Joint subtree distributions under two evolutionary tree models

Symposium in Memory of Charles Stein [1920 - 2016]

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Joint work with
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Outline

1. Introduction

2. Joint subtree distributions under two evolutionary models

3. Discrimination Efficiency

4. Work in Progress

1. Introduction

- Trees provide visual representation of the evolutionary relatedness among organisms, species, or genes.
- Phylogenetic tree has become a powerful tool in studying evolution and diversification in Biology.
- It finds wide applications in evolutionary biology, developmental biology (cell lineages) and epidemiology. Such as
  - Inferring evolutionary process from phylogenetic tree shape[1];
  - Studying diversification[2];
  - Study of pathogens[3,3a].
- Tree shape is the signature of the forces that produce biodiversity[4]
- Fitting stochastic models to tree data helps infer macro-evolutionary processes such as speciation and extinction rates.

[1] Mooers & Heard (1997). Inferring evolutionary process from phylogenetic tree shape. *Quart. Review Biol.*, **72**, 31-54.

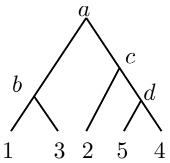
[2] Morlon (2014). Phylogenetic approaches for studying diversification. *Ecology Letters*, **17**, 508-525.

[3] Poon et al. (2013). Mapping the Shapes of Phylogenetic Trees from Human and Zoonotic RNA Viruses. *PLoS One*

[3a] Colijin & Plazzotta (2017). A metric on phylogenetic tree shapes. *Syst. Biol.*, **11**, 113-126.

[4] Mooers & Heard (2002). Using Tree shape. *Sys. Biol.*, **51**, 833-834.

1. Introduction



T

- T is a phylogenetic tree on $\mathscr{X} = \{1, \ldots, 5\}$, the set of leaves.
- All edges are directed away from the root, a (arrows not drawn).
- Binary tree $(V(T), E(T))$, set of pendant edges denoted by $E^*(T)$.
- Each node is either of

  degree 1 (for leaves);

  degree 2 (root); or

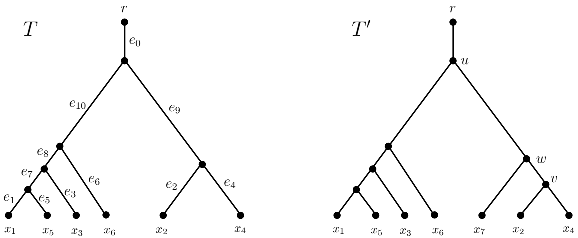
  degree 3 (the rest of internal nodes).

Our objectives

- Given a tree T, to infer if this tree is more likely generated by YHK model than by PDA model.
- Given a “tree feature” (index), to assess how good this feature in discriminating one generative model from another.
  - YHK trees are observed to be more symmetric. Many tree indices have been proposed to measure tree balance.
  - Examples: Colless index and Sackin index

1.2 Two random generative tree models: YHK & PDA

- Two common generative tree models: YHK (Yule-Harding-Kingsman) model and PDA (Proportional-to-Distinguishable-Arrangements) model



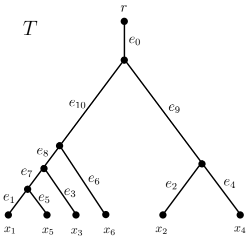
- YHK: Choose a pendant edge at random in T to form T'.
- PDA: Choose an edge at random from all edges in T to form T'.
- In this figure, the PDA model: $T' = T[e_9; x_7]$ is obtained from T by attaching the leaf labelled x_7 to edge e_9.

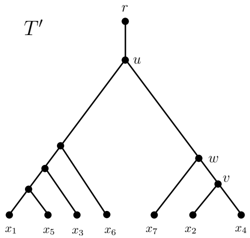
1.2 Two generative tree models: YHK & PDA

Starting with a tree of 2 leaves, iteratively attach (manner to be specified) one leaf at a time to grow the tree to its desired size.

- YHK, also known as equal-rates-Markov model: all extant lineages have equal probabilities of speciating at an instant.
  - Uniformly sample a pendant edge from the tree's pendant edges, and attach a new leaf to it.
- PDA: Each "possible arrangement" of n leaves into a tree is equally likely.
  - Uniformly sample an edge from the present tree's edges, and attach a new leaf to it.

