●●●

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4.11.2016

The Question(s)

- What is the ancestral state for squamate parity?
- How many times has the alternative state evolved from that?
- Have there been reversals back to the ancestral state?

The Set-Up

- Pyron and Burbrink 2014 (http://onlinelibrary.wiley.com/doi/10.1111/ele.12168/full)

The Set-Up

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- 8000 species classified by parity mode

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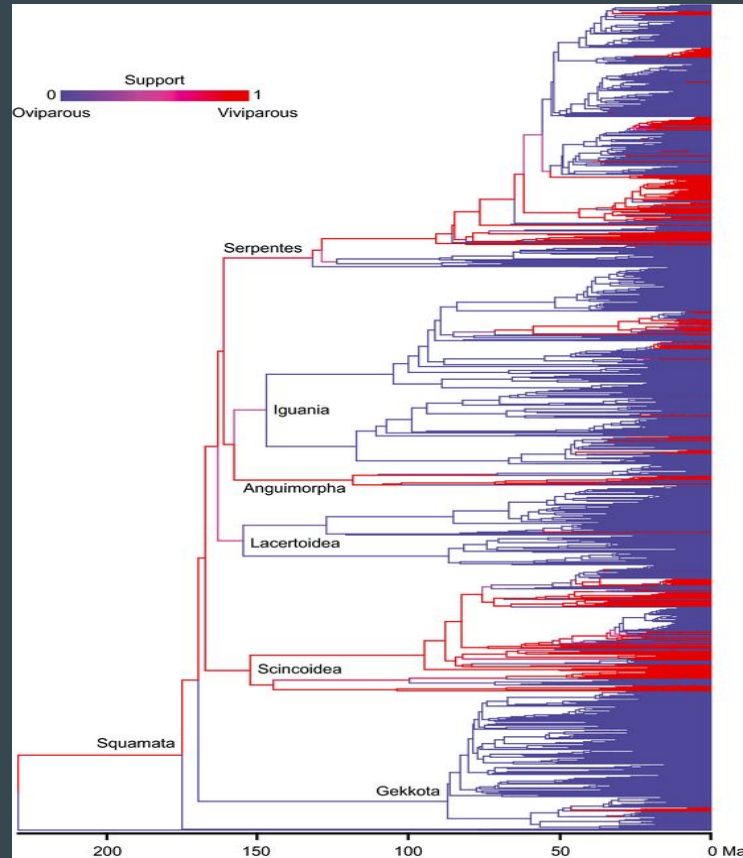 - 12 species were bimodal

The Set-Up

- Fit a model of speciation and extinction to these data
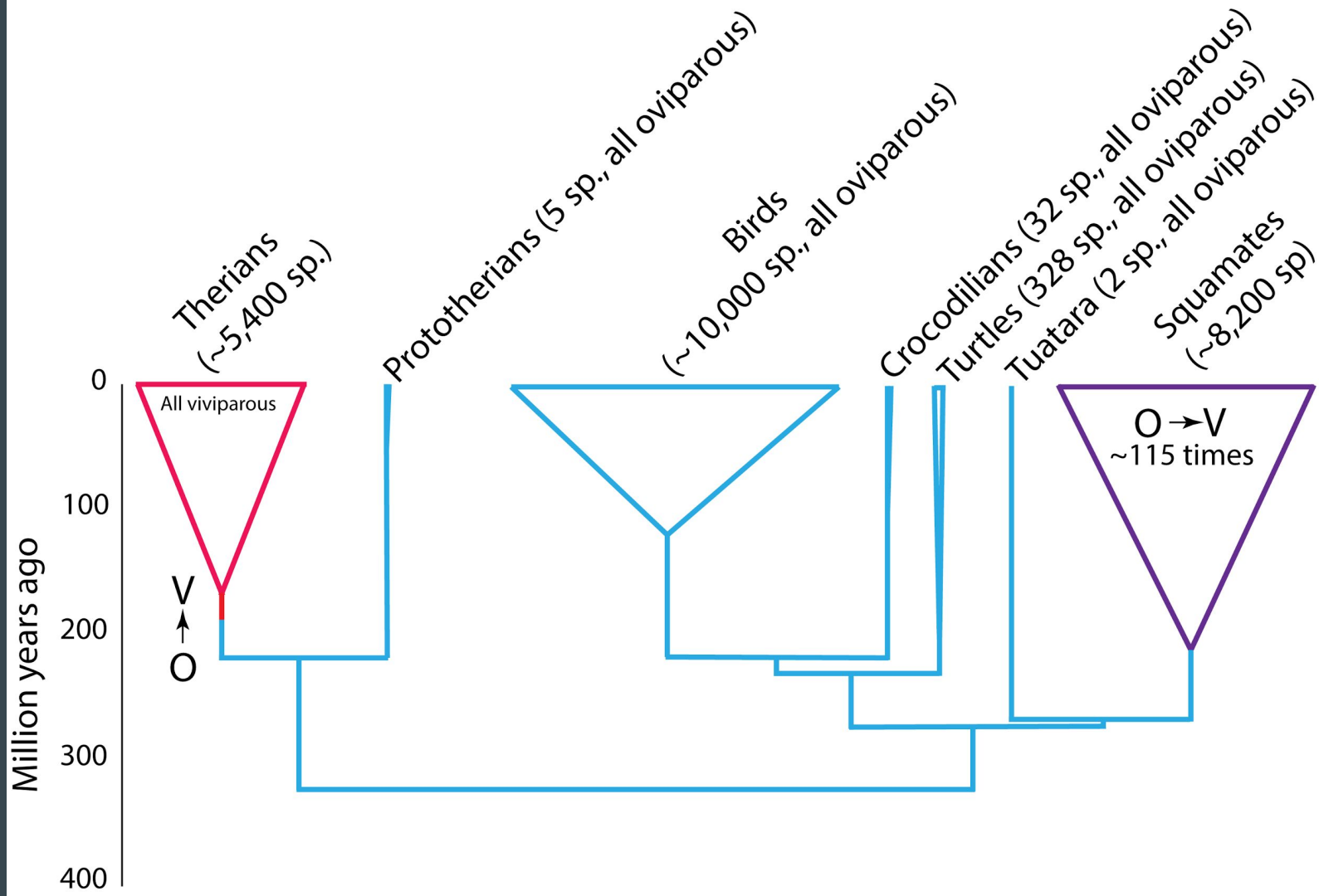
The Set-Up

