# Greedy algorithms

CMPSC 465 - Yana Safonova

# Disjoint sets or union-find sets or merge-find sets

## Optimized disjoint set - implementation

```
#finding root of an element
def root(Arr, i):
    while Arr[ i ] != i:
        i = Arr[ i ]
    return i
def union(Arr, A, B):
    root A = root(Arr, A)
    root B = root(Arr, B)
    Arr[ root_A ] = root_B
def find(Arr, A, B):
    return root(Arr, A)==root(Arr, B)
```

## Optimized disjoint set - only a half-way through!

```
#finding root of an element
A loop is
         def root(Arr, i):
hidden
              while Arr[ i ] != i:
here
              i = Arr[ i ]
               return i
          def union(Arr, A, B):
              root_A = root(Arr, A)
We don't
have a
             root_B = root(Arr, B)
loop here
             Arr[ root_A ] = root_B
anymore
```

```
def find(Arr, A, B):
    return root(Arr, A)==root(Arr, B)
```

0	1	2	3	4	5
0	1	2	3	4	5

0	1	2	3	4	5
0	0	2	3	4	5

Union(1, 0)

0	1	2	3	4	5
2	0	2	3	4	5

Union(1, 0) Union(0, 2)

0	1	2	3	4	5
2	0	3	3	4	5

Union(1, 0)

Union(0, 2)

Union(2, 3)

0	1	2	3	4	5
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Union(1, 0)

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Union(2, 3)

Union(3, 4)

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2	0	3	4	5	5

Union(1, 0)

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Union(3, 4)

Union(4, 5)

0	1	2	3	4	5
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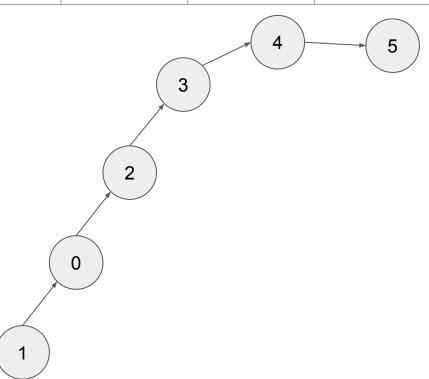
Union(1, 0)

Union(0, 2)

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0	1	2	3	4	5
2	0	3	4	5	5

Union(1, 0)

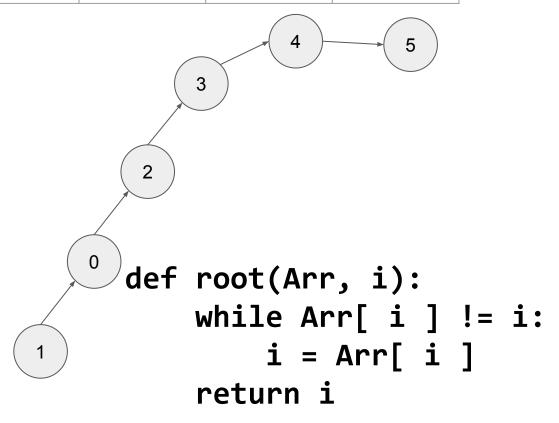
Union(0, 2)

Union(2, 3)

Union(3, 4)

Union(4, 5)

Still O(N)!



# **Disjoint sets**

- Stores non-overlapping sets
- Union(a, b) = merges sets where a and b are located
- Find(a, b) = tells whether or not a and b are located in the same set

	Naive implementation	Semi-optimized implementation
Find	O(1)	O(N) - uses root
Union	O(N)	O(N) - uses root
Union for all elements	O(N <sup>2</sup> )	O(N <sup>2</sup> )
Root	-	O(N)

## From semi-optimal to optimized implementation

Consecutive merging elements from left to right (or vice versa) is the worst case scenario for the semi-optimized implementation

The tree representing all unions looks like a single branch in this case

```
3
def root(Arr, i):
    while Arr[ i ] != i:
        i = Arr[ i ]
    return i
```

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Do we really care about the shape of the tree representing elements of the same set?

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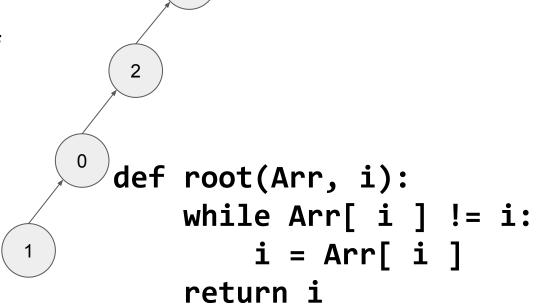
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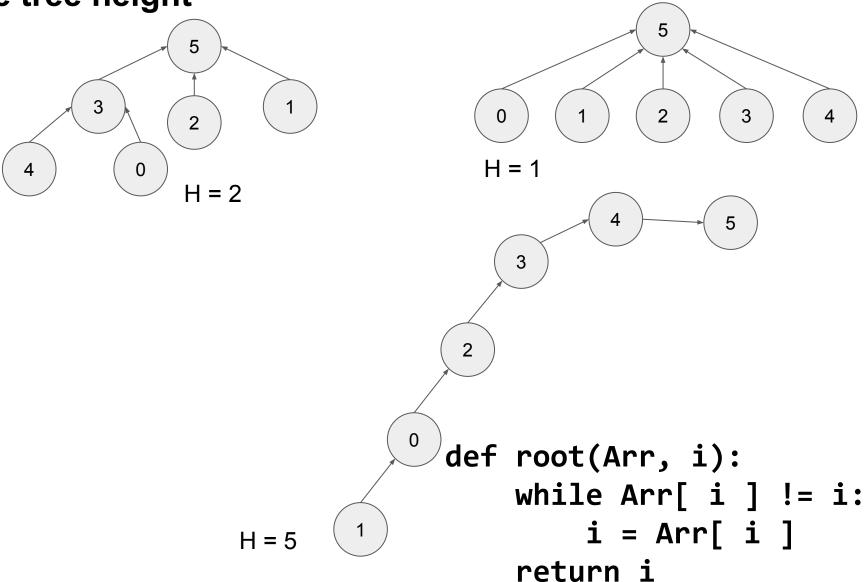
Do we really care about the shape of the tree representing elements of the same set?

No!