2.1 Subtree





- A cherry–a subtree with two leaves.

  For examples,

  $\{x_1, x_5\}$ (together with their parent) forms a cherry, and we think of three edges: e_7, e_1, e_5

  $\{x_2, x_4\}$ forms another cherry with edges: e_9, e_2, e_4.

- A pitchfork–a subtree with three leaves.

  E.g., $\{x_1, x_5, x_3\}$ with their most recent common ancestor; 5-edge: e_8, e_7, e_3, e_1, e_5.

2.2 Subtrees of sizes 2 and 3 (Cherry and Pitchfork)

- It has been observed that YHK generated trees are more “symmetric”: and hence contain more cherries.

Definitions

- A_n: Number of pitchforks in a tree with n leaves
- C_n: Number of cherries in a tree with n leaves
- Let h_n denote the joint pmf of A_n and C_n under the YHK model. That is,

$$h_n(a, c) = P_Y[A_n = a, C_n = c].$$

- Let f_n be the pmf of A_n; and g_n pmf of C_n under the YHK model.
- Denote $\widetilde{h}_n, \widetilde{f}_n, \widetilde{g}_n$ the counterparts under the PDA model.

Thm 1 We have the following recurrence relations.

(a) YHK Model

For $n \geq 3$,

$$\begin{aligned} h_{n+1}(a,c) \quad &= \quad \frac{2a}{n} h_n(a,c) + \frac{a+1}{n} h_n(a+1,c-1) \\ &\quad + \frac{2(c-a+1)}{n} h_n(a-1,c) + \frac{n-a-2c+2}{n} h_n(a,c-1); \end{aligned}$$

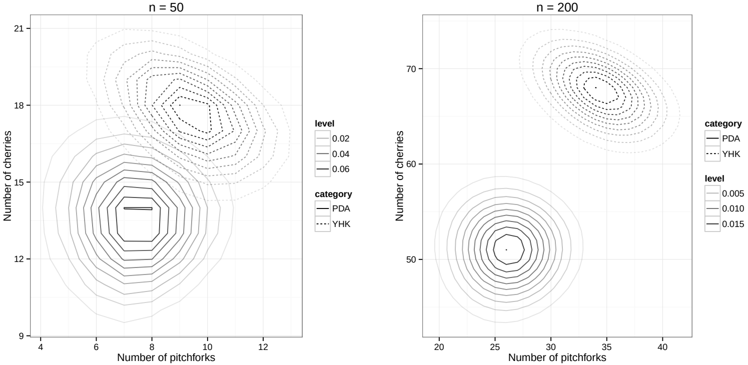
and $h_3(1,1) = 1$, and $h_3(a,c) = 0$ if $(a,c) \neq (1,1)$.

(b) PDA Model

For $n \geq 3$,

$$\begin{aligned} \widetilde{h}_{n+1}(a,c) \quad &= \quad \frac{n+3a-c-1}{2n-1} \widetilde{h}_n(a,c) + \frac{a+1}{2n-1} \widetilde{h}_n(a+1,c-1) \\ &\quad + \frac{3(c-a+1)}{2n-1} \widetilde{h}_n(a-1,c) + \frac{n-a-2c+2}{2n-1} \widetilde{h}_n(a,c-1); \end{aligned}$$

and $\widetilde{h}_3(1,1) = 1$, and $\widetilde{h}_3(a,c) = 0$ if $(a,c) \neq (1,1)$.


n = 50
Number of cherries
21
18
15
12
9
4
6
8
10
12
Number of pitchforks
level
0.02
0.04
0.06
category
PDA
YHK
n = 200
Number of cherries
70
60
50
20
25
30
35
40
Number of pitchforks
category
PDA
YHK
level
0.005
0.010
0.015

Key step in the proof of Thm 1

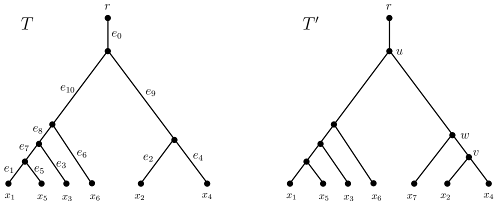
Edge decomposition for a PDA tree: Partition $E(T)$ into

