

The end is near!



© Dan Tague

Mudd Summer Research Info Session

Is summer research the right move for me?
How do I know which lab to join?
How do I apply?

Come to the info session to learn about summer research at HMC!

Thursday Nov 18, 4:30-5:30 pm
The info session will be recorded for
those who can't attend.

Sign up through Handshake, or use
the Zoom info below.
Meeting ID: 994 5831 3034
Passcode: 728687



What's coming next...

- Tuesday: Projects showcase!
- After break
 - 11/30, 12/2 and 12/7 lecture in BECKMAN B126 (big Beckman)
 - Class material: The limits of computation!
 - 12/9 we're back "home" in Shan 2460 for a final lecture
 - Work on your project (milestone + final project)
 - Labs are just for working and getting help on projects (will be at normal time and place with the three of us)

Why are dictionaries fast?

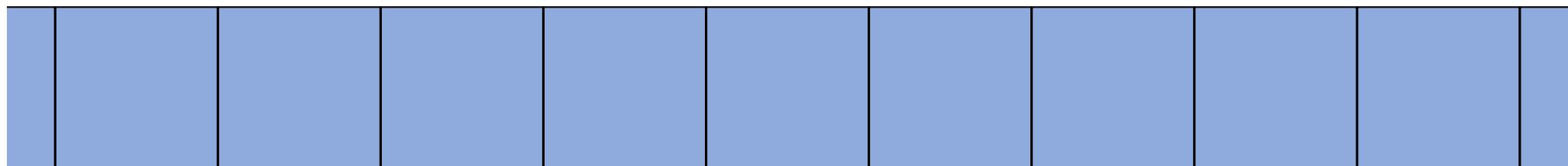
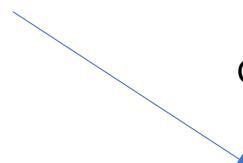
```
>>> D={ }  
>>> D['gene4242'] = ['gene21', 'gene5000', 'gene1987']
```



hash ('gene4242')

4192264438798265428

Go to memory location based on hash





CS 5 Green

Plan for today

- Describe inheritance and its benefits
- An aside on Prof Bush's research, with examples of OOPs

Inheritance (inherit s!)

```
class Person:

    def __init__(self, first_name, last_name):
        self.first_name = first_name
        self.last_name = last_name

    def __repr__():
        return self.first_name + " " + self.last_name

    def is_asleep(self, time):
        return 0 <= time <= 8 # using 24hr time format
```

```
>>> eliot = Person("Eliot", "Bush")
>>> eliot
Eliot Bush
>>> eliot.is_asleep(2)
True
```

```

class Person:

    def __init__(self, first_name, last_name):
        self.first_name = first_name
        self.last_name = last_name

    def __repr__(self):
        return self.first_name + " " + self.last_name

    def is_asleep(self, time):
        return 0 <= time <= 8

class Student(Person):

    def __init__(self, first_name, last_name, age):
        Person.__init__(self, first_name, last_name) # call base class constructor
        self.age = age

    def __repr__(self):
        return Person.__repr__(self) + ", " + str(self.age) + " years old"

    def is_asleep(self, time):
        return 3 <= time <= 11

```

Inheritance!

Read as: Student “is a” Person
 Person is the **base class**.
 Student is the **derived class**.
 Student **inherits** all attributes and methods from Person.

Function Overriding!



Sleeping until 11 AM!?

```

>>> s = Student("Sue", "Persmart", 18)
>>> s
Sue Persmart, 18 years old
>>> s.is_asleep(2)
False

```

```

class Person:
    def __init__(self, first_name, last_name):
        self.first_name = first_name
        self.last_name = last_name

    def __repr__(self):
        return self.first_name + " " + self.last_name

    def is_asleep(self, time):
        return 0 <= time <= 8

class Student(Person):
    def __init__(self, first_name, last_name, age):
        Person.__init__(self, first_name, last_name)
        self.age = age

    def __repr__(self):
        return Person.__repr__(self) + ", " + \
            str(self.age) + " years old"

    def is_asleep(self, time):
        return 3 <= time <= 11

class Mudder(Student):
    def __init__(self, first_name, last_name, age, dorm):
        Student.__init__(self, first_name, last_name, age)
        self.dorm = dorm

    def is_asleep(self, time):
        return False

```



```

>>> wally = Mudder("wally", "wart",
                     42, "west")
>>> wally
?
>>> wally.is_asleep(10)
?

```



Get some sleep!!!

Objects are self-ish

```
class Person:
```

```
    ...
```

```
def rename(self,
           new_first_name,
           new_last_name):
    self.first_name = new_first_name
    self.last_name = new_last_name
```



```
def rename(self,
           new_first_name,
           new_last_name):
    self = Person(new_first_name,
                  new_last_name)
```



Polite Lists

```
>>> p = polite()
Thank you for using polite lists!
>>> p.append(42)
>>> p.append(50)
>>> p[0] += 1
>>> p
This polite list contains [43, 50]
>>> p[3] = 100
Pardon me, but your index is out of bounds
>>> p[3]
Pardon me, but your index is out of bounds
```

Polite Lists



We are inheriting
from the `list` class!

```
class polite(list): ←  
    def __init__(self):  
        print("Thank you for using polite lists!")  
  
    def __repr__(self):  
        return "This polite list contains " + list.__repr__(self)  
  
    def __setitem__(self, index, value):  
        if index >= len(self):  
            print("Pardon me, but your index is out of bounds")  
        else:  
            list.__setitem__(self, index, value)  
  
    def __getitem__(self, index):  
        if index >= len(self):  
            print("Pardon me, but your index is out of bounds")  
        else:  
            return list.__getitem__(self, index)
```



Q

```
class polite(list):
    def __init__(self):
        print("Thank you for using polite lists!")

    def __repr__(self):
        return "This polite list contains " + list.__repr__(self)

    def __setitem__(self, index, value):
        if index >= len(self):
            print("Pardon me, but your index is out of bounds")
        else:
            list.__setitem__(self, index, value)

    def __getitem__(self, index):
        if index >= len(self):
            print("Pardon me, but your index is out of bounds")
        else:
            return list.__getitem__(self, index)
```

What does this do?

```
def __add__(self, other):
    output = polite()
    for x in self:
        output.append(x)
    if isinstance(other, int):
        output.append(other)
    elif isinstance(other, list):
        output.extend(other)
    else:
        print("Pardon me, but your other is confusing")
    return output
```

```
>>> L = polite()
Thank you for using polite lists!
>>> L.append(42)
>>> L.append(47)
>>> L

>>> M = L + 5

>>> M

>>> N = M + [50]

>>> N
```



S

```
class polite(list):
    def __init__(self):
        print("Thank you for using polite lists!")

    def __repr__(self):
        return "This polite list contains " + list.__repr__(self)

    def __setitem__(self, index, value):
        if index >= len(self):
            print("Pardon me, but your index is out of bounds")
        else:
            list.__setitem__(self, index, value)

    def __getitem__(self, index):
        if index >= len(self):
            print("Pardon me, but your index is out of bounds")
        else:
            return list.__getitem__(self, index)
```

What does this do?

```
def __add__(self, other):
    output = polite()
    for x in self:
        output.append(x)
    if isinstance(other, int):
        output.append(other)
    elif isinstance(other, list):
        output.extend(other)
    else:
        print("Pardon me, but your other is confusing")
    return output
```

```
>>> L = polite()
Thank you for using polite lists!
>>> L.append(42)
>>> L.append(47)
>>> L
This polite list contains [42, 47]
>>> M = L + 5
Thank you for using polite lists!
>>> M
This polite list contains [42, 47, 5]
>>> N = M + [50]
Thank you for using polite lists!
>>> N
This polite list contains [42, 47, 5, 50]
```

