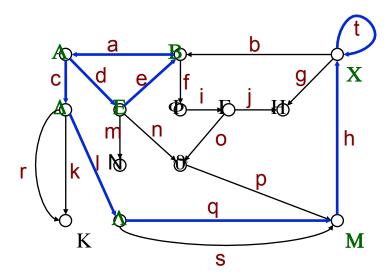
Closed walk

A closed walk is a walk whose initial and final vertices are identical (e.g.: d, e, a, d, n,p,h,t,t,t,b,a)



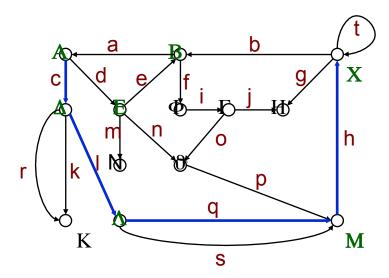
Trail

- A trail is a walk with no repeated edges (e.g.: d, e, a, c,l,q,h,t)
- Remark: a vertex can appear repeatedly in the same traiL (e.g.: α and χ on the figure)



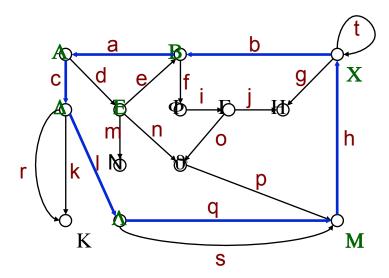
Path

A path is a trail with no repeated vertices, except possibly the initial and final vertex (e.g. c,l,q,h)



Path

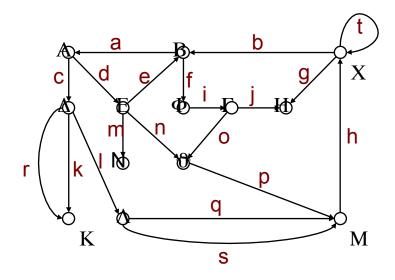
A cycle is a closed path with at least one edge (e.g. c,l,q,h,b,a)



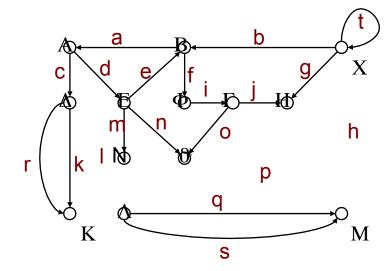
Connected graph

 a connected graph is a graph in which there is a walk between every pair of distinct vertices

Connected graph



Non-connected graph



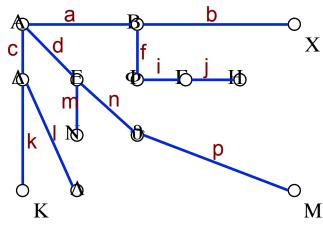
Basic concepts of graph theory

Trees

Tree

a *tree* is a connected graph that has no cycles

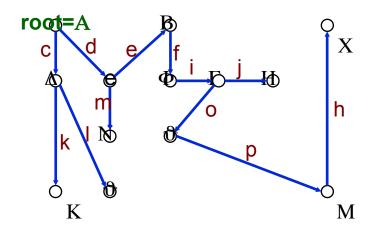
Tree

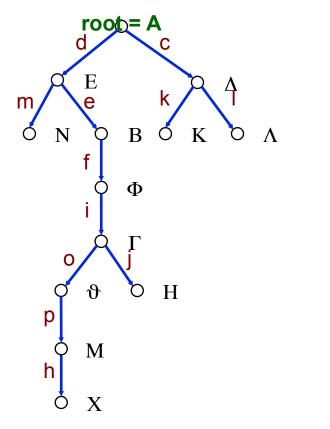


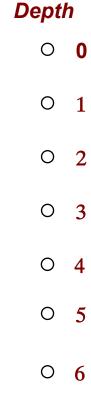
Rooted tree

- A **rooted tree** is a directed tree having a distinguished vertex *r* called the **root** such that for each other vertex *v*, there is a directed path from the root to *v*
- Each non-root node has a single parent

Rooted tree





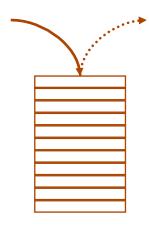


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0

Queue and stack

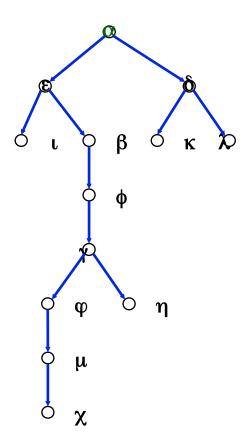




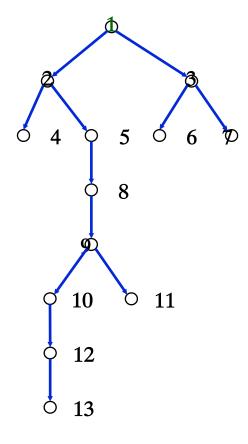
- A queue is a sequence of elements such that each new element is addeD (enqueued) to one end, called the back of the queue, and an element is removeD (dequeued) from the other end, called the front
- A stack is a sequence of elements such that each new element is addeD (or pushed) onto one end, called the top, and an element is removeD (popped) from the same end

Level-order tree traversal with a queue

- Enqueue root
- While queue is not empty
 - Dequeue a vertex and write it to the output list
 - Enqueue its children left-to-right

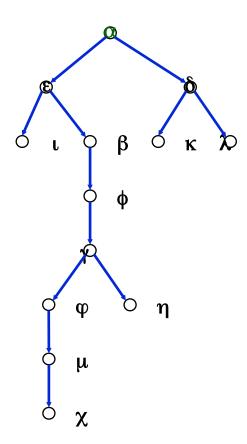


Step	Output	Queue
0		α
1	α	ε,δ
2	3	δ , ι , β
3	δ	ι,β,κ,λ
4	l	β,κ,λ
5	β	κ,λ,φ
6	ĸ	λ,φ
7	λ	φ
8	φ	γ
9	γ	φ,η
10	φ	η,μ
11	η	μ,χ
12	μ	χ
13	χ.	

