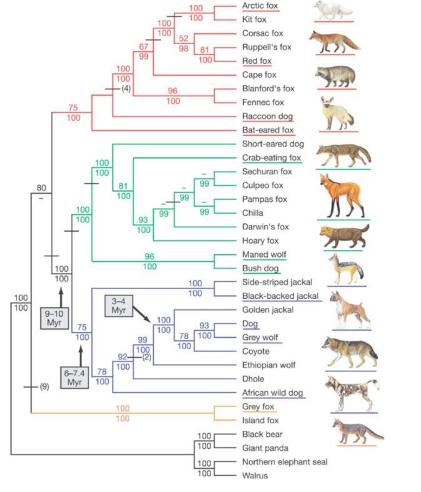
"I wonder about Trees" –Robert Frost



"We wonder about Robert Frost" - Trees

Hey! How come no turtles in this tree?

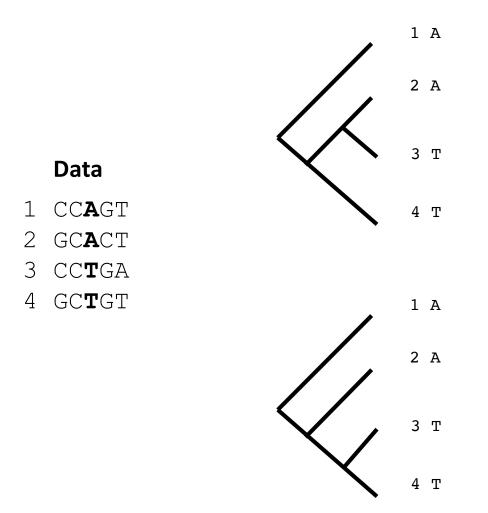




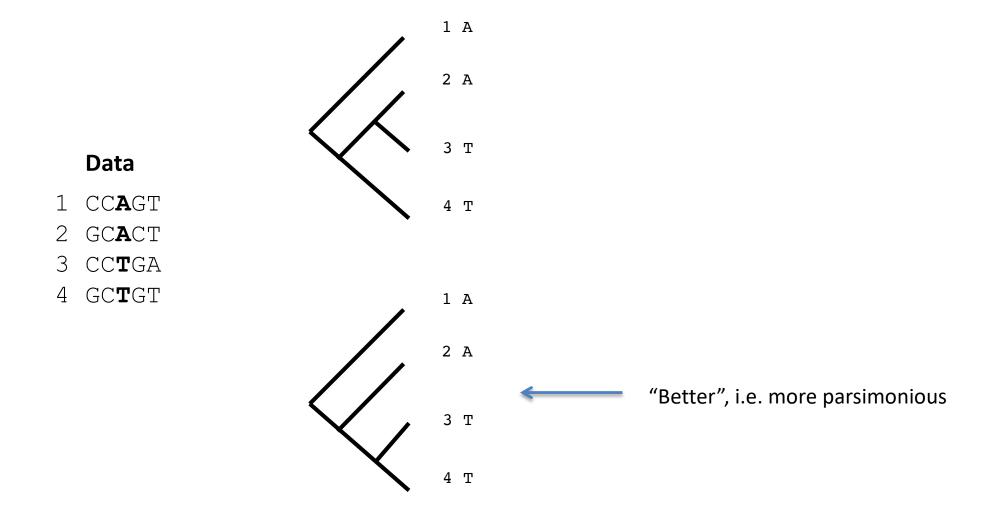
Learning Goals

- Describe the parsimony principle
- Introduce method for enumerating all trees

Trees and the parsimony principle

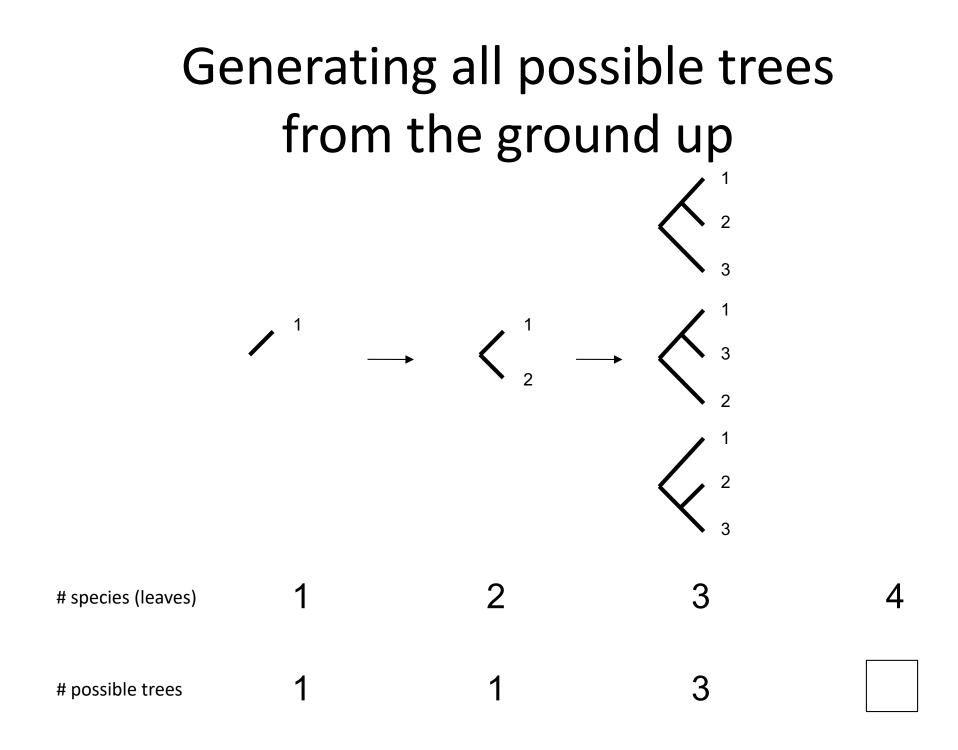


Trees and the parsimony principle