- Fit a model of speciation and extinction to these data
- This model, internally, estimates ancestral states

Early origin of viviparity and multiple reversions to oviparity in squamate reptiles

The Set-Up

- 34 origins of oviparity
- 56 reversals to oviparity

What we'll do today

- Large tree inference
- State-dependent diversification models

http://people.sc.fsu.edu/~dswofford/paup_test/

http://tree.bio.ed.ac.uk/software/figtree/

website

paup

execute infile.nex;

set criterion = distance;

hs;

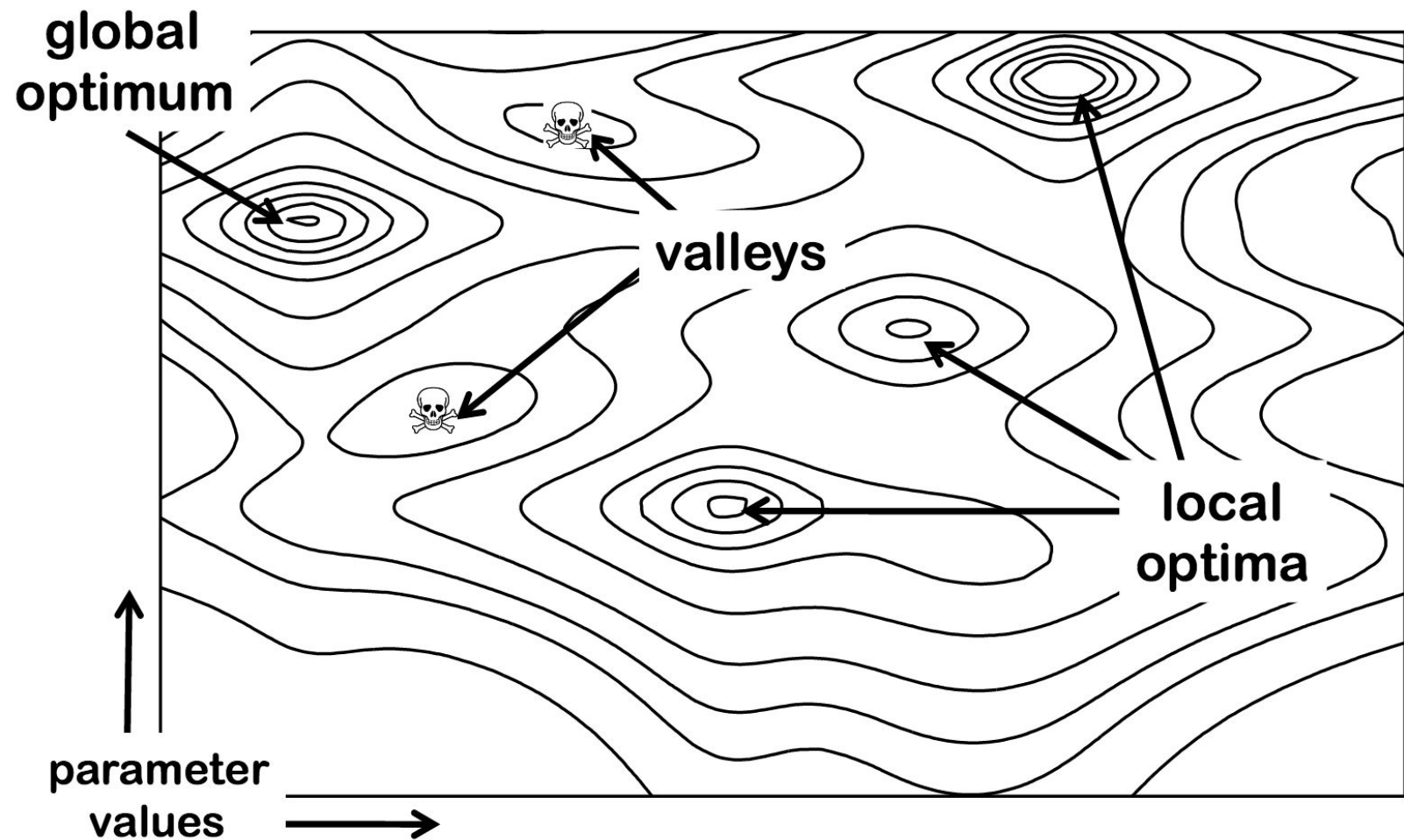This will run 10 ish minutes.

