

# Workflow

Ecology



Lambda = ?

Molecular data

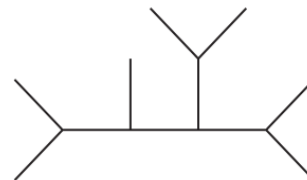
```
.GCTACCTTTATCCCTAGCCCCCTGCGCCCG  
GTGAGGTCTGCTCTGGGTCCCTCGCCACC  
CCCTAGCTCCGTGCGCCACTCCGGCGGGCC  
CCGGACTACGGTGGTTACCACGTGGCGGG
```



Alignment

-	V	H	L	T	A	D	E	K	A	A	V	T	A	L	W	G	K	V	N	
-	V	H	L	T	G	E	E	K	A	A	A	V	T	A	L	W	G	K	V	N
M	V	H	L	T	P	E	E	K	N	A	A	V	T	T	L	W	G	K	V	N
M	V	H	L	T	P	E	E	K	S	A	A	V	T	A	L	W	G	K	V	N

Phylogeny



Parameter estimates

Lambda = 0.5



# Multi-step

Ecology



Lambda = ?

Molecular data

```
.GCTACCTTTATCCCTAGCCCCCTGCGCCCG  
GTGAGGTCTGCTCTGGGTCCCTCGCCACCG  
CCCTAGCTCCGTGCGCCACTCCGGCGGGCC  
CCGGACTACGGTGGTTACCACGTGGCGGG
```



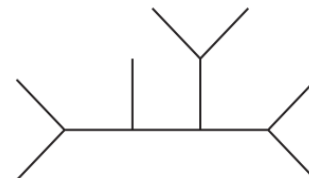
Alignment

Use best

-	V	H	L	T	A	D	E	K	A	A	V	T	A	L	W	G	K	V	N	
-	V	H	L	T	G	E	E	K	A	A	A	V	T	A	L	W	G	K	V	N
M	V	H	L	T	P	E	E	K	N	N	A	V	T	T	L	W	G	K	V	N
M	V	H	L	T	P	E	E	K	S	S	A	V	T	A	L	W	G	K	V	N

Phylogeny

Use best



Parameter estimates

Use best

Lambda = 0.5 +/- 0.01



# Joint inference

Ecology



Lambda = ?

Molecular data

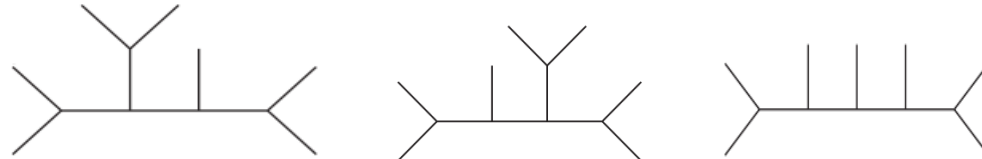
```
.GCTACCTTTATCCCTAGCCCCCTGCGCCCG  
GTGAGGTCTGCTCTGGGTCCCTCGCCACC  
CCCTAGCTCCGTGCGCCACTCCGGCGGGCC  
CCGGACTACGGTGGTTACCACGTGGCGGG
```



Alignments

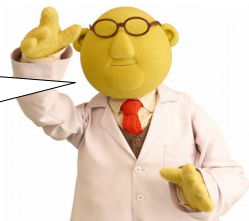
T	A	D	E	K	A	-	V	H	L	T	A	D	E	A	A	V	T	A	L	
T	G	E	E	K	A	-	V	H	L	T	G	E	E	A	A	A	V	T	A	L
T	P	E	E	K	N	M	V	H	L	T	P	E	E	N	A	V	T	T	L	
T	P	E	E	K	S	M	V	H	L	T	P	E	E	S	A	V	T	A	L	