Worksheet

Q

```
class polite(list):
    def __init__(self):
        print("Thank you for using polite lists!")

    def __repr__(self):
        return "This polite list contains " + list.__repr__(self)

    def __setitem__(self, index, value):
        if index >= len(self):
            print("Pardon me, but your index is out of bounds")
        else:
            list.__setitem__(self, index, value)

    def __getitem__(self, index):
        if index >= len(self):
            print("Pardon me, but your index is out of bounds")
        else:
            return list.__getitem__(self, index)
```

Complete the function

```
def __mul__(self, other):
```

```
>>> L = polite()
Thank you for using polite lists!
>>> L.append(42)
>>> L.append(47)
>>> L.append(23)
>>> M = polite()
Thank you for using polite lists!
>>> M.append(5)
>>> M.append(6)
>>> N = L * M # same as N = L.__mul__(M)
Thank you for using polite lists!
>>> N
This polite list contains [(42, 5), (42, 6), (47, 5), (47, 6), (23, 5), (23, 6)]
```

Worksheet

S

```
class polite(list):
    def __init__(self):
        print("Thank you for using polite lists!")

    def __repr__(self):
        return "This polite list contains " + list.__repr__(self)

    def __setitem__(self, index, value):
        if index >= len(self):
            print("Pardon me, but your index is out of bounds")
        else:
            list.__setitem__(self, index, value)

    def __getitem__(self, index):
        if index >= len(self):
            print("Pardon me, but your index is out of bounds")
        else:
            return list.__getitem__(self, index)
```

Complete the function

```
def __mul__(self, other):
    output = polite()
    for x in self:
        for y in other:
            output.append((x,y))
    return output
```

```
>>> L = polite()
Thank you for using polite lists!
>>> L.append(42)
>>> L.append(47)
>>> L.append(23)
>>> M = polite()
Thank you for using polite lists!
>>> M.append(5)
>>> M.append(6)
>>> N = L * M # same as N = L.__mul__(M)
Thank you for using polite lists!
>>> N
This polite list contains [(42, 5), (42, 6), (47, 5), (47, 6), (23, 5), (23, 6)]
```



Q

```
class polite(list):
    def __init__(self):
        print("Thank you for using polite lists!")

    def __repr__(self):
        return "This list contains " + list.__repr__(self)

    def __setitem__(self, index, value):
        if index >= len(self):
            print("Pardon me, but your index is out of bounds")
        else:
            list.__setitem__(self, index, value)

    def __getitem__(self, index):
        if index >= len(self):
            print("Pardon me, but your index is out of bounds")
        else:
            return list.__getitem__(self, index)
```

What needs to be done to do this?

```
>>> L = polite([1, 2, 3, 4])
Thank you for using polite
lists!
>>> L
This polite list contains [1,
2, 3, 4]
>>> 3 in L
True
```



S

```
class polite(list):
    def __init__(self):
        print("Thank you for using polite lists!")

    def __repr__(self):
        return "This list contains " + list.__repr__(self)

    def __setitem__(self, index, value):
        if index >= len(self):
            print("Pardon me, but your index is out of bounds")
        else:
            list.__setitem__(self, index, value)

    def __getitem__(self, index):
        if index >= len(self):
            print("Pardon me, but your index is out of bounds")
        else:
            return list.__getitem__(self, index)
```

What needs to be done to do this?

```
>>> L = polite([1, 2, 3, 4])
Thank you for using polite
lists!
>>> L
This polite list contains [1,
2, 3, 4]
>>> 3 in L
True
```

```
def __init__(self, lst=[]):
    print("Thank you for using polite lists!")
    list.__init__(self, lst)

# nothing needs to be done
# polite is a list
# list knows in (__contains__)
```

Default Arguments

```
class Person:  
    def __init__(self, ...):  
    def __repr__(self):  
    def is_asleep(self):  
  
class Student(Person):  
    def __init__(self,  
                 first_name,  
                 last_name,  
                 school = "Claremont Colleges",  
                 major = "undeclared"):  
        self.first_name = first_name  
        self.last_name = last_name  
        self.college = school  
        self.major = major  
  
>>> wally = Student("Wally", "Wart", "Harvey Mudd")  
>>> cecil = Student("Cecil", "Sagehen", "Pomona", "Biology and Mathematics")  
>>> la_semeuse = Student("La", "Semeuse", school="Scripps")  
>>> sammy = Student("Sammy", "the Owl", major="Engineering")  
>>> elmo = Student("Elmo")
```



In my experience, arguments
are usually default of
deperson who started dem!



