



A consistent estimator of the evolutionary rate



Krzysztof Bartoszek^a, Serik Sagitov^{b,*}

^a Department of Mathematics, Uppsala University, 751 06, Uppsala, Sweden

^b Mathematical Sciences, Chalmers University of Technology and University of Gothenburg, 412 96 Gothenburg, Sweden

HIGHLIGHTS

- Estimation of the evolutionary rate without knowing the phylogenetic tree.
- We study a tree-free evolutionary model based on the Yule process and Brownian motion.
- We compute the asymptotic variance of the trait disparity for phylogenetically correlated samples.

ARTICLE INFO

Article history:

Received 16 September 2014

Received in revised form

14 January 2015

Accepted 18 January 2015

Available online 28 January 2015

Keywords:

Branching Brownian motion

Conditioned branching process

Tree-free phylogenetic comparative method

Quantitative trait evolution

Yule process

ABSTRACT

We consider a branching particle system where particles reproduce according to the pure birth Yule process with the birth rate λ , conditioned on the observed number of particles to be equal to n . Particles are assumed to move independently on the real line according to the Brownian motion with the local variance σ^2 . In this paper we treat n particles as a sample of related species. The spatial Brownian motion of a particle describes the development of a trait value of interest (e.g. log-body-size). We propose an unbiased estimator R_n^2 of the evolutionary rate $\rho^2 = \sigma^2/\lambda$. The estimator R_n^2 is proportional to the sample variance S_n^2 computed from n trait values. We find an approximate formula for the standard error of R_n^2 based on a neat asymptotic relation for the variance of S_n^2 .

© 2015 Elsevier Ltd. All rights reserved.

1. Introduction

Biodiversity within a group of n related species could be quantified by comparing suitable trait values. For some key trait values like log-body-size, researchers apply the Brownian motion model proposed by Felsenstein (1985). It is assumed that the current trait values $(X_1^{(n)}, \dots, X_n^{(n)})$ have evolved from the common ancestral state X_0 as a branching Brownian motion with the local variance σ^2 . Given a phylogenetic tree describing the ancestral history of the group of species the Brownian trajectories of the trait values for sister species are assumed to evolve independently after the ancestor species splits in two daughter species. The resulting phylogenetic sample $(X_1^{(n)}, \dots, X_n^{(n)})$ consists of identically distributed normal random variables with a dependence structure caused by the underlying phylogenetic signal.

A mathematically appealing and biologically motivated version of the phylogenetic sample model assumes that the phylogenetic

tree behind the normally distributed trait values $(X_1^{(n)}, \dots, X_n^{(n)})$ is unknown. As a natural first choice to model the unknown species tree, we use the Yule process with birth rate λ (see Yule, 1924). Since the phylogenetic sample size is given, n , the Yule process should be conditioned on having n tips: such conditioned branching processes have received significant attention in recent years, due to e.g. Aldous and Popovic (2005), Gernhard (2008), Mooers et al. (2012), Stadler (2009, 2011), and Stadler and Steel (2012). This “tree-free” approach for phylogenetic comparative methods was previously addressed by Sagitov and Bartoszek (2012), Crawford and Suchard (2013) and Mulder and Crawford (2015) (much earlier Edwards, 1970 used a related branching Brownian process as a population genetics model).

In our work we show that a properly scaled sample variance is an unbiased and consistent estimator of the compound parameter $\rho^2 = \sigma^2/\lambda$ which we call the evolutionary rate of the trait value in question. Our main mathematical result, Theorem 2.1, gives an asymptotic expression for the variance of the phylogenetic sample variance. This result leads to a simple asymptotic formula for the estimated standard error of our estimator. Our result is in agreement with the work of Crawford and Suchard (2013) whose simulations indicate that their approximate maximum likelihood

* Corresponding author at: Mathematical Sciences, Chalmers University of Technology, 412 96 Gothenburg, Sweden. Tel.: +46 31772 5351; fax: +46 31772 3508.

E-mail address: serik@chalmers.se (S. Sagitov).

procedure yields an unbiased consistent estimator of σ^2 . This is illustrated using the example of the Carnivora order studied previously by Crawford and Suchard (2013).

The phenotype modelled by a Brownian motion is usually interpreted as the case of neutral evolution with a random noise around the ancestral state. This model was later developed into an adaptive evolutionary model based on the Ornstein–Uhlenbeck process by Felsenstein (1988), Hansen (1997), Butler and King (2004), Hansen et al. (2008), and Bartoszek et al. (2012). The tree-free setting using the Ornstein–Uhlenbeck process was addressed by Bartoszek and Sagitov (2015) where for the Yule–Ornstein–Uhlenbeck model, some phylogenetic confidence intervals for the optimal trait value were obtained via three limit theorems for the phylogenetic sample mean. Furthermore, it was shown that the phylogenetic sample variance is an unbiased consistent estimator of the stationary variance of the process.

At the end of their discussion Crawford and Suchard (2013) write that as the tree of life is refined interest in “tree-free” estimation methods may diminish. They however indicate that “tree-free” estimates may be useful to calculate starting points for simulation analysis. We certainly agree with the second statement but believe that development of “tree-free” methods should proceed alongside that of “tree-based” ones.

One of the most useful features of the “tree-free” comparative models is that they offer a natural method of tree growth allowing for study of theoretical properties of phylogenetic comparative models. This is a field receiving more and more attention in recent years (e.g. Gascuel and Steel, 2014; Ho and Ané, 2014a,b). A fundamental setup to consider is the pure-birth Yule tree. Statistical results for processes evolving on top of such a tree is developed in this work (and also Sagitov and Bartoszek, 2012; Crawford and Suchard, 2013; Bartoszek, 2014; Mossel and Steel, 2014; Bartoszek and Sagitov, 2015). Another alternative to studying estimators of parameters of such processes is the tree growth model proposed by Ané (2008), Ho and Ané (2013), and Ané et al. (2014). In this setup the total height of the tree is kept fixed and new tips are added to randomly chosen branches (however Ané et al., 2014 also discuss more general setups). These two approaches seem to be in agreement, at least up to the second moments, since e.g. they agree on the lack of consistency of estimating X_0 . In Sagitov and Bartoszek (2012) we showed that under the Yule Brownian motion model $\text{Var}[\bar{X}_n] \rightarrow 2\sigma^2$.

In a practical situation “tree-free” methods can be used for a number of purposes. Firstly as pointed out by Crawford and Suchard (2013) they can be useful for calculating starting points for further numerical estimation procedures or defining prior distributions in a Bayesian setting. Secondly they have to be used in a situation where the tree is actually unknown, e.g. when we are studying fossil data or nearly very difficult to infer. For example, the phylogenies of insects are characterized by multiple recent radiations. In such a situation the support of many internal nodes can be close to zero—we do not have enough signal to place them even though we do not suspect polytomies. Piwczyński et al.'s (2014) molecular phylogeny of flesh flies can serve as a model example—their Bayesian analysis could not converge, while maximum likelihood trees had very low support for many internal nodes. Thirdly “tree-free” methods can be useful for making predictive statements about future phenotypes, e.g. development of viruses. Finally they can be used for various sanity checks. If they contradict “tree-based” results this could indicate that the numerical method fell into a local maximum.