Phylogenies



Parameter estimates

This alignment, this phylogeny  
and lambda = 0.5 have a 90% probability

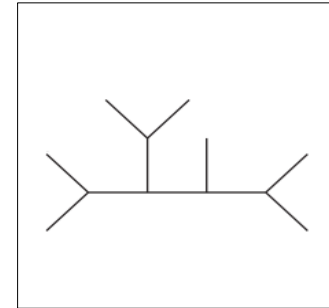






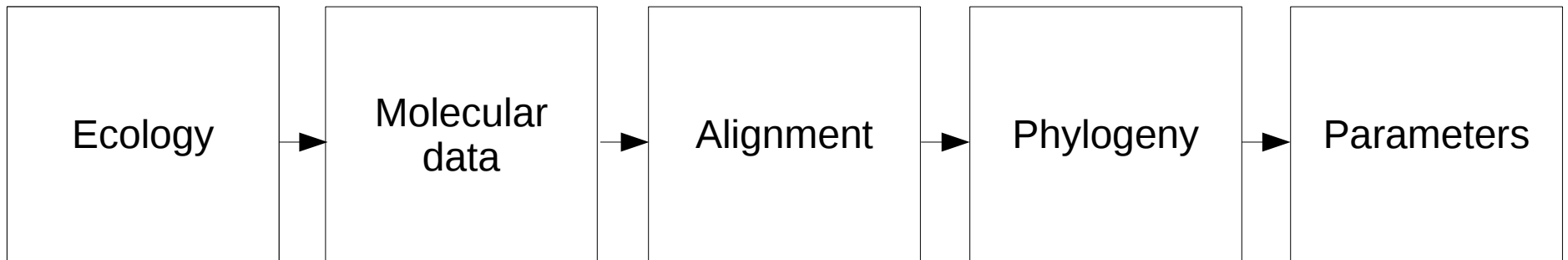
GCTACCTT  
GTGAGGTC  
CCCTAGCTC  
CCGGACTAC

T	A	D	E	K	A
T	G	E	E	K	A
T	P	E	E	K	N
T	P	E	E	K	S

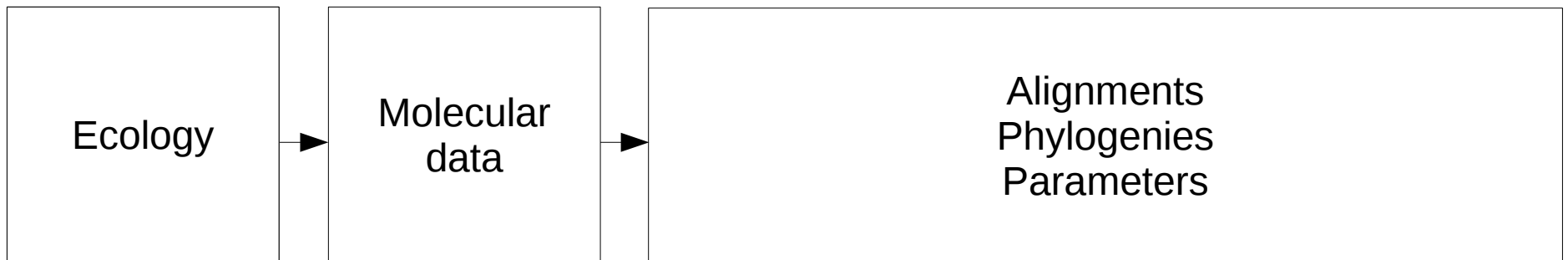


Lambda = 0.5

Multi-step method



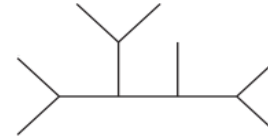
Joint inference





GCTACCTT  
GTGAGGTC  
CCCTAGCTC  
CCGGACTAC

T	A	D	E	K	A
T	G	E	E	K	A
T	P	E	E	K	N
T	P	E	E	K	S



Lambda = 0.5

Multi-step method

Ecological  
model

Molecular  
data

Alignment

Phylogeny

Parameters

Joint inference

Ecological  
model

Molecular  
data

Alignments  
Phylogenies  
Parameters