

SUBSTITUTION MODELS

SHORT RECAP + MODELTEST PAPER DISCUSSION



AARHUS
UNIVERSITY
DEPARTMENT OF MOLECULAR BIOLOGY AND GENETICS

EVOLUTIONARY THINKING 2023
WEEK 36

CALIN PANTEA
PHD STUDENT



EVENT MODELLING

- Basic nucleotide substitution models
- Appropriateness
- Gamma distribution
- Model selection (AIC and BIC)

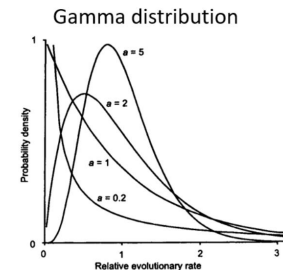
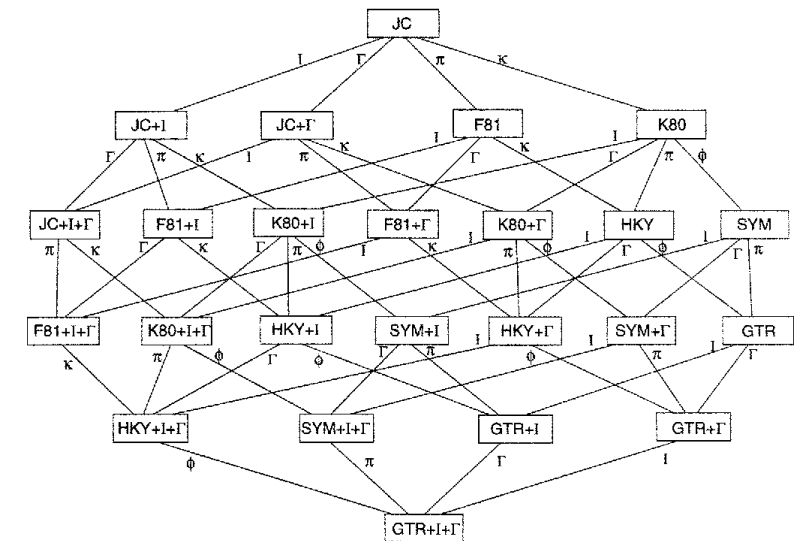
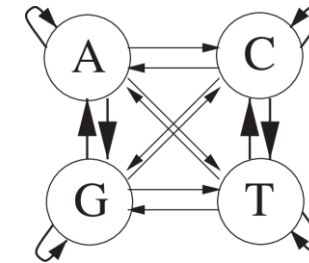


FIGURE 2.3. Gamma distributions of substitution rates among sites for different gamma parameters (α 's).