The paper has the following structure. Section 2 presents the model, the main results and an application. In Section 3 we state two lemmas characterizing the coalescent time of a Yule tree needed for the proof of Proposition 4.1. Section 4 states two further lemmas and a proposition directly yielding the assertion of Theorem 2.1. Proposition 4.1 deals with the covariances between coalescent times for randomly chosen pairs of tips from a random Yule n -tree.

2. The main results

The basic evolutionary model considered in this paper is characterized by four parameters $(\lambda, n, X_0, \sigma^2)$ and consists of two stochastic components: a random phylogenetic tree defined by parameters (λ, n) and a trait evolution process along a lineage defined by parameters (X_0, σ^2) . The first component, species tree connecting n extant species, is modelled by the pure birth Yule process (Yule, 1924) with the birth (speciation) rate λ and conditioned on having n tips (Gernhard, 2008). For the second component we adapt the approach by assuming that for a given $i = 1, \dots, n$, the current trait value $X_i^{(n)}$ has evolved from the

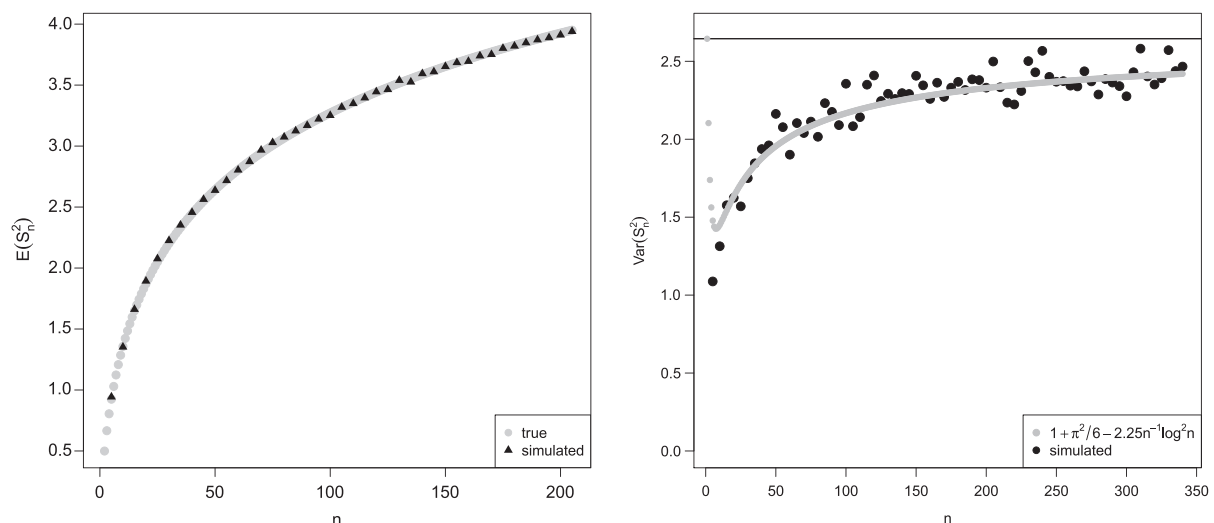


Fig. 1. Left: True and simulated values of $E[S_n^2]$, right: simulated values of $\text{Var}[S_n^2]$ with limit equalling $\pi^2/6 + 1$. Each point comes from 10 000 simulated Yule trees and Brownian motions on top of them. Parameters used in simulations are $\lambda = 1$, $X_0 = 0$ and $\sigma^2 = 1$. The grey line on the right panel fits a curve based on the convergence rate $O(n^{-1}\log^2 n)$.

ancestral state X_0 according to the Brownian motion with the local variance σ^2 .

Treating the collection of the current trait values $(X_1^{(n)}, \dots, X_n^{(n)})$ generated by such a process as a sample of identically distributed, but dependent, observations, we are interested in the properties of the basic summary statistics:

$$\bar{X}_n = \frac{X_1^{(n)} + \dots + X_n^{(n)}}{n}, \quad S_n^2 = \frac{1}{n-1} \sum_{i=1}^n (X_i^{(n)} - \bar{X}_n)^2,$$

the sample mean and sample variance.

According to Sagitov and Bartoszek (2012) we have

$$E[S_n^2] = \left(\frac{n+1}{n-1} H_n - 2 \frac{n}{n-1} \right) \frac{\sigma^2}{\lambda}, \quad H_n = \sum_{i=1}^n \frac{1}{i},$$

see Fig. 1, left panel (all simulations are produced using the TreeSim, Stadler, 2009, 2011, and mvSLOUCH, Bartoszek et al., 2012 and R Core Team, 2013 packages). It follows that the normalized sample variance

$$R_n^2 = \left(\frac{n+1}{n-1} H_n - 2 \frac{n}{n-1} \right)^{-1} S_n^2 \quad (1)$$

gives an unbiased estimator of the compound parameter $\rho^2 := \sigma^2/\lambda$ for the Yule–Brownian-motion model, see Fig. 2. In the phylogenetic comparative methods framework the ratio ρ^2 can be called the *evolutionary rate* as it measures the speed of change in the trait value when the time scale is such that we expect one speciation event per unit of time and per species. The next theorem is the main asymptotic result of this paper, illustrated in Fig. 1, right panel.

Theorem 2.1. Consider the sample variance S_n^2 for the Yule–Brownian-motion model with parameters $(\lambda, n, X_0, \sigma^2)$. Its variance satisfies the following asymptotic relation:

$$\text{Var}[S_n^2/\rho^2] = 1 + \frac{\pi^2}{6} + O(n^{-1} \log^2 n), \quad n \rightarrow \infty.$$

In terms of our estimator equation (1), Theorem 2.1 yields

$$\text{Var}[R_n^2/\rho^2] = \frac{1 + \frac{\pi^2}{6}}{(\log n + \gamma - 2)^2} + O(n^{-1}),$$

where $\gamma \approx 0.577$ is the Euler constant, implying that R_n^2 is a consistent estimator of the evolutionary rate ρ^2 . It follows that for large n , the standard error (estimated standard deviation) of the unbiased estimator R_n^2 can be approximated by

$$\text{SE}(R_n^2) \approx \sqrt{1 + \frac{\pi^2}{6}} \cdot \frac{R_n^2}{\log n + \gamma - 2} \approx \frac{1.626}{\log n - 1.423} \cdot R_n^2. \quad (2)$$

The estimator of Eq. (1) should be compared to the approximate maximum-likelihood estimator for the local variance σ^2 recently proposed by Crawford and Suchard (2013) in the same framework of the Yule–Brownian-motion model. The main difference between two approaches is that in Crawford and Suchard (2013) it is assumed that one knows both the number of tips and the total height of the otherwise unknown species tree. The Crawford–Suchard estimator is based on a closed form of the distribution of phylogenetic diversity—the sum of branch lengths connecting the species in a clade.

