

#Orthologs and Paralogs

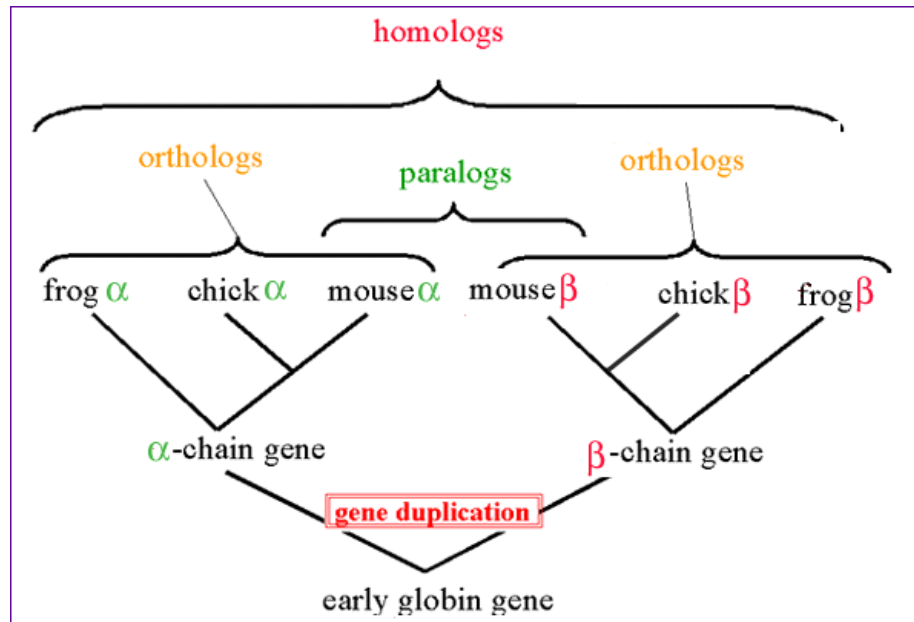
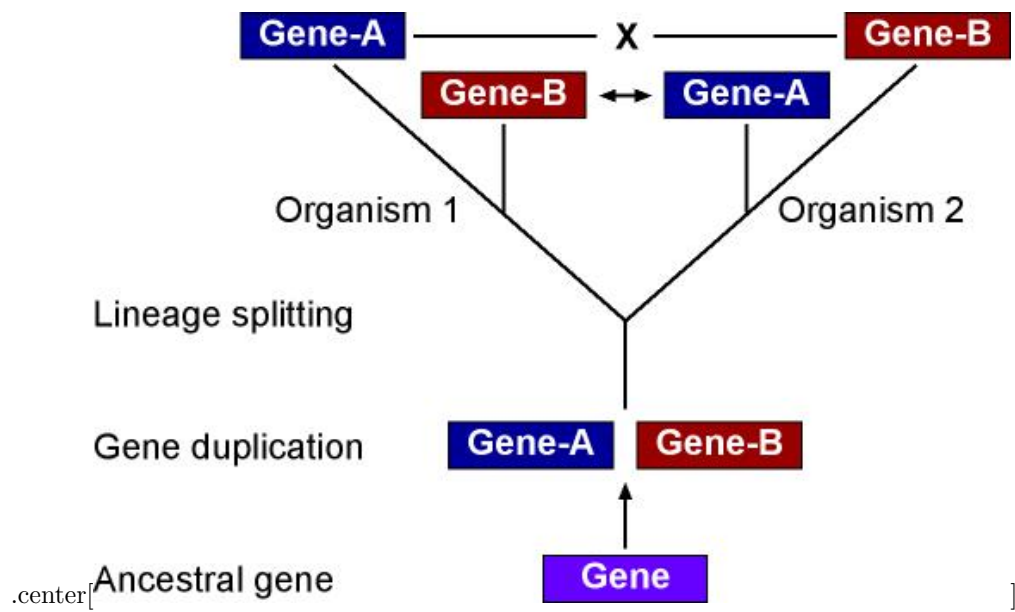