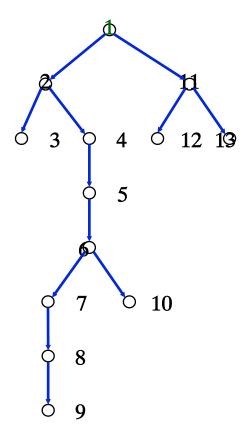


Pre-order tree traversal with a stack

- Push root onto the stack
- While stack is not empty
 - Pop a vertex off stack, and write it to the output list
 - Push its children right-to-left onto stack



Step	Output	Stack
0		α
1	α	δ,ε
2	ε	δ,β,ι
3	ı	δ,β
4	β	δ,φ
5	ф	δ,γ
6	γ	δ,η,φ
7	φ	δ,η,μ
8	$\overset{\cdot}{\mu}$	δ,η,χ
9	χ	δ,η
10	η	δ
11	δ	λ,κ
12	ĸ	λ
13	λ	



Basic concepts of graph theory

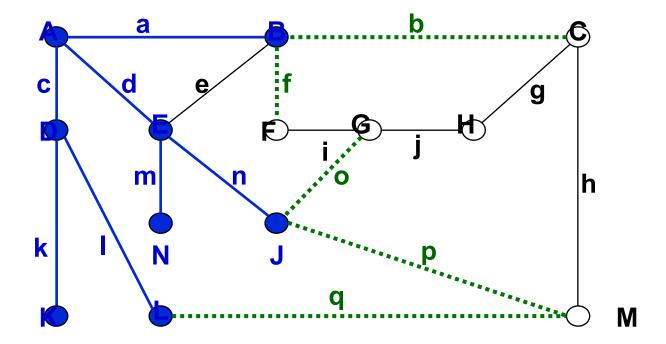
Path finding

Path finding in biochemical networks

- 2-ends path finding
 - Find all pathways from compound A to compound B
- 1-end path finding
 - Find all genes regulated by a membrane receptor via a signal transduction pathway
- 1-end path finding, reverse
 - Find all proteins and compounds exerting a direct or indirect action on the level of expression of a given gene
- Circuit finding
 - Find all feed-back loops
- Subgraph extraction
 - Starting from a set of n seed nodes, extract a subgraph that joins "at best" the seeds.
 - Unweighted graphs: minimize the number of edges of the subgrpah
 - Weighted graphs: minimize the weight of the subgraph

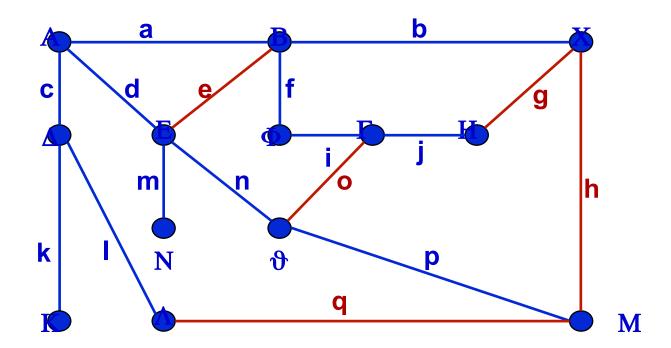
Tree in a graph

- A tree T in a graph G is a connected subgraph which contains no cycle
- The edges and vertices of T are called *tree-edges* and *tree-vertices*
- A frontier-edge is a non-tree edge with one endpoint in T and one endpoint not in T.



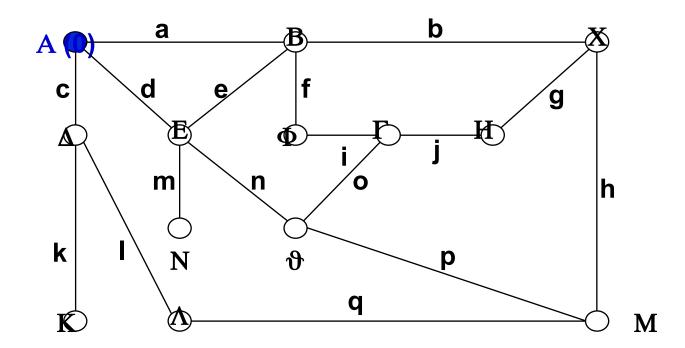
Spanning tree

- A spanning tree is a tree which contains all the vertices of a graph
- A spanning tree does not necessarily contain all the edges
- A fundamental cycle in the graph G is the unique cycle which is created when a non-tree edge is added to the spanning tree T
- Each non-tree edge corresponds to a fundamental cycle in the graph

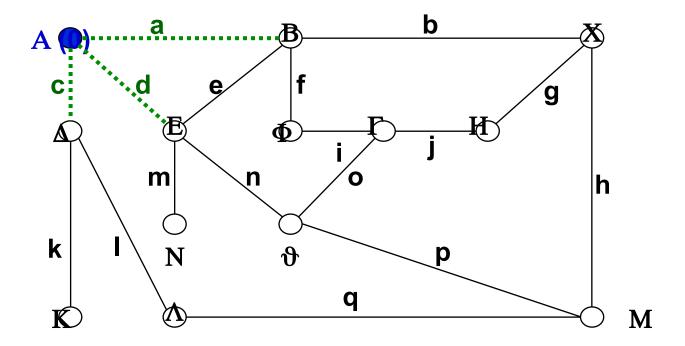


Depth-first-searcH (DFS)

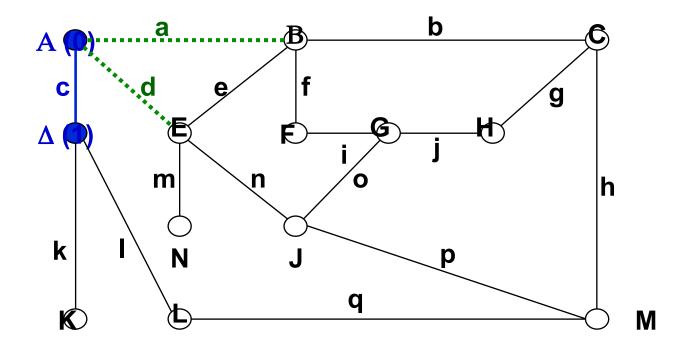
- Initialize tree at a given vertex (for example a)
- Initialize the set of frontier edges as empty
- Set dfnumber(a) to 0
- Initialize label counter i to 1