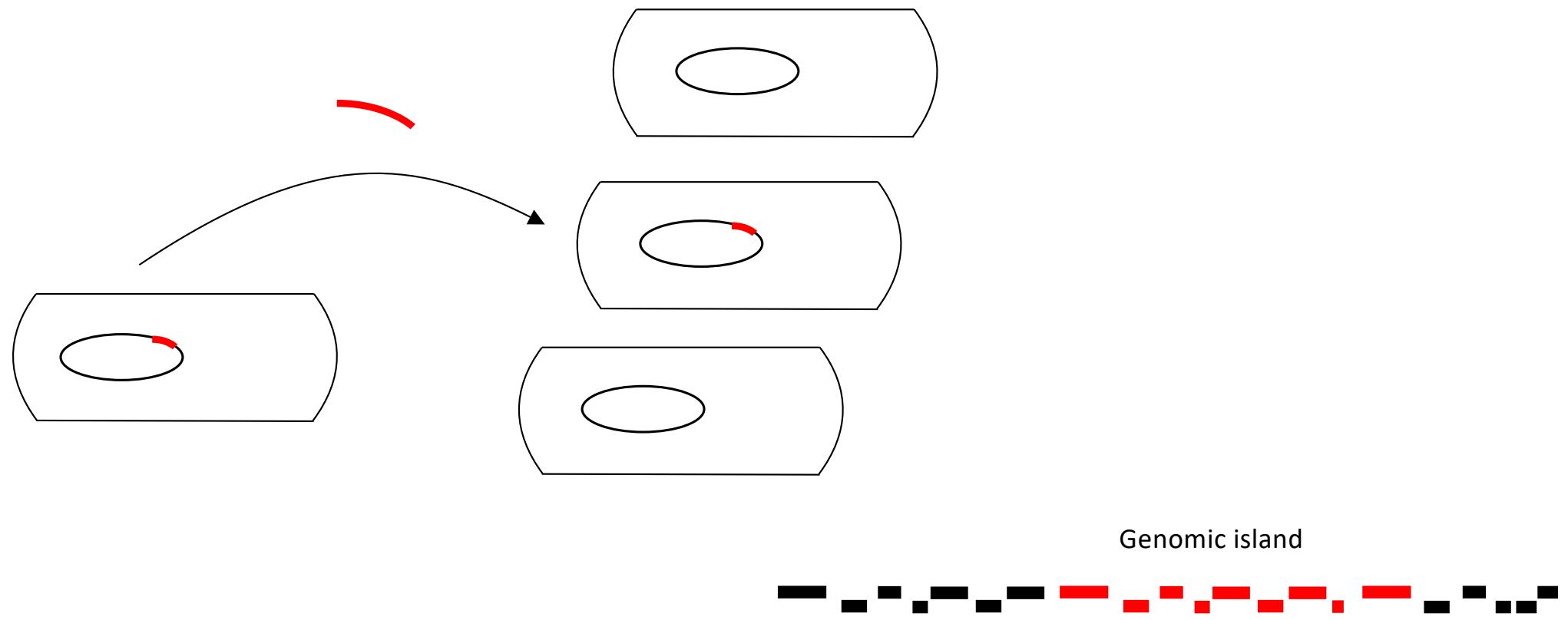


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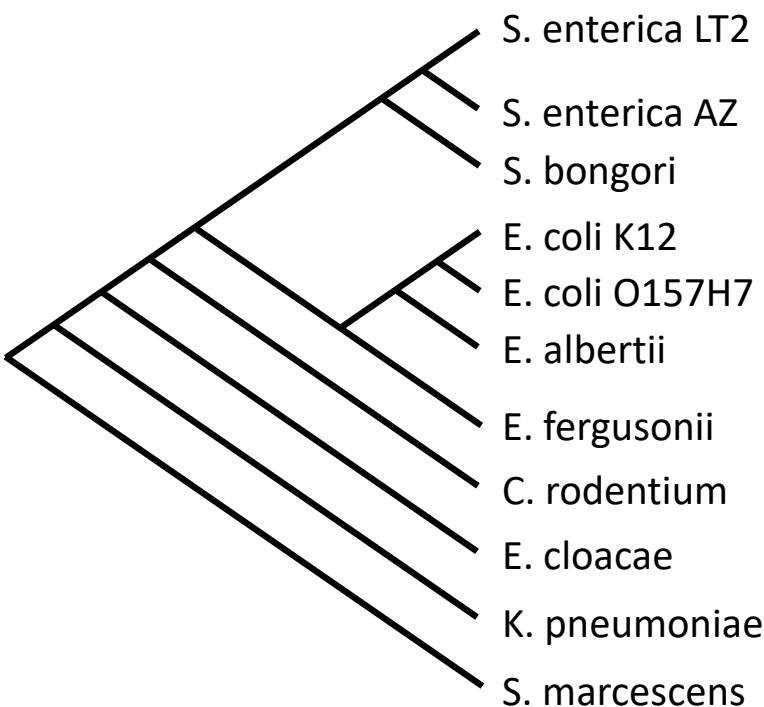
Plan for today

- Describe inheritance and its benefits
- An aside on Prof Bush's research, with examples of OOPs

Horizontal transfer plays a large role in microbial genome evolution



The problem: placing genomic islands in their phylogenetic context

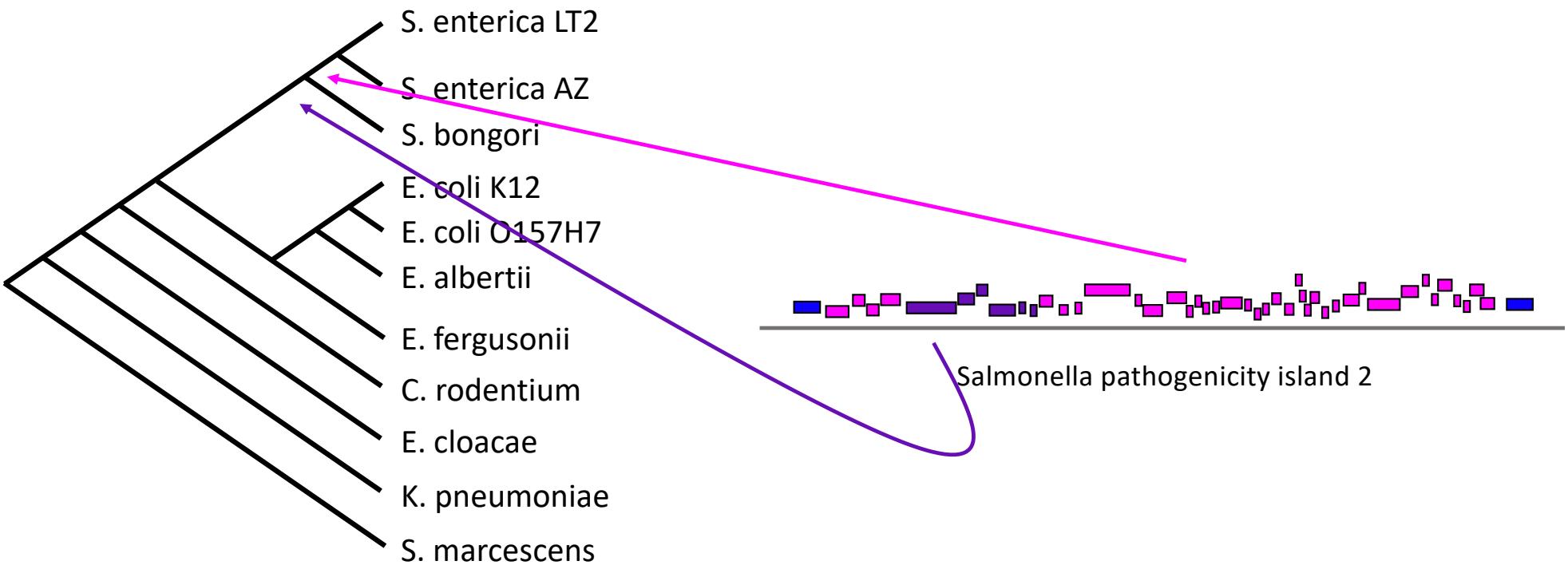


In the geneFinder assignment, you identified genes from Salmonella pathogenicity island 1



Salmonella pathogenicity island 2

The problem: placing genomic islands in their phylogenetic context

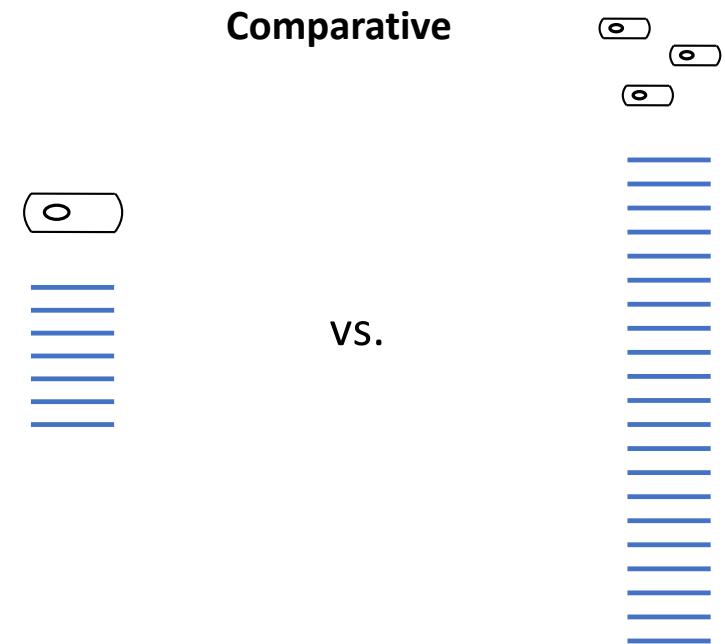


Previously existing automated methods don't identify islands in their phylogenetic context