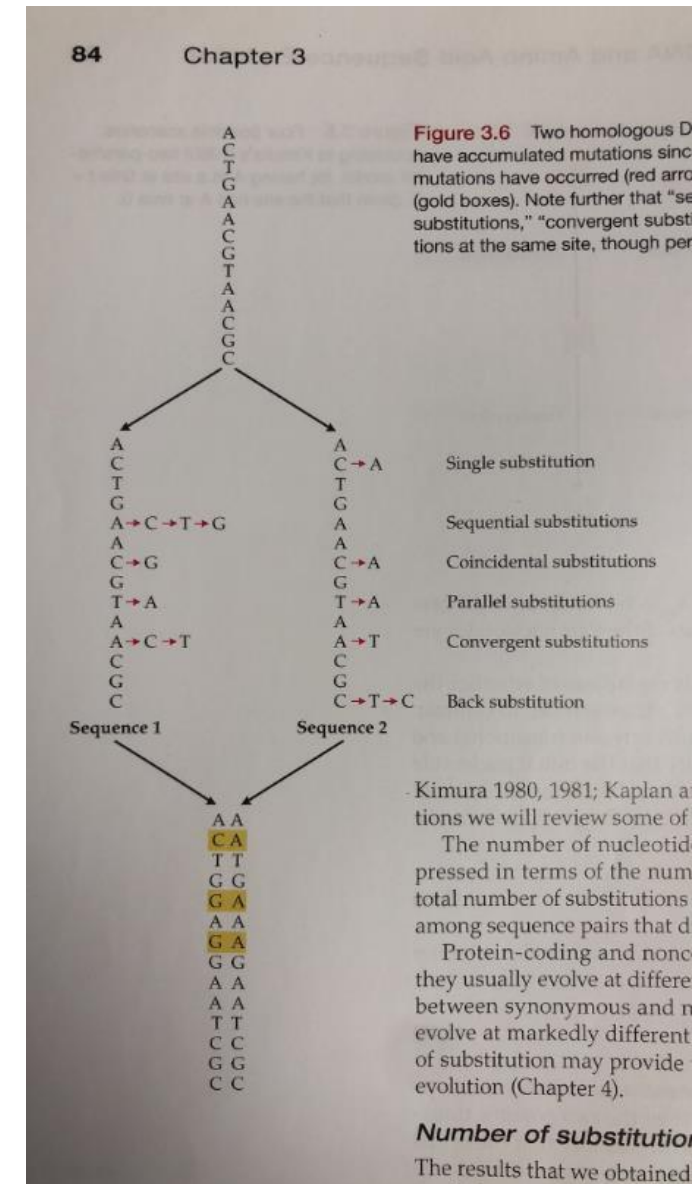


NUCLEOTIDE SUBSTITUTION

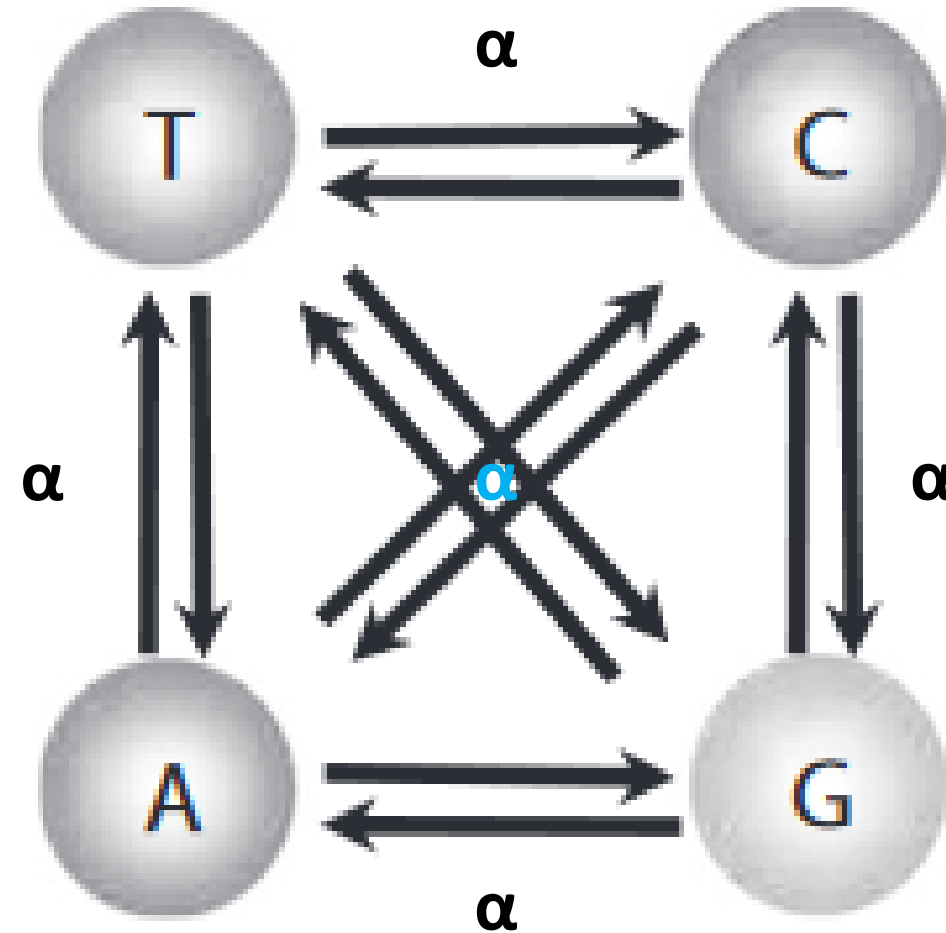
- divergent sequences

AGATGCTAGCATCGACTAGCATCAGCTGACCCCGCGCGCGCAT

