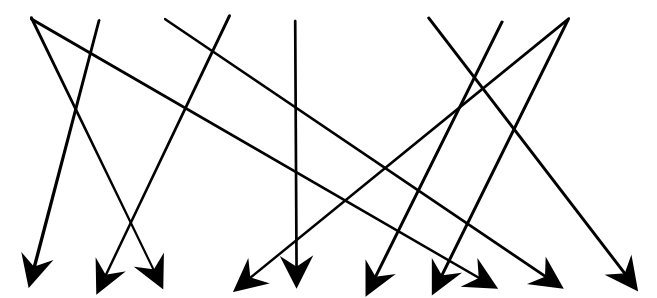


# Topological Support (ML)

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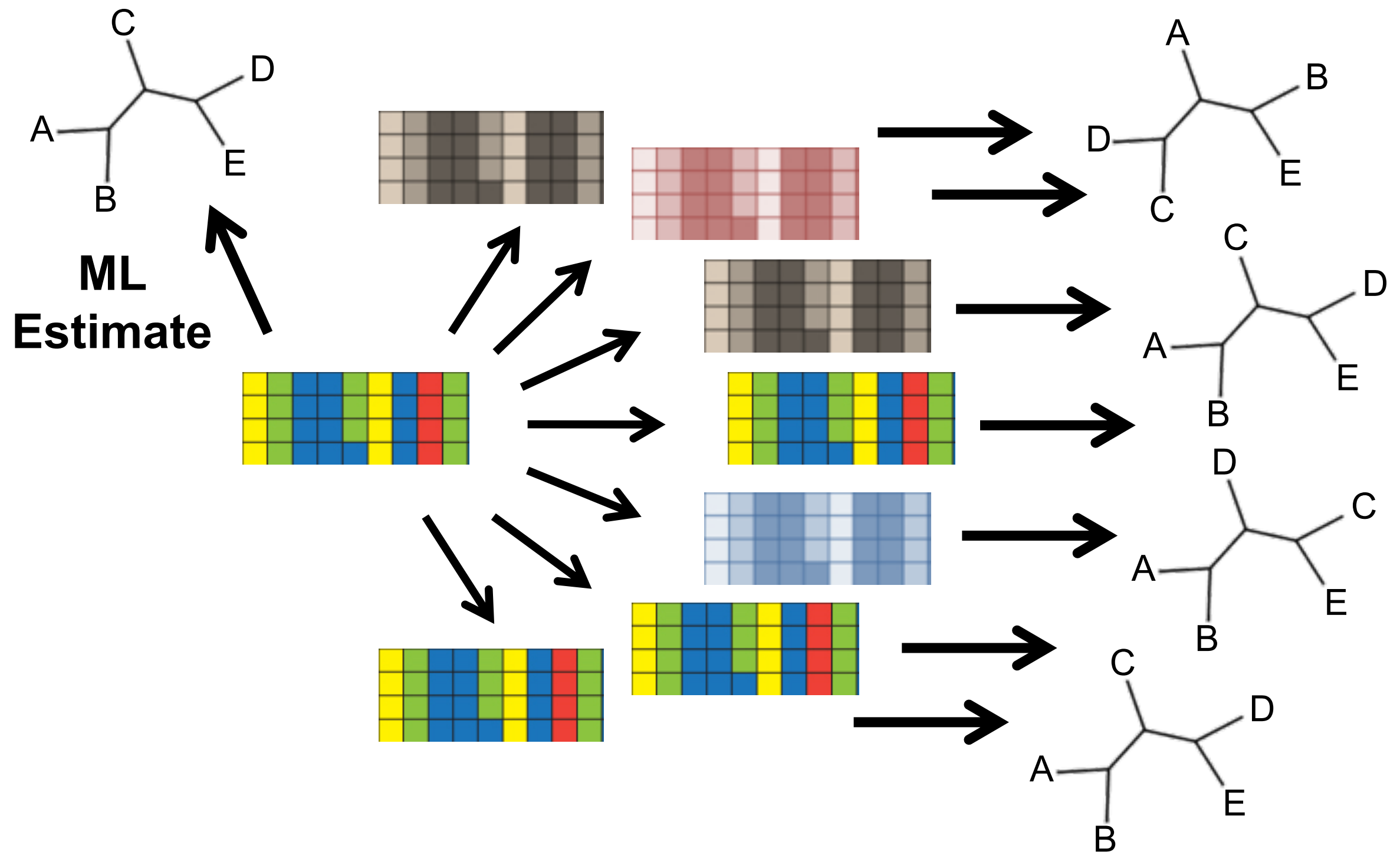
# Bootstrapping

