The Critical Beta-Splitting Random Tree Model: Results and Open Problems

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This talk is about properties of one specific "new" model. Why might one care?

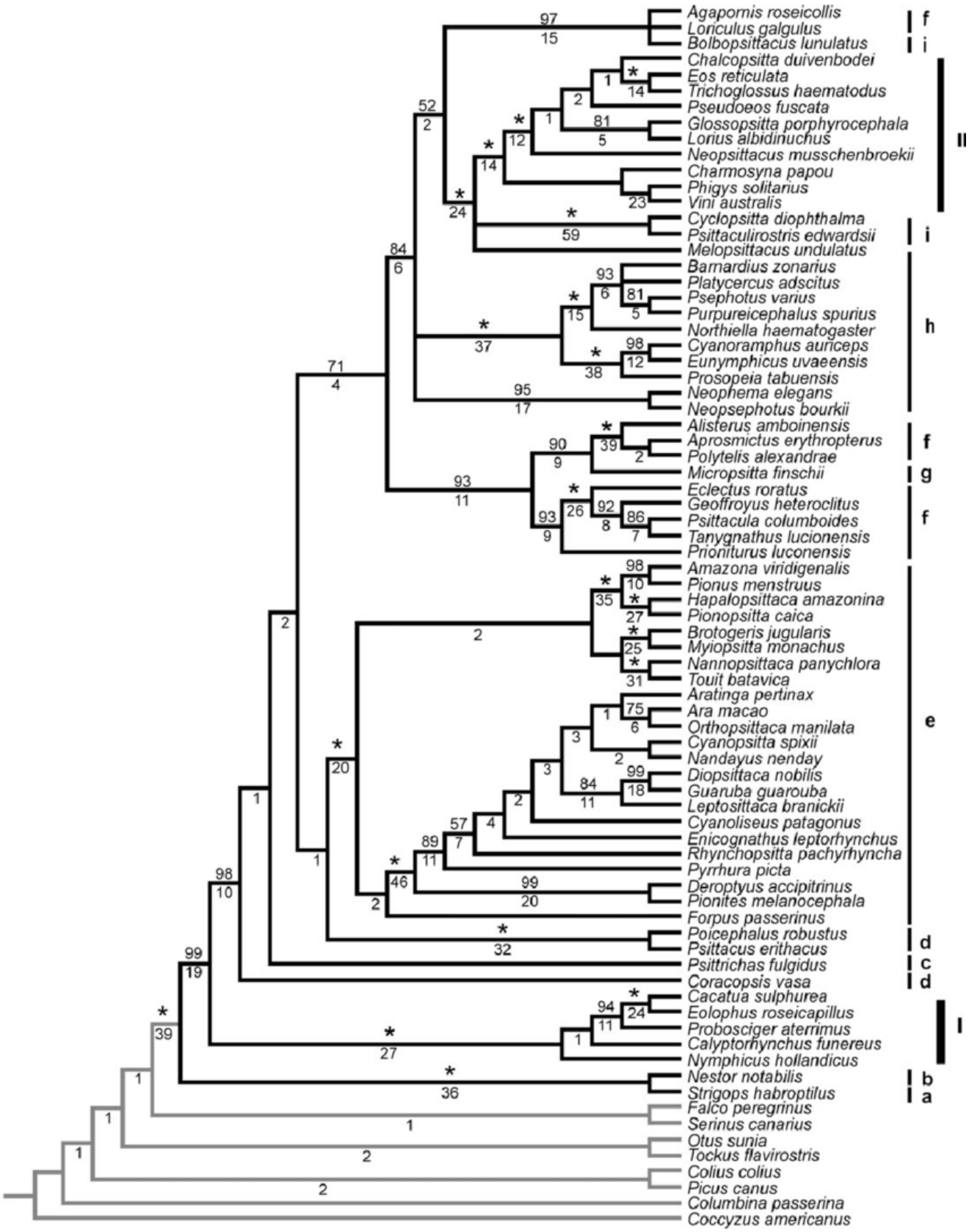
- Some (weak) real-world motivation.
- Being a "random tree" model, there are many aspects to study; we have some results and many open problems. Will suggest 4 specific **challenges**.
- Can compare and contrast with the known continuum random tree limits of other models.
- Friendly competition between probabilistic and analysis-of-recursions techniques (ongoing work with co-author Boris Pittel).

2 long preprints on arXiv
The Critical Beta-splitting Random Tree, I and II

Digression: A something completely different problem

Take a probability measure μ on a complete separable metric space (S, d). Take 2 independent samples ξ_1, ξ_2 from μ. The r.v. $d(\xi_1, \xi_2)$ has some distribution θ on $[0, \infty)$.

What distributions θ arise in this way?


Agapornis roseicollis
Loriculus galgulus
Bolbopsittacus lunulatus
Chalcopsitta duivenbodei
Eos reticulata
Trichoglossus haematodus
Pseudoeos fuscata
Glossopsitta porphyrocephala
Lorius albidinuchus
Neopsittacus musschenbroekii
Charmosyna papou
Phigys solitarius
Vini australis
Cyclopsitta diophthalma
Psittaculirostris edwardsii
Melopsittacus undulatus
Barnardius zonarius
Platycercus adscitus
Psephotus varius
Purpureicephalus spurius
Northiella haematogaster
Cyanoramphus auriceps
Eunymphicus uvaeensis
Prosopeia tabuensis
Neophema elegans
Neopsephotus bourkii
Alisterus amboinensis
Aprosmictus erythropterus
Polytelis alexandrae
Micropsitta finschii
Eclectus roratus
Geoffroyus heteroclitus
Psittacula columboides
Tanygnathus lucionensis
Prioniturus luconensis
Amazona viridigenalis
Pionus menstruus
Hapalopsittaca amazonina
Pionopsitta caica
Brotogeris jugularis
Myiopsitta monachus
Nannopsittaca panychlora
Touit batavica
Aratinga pertinax
Ara macao
Orthopsittaca manilata
Cyanopsitta spixii
Nandayus nenday
Diopsittaca nobilis
Guaruba guarouba
Leptosittaca branickii
Cyanoliseus patagonus
Enicognathus leptorhynchus
Rhynchopsitta pachyrhyncha
Pyrrhura picta
Deroptyus accipitrinus
Pionites melanocephala
Forpus passerinus
Poicephalus robustus
Psittacus erithacus
Psittrichas fulgidus
Coracopsis vasa
Cacatua sulphurea
Eolophus roseicapillus
Probosciger aterrimus
Calyptorhynchus funereus
Nymphicus hollandicus
Nestor notabilis
Strigops habroptilus
Falco peregrinus
Serinus canarius
Otus sunia
Tockus flavirostris
Colius colius
Picus canus
Columbina passerina
Coccyzus americanus
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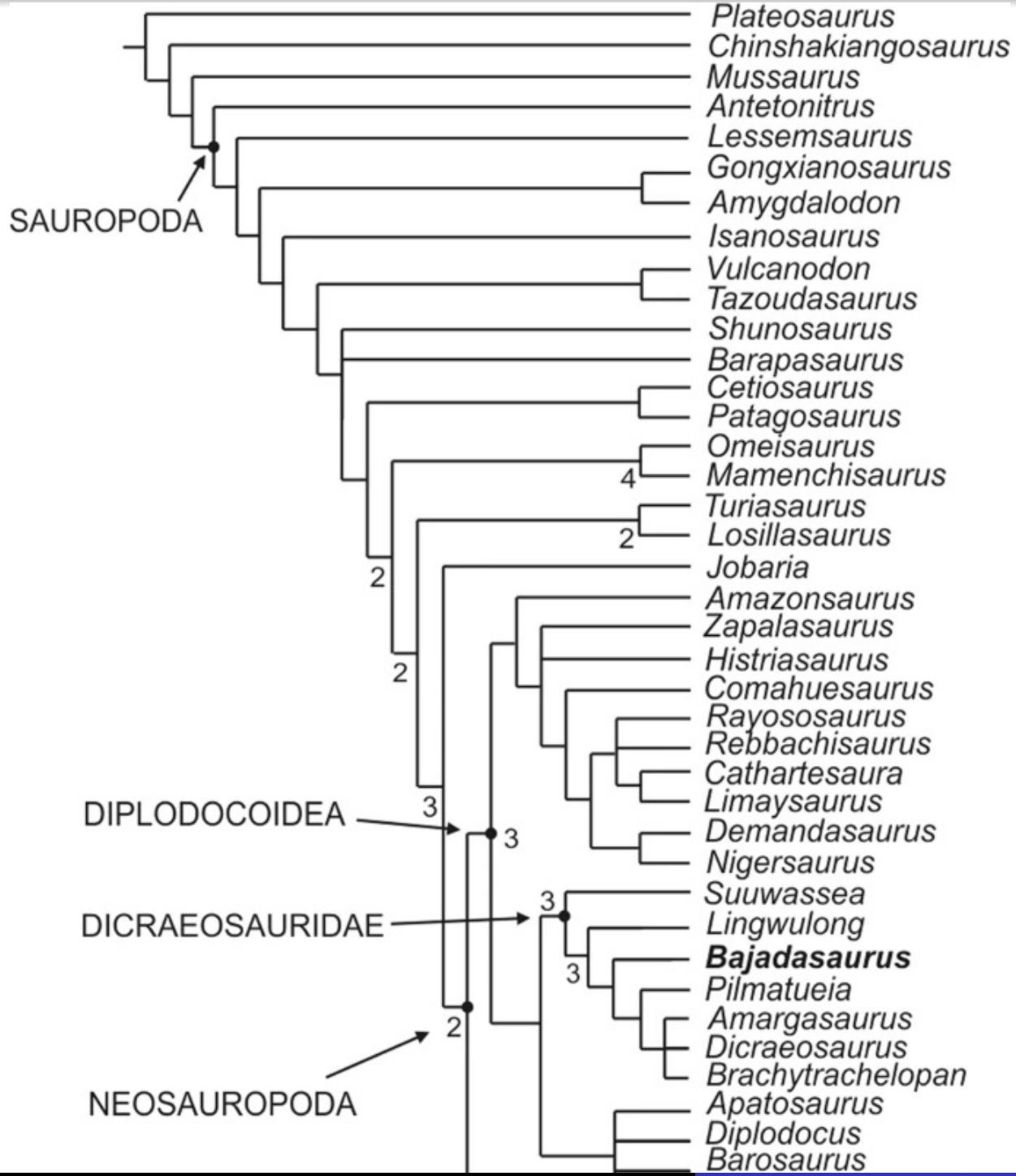
This "uneven split" property holds for most phylogenies – just type "xxx phylogeny" into Google Images.

