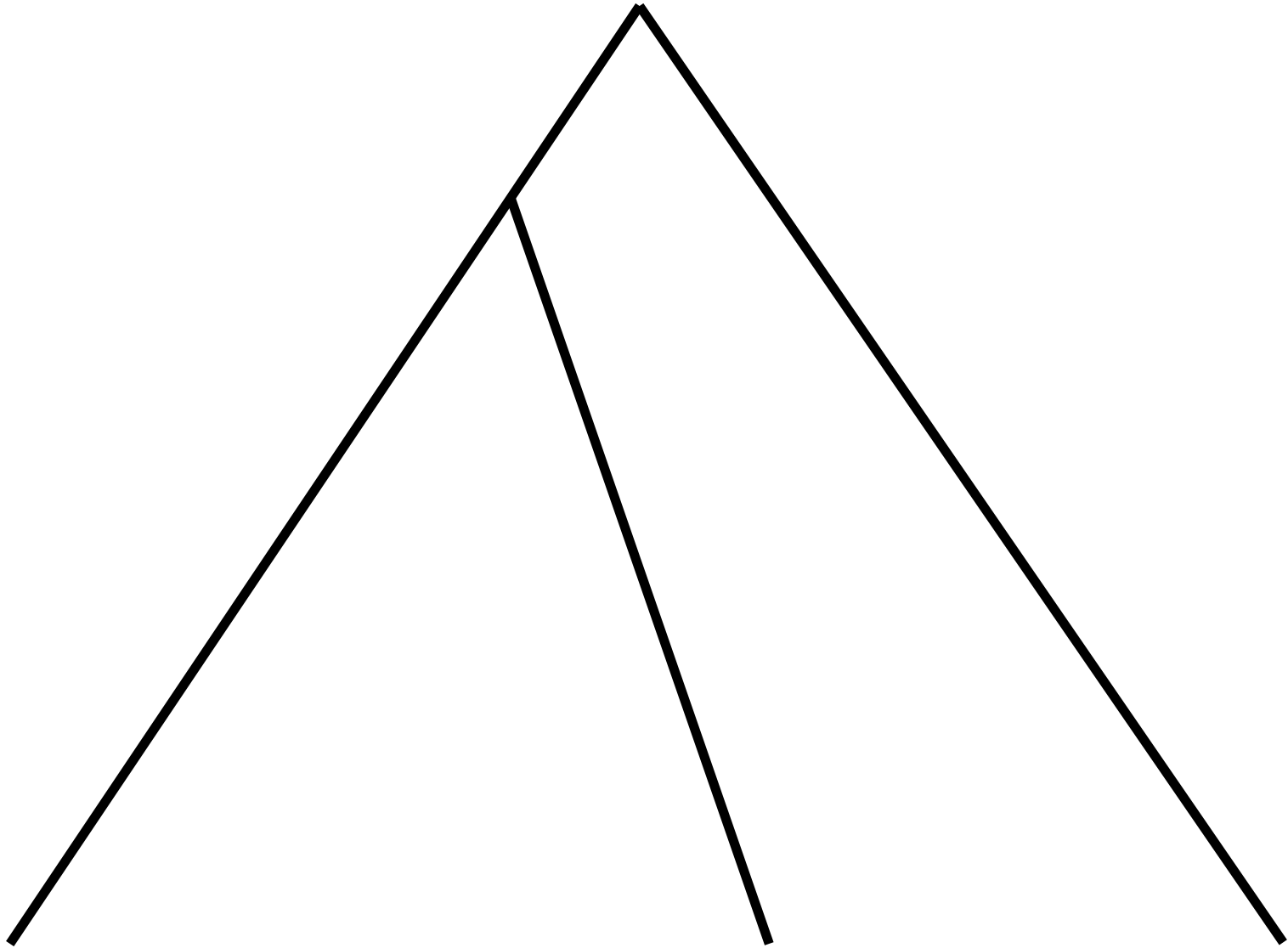