showdist;

What do we observe?

What do we observe?

- Massive amounts of missing data

What do we observe?

- Massive amounts of missing data
- ⅛ of taxon pairs have no data that can be used to evaluate them with respect to one another

Tips	Number of unrooted (binary) trees	
4	3	
5	15	
6	105	
7	945	
8	10,395	
9	135,135	
10	2,027,025	
11	34,459,425	
12	654,729,075	
13	13,749,310,575	
14	316,234,143,225	
15	7,905,853,580,625	
16	213,458,046,676,875	
17	6,190,283,353,629,375	
18	191,898,783,962,510,625	
19	6,332,659,870,762,850,625	
20	22,164,309,5476,699,771,875	
21	8,200,794,532,637,891,559,375	
22	319,830,986,772,877,770,815,625	
23	13,113,070,457,687,988,603,440,625	> 21 moles of trees
24	563,862,029,680,583,509,947,946,875	

Missing data and topology estimation

- Random missing data are generally not a problem, if the sample size is large

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  - = reducing sample size

Missing data and topology estimation

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- Biased missing data tend to cause a big problem

Tree estimation

- Maximum likelihood

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Tree estimation

- Maximum likelihood
  - RAxML
  - Bootstraps

Branch Lengths
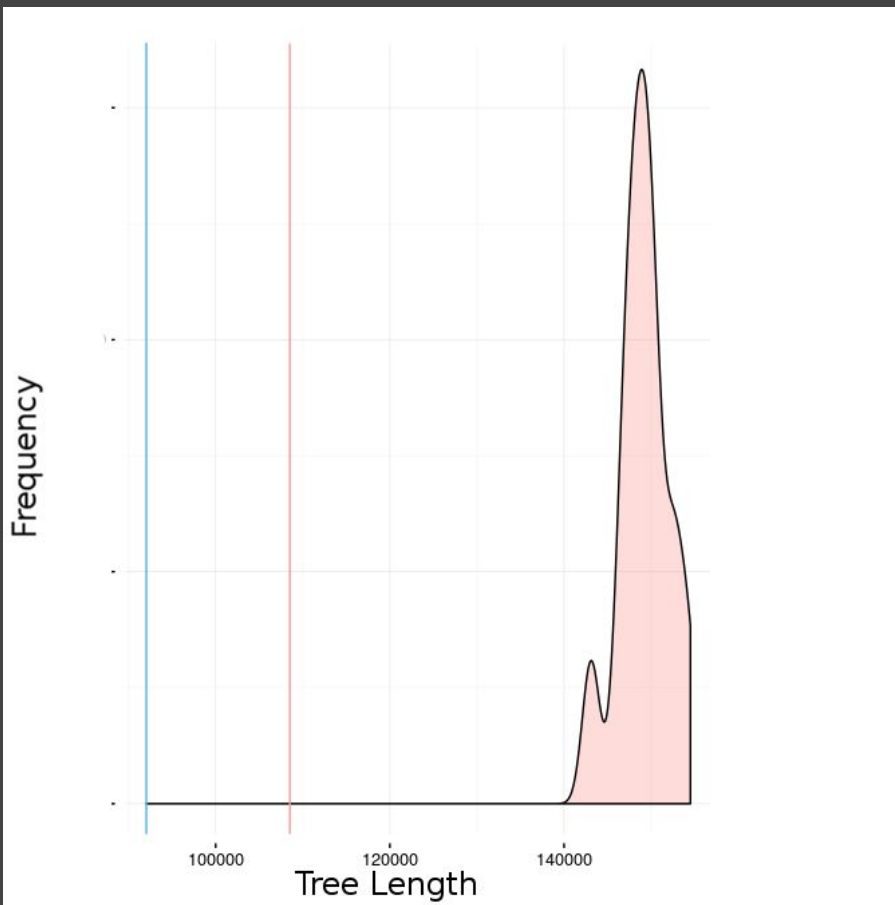
Tree estimation

- So we compromised

Tree estimation

- So we compromised
  - First pass estimation in RAxML
  - Optimization in Garli
    - For just branch lengths
    - For BL + topology

Anguimorpha

Iguania

Serpentes

Sphenodon punctatus

Dibamidae

Gekkota

Lacertoidea

Scincomorpha

20.0

Wright et al. 2015

Tree
Ln Likelihood

Pyron and Burbrink
-2,676,499
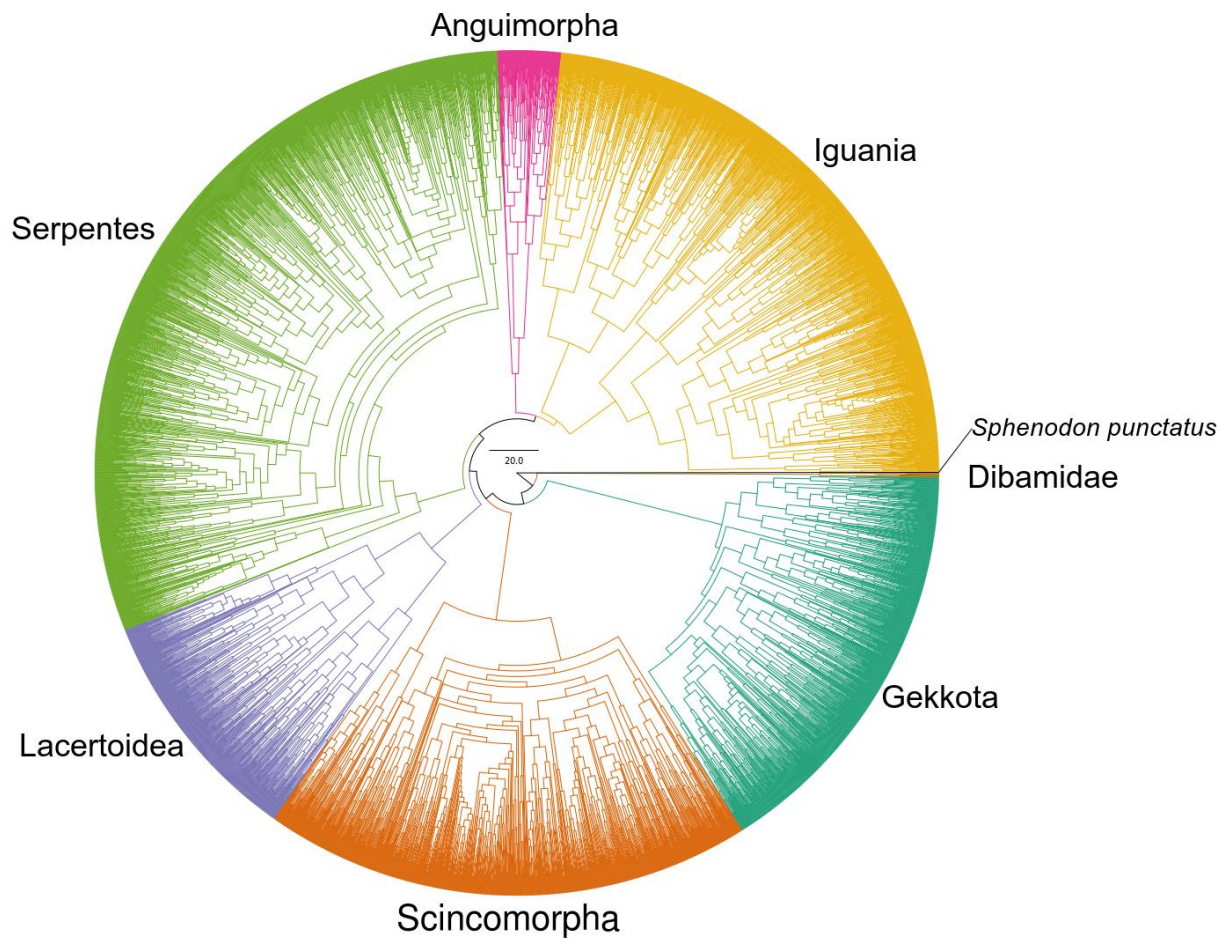
ExaML Best-Scoring
-2,598,386
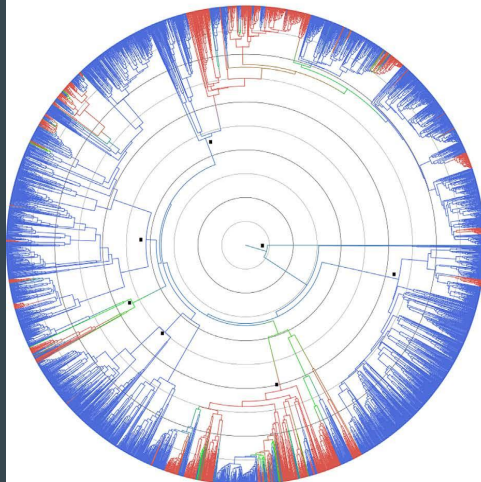
Tree
Ln Likelihood
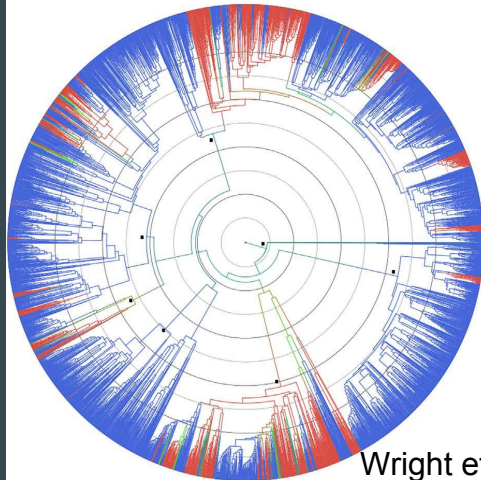
Branch Length Improved
-2,595,843
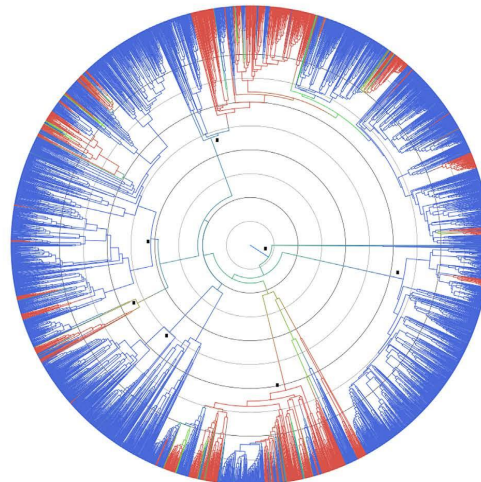
Branch Length and Topology Improved
-2,592,703