To demonstrate, having already said "dead parrot" and "something completely different" let's continue the Monty Python theme by showing phylogenetic trees for

- Brontosaurus
- Swallows
- Pythons


Plateosaurus
Chinshakiangosaurus
Mussaurus
Antetonitrus
Lessemsaurus
Gongxianosaurus
Amygdalodon
Isanosaurus
Vulcanodon
Tazoudasaurus
Shunosaurus
Barapasaurus
Cetiosaurus
Patagosaurus
Omeisaurus
Mamenchisaurus
Turiasaurus
Losillasaurus
Jobaria
Amazonsaurus
Zapalasaurus
Histriasaurus
Comahuesaurus
Rayososaurus
Rebbachisaurus
Cathartesaura
Limaysaurus
Demandasaurus
Nigersaurus
Suuwassea
Lingwulong
Bajadasaurus
Pilmatueia
Amargasaurus
Dicraeosaurus
Brachytrachelopan
Apatosaurus
Diplodocus
Barosaurus
SAUROPODA
DIPLODOCOIDEA
DICRAEOSAURIDAE
NEOSAUROPODA
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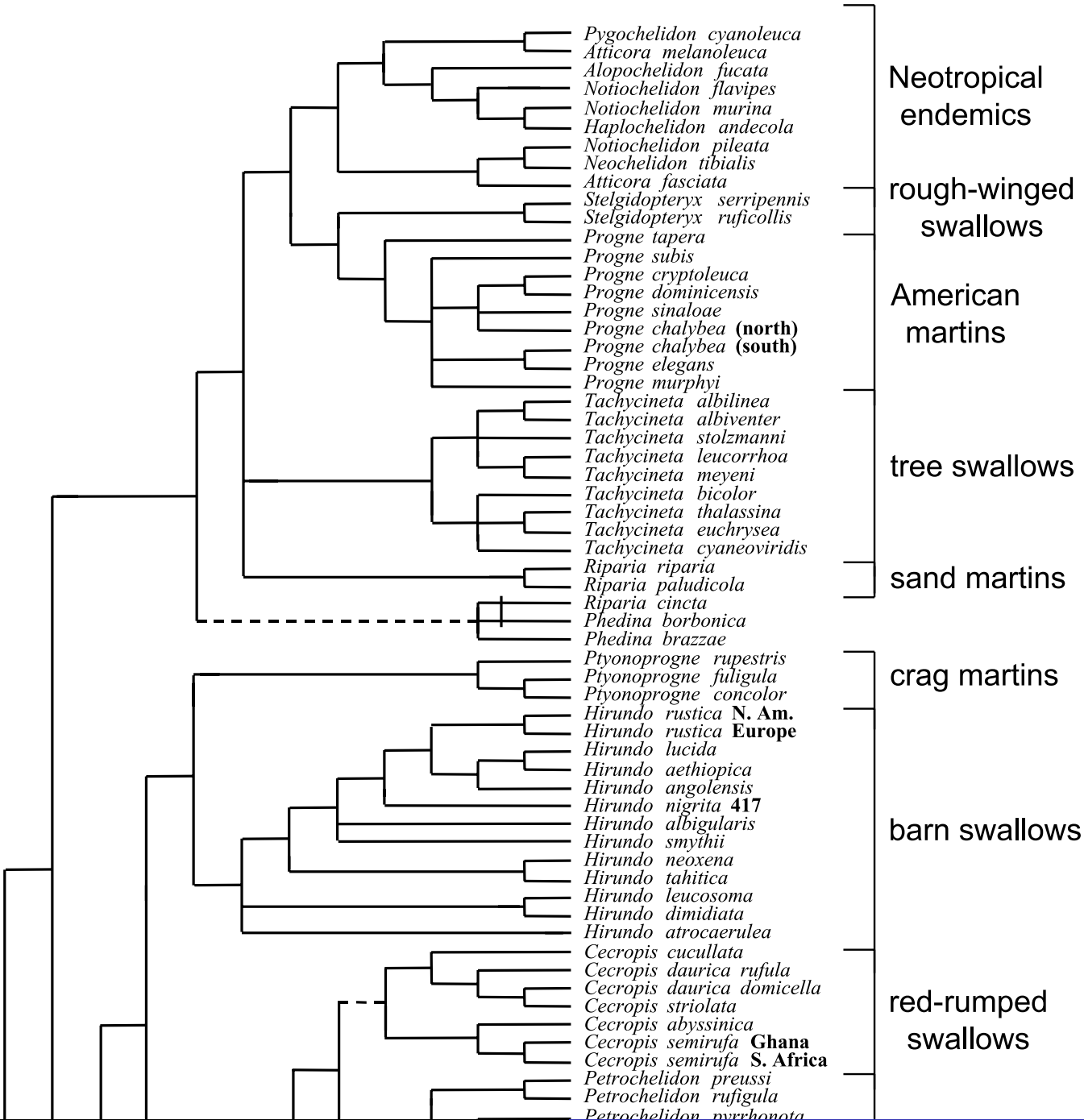
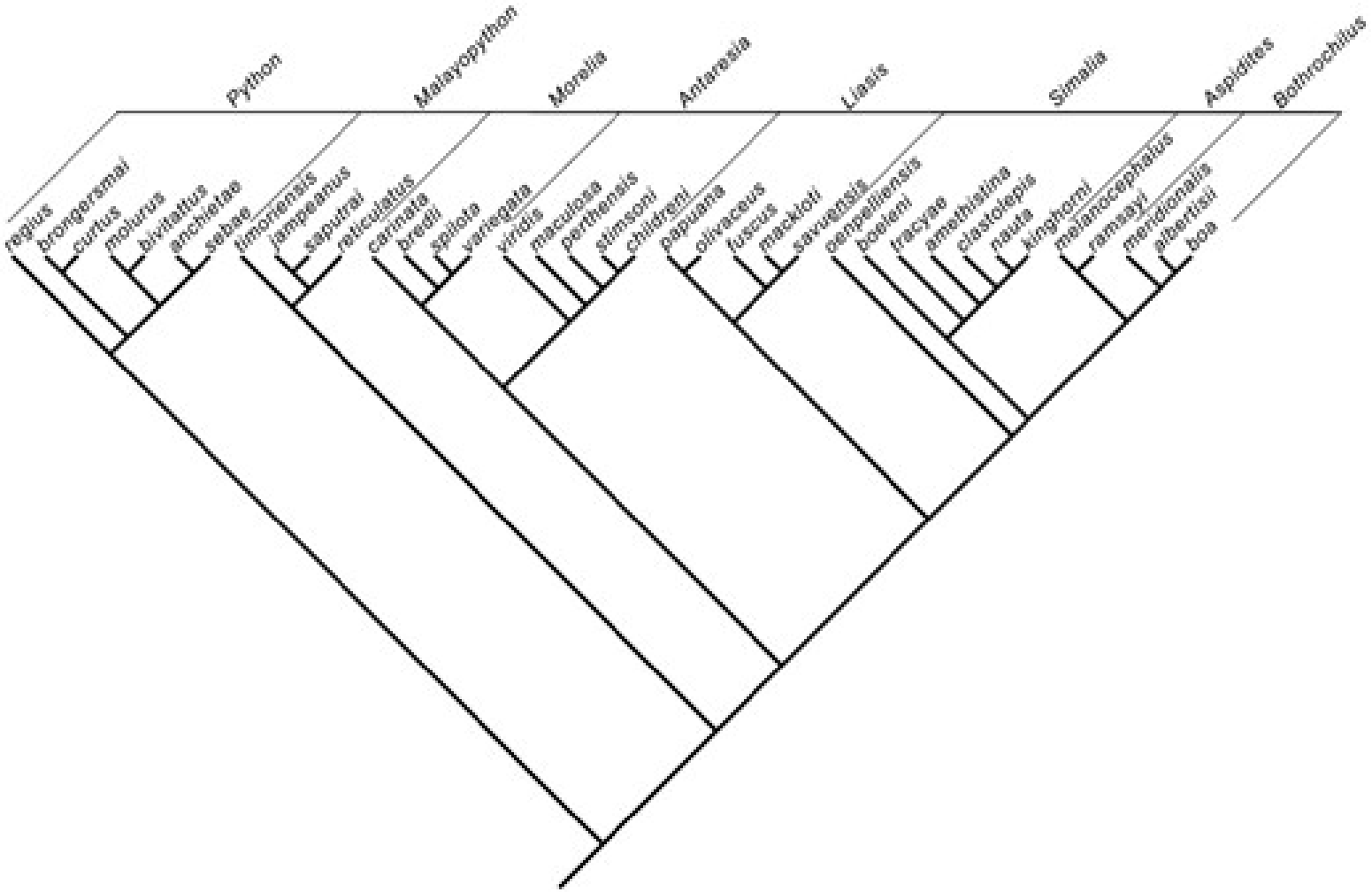