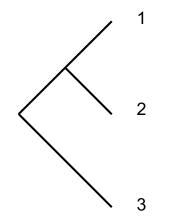
Another general strategy for inferring phylogenies

- Generate all possible trees
- Pick the most parsimonious given some data

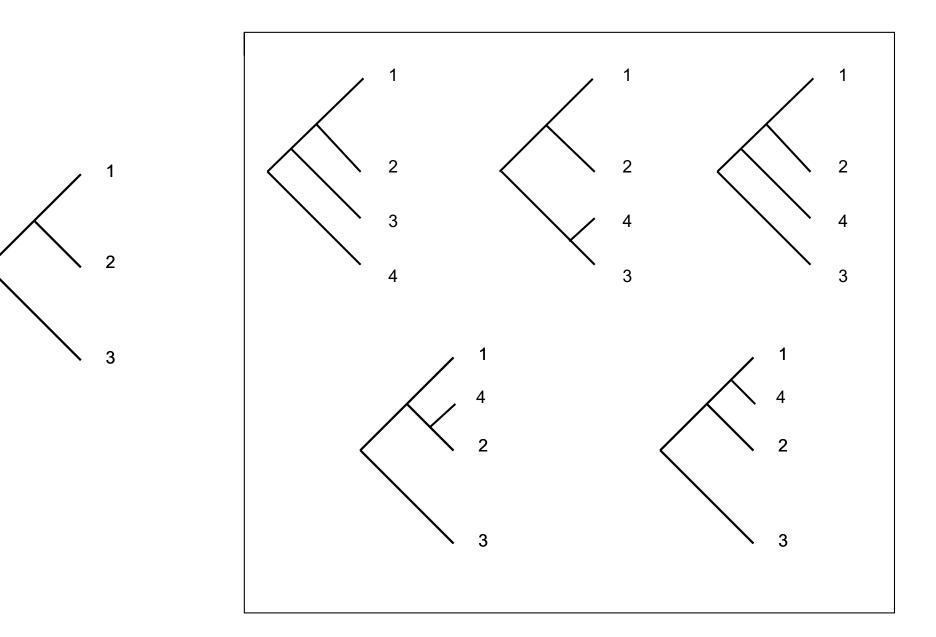


Draw all possible trees that result from adding a species 4 to this tree.

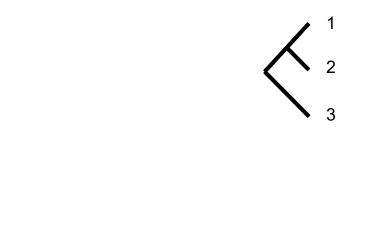


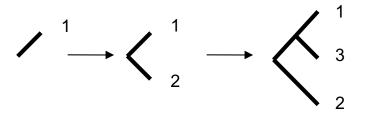


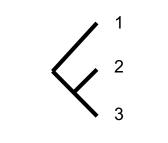
Draw all possible trees that result from adding a species 4 to this tree.