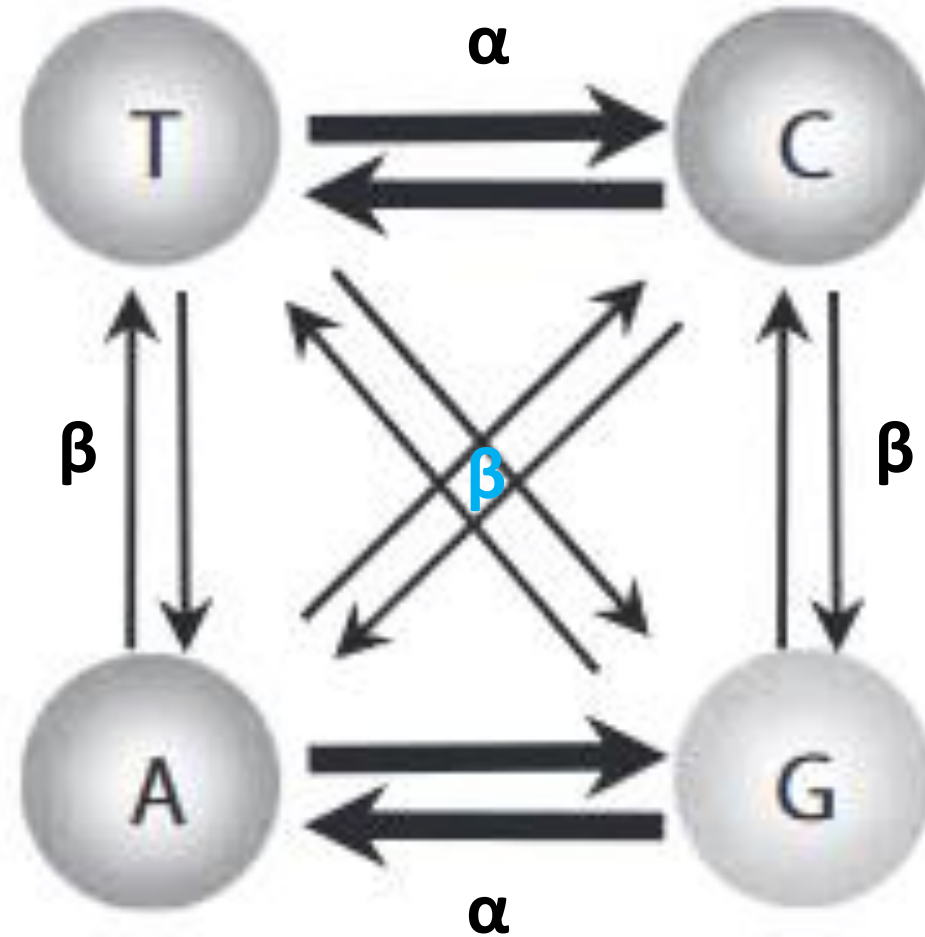
AGATAA TAGCATCGACTAGCATCAGCGGACCCCGCGCGCGCAC



JUKES-CANTOR (JC69)



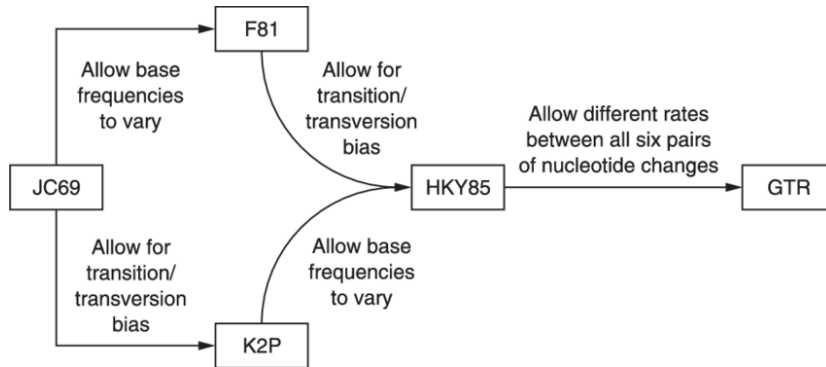
KIMURA (K2P)



OTHER MODELS

Which model is the best?