$E_1(T)$: pendant edges that are contained in a pitchfork but not in a cherry;

$E_2(T)$: edges that are contained in a cherry but not in a pitchfork;

$E_3(T)$: pendant edges that are contained in neither a pitchfork nor a cherry;

$E_4(T) = E(T) \setminus (E_1(T) \cup E_2(T) \cup E_3(T))$.



$$E_1(T) = \{e_3\}, \qquad E_2(T) = \{e_2, e_4, e_9\}, \qquad E_3(T) = \{e_6\},$$
$$E_4(T) = \{e_0, e_1, e_5, e_7, e_8, e_{10}\}.$$

Key step in the proof of Thm 1

Edge decomposition for a PDA tree

- Track the changes in the numbers of pitchforks and cherries when a new leaf join the tree T at $E_i(T)$:

$$(A(T'),C(T')) = \begin{cases} (A(T)-1, C(T)+1), & e \in E_1(T), \\ (A(T)+1, C(T)), & e \in E_2(T), \\ (A(T), C(T)+1), & e \in E_3(T), \\ (A(T), C(T)), & e \in E_4(T), \end{cases}$$

and

$$\begin{aligned} |E_1(T)| &= A(T), \\ |E_2(T)| &= 3(A(T)-C(T)), \\ |E_3(T)| &= n-A(T)-2C(T), \\ |E_4(T)| &= n-1+3A(T)-C(T). \end{aligned}$$

Thm 2 Denote expectation under YHK (resp., PDA) model by $\mathbb{E}_Y$ (resp., $\mathbb{E}_U$). Let $\phi : \mathbb{R} \times \mathbb{R} \longrightarrow \mathbb{R}$. Then, for $n \geq 4$,

$$\begin{aligned}
n\mathbb{E}_Y[\phi(A_{n+1}, C_{n+1})] &= 2\mathbb{E}_Y[A_n\phi(A_n, C_n)] \\
&\quad +\mathbb{E}_Y[A_n\phi(A_n - 1, C_n + 1)] \\
&\quad +2\mathbb{E}_Y[(C_n - A_n)\phi(A_n + 1, C_n)] \\
&\quad +\mathbb{E}_Y[(n - A_n - 2C_n)\phi(A_n, C_n + 1)];
\end{aligned}$$

$$\begin{aligned}
(2n-1)\mathbb{E}_U[\phi(A_{n+1}, C_{n+1})] &= \mathbb{E}_U[(n + 3A_n - C_n - 1)\phi(A_n, C_n)] \\
&\quad +\mathbb{E}_U[A_n\phi(A_n - 1, C_n + 1)] \\
&\quad +3\mathbb{E}_U[(C_n - A_n)\phi(A_n + 1, C_n)] \\
&\quad +\mathbb{E}_U[(n - A_n - 2C_n)\phi(A_n, C_n + 1)].
\end{aligned}$$

Special cases

(1) Let $\psi : \mathbb{R} \longrightarrow \mathbb{R}$ be any function.

(a) Define $\phi(x,y) = \psi(y)$, we have

$$\begin{aligned} n\mathbb{E}_Y[\psi(C_{n+1})] &= \mathbb{E}_Y[2C_n\psi(C_n) + (n-2C_n)\psi(C_n+1)]; \\ (2n-1)\mathbb{E}_U[\psi(C_{n+1})] &= \mathbb{E}_U[(n+2C_n-1)\psi(C_n) \\ &\qquad +(n-2C_n)\psi(C_n+1)]. \end{aligned}$$

(b) Define $\phi(x,y) = I_k(y)$, we have

$$\begin{aligned} ng_{n+1}(k) &= 2k\,g_n(k) + (n-2k+2)g_n(k-1); \\ (2n-1)\widetilde{g}_{n+1}(k) &= (n+2k-1)\,\widetilde{g}_n(k) + (n-2k+2)\widetilde{g}_n(k-1), \end{aligned}$$

for $n \geq 3$ and $k \geq 1$.