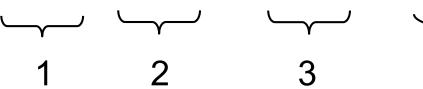






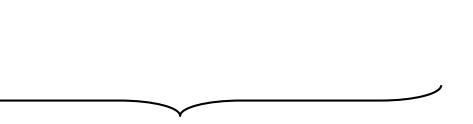


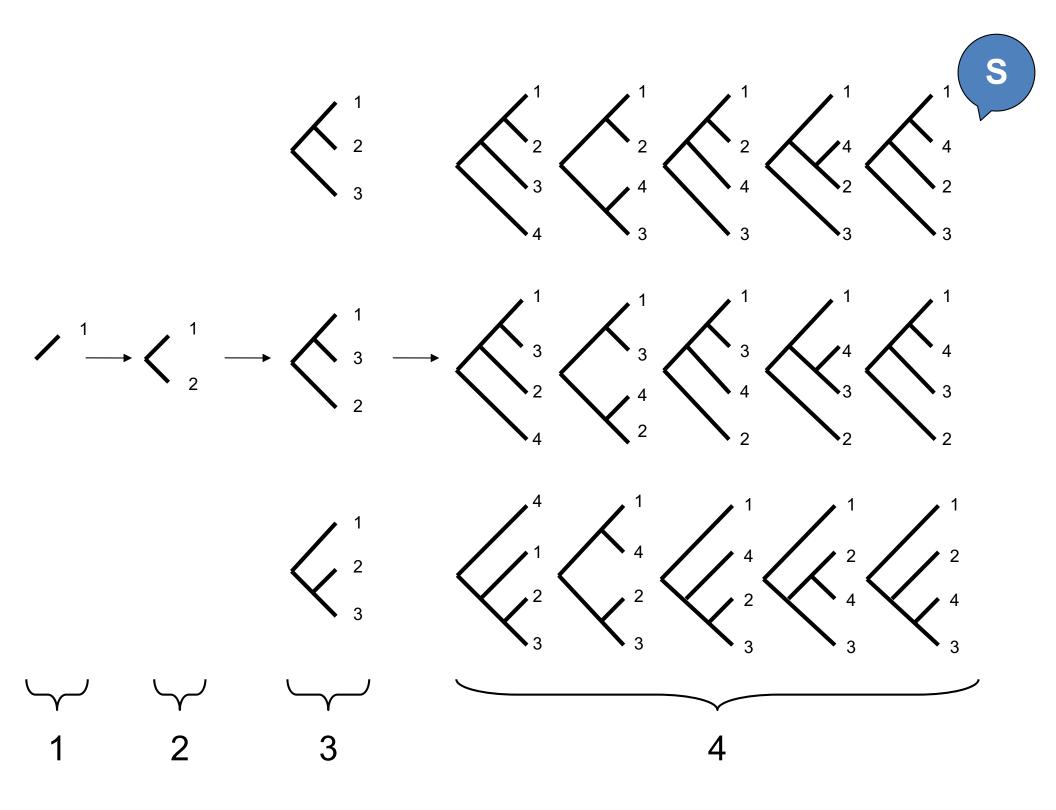






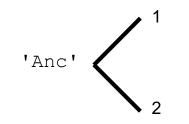




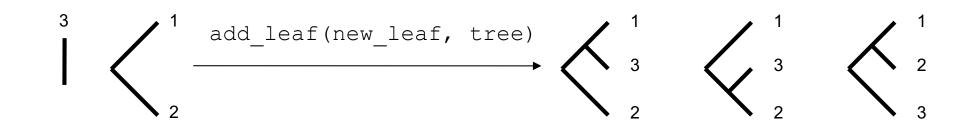


A convention for naming internal/ancestral nodes

tree = ('Anc', (1, (), ()), (2, (), ()))

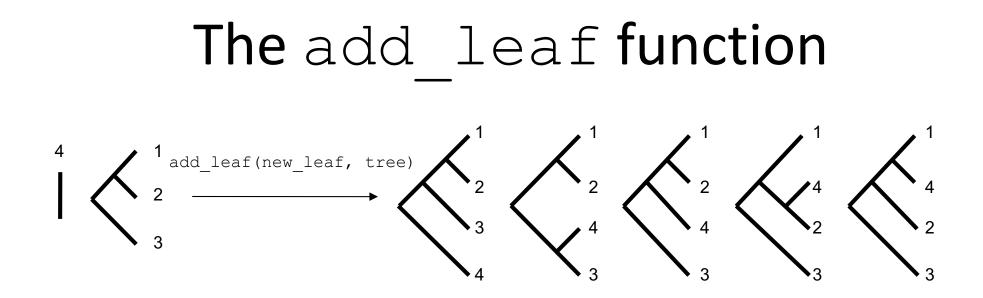


The add leaf function



```
>>> leaf = ( 3, (), () )
>>> tree = ( 'Anc', (1,(),()) , (2,(),()) )
>>> add_leaf(leaf, tree)
[
    ('Anc', (3, (), ()) , ('Anc', (1, (), ()), (2, (), ())) ),
    ('Anc', ('Anc', (3, (), ()), (1, (), ())), (2, (), ()) ),
    ('Anc', (1, (), ()), ('Anc', (3, (), ()), (2, (), ())) ),
]
```

Which illustration does the last tuple tree correspond to?

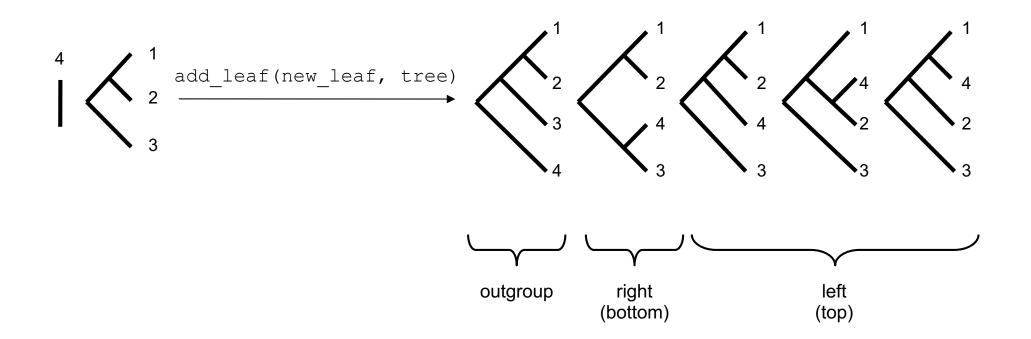


```
def add_leaf(new_leaf, tree):
    """Returns a list of all possible trees that result from
    adding new_leaf to tree."""
    root, left, right = tree
    anc = "Anc"
```

```
def add_leaf(new_leaf, tree):
    """Returns a list of all possible trees that result from
    adding new_leaf to tree."""
    root, left, right = tree
    anc = "Anc"
    if left == (): # a leaf.
        new_tree = (anc, new_leaf, tree)
        return [new_tree] # wrap it in a list!
```