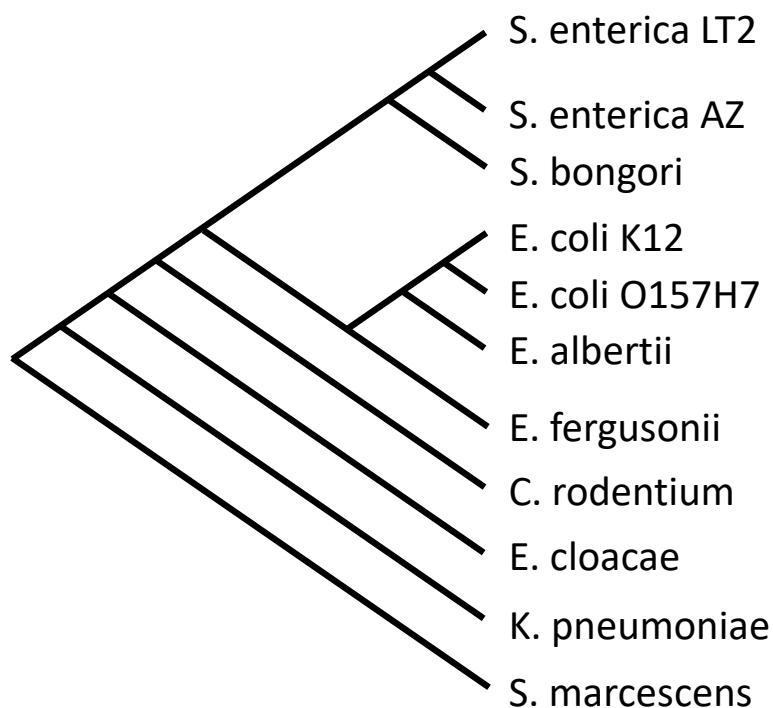
Sequence composition based

```
GTGGTAACGTTGGTTAGTGGTTGAAAGTAAACCCGGTGGCA  
GCAGCACATGAACAAGTTCGTCAGGTTAATAAATCAAATA  
TTTATTGACTTAGGTCAACCAGATACTTAACCAATAGAGAC  
ACACAGCACAGACAGATAAAAATTACAGAGTACACAACATC  
CATGAAACGCATCAGCACCACTATTACCACCAACCCA  
TTACACAGGTAACGGTGCAGGCTGACCGTACAGGAAATA  
CAGAAAAAAAGCCCGCACCTGAACAGTGCAGGCTTTTTTC  
GACCAAAGTTAACGAGGTAACAACCATGCGAGTGTGAAGT  
TCGGCGGTACGTCACTGGCAAATGCAGAACGGTTCTGCGG  
GTTGCCGATATTCTGGAAAGCAATGCCAGGCAGGGCAGGT  
AGCGACCGTACTTCTGCCCGCAAAAATTACCAACCACC  
TGGTGGCGATGATTGAAAAGACTATCGGC...
```

Comparative



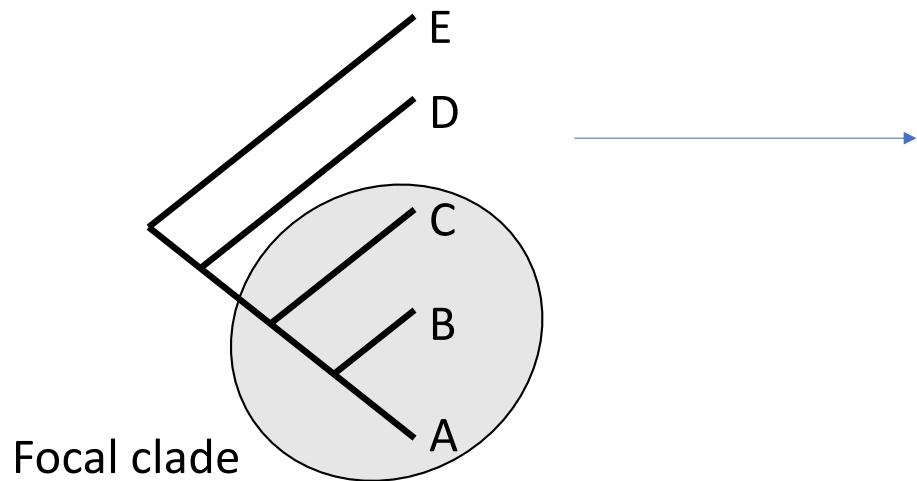
xenoGI: an automated approach to reconstructing the history of GI insertions into a clade



- Determine which genes were present in the MRCA, and which arrived via horizontal transfer
- Group genes with common origin into islands
- Map island insertion events onto the phylogenetic tree

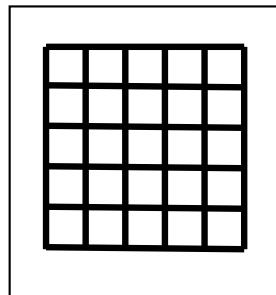
xenoGl: inputs and outputs

- A set of genomes in genbank format
- A phylogenetic tree for the species
- Text output specifying the origin of each gene
- Bed files to visualize islands in a genome browser

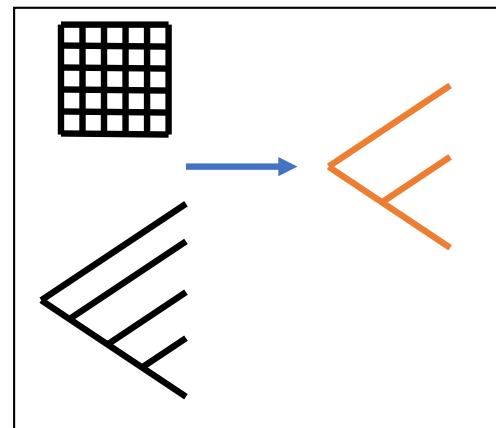


xenoGI: the general approach

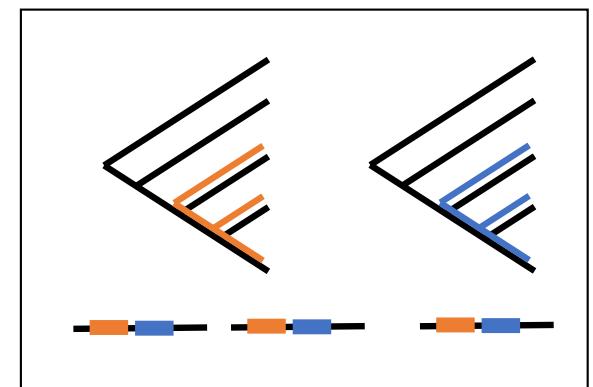
Calculate similarity scores



Form gene families



Group families into islands



Calculate similarity scores between genes

- All vs. all protein blast
- Global-alignment-based protein similarity score (raw score)
- Synteny scores

Raw score

E_coli_K12-AA	1 MRVLKFGGTSVANAERFLRVADILESNDARQGVATVLSAPAKITNHLVAM	50
E_albertii-BA	1 MRVLKFGGTSVANAERFLRVADILESNDARQGVATVLSAPAKITNHLVAM	50
E_coli_K12-AA	51 IEKTISGQDALPNISDAERIFAELLTGLAAAQPGFPLAQLKTFVDQEFAQ	100
E_albertii-BA	51 IEKTISGQDALPNISDAERIFAELLTGLADAQPGFPLAQLKTFVDLEFAQ	100
E_coli_K12-AA	101 IKHVLHGISLLGQCPDSINAALICRGEKMSIAIMAGVLEARGNVTVIDP	150
E_albertii-BA	101 IKHVLHGISLLGQCPDSINAALICRGEKMSIAIMAGVLEARGNVTVIDP	150

- Based on global alignment
- Uses parasail python package

Local synteny score

Gene X in one strain



Gene Y in another strain



There's a Score class...