Wright et al. 2015
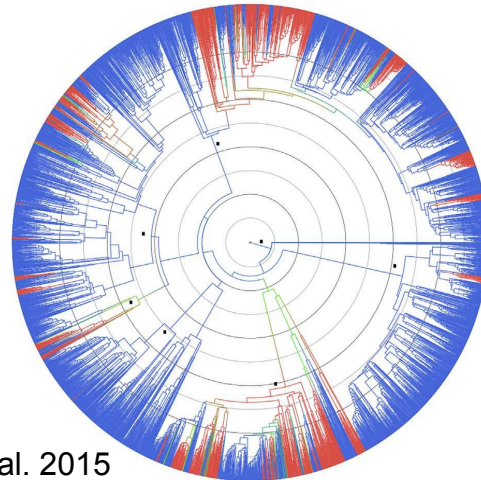
iPython Notebook

RF_Checking

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RF_Checking

- What I want you to note is that there are 854 differences between the Pyron and Burbrink tree and our best one.

iPython Notebook

RF_Checking

- What I want you to note is that there are 854 differences between the Pyron and Burbrink tree and our best one.
    - Total possible differences 8118
    - About 10% of the tree is different

Anguimorpha

Iguania

Serpentes

Sphenodon punctatus

20.0

Dibamidae

Gekkota

Lacertoidea

Scincomorpha

Wright et al. 2015
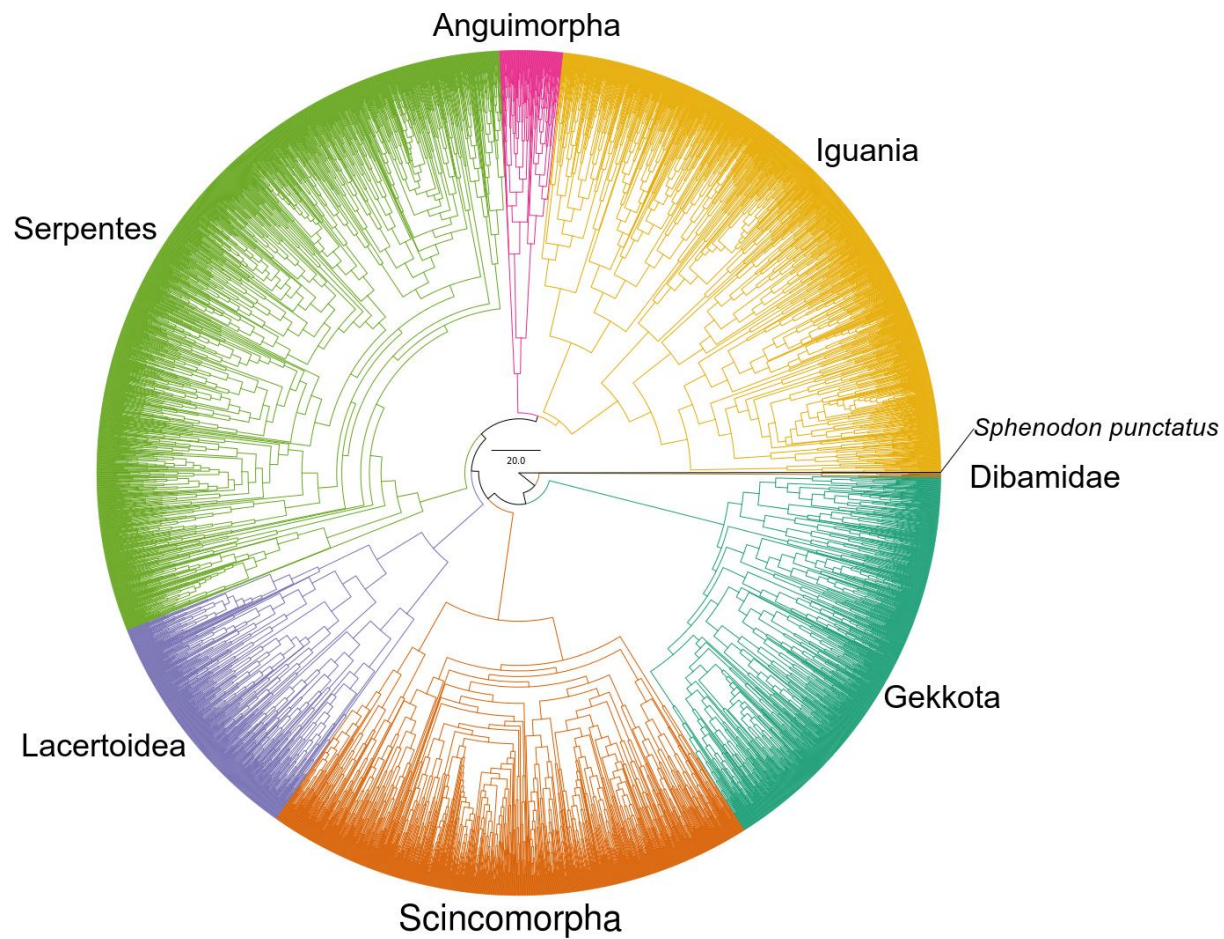
State-dependent diversification models

State-dependent diversification models

- Full BiSSe model
  - Two speciation parameters

  - Two extinction parameters

  - Two transition rates

State-dependent diversification models

- Full BiSSe model
  - Two speciation parameters
  - Two extinction parameters
  - Two transition rates

One of each parameter for oviparity and viviparity

State-dependent diversification models

- R CMD BATCH bisse.R

Let's look inside the script

Heatmaps

Show that 4-tree figure again, zoom in on one.

Show that 4-tree figure again, zoom in on one.

- yes ma'am.