As an application of their estimator, Crawford and Suchard (2013) study different families of the Carnivora order, estimating σ^2 for each of the 12 clades. The data for the log-body-size disparities was taken from the PanTHERIA database (Jones et al., 2009). The data summary and the Crawford–Suchard estimates are shown in the left part of Table 1. In the right part of Table 1 we present our estimates $\hat{\rho}^2$ for the evolutionary rate parameter $\rho^2 = \sigma^2/\lambda$ for each of the 12 families in the Carnivora order. The standard error is computed using Eq. (2). We note that the data does not take into account the newly described species *Bassaricyon neblina* from the Procyonidae family (Helgen et al., 2013).

In the next-to-last column we list the ratios demonstrating a surprisingly good agreement between our and Crawford–Suchard estimates. The ratio is taken between two products: $\hat{\rho}^2 u_n$ on one hand, and $\hat{\sigma}^2 t_n$ on the other. Here $u_n = E[U_n]$ is the expected age of the conditioned standard Yule process with $\lambda = 1$, while t_n is the clade age assumed to be known in the Crawford–Suchard framework. Both $\hat{\rho}^2 u_n$ and $\hat{\sigma}^2 t_n$ estimate the same quantity—the variance in the trait values for the evolution of the corresponding clade. Therefore, one should expect these ratios to be close to one. And indeed, the 12 ratios have mean 0.97 and standard deviation 0.20.

Our estimator and its standard error are computed by simple formulae given above. A major weakness of our estimator is relatively big standard error for realistic richness values, see the

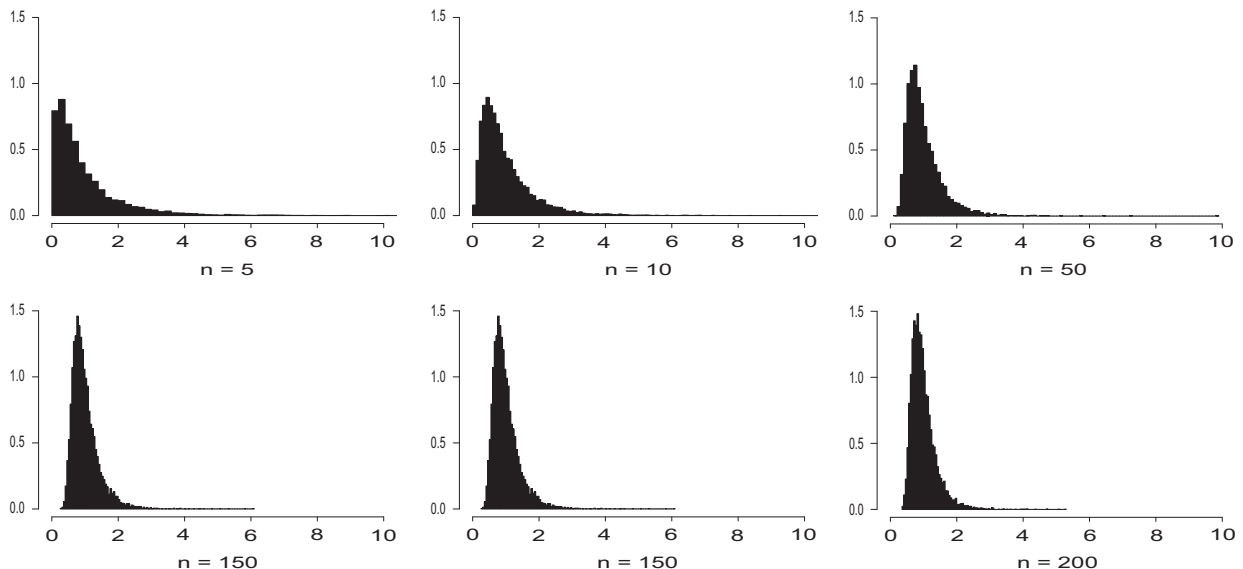


Fig. 2. Histograms of R_n^2 for left to right top $n = 5, 10, 50$ and bottom $n = 100, 150, 200$. Parameters used in simulations are $\lambda = 1$, $X_0 = 0$ and $\sigma^2 = 1$.

Table 1
Data summary. 2nd column: clade richness (number of missing trait values); 3rd column: the clade age in millions of years; 4th column: $(n-1)/n \cdot S_n^2$ trait disparity; 6th column: the expected age $u_n = E[U_n]$ of the conditioned standard Yule process with $\lambda = 1$.

Family	n	t_n	Disparity	$\hat{\sigma}^2$ (SE)	u_n	$\hat{\rho}^2$ (SE)	$\frac{\hat{\rho}^2 u_n}{\hat{\sigma}^2 t_n}$	$\frac{\hat{\rho}^2}{\hat{\sigma}^2/\lambda}$
Felidae	40 (7)	33.3	1.588	0.080 (0.009)	4.279	0.649 (0.466)	1.042	0.560
Viverridae	35 (6)	37.4	0.662	0.029 (0.004)	4.147	0.284 (0.217)	1.086	0.676
Herpestidae	33 (4)	25.5	0.482	0.030 (0.003)	4.089	0.211 (0.166)	1.128	0.485
Eupleridae	8 (0)	25.5	0.916	0.079 (0.010)	2.718	0.758 (1.72)	1.023	0.662
Hyaenidae	4 (0)	32.2	0.805	0.122 (0.005)	2.083	0.999(19.5)	0.530	0.565
Canidae	35 (3)	48.9	0.678	0.030 (0.004)	4.147	0.290 (0.221)	0.825	0.667
Ursidae	8 (0)	42.6	0.303	0.024 (0.002)	2.718	0.251 (0.569)	0.667	0.722
Otariidae	16 (2)	24.5	0.386	0.028 (0.003)	3.381	0.227 (0.274)	1.119	0.559
Phocidae	19 (0)	24.5	0.751	0.052 (0.005)	3.548	0.410 (0.438)	1.142	0.544
Mephitidae	12 (3)	32.0	0.570	0.039 (0.005)	3.103	0.384 (0.588)	0.955	0.679
Mustelidae	59 (10)	27.4	2.263	0.126 (0.014)	4.663	0.811 (0.497)	1.095	0.444
Procyonidae	14 (1)	27.4	0.531	0.037 (0.004)	3.252	0.332 (0.444)	1.065	0.619