Figure 1: Orthologs

## Gene families and Orthology

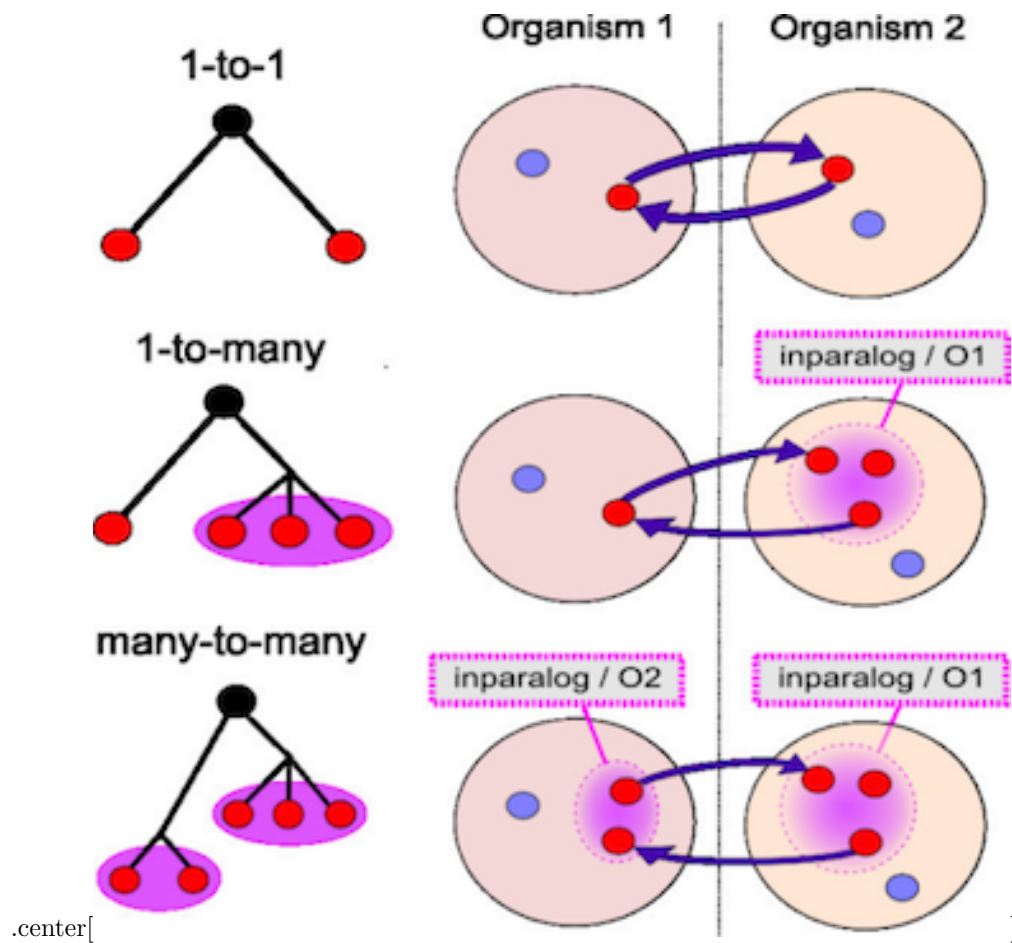
Problem: How to find “same” genes across multiple species.

Genes can duplicate (Paralogs) and can be identical due to descent (Ortholog)



## Methods

- BLAST: 1 way BLAST (Gene A in Species X, what is best hit in Species Y)
- BLAST: reciprocal BLAST



## Trees can help resolve relationships

Best hits can sometimes be wrong (B) though it can be resolved with phylogenetics.

## Reciprocal Searches

- Bi-directional or Reciprocal BLAST

## Implement Bidirectional

Method to find best top hit in one direction and the reverse.