S

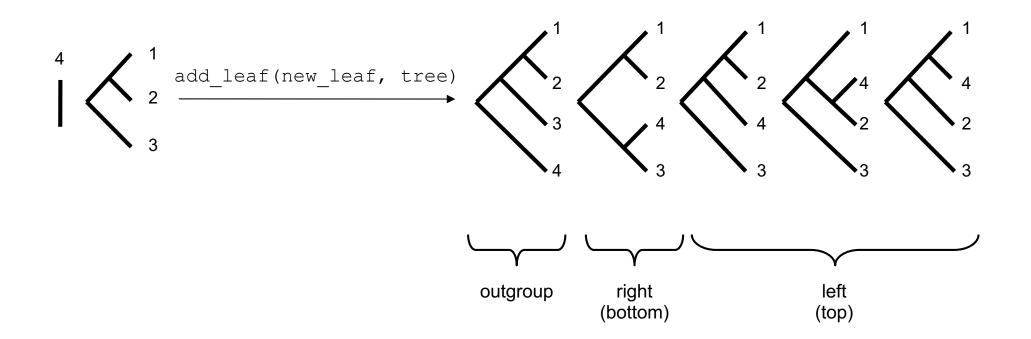
General case: three steps at each node



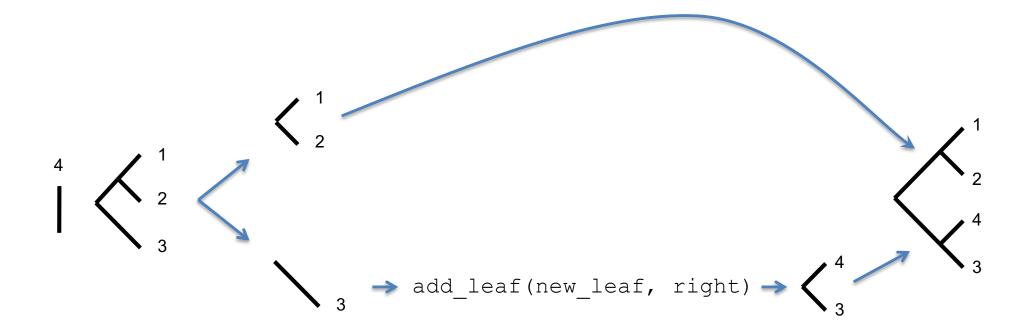
```
def add_leaf(new_leaf, tree):
    """Returns a list of all possible trees that result from
    adding new_leaf to tree."""
    root, left, right = tree
    anc = "Anc"
    if left == (): # a leaf.
        new_tree = (anc, new_leaf, tree)
        return [new_tree] # wrap it in a list!
else:
        output_trees = []
        # put new_leaf as outgroup
        output_trees.append((anc, new_leaf, tree))
```

S

General case: three steps at each node



The add leaf chop shop: right tree





http://bananajams.wordpress.com/

The add leaf chop shop: left tree $\bigwedge_{\substack{2\\4}}^{1} \twoheadrightarrow \bigwedge_{\substack{2\\4\\2}}^{1}$ $\left\langle \begin{array}{c} 1\\2 \end{array} \right\rangle \Rightarrow \operatorname{add_leaf(new_leaf, left)} \Rightarrow \left\langle \begin{array}{c} 1\\2\\4 \end{array} \right\rangle \Rightarrow \left\langle \begin{array}{c} 2\\4\\4 \end{array} \right\rangle$ $\bigwedge_{4}^{1} \rightarrow \bigwedge_{2}^{1}$ http://bananajams.wordpress.com/

```
def add_leaf(new_leaf, tree): Worksheet
  """Returns a list of all possible trees that result from
  adding new_leaf to tree."""
  root, left, right = tree
  anc = "Anc"
  if left == (): # a leaf.
    new_tree = (anc, new_leaf, tree)
    return [new_tree] # wrap it in a list!
else:
    output_trees = []
    # put new_leaf as outgroup
```

```
output_trees.append((anc, new_leaf, tree))
```

```
Worksheet
def add leaf(new leaf, tree):
                                                                    S
    """Returns a list of all possible trees that result from
    adding new leaf to tree."""
    root, left, right = tree
    anc = "Anc"
    if left == (): # a leaf.
        new tree = (anc, new leaf, tree)
        return [new tree] # wrap it in a list!
    else:
        output trees = []
        # put new leaf as outgroup
        output trees.append((anc, new leaf, tree))
        # recur to add new leaf on branches of right subtree
        temp right trees = add leaf(new leaf, right)
        for temp right tree in temp right trees:
            new tree = (anc, left, temp right tree)
            output trees.append(new tree)
```

```
Worksheet
def add leaf(new leaf, tree):
                                                                    S
    """Returns a list of all possible trees that result from
    adding new leaf to tree."""
    root, left, right = tree
    anc = "Anc"
    if left == (): # a leaf.
        new tree = (anc, new leaf, tree)
        return [new tree] # wrap it in a list!
    else:
        output trees = []
        # put new leaf as outgroup
        output trees.append((anc, new leaf, tree))
        # recur to add new leaf on branches of right subtree
        temp right trees = add leaf(new leaf, right)
        for temp right tree in temp right trees:
            new tree = (anc, left, temp right tree)
            output trees.append(new tree)
        # recur to add new leaf on branches of left subtree
        temp left trees = add leaf(new leaf, left)
        for temp left tree in temp_left_trees:
            new tree = (anc, temp left tree, right)
            output trees.append(new tree)
```

```
return output trees
```

