## Quiz Section Week 5 April 26, 2018

Review

#### Topics (not guaranteed to be comprehensive!)

#### Alignments

- Reasons to align sequences
- Needleman-Wunsch algorithm
- Smith-Waterman algorithm
- Effects of parameter variation (including gap penalties)
- Testing for statistical significance of an alignment

#### Phylogenetic trees

- Rooted and unrooted topologies
- Defining the best tree with UPGMA and Neighbor Joining
- Concept of parsimony
- Fitch algorithm: quantifying how parsimonious a tree is, assigning internal states
- Finding the most parsimonious tree: Hill climbing w/ Nearest-Neighbor interchanges
- Bootstrapping to quantify confidence in tree partitions

#### Clustering

- Defining a clustering problem
- Hierarchical clustering
  - Impact of using single/complete/average linkage
- K-means: Objective and algorithm

#### Networks

- Reasons to make and analyze networks
- Basic network definitions
- Dijkstra's Algorithm
- Network motifs and their uses

### Phylogenetic trees

#### **UPGMA/Neighbor Joining**

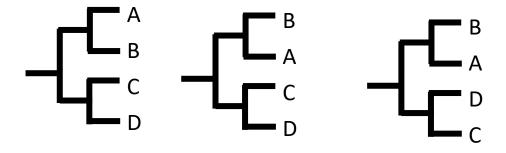
- Define the best tree: based on distance between leaves
- Find the best tree using: polynomial time algorithm to construct the best tree from a distance matrix

#### Parsimony approach

- Define the best tree: Minimum # of mutations required to traverse tree
- Find the best tree: by enumerating all trees (exhaustive search), or by heuristic approach like Nearest-Neighbor Interchange Hill-Climbing

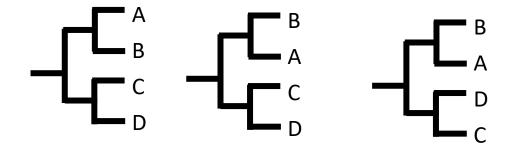
## Tree topologies

Are these the same tree?

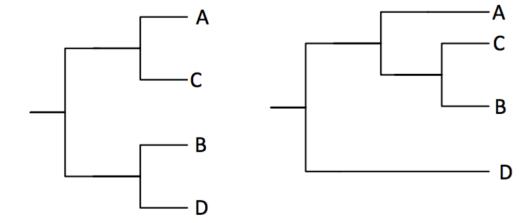


## Tree topologies

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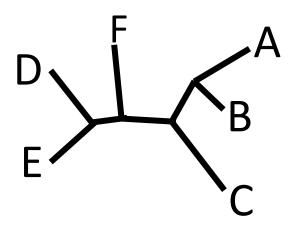
How about these?



For N leaves

```
# of unrooted topologies = 3*5*7*...*(2N-5)
# of branches = 2N-3
```

E.g. an unrooted tree with 6 nodes

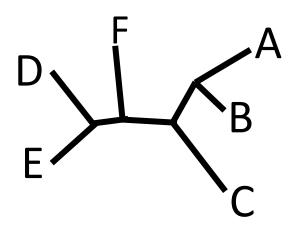


How many different topologies?

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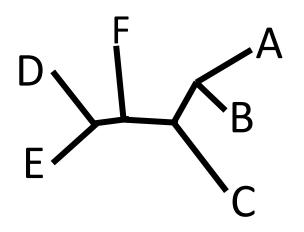


How many different topologies? 3\*5\*7 = 105

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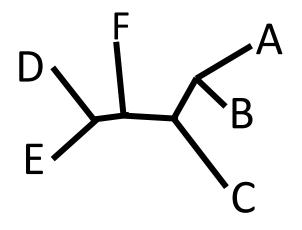


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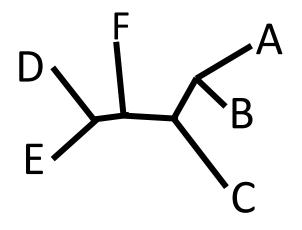
How many different topologies?

$$2N-3 = 9$$

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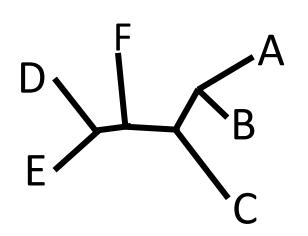


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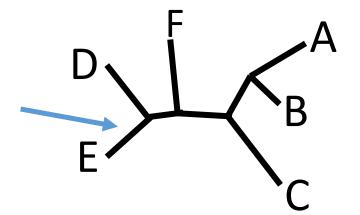
### The root could be placed on any branch

