# Ancestral character estimations of endochondral bone presence (character 4)

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#### Data and package

## Loading required package: Rcpp

#### Running the ancestral character estimation (ACE)

Here we run the ancestral character estimation with an equal rates (ER) and all rates different (ARD) on a random parsimony tree and a random resolution (dichotomous) of the Bayesian consensus tree.

#### Extracting the models informations

Extracting the AICs, logged likelihood (global) and the scaled likelihood for each state at the node of interest (MRCA between *Mininjinia* and *Helodus*) for all the ancestral character estimations.s

#### Result tables

Displaying the results into a table

Table 1: Tree distribution (100) ancestral states estimation results. ER = Equal rates model; ARD = All Rates Different model. The columns AIC and log.lik represent the median AIC and log.lik across the 100 parsimony and bayesian trees (for both models). The columns Absent and Present represent the median scaled likelihood for the endochondral bone state. The 2.5%, 25%, 75% and 97.5% represent the confidence intervals values for each estimated parameter (log.lik, AIC, Present and Absent endochondral bone).

Trees	Model	Median	2.5%	25%	75%	97.5%
Parsimony Implied Weights		log.lik.				
	$\operatorname{ER}$	-30.6	-30.61	-30.6	-30.57	-30.54
	ARD	-27.52	-27.53	-27.53	-27.52	-27.51
		AIC				
	$\operatorname{ER}$	63.2	63.08	63.14	63.2	63.21
	ARD	59.04	59.03	59.04	59.05	59.05
		Absent				
	$\operatorname{ER}$	0.92	0.92	0.92	0.92	0.93

Trees	Model	Median	2.5%	25%	75%	97.5%
	ARD	0.38 Present	0.38	0.38	0.4	0.42
	$\operatorname{ER}$	0.08	0.07	0.08	0.08	0.08
	ARD	0.62	0.58	0.6	0.62	0.62
Parsimony Equal Weights		log.lik.				
	$\operatorname{ER}$	-30.8	-30.95	-30.85	-30.74	-30.7
	ARD	-27.51	-27.61	-27.56	-27.48	-27.47
		AIC				
	$\operatorname{ER}$	63.59	63.4	63.48	63.7	63.9
	ARD	59.01	58.94	58.96	59.11	59.21
		Absent				
	$\operatorname{ER}$	0.78	0.77	0.78	0.78	0.79
	ARD	0.2	0.19	0.2	0.2	0.21
		Present				
	$\operatorname{ER}$	0.22	0.21	0.22	0.22	0.23
	ARD	0.8	0.79	0.8	0.8	0.81
Bayesian Partitioned		log.lik.				
	$\operatorname{ER}$	-32.72	-36.28	-33.74	-31.83	-30.44
	ARD	-29.61	-33.61	-30.42	-28.71	-27.49
		AIC				
	$\operatorname{ER}$	67.43	62.88	65.67	69.48	74.57
	ARD	63.21	58.98	61.41	64.83	71.22
		Absent				_
	ER	0.84	0.12	0.58	0.99	1
	ARD	0.26	0.01	0.05	0.81	1
		Present				
	ER	0.16	0	0.01	0.42	0.88
	ARD	0.74	0	0.19	0.95	0.99
Bayesian Unpartitioned		log.lik.		22.12		
	ER	-32.55	-35.58	-33.49	-31.75	-30.2
	ARD	-29.22	-32.66	-30.35	-28.59	-26.58
	- DD	AIC	00.00	25.5	ao o=	-0.40
	ER	67.1	62.39	65.5	68.97	73.16
	ARD	62.44	57.15	61.19	64.71	69.33
	- DD	Absent	0 0 F	0.00	0.00	_
	ER	0.73	0.05	0.38	0.98	1
	ARD	0.14	0	0.04	0.79	1
	ED	Present	0	0.00	0.00	0.05
	ER	0.27	0	0.02	0.62	0.95
	ARD	0.86	0	0.21	0.96	1

Table 2: Tree distribution (100) ancestral states estimation results. ER = Equal rates model; ARD = All Rates Different model. The columns AIC and log.lik represent the median AIC and log.lik across the 100 parsimony and bayesian trees (for both models). The columns Absent and Present represent the median scaled likelihood for the endochondral bone state.

Trees	Model	log.lik.	log.ratio	AIC	Absent	Present
Parsimony Implied Weights	ER	-30.6	6.16	63.2	0.92	0.08
	ARD	-27.52		59.04	0.38	0.62

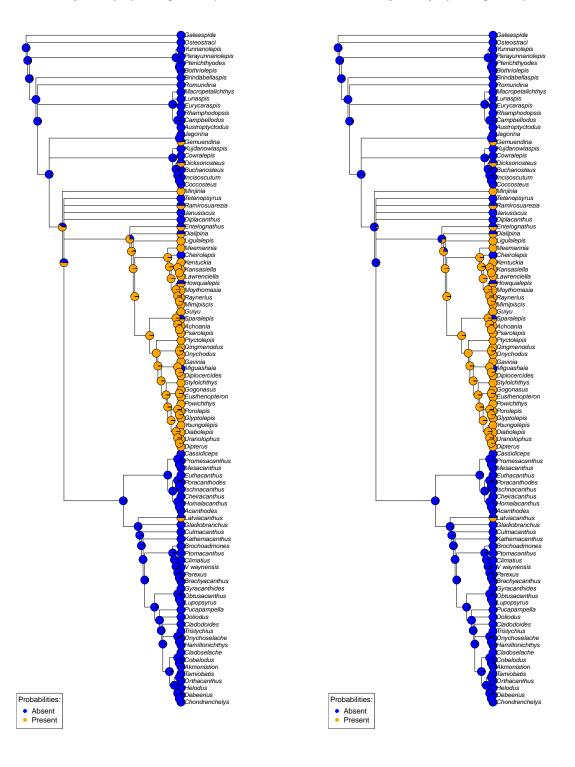
Trees	Model	log.lik.	log.ratio	AIC	Absent	Present
Parsimony Equal Weights	ER ARD	-30.8 -27.51	6.58	63.59 59.01	0.78	0.22
Bayesian Partitioned	ER ARD	-32.72 -29.61	6.22	67.43 63.21	0.84 0.26	0.16 0.74
Bayesian Unpartitioned	ER ARD	-32.55 -29.22	6.66	67.1 62.44	0.20 0.73 0.14	0.74 $0.27$ $0.86$

