1 **Electronic supplementary file for "Evolutionary models demonstrate rapid and**
2 **adaptive diversification of Australo-Papuan pythons"**
3
4 Damien Esquerré, Ian G. Brennan, Stephen Donnellan, & J. Scott Keogh
5
6 **Supplementary phylogenetic reconstruction methods:**
7
8 Three of the previously unsampled species in the phylogeny were taken from Reynolds et al.
9 2014 (*Python anchietae, P. sebae, P. molurus* and *Simalia clastolepis*) and an additional one
10 was sequenced for cytochrome b following Esquerré et al. 2021 (*Antaresia papuensis*). There
11 is only one species that is only in the nuclear alignment (*P. breitensteini*). Taxonomic
12 changes since Esquerré et al. 2020 include the lumping of six *Leiopython* species into two
13 (Natusch et al. 2021), the synonymy of *Antaresia stimsoni* with *A. childreni* and the
14 description of *A. papuensis* (Esquerré et al. 2021). For the MCMCTree dating analysis we
15 estimated branch lengths using BASEML from the PAML package, splitting the molecular
16 data into three alignments: first two codon positions for the nuclear exons, third codon
17 position for the nuclear exons, and the mitochondrial data. We used the date crown age of
18 pythons inferred by Esquerré et al. (2020) as a secondary calibration point, with a Skew
19 Normal distribution with a mean of 43 million years with a scale of 0.01 and an *alpha* (slant
20 parameter) of 1. We set the root (the split between python and Loxocemidae) to be no older
21 than 80 million years. We used the independent log-normal clock rates model to set the priors
22 on internal nodes and an HKY substitution model, and set the birth–death parameter priors to
23 a uniform distribution. We ran two independent chains with a burnin of 10,000 iterations,
24 then sampling every 50 iterations until we the chains collected 20,000 samples, which was
25 more than enough to reach convergence.
26
27 **References**
28

29 Esquerré D, Donnellan S, Brennan IG, Lemmon AR, Lemmon EM, Zaher H, Grazziotin FG,
30 Keogh JS. 2020 Phylogenomics, biogeography, and morphometrics reveal rapid phenotypic
31 evolution in pythons after crossing Wallace's line. *Syst Biol* 69, 1039–1051.
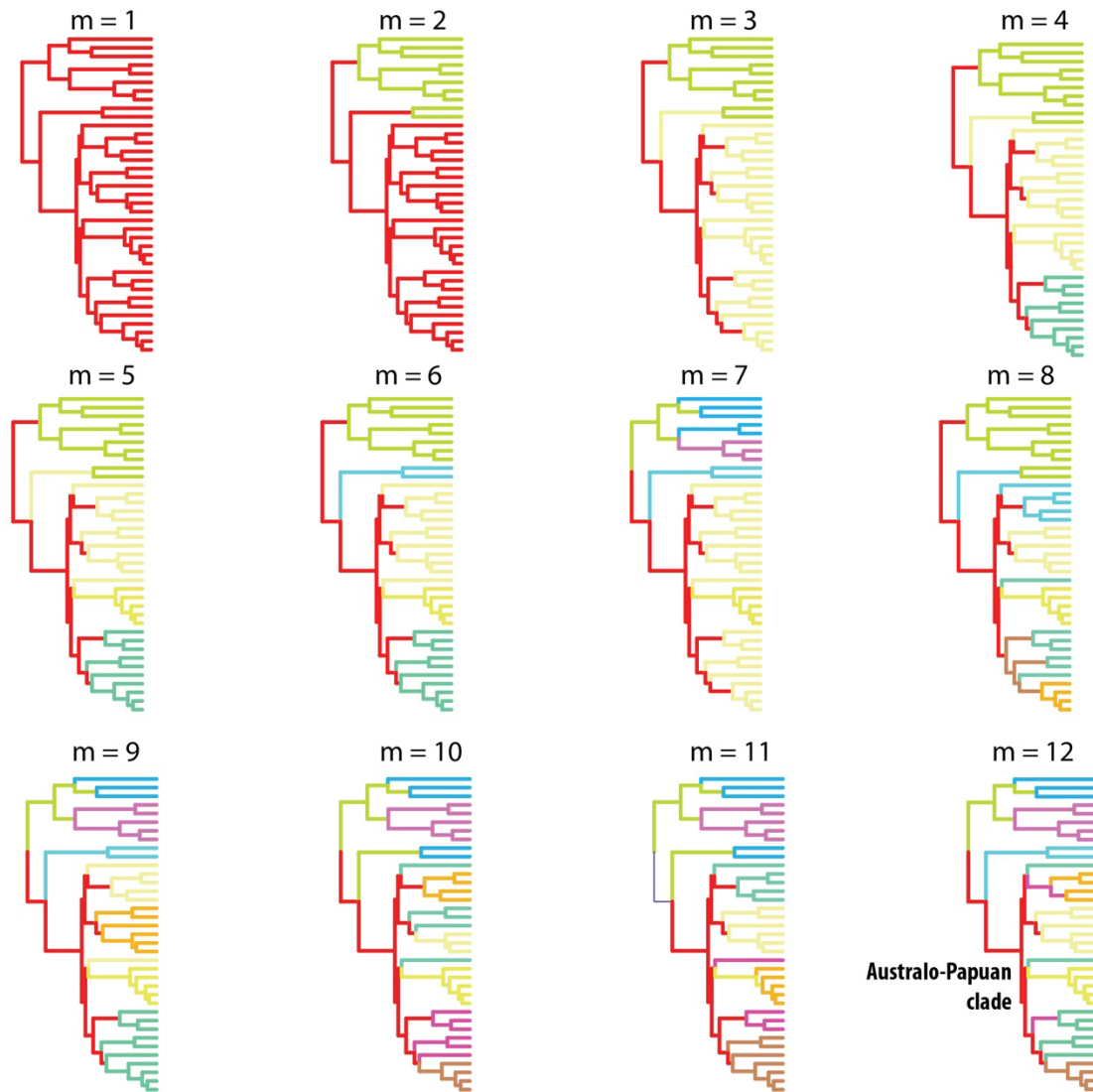32
33 Esquerré D, Donnellan SC, Pavón-Vázquez CJ, Fenker J, Keogh JS. 2021 Phylogeography,
34 historical demography and systematics of the world's smallest pythons (Pythonidae,
35 Antaresia). *Mol Phylogenet Evol* 161, 107181.
36
37 Natusch DJD, Esquerré D, Lyons JA, Hamidy A, Lemmon AR, Lemmon EM, Riyanto A,
38 Keogh JS, Donnellan S. 2021 Phylogenomics, biogeography and taxonomic revision of New
39 Guinean pythons (Pythonidae, Leiopython) harvested for international trade. *Mol Phylogenet*
40 *Evol* 158, 106960.
41
42 Reynolds GR, Niemiller ML, Revell LJ. 2014 Toward a tree-of-life for the boas and pythons:
43 Multilocus species-level phylogeny with unprecedented taxon sampling. *Molecular*
44 *Phylogenetics and Evolution* 71, 201–213.
45

46

47 **Figure S1**. Pythonidae tree painted with different diversification modalities estimated from

48 its spectral distances profile. The optimal number of modalities is 12, but we present trees

49 with 1:12 modalities to visualize consistent diversification modalities across the tree, in

50 particular the one at the base of the Australo-Papuan radiation.

51

52