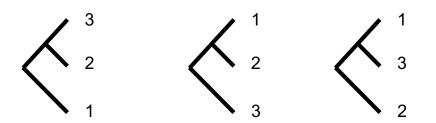
Demo!

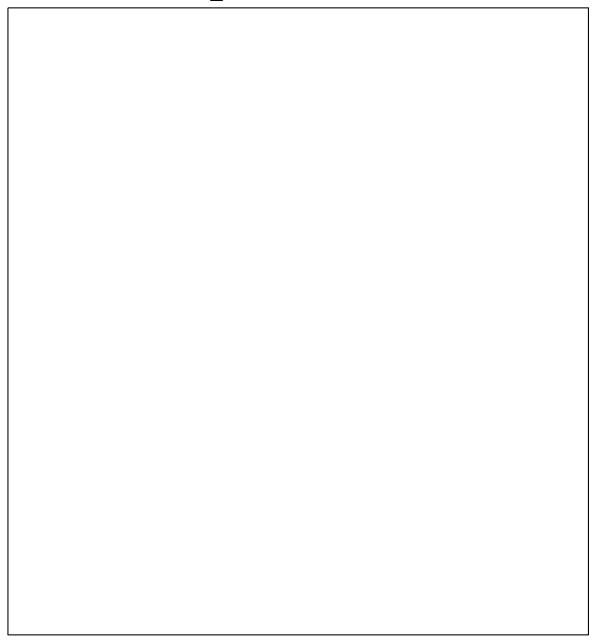


(Bonus) homework problem: all_trees

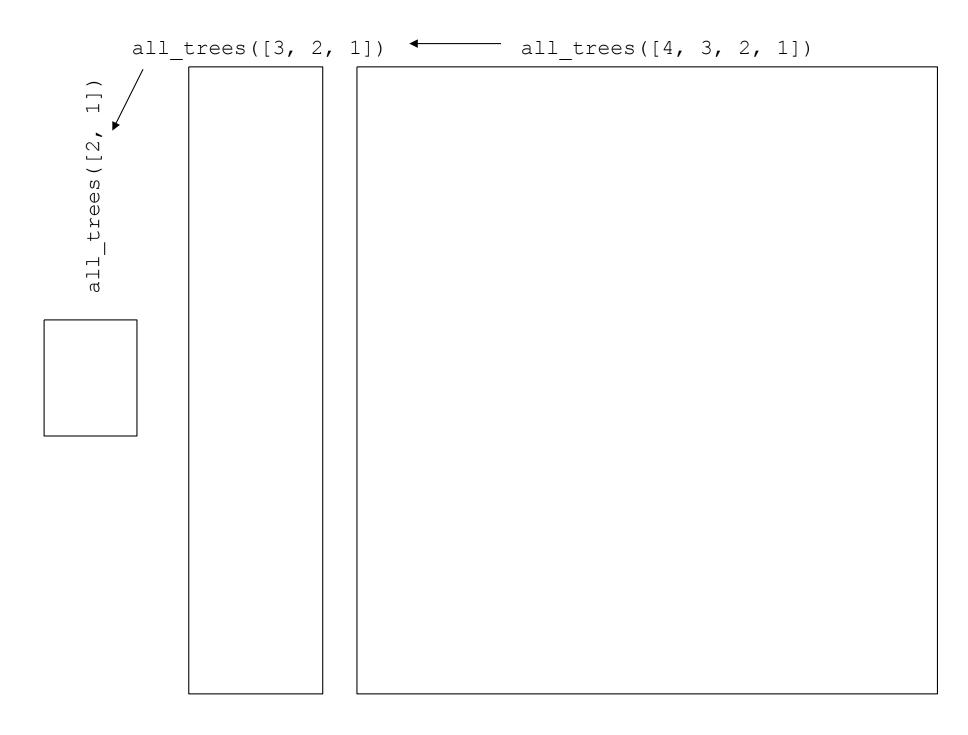
```
def all_trees(leaf_names):
    """Given a list of species, returns a list of all
    possible tree topologies."""
```