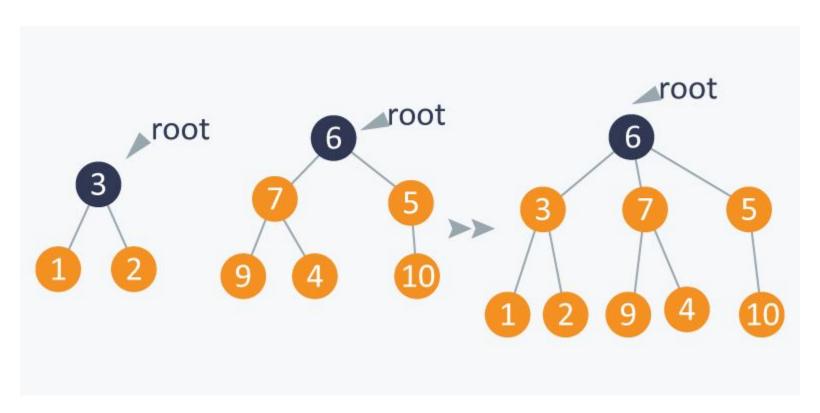


3

The running time of the "root" procedure is defined as the tree height



## Optimized disjoint set: weighted-union operation



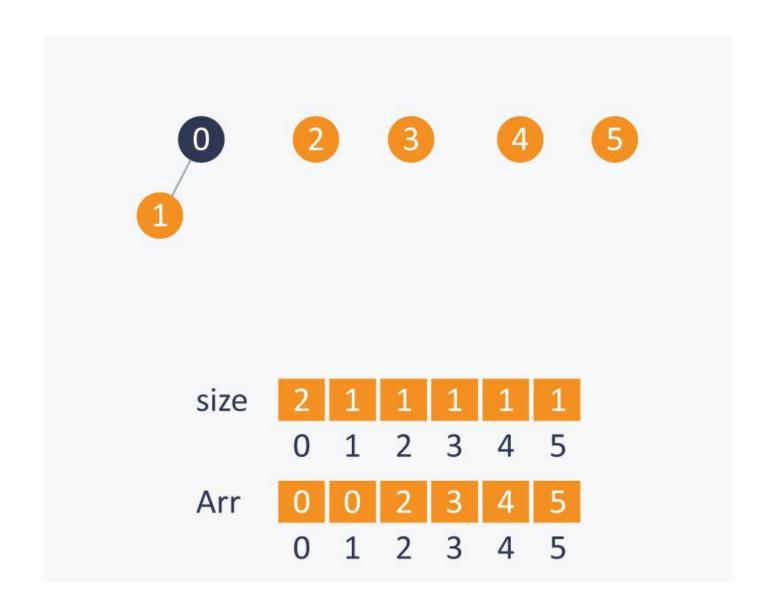
Union(A, B): instead of always merging the left set with the right set, let's merge the smallest set with the biggest one

In terms of trees representing sets, it would mean rerooting the smallest tree

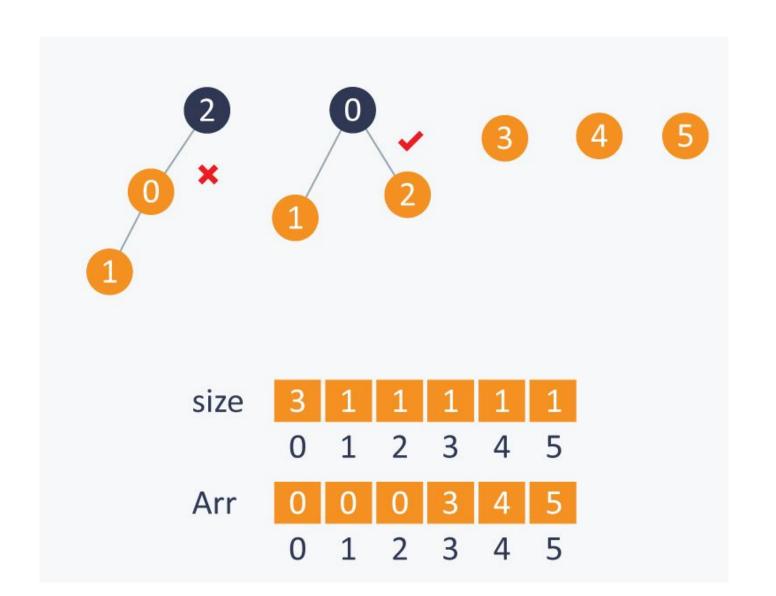
# Weighted-union operation



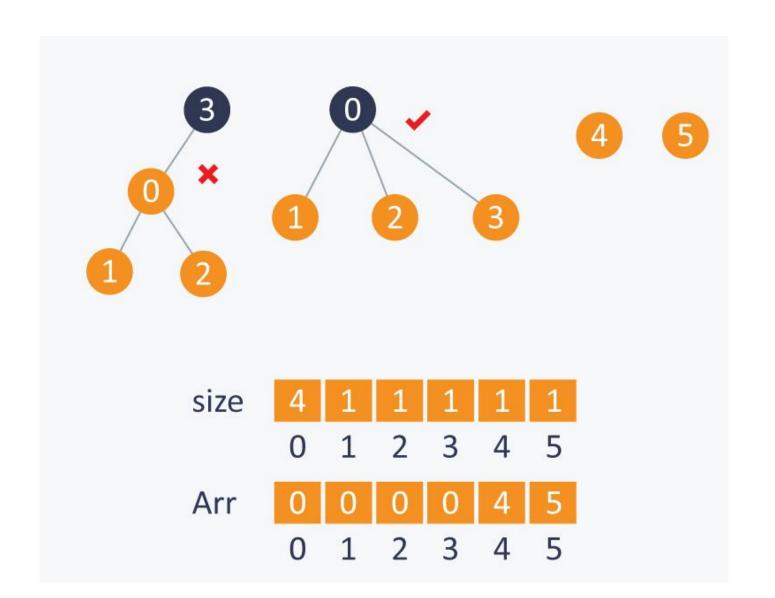
# Weighted-union operation - union(0, 1)



# Weighted-union operation - union(1, 2)



# Weighted-union operation - union(3, 2)



# Weighted-union operation

```
def initialize(Arr, size, N):
    for i in range(N):
        Arr[ i ] = i
        size[ i ] = 1
def weighted_union(Arr, size, A, B):
    root A = root(Arr, A)
    root B = root(Arr, B)
    if size[root_A] < size[root_B]:</pre>
        Arr[root_A] = Arr[root_B]
        size[root B] += size[root A]
    else:
        Arr[root_B] = Arr[root_A]
        size[root A] += size[root B]
```

 If we merge sets represented by trees of different heights, then the height of the resulting tree (tree tree after union) doesn't change

• ?: If we merge sets of the same height H, what would be the height of the resulting tree?