Pygochelidon cyanoleuca
Atticora melanoleuca
Alopochelidon fucata
Notiochelidon flavipes
Notiochelidon murina
Haplochelidon andecola
Notiochelidon pileata
Neochelidon tibialis
Atticora fasciata
Stelgidopteryx serripennis
Stelgidopteryx ruficollis
Progne tapera
Progne subis
Progne cryptoleuca
Progne dominicensis
Progne sinaloae
Progne chalybea (north)
Progne chalybea (south)
Progne elegans
Progne murphyi
Tachycineta albilinea
Tachycineta albiventer
Tachycineta stolzmanni
Tachycineta leucorrhoa
Tachycineta meyeni
Tachycineta bicolor
Tachycineta thalassina
Tachycineta euchrysea
Tachycineta cyaneoviridis
Riparia riparia
Riparia paludicola
Riparia cincta
Phedina borbonica
Phedina brazzae
Ptyonoprogne rupestris
Ptyonoprogne fuligula
Ptyonoprogne concolor
Hirundo rustica N. Am.
Hirundo rustica Europe
Hirundo lucida
Hirundo aethiopica
Hirundo angolensis
Hirundo nigrita 417
Hirundo albigularis
Hirundo smythii
Hirundo neoxena
Hirundo tahitica
Hirundo leucosoma
Hirundo dimidiata
Hirundo atrocaerulea
Cecropis cucullata
Cecropis daurica rufula
Cecropis daurica domicella
Cecropis striolata
Cecropis abyssinica
Cecropis semirufa Ghana
Cecropis semirufa S. Africa
Petrochelidon preussi
Petrochelidon rufigula
Neotropical endemics
rough-winged swallows
American martins
tree swallows
sand martins
crag martins
barn swallows
red-rumped swallows


Python
Malayopython
Morelia
Antaresia
Liasis
Simalia
Aspidites
Bothrochilus
regius
brongersmai
curtus
molurus
bivittatus
anchietae
sebae
timorensis
jampeanus
saputrai
reticulatus
carinata
oenpelliensis
spilota
variegata
viridis
maculosa
perthensis
stimsoni
childreni
papuana
olivaceus
fuscus
mackloti
savuensis
boeleni
fraenata
amethistina
clastolepis
nauta
kinghorni
melanocephalus
ramsayi
meridionalis
albertisii
boa

- Is there a simple probability model that replicates this "uneven splits" aspect of real cladograms?

At each split within a cladogram, a clade (sub-tree) of size m species is split into clades of sizes i and $m - i$. Data often shows (Aldous, Stat. Sci, 2001) that the median size of the smaller subtree scales as roughly $m^{1/2}$. Simple probability models used before 2000 would predict median size $O(1)$ or $O(\log m)$ or $\Omega(m)$.

One could invent models with several real parameters, and then see if any parameter values gave order $m^{1/2}$.

- Is there a simple model that predicts $m^{1/2}$?

A class of probability models for n-leaf rooted binary trees.

For each $m \geq 2$, specify a probability distribution $(q(m,i), 1 \leq i \leq m-1)$ with the symmetry condition $q(m,i) \equiv q(m,m-i)$.

Given n, construct the random tree by specifying that there is a left edge and a right edge at the root, leading to a left subtree which will have L_n leaves and a right subtree which will have $R_n = n - L_n$ leaves, where L_n (and also R_n, by symmetry) has distribution $q(n,\cdot)$.

Continue recursively; a subtree which will have $m \geq 2$ leaves is split into two subtrees of random size from the distribution $q(m,\cdot)$; continue until reaching subtrees of size 1, which are leaves.

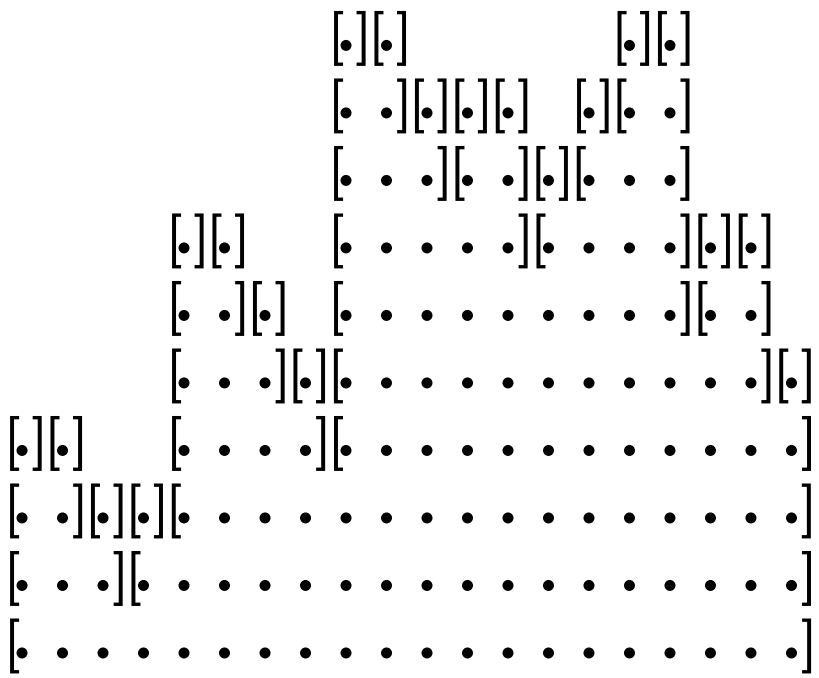


Figure: Representation as discrete interval-splitting

Specialize to a 1-parameter family, which we call *beta*-splitting: roughly it is

$$q(n,i) \propto i^{\beta}(n-i)^{\beta}$$

defined for $-2 \leq \beta \leq \infty$.

In this model the height of a typical leaf (number of edges to the root) grows as

$(\beta > -1)$: order $\log n$

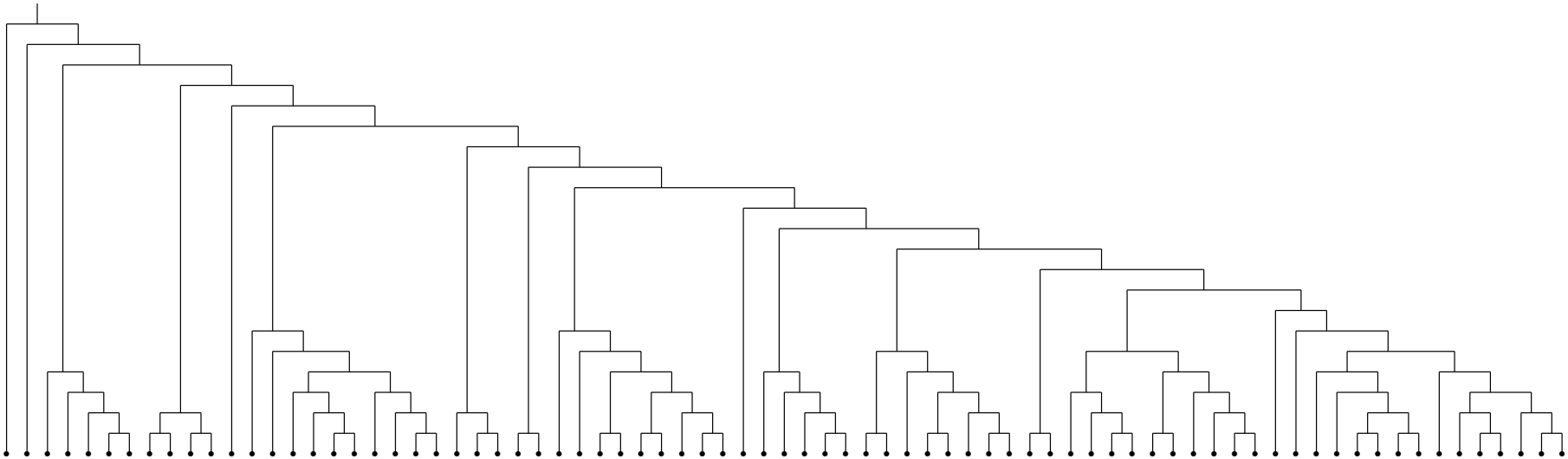
$(\beta < -1)$: order $n^{-\beta-1}$.