- Simple models
 - Few parameters (LOW sampling variance)
 - Perform poorly for large distance
- Complex models
 - Many parameters (LARGE sampling variance)
 - Better behaved for large divergence
 - Require LOTS of data
- What is the true patterns of substitution ?



Gamma distribution

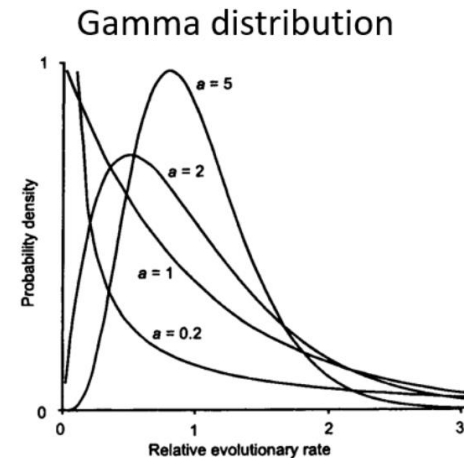
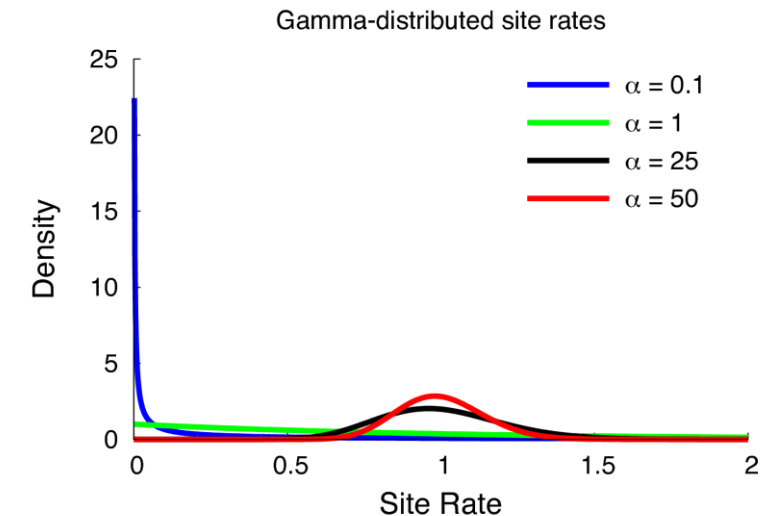