Azemiops feae
Tropidolaemus wagleri
Deinagkistrodon acutus
Calloselasma rhodostoma
Hypnale nepa
Hypnale hypnale
Hypnale zara
Trimeresurus puniceus
Trimeresurus borneensis
Trimeresurus malabaricus
Trimeresurus gramineus
Trimeresurus trigonocephalus
Parias hageni
Parias malcolmi
Parias flavomaculatus
Parias sumatranus
Parias schultzei
Himalayophis tibetanus
Popeia popeiorum
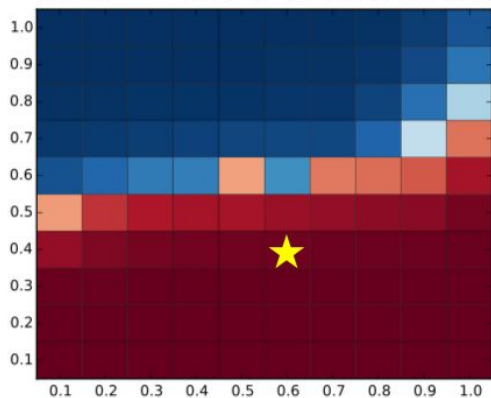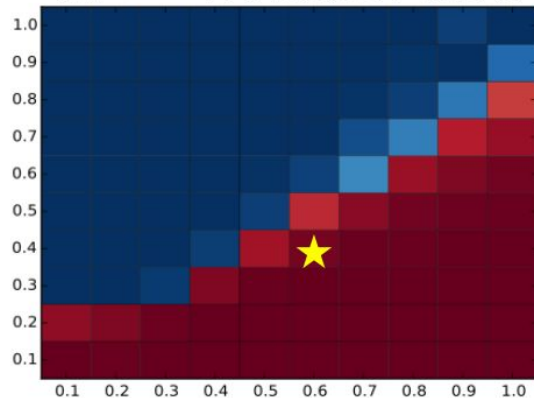Viridovipera medoensis
Viridovipera yunnanensis
Viridovipera gumprechti
Viridovipera vogeli
Viridovipera stejnegeri
Cryptelytrops kanburiensis
Cryptelytrops macrops
Cryptelytrops venustus
Cryptelytrops insularis
Cryptelytrops fasciatus
Cryptelytrops andersoni
Cryptelytrops septentrionalis
Cryptelytrops albolabris
Cryptelytrops cantori
Cryptelytrops erythrurus
Cryptelytrops purpureomaculatus
Trimeresurus gracilis
Ovophis okinavensis
Gloydius tsushimaensis
Gloydius brevicaudus
Gloydius blomhoffi
Gloydius ussuriensis
Gloydius strauchi
Gloydius halys
Gloydius shedaoensis
Gloydius saxatilis
Gloydius intermedius
Ovophis monticola
Ovophis tonkinensis
Ovophis zayuensis
Triceratolepidophis sieversorum
Protobothrops kaulbacki
Zhaoermia mangshanensis
Protobothrops cornutus
Protobothrops xiangchengensis
Protobothrops flavoviridis
Protobothrops tokarensis
Protobothrops mucrosquamatus
Protobothrops elegans
Atropoides occiduus
Atropoides nummifer
Atropoides olmec
Atropoides picadoi
Cerrophidion godmani
Cerrophidion tzotzilorum
Cerrophidion petlalcalensis
Porthidium ophryomegas
Porthidium dunni
Porthidium yucatanicum
Porthidium nasutum