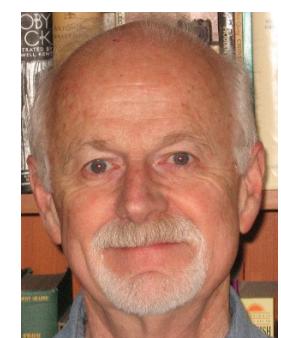
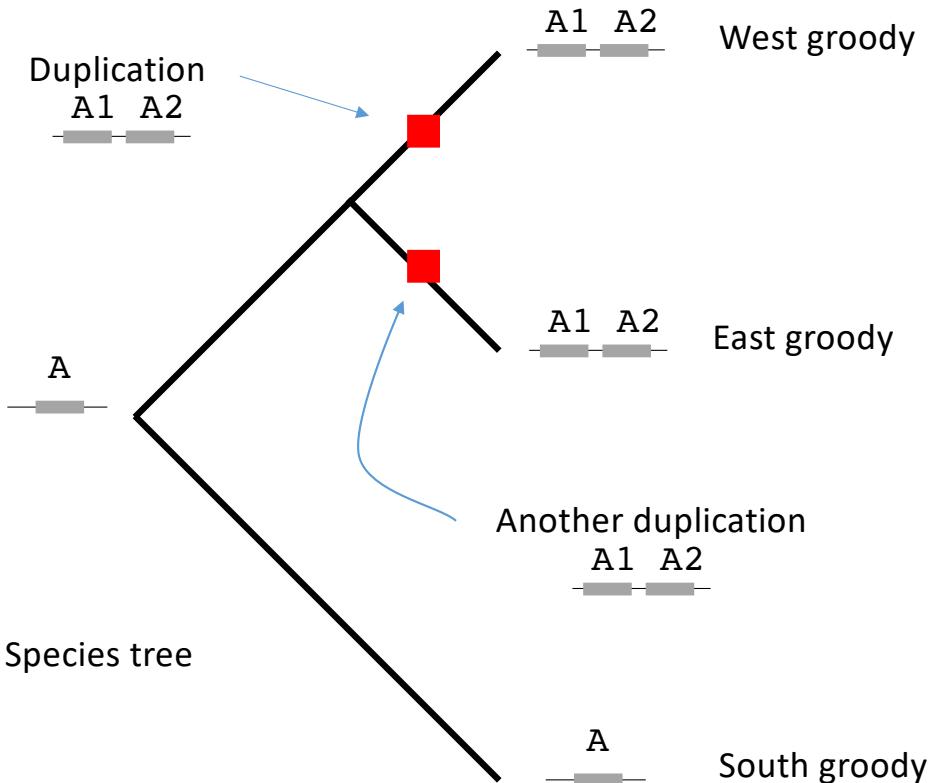
```
class Score:

    def __init__(self):
        '''Create an object for storing scores.'''

        self.endNodesToEdgeD = {}
        self.numEdges = 0 # to start out
        self.strainPairScoreLocationD = {}
        self.scoreD = {}

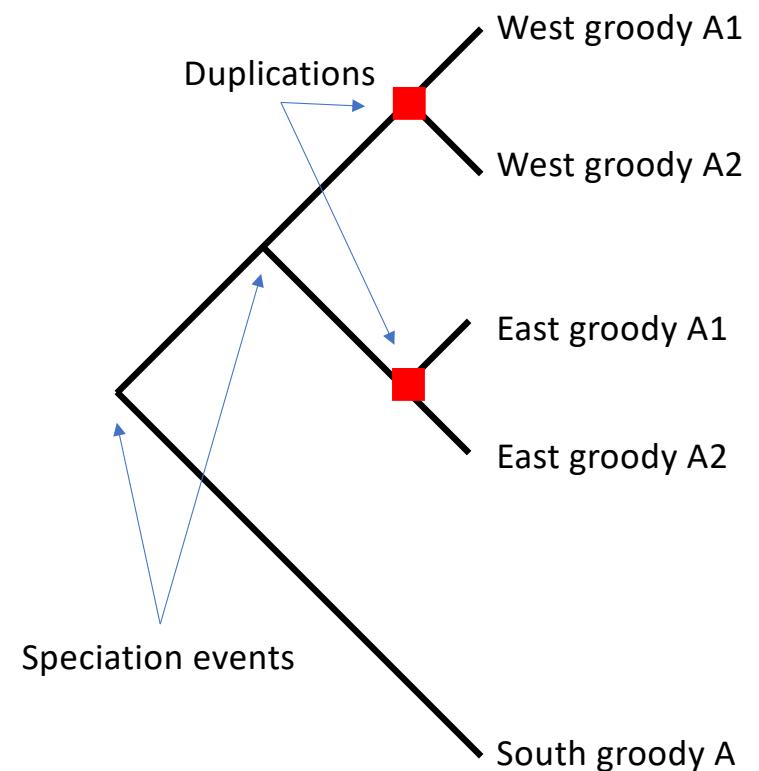
    def initializeDataAttributes(self,blastFnL,paramD,strainNamesT):
        '''This method takes a new, empty object and fills the data attributes
        by reading through blast files to identify pairs of genes with
        edges. Also creates the array for storing raw scores, initialized to
        0. Arrays for other score types will be created later. The genes
        included here depend on what is found in the blast files in blastFnL.
```

Evolution of the “A” gene family

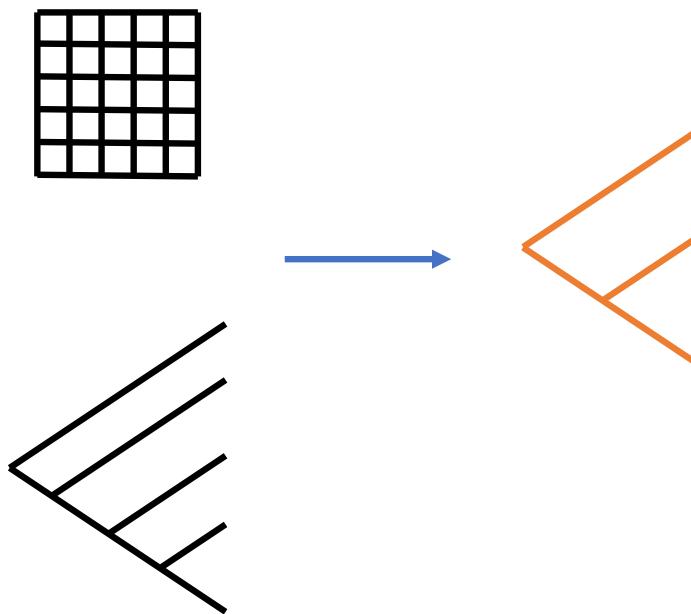


A gene tree

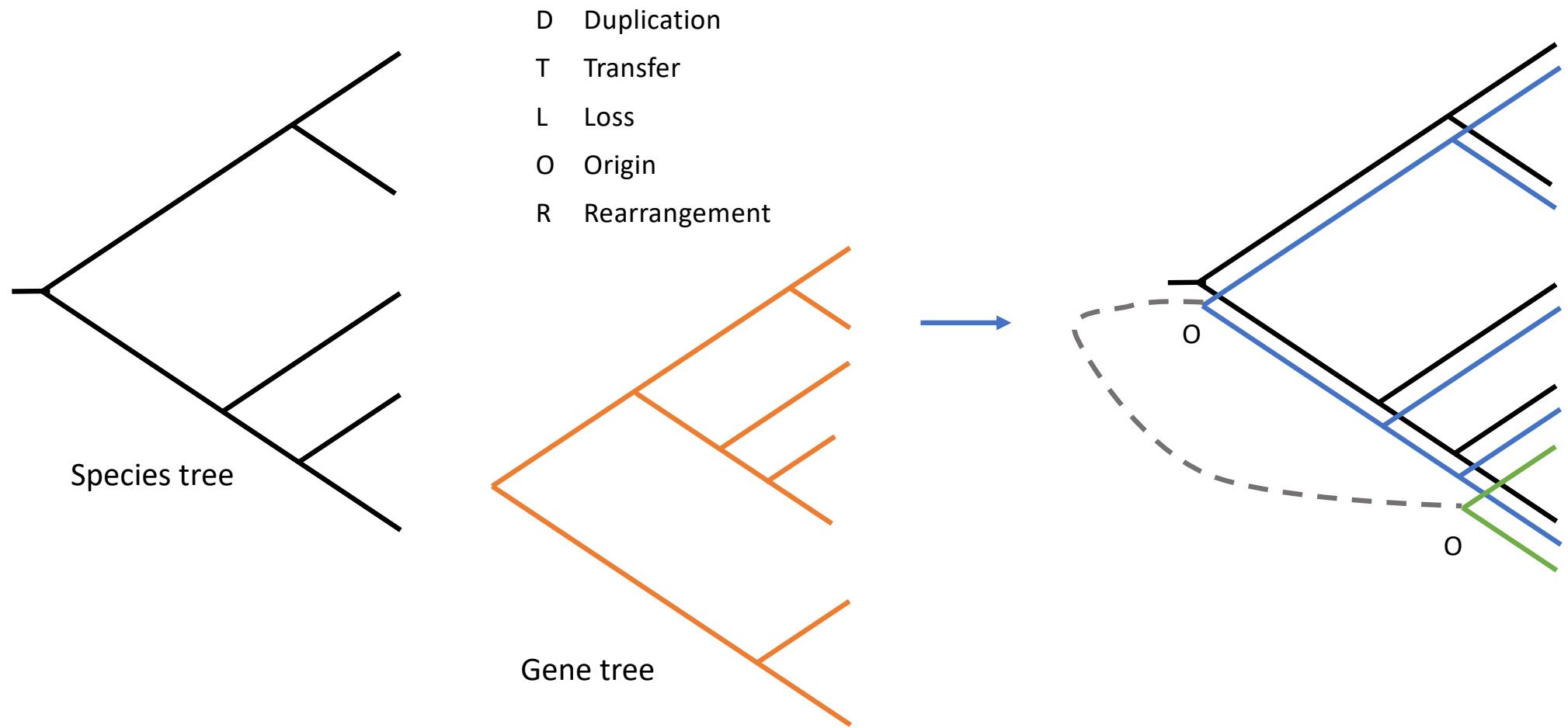
- Tips are genes
- Internal nodes may be speciation events **or** duplication events