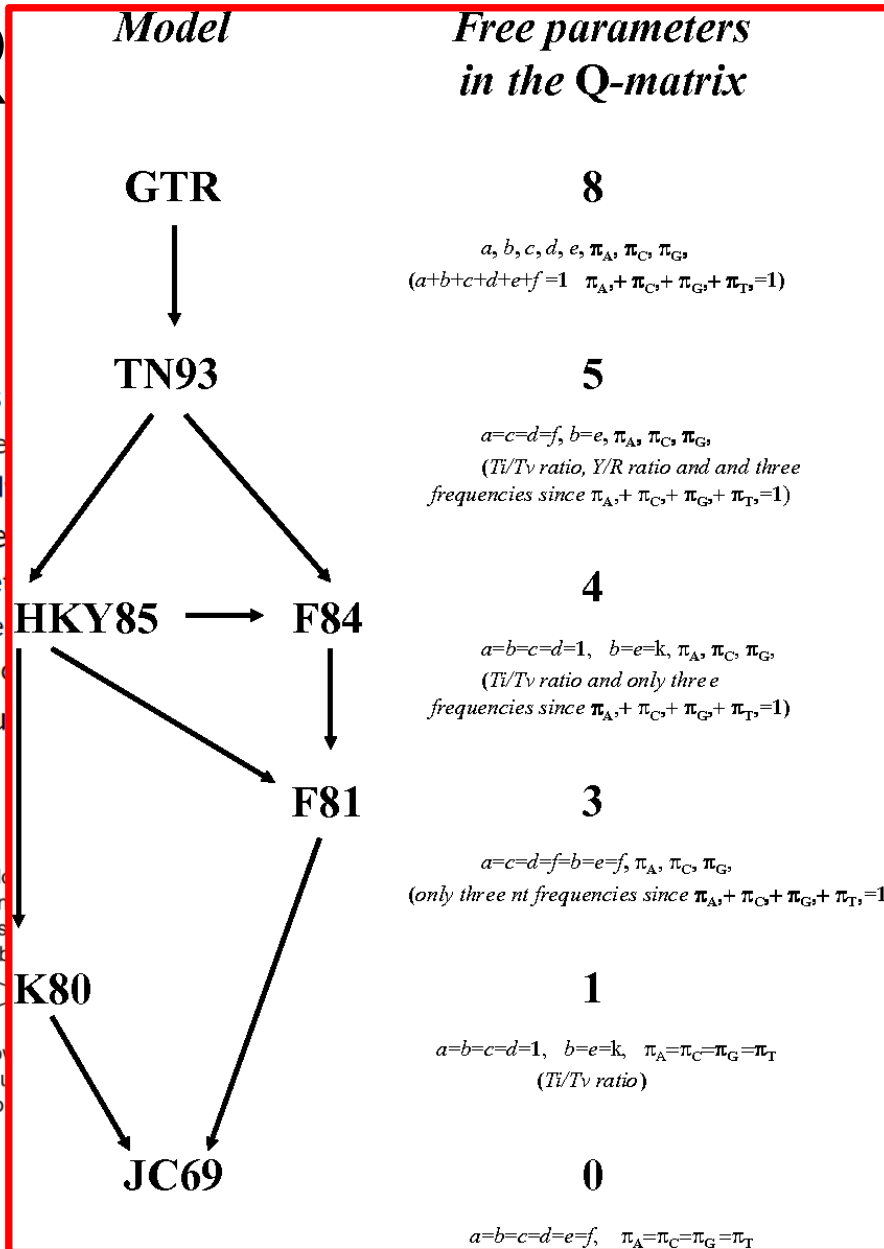
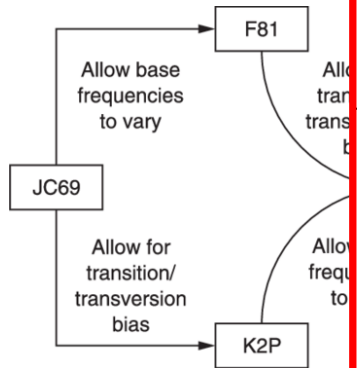
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OTHER

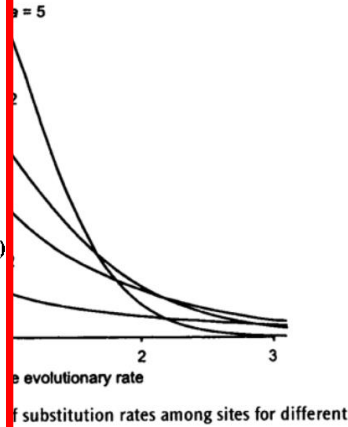
Which

- Simple models
 - Few parameters
 - Perform poorly
- Complex models
 - Many parameters
 - Better behavior
 - Require LOTS of data
- What is the truth?