Porthidium lansbergii
Porthidium porrasi
Ophryacus undulatus
Cerrophidion barbouri
Ophryacus melanurus
Lachesis muta
Lachesis stenophrys
Bothriechis schlegelii
Bothriechis nigroviridis
Bothriechis lateralis
Bothriechis bicolor
Bothriechis aurifer
Bothriechis rowleyi
Bothriechis thalassinus
Bothriechis marchi
Bothrops pictus
Bothrocophias campbelli
Bothrocophias hyoprora
Bothrocophias microphthalmus
Bothrops ammodytoides
Bothrops fonsecai
Bothrops cotiara
Bothrops itapetiningae
Bothrops alternatus
Bothriopsis pulchra
Bothriopsis chloromelas
Bothriopsis taeniata
Bothriopsis bilineata
Bothrops erythromelas
Bothrops diporus
Bothrops neuwiedi
Bothrops jararaca
Bothrops insularis
Bothrops alcatraz
Bothrops brazili
Bothrops jararacussu
Bothrops punctata
Bothrops caribbaeus
Bothrops lanceolatus
Bothrops asper
Bothrops marajoensis
Bothrops colombiensis
Bothrops atrox
Bothrops leucurus
Bothrops moojeni
Agkistrodon contortrix
Agkistrodon piscivorus
Agkistrodon bilineatus
Agkistrodon taylori
Sistrurus miliarius
Sistrurus catenatus
Crotalus pricei
Crotalus intermedius
Crotalus transversus
Crotalus tancitarensis
Crotalus lepidus
Crotalus aquilus
Crotalus triseriatus
Crotalus pusillus
Crotalus ravus
Crotalus cerastes
Crotalus enyo
Crotalus polystictus
Crotalus horridus
Crotalus willardi
Crotalus simus
Crotalus durissus
Crotalus basiliscus
Crotalus molossus
Crotalus totonacus
Crotalus ruber
Crotalus catalinensis
Crotalus atrox
Crotalus tortugensis
Crotalus mitchellii
Crotalus tigris
Crotalus adamanteus
Crotalus scutulatus
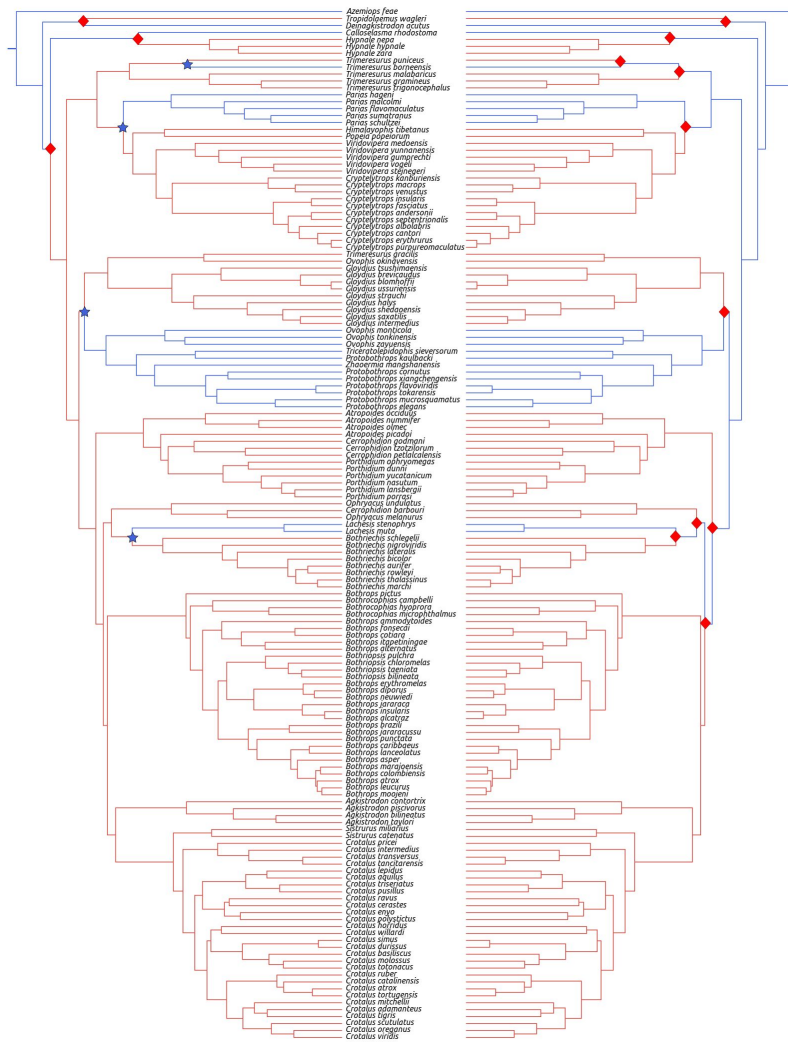Crotalus oreganus
Crotalus viridis