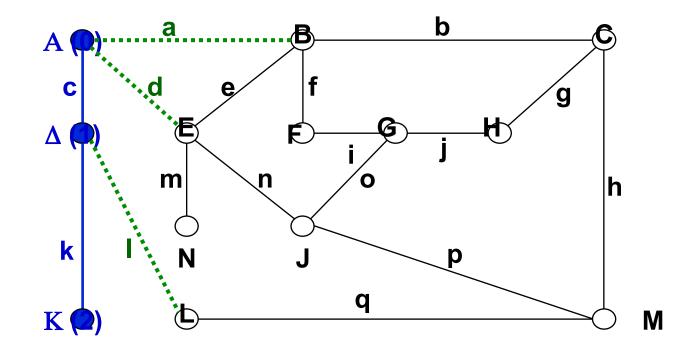
- While T does not span G
 - update the set of frontier edges



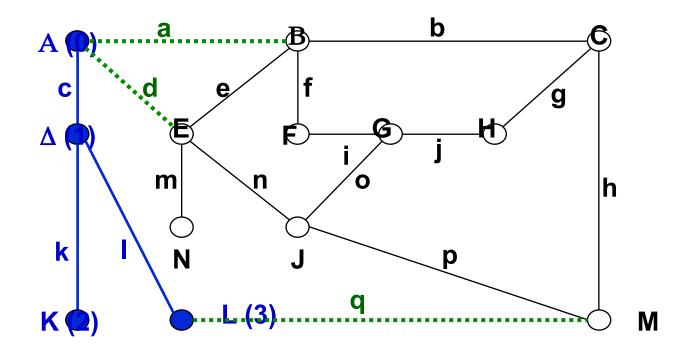
- While T does not span G
 - update the set of frontier edges
 - select a frontier edge whose labelled endpoint has the largest possible dfnumber
 - add this edge to the tree
 - select the unlabelled endpoint of this edge, and set its dfnumber to i
 - □ i := i+1