(c) Take $\phi(x,y) = y$ to derive $\mathbb{E}_Y[C_n]$ and $\mathbb{E}_U[C_n]$;

(d) $\phi(x,y) = y^2$ to derive $Var_Y[C_n]$ and $Var_U[C_n]$.

On the average

- more cherries with less variation in a YHK tree than in a PDA tree:

$$\begin{aligned} \mathbb{E}_Y[C_n] = \tfrac{n}{3} \quad &> \quad \mathbb{E}_U[C_n] = \frac{n(n-1)}{2(2n-3)} \sim \frac{n}{4}; \\ Var_Y[C_n] = \tfrac{2n}{45} \quad &< \quad Var_U[C_n] = \frac{n(n-1)(n-2)(n-3)}{2(2n-3)^2(2n-5)} \sim \frac{n}{16}; \end{aligned}$$

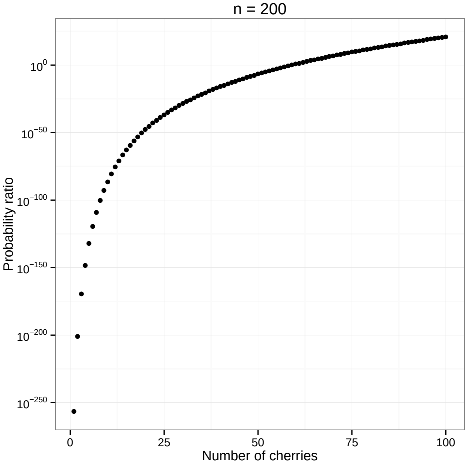
- more pitchforks but also with more variation in a YHK tree than in a PDA tree:

$$\begin{aligned} \mathbb{E}_Y[A_n] = \tfrac{n}{6} \quad &> \quad \mathbb{E}_U[A_n] = \frac{n(n-1)(n-2)}{2(2n-3)(2n-5)} \sim \frac{n}{8} \\ Var_Y[A_n] = \tfrac{23n}{420} \quad &> \quad Var_U[A_n] = \frac{3n(n-1)(n-2)(n-3)(4n^3-40n^2+123n-110)}{4(2n-3)^2(2n-5)^2(2n-7)(2n-9)} \sim \frac{3n}{64}; \end{aligned}$$

- Correlation of numbers of cherries and pitchforks is constant (independent of n) under YHK; whereas correlation $= O(1/n)$ under PDA:

$$Cor_Y(A_n, C_n) = -\sqrt{\frac{14}{69}}; \quad Cor_U(A_n, C_n) \sim \frac{-1}{\sqrt{3}\,n}.$$

We examine the likelihood ratio of the number of cherries under YHK versus PDA: $f_n(k)/\widetilde{f}_n(k)$. It is monotone in k for fixed n.



3.1 Model-based total variation distance between YHK and PDA

- **Definition** We define a total variation distance between YHK model and PDA model on the collection of trees with n leaves as

$$mtv_n(YHK, PDA) := \frac{1}{2} \sum_{T \in \mathscr{T}_n} |P_Y(T) - P_U(T)|.$$

- For $T \in \mathscr{T}_n$, it is known

$$P_U(T) = \frac{1}{(2n-3)!!} \quad \text{and} \quad P_Y(T) = \frac{2^{n-1}}{n!\pi(T)}$$

where

$$\pi(T) := \prod_{v \in \overset{\circ}{V}} (\Lambda(v) - 1)$$

where $\overset{\circ}{V}$ denotes the set of internal nodes of T, and $\Lambda(v)$ is the number of descendants of v (Semple & Steel, 2003).

- An application: $H_0 : YHK$ vs $H_1 : PDA$,

$$\text{power } \leq \alpha + mtv_n(YHK, PDA).$$

- By exhaustive enumeration, we computed the numerical values of $mtv_n(YHK, PDA)$ for $n = 3, \ldots, 20$.
- For larger n, we estimate $mtv_n(YHK, PDA)$ by simulation.

  Rewrite

$$
\begin{aligned}
mtv_n(YHK, PDA) &= \sum_{T \in \mathscr{T}_n} [P_Y(Y) - P_U(T)]_+ \\
&= \sum_{T \in \mathscr{T}_n} \left[\frac{P_Y(Y)}{P_U(T)} - 1 \right]_+ P_U(T) = \mathbb{E}_U[R]
\end{aligned}
$$

where $R : \mathscr{T}_n \to \mathbb{R}$ defined as $R(T) = \left[\frac{P_Y(Y)}{P_U(T)} - 1 \right]_+$.