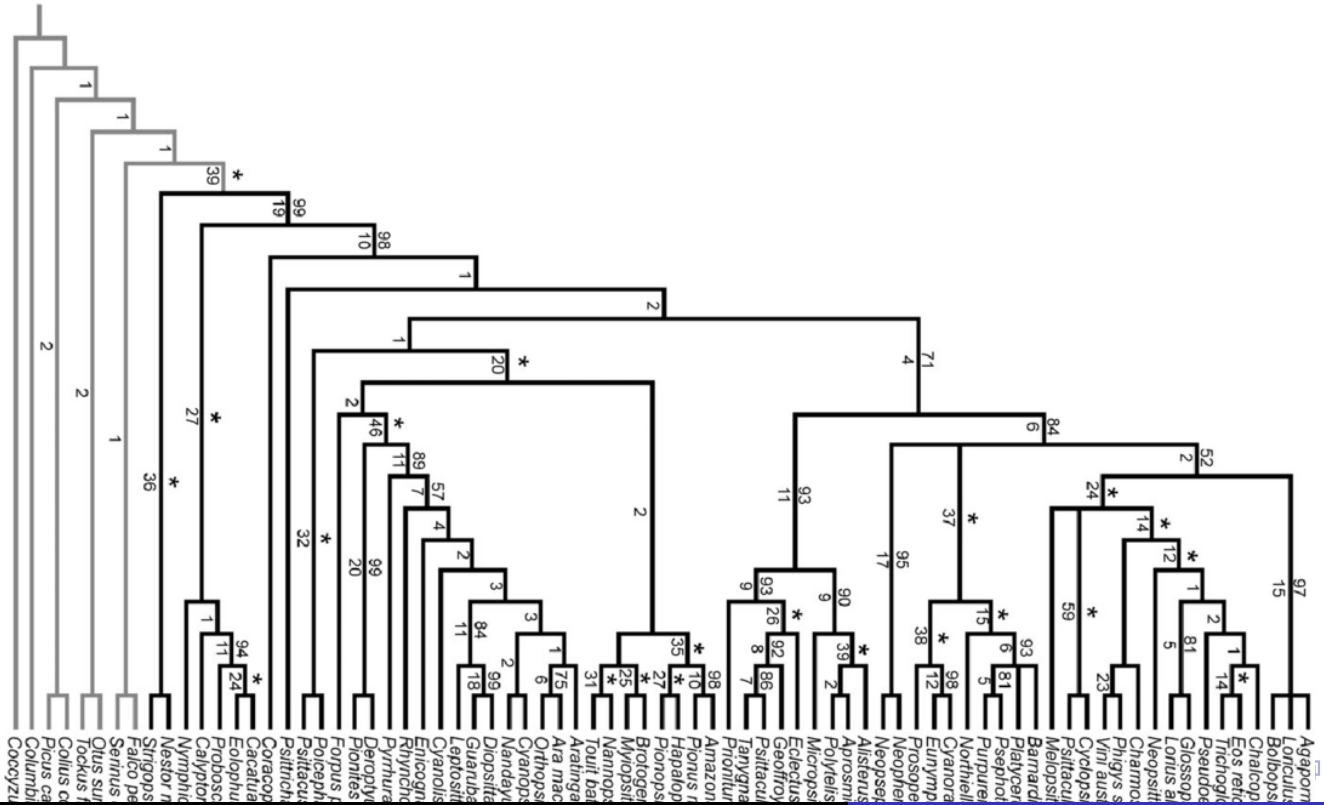
We will study the *critical* case $\beta = -1$.

Two motivations:
(i) Will fit the order $m^{1/2}$ data.
(ii) A stochastic model, with a "phase transition" separating qualitatively different behaviors, often has mathematically interesting special properties at the critical value of the parameter.

This project was mentioned in (Aldous, Probability Distributions on Cladograms, 1995) but not followed up.

Simulation of model, drawn as cladogram.





OK, forget the biology, now onto the mathematics.

Our model: splitting probability $q(n,i) \propto \frac{1}{i(n-i)}$.
Note $\frac{1}{i(n-i)} = \frac{1}{n}(\frac{1}{i} + \frac{1}{n-i})$, so we get the normalization constant

$$q(n,i) = \frac{n}{2h_{n-1}} \; \frac{1}{i(n-i)}, \quad 1 \le i \le n-1$$

where $h_n = \sum_{i=1}^{n} \frac{1}{i} \sim \log n$. So the median size of the smaller split is essentially $n^{1/2}$ because when we sum over $1 \le i \le n^{1/2}$

$$2 \times \frac{1}{2h_{n-1}} \times \sum_{i=1}^{n^{1/2}} \frac{1}{i} \approx \frac{1}{\log n} \times \log n^{1/2} \approx \frac{1}{2}.$$

So now, what does the random tree look like drawn from the root? First we have to think how we will draw a tree.

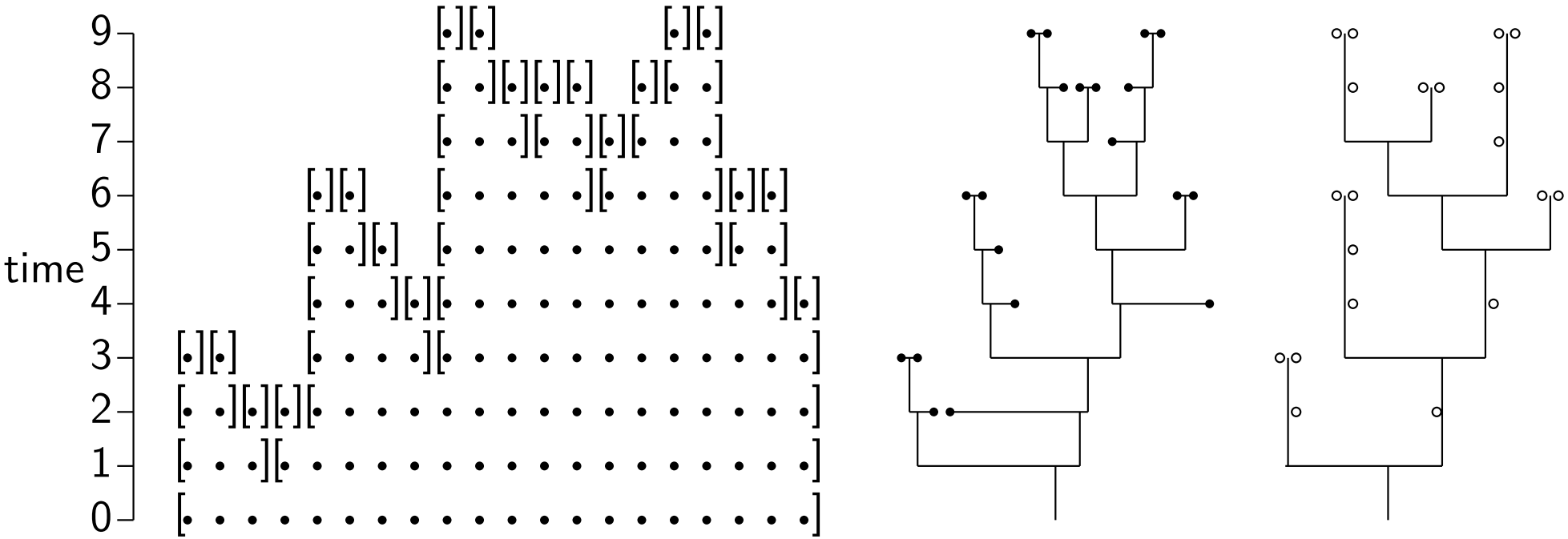


Figure: Equivalent representations of a realization of DTCS(20).

The tree on the right has some specific structure: leaves occur as pairs at the end of a stem, or as a singleton on one side of a branch. This "pruned" form turns out to be mathematically convenient when we switch to continuous time.

Overview of results

- There is a canonical way to embed the discrete-time model into a continuous-time model (which we call CTCS(n)) by specifying that a clade of size $m \geq 2$ is split at rate h_{m-1}.
- For the height (time reached) D_n of a uniform random leaf in the CTCS(n) model, $\mathbb{E}[D_n] \sim \frac{6}{\pi^2} \log n$ and also there is a Gaussian limit distribution. **Many related results of surprising sharpness can be obtained via analysis of recursions**.
- We can describe the limit fringe distribution of CTCS(n), that is the local weak limit relative to a random leaf.
- There is a non-obvious consistency property of $(CTCS(n), n \geq 2)$ in its "pruned" form: given CTCS(n+1), delete a random leaf and prune; this gives CTCS(n). In reverse this gives an explicit algorithm for growing CTCS(n+1) from CTCS(n).
- There is a scaling limit of $(\text{CTCS(n)}, n \geq 2)$, as a process of splitting the continuous interval $(0, 1)$, with a corresponding continuum tree. The pruned spanning tree on n random points is CTCS(n).