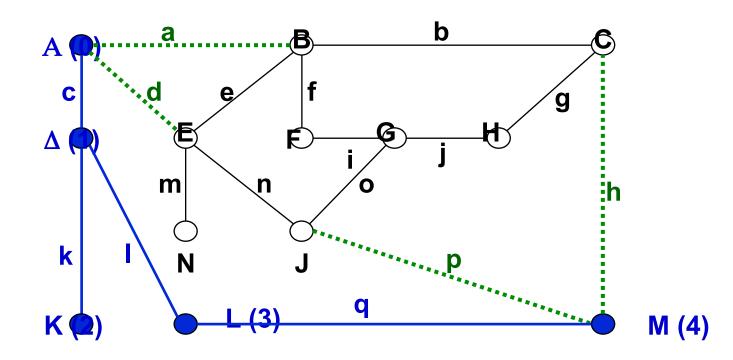
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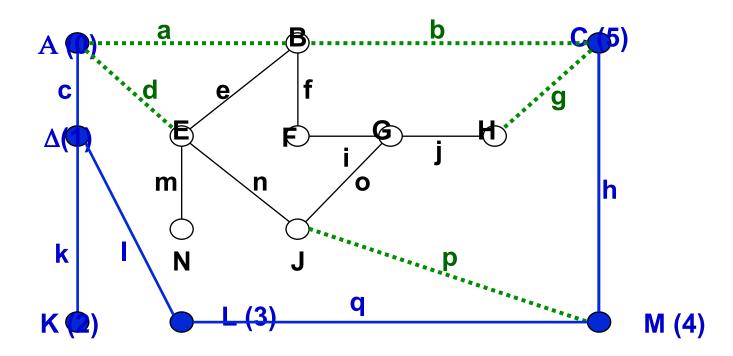
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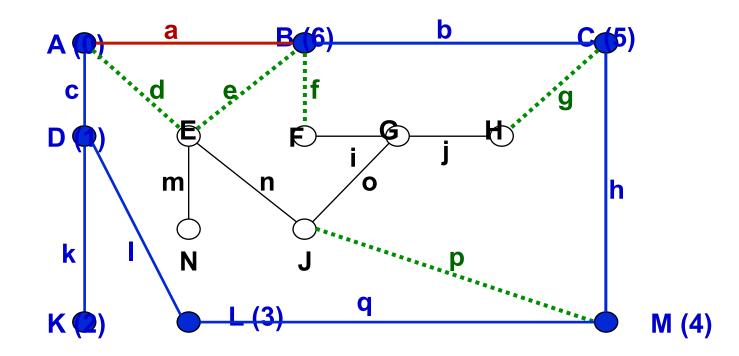
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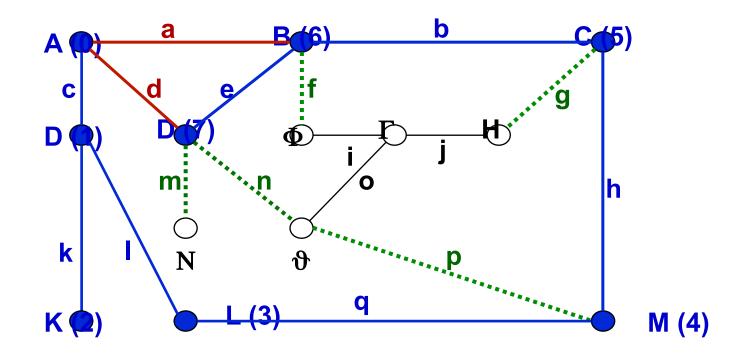
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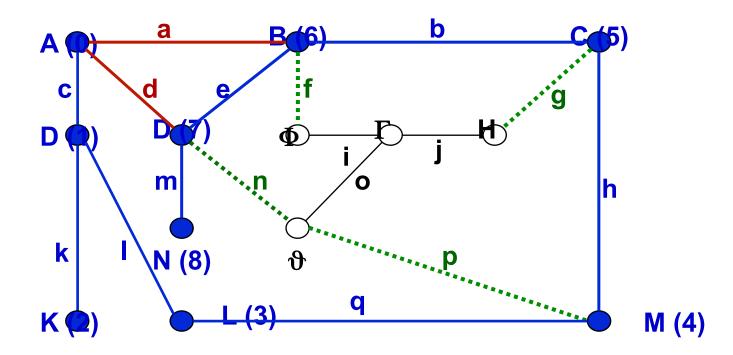
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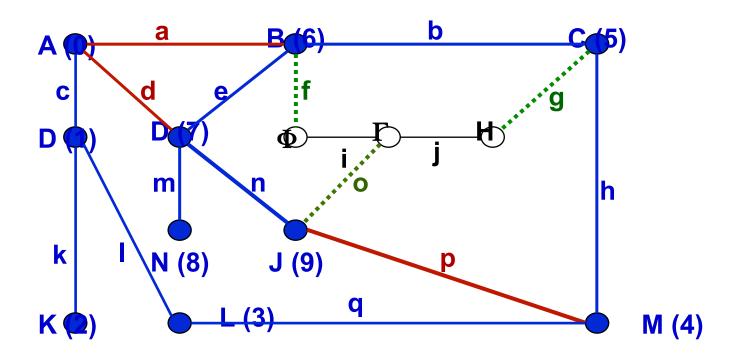
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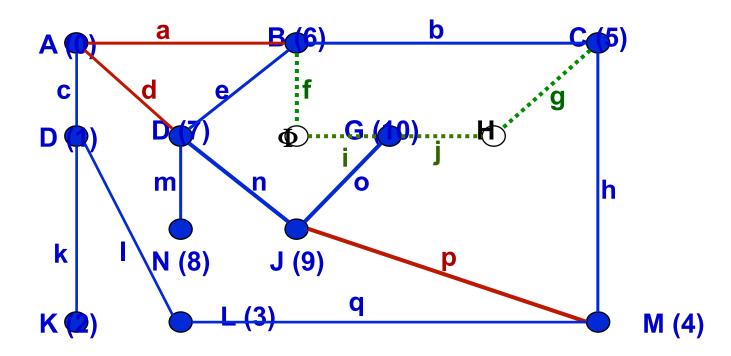
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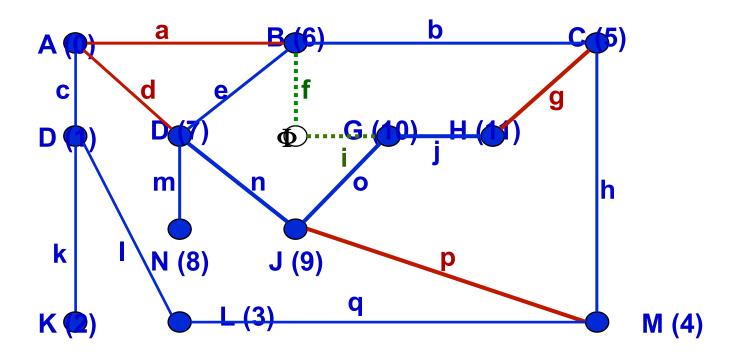
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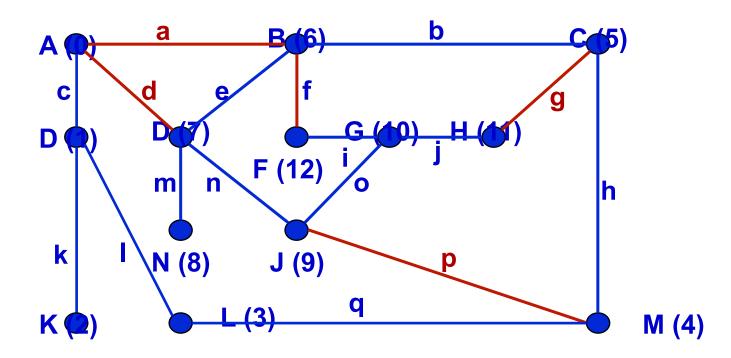
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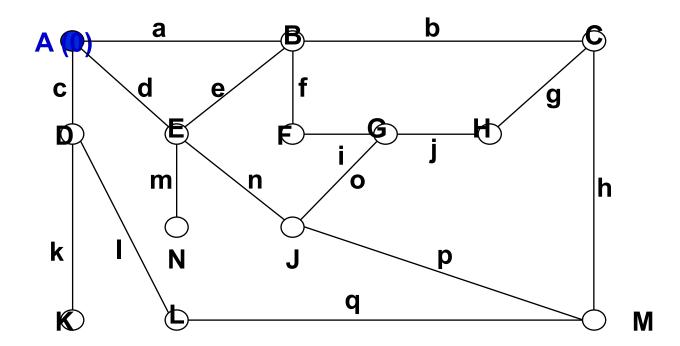


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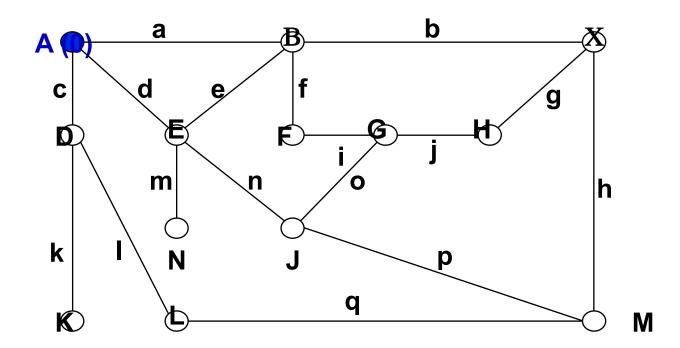
Breadth-first-searcH (BFS)

- Initialize tree at a given vertex (for example a)
- Initialize the set of frontier edges as empty
- Write label 0 on vertex a
- Initialize label counter i to 1