Sample $T_1, T_2, \ldots, T_m$ from $\mathscr{T}_n$ according to the PDA model. Compute $R(T_1), R(T_2), \ldots, R(T_m)$. And

$$
\frac{1}{m} \sum_{i=1}^{m} R(T_i) \approx \mathbb{E}_U[R] = mtv_n(YHK, PDA).
$$

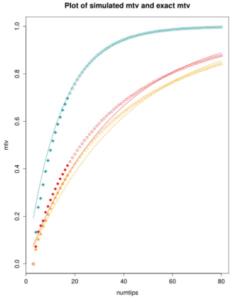


FIGURE 1. Exact and approximate total variation distances between tree models. Blue diamonds, red circles and orange triangles denote $mtv(n; YHK, PDA)$, $mtv(n; YHK, AB)$ and $mtv(n; PDA, AB)$ respectively. Solid plotting characters and hollow plotting characters indicate exact values and approximate values by simulation respectively. The lines denote the fitted curves by regression.

- Simulation is conducted up to $n = 80$.
- We plot $-\log(1 - mtv_n(YHK, PDA))$ as a function of n, suggesting

$$mtv_n(YHK, PDA) \approx 1 - e^{-\alpha - \beta n}.$$

3.2 Discrimination Efficiency

- For a chosen feature of a tree $T \in \mathscr{T}_n$, we propose a score, discrimination efficiency (DE), to assess the extent this feature is able to discriminate *YHK* from *PDA*.

- For examples,
  - Colless index of balanced tree

$$Colless(T) = \sum_{v \in \overset{\circ}{V}} |R(v) - L(v)|$$

    where $\overset{\circ}{V}$ denotes the set of interior vertices; $R(v)$ (resp., $L(v)$) denotes the number of descendants by the right (left) child of v.

  - Number of cherries in T, $C_n(T)$
  - Joint numbers of cherries and pitchforks in T, $(A_n(T), C_n(T))$

3.2 Discrimination Efficiency

- Suppose we consider a tree index I_n on $\mathscr{T}_n$

  $$\begin{aligned} mtv_{I_n}(YHK, PDA) &:= d_{tv}(\mathscr{L}(I_n|YHK), \mathscr{L}(I_n|PDA)) \\ &= \frac{1}{2}\sum_a |g_n(a) - \widetilde{g}_n(a)| \end{aligned}$$

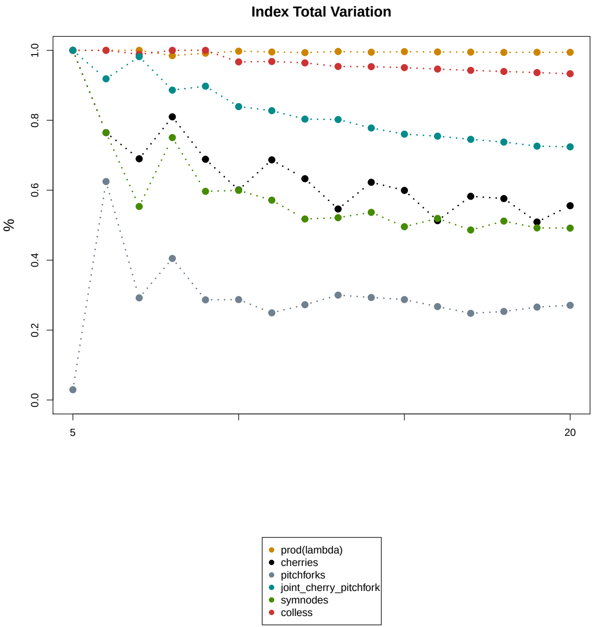
  where $g_n(a) = \sum P_y(T)$ where the sum is taken over all $T \in \mathscr{T}_n$ with $I_n(T) = a$.