E.g. an unrooted tree with 6 nodes



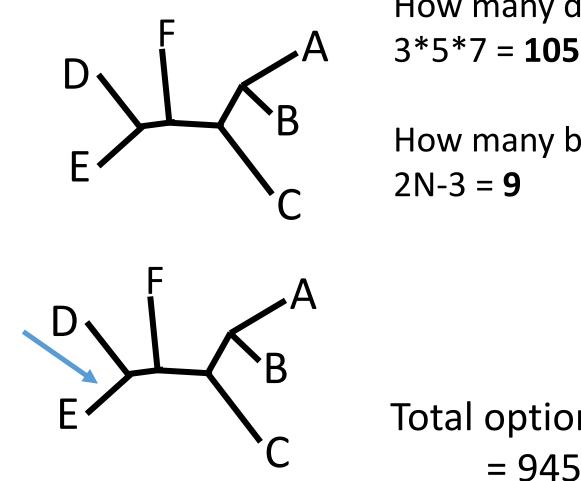
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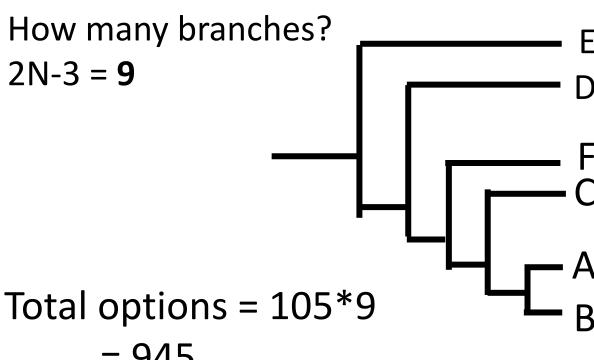


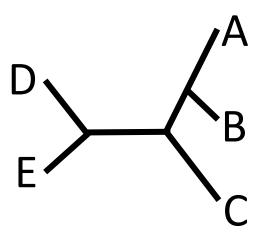
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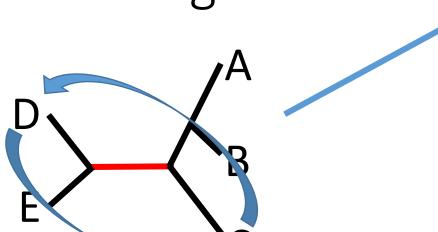
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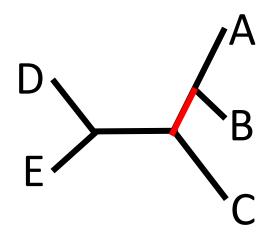


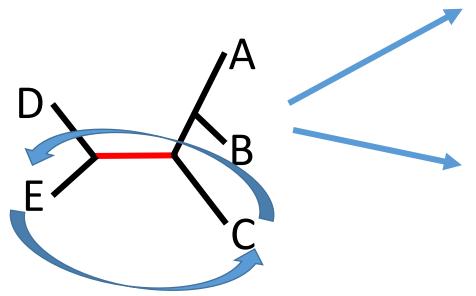
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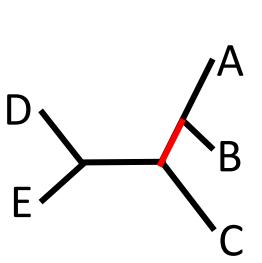