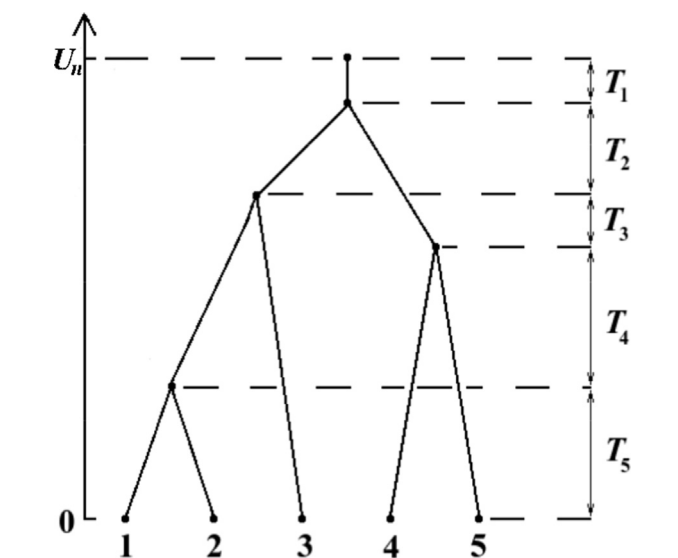


Fig. 3. An example of a standard Yule n -tree with $n=5$. The tree height is $U_n = T_1 + \dots + T_n$, where T_i are the times between the consecutive speciation events. The 10 pairwise coalescent times $\tau_{ij}^{(n)}$ for the tips of the tree are $\tau_{12}^{(5)} = T_5$, $\tau_{45}^{(5)} = T_5 + T_4$, $\tau_{13}^{(5)} = \tau_{23}^{(5)} = T_5 + T_4 + T_3$, and $\tau_{14}^{(5)} = \tau_{24}^{(5)} = \tau_{34}^{(5)} = \tau_{15}^{(5)} = \tau_{25}^{(5)} = \tau_{35}^{(5)} = T_5 + T_4 + T_3 + T_2$.

7th column in Table 1. This can be explained by the fact that we do not use an additional information about the species tree, like the height of the tree used in the Crawford–Suchard estimator.

This close agreement is obtained despite a number of features that complicates the comparison between two methods. Our approach in its current form does not allow us to take into account the fact that some trait values are missing. We calculated $\hat{\rho}^2$ for the trait disparity as if it was computed using all n trait values. Moreover, it is not clear how to take into account the measurement variance. As shown by Hansen and Bartoszek (2012) even with a known tree, the measurement error can cause very diverse effects. Therefore we would expect the situation to be even more interesting when we integrate the phylogeny out.

In their work Crawford and Suchard (2013) estimated the overall speciation rate to be $\hat{\lambda} = 0.069$ per million years. The last column of Table 1 demonstrates that using this common value for the speciation rate λ produces huge discrepancy between our estimates $\hat{\rho}^2$ for the rates of evolution $\rho^2 = \sigma^2/\lambda$ and the rates of evolution computed using the Crawford–Suchard estimates for σ^2 . This observation points out that a fair direct comparison of $\hat{\rho}^2$ and $\hat{\sigma}^2/\lambda$ would require specific estimates of the speciation rate λ for each of the 12 clades.

3. Coalescent indices of the standard Yule n -tree

Following the standard ($\lambda = 1$) Yule n -tree from its root toward the tips we label the consecutive splittings by indices $1, \dots, n-1$: splitting k is the vertex when $k-1$ branches turn into k branches. We define three random splitting indices (as we are interested in four randomly chosen tips out of n available):

- K_n is the index of the splitting where two randomly chosen tips coalesce,
- L_n is the index of the splitting where the first coalescent among three randomly chosen tips takes place,
- M_n is the index of the splitting where the first coalescent among four randomly chosen tips takes place.

To avoid multilevel indices in the forthcoming formulae, we will often use the following notational convention:

$$KL_n := K_{L_n}, \quad LM_n := L_{M_n}, \quad KLM_n := K_{LM_n}.$$

To illustrate these indices, turn to Fig. 3. If the two randomly chosen tips are (1, 2), then $K_n = 4$. If the three randomly chosen tips are (2, 3, 4), then $L_n = 2$, $K_{L_n} = 1$. If the four randomly chosen tips are (2, 3, 4, 5), then $M_n = 3$, $L_{M_n} = 2$, $K_{LM_n} = 1$.

The importance of these random indices comes from the following representations for the standard Yule n -tree. Denote $U_k^{(n)} := T_{k+1} + \dots + T_n$ the sum of adjacent times between splittings in the tree, and for a quadruplet (i, j, k, l) of tips randomly sampled without replacement out of n tree tips, define

$$\tau_1^{(n)} = \tau_{ij}^{(n)}, \quad \tau_2^{(n)} = \tau_{ik}^{(n)}, \quad \tau_3^{(n)} = \tau_{lk}^{(n)}, \quad \tau_4^{(n)} = \tau_{jk}^{(n)}, \quad \tau_5^{(n)} = \tau_{jl}^{(n)}, \quad \tau_6^{(n)} = \tau_{kl}^{(n)}. \quad (3)$$

Clearly,

$$\tau_1^{(n)} \stackrel{d}{=} U_{K_n}^{(n)}, \quad \tau_1^{(n)} \wedge \tau_2^{(n)} \stackrel{d}{=} U_{L_n}^{(n)}, \quad \tau_1^{(n)} \vee \tau_2^{(n)} \stackrel{d}{=} U_{KL_n}^{(n)}, \quad \tau_1^{(n)} \vee \tau_3^{(n)} \stackrel{d}{=} U_{KLM_n}^{(n)}. \quad (4)$$

To prove our key Proposition 4.1 we need to know the distributions of these random splitting indices which are given in the next two lemmas. We remind the reader that the properties of the coalescent of a single random pair were previously studied by e.g. Steel and McKenzie (2001) and Sagitov and Bartoszek (2012).

Lemma 3.1. *The above defined random splitting indices have the following distributions:*

$$P(K_n = k) = \frac{n+1}{n-1} \cdot \frac{2}{(k+1)(k+2)}, \quad k = 1, \dots, n-1,$$

$$P(L_n = k) = \frac{(n+1)(n+2)}{(n-1)(n-2)} \cdot \frac{6(k-1)}{(k+1)(k+2)(k+3)}, \quad k=2, \dots, n-1,$$

$$P(M_n = k) = \frac{(n+1)(n+2)(n+3)}{(n-1)(n-2)(n-3)} \cdot \frac{12(k-1)(k-2)}{(k+1)(k+2)(k+3)(k+4)},$$

$$k=3, \dots, n-1.$$

Proof. From the definition of K_n it is easy to see that, for $k=2, \dots, n$,

$$P(K_n < k-1 | K_n < k) = 1 - \frac{1}{\binom{k}{2}} = \frac{(k+1)(k-2)}{k(k-1)}.$$

Therefore,

$$P(K_n < k-1) = \frac{(n+1)(n-2)}{n(n-1)} \cdot \frac{n(n-3)}{(n-1)(n-2)} \cdot \frac{(n-1)(n-4)}{(n-2)(n-3)} \cdots \frac{(k+1)(k-2)}{k(k-1)}$$

$$= \frac{(n+1)(k-2)}{(n-1)k},$$

$$P(K_n = k-1) = \frac{(n+1)(k-1)}{(n-1)(k+1)} - \frac{(n+1)(k-2)}{(n-1)k} = \frac{n+1}{n-1} \cdot \frac{2}{(k+1)k}.$$