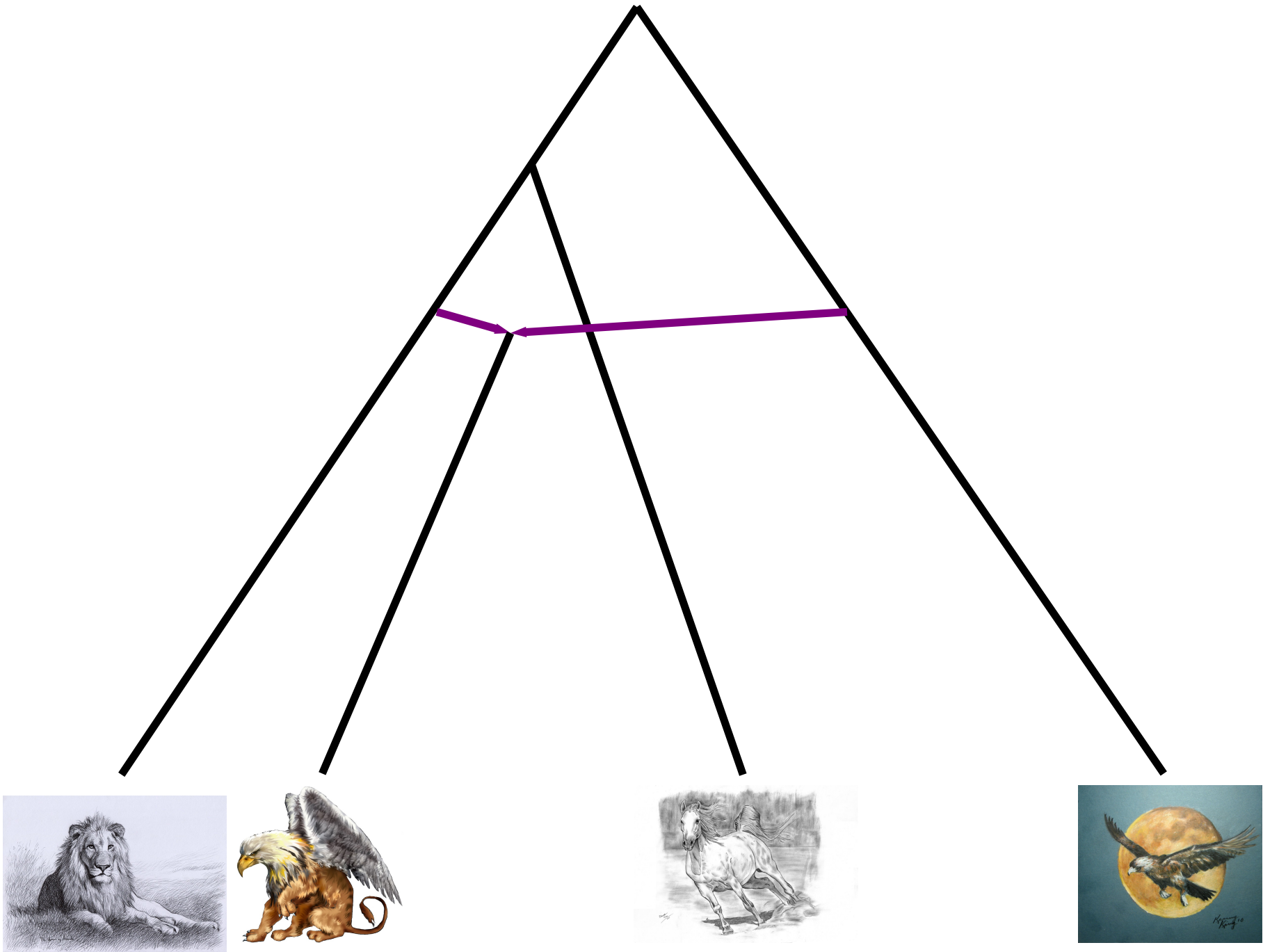