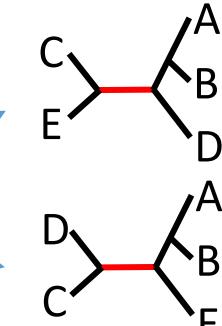


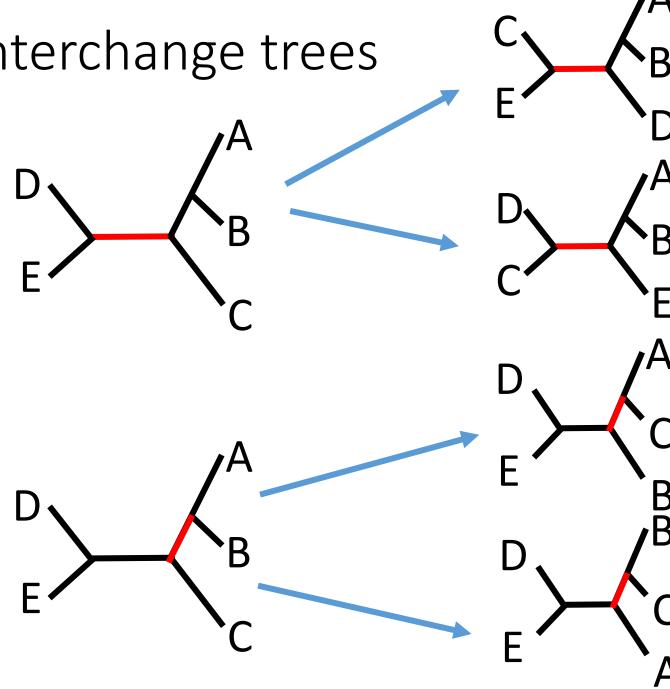




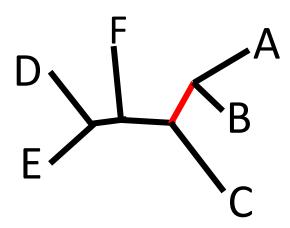




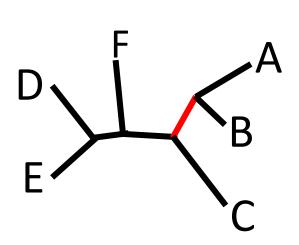


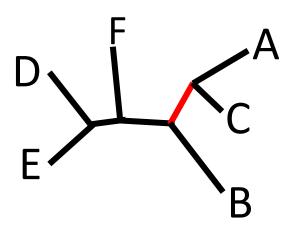


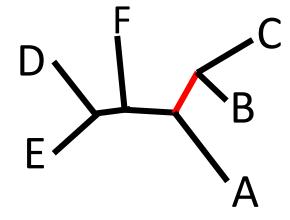
NN Practice: Draw both interchanges from swapping this branch



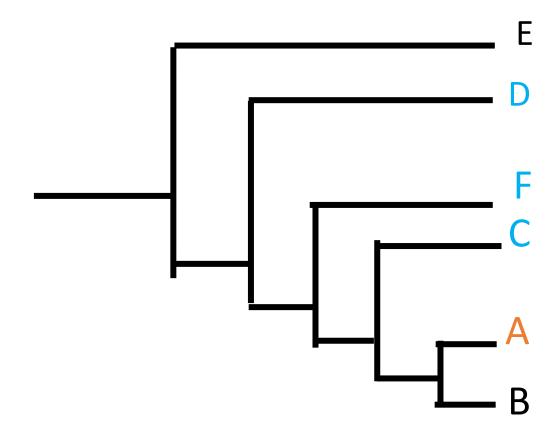
# NN Practice: Draw both interchanges from swapping this branch