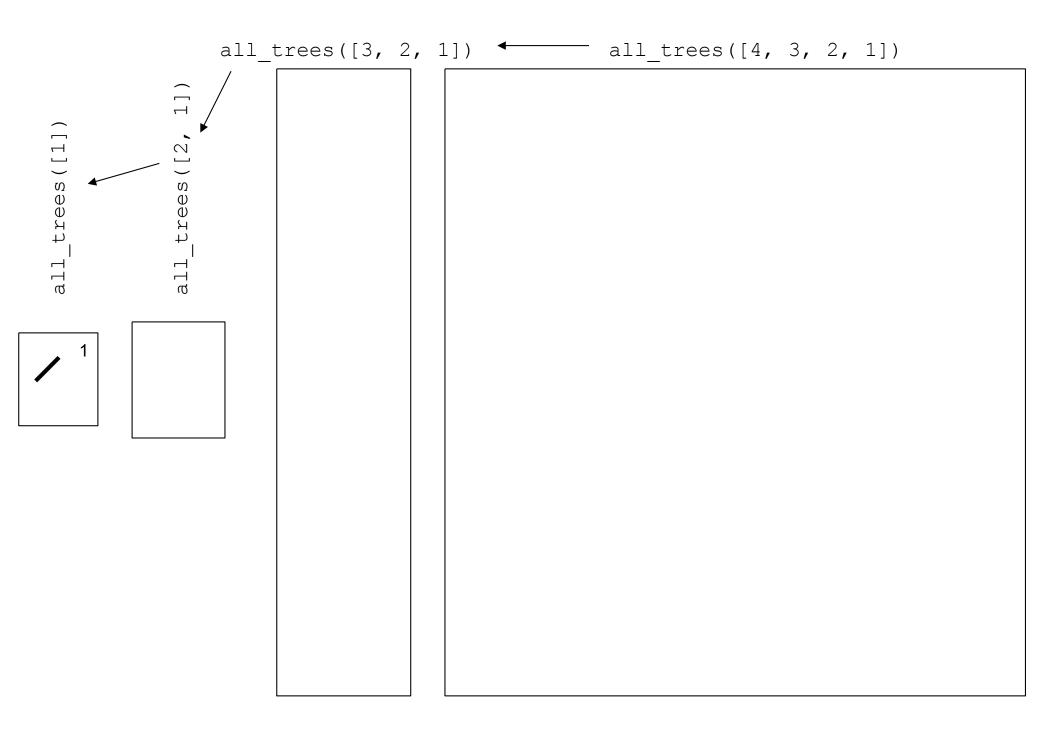
```
>>> all_trees( [1,2,3] )
[
    ('Anc', (1, (), () ) , ('Anc', (2, (), ()), (3, (), ()))),
    ('Anc', ('Anc', (1, (), ()), (2, (), ())), (3, (), ())),
    ('Anc', (2, (), ()), ('Anc', (1, (), ()), (3, (), ())))
]
```