# Phylogeny and Sequence Simulation with Hybridization

Michael Woodhams  
School of Mathematics and Physics, University of Tasmania





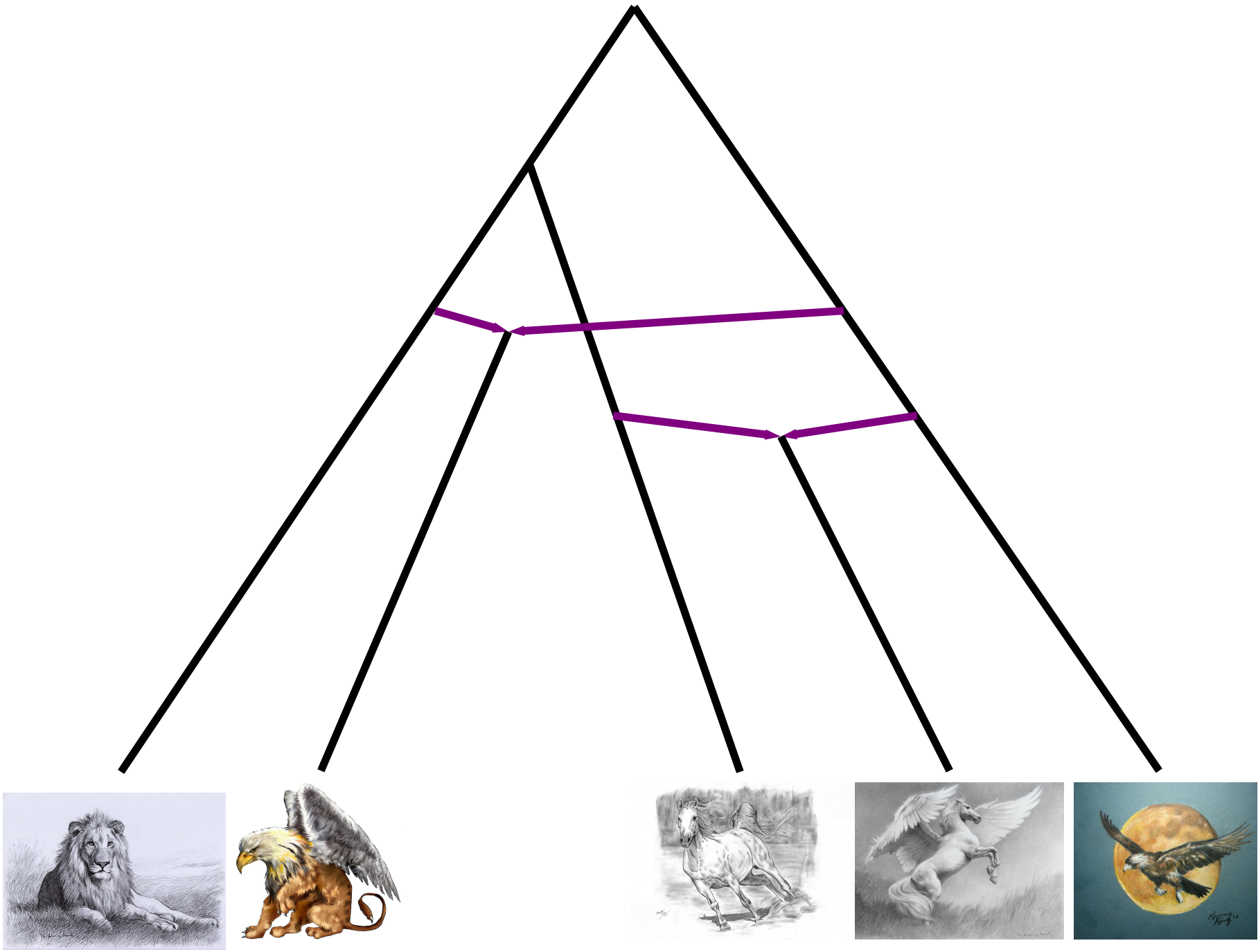
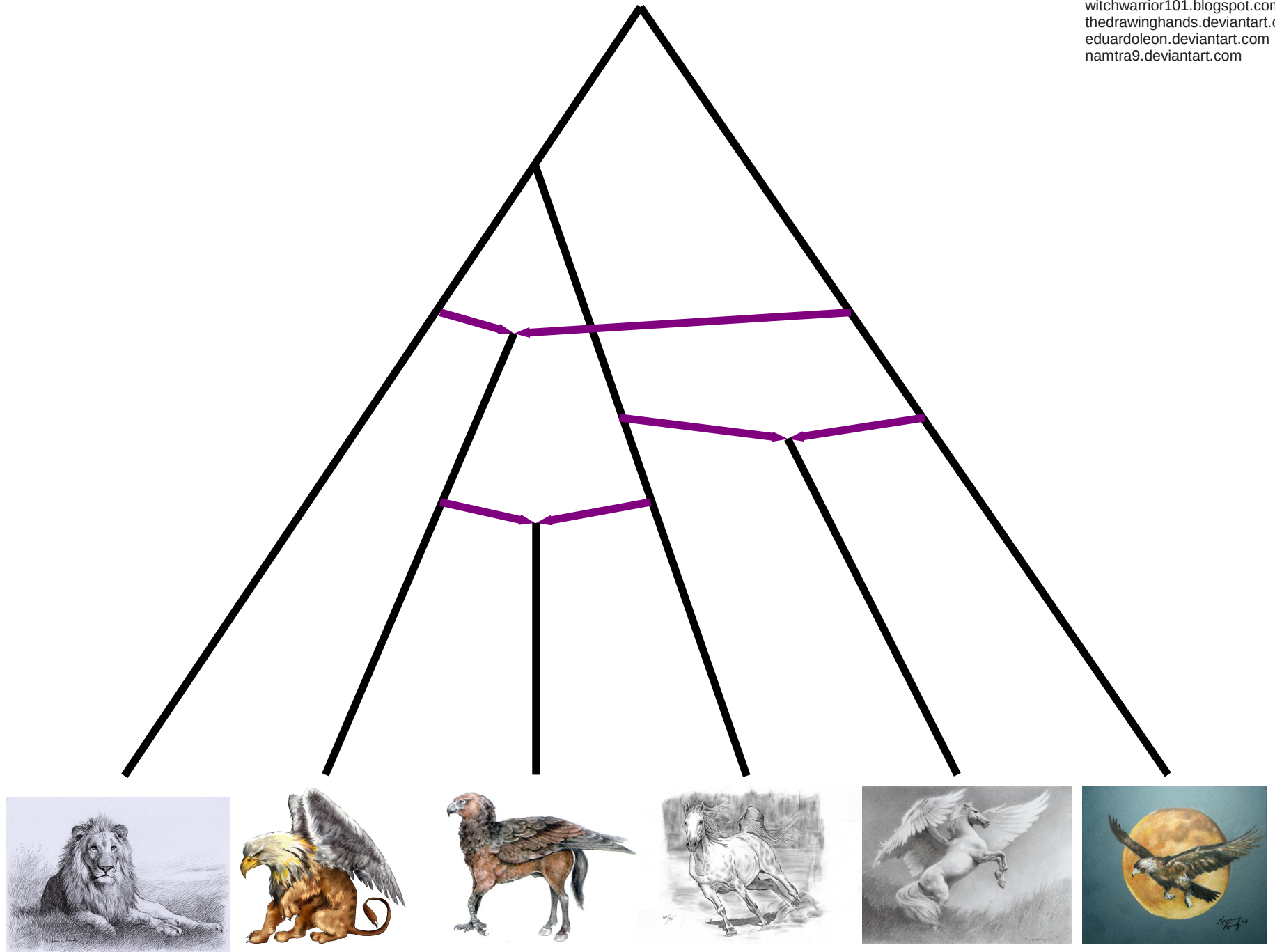
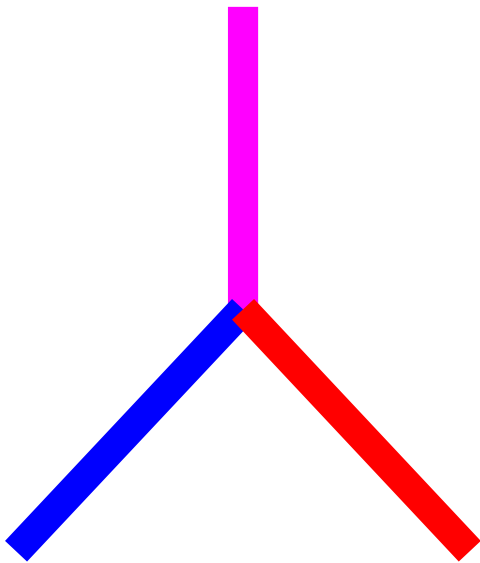