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Original alignment	Site	1	2	3	4	5	6	7	8	9	10
	human	N	E	N	L	F	A	S	F	I	A
	chimpanzee	N	E	N	L	F	A	S	F	A	A
	bonobo	N	E	N	L	F	A	S	F	A	A
	gorilla	N	E	N	L	F	A	S	F	I	A
	orangutan	N	E	D	L	F	T	P	F	T	T
	Sumatran	N	E	S	L	F	T	P	F	I	T
	gibbon	N	E	N	L	F	T	S	F	A	T
Bootstrap sample											
	Site	2	4	1	9	5	8	9	1	3	7
	human	E	L	N	I	F	F	I	N	N	S
	chimpanzee	E	L	N	A	F	F	A	N	N	S
	bonobo	E	L	N	A	F	F	A	N	N	S
	gorilla	E	L	N	I	F	F	I	N	N	S
	orangutan	E	L	N	T	F	F	T	N	D	P
	Sumatran	E	L	N	I	F	F	I	N	S	P
	gibbon	E	L	N	A	F	F	A	N	N	S

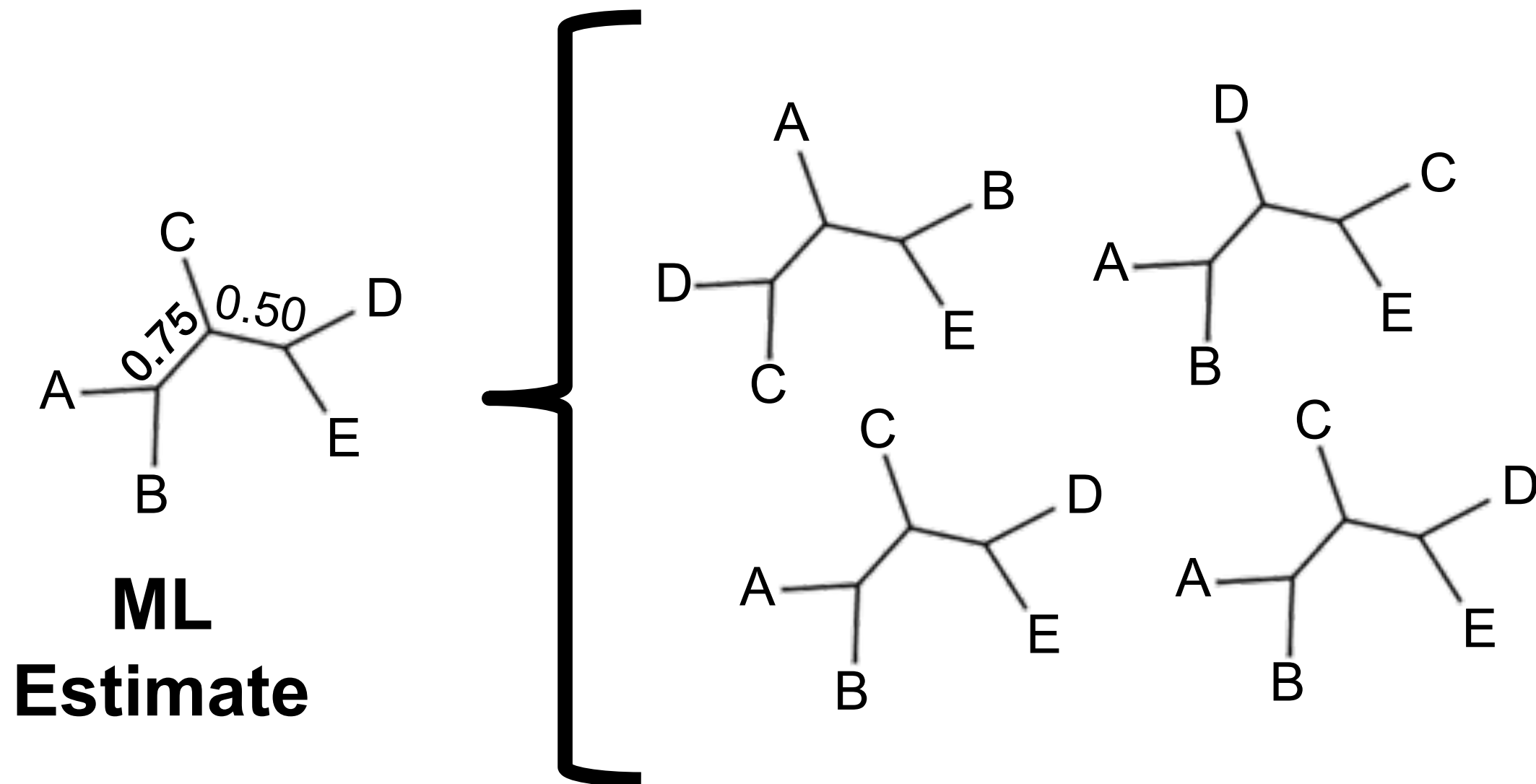