#### Visualisation on the consensus trees

We can then visualise all the results on the consensus trees

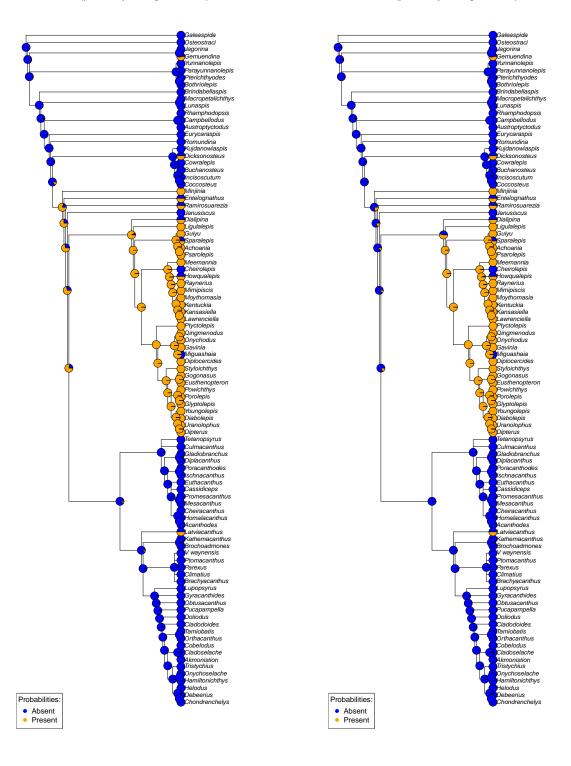
### Endochondral bone estimation (parsimony implied weights – ARD)

### Endochondral bone estimation (parsimony implied weights - ER)



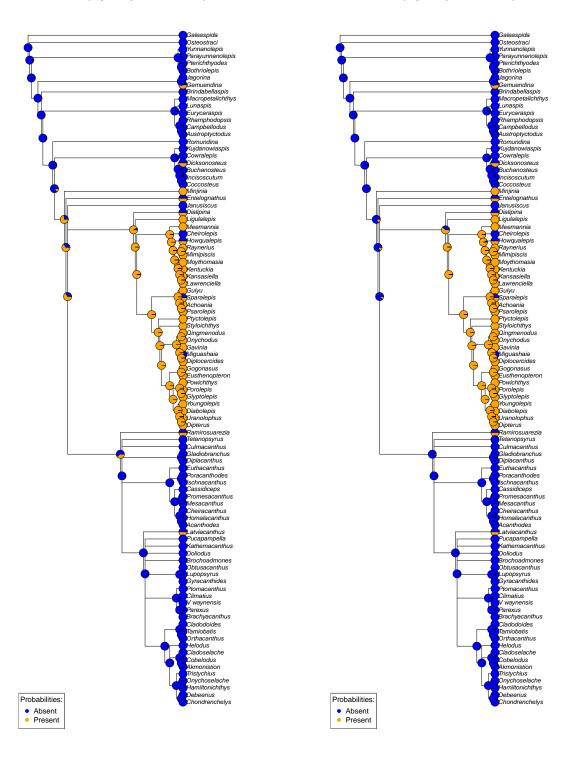
### Endochondral bone estimation (parsimony unweighted – ARD)

# Endochondral bone estimation (parsimony unweighted – ER)



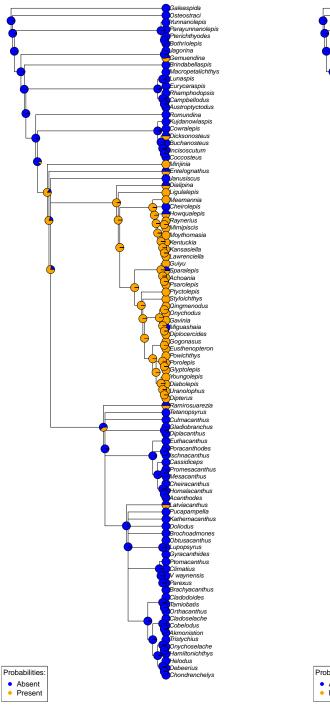
# Endochondral bone estimation (Bayesian partitioned – ARD)

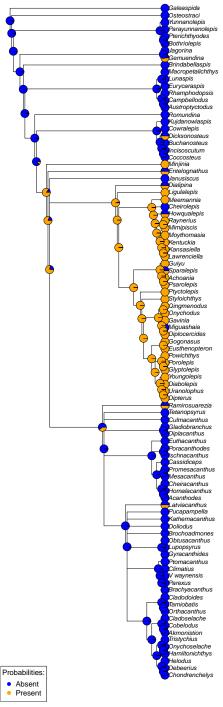
# Endochondral bone estimation (Bayesian partitioned – ER)



### Endochondral bone estimation (Bayesian unpartitioned – ARD)

# Endochondral bone estimation (Bayesian unpartitioned – ER)





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