Form gene families taking account of the species tree and synteny information

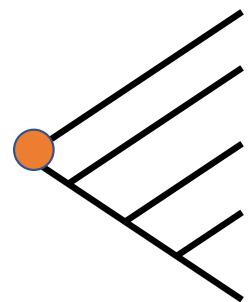


Use custom DTLOR reconciliation algorithm to make gene families

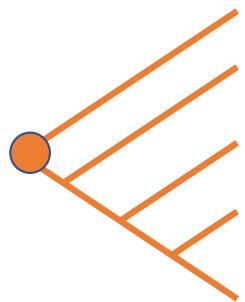
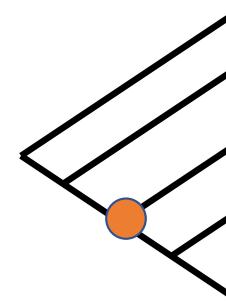


An “origin” family descends from a single ancestor gene within the species tree

Core gene family



HGT gene family



```

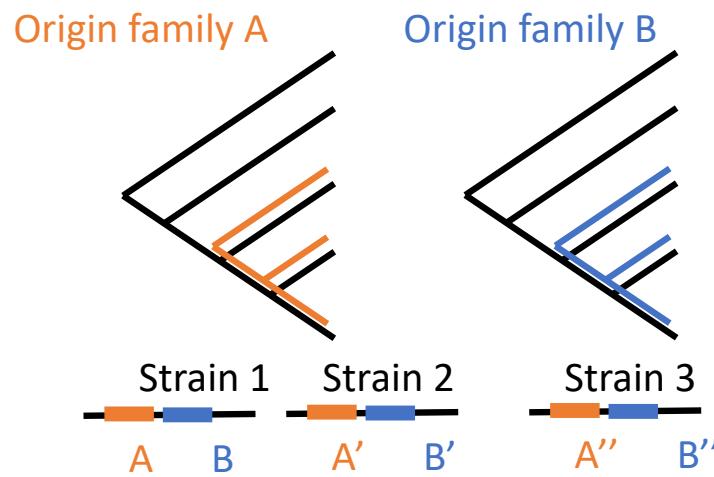
class Family:
    def __init__(self,famNum,mrca,geneTree0=None,dtlorMprD=None,sourceFam=None):
        '''Base class to be inherited by initialFamily and originFamily.'''
        self.famNum = famNum
        self.mrca = mrca
        self.locusFamiliesL = [] # will contain locusFamily objects for this family
        self.geneTree0 = geneTree0 # gene tree object
        self.dtlorMprD = dtlorMprD # mpr dict
        self.sourceFam = sourceFam # specifies the corresponding fource fam (blast or ifam)
        # rest not shown...

class initialFamily(Family):
    def __init__(self,famNum,mrca,geneTree0=None,dtlorCost=None,dtlorGraphD=None,dtlorMprD=None,sourceFam=None,productFamT=None):
        '''Initialize an object of class initialFamily.'''
        super().__init__(famNum,mrca,geneTree0,dtlorMprD,sourceFam)
        # dtlorCost is cost from dtlor alg. A positive integer. In
        # the case where a family was re-run with permissive origin
        # costs, we make this value negative.
        self.dtlorCost = dtlorCost
        self.dtlorGraphD = dtlorGraphD
        self.productFamT = productFamT # ids of origin families made from this ifam
        # rest not shown...

class originFamily(Family):
    def __init__(self,famNum,mrca,geneTree0=None,dtlorMprD=None,sourceFam=None):
        '''Initialize an object of class originFamily.'''
        super().__init__(famNum,mrca,geneTree0,dtlorMprD,sourceFam)
        # rest not shown...

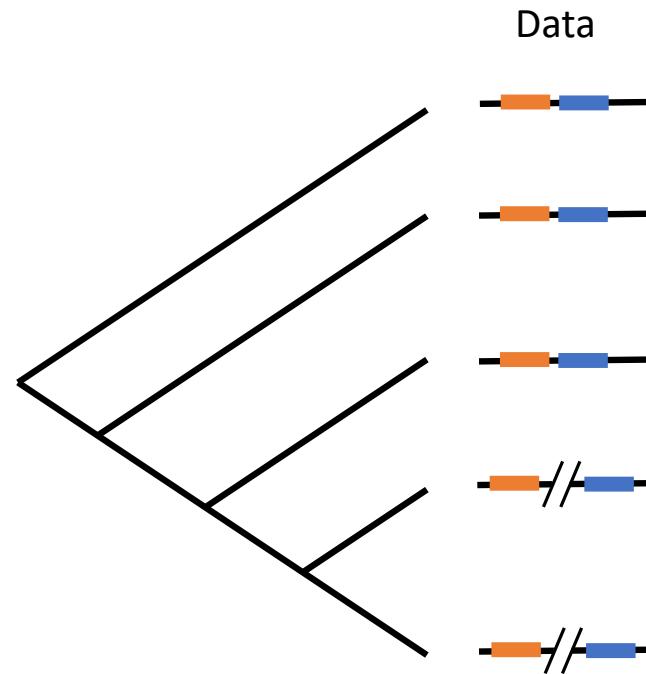
```

Merge origin families with a common origin into islands



A case where we'd like to merge families into an island.

Parsimony based cost with a simple model of genome evolution



Assuming in ancestor: cost = 1

Assuming in ancestor: cost = 3

- Create Island data structure. Initially, each island contains one family
- Calculate rearrangement score between all pairs of islands

$$\text{Rearrangement score} = \text{Cost assuming } \textcolor{orange}{-}/\textcolor{blue}{-} \text{ in ancestor} - \text{Cost assuming } \textcolor{orange}{-}\textcolor{blue}{-} \text{ in ancestor}$$

- Greedily merge islands

```
class LocusIsland:

    def __init__(self, idnum, mrca, locusFamilyL):
        '''Create a LocusIsland object.'''
        self.id = idnum
        self.mrca = mrca
        self.locusFamilyL=locusFamilyL # list of locus family numbers in the island, in order

    def __repr__(self):
        return "<id:"+str(self.id)+", mrca:"+str(self.mrca)+", locusFamilyL:"+str(self.locusFamilyL)+">"

    def __len__(self):
        return len(self.locusFamilyL)

# rest not shown...
```