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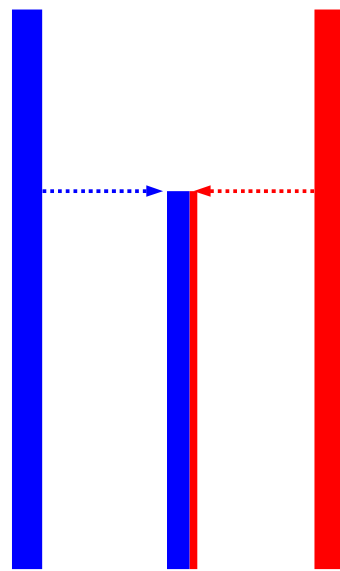


# Speciation



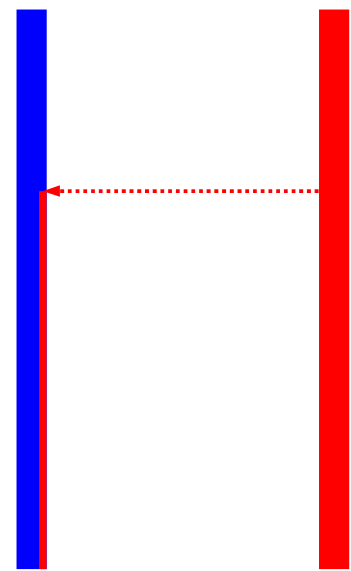
Rate:  
Base  
 $\times$   
 $N$

# Hybridization

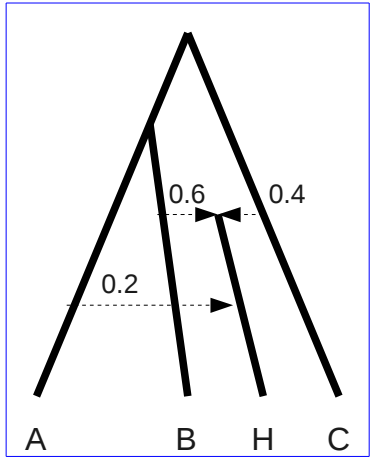


Base  
 $\times$   
 $N(N-1)$   
 $\times$   
Success chance

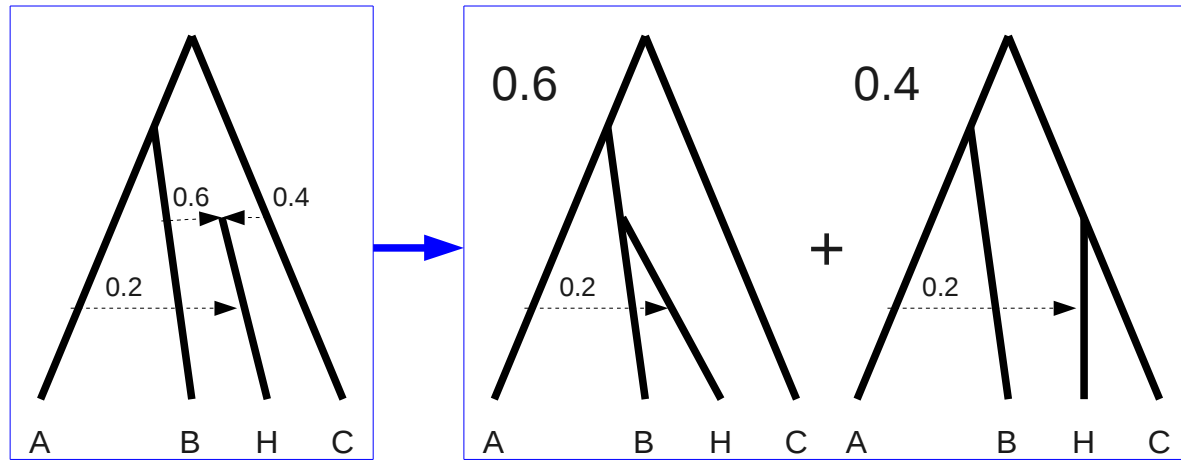
# Introgression



Base  
 $\times$   
 $N(N-1)$   
 $\times$   
Success chance

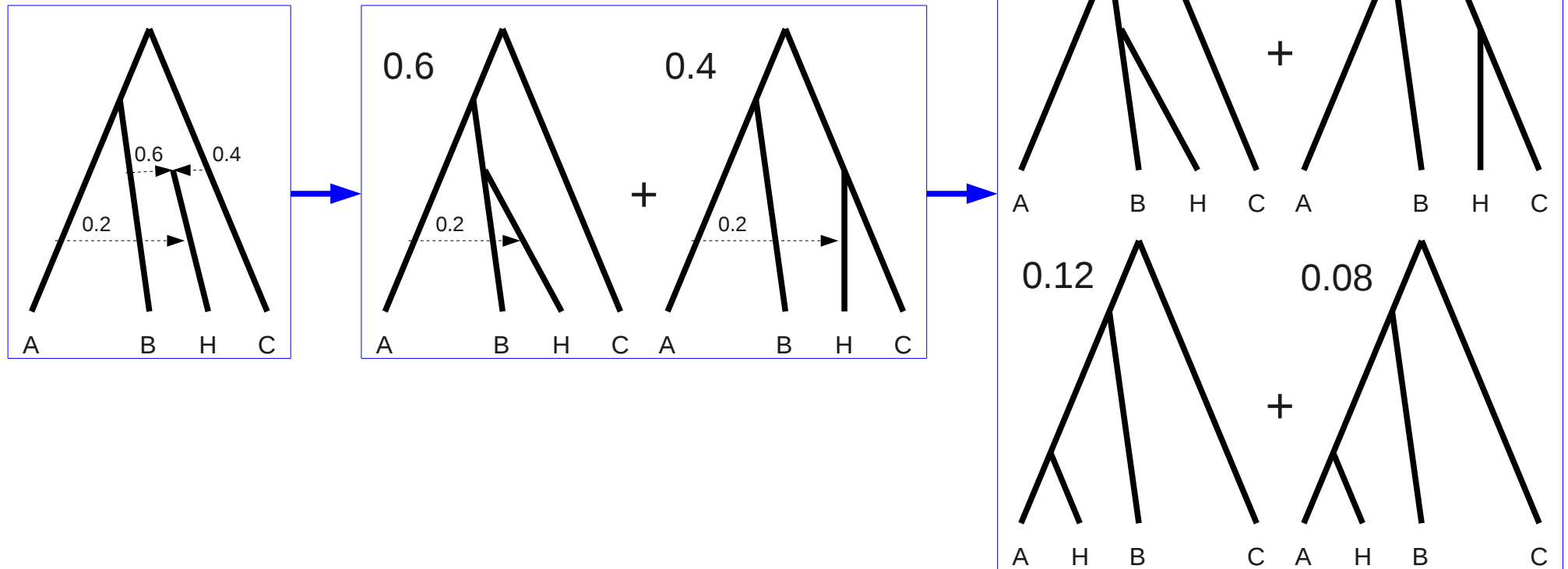


Decomposing a hybrid network to weighted trees.



Decomposing a hybrid network to weighted trees.