Similarly, for $k=3, \dots, n$,

$$P(L_n < k-1 | L_n < k) = 1 - \frac{3}{\binom{k}{2}} = \frac{(k+2)(k-3)}{k(k-1)},$$

$$P(L_n < k-1) = \frac{(n+2)(n-3)(n+1)(n-4)}{n(n-1)} \cdot \frac{n(n-5)}{(n-1)(n-2)(n-3)} \cdots \frac{(k+2)(k-3)}{k(k-1)}$$

$$= \frac{(n+2)(n+1)(k-2)(k-3)}{(n-1)(n-2)(k+1)k},$$

$$P(L_n = k-1) = \frac{(n+2)(n+1)(k-1)(k-2)}{(n-1)(n-2)(k+2)(k+1)} - \frac{(n+2)(n+1)(k-2)(k-3)}{(n-1)(n-2)(k+1)k}$$

$$= \frac{6(n+2)(n+1)(k-2)}{(n-1)(n-2)(k+2)(k+1)k},$$

and, for $k=4, \dots, n$,

$$P(M_n < k-1 | M_n < k) = 1 - \frac{6}{\binom{k}{2}} = \frac{(k+3)(k-4)}{k(k-1)},$$

$$P(M_n < k-1) = \frac{(n+3)(n+2)(n+1)(k-2)(k-3)(k-4)}{(n-1)(n-2)(n-3)(k+2)(k+1)k},$$

$$P(M_n = k-1) = \frac{12(n+3)(n+2)(n+1)(k-2)(k-3)}{(n-1)(n-2)(n-3)(k+3)(k+2)(k+1)k}. \quad \square$$

Lemma 3.2. The random numbers $K_{L_n}, L_{M_n}, K_{LM_n}$ have the following distributions:

$$P(K_{L_n} = k) = \frac{n+1}{(n-1)(n-2)} \cdot \frac{12}{(k+1)(k+2)} \left(\frac{n+2}{k+3} - 1 \right), \quad k=1, \dots, n-2,$$

$$P(L_{M_n} = k) = \frac{(n+1)(n+2)}{(n-1)(n-2)(n-3)} \cdot \frac{72(k-1)}{(k+1)(k+2)(k+3)} \left(\frac{n+3}{k+4} - 1 \right),$$

$$k=2, \dots, n-2,$$

$$P(K_{LM_n} = k) = \frac{n+3}{(n-1)(n-2)(n-3)} \cdot \frac{72}{(k+1)(k+2)} \left(\frac{(n+1)(n+2)}{(k+3)(k+4)} - 1 \right)$$

$$- \frac{n+2}{(n-1)(n-2)(n-3)} \cdot \frac{144}{(k+1)(k+2)} \left(\frac{n+1}{k+3} - 1 \right),$$

$$k=1, \dots, n-3.$$

Proof. Clearly,

$$P(K_{L_n} = k) = \sum_{l=k+1}^{n-1} P(K_l = k) P(L_n = l)$$

$$= \frac{(n+1)(n+2)}{(n-1)(n-2)} \cdot \frac{12}{(k+1)(k+2)} \sum_{l=k+1}^{n-1} \frac{1}{(l+2)(l+3)}$$

leads to the first assertion. Further,

$$P(L_{M_n} = k) = \frac{(n+1)(n+2)(n+3)}{(n-1)(n-2)(n-3)} \times \sum_{m=k+1}^{n-1} \frac{12(m-1)(m-2)(m+1)(m+2)}{(m+1)(m+2)(m+3)(m+4)(m-1)(m-2)}$$

$$\cdot \frac{6(k-1)}{(k+1)(k+2)(k+3)},$$

and

$$P(L_{M_n} = k) = \frac{(n+1)(n+2)(n+3)}{(n-1)(n-2)(n-3)} \cdot \frac{72(k-1)}{(k+1)(k+2)(k+3)} \sum_{m=k+1}^{n-1} \frac{1}{(m+3)(m+4)}$$

$$= \frac{(n+1)(n+2)(n+3)}{(n-1)(n-2)(n-3)} \cdot \frac{72(k-1)}{(k+1)(k+2)(k+3)} \left(\frac{1}{k+4} - \frac{1}{n+3} \right).$$

Finally,

$$P(K_{LM_n} = k) = \sum_{m=k+1}^{n-2} \frac{(n+1)(n+2)(n+3)}{(n-1)(n-2)(n-3)} \cdot \frac{72(m-1)}{(m+1)(m+2)(m+3)(m+4)} \cdot \frac{m+1}{m-1} \cdot \frac{2}{(k+1)(k+2)}$$

$$- \sum_{m=k+1}^{n-2} \frac{(n+1)(n+2)}{(n-1)(n-2)(n-3)} \cdot \frac{72(m-1)}{(m+1)(m+2)(m+3)} \cdot \frac{m+1}{m-1}$$

$$\cdot \frac{2}{(k+1)(k+2)}$$

$$= \frac{(n+1)(n+2)(n+3)}{(n-1)(n-2)(n-3)} \cdot \frac{144}{(k+1)(k+2)} \sum_{m=k+1}^{n-2} \frac{1}{(m+2)(m+3)(m+4)}$$

$$- \frac{(n+1)(n+2)}{(n-1)(n-2)(n-3)} \cdot \frac{144}{(k+1)(k+2)} \sum_{m=k+1}^{n-2} \frac{1}{(m+2)(m+3)},$$

and therefore, it remains to use the equalities:

$$\sum_{m=k+1}^{n-2} \frac{1}{(m+2)(m+3)} = \frac{1}{k+3} - \frac{1}{n+1},$$

$$\sum_{m=k+1}^{n-2} \frac{2}{(m+2)(m+3)(m+4)} = \frac{1}{(k+3)(k+4)} - \frac{1}{(n+1)(n+2)}. \quad \square$$

4. Proof of Theorem 2.1

In terms of the sample variance

$$D_n^2 = \frac{1}{n-1} \sum_{i=1}^n (Y_i - \bar{Y})^2, \quad \bar{Y} = n^{-1} \sum_{i=1}^n Y_i,$$

for the scaled trait values

$$Y_i := Y_i^{(n)} = \frac{X_i^{(n)} - X_0}{\sigma/\sqrt{\lambda}}, \quad i=1, \dots, n, \quad (5)$$

we have $S_n^2 = \sigma^2 D_n^2 / \lambda$, and to prove Theorem 2.1 we have to verify that

$$\text{Var}[D_n^2] = 1 + \frac{\pi^2}{6} + O(n^{-1} \log^2 n). \quad (6)$$

The standard Yule n -tree underlying the set of scaled values equation (5) has unit speciation rate and we denote by \mathcal{Y}_n the σ -algebra generated by all the information describing this random tree. Under the Brownian motion assumption the trait values equation (5) is conditionally normal with

$$E[Y_i | \mathcal{Y}_n] = 0, \quad \text{Var}[Y_i | \mathcal{Y}_n] = U_n,$$

where U_n is the height of the standard Yule n -tree, see Fig. 3. Moreover, we have

$$\text{Cov}[Y_i Y_j | y_n] = U_n - \tau_{ij}^{(n)}, \quad (7)$$

where $\tau_{ij}^{(n)}$ is the backward time to the most recent common ancestor for a pair of distinct tips (i, j) in the standard Yule n -tree, see Fig. 3.