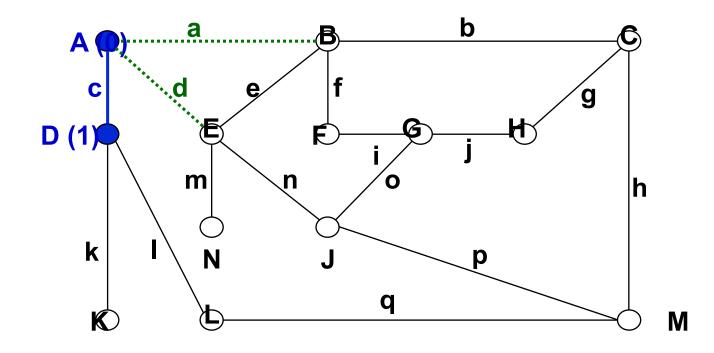


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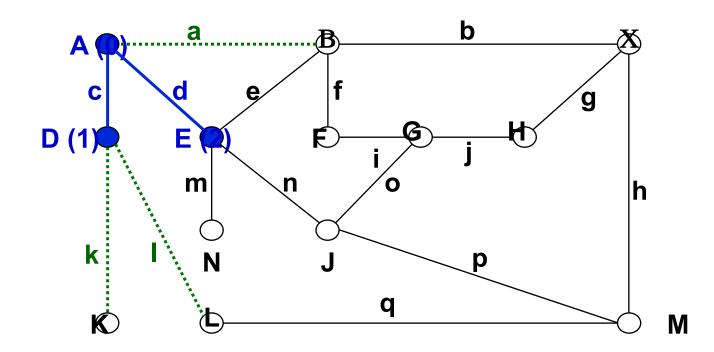
- While T does not span G
 - update the set of frontier edges
 - select a frontier edge for which the labeled endpoint has the smallest possible label
 - add edge to the tree T
 - select the unlabelled vertex of the edge and set its label to i
 - increment N (i := 1+1)



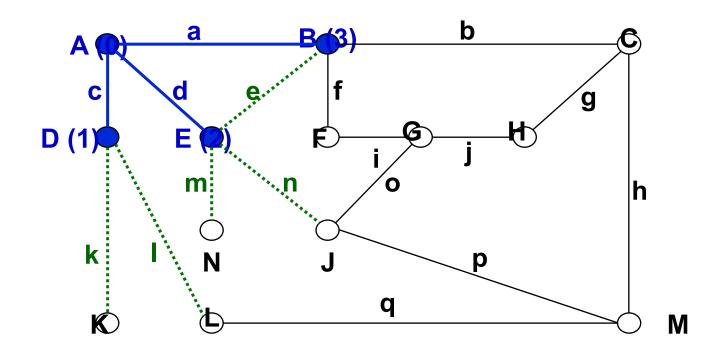
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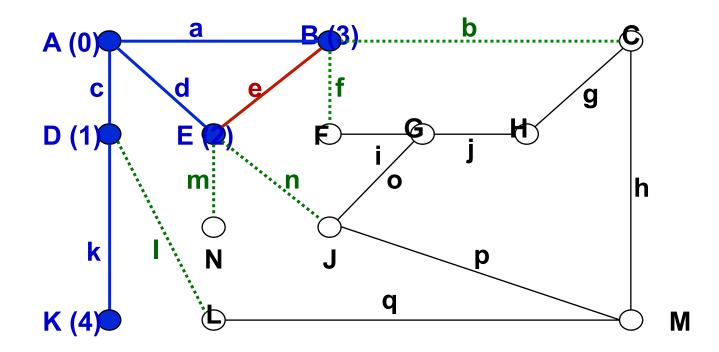
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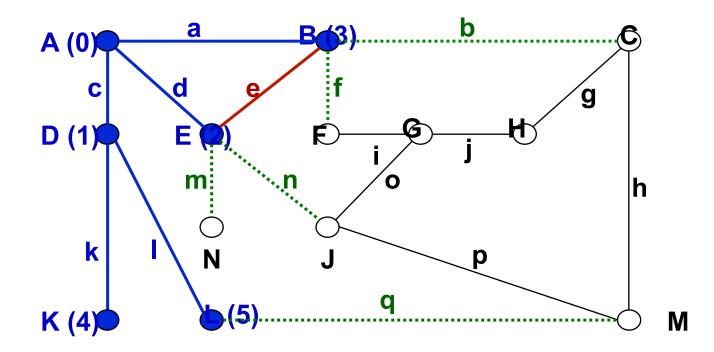
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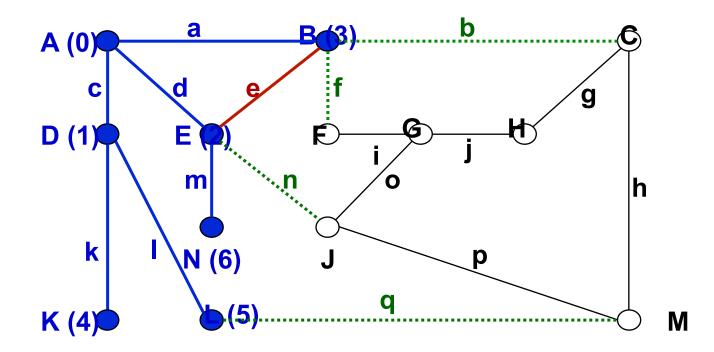
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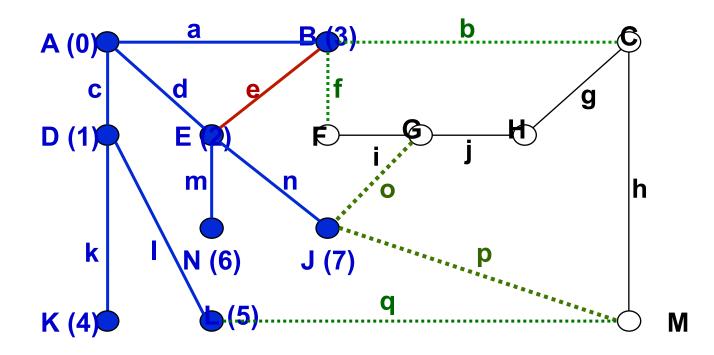
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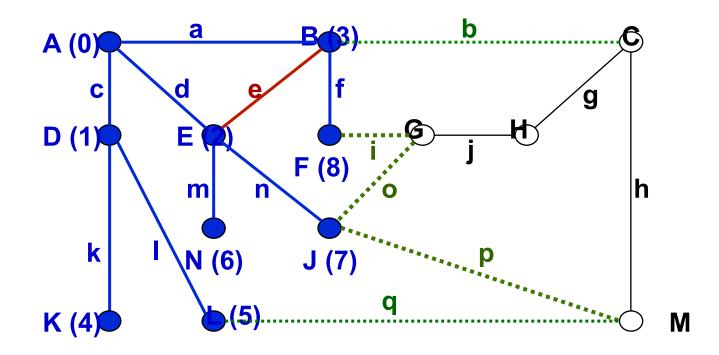
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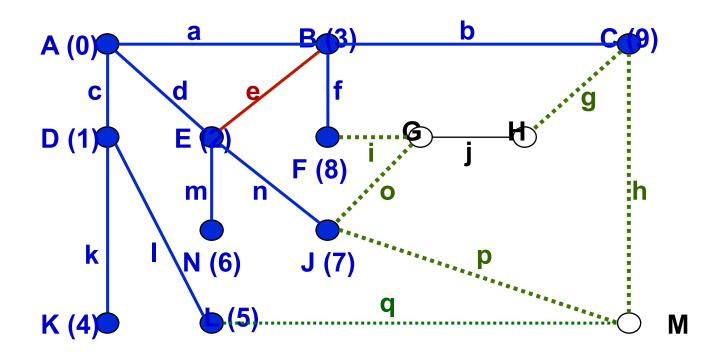
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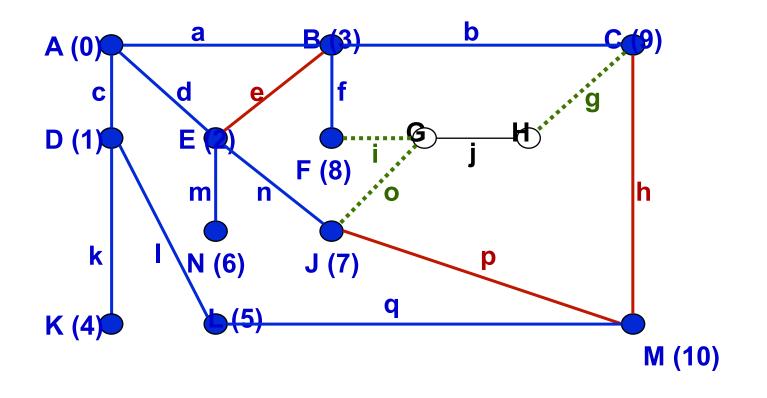
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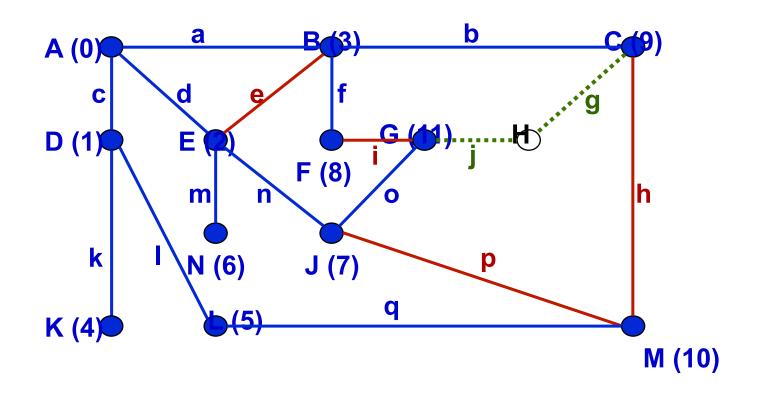