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By merging two elements, we increased the maximum height

 If we merge sets represented by trees of different heights, then the height of the resulting tree (tree tree after union) doesn't change

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To increase the max height further, we need to merge the red set with another set of the same height

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To increase the max height further, we need to merge the red set with another set of the same height > we need to construct it!

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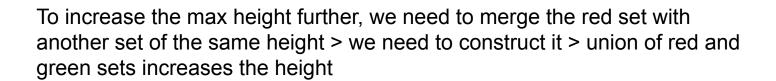
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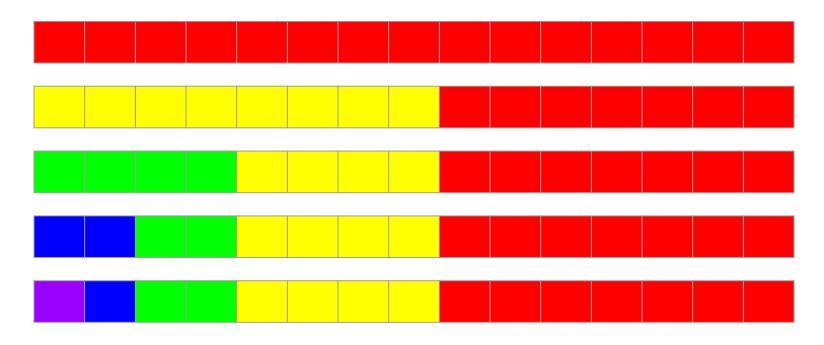
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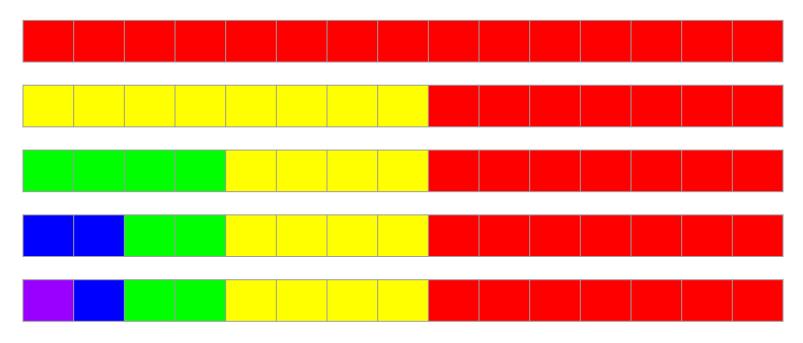
 ?: If we merge sets of the same height H, what would be the height of the resulting tree? (H + 1)

The maximum height is achieved when we merge "similar" sets: represented by trees of the same heights and in the worst case having the same numbers of elements



#### Running time of the "root" procedure

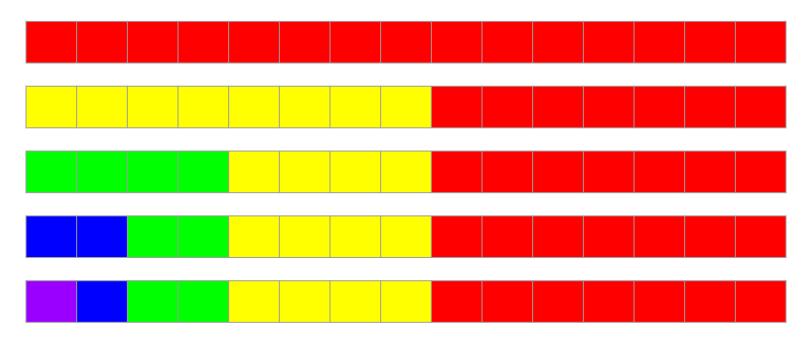
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?: what is the maximum number of unions of sets of the same sizes?

#### Running time of the "root" procedure

The maximum height is achieved when we merge "similar" sets: represented by trees of the same heights and in the worst case having the same numbers of elements



?: what is the maximum number of unions of sets of the same sizes? O(log N)

### **Disjoint sets**

- Stores non-overlapping sets
- Union(a, b) = merges sets where a and b are located
- Find(a, b) = tells whether or not a and b are located in the same set

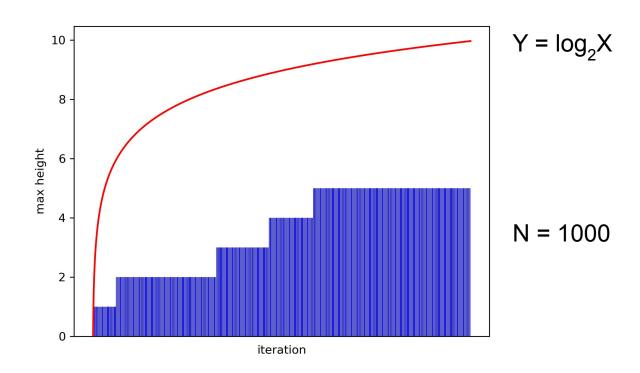
	Naive implementation	Semi-optimized implementation	Weighted-union implementation
Find	O(1)	O(N)	O(logN)
Union	O(N)	O(N)	O(logN)
Union for all elements	O(N <sup>2</sup> )	O(N <sup>2</sup> )	O(NlogN)
Root	-	O(N)	O(logN)