The proof of (6) is structured as follows. We start with a general observation, Lemma 4.1, concerning the sample variance D_n^2 of possibly dependent and not necessarily identically distributed, observations (Y_1, \dots, Y_n) . Together with Lemma 4.2, it shows that to establish (6) it is enough to verify the next asymptotical results, having interest on its own.

Proposition 4.1. Consider the coalescent times equation (3). As $n \rightarrow \infty$,

$$\begin{aligned} \text{Var}[\tau_1^{(n)}] &= \frac{\pi^2}{6} + O(n^{-1} \log^2 n), \\ \text{Cov}[\tau_1^{(n)}, \tau_2^{(n)}] &= 2 - \frac{\pi^2}{6} + O(n^{-1} \log^2 n), \\ \text{Cov}[\tau_1^{(n)}, \tau_3^{(n)}] &= 3 - \frac{5\pi^2}{18} + O(n^{-1} \log^2 n). \end{aligned}$$

Notice that these asymptotic relations concern only the first component of the evolutionary model we study—the standard Yule n -tree. For the standard Yule n -tree it is well known that the times between the consecutive speciation events (T_1, \dots, T_n) are independent exponentials with parameters $(1, \dots, n)$ respectively, see Fig. 3. As shown by Gernhard (2008), this property corresponds to the unit rate Yule process conditioned on having n tips at the moment of observation, assuming that the time to the origin has the improper uniform prior (see also Feller, 1971).

In view of Eq. (4), the harmonic numbers

$$H_n = \sum_{k=1}^n k^{-1}, \quad \bar{H}_n = \sum_{k=1}^n k^{-2} \quad (8)$$

play an important role in our calculations as

$$\begin{aligned} E[U_k^{(n)}] &= H_n - H_k, \\ E[(U_k^{(n)})^2] &= \bar{H}_n - \bar{H}_k + (H_n - H_k)^2 = H_n^2 - 2H_n H_k + \bar{H}_n + H_k^2 - \bar{H}_k. \end{aligned}$$

According to Lemma 4.3, the joint moments of coalescent times in Proposition 4.1 can be expressed in terms of the expectations of the harmonic numbers indexed by random numbers introduced in Section 3. The required asymptotic analysis of such expectations is performed in Lemmas 4.4–4.5 using the following properties of harmonic numbers:

$$\begin{aligned} \sum_{k=1}^{n-1} \frac{H_k}{k(k+1)} &= \bar{H}_n - \frac{H_n}{n} \xrightarrow{n \rightarrow \infty} \frac{\pi^2}{6}, \\ \sum_{k=1}^{n-1} \frac{H_k}{(k+m)(k+m+1)} &= \frac{H_m}{m} - \frac{H_{n+m} - H_n}{m} \xrightarrow{n \rightarrow \infty} \frac{H_m}{m}, \quad m \geq 1, \\ \sum_{k=1}^{n-1} \frac{\bar{H}_k}{(k+m)(k+m+1)} &= \frac{n\bar{H}_n}{(n+m)m} - \frac{H_m}{m^2} + \frac{H_{n+m} - H_n}{m^2} \xrightarrow{n \rightarrow \infty} \frac{\pi^2}{6m} - \frac{H_m}{m^2}, \quad m \geq 1, \\ \sum_{k=1}^{n-1} \frac{H_k^2}{(k+1)(k+2)} &= \bar{H}_n + \frac{n - H_n^2 - 2H_n}{n+1} \xrightarrow{n \rightarrow \infty} \frac{\pi^2}{6} + 1, \\ \sum_{k=1}^{n-1} \frac{H_k^2}{(k+2)(k+3)} &= \bar{H}_n + \frac{11n^2 + 21n}{8(n+1)(n+2)} - \frac{H_n(2n+3)}{(n+1)(n+2)} - \frac{H_n^2}{n+2} \xrightarrow{n \rightarrow \infty} \frac{\pi^2}{12} + \frac{11}{8}, \\ \sum_{k=1}^{\infty} \frac{H_k^2}{(k+m)(k+m+1)} &= \frac{1}{m} \left(\frac{\pi^2}{6} + H_m^2 + \bar{H}_m - \frac{H_m}{m} \right), \quad m \geq 1. \end{aligned} \quad (9)$$

Some of these properties can be found in Adamchik (1997) and Sofo (2011, 2012, 2013).

Lemma 4.1. If (W_1, W_2, W_3, W_4) is a random variable sampled without replacement from random values (Y_1, \dots, Y_n) , then

$$\text{Var}[D_n^2] = \text{Cov}[W_1^2, W_2^2] - 2\text{Cov}[W_1^2, W_2 W_3] + \text{Cov}[W_1 W_2, W_3 W_4] + n^{-1} B_n, \quad (10)$$

where

$$\begin{aligned} |B_n| &< E[W_1^4] + 4E[W_1^3 W_2] + E[W_1^2 W_2^2] + 6E[W_1^2 W_2 W_3] \\ &\quad + 4E[W_1 W_2 W_3 W_4]. \end{aligned}$$

Proof. Using the representation

$$D_n^2 = \frac{n}{n-1} \left(\frac{1}{n} \sum_{i=1}^n Y_i^2 - \bar{Y}_n^2 \right) = \frac{1}{n} \sum_{i=1}^n Y_i^2 - \frac{1}{n(n-1)} \sum_{i \neq j} Y_i Y_j$$

we find that

$$\begin{aligned} E[D_n^4] &= \frac{1}{n^2} \left(\sum_i E[Y_i^4] + \sum_{i \neq j} E[Y_i^2 Y_j^2] \right) \\ &\quad - \frac{2}{n^2(n-1)} \left(\sum_{i \neq j} E[Y_i^3 Y_j] + \sum_{i \neq j} E[Y_i Y_j^3] \right. \\ &\quad \left. + \sum_{i \neq j \neq k \neq i} E[Y_i^2 Y_j Y_k] \right) + \frac{1}{n^2(n-1)^2} \left(\sum_{i \neq j} E[Y_i^2 Y_j^2] \right. \\ &\quad \left. + \sum_{i \neq j \neq k \neq i} E[Y_i^2 Y_j Y_k] + \sum_{i \neq j \neq k \neq i} E[Y_i Y_j^2 Y_k] \right. \\ &\quad \left. + \sum_{i \neq j \neq k \neq l \neq i} E[Y_i Y_j Y_k Y_l] \right). \end{aligned}$$

If (W_1, W_2, W_3, W_4) is a random sample without replacement of four out of n trait values, then

$$\begin{aligned} E[W_1^4] &= n^{-1} \sum_i E[Y_i^4], \\ E[W_1^3 W_2] &= \frac{1}{n(n-1)} \sum_{i \neq j} E[Y_i^3 Y_j], \\ E[W_1^2 W_2^2] &= \frac{1}{n(n-1)} \sum_{i \neq j} E[Y_i^2 Y_j^2], \end{aligned}$$

and

$$\begin{aligned} E[W_1^2 W_2 W_3] &= \frac{1}{n(n-1)(n-2)} \sum_{i \neq j \neq k \neq i} E[Y_i^2 Y_j Y_k], \\ E[W_1 W_2 W_3 W_4] &= \frac{1}{n(n-1)(n-2)(n-3)} \sum_{i \neq j \neq k \neq l \neq i} E[Y_i Y_j Y_k Y_l]. \end{aligned}$$