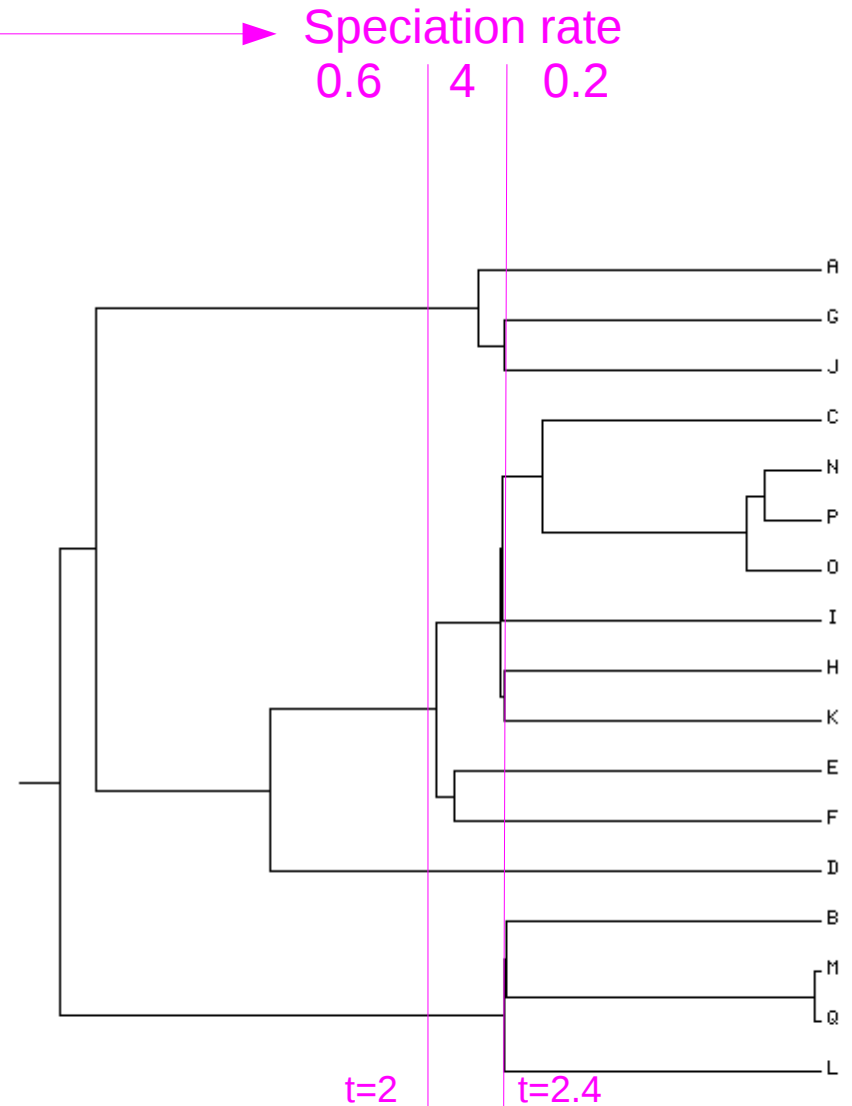




Decomposing a hybrid network to weighted trees.

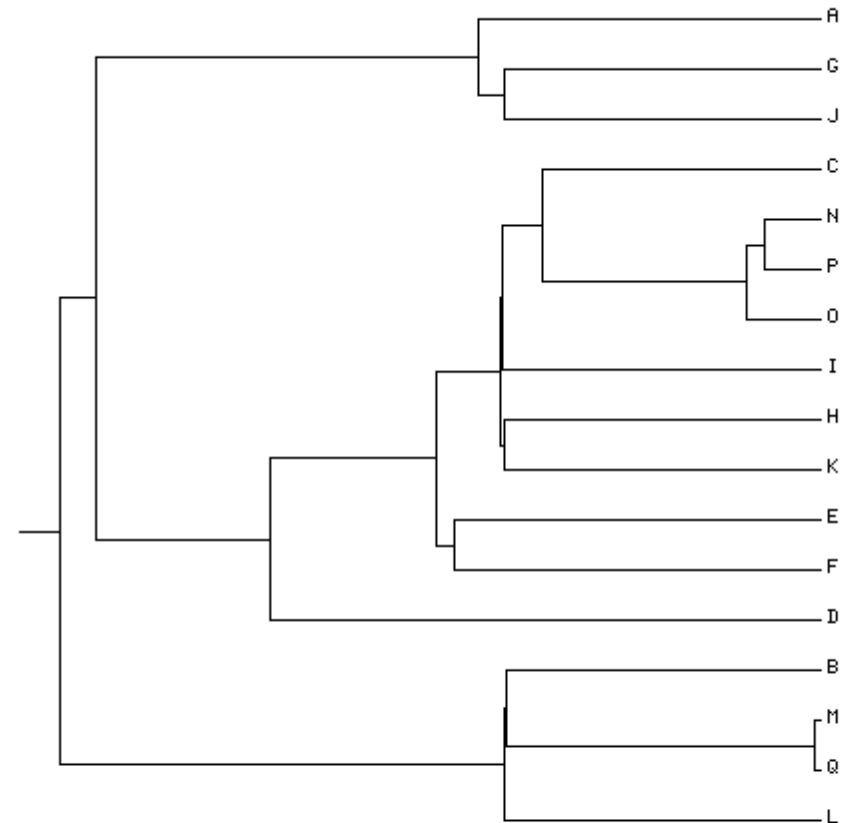
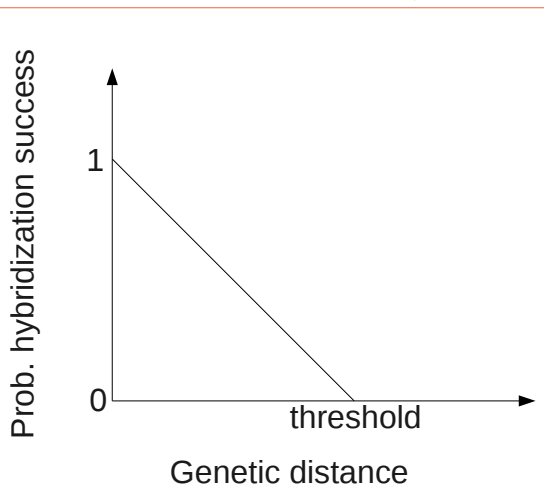
# Input Parameters

```
speciation rate = (0.6,2,4,2.4,.2)
speciation function = linear
hybridization rate = 0
hybridization function = quadratic
introgression rate = 0
introgression function = quadratic
hybridization distribution = (0.25,1) (0.5,2) (0.75,1)
introgression distribution = (0.4,1) (0.5,2) (0.6,1)
halt time = 4
halt taxa = 30
halt hybrid = 30
seed = 4
hybridization threshold = .5
dollo rate = 0.06
dollo sites = 0
filo sites = 0
```



# Input Parameters

```
speciation rate = (0.6,2,4,2.4,.2)
speciation function = linear
hybridization rate = 0
hybridization function = quadratic
introgression rate = 0
introgression function = quadratic
hybridization distribution = (0.25,1) (0.5,2) (0.75,1)
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halt time = 4
halt taxa = 30
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hybridization threshold = .5
dollo rate = 0.06
dollo sites = 0
filo sites = 0
```