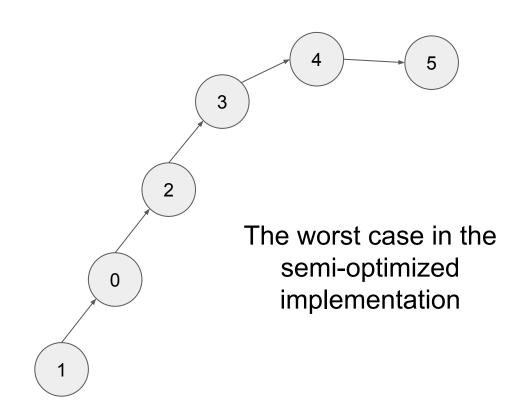
#### **Example - random case**

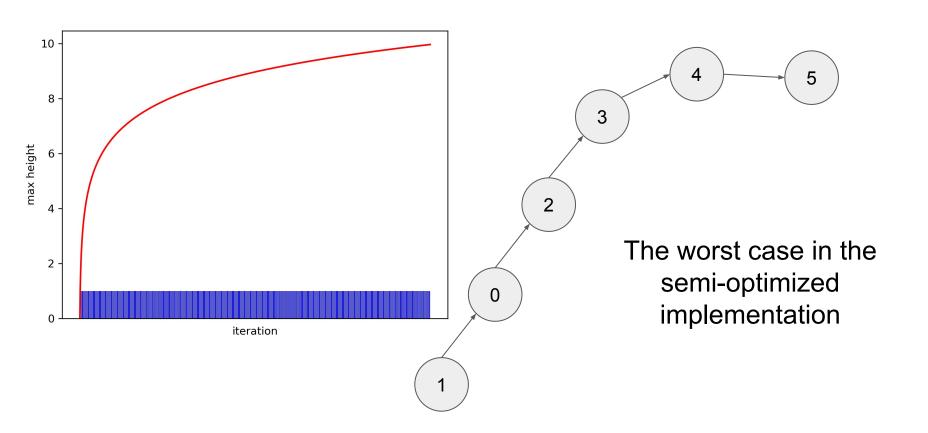
Let's start with N elements and at each step merge two randomly chosen elements

#### **Example - random case**

Let's start with N elements and at each step merge two randomly chosen elements

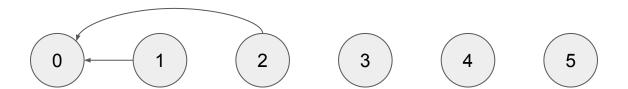


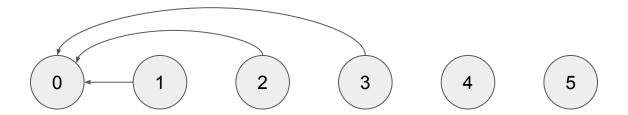


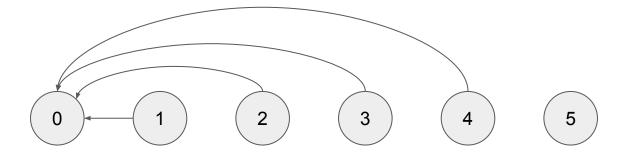


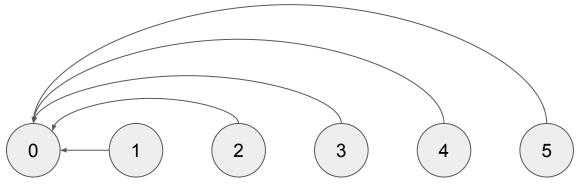


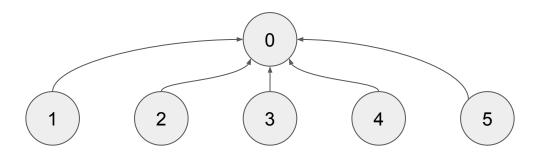












#### Example: how to compute the maximum tree height?

```
def root(Arr, i):
    while Arr[ i ] != i:
        i = Arr[ i ]
    return i
```

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```
def root(Arr, i):
    while Arr[ i ] != i:
        i = Arr[ i ]
    return i
def height(Arr, i):
    H = 0
    while Arr[ i ] != i:
        H += 1
        i = Arr[ i ]
    return H
```

#### Example: how to compute the maximum tree height?

```
def height(Arr, i):
    H = 0
    while Arr[ i ] != i:
        H += 1
        i = Arr[ i ]
    return H