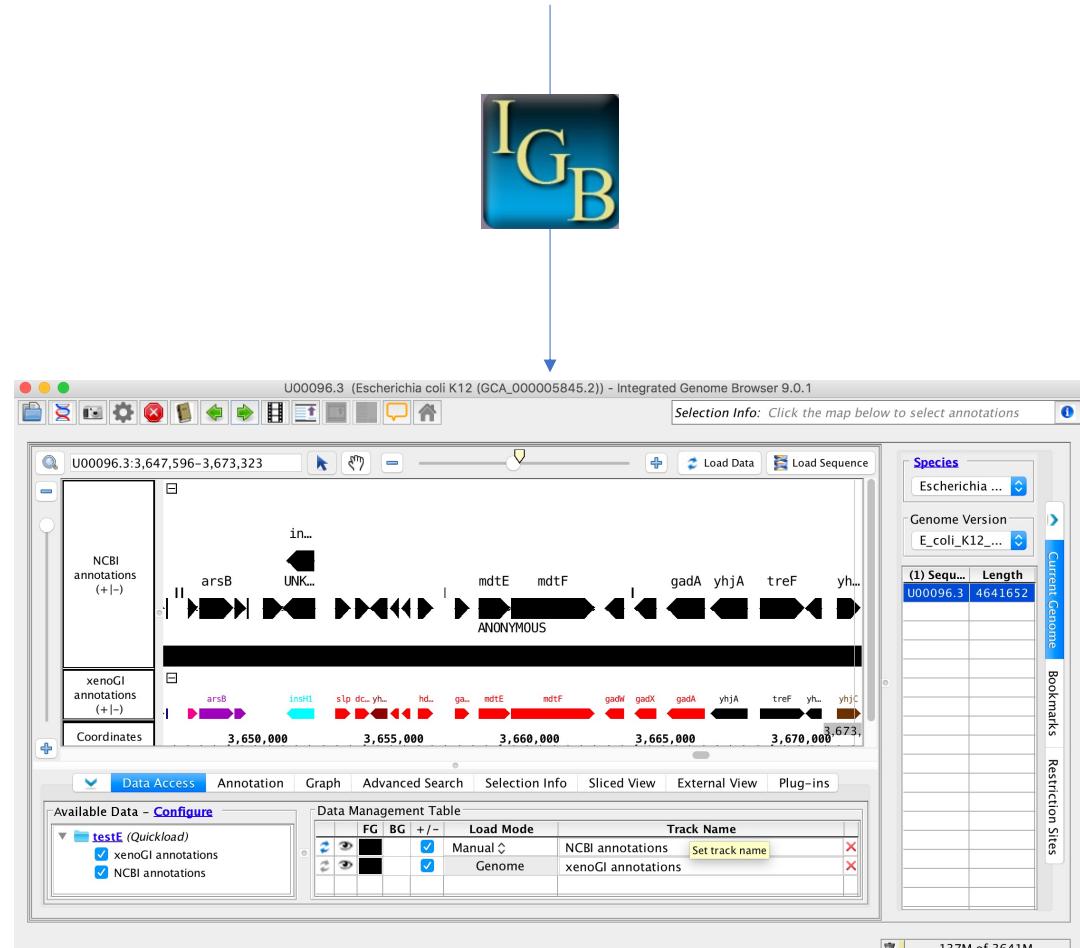
Output

- Text based
 - Organized by species tree node
 - Organized by gene
- Bed file for visualization in a genome browser

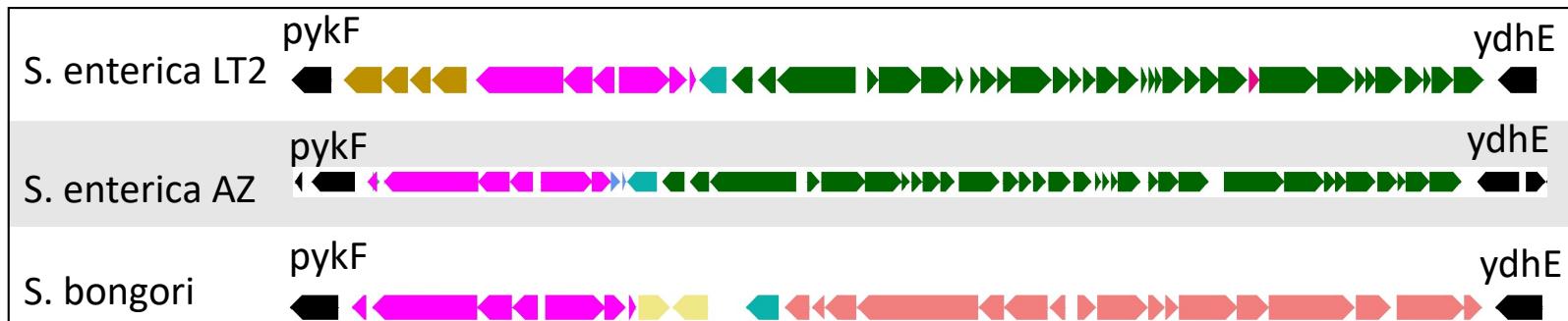
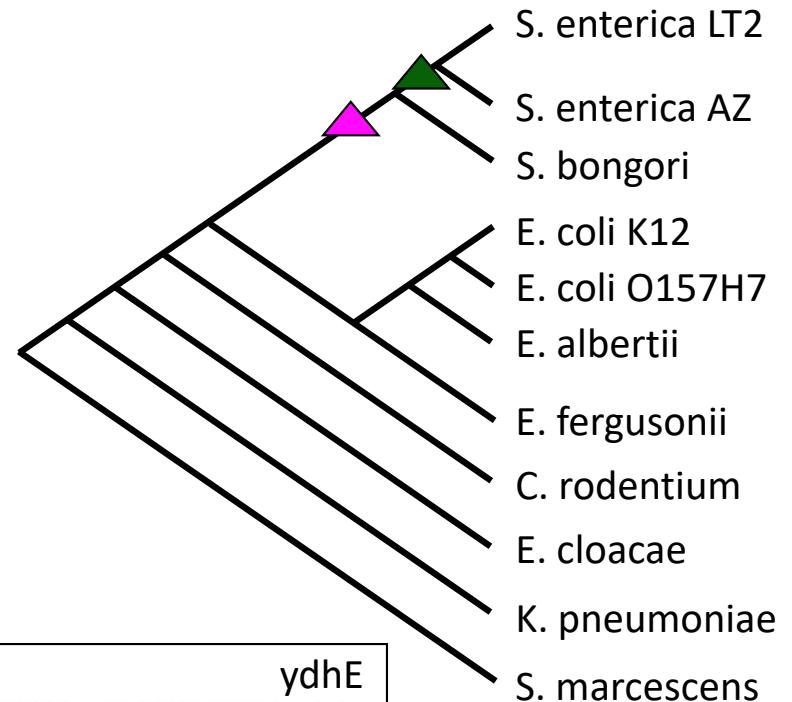
```
##### Islands at node i0

---
Island 3456
Family | E_coli_K12 | E_albertii
3456 | E_coli_K12-AAC76118.1(higB) | E_albertii-BAT45100.1
3586 | E_coli_K12-AAC76117.1(higA) | E_albertii-BAT45099.1(ygjM)
3559 | E_coli_K12-AAC76116.1(fadH) | E_albertii-BAT45098.1(fadH)
3520 | E_coli_K12-AAC76115.1(ygjK) | E_albertii-BAT45097.1(ygjK)
3532 | E_coli_K12-AAC76114.1(ygjJ) | E_albertii-BAT45096.1(ygjJ)
3497 | E_coli_K12-AAT48165.1(ygjI) | E_albertii-BAT45095.1(ygjI)
3484 | E_coli_K12-AAC76112.1(ebgC) | E_albertii-BAT45094.1(ebgC)
3562 | E_coli_K12-AAT48164.1(ebgA) | E_albertii-BAT45093.1(ebgA)
3564 | E_coli_K12-AAC76110.1(ebgR) | E_albertii-BAT45092.1(ebgR)
3533 | E_coli_K12-AAC76109.1(ygjH) | E_albertii-BAT45091.1(ygjH)
3472 | E_coli_K12-AAC76108.3(patA) | E_albertii-BAT45090.1(ygjG)
```

```
track name=E_coli_K12 type=bedDetail visibility=full itemRgb="On" useScore=0
U00096.3      189     255     thrL    0      +      189     189     245,130,48 ...
U00096.3      336     2799    thrA    0      +      336     336     0,0,0   ...
...
```