# Bootstrapping

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# Bootstrapping

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# Bootstrapping

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Interpretations of the bootstrap:

- Repeatability

- 1 – False Positive Rate from a polytomy

- Probability branch is true

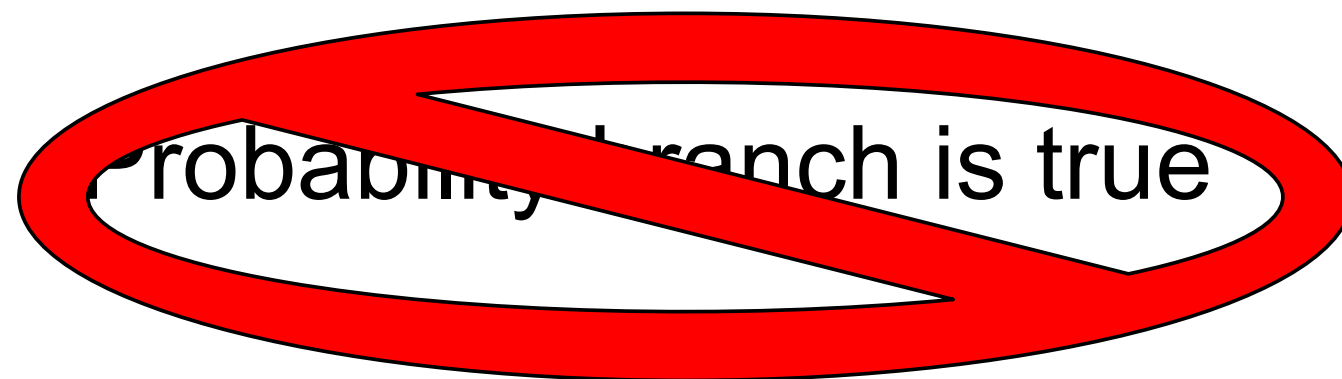
# Bootstrapping

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Interpretations of the bootstrap:

-Repeatability

-1 – False Positive Rate from a polytomy



# Bootstrapping

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Cool bootstrapping simulation by Mark Holder.