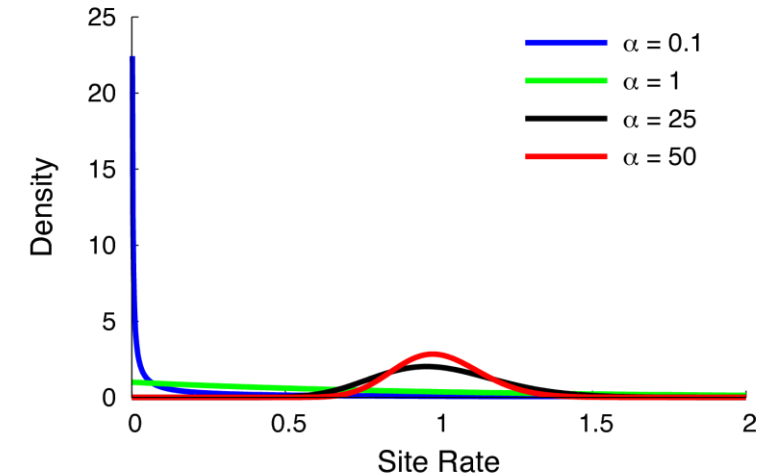


Gamma distribution

distribution



Gamma-distributed site rates

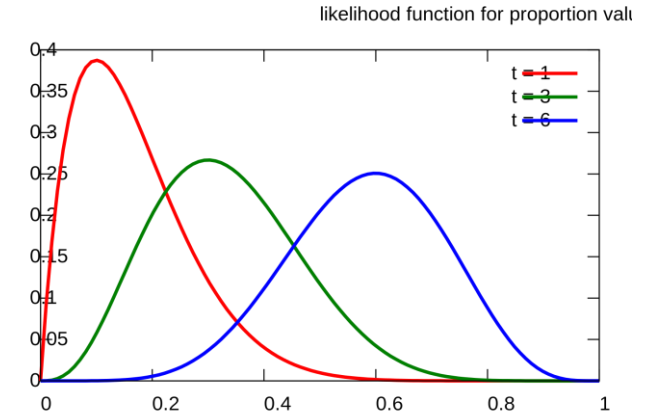


LIKELIHOOD FUNCTION AND MLE

Likelihood function

$$\mathcal{L}(\theta | x)$$

- describes the distribution of probabilities that a model fitted to data describes it well



MLE (maximum likelihood estimation) – maximum value of the likelihood function for model describing studied data

- basically – highest possible probability for the fitted model to really described the data

-> but more complex models are more prone to **overfitting**!

AIC AND BIC

k = number of model parameters; n = number of observations

Bayesian information criterion (BIC)

$$\text{BIC} = k \ln(n) - 2 \ln(\hat{L})$$

- depends on sample size 'n'
- can only be reliable as long as $n \gg k$

Akaike information criterion (AIC)

$$\text{AIC} = 2k - 2 \ln(\hat{L})$$

- somewhat more permissive
- sometimes more reliable
- better choice than BIC for $n \not\gg k$

MODELTEST PAPER

- Introduces an early solution for substitution model choice: simple model likelihood pairwise comparison
- Old and plain; but still a solid early paper discussion resource
- Why?
 - Practice paper discussion
 - Insight into scientific thinking
 - Useful for exam mindset <and> future research work

Course week	Week number	Lecture Monday	Readings	TA Wednesday	TA Friday	Hand-ins
1	35	Origin of life substitution models	Yang, pp 1-23 and originoflife paper	Tree pretest exercise (pen and paper) Installing MEGA11	MEGA11 exercises: retrieve sequences, alignment and distance matrix	
2	36	Phylogenetic tree reconstruction	Yang pp 23-50, graur 165-178	Paper discussion: Modeltest paper, Yang problems	MEGA11 exercises: substitution models	
3	37	Trees continued plus Molecular clocks	Graur 165-209	Paper discussion: Zoonomia paper	Work on Hand in I	Hand-in I: Phylogenetic tree analysis
4	38	Student presentations and work on hand in I	Yang 361-368	Paper discussion: HIV infection on a dental clinic	Introduction to R using phylogenetics	Hand-in I deadline
5	39	Basics of population genetics	NS 2,3, Charlesworth	Problems NS 1,2,3 Hand-in I correction	Wright-Fisher and Coalescent simulator exercises (R)	
6	40	The coalescent continued	NS 4,5,6, Ellegren paper	Problems NS 4,5,6	Problems NS 4,5,6	
7	41	Tests of neutrality	NS 7,8,9, Vicoso paper	Problems NS 7,8	R exercise: detecting positive selection using dn/ds. Jeopardy	Hand-in II: NORC
-	42	Autumn Break		Autumn Break	Autumn Break	Autumn Break
8	43	Incomplete lineage sorting	Mallund et al.	Paper discussion: Iker Rivas Gonzalez et al	Hand-in II correction	Hand-in II deadline
9	44	Comparative genomics and X chromosomes	Review	Paper discussion:	Chatgpt driven phylogenetics exercise in R	
10	45	Genome scans and primate genomics,	Marques-Bonet et al and Kuderna et al	Paper discussion: Gao et al.	R exercise	
11	46	Ancient DNA	Rasmussen et al.	Paper discussion: Green et al.	Update: MEGA11 exercise with data	
12	47	Genome evolution, mutation		Paper discussion: Bergeron et al	Ancient DNA exercise Work on Hand-in III	Hand-in III: Ancient DNA
13	48	Genome evolution, TE		Paper discussion: Hallast et al. Self-test	Self-test	Hand-in III deadline
14	49	Evaluation	none	Hand-in III correction/discussion	Summary of the exercises/discussion	