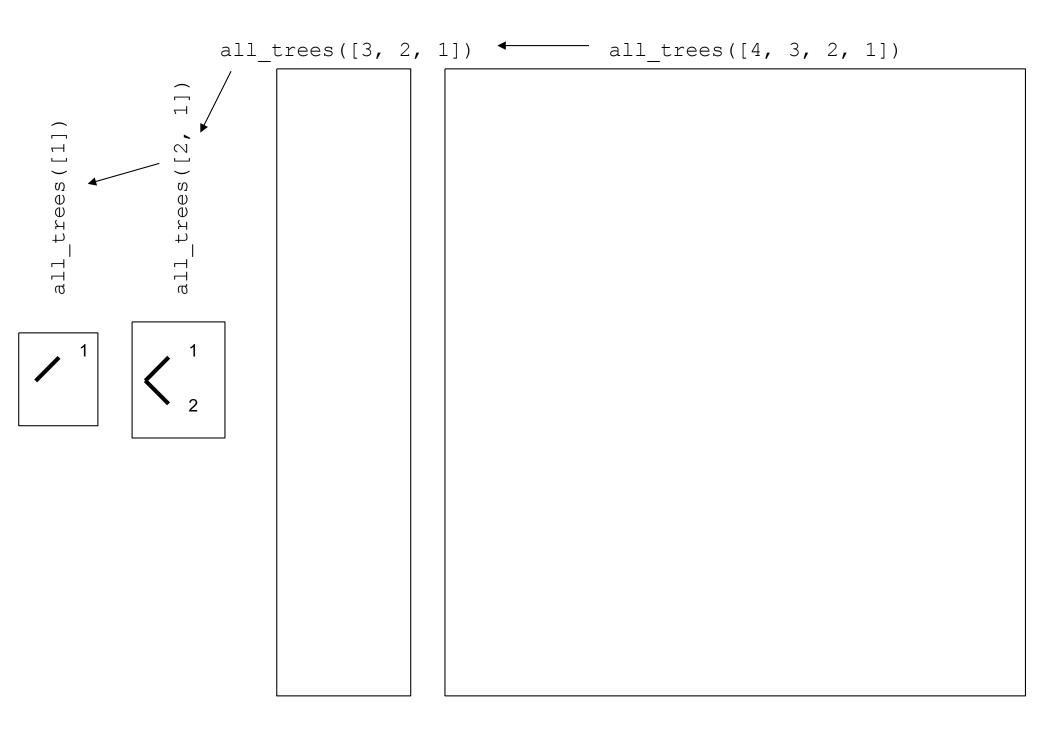


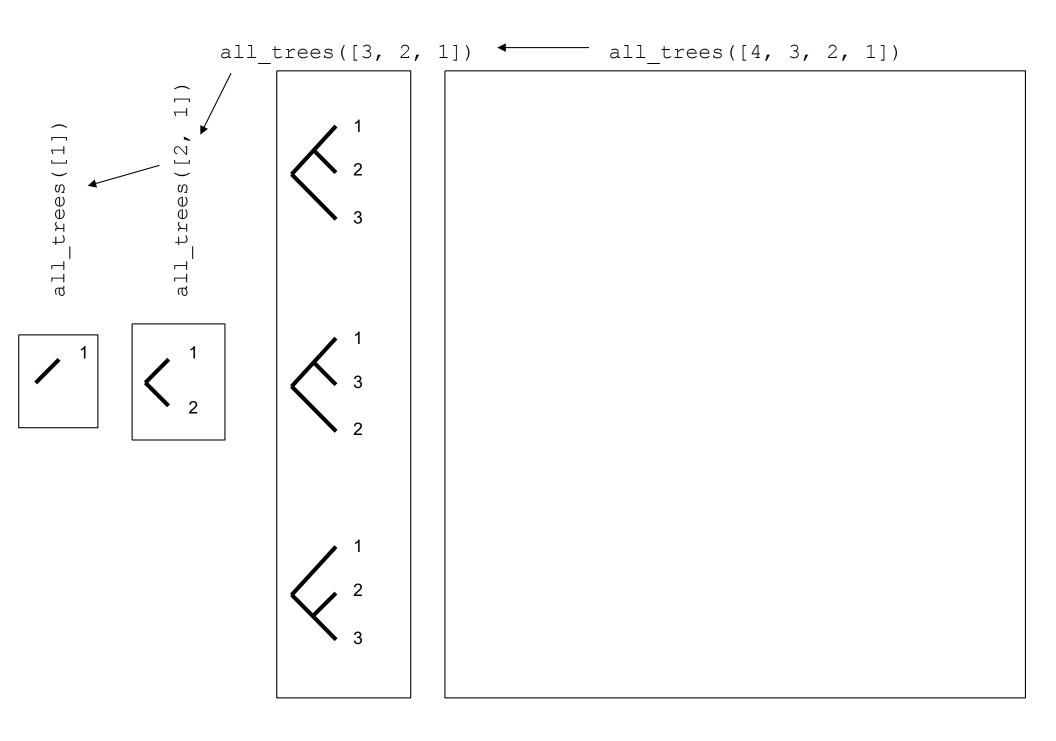


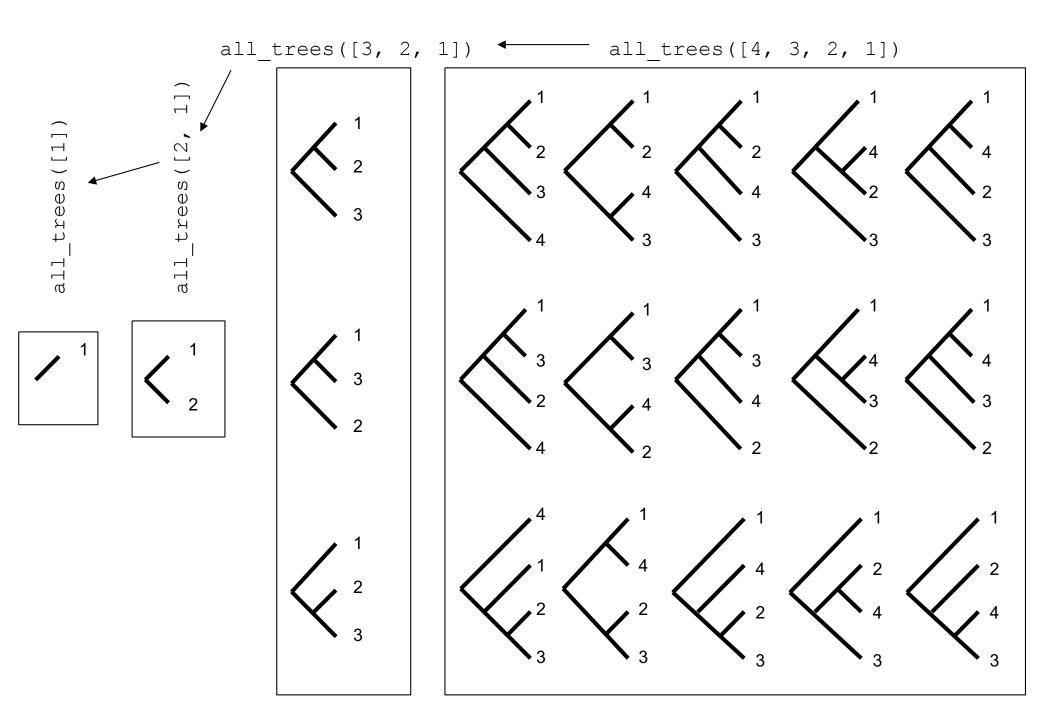
all_trees([3, 2,	1])	all_trees([4,	3, 2, 1])