Our discrete time construction was:

At each unit time, split a size m clade into $(i, m-i)$ clades with probability

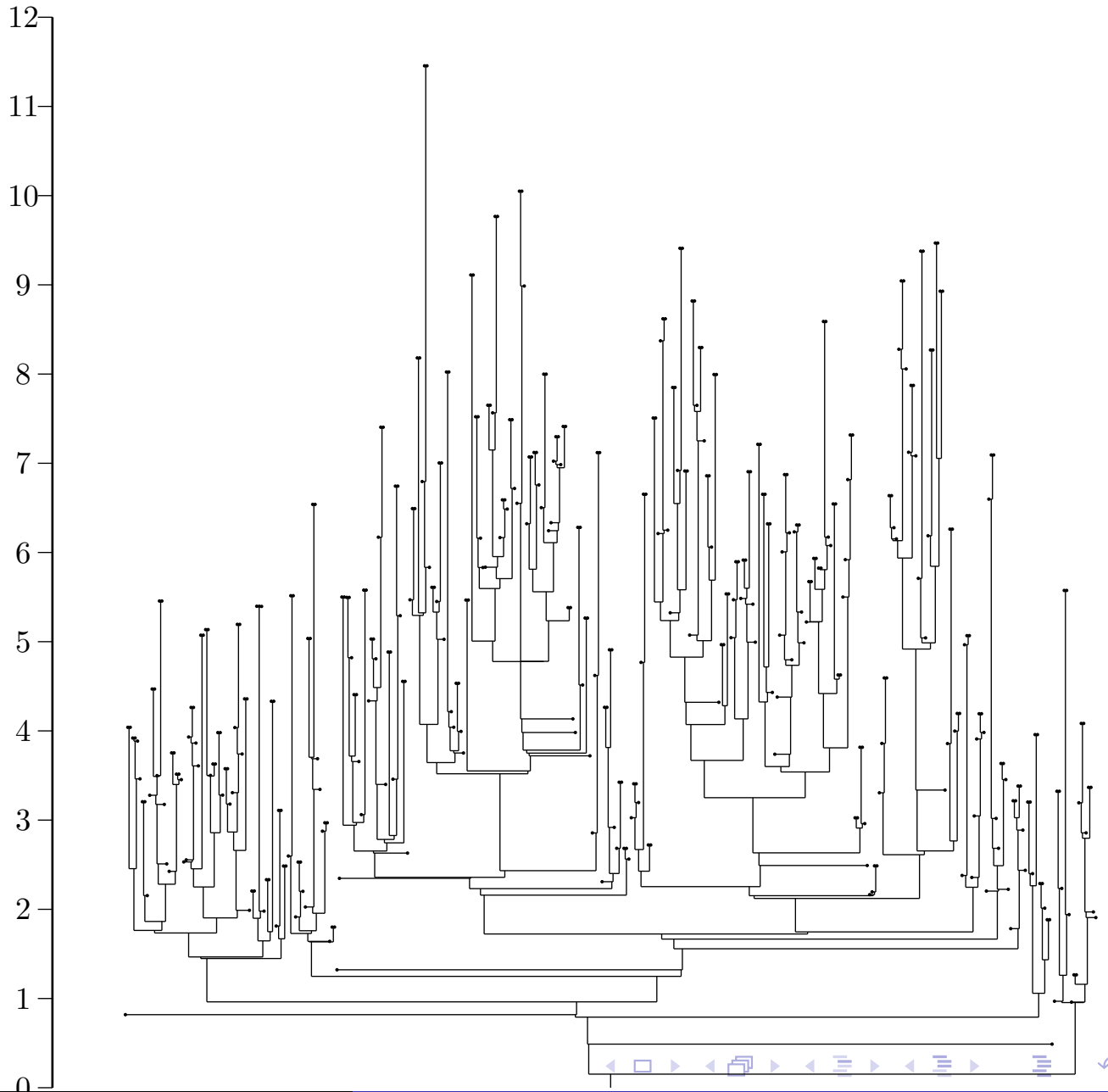
$$q(m,i) = \frac{m}{2h_{m-1}} \; \frac{1}{i(m-i)}, \quad 1 \le i \le m-1$$

Instead we will work with a continuous time model CTCS(n) where we split size m clades at rate h_{m-1} instead. That is:

Split rate is $= \frac{m}{2} \; \frac{1}{i(m-i)}, \quad 1 \le i \le m-1$

This turns out to be mathematically more tractable.

We will mostly be doing $n \to \infty$ asymptotics, so what does a tree on 400 leaves look like?


12
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The consistency property

Important that in our discrete-time model, there's no direct relation between the trees for n and $n+1$, we have to start over with the construction. Somewhat magically, there is a simple connection for the continuous-time model:

Given CTCS(n+1), delete a random leaf and prune; this gives CTCS(n).

Here's a discussion.

To formulate a consistency property, first consider spanning sub-trees on a given set of leaves within a large tree.

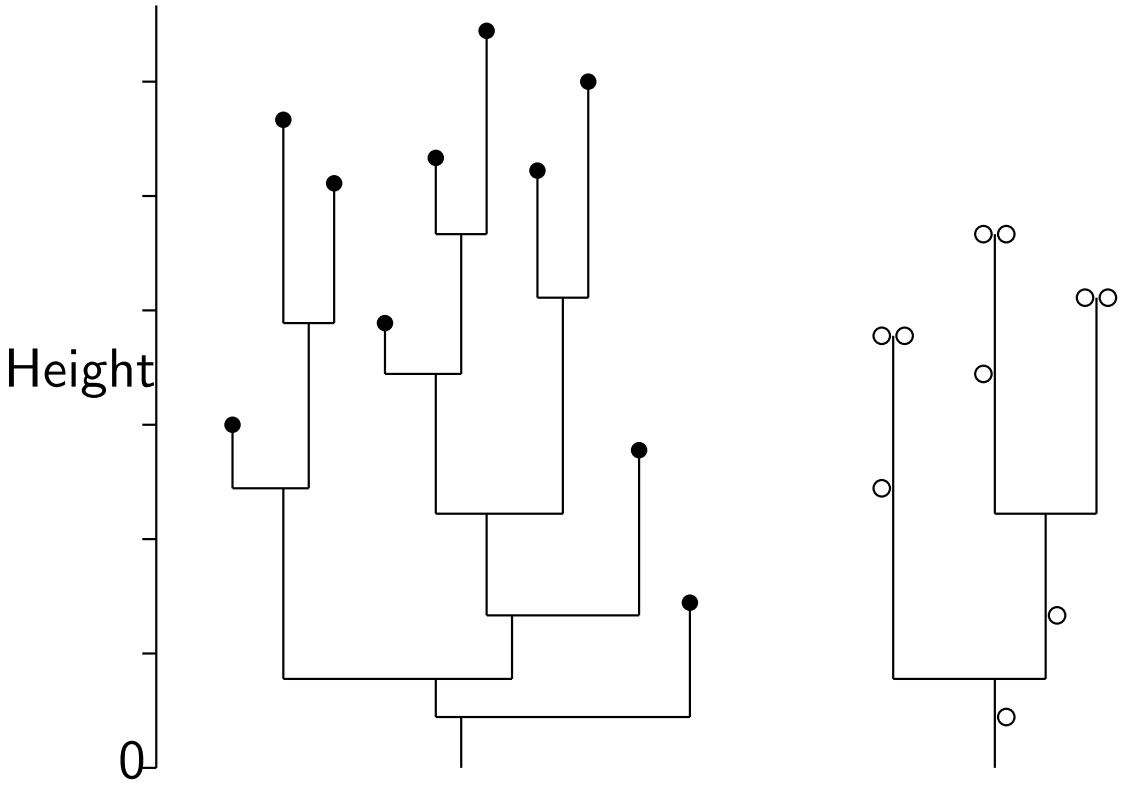


Figure: A spanning tree on $k = 10$ leaves within CTCS(n) for some $n \gg k$ (left) and the corresponding pruned tree PRU(n,k) (right).

The key consequence of the continuous-time embedding is (via a simple calculation)

(*) Within CTCS(n), the time S_n at which the paths to 2 different random leaves diverge satisfies

$$(*) \quad S_n \text{ has exactly Exponential(1) distribution.}$$

This makes it intuitively clear that, for the pruned tree PRU(n,k) on k random leaves, there must be some limit

$$\text{PRU(n,k)} \to \mathbb{T}(k) \text{ as } n \to \infty$$

because (*) says we already did the right order of scaling. By construction, the family $(\mathbb{T}(k), k \geq 2)$ must be consistent under "delete random leaf and prune".

Is this $\mathbb{T}(k)$ the same as CTCS(k)?

Is this $\mathbb{T}(k)$ the same as CTCS(k)?

Yes: there is an abstract-but-strangely-unconvincing proof. This implies the family is consistent under "delete random leaf and re-prune". But more informative to check by explicit formulas for the distribution of shape/density-of-edge-lengths, which leads to the following inductive construction of (CTCS(n), $n \geq 2$)

Algorithm: given CTCS(k)

- Pick uniform random leaf; move up path from root toward that leaf. A "stop" event occurs at rate $= 1/$(size of subclade from current position).
- If "stop" before reaching target leaf, make a side-leaf.
- Otherwise, extend target leaf into a twig of Exponential(1) length to make a leaf-pair.