PAPER QUESTIONS

Group 1

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Charlton, Chester Henry, au747556, 747556
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Kongsgaard, Viktor, au661991, 661991
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Sucipto, Abby Kurniawati, au747615, 747615
Wahab, Adam Faraidon, au667387, 667387

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Guo, Jiahui, au747088, 747088
Lütken, Gorm Hjorth, au681865, 681865

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Nikolaidou, Eleni, au752666, 752666
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Gálfalvy, Nóra, au752687, 752687
Jørgensen, Carolina Ferreira, au590004, 590004
Ulstrup, Johan Christensen, au664823, 664823

1-6

7-11



YOUR QUESTIONS ABOUT PAPER QUESTIONS



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7-11

QUESTIONS ABOUT PAPER QUESTIONS





Google Docs

QUIZ TIME!

questions

and

feedback



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Feedback

Strongly disagree		Strongly agree
	The paper was interesting	
	The fixed questions format feels appropriate	
	The recap was too damn long	



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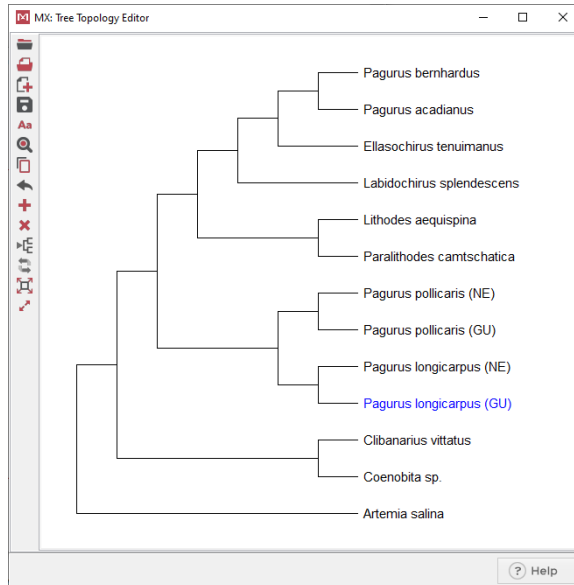
POTENTIAL LECTURE CHANGES

Monday 18th Sept (Week 38) – No
lecture (Mikkel is away)

Possibly moved the week before, on
Friday the 15th Sept!

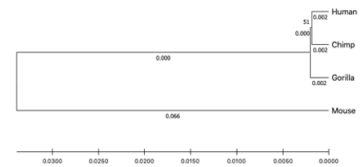
SEE YOU ON FRIDAY FOR SOME MORE DELIGHTFUL MEGA SHENANIGANS

MEGA tree building!

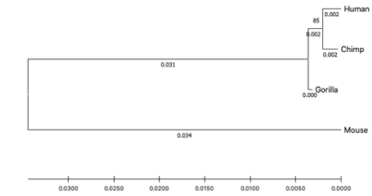


FOXP2

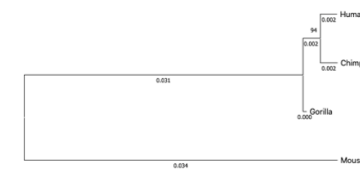
UPGMA



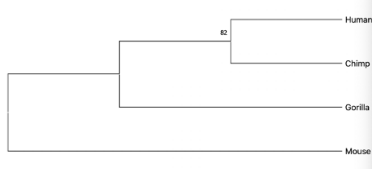
NJ



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