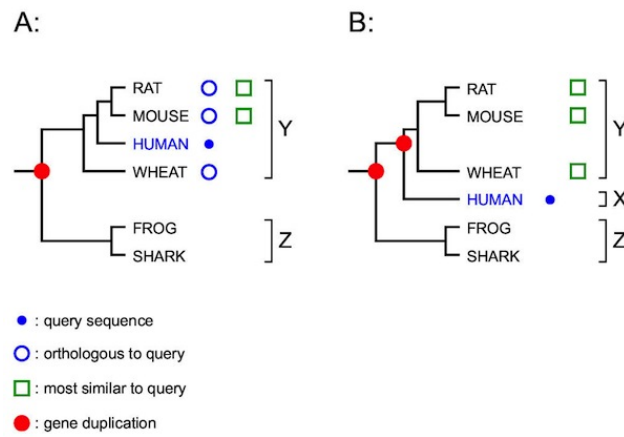


Figure 2: RIO

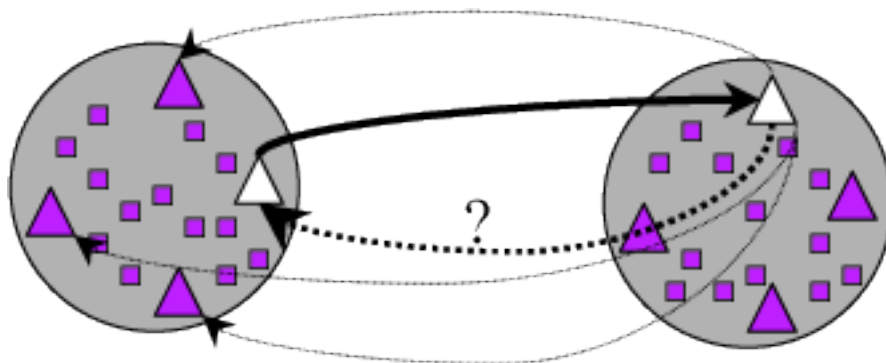


Figure 3: BRH

Let's walk through the [code](#)

*Will write this in Python in Class*

## Clustering

- Lumping genes together based on similarity linkage
- Single-linkage means if there is a link between A-B then they are in a cluster