<http://phylo.bio.ku.edu/mephytis/boot-sample.html>

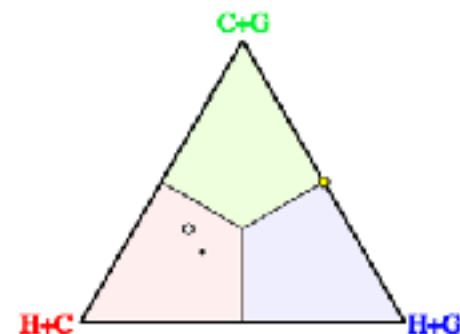
Human	G	C	C	A	G	C	T	G	C	T
Chimp	G	C	C	G	G	G	T	A	T	T
Gorilla	G	T	C	A	A	C	T	A	T	G
Orang	C	T	C	A	A	G	T	G	C	G

Acid 1 bootstrap rep

Human	G	T	C	G	T	C	C	C	C	C
Chimp	G	T	G	G	T	G	T	T	T	G
Gorilla	G	T	C	G	T	C	T	T	T	C
Orang	C	T	G	C	T	G	C	C	C	G

4 replicates:

H+C tree tied with C+G tree on this rep.  
C+G 37.5%    E+G 0.0%    H+C 52.5%



# Bootstrapping

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Human	G	C	C	A	G	C	T	G	C	T
Chimp	G	C	C	G	G	G	T	A	T	T
Gorilla	G	T	C	A	A	C	T	A	T	G
Orang	C	T	C	A	A	G	T	G	C	G

Add 1 bootstrap rep

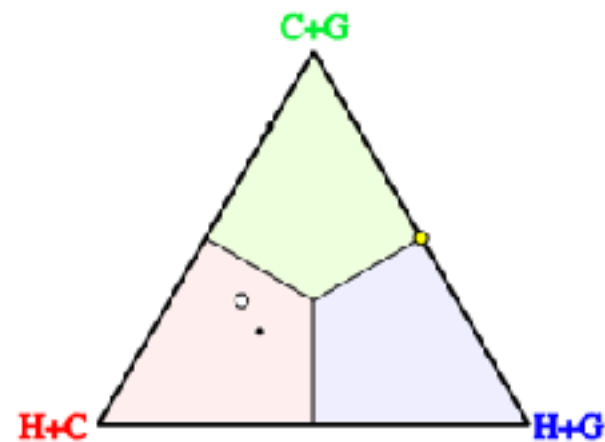
Human	G	T	C	G	T	C	C	C	C	C
Chimp	G	T	G	G	T	G	T	T	T	G
Gorilla	G	T	C	G	T	C	T	T	T	C
Orang	C	T	G	C	T	G	C	C	C	G

Run this 20 times and  
let's compare results.

4 replicates:

H+C tree tied with C+G tree on this rep.

C+G 37.5%      H+G 0.0%      H+C 62.5%





# IQTree

**IQ-TREE**[Download](#)[News](#)[Web server](#)[Docs](#)[Workshop](#)[About](#)

## IQ-TREE

Efficient software for phylogenomic inference

Latest version 1.6.10 (February 19, 2019)

[Download v1.6.10 for macOS](#)

[All Downloads](#) [Documentation](#)

### LATEST NEWS

We are teaching IQ-TREE in [various Workshops detailed here](#)  
Mesquite software 3.5 allows to run IQ-TREE with a package installed via Zephyr

### IQ-TREE key features



#### IQ-TREE - Efficient Tree Reconstruction

A fast and effective stochastic algorithm to infer phylogenetic trees by maximum likelihood. *IQ-TREE* compares favorably to *RAxML* and *PhyML* in terms of likelihoods with similar computing time ([Nguyen et al., 2015](#)).



#### ModelFinder - Fast and Accurate Model Selection

ModelFinder ([Kalyaanamoorthy et al., 2017](#)) enables a free rate variation model and is 10 to 100 times faster than *JModelTest* and *ProtTest*. It also finds best-fit partitioning scheme like [PartitionFinder](#).