def max_height(Arr, N):
    return max([height(Arr, i) for i in range(N)])
```

### Further optimization of disjoint set

Path compression: requires additional memory but speed up the "find" procedure

Path compression + weighted union:

the amortized time complexity is  $O(\alpha(n))$ ,

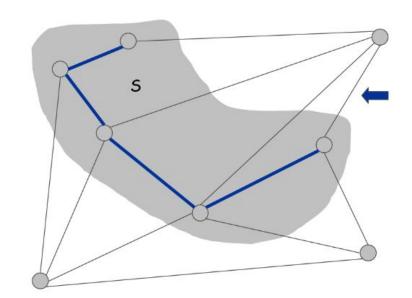
 $\alpha(n)$  is the inverse Ackermann function (a very slowly growing function)

#### Prim's algorithm

Prim's algorithm. Start with some root node s and greedily grow a tree T from s outward. At each step, add the cheapest edge e to T that has exactly one endpoint in T.

- Initialize S = any node.
- Apply cut property to S.
- Add min cost edge in cutset corresponding to S to T, and add one new explored node u to S.

Implementation uses the priority queue similar to the one in Dijkstra algorithm



### Maximum spanning tree?

The algorithms are similar except for:

- Kruskal's algorithm: sort edges in the decreasing order of the weights
- Prim's algorithm: choose the max weight edge
- The cut property: the max weight edge in a cutset is in the MST
- The cycle property: the min weight edge in a cycle is not in the MST

# MST and clustering

### **Application: clustering**

You're given n items and the distance d(u, v) between each of pair.