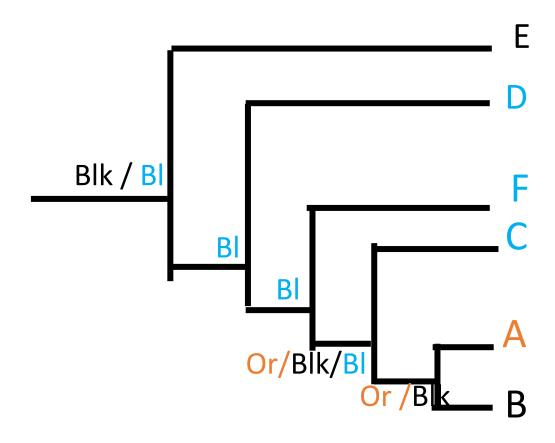




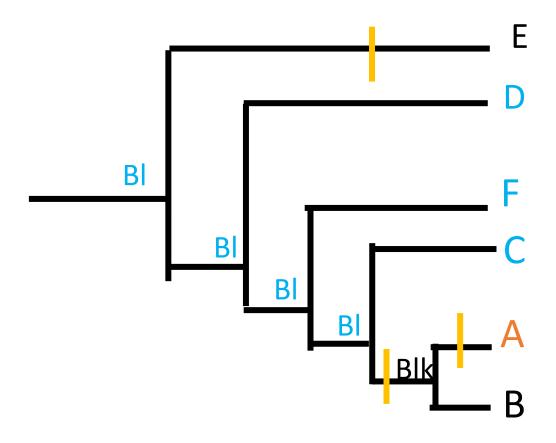
## Fitch algorithm practice



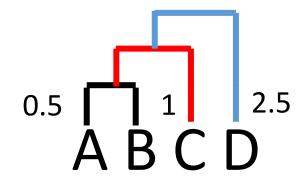
### Fitch algorithm practice: bottom-up



### Fitch algorithm practice: top-down



# Hierarchical clustering with complete linkage example

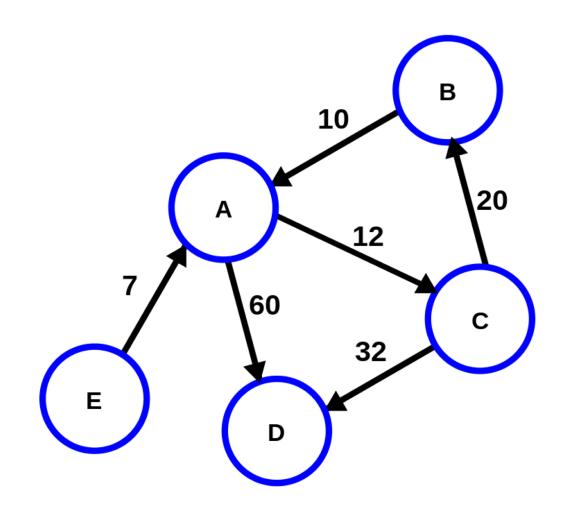


	A	В	C	D
A	0 (	(1)	2	4
В	1	0	2	5
C	2	2	0	5
D	4	5	5	0

	A,B	C	D
A,B	0 (	2	5
C	2	0	5
D	5	5	0

	A,B,C	D
A,B,C	0	5
D	5	0

## Dijkstra's Algorithm



#### Another data type: Dictionaries

- a data structure that consists of an unordered set of key:
   value pairs
  - think of as word: definition pairs!

Q: How could we encode the entire genetic code?

## Dictionaries: How could we encode the entire genetic code?

```
>>> genetic code = {"ATG": "Start", "TGA": "Stop", "TAG":
"Stop" }
>>> genetic code["TAA"] = "Stop"
>>> genetic code.get("TGA")
'Stop'
>>> genetic code["TGA"]
'Stop'
>>> genetic code.get("sss") #nothing or 'None' if not defined
>>> genetic code["sss"]
KeyError: 'ttt'
```

#### Creating a dictionary

```
#create an empty dictionary
myDict = {}
#create a dictionary with three entries
myDict = {"Curly":4123, "Larry":2057, "Moe":1122}
#add another entry
myDict["Shemp"] = 2232
#change Moe's phone number
myDict["Moe"] = 4040
#delete Moe from dictionary
del myDict["Moe"]
```

#### Rules for dictionaries

- The first item is a key.
- Each key can appear only once in a dict.
- A key must be an <u>immutable</u> object: number, string, or tuple.
- Lists cannot be keys (they are mutable).
- The key is the item you'll use to do look-ups.
- Each key is paired with a value.

#### Some useful dictionary methods

```
>>> genetic_code.items()
[('TAA', 'Stop'), ('TGA', 'Stop'), ('ATG', 'Start')]
>>> genetic_code.keys()
['TAA', 'TGA', 'TAG', 'ATG']
>>> genetic_code.values()
['Stop', 'Stop', 'Stop', 'Start']
```

# Another use of dictionaries: store counts of named elements

Example: Calculate # of each nucleotide in a sequence

```
sequence = "GACCCT"
nuc_counts = {'A': 0, 'C': 0, 'T':0, 'G': 0}
for nuc in sequence:
    #Add to the count for the given nucleotide
```

# Another common use of dictionaries: store counts of named elements

Calculate # of each nucleotide in a sequence

```
sequence = "GACCCT"
nuc_counts = {'A': 0, 'C': 0, 'T':0, 'G': 0}
for nuc in sequence:
   nuc_counts[nuc] = nuc_counts[nuc] + 1
```

#### Traversing a dictionary by key

```
# birthdays is a dictionary with names as keys
# and birth dates as values

for person in birthdays.keys():
    print "Send", person, "a card on", birthdays[person]
```

#### dictionary basics

```
D = {'dna':'T','rna':'U'} # dictionary literal assignment
D = {} # make an empty dictionary
D.keys() # get the keys as a list
D.values() # get the values as a list
D['dna'] # get a value based on key
D['dna'] = 'T' # set a key:value pair
del D['dna'] # delete a key:value pair
'dna' in D # True if key 'dna' is found in D, else False
```

The keys must be immutable objects (e.g. string, int, tuple).

The values can be anything (including a list or another dictionary).

The order of elements in the list returned by **D.keys()** or **D.values()** is arbitrary (effectively random).

Each key can be stored only once in the dictionary, so if you set the value for a key for a second time it OVERWRITES the old value!