One general strategy for inferring phylogenies

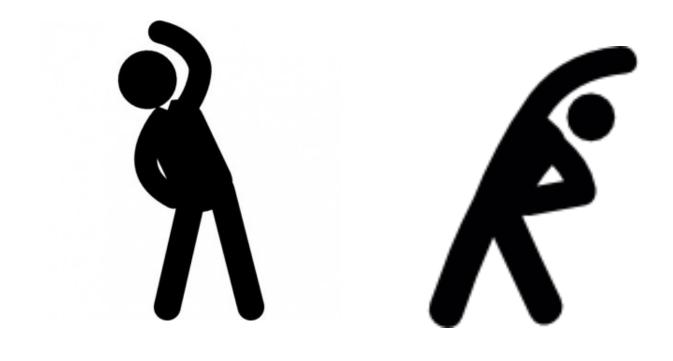
- Generate all possible trees
- Pick the most parsimonious given some data

The number of trees grows quickly...

# species (leaves)	1	5	10	15	20	25
# possible trees	1	105	34,459,425	2.13458 x 10^14	8.200795 x 10^21	1.192568 x 10^30







Programming motifs: all vs. all

protsA = ['PLLYK', 'QSTE', 'NITQIVG', 'INE', 'QVAEA', 'YMSA']
protsB = ['LAGADLEQ', 'LAL', 'EAMERY', 'ENLEL']

	B1	B2	B3	B4
A1				
A2				
A3				
A4				
A5				
A6				

d = {}
for pA in protsA:
 for pB in protsB:
 d[(pA,pB)] = memoAlignScore(pA, pB, -9, blosum62, {})

Programming motifs: running the gauntlet

rnas = ['AUGACGCAGUAGUCA', 'UAGACAGUA', 'AGGUACAUC'...]

- If no RNA has a fold score above 7, return False
- Otherwise return True

```
for rna in rnas:
    if fold(rna) > 7:
        return True
return False
```

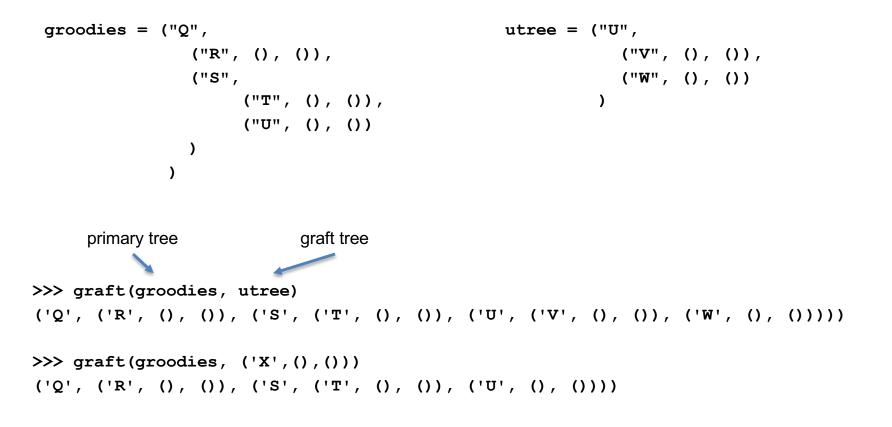
Programming motifs: finding extremz

dictionary = ["abdomen", "abdominal", "abduct", "abduction," "aberration," "abet," "abhor," "abhorrence," "abhorrent," "abide," "abiding," "ability," "abject," "ablaze," ... ••• etc.]

```
def z(input):
    '''Count z's in a string'''
    counter = 0
    for symbol in input:
        if symbol == 'z':
            counter = counter + 1
    return counter
```

```
def extremz(words):
    '''Find and return the word with the most z's'''
    best_count = 0
    best_word = ""
    for word in words:
        count = z(word)
        if count > best_count:
            best_count = count
            best_word = word
    return best word
```

Recursion on trees: graft



- <u>At most one leaf of primary tree has the same name as the root of graft tree.</u>
- If there is one such match, the function returns a new tree that is identical to primary_tree but with that leaf in primary tree replaced by the entire graft tree.
- If there is no leaf in primary_tree that matches the name of the root of graft_tree, the function simply returns primary_tree.
- No internal node of the primary_tree will have a name that matches the root of the graft_tree.



def graft(primary_tree, graft_tree):

"""If primary_tree has a leaf whose name is the same as the root of graft_tree then we return a new tree identical to primary_tree except with that leaf replaced by graft_tree. Otherwise, we just return primary_tree."""

```
def graft(primary_tree, graft_tree):
    """If primary_tree has a leaf whose name is the same as the root of
    graft_tree then we return a new tree identical to primary_tree
    except with that leaf replaced by graft_tree. Otherwise, we
    just return primary_tree."""
    root, left, right = primary_tree
    if root == graft_tree[0]:
        return graft_tree
    elif left == ():
        return primary_tree
    elif_graft = graft(left, graft_tree)
        right_graft = graft(right, graft_tree)
```

```
return (root, left_graft, right_graft)
```

Reminder:

 Lecture feedback form (<u>https://forms.gle/aPmkpXDUTp4Xo4CV7</u>)