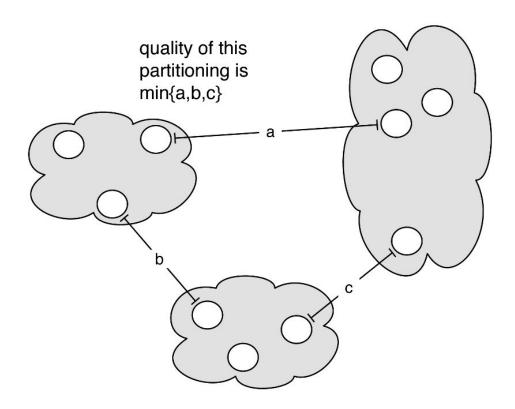
d(u, v) may be an actual distance, or some abstract representation of how dissimilar two things are.

(What's the "distance" between two species?)

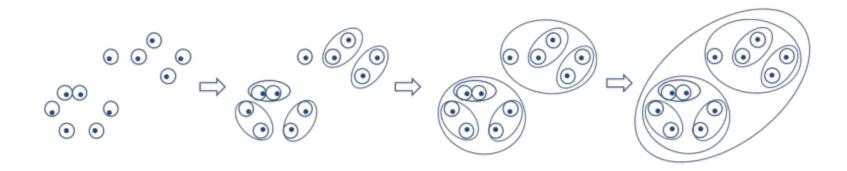
**Our Goal:** Divide the n items up into k groups so that the minimum distance between items in different groups is maximized.

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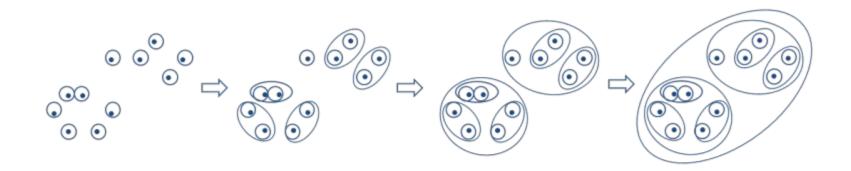


#### Agglomerative clustering: from bottom to top



- 1. Compute distance between each pairs of objects
- 2. Choose a pair (A, B) with the shortest distance
- 3. Combine A & B into the same cluster A'
- 4. Remove A and B from the distance matrix and add A'
- 5. Compute distances from A' to all other objects
- 6. Repeat from 2

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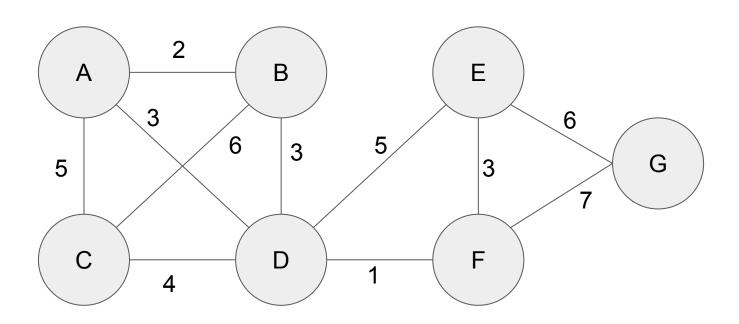


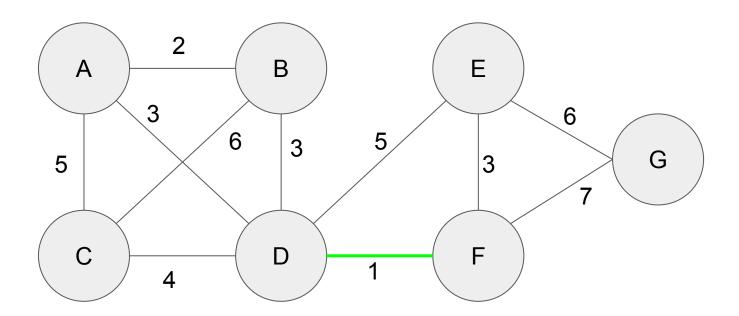
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Single linkage: min{ d(x, y): x in A, y in B }

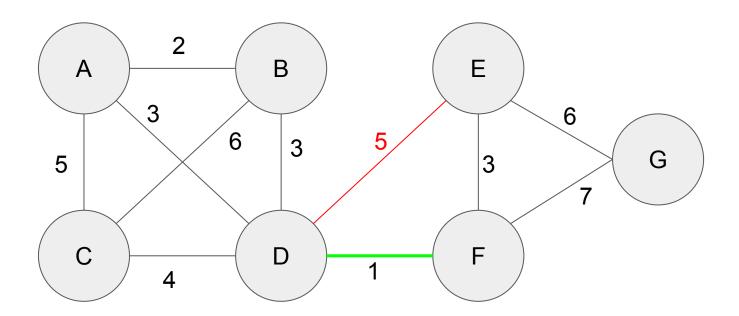
Average clustering: sum{ d(x, y): x in A, y in B } / |A| / |B|

# Kruskal's algorithm aka single-linkage clustering

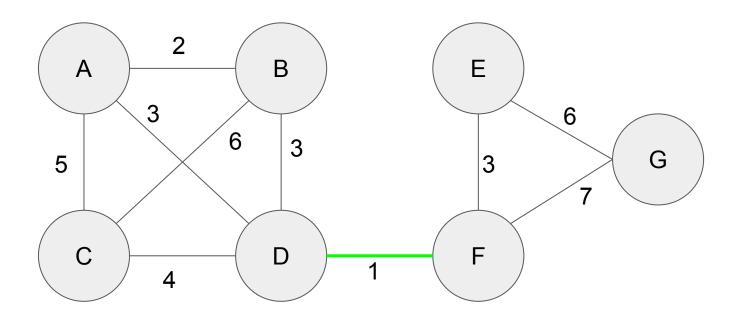




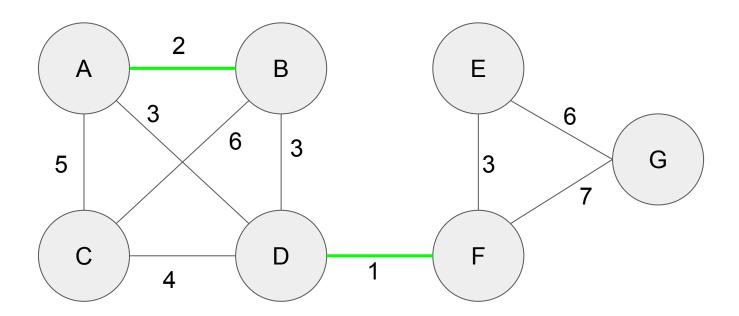


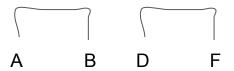