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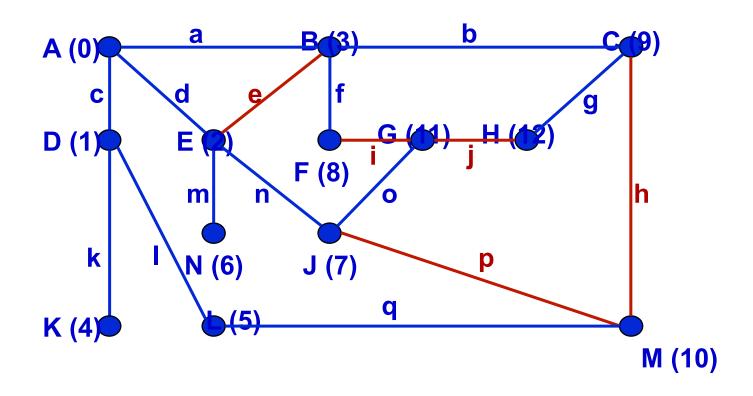


i=11

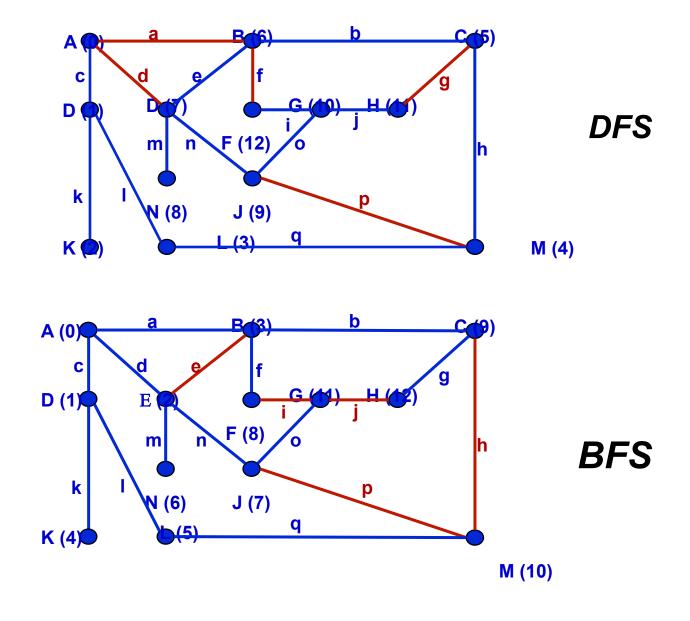
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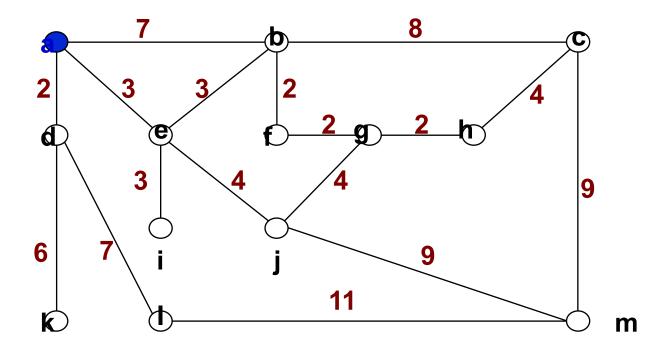
- While T does not span G
 - update the set of frontier edges
 - select a frontier edge for which the labeled endpoint has the smallest possible label
 - add edge to the tree T
 - select the unlabelled vertex of the edge and set its label to i
 - increment N (i := i+1)