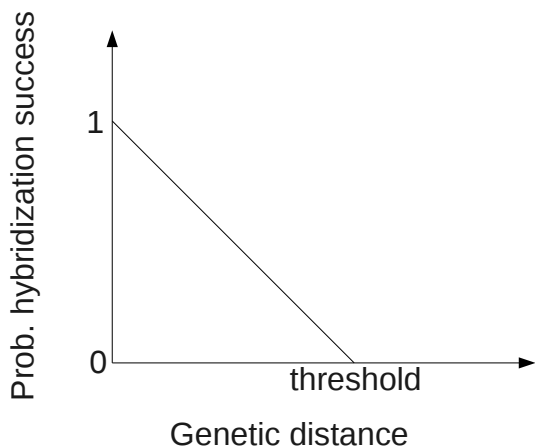
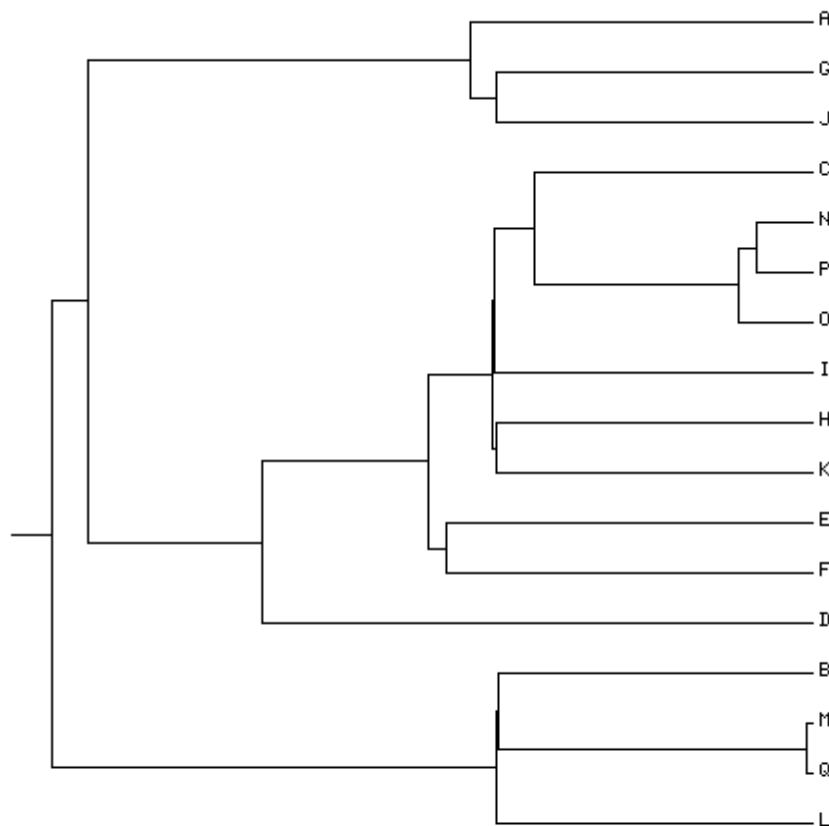
# Input Parameters

```

speciation rate = (0.6,2,4,2.4,.2)
speciation function = linear
hybridization rate = 0
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halt time = 4
halt taxa = 30
halt hybrid = 30
seed = 4
hybridization threshold = .5
dollo rate = 0.06
dollo sites = 0
filo sites = 0
    
```

Genetic contribution  
of first species

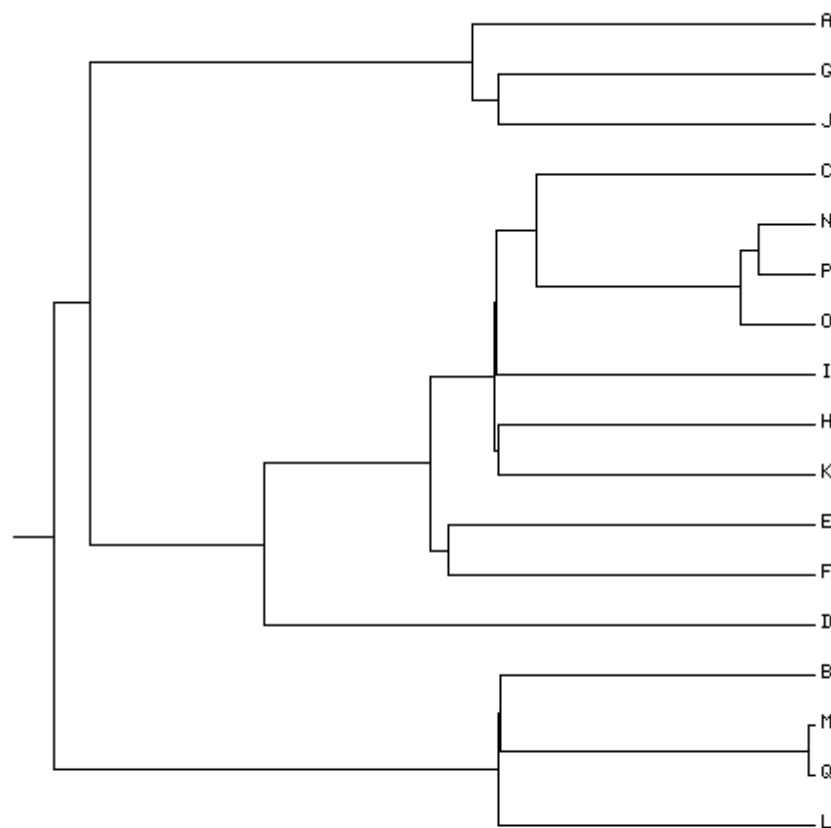
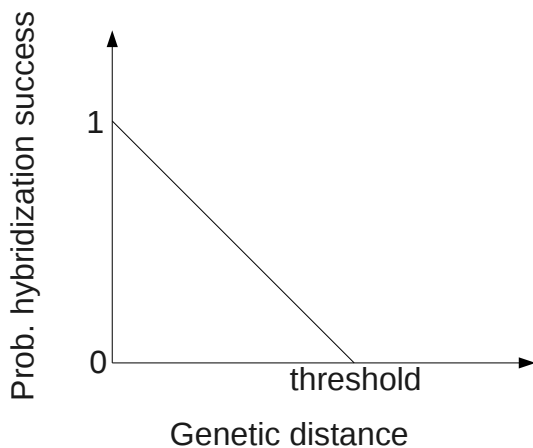
Weights