- Triangle inequality implies

  $$0 \leq mtv_{I_n}(YHK, PDA) \leq mtv_n(YHK, PDA).$$

- Define discrimination efficiency of index I_n:

  $$DE(C_n) := mtv_{C_n}(YHK, PDA)/mtv_n(YHK, PDA) \in [0, 1].$$


Index Total Variation
%
1.0
0.8
0.6
0.4
0.2
0.0
5
20
prod(lambda)
cherries
pitchforks
joint_cherry_pitchfork
symnodes
colless

3.2 Discrimination Efficiency

- Write $\mathscr{T}_n(a) = \{T \in \mathscr{T}_n : I_n(T) = a\}$.
- Since

$$mtv_{I_n}(YHK, PDA) = \frac{1}{2}\sum_a \left| \sum_{T \in \mathscr{T}_n(k)} [P_y(T) - P_U(T)] \right|,$$

index I_n is optimal

$\Leftrightarrow$ for each a, $P_y(T) - P_U(T)$ is of the same sign for all $T \in \mathscr{T}_n(a)$

$\Leftrightarrow$ for each a, $P_y(T)$ is a constant

$\Leftrightarrow$ for each a, $\pi(T) = \prod_{v \in \overset{\circ}{V}} (\Lambda(v) - 1)$ is a constant

- This leads to the tree index: $\sum_{v \in \overset{\circ}{V}} \log(\Lambda(v) - 1)$ one that is proposed by Blum and Francois (2006)[5].

[5] Which random processes describe the tree of life? A large scale study of phylogenetic tree imbalance. *Sys. Biol.*, **55**, 685-691

4 Work in progress

4.1 Extend the results to unrooted trees

- Studying unrooted trees is of interest: many inference methods return unrooted trees first. Then some ways to root this tree if a rooted tree is desired.

- C + Thompson + Wu observed the edge decomposition step can be modified to handle unrooted tree.

4 Work in progress

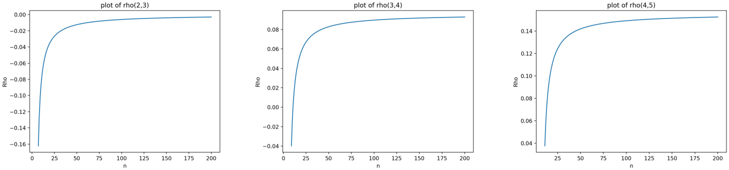
4.2 We are interested in the correlation of the number of nodes with *a*-descendants and the number of nodes of *b*-descendants

Number of cherries = Number of nodes with 2-descendants;
Number of pitchforks = Number of nodes with 3-descendants.

- Recall YHK: $\rho_{n,YHK}(2,3)$ is a constant in n.

  C + Wu proved that the same is true for general a and b.

Under PDA model: correlation can be positive!



Left panel: $a = 2, b = 3$, the correlation is negative for all n.

Middle panel: $a = 3, b = 4$, the correlation changes sign from $-$ve to $+$ve.

Right panel: $a = 4, b = 5$, the correlation is positive for all n.

C + Wu gave a characterization for which pair (a, b) will lead to left panel and right panel.

4 Work in progress

4.3 Two one-parameter families of evolutionary models

4.3.a. Aldous' β-branch split model (1996, 2001)

- Prob of left sister clade and right sister clade ontain i leaves and $n-i$ leaves respectively is

$$p_\beta(i|n) = \frac{1}{a_n(\beta)} \frac{\Gamma(\beta+i+1)\Gamma(\beta+n-i+1)}{\Gamma(i+1)\Gamma(n-i+1)}, \quad 1 \le i \le n-1.$$

  - $\beta = 0$: YHK
    $\beta = -\frac{3}{2}$: PDA
  - Yule model did not fit the empirical tree data well.
  - Many empirical trees are consistent with Aldous' branch split model: $\beta \approx -1$.[6]

[6] AB model in previous plot corresponds to $\beta = -1$

4 Work in progress

4.3 Two one-parameter families of generative models

4.3.b. Ford's α model (2005)

- Starting with a small tree, grow it to the desired size by adding one leaf at a time.
- Fix $\alpha \in [0,1]$.

  Attach a new leaf to the current tree's internal edge with probability α; and to a pendant edge $1-\alpha$.
- YHK: $\alpha = 0$;

  PDA: $\alpha = \frac{1}{2}$.