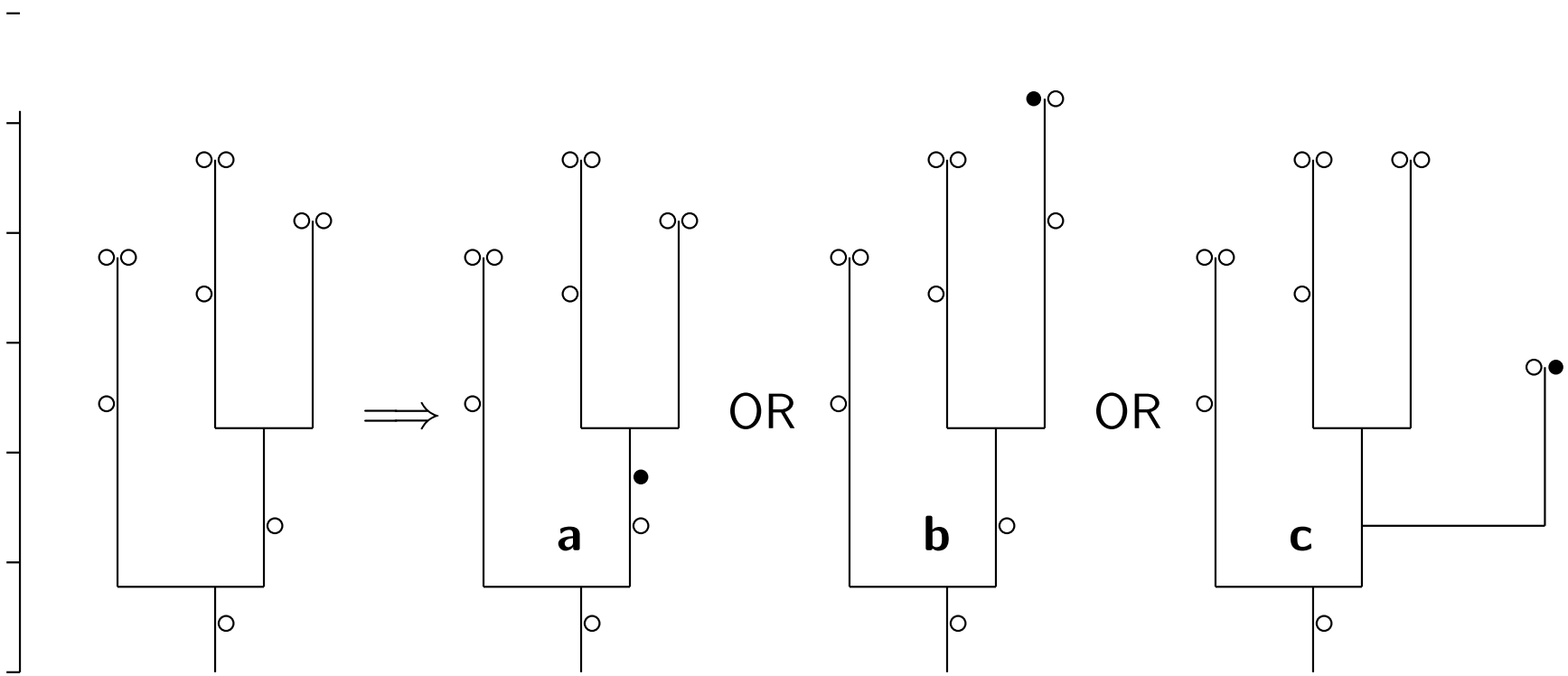


Figure: The possible transitions from CTCS(10) to CTCS(11): the added leaf is •.

Challenge #1. Is this construction useful for doing calculations? Is there some relevant martingale?

Height of leaves

Most of our (ongoing collaboration with Boris Pittel) actual results start from detailed study of

$$D_n := \textbf{height of random leaf } \ell \textbf{ in CTCS(n).}$$

Along the path from the root to ℓ, at each time t we are in a clade of some size X_t. By size-biasing of the split probabilities $q(m,i)$ we find that the process X_t is the decreasing continuous-time Markov chain on $\{n, n-1, n-2, \ldots, 1\}$ started at n, absorbing at 1, with transition rates

$$\lambda(j,i) = \frac{1}{j-i}, \quad 1 \le i < j \le n.$$

Let's call X_t the explorer chain.

[Needs a better name. Has it been studied before in some other context ???]

A very simple calculation

From the transition rates for our explorer chain $(X_t, 0 \le t < \infty)$ started at $X_0 = n$, for $j > i \ge 1$

$$\mathbb{E}[dX_t | X_t = j] = \sum_{i=1}^{j-1} \tfrac{1}{j-i}(i-j)\ dt = -(j-1)dt \text{ on } \{X_t \ge 2\}.$$

So setting $Y_t := X_t - 1$ we have $Y_0 = n - 1$ and

$$\mathbb{E}[dY_t | \mathcal{F}_t] = -Y_t\ dt,\ 0 \le t < \infty.$$

So, taking expectations, $d\mathbb{E}[Y_t] = -\mathbb{E}[Y_t]dt$ and so

$$\mathbb{E}[Y_t] = (n-1)e^{-t}; \quad \mathbb{E}[X_t] = 1 + (n-1)e^{-t}.$$

Because $\mathbb{P}(D_n > t) = \mathbb{P}(X_t - 1 \geq 1)$ we easily deduce an inequality

$$(*) \qquad \mathbb{E}[D_n] \leq 1 + \log(n-1).$$

In fact this is not the right way to study $\mathbb{E}[D_n]$, but allows me to introduce an alternative proof of (*) via recursions.

Because of the recursive structure of the model, $\mathbb{E}[D_n]$ is determined by a certain recurrence:

$$\mathbb{E}[D_1] = 0$$

$$\mathbb{E}[D_n] = \tfrac{1}{h_{n-1}} \left(1 + \sum_{k=1}^{n-1} \tfrac{\mathbb{E}[D_k]}{n-k} \right), \quad n \geq 2. \tag{1}$$

We will prove

$$\mathbb{E}[D_n] \leq f(n) := 1 + \log(n-1). \tag{2}$$

It is enough to show that $f(n)$ satisfies

$$f(n) \geq \frac{1}{h_{n-1}} \left(1 + \sum_{i=1}^{n-1} \tfrac{f(i)}{n-i} \right), \quad n \geq 2. \tag{3}$$

Since $f(x)$ is *concave* for $x > 1$, we have

$$\begin{aligned} \frac{1}{h_{n-1}} \left(1 + \sum_{i=1}^{n-1} \tfrac{f(i)}{n-i} \right) &\leq \tfrac{1}{h_{n-1}} + f\left(\sum_{i=1}^{n-1} \tfrac{i}{n-i} \right) \\ &= \tfrac{1}{h_{n-1}} + f\left(n - \tfrac{n-1}{h_{n-1}}\right) \leq \tfrac{1}{h_{n-1}} + f(n) - f'(n)\left(\tfrac{n-1}{h_{n-1}}\right), \end{aligned}$$

which is exactly $f(n)$, since $f'(x) = \frac{1}{x-1}$ for $x > 1$.

To most of this audience, that "recurrence" argument is less informative/natural than the "probability" argument, which established an exact result on the way. But the simplicity of the probability argument in this case is purely lucky.

In the context of probability-on-trees, (and many analysis-of-algorithms settings), one can often set up such recurrences. And anything defined by a recurrence can in principle be bounded by inductively verifying a bound.

This talk focusses on probabilistic proofs (in preprint #2), whereas preprint #1 proves a variety of refinements based on the recurrence method above.

A key insight is that the explorer chain X_t is decreasing in some "multiplicative" way. Recall the elementary textbook example:

What is the behavior of $M_n := \prod_{i=1}^n U_i$ *for i.i.d.U[0,1] RVs* U_i *?*

First answer: $\mathbb{E}[M_n] = 2^{-n}$.

Better answer: $M_n \approx e^{-n}$ because $\log M_n = \sum_{i=1}^n \log U_i$ and so $n^{-1} \log M_n \to \mathbb{E}[\log U] = e^{-1}$.

So let's go back to our explorer chain and take *logs*.

$X(t)$ is the continuous-time Markov chain on $\{1, 2, 3, \ldots, n\}$ started at n, absorbing at 1, with rates

$$\lambda(j, i) = \frac{1}{j - i}, \quad 1 \le i < j \le n.$$

Study $Z(t) := \log X(t)$. A transition $z \to z - a$ is a transition

$$x = e^z \to e^{z-a} = xe^{-a} = x - x(1 - e^{-a}).$$

So rate of transitions $z \to [0, z - a]$ is

$$\sum_{i=x(1-e^{-a})}^{x} 1/i \sim -\log(1 - e^{-a}).$$

which does not depend on z.
This says that the process $\log X(t)$ is essentially just a (continuous time) random walk. More specifically:

There is a σ-finite measure ψ on $(0, \infty)$ with $\psi[a, \infty) = -\log(1 - e^{-a})$. Write $Y(t)$ for the subordinator with Levy measure ψ. Then, for $X^{(n)}(t)$ the chain started at n,

$$\log X^{(n)}(t) \approx \log n - Y(t) \text{ until this is } O(1). \tag{4}$$

We are studying

$$D_n := \inf\{t : X^{(n)}(t) = 1\}.$$

But we have a SLLN and CLT for the subordinator. Assuming the approximation (4) is good enough:

$$t^{-1} Y(t) \to \rho := \int_0^\infty \psi[a, \infty) \, da$$

and so $D_n \sim \rho^{-1} \log n$. By a classical identity $\rho = \zeta(2) = \pi^2/6$ so our simple bound $\mathbb{E} D_n \le 1 + \log(n-1)$ is upgraded to $\mathbb{E} D_n \sim 6\pi^{-2} \log n$. And finally the CLT:

Theorem

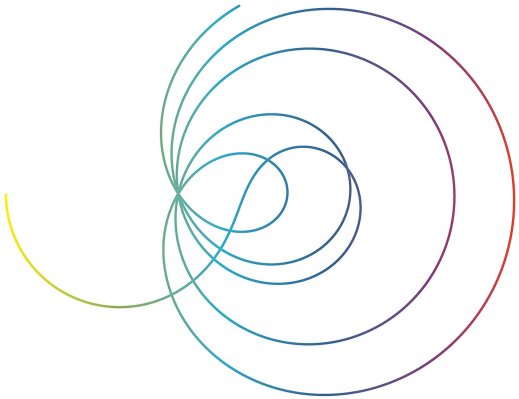
$$\frac{D_n - \mu \log n}{\sqrt{\log n}} \to_d \text{Normal}(0, \mu^3 \sigma^2)$$

where

$$\mu := 1/\zeta(2) = 6/\pi^2 = 0.6079...; \quad \sigma^2 := 2\zeta(3) = 2.4040.....$$

So in outline this is just the textbook CLT for renewal processes, but the technical work is in justifying the approximation (4). Our proof (preprint # 2) seems a Horrible Hack: there must be some better way . . . . . .
Challenge #2.

