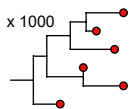
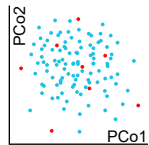


0	1	1	1	0	0	0	1	0
1	0	1	1	0	0	0	1	0
0	0	1	0	0	0	0	1	1
0	1	1	0	0	0	0	1	1
0	1	1	0	0	0	0	0	0
1	0	1	1	0	1	0	0	0
1	1	1	0	1	1	0	0	0

(a) update belemnite character matrix

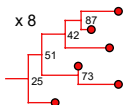
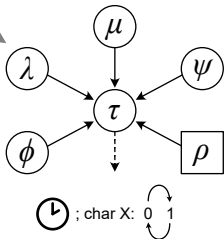


(c) posterior tree sample

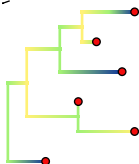


(d) multidimensional tree space

(b) FBD model



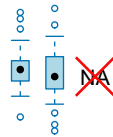
(e) representative trees



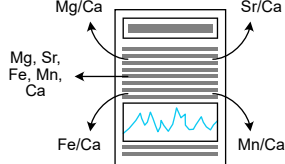
(k) ancestral state reconstruction

$$E/Ca = 0.1 \times \frac{E [\mu\text{g/g}]}{A_r(E)} / \frac{Ca [\text{wt\%}]}{A_r(Ca)}$$

(g) calculate missing values



(h) data exploration / cleaning

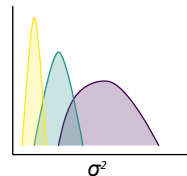
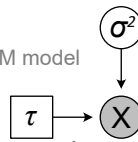


(f) literature data

<i>Acrocoelites</i>	15.30
<i>Belemnopsis</i>	4.41
<i>Cylindroteuthis</i>	5.10
<i>Dimitobelus</i>	11.35
<i>Hibolites</i>	12.74
...	...

(i) mean values per genus

(j) BM model



(l) evolutionary rate estimation