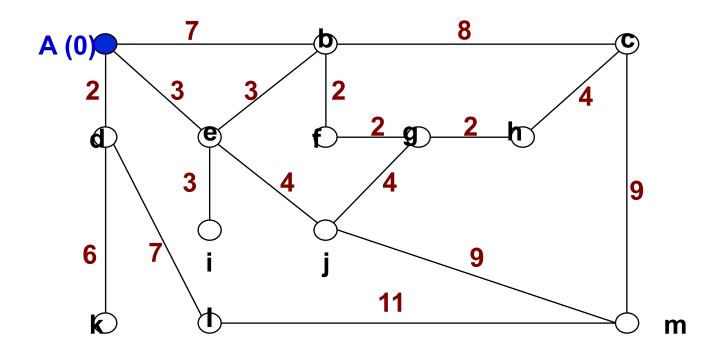
Result comparison : DFS versus BFS



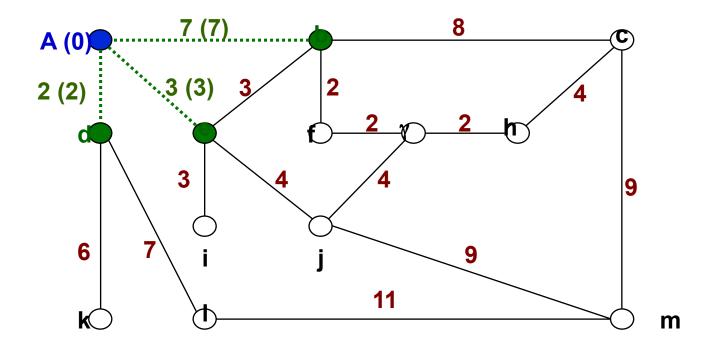
- Input: a weighted connected graph G whose edge-weights are non-negative, and a starting vertex a
- Output: a spanning tree, rooted at a, whose path from each vertex v is the shortest path from a to v in G; the vertex-labelling gives the distance from s to each vertex



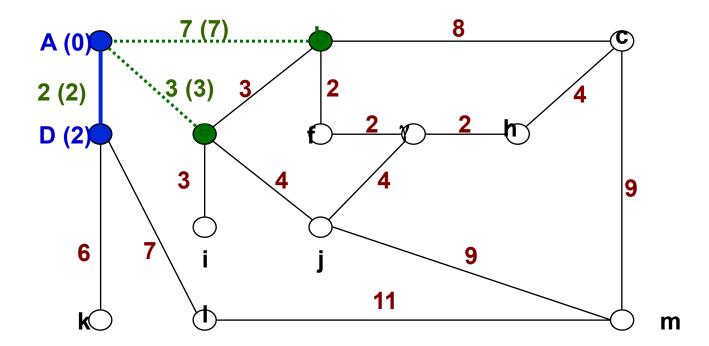
- Initialise the Dijkstra tree T as vertex a
- dist[a] = 0
- write label 0 on vertex a



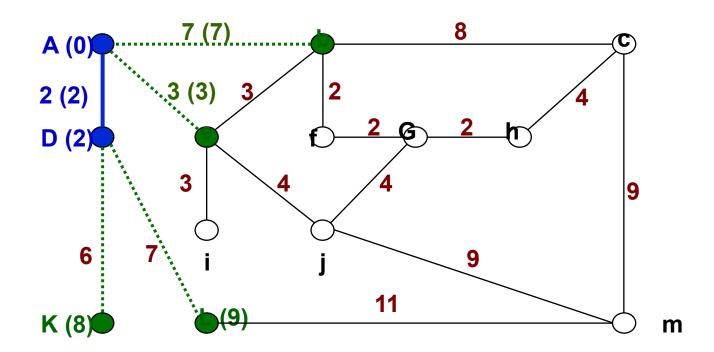
- While T does not span G
 - Update frontier edges
 - For each frontier edge e
 - let x be the labelled and y the unlabelled endpoints of e
 - set **D(e)** = dist[x] + w(e)



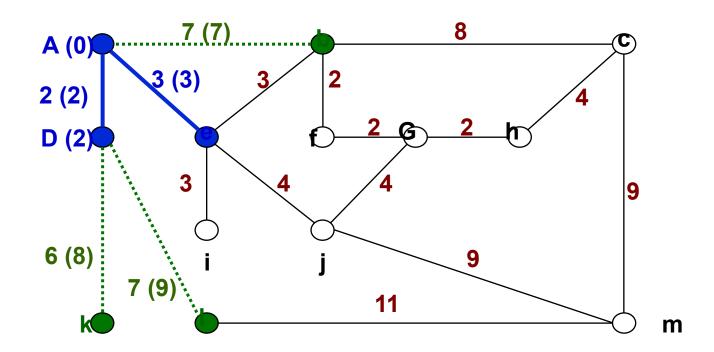
- While T does not span G
 - Update frontier edges
 - For each frontier edge e
 - let x be the labelled and y the unlabelled endpoints of e
 - set **D(e)** = dist[x] + w(e)
 - Let e be a frontier edge that has the smallest D-value
 - Add edge e to T, and set dist[y] = D(e)