In parallel, preprint #1 gives an analytic proof based on the recurrence for the Laplace transform. But also technically intricate.



In Pursuit of Zeta-3

The World's Most Mysterious Unsolved Math Problem

Paul J. Nahin

Sharp results by analysis of recurrences

$\mathbb{E}[D_n]$ is determined by the recurrence: $\mathbb{E}[D_1] = 0$ and

$$\mathbb{E}[D_n] = \frac{1}{h_{n-1}} \left(1 + \sum_{k=1}^{n-1} \frac{\mathbb{E}[D_k]}{n-k} \right), \quad n \geq 2. \tag{5}$$

Theorem

$$\mathbb{E}[D_n] = \frac{6}{\pi^2} \log n + O(1) \text{ as } n \to \infty.$$

Proposition

Assuming the h-ansatz, there exists a constant c_0 such that

$$\mathbb{E}[D_n] = \frac{6}{\pi^2} \log n + c_0 - \frac{3}{\pi^2} n^{-1} + O(n^{-2}). \tag{6}$$

One can calculate $\mathbb{E}[D_n]$ numerically via the basic recurrence, and doing so up to $n = 400,000$ gives a good fit to (6) with $c_0 = 0.7951556604.....$
Yes, really 10 significant digits .....

Proofs are long and technical; they depend on sharp estimates like

Lemma

$$\sum_{k=1}^{n-1} \frac{\log(k/n)}{n-k} = -\frac{\pi^2}{6} + \frac{\log(2\pi e)}{2n} + \frac{\log n}{12n^2} + O(n^{-2}).$$

which are proved, in the spirit of Knuth's *Concrete Mathematics*, via ingredients such as Euler's summation formula: if $f(x)$ is a smooth differentiable function for $x \in [a, b]$ such that the even derivatives $f^{(2)}, f^{(4)}, \ldots$ are all of the same sign, then for every $m \geq 1$

$$\begin{aligned} \sum_{a \leq k < b} f(k) &= \int_a^b f(x)\,dx - \tfrac{1}{2} f(x)\Big|_a^b \\ &+ \sum_{\ell=1}^{m} \frac{B_{2\ell}}{(2\ell)!} f^{(2\ell-1)}(x)\Big|_a^b + \theta_m \frac{B_{2m+2}}{(2m+2)!} f^{(2m+1)}(x)\Big|_a^b. \quad (7) \end{aligned}$$

Here θ_m is some real in $(0, 1)$ and the $\{B_{2\ell}\}$ are the even Bernoulli numbers, defined by $\frac{z}{e^z - 1} = \sum_{\mu \geq 0} B_\mu \frac{z^\mu}{\mu!}$.

In the tree model, D_n arises from two levels of randomness, as the distance $d(U_n, \mathbb{T}_n)$ within a random tree $\mathbb{T}_n$ from the root to a uniform random leaf U_n of that tree. Write $a(\mathbb{T}_n)$ for the average height of the n leaves of $\mathbb{T}_n$. The law of total variance says

$$\mathrm{var}[D_n] = \mathbb{E}[\mathrm{var}(d(U_n, \mathbb{T}_n)|\mathbb{T}_n)] + \mathrm{var}[a(\mathbb{T}_n)]. \tag{8}$$

As statisticians say, the first term of the right indicates the "within tree" variability of leaf height, and the second term indicates the "between trees" variability. As a standard technique, one can calculate the proportion of "between trees" variance

$$r_n := \frac{\mathrm{var}[a(\mathbb{T}_n)]}{\mathrm{var}[D_n]}$$

because it is essentially the correlation between the D's of two random leaves from the same realization of $\mathbb{T}_n$.

Theorem

Assuming the h-ansatz: for Euler's constant γ

$$\lim_{n\to\infty} r_n = \frac{\gamma\,\zeta(2)}{2\zeta(3)} = 0.3949404179\ldots,$$

Theorem

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$$\lim_{n\to\infty} r_n = \frac{\gamma\,\zeta(2)}{2\zeta(3)} = 0.3949404179\ldots,$$

If we could find a nicer "probability" proof of the CLT for D_n, that could presumably be extended to a bivariate Gaussian limit in this setting.

Consider the height D_n^* of the random tree CTCS(n) itself, that is the maximum leaf height. The naive argument is that D_n^* behaves as the maximum of n i.i.d. samples from the approximating distribution $D_n \approx_d$ Normal$(\mu \log n, \mu^3 \sigma^2 \log n)$, which would give

$$D_n^* \approx \mu \log n + \sqrt{2 \log n} \times \sqrt{\mu^3 \sigma^2 \log n} \approx (\mu + 1.04) \log n. \qquad (9)$$

However the tail of the distribution of D_n might be fatter than Normal, or the dependence between leaf heights might be stronger, so the constant might be larger or smaller than $(\mu + 1.04)$.

Another approach: there are order n edges to leaves, which have independent Exponential(1) lengths, so their max length is $\sim 1 \cdot \log n$. Consider the corresponding leaf: it attaches to a branch whose height has the Normal distribution, so that leaf's height is at least $(\mu + 1) \log n$.

Challenge #3. What is the right constant?

[repeat earlier slide]

Overview of results/problems

- ✓ There is a canonical way to embed the discrete-time model into a continuous-time model (which we call CTCS(n)) by specifying that a clade of size $m \geq 2$ is split at rate h_{m-1}.
- ✓ For the height (time reached) D_n of a uniform random leaf in the CTCS(n) model, $\mathbb{E}[D_n] \sim \frac{6}{\pi^2} \log n$ and also there is a Gaussian limit distribution. Many related results of surprising sharpness can be obtained via analysis of recursions.
- We can describe the limit fringe distribution of CTCS(n), that is the local weak limit relative to a random leaf.
- ✓ There is a non-obvious consistency property of $(CTCS(n), n \geq 2)$ in its "pruned" form: given CTCS(n+1), delete a random leaf and prune; this gives CTCS(n). In reverse this gives an explicit algorithm for growing CTCS(n+1) from CTCS(n).
- There is a scaling limit of $(\text{CTCS(n)}, n \geq 2)$, as a process of splitting the continuous interval $(0, 1)$, with a corresponding continuum tree. The pruned spanning tree on n random points is CTCS(n).

The fringe process

Consider the quantity

$$a(n,i) := \mathbb{P}(\textit{explorer chain started at state } n \textit{ is ever in state } i)$$

[same for the discrete or continuous models.] By a coupling argument

Proposition

The limit $a(i) := \lim_{n\to\infty} a(n,i)$ *exists,* $i = 1, 2, \ldots$.

But the proof does not give any useful quantitative information about the limit $(a(i), i = 1, 2, \ldots)$. The limit must satisfy the system of equations,

$$a_i = \sum_{j>i} a_j (q(j,i) + q(j,i-j))i/j, \quad i \geq 1$$

with $a_1 = 1$, using the transition probabilities

$$q(n,i) = \frac{n}{2h_{n-1}} \; \frac{1}{i(n-i)}, \quad 1 \leq i \leq n-1.$$

Presumably it is the *unique* solution of these equations, but we do not have a proof.