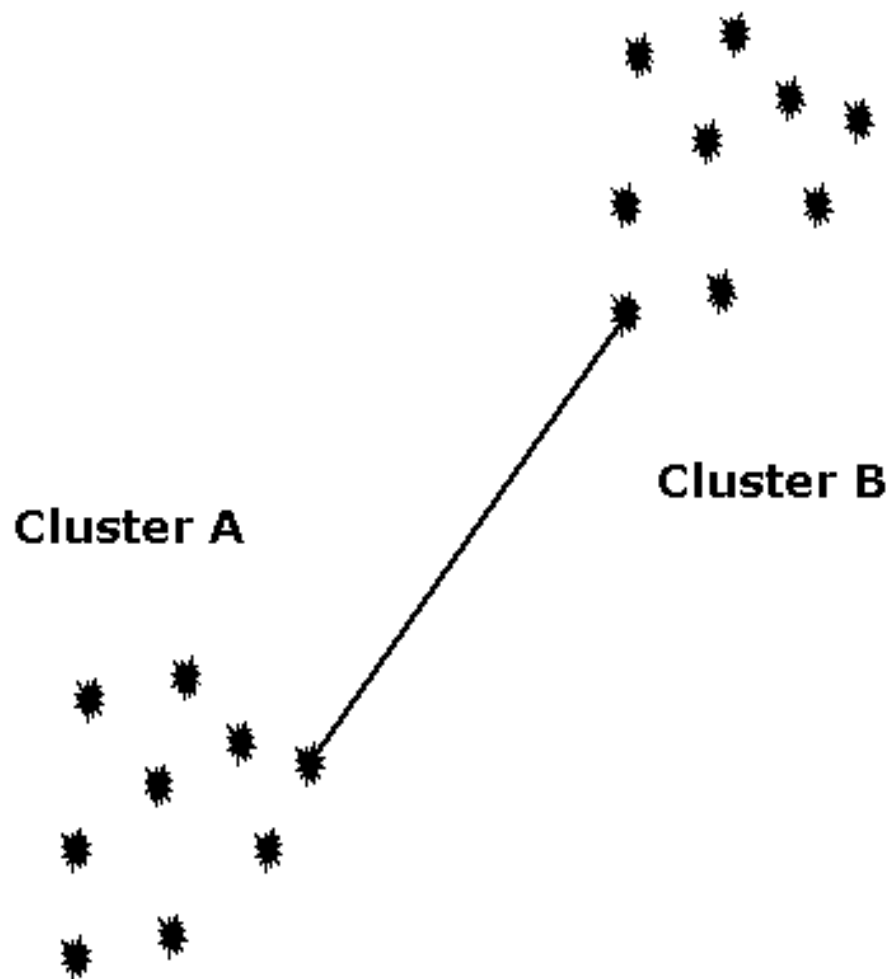


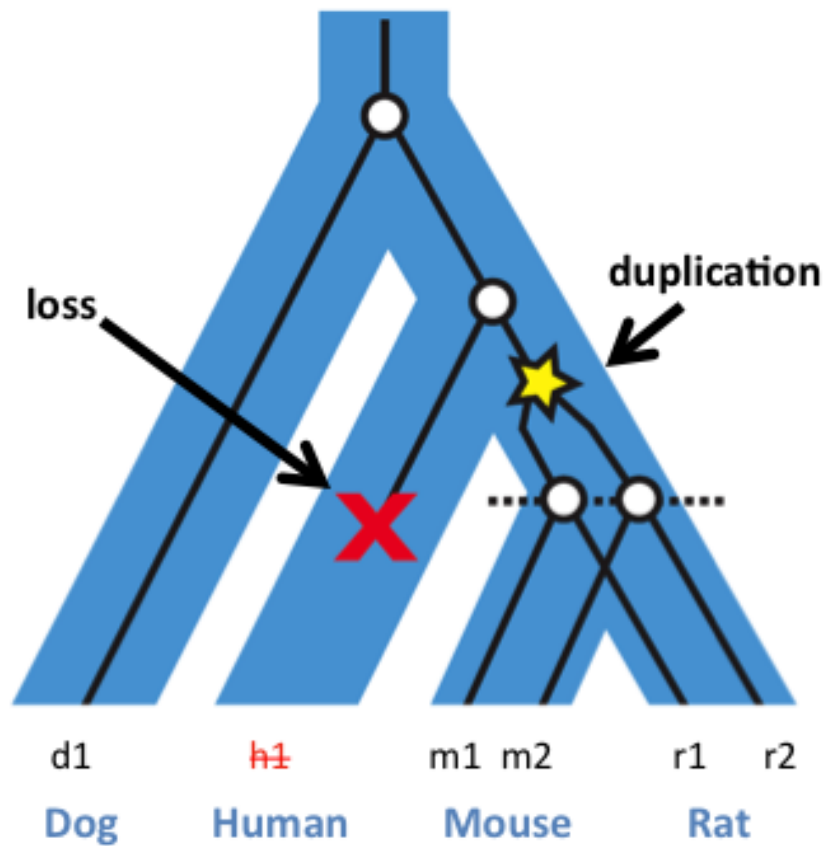
Figure 4: SingleLinkage

## Code up single-linkage

Let's look at some [code](#).

*Will write this in Python in Class*

## Issues



.center[ ]

## Existing solution

- OrthoMCL - requires SQL Database
- Orthagogue - nearly identical results but runs w/o DB