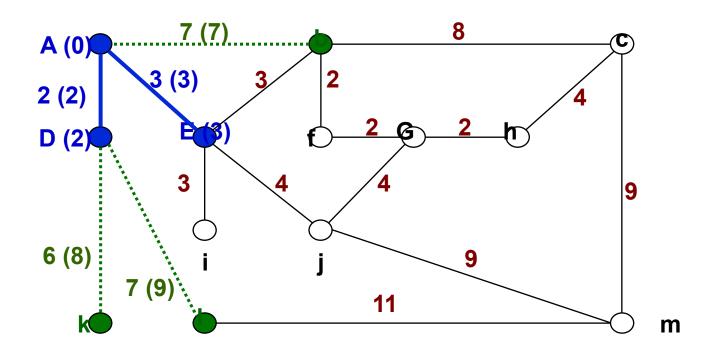
- While T does not span G
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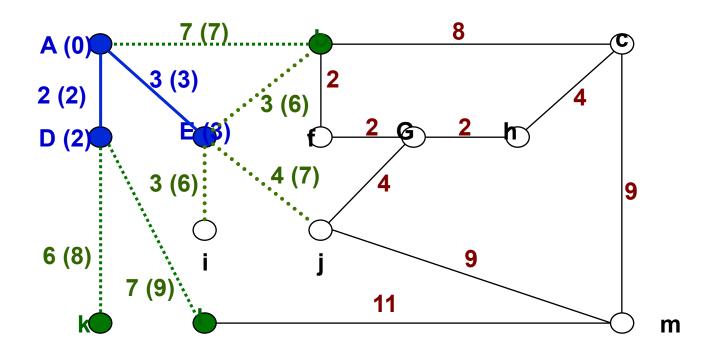
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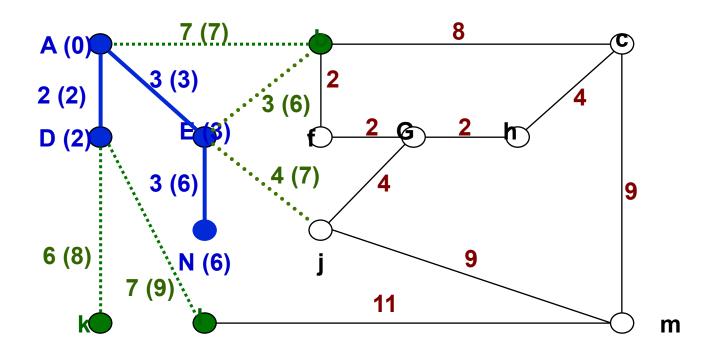
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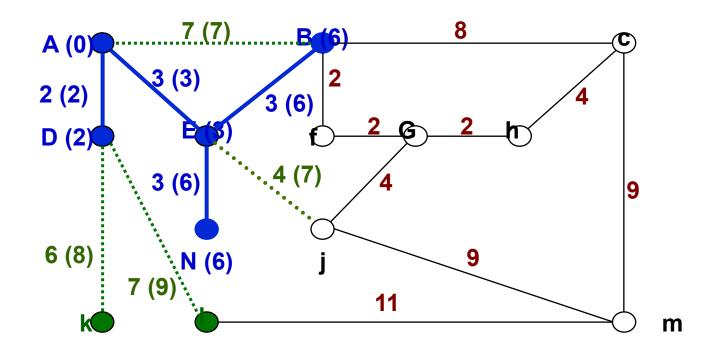
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Exercise

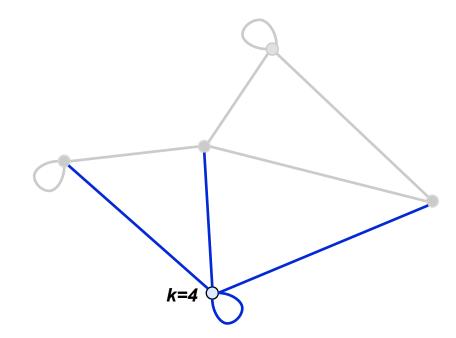
 Follow the Dijkstra algorithm until all the vertices of the preceding graph are labelled.

Graph topology

Degree - definition

- In a non-directed graph
 - \Box The degree (k) of a node is the number of edges for which it is an endpoint.
- In a directed graph
 - The in-degree (k_{in}) of a node is the number of arcs for which it is the tail.
 - \Box The out-degree (k_{out}) of a node is the number of arcs for which it is the head.
 - □ The total degree (k) of a node is the sum of in-degree and out-degree

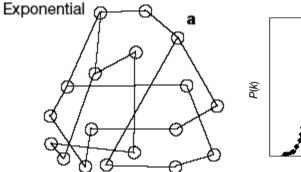
•
$$k=k_{in}+k_{out}$$

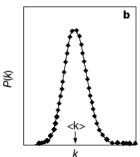


Stochastic models for the degree distribution of a graph

Homogeneous networks

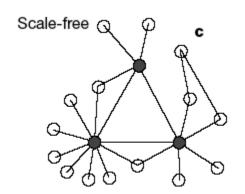
- Erdös-Rényi model (ER model)
- Pairs of nodes are connected with a constant random probability
- The connectivity follows a Poisson law
 - $P(k) \sim \lambda^k e^{-\lambda}/k!$
 - λ mean number of connections per node
 - k number of connections for a given node
- The probability of finding a highly connected node decreases exponentially with connectivity.

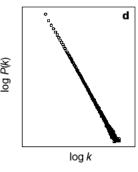




Scale-free networks

- A few nodes are highly connected, most nodes are poorly connected.
- Can be generated randomly with a model where new nodes are preferentially connected to already established nodes
- The connectivity follows a power law
 - $P(k) = Ck^{-\gamma} <=> log(P) = -y * log(k) + log(C)$
 - γ the slope of the distribution in a log-log graph.
 - k number of connections for a given node

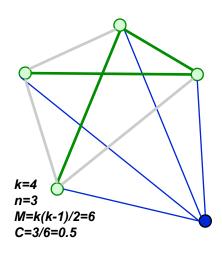




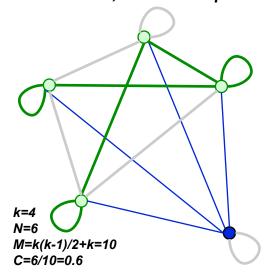
Clustering coefficient

- The clustering coefficient of a node i indicates the density of arcs among its neighbours.
- It is computed as the ratio between the number of arcs
 (n) between the neighbours, and the maximal number
 of such arcs (M).
- The maximal number of arcs depends on the graph type
 - Directed or undirected
 - With or without self-loops

Undirected, without self-loops



Undirected, with self-loops



$$C_i = \frac{n}{M}$$

Directed, self - loops

$$C_i = \frac{n}{k_i^2}$$

Directed, no self - loop

$$C_i = \frac{n}{k_i(k_i - 1)}$$

Undirected, self - loops

$$C_i = \frac{n}{M} = \frac{2n}{k_i(k_i + 1)}$$

Undirected, no self - loop

$$C_i = \frac{n}{M} = \frac{2n}{k_i(k_i - 1)}$$

Suggested readings

 Gross, J. & Yellen, J. (1999). Graph theory and its applications. Discrete mathematics and its applications (Rosen, K. H., Ed.), CRC press, London