Our results (that $\log X_t$ deceases at speed $\pi^2/6$) imply that $\sum_{j=2}^{m} a(j)/h_{j-1} \sim (6/\pi^2) \log m$ and so it is very natural to make

Conjecture

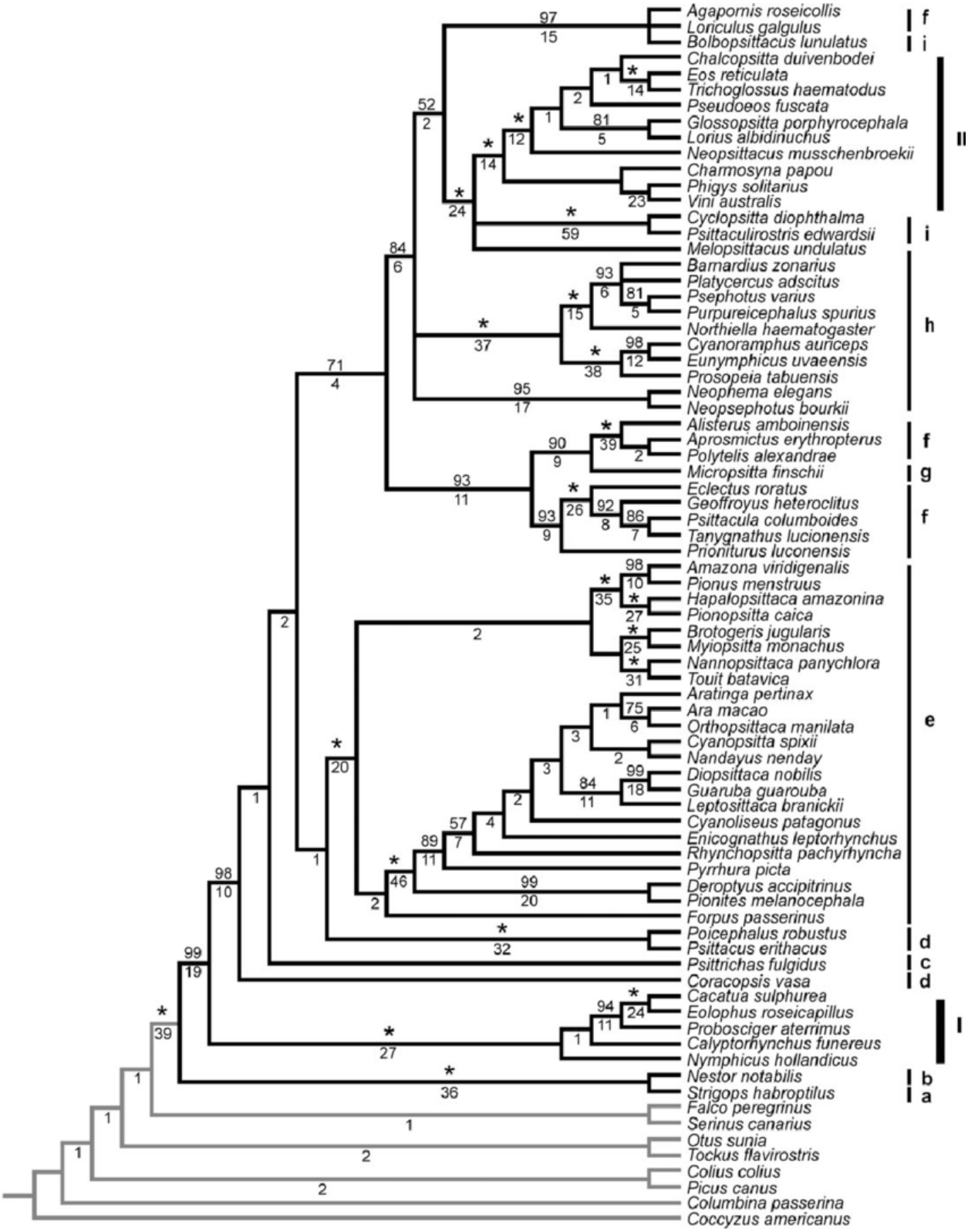
$a(j) \sim \frac{6}{\pi^2} \frac{\log j}{j}$ *as* $j \to \infty$.

The motivation for Proposition 2 involves the *fringe distribution* for the tree model, that is the description of the tree relative to a typical leaf, which (by Bayes rule) can be described in terms of the a_i. In particular, a leaf in the DTCS(n) model arises from a split of some size $W_n \geq 2$, and so Proposition 2 implies that $W_n \to_d W$ where

$$\mathbb{P}(W = i) = a_i(q(i,1) + q(i,i-1))/i, \quad i \geq 2. \tag{10}$$

The Conjecture would then lead to

$$\mathbb{P}(W = i) \sim \frac{12}{\pi^2} \frac{1}{i^2}.$$


Agapornis roseicollis
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Bolbopsittacus lunulatus
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Eos reticulata
Trichoglossus haematodus
Pseudoeos fuscata
Glossopsitta porphyrocephala
Lorius albidinuchus
Neopsittacus musschenbroekii
Charmosyna papou
Phigys solitarius
Vini australis
Cyclopsitta diophthalma
Psittaculirostris edwardsii
Melopsittacus undulatus
Barnardius zonarius
Platycercus adscitus
Psephotus varius
Purpureicephalus spurius
Northiella haematogaster
Cyanoramphus auriceps
Eunymphicus uvaeensis
Prosopeia tabuensis
Neophema elegans
Neopsephotus bourkii
Alisterus amboinensis
Aprosmictus erythropterus
Polytelis alexandrae
Micropsitta finschii
Eclectus roratus
Geoffroyus heteroclitus
Psittacula columboides
Tanygnathus lucionensis
Prioniturus luconensis
Amazona viridigenalis
Pionus menstruus
Hapalopsittaca amazonina
Pionopsitta caica
Brotogeris jugularis
Myiopsitta monachus
Nannopsittaca panychlora
Touit batavica
Aratinga pertinax
Ara macao
Orthopsittaca manilata
Cyanopsitta spixii
Nandayus nenday
Diopsittaca nobilis
Guaruba guarouba
Leptosittaca branickii
Cyanoliseus patagonus
Enicognathus leptorhynchus
Rhynchopsitta pachyrhyncha
Pyrrhura picta
Deroptyus accipitrinus
Pionites melanocephala
Forpus passerinus
Poicephalus robustus
Psittacus erithacus
Psittrichas fulgidus
Coracopsis vasa
Cacatua sulphurea
Eolophus roseicapillus
Probosciger aterrimus
Calyptorhynchus funereus
Nymphicus hollandicus
Nestor notabilis
Strigops habroptilus
Falco peregrinus
Serinus canarius
Otus sunia
Tockus flavirostris
Colius colius
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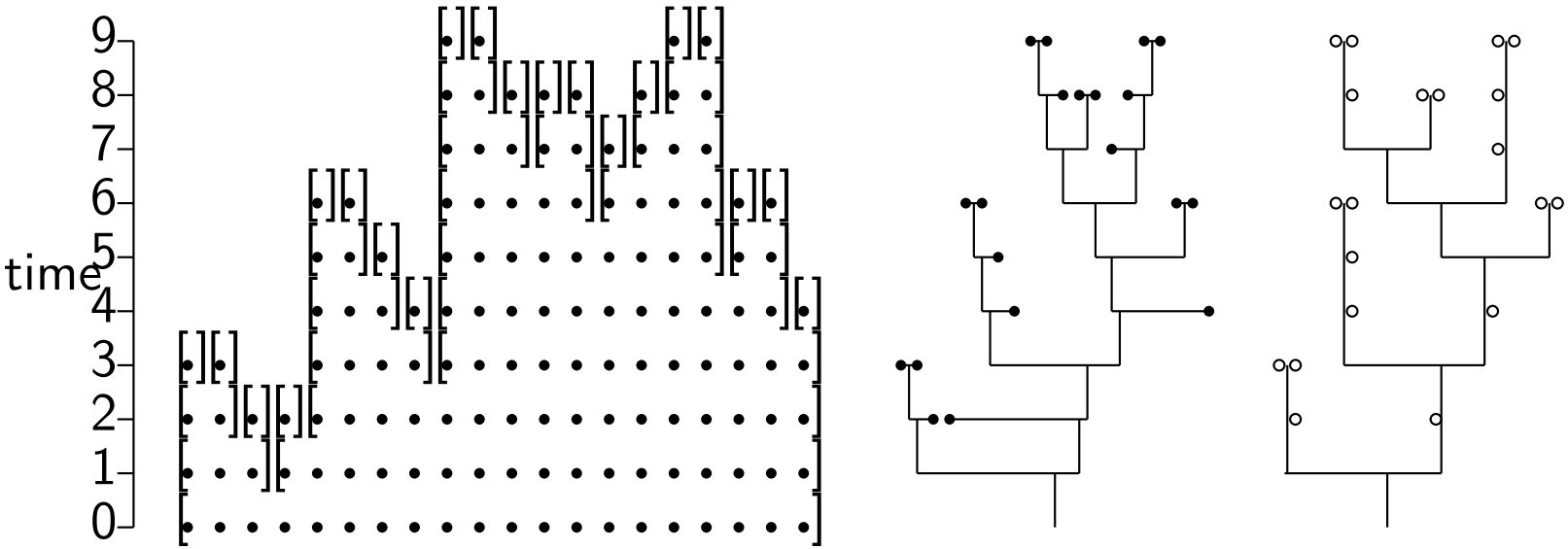
The scaling limit

- Heuristically, there is a scaling limit of (CTCS(n), $n \geq 2$), as a process of splitting the continuous interval $(0, 1)$, with a corresponding continuum tree. The pruned spanning tree on n random points is CTCS(n).

Challenge #4.. Think rigorously about this, and connections with below.

- There is a classical "applied probability" literature on interval-splitting, focussed on the distribution of fragment lengths, which in our model would be clade sizes at a given time.
- A more recent approach is via exchangeable partitions, see e..g. Haas - Miermont - Pitman - Winkel 2008.



Consider a process of splitting the continuous unit interval $[0, 1]$.

An interval of length x is split into sub-intervals of lengths $(y, x - y)$ at σ-finite rate $\frac{x}{2y(x-y)}\, dy$. Hard to draw a good picture, but the induced spanning tree on k points has the previous type of structure (right side).

There are many analogs/differences between this setting and the theory around the Brownian CRT. Perhaps a "Cauchy" analog?