## Steps to build orthologs on cluster

Make sure genome protein FASTA file is

```
>SPECIESPREFIX|GENENAME
```

See [https://github.com/biodataprogram/GEN220\\_2019\\_examples/tree/master/Bioinformatics\\_1](https://github.com/biodataprogram/GEN220_2019_examples/tree/master/Bioinformatics_1) for example script for running orthofinder.

```
#!/usr/bin/bash
#SBATCH --ntasks 16 --mem 8G -p short
module load ncbi-blast
module load orthofinder
module load miniconda2
CPU=8

mkdir -p cyanobacteria
cd cyanobacteria
curl -L -O ftp://ftp.ensemblgenomes.org/pub/bacteria/release-45/fasta/bacteria_10_collection
curl -L -O ftp://ftp.ensemblgenomes.org/pub/bacteria/release-45/fasta/bacteria_0_collection
curl -L -O ftp://ftp.ensemblgenomes.org/pub/bacteria/release-45/fasta/bacteria_4_collection

for file in *.fa.gz
do
  m=$(basename $file .pep.all.fa.gz)
  pigz -dc $file > $m.fasta
done
pigz -k *.fa.gz
cd ..

orthofinder.py -a $CPU -f cyanobacteria
```

## Ortholog results

Opening the file cyanobacteria/Results\_\_Nov08/Orthogroups.txt

### Format

GroupName\tSp1\_Gene1, Sp1\_Gene2\tSp2\_Gene1, Sp2\_Gene2\tSp3\_Gene1, Sp3\_Gene2

```
Cyanobacterium_aponinum_pcc_10605.ASM31767v1    Nostoc_punctiforme_pcc_73102.ASM2002v1
OG00000000    EKQ66605, EKQ66611, EKQ66662, EKQ66782, EKQ66954, EKQ66984, EKQ67084, EK
EKQ67433, EKQ67590, EKQ67680, EKQ67799, EKQ67807, EKQ67983, EKQ68026, EKQ68032, EKQ68054, EK
EKQ69279, EKQ69300, EKQ69345, EKQ69368, EKQ69506, EKQ69549, EKQ69629, EKQ69630, EKQ69655, EK
EKQ70786, EKQ70840, EKQ70870, EKQ70894, EKQ71088, EKQ71090, EKQ71265, EKQ71335
```

OG0000001 AFZ52442, AFZ54265, AFZ54640 ACC78968, ACC78978, ACC79054, ACC79090, ACC79138  
 81797, ACC82091, ACC82628, ACC82978, ACC83035, ACC83215, ACC83711, ACC84528, ACC84844, ACC84  
 69971, EKQ69995, EKQ70003, EKQ70556, EKQ70833, EKQ71286  
 OG0000002 AFZ55137 ACC79344, ACC80485, ACC80595, ACC82143, ACC82836, ACC82962, ACC83845  
 ACC84972, ACC84974, ACC84981, ACC84982, ACC84983, ACC85032 EKQ66950, EKQ67597, EKQ67615, EK  
 OG0000003 AFZ53198 ACC78875, ACC78976, ACC79256, ACC79524, ACC79759, ACC80145, ACC80528  
 ACC82769, ACC83025, ACC83081, ACC83457, ACC83602, ACC83721, ACC83749, ACC84422, ACC85331  
 OG0000004 ACC80422, ACC80525, ACC80662, ACC80851, ACC80857, ACC80914, ACC81440, ACC815  
 6, ACC83981, ACC84622, ACC84732, ACC85457 EKQ66830, EKQ66911, EKQ67039, EKQ67311, EKQ69997  
 OG0000005 AFZ52318, AFZ52611, AFZ52613, AFZ52925, AFZ52973, AFZ53626, AFZ53840, AFZ53841,  
 CC82559, ACC83603, ACC83674, ACC85005, ACC85009 EKQ67574, EKQ67809, EKQ69976  
 OG0000006 AFZ52319, AFZ53394, AFZ54017, AFZ54472 ACC79360, ACC79745, ACC79853, ACC80832,  
 478, EKQ67551, EKQ67724, EKQ67810, EKQ68266  
 OG0000007 AFZ53704, AFZ54461, AFZ54462 ACC79786, ACC80242, ACC80282, ACC80538, ACC80768  
 2, EKQ68369, EKQ70142, EKQ70145, EKQ71300

## Write script to turn this into a table

ORTHOLOG_GRP	SP1	SP2	SP3
ORTHO_0001	10	5	
ORTHO_0002	1	1	