Therefore, we have

$$\begin{aligned} E[D_n^4] &= n^{-1} E[W_1^4] - 4n^{-1} E[W_1^3 W_2] + \frac{n^2 - 2n + 2}{n(n-1)} E[W_1^2 W_2^2] \\ &\quad - \frac{2(n-2)^2}{n(n-1)} E[W_1^2 W_2 W_3] + \frac{(n-2)(n-3)}{n(n-1)} E[W_1 W_2 W_3 W_4]. \end{aligned} \quad (11)$$

Since

$$E[D_n^2] = E[W_1^2] - E[W_1 W_2],$$

we conclude

$$\begin{aligned} \text{Var}[D_n^2] &= n^{-1} E[W_1^4] - 4n^{-1} E[W_1^3 W_2] + \text{Cov}[W_1^2, W_2^2] \\ &\quad - \frac{n-2}{n(n-1)} E[W_1^2 W_2^2] - 2\text{Cov}[W_1^2, W_2 W_3] \\ &\quad + \frac{2(3n-4)}{n(n-1)} E[W_1^2 W_2 W_3] \\ &\quad + \text{Cov}[W_1 W_2, W_3 W_4] - \frac{2(2n-3)}{n(n-1)} E[W_1 W_2 W_3 W_4]. \end{aligned}$$

The stated relations follow with

$$B_n = E[W_1^4] - 4E[W_1^3 W_2] - \frac{n-2}{n-1}E[W_1^2 W_2^2] + \frac{2(3n-4)}{n-1}E[W_1^2 W_2 W_3] - \frac{2(2n-3)}{n-1}E[W_1 W_2 W_3 W_4]. \quad \square$$

Lemma 4.2. Let (W_1, W_2, W_3, W_4) be a random sample without replacement of four trait values out of n random values defined by Eq. (5). Then in terms of the coalescent times equation (3) we have

$$\begin{aligned} \text{Cov}[W_1^2, W_2^2] - 2\text{Cov}[W_1^2, W_2 W_3] + \text{Cov}[W_1 W_2, W_3 W_4] \\ = 2\text{Var}[\tau_1^{(n)}] - 4\text{Cov}[\tau_1^{(n)}, \tau_2^{(n)}] + 3\text{Cov}[\tau_1^{(n)}, \tau_3^{(n)}]. \end{aligned}$$

Proof. Denote by $Y_{ij}^{(n)}$ the normalized trait value of the most recent common ancestor of the tips (i, j) . Let $\mathcal{Y}_{ij}^{(n)}$ stand for the σ -algebra generated by the pair $(\mathcal{Y}_n, Y_{ij}^{(n)})$, then

$$\begin{aligned} E[Y_i | \mathcal{Y}_{ij}^{(n)}] &= E[Y_j | \mathcal{Y}_{ij}^{(n)}] = Y_{ij}^{(n)}, \\ \text{Var}[Y_i | \mathcal{Y}_{ij}^{(n)}] &= \text{Var}[Y_j | \mathcal{Y}_{ij}^{(n)}] = \tau_{ij}^{(n)}, \\ \text{Cov}[Y_i, Y_j | \mathcal{Y}_{ij}^{(n)}] &= 0, \end{aligned}$$

implying Eq. (7)

$$\text{Cov}[Y_i Y_j | \mathcal{Y}_n] = \text{Var}[Y_{ij}^{(n)} | \mathcal{Y}_n] = U_n - \tau_{ij}^{(n)}.$$

By Eq. (13) of [Bohrnstedt and Goldberger \(1969\)](#), we have

$$\text{Cov}[Z_i Z_j, Z_k Z_l] = m_i m_k c_{jl} + m_i m_l c_{jk} + m_j m_k c_{il} + m_j m_l c_{ik} + c_{ik} c_{jl} + c_{il} c_{jk}$$

for any sequence of normally distributed random values Z_1, Z_2, \dots with means $E[Z_i] = m_i$ and covariances $\text{Cov}[Z_i, Z_j] = c_{ij}$. In the special case with $m_i = 0$ it follows

$$\begin{aligned} \text{Cov}[Z_i Z_j, Z_k Z_l] &= c_{ik} c_{jl} + c_{il} c_{jk}, \\ \text{Cov}[Z_i^2, Z_j Z_k] &= 2c_{ij} c_{ik}, \\ \text{Cov}[Z_i^2, Z_j^2] &= 2c_{ij}^2. \end{aligned}$$

Using conditional normality of Y_i and putting $c_{ij} = U_n - \tau_{ij}^{(n)}$, we derive from these relations that

$$\begin{aligned} \text{Cov}[Y_i^2 Y_j^2 | \mathcal{Y}_n] &= 2(U_n - \tau_{ij}^{(n)})^2, \\ \text{Cov}[Y_i^2 Y_j Y_k | \mathcal{Y}_n] &= 2(U_n - \tau_{ij}^{(n)})(U_n - \tau_{ik}^{(n)}), \\ \text{Cov}[Y_i Y_j Y_k Y_l | \mathcal{Y}_n] &= (U_n - \tau_{ik}^{(n)})(U_n - \tau_{jl}^{(n)}) + (U_n - \tau_{il}^{(n)})(U_n - \tau_{jk}^{(n)}) \end{aligned}$$

yielding in terms of Eq. (3),

$$\begin{aligned} \text{Cov}[W_1^2 W_2^2 | \mathcal{Y}_n] &= 2(U_n - \tau_1^{(n)})^2, \\ \text{Cov}[W_1^2 W_2 W_3 | \mathcal{Y}_n] &= 2(U_n - \tau_1^{(n)})(U_n - \tau_2^{(n)}), \\ \text{Cov}[W_1 W_2 W_3 W_4 | \mathcal{Y}_n] &= (U_n - \tau_2^{(n)})(U_n - \tau_3^{(n)}) + (U_n - \tau_3^{(n)})(U_n - \tau_4^{(n)}). \end{aligned}$$

By the total covariance formula, we derive

$$\begin{aligned} \text{Cov}[W_1^2, W_2^2] &= 2E[(U_n - \tau_1^{(n)})^2] + \text{Var}[U_n], \\ \text{Cov}[W_1^2, W_2 W_3] &= 2E[(U_n - \tau_1^{(n)})(U_n - \tau_2^{(n)})] + \text{Cov}[U_n, U_n - \tau_1^{(n)}], \\ \text{Cov}[W_1 W_2, W_3 W_4] &= 2E[(U_n - \tau_1^{(n)})(U_n - \tau_3^{(n)})] + \text{Cov}[U_n - \tau_1^{(n)}, U_n - \tau_3^{(n)}] \\ &= 3E[(U_n - \tau_1^{(n)})(U_n - \tau_3^{(n)})] - (E[U_n - \tau_1^{(n)}])^2. \end{aligned}$$