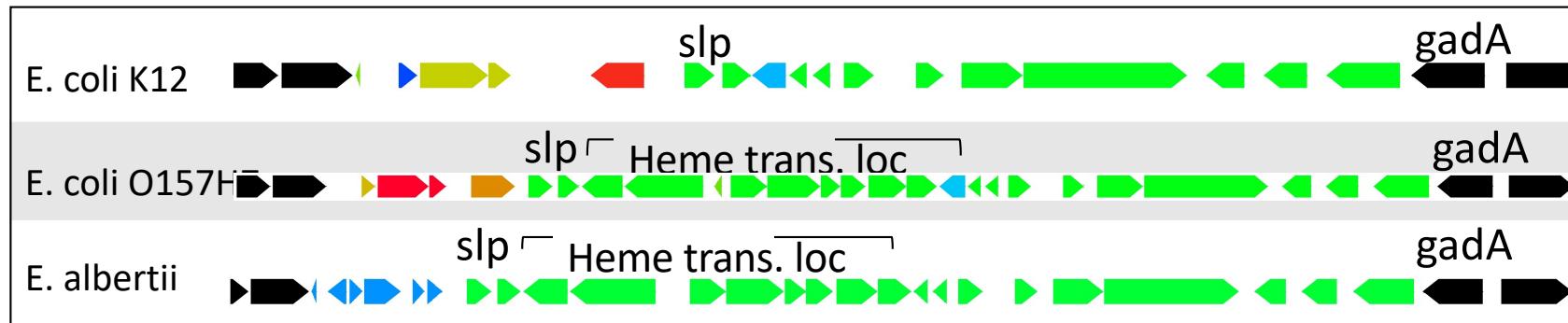
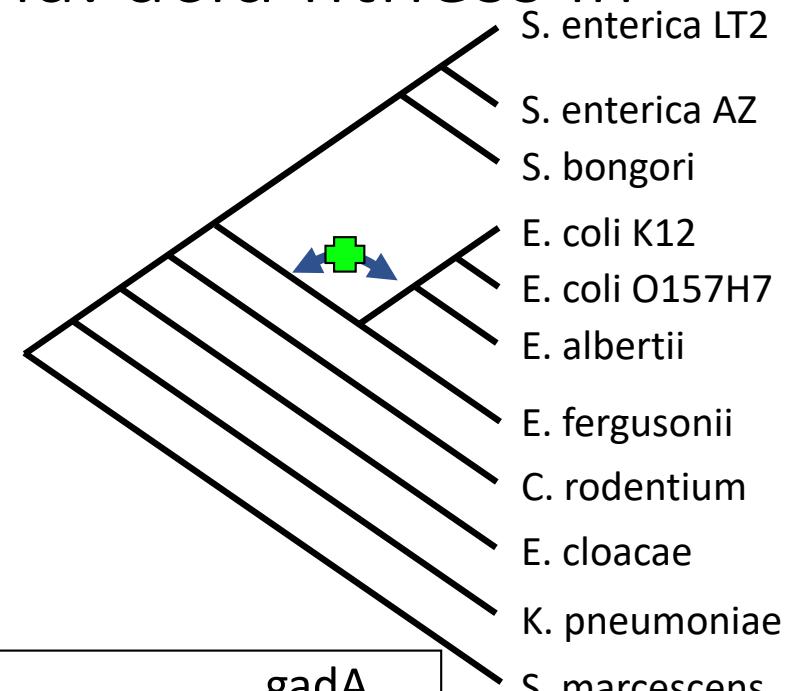


Examples from enteric bacteria: Salmonella pathogenicity island 2

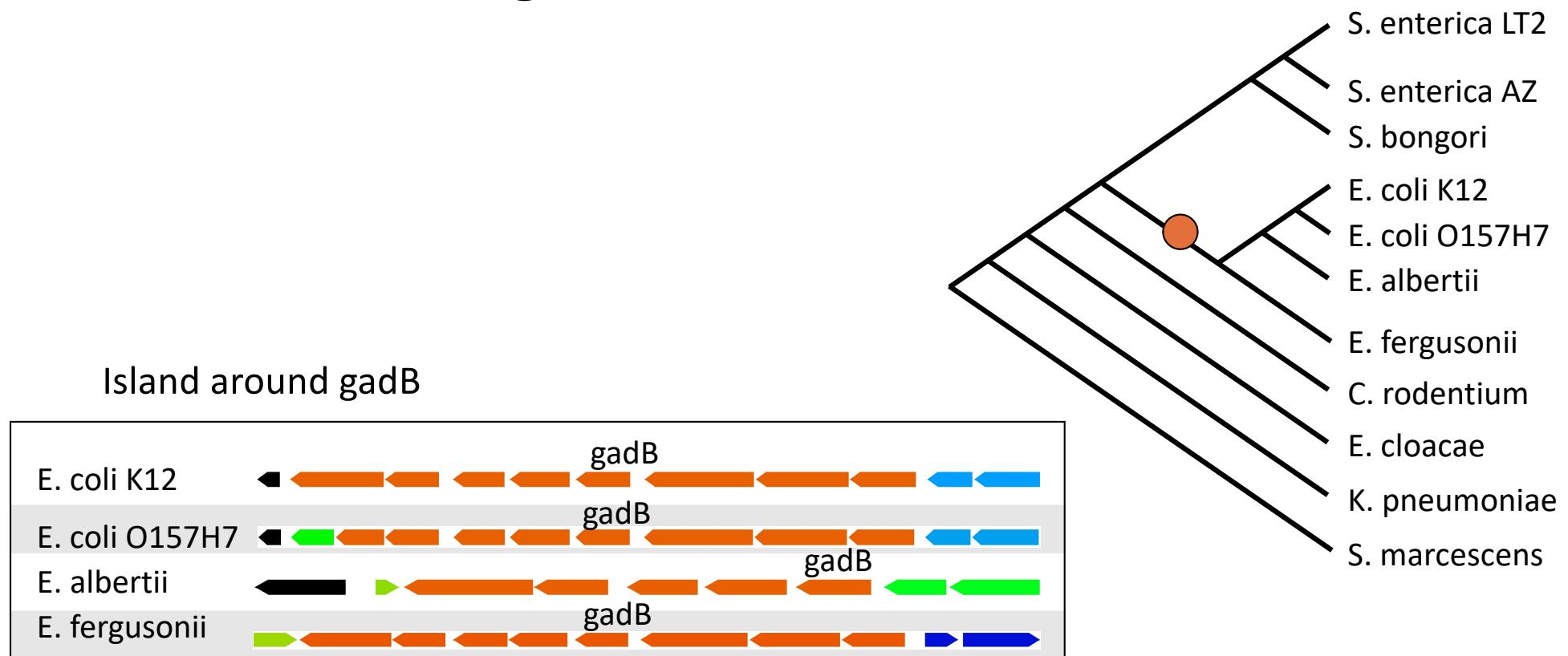


Examples from enteric bacteria: acid fitness in the Escherichia clade

- AFI correctly identified
- Co-localized with heme transport locus
- Timing



Example from enteric bacteria: the genomic island around gadB



Resources

Available as a pip installable python package.

Code :

<https://github.com/ecbush/xenoGI>

A simple web service:

<http://www.cs.hmc.edu/xgiWeb/>

Upload files for xenoGI

Note that we limit runs on the web server to 12 species. If you need to do more than that, then you should run xenoGI locally.

Select a tree file to upload: No file chosen

Select genbank gbff files to upload:

No file chosen

Enter the name of root focal clade

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