Table 2. Number of changes to viviparity and oviparity, and support for the root state, as estimated across four trees and three methods of taxon-sampling correction.

Tree	Origins of viviparity	Minimum number of reversals to oviparity				Root state (% support for oviparity)		
		1X	2X	3X	4X	No sampling correction	One term correction	Two term correction
Pyron and Burbrink tree	106–129	13	2	1	0	80.8	7.2	7.4
ExaML tree	103–126	12	3	1	0	75.0	87.9	11.2
Branch-length improved tree	103–124	12	3	1	0	90.4	97.5	24.4
Best tree	98–129	18	3	0	0	88.6	94.5	14.3

The ranges for origins of viviparity indicate the number of origins under the equal weighted model to the number of origins assuming no reversals to oviparity. Reversals to oviparity are shown for four models of character change: 1X = equal weighting of changes between viviparity and oviparity; 2X = twofold greater penalty of reversals to oviparity; 3X = threefold greater penalty of reversals to oviparity; 4X = fourfold greater penalty of reversals to oviparity.

Conclusions

The story we tell about this trait depends on:

Conclusions

The story we tell about this trait depends on:

- The tree we use

Conclusions

The story we tell about this trait depends on:

- The tree we use
- The model we use

Conclusions

The story we tell about this trait depends on:

- The tree we use
- The model we use
- How we parse teh model output

Future Directions

- Threshold model