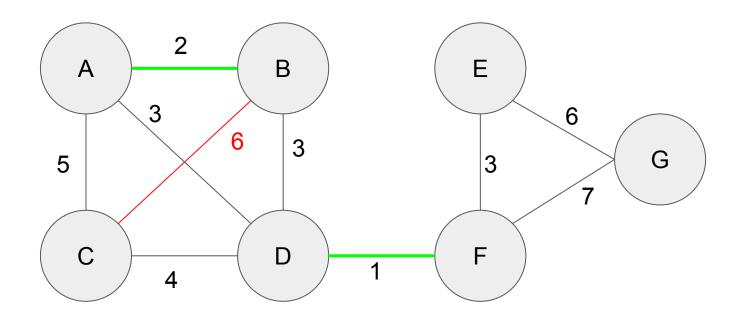


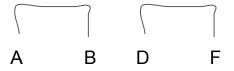


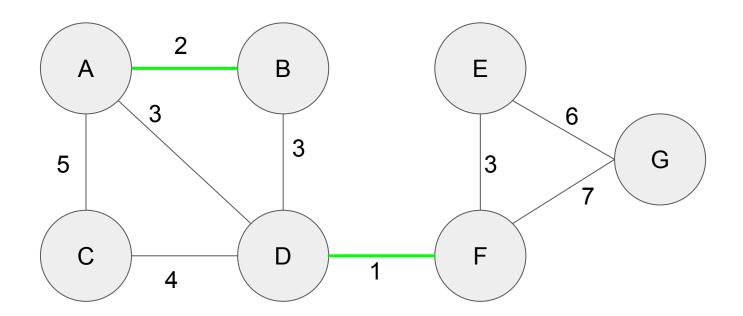


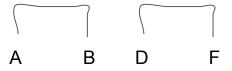


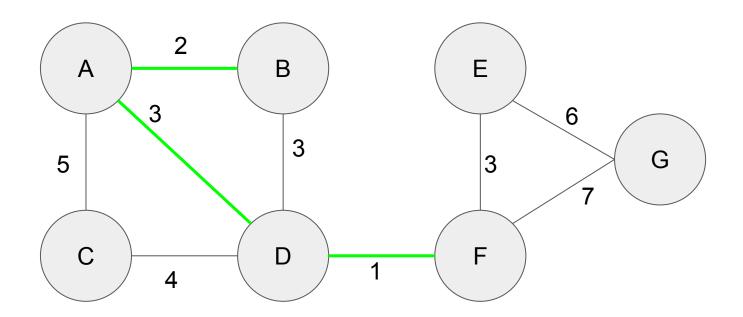


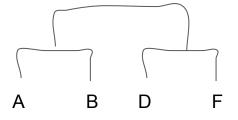


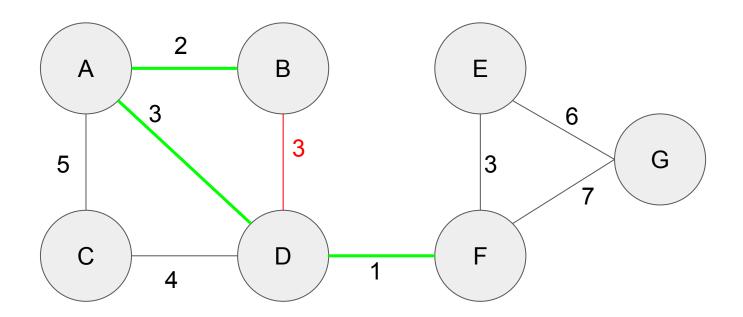


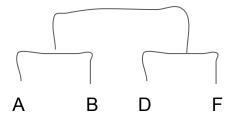


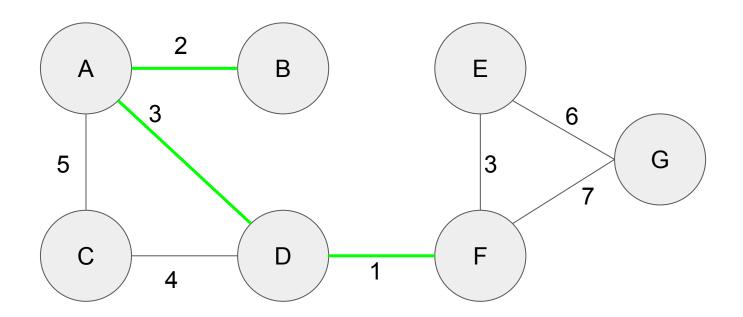


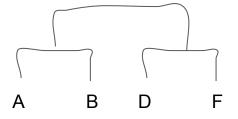


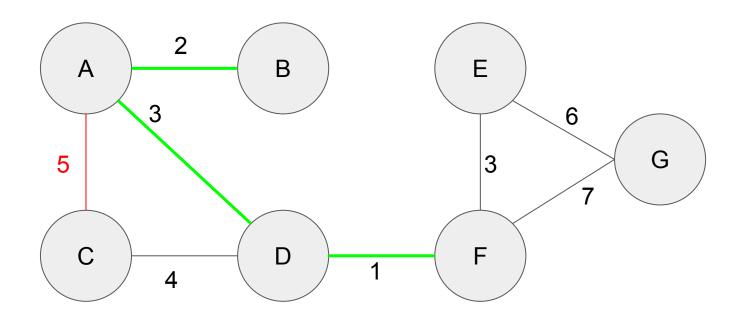


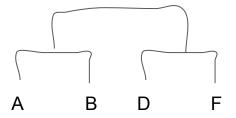


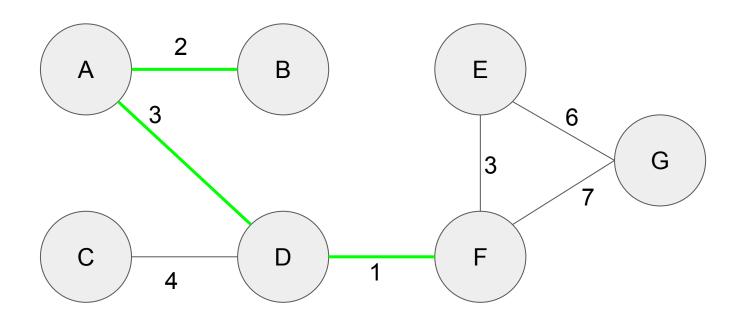


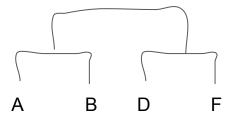


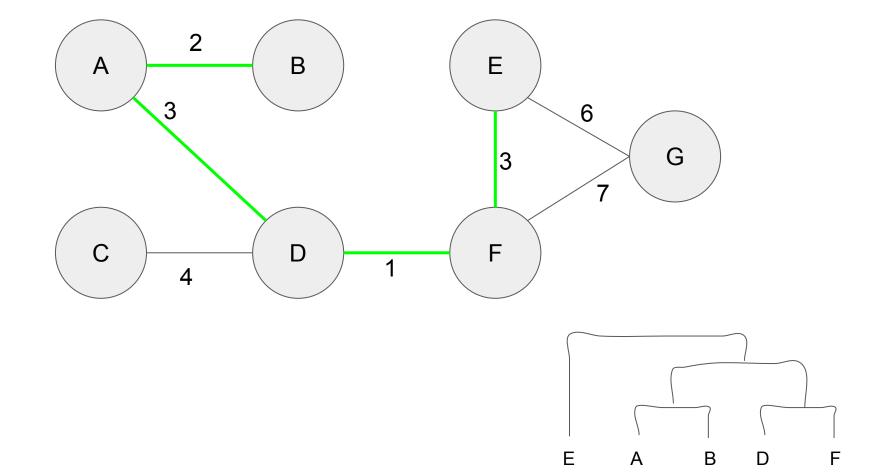


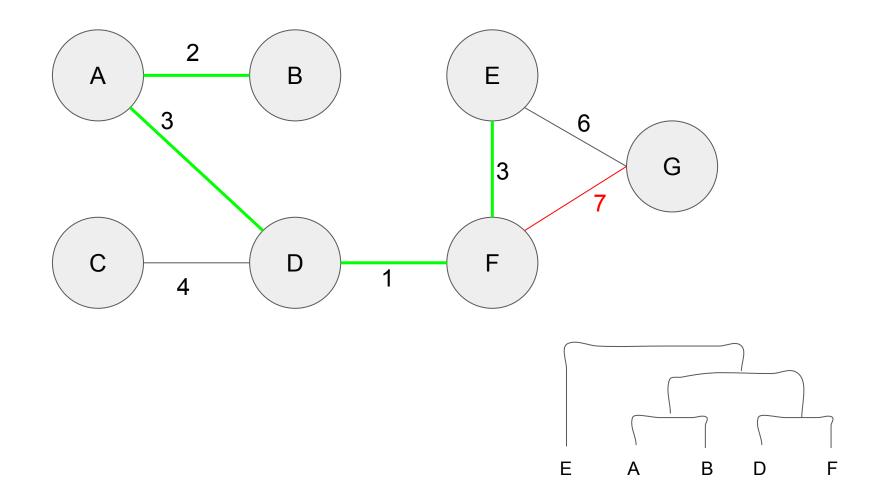


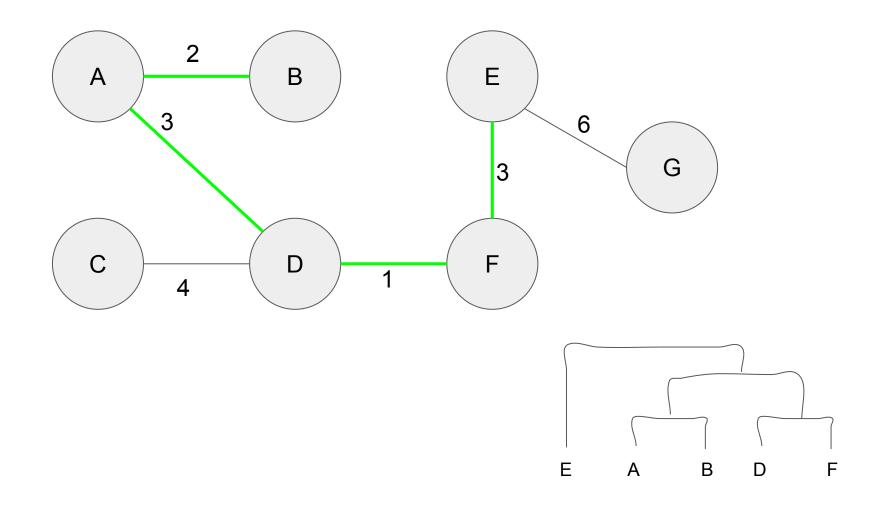


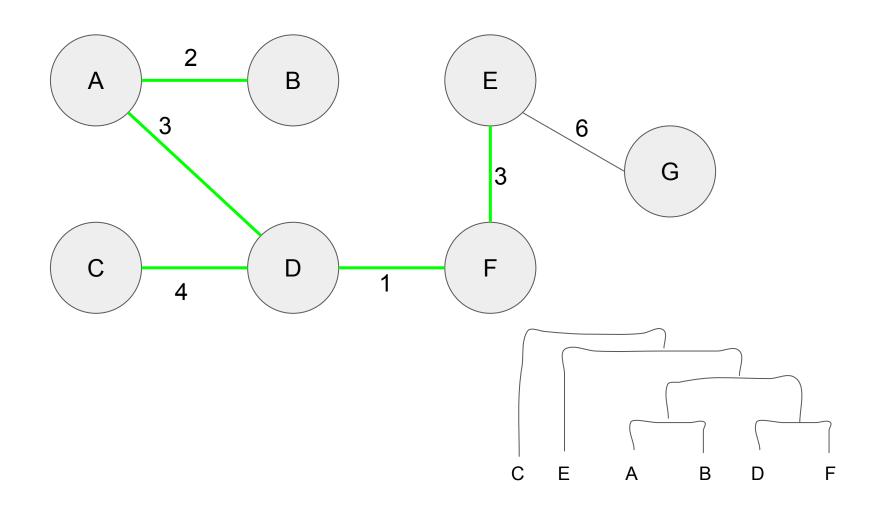


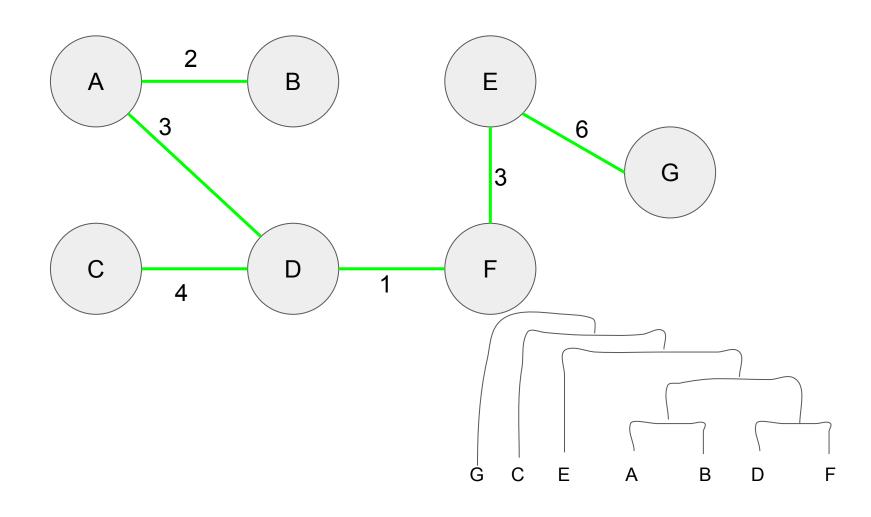








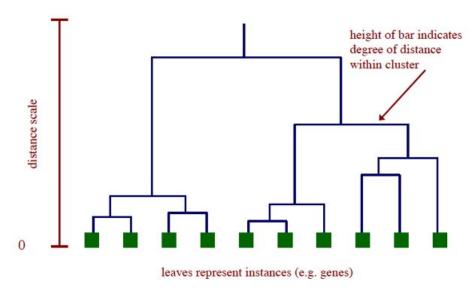




#### Dendrogram

Dendrogram. Scientific visualization of hypothetical sequence of evolutionary events.

- Leaves = genes.
- Internal nodes = hypothetical ancestors.



Reference: http://www.biostat.wisc.edu/bmi576/fall-2003/lecture13.pdf









#### Morphological features

Dolphin (D): aquatic, eats fish

Seal (S): semi-aquatic, eats fish

Cow (C): terrestrial, eats grass

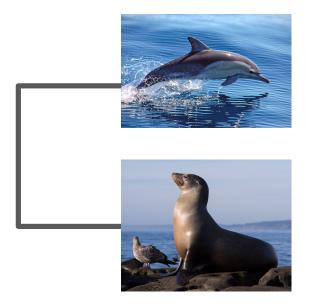