# Input Parameters

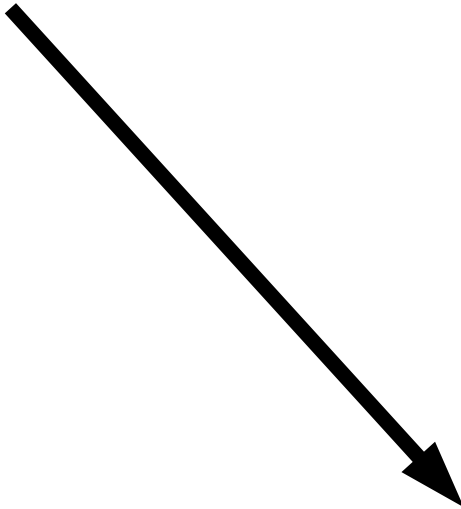
Halts when any one of these criteria is met.

speciation rate = (0.6,2,4,2.4,.2)  
speciation function = linear  
hybridization rate = 0  
hybridization function = quadratic  
introgression rate = 0  
introgression function = quadratic  
hybridization distribution = (0.25,1) (0.5,2) (0.75,1)  
introgression distribution = (0.4,1) (0.5,2) (0.6,1)  
halt time = 4  
halt taxa = 30  
halt hybrid = 30  
seed = 4  
hybridization threshold = .5  
dollo rate = 0.06  
dollo sites = 0  
filo sites = 0



# Filo feature

```
#NEXUS
begin filo;
  output
    format = fasta, nexus, raw
    filename = hybridoutput
    precision 5
  ;
  params
    indel 0
    ntrials = 10
  ;
  matrix HKY = HKY85 0.2 0.5 [ 0.25 0.05 0.25 0.45 ];
run;
end;
```



```
#NEXUS
begin filo;
  output
    format = fasta, nexus, raw
    filename = hybridoutput
    precision 5
  ;
  params
    indel 0
    ntrials = 10
  ;
  matrix HKY = HKY85 0.2 0.5 [ 0.25 0.05 0.25 0.45 ];
  tree T0 = ((A:0.45,C:0.45):0.06,(B:0.19,(D:0.15,E:0.15):0.03):0.32);
  treeparams T0
    1 54
  ;
  tree T1 = ((A:0.45,(C:0.15,E:0.15):0.30):0.06,(B:0.19,D:0.19):0.32);
  treeparams T1
    1 14
  ;
  tree T2 = ((A:0.45,(C:0.19,(D:0.15,E:0.15):0.03):0.26):0.06,B:0.51);
  treeparams T2
    1 28
  ;
  tree T3 = ((A:0.45,((C:0.15,E:0.15):0.03,D:0.19):0.26):0.06,B:0.51);
  treeparams T3
    1 4
  ;
run;
end;
```

# Dollo

```
>A
0111111111011101111111110111110011111111110011101110101111
>B
0111011101101101111111111011111011111111101011001110101110
>C
111111101101101011011111111111100011111100011001100101101
>D
01110111011011010111111111111011111111101010001110101110
>E
01110111011110111111111111111011011111100011011110111110
```

All characters have same loss rate.

Gain location chosen randomly to keep number of characters present in equilibrium over the tree.

# Input Parameters

Halts when any one of these criteria is met.

speciation rate = (0.6, 2, 4, 2.4, .2)  
 speciation function = linear  
 hybridization rate = 0  
 hybridization function = quadratic  
 introgression rate = 0  
 introgression function = quadratic  
 hybridization distribution = (0.25, 1) (0.5, 2) (0.75, 1)  
 introgression distribution = (0.4, 1) (0.5, 2) (0.6, 1)

halt time = 4  
 halt taxa = 30  
 halt hybrid = 30

seed = 4

hybridization threshold = .5

dollo rate = 0.06  
 dollo sites = 0  
 filo sites = 0

Genetic contribution of first species

Weights

Speciation rate  
 0.6 | 4 | 0.2