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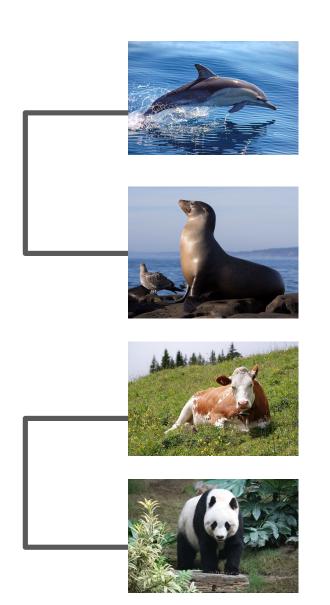
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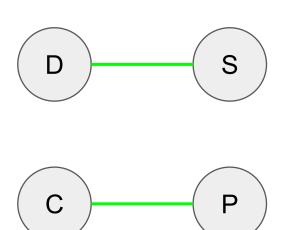
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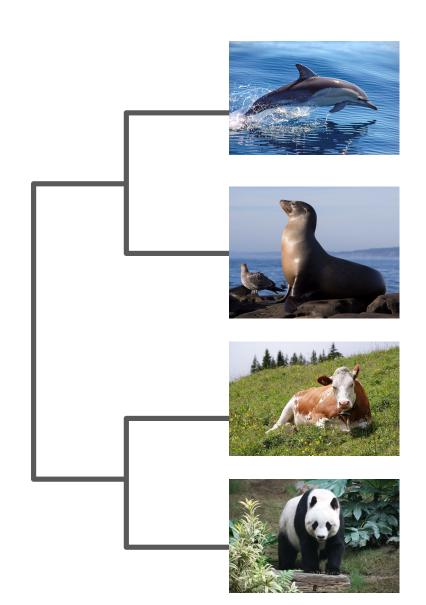
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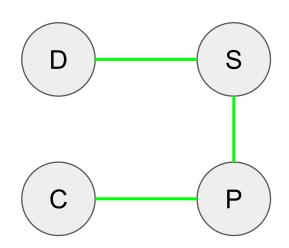
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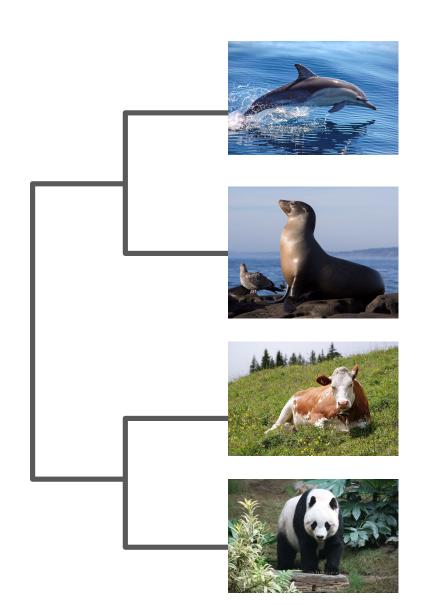
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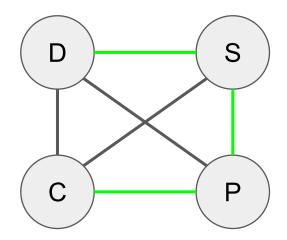
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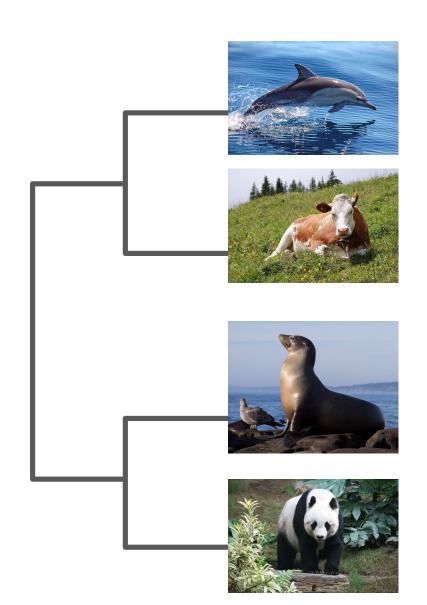
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Panda (P): terrestrial, eats grass

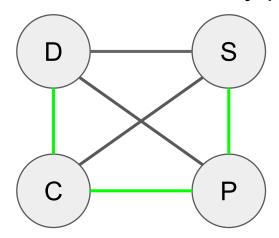


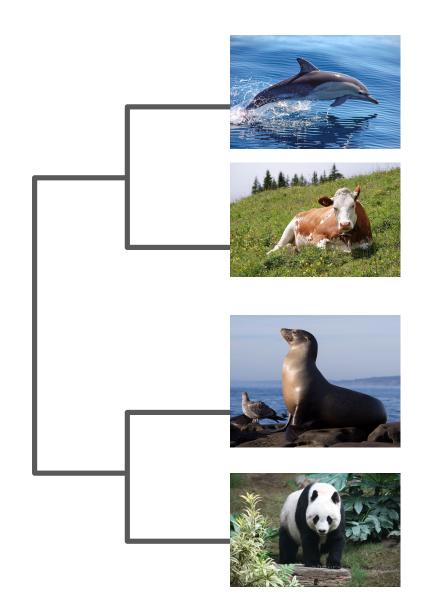


#### Morphological features

Dolphin (D): aquatic, eats fish
Seal (S): semi-aquatic, eats fish
Cow (C): terrestrial, eats grass
Panda (P): terrestrial, eats grass

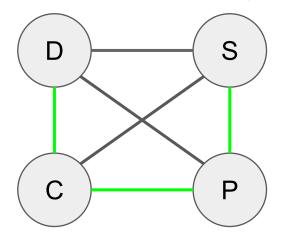
Genetic MST (the actual evolutionary path):





Computing genetic distances will be discussed in the dynamic programming section

Genetic MST (the actual evolutionary path):



#### **Applications in data analysis**

Tumors in similar tissues cluster together.