Combining these relations we get

$$\text{Cov}[W_1^2, W_2^2] - 2\text{Cov}[W_1^2, W_2 W_3] + \text{Cov}[W_1 W_2, W_3 W_4]$$

$$\begin{aligned} &= 2E[(U_n - \tau_1^{(n)})^2] - 4E[(U_n - \tau_1^{(n)})(U_n - \tau_2^{(n)})] \\ &\quad + 3E[(U_n - \tau_1^{(n)})(U_n - \tau_3^{(n)})] \\ &\quad + \text{Var}[U_n] - 2\text{Cov}[U_n, U_n - \tau_1^{(n)}] - (E[U_n - \tau_1^{(n)}])^2. \end{aligned}$$

This together with

$$\begin{aligned} \text{Var}[U_n] - 2\text{Cov}[U_n, U_n - \tau_1^{(n)}] - (E[U_n - \tau_1^{(n)}])^2 \\ = E[U_n^2] - E[U_n]^2 - 2E[U_n(U_n - \tau_1^{(n)})] + 2E[U_n]E[U_n - \tau_1^{(n)}] \\ - (E[U_n - \tau_1^{(n)}])^2 = E[U_n^2] - 2E[U_n(U_n - \tau_1^{(n)})] - E[\tau_1^{(n)}]^2 \\ = E[(\tau_1^{(n)})^2] - E[\tau_1^{(n)}]^2 - E[(U_n - \tau_1^{(n)})^2] \end{aligned}$$

implies the assertion of [Lemma 4.2](#)

$$\begin{aligned} \text{Cov}[W_1^2, W_2^2] - 2\text{Cov}[W_1^2, W_2 W_3] + \text{Cov}[W_1 W_2, W_3 W_4] \\ = E[(U_n - \tau_1^{(n)})^2] + E[(\tau_1^{(n)})^2] - E[\tau_1^{(n)}]^2 \\ - 4E[(U_n - \tau_1^{(n)})(U_n - \tau_2^{(n)})] + 3E[(U_n - \tau_1^{(n)})(U_n - \tau_3^{(n)})] \\ = E[(U_n - \tau_1^{(n)})^2] + \text{Var}[\tau_1^{(n)}] - E[(U_n - \tau_1^{(n)})U_n] + E[U_n \tau_1^{(n)}] \\ - 4E[\tau_1^{(n)} \tau_2^{(n)}] + 3E[\tau_1^{(n)} \tau_3^{(n)}] \\ = 2\text{Var}[\tau_1^{(n)}] - 4\text{Cov}[\tau_1^{(n)}, \tau_2^{(n)}] + 3\text{Cov}[\tau_1^{(n)}, \tau_3^{(n)}]. \quad \square \end{aligned}$$

Lemma 4.3. We have

$$\begin{aligned} E[\tau_1^{(n)}] &= H_n - E[H_{K_n}], \\ E[(\tau_1^{(n)})^2] &= H_n^2 - 2H_n E[H_{K_n}] + \overline{H}_n + E[H_{K_n}^2 - \overline{H}_{K_n}], \\ E[\tau_1^{(n)} \tau_2^{(n)}] &= H_n^2 - H_n E\left[\frac{2H_{L_n} + 4H_{KL_n}}{3}\right] + \overline{H}_n + E\left[\frac{2H_{L_n} H_{KL_n} + H_{KL_n}^2 - 2\overline{H}_{L_n} - \overline{H}_{KL_n}}{3}\right], \\ E[\tau_1^{(n)} \tau_3^{(n)}] &= H_n^2 - H_n E\left[\frac{3H_{M_n} + 5H_{LM_n} + 10H_{KLM_n}}{9}\right] + \overline{H}_n - \frac{1}{3}E[\overline{H}_{M_n}] \\ &\quad + \frac{1}{9}E[H_{M_n} H_{LM_n} + 2H_{M_n} H_{KLM_n} + 4H_{LM_n} H_{KLM_n} \\ &\quad + 2H_{KLM_n}^2 - 4\overline{H}_{LM_n} - 2\overline{H}_{KLM_n}]. \end{aligned}$$

Proof. We have

$$E[\tau_1^{(n)}] = E[U_{K_n}^{(n)}] = H_n - E[H_{K_n}],$$

and

$$E[(\tau_1^{(n)})^2] = E[(U_{K_n}^{(n)})^2] = \overline{H}_n + H_n^2 - E[\overline{H}_{K_n} + 2H_{K_n} H_n - H_{K_n}^2].$$

Further, using Eq. (4) and $U_{KL_n}^{(n)} = U_{L_n}^{(n)} + U_{KL_n}^{(L_n)}$, we get

$$\begin{aligned} E[\tau_1^{(n)} \tau_2^{(n)}] &= \frac{1}{3}E[(U_{KL_n}^{(n)})^2] + \frac{2}{3}E[U_{KL_n}^{(n)} U_{L_n}^{(n)}] \\ &= E[(U_{L_n}^{(n)})^2] + \frac{4}{3}E[U_{L_n}^{(n)} U_{KL_n}^{(L_n)}] + \frac{1}{3}E[(U_{KL_n}^{(L_n)})^2]. \end{aligned}$$

Thus

$$\begin{aligned} E[\tau_1^{(n)} \tau_2^{(n)}] &= H_n^2 - 2H_n E[H_{L_n}] + \overline{H}_n + E[H_{L_n}^2 - \overline{H}_{L_n}] + \frac{4}{3}E[(H_n - H_{L_n})(H_{L_n} - H_{KL_n})] \\ &\quad + \frac{1}{3}E[H_{L_n}^2 - 2H_{L_n} H_{KL_n} + \overline{H}_{L_n} + H_{KL_n}^2 - \overline{H}_{KL_n}] \\ &= H_n^2 - H_n E\left[\frac{2H_{L_n} + 4H_{KL_n}}{3}\right] + \overline{H}_n + E\left[\frac{2H_{L_n} H_{KL_n} + H_{KL_n}^2 - 2\overline{H}_{L_n} - \overline{H}_{KL_n}}{3}\right]. \end{aligned}$$

Finally, for two pairs of sampled tips, we have three coalescent events to consider: going from four to three selected nodes, $4 \rightarrow 3$, going from three to two selected nodes, $3 \rightarrow 2$, and going from two to one selected nodes, $2 \rightarrow 1$. The coalescent $4 \rightarrow 3$ holds across the two pairs with probability $\frac{4}{2} = \frac{2}{3}$ and within a pair with probability $\frac{1}{3}$.

Given the former outcome, the coalescent $3 \rightarrow 2$ holds again across the pairs with probability $\frac{1}{3}$ and within a pair with probability $\frac{2}{3}$. Otherwise, the coalescent $3 \rightarrow 2$ holds across the pairs with probability $\frac{2}{3}$ and within the second pair with probability $\frac{1}{3}$. The four possibilities ($\frac{2}{3} \times \frac{1}{3}$, $\frac{2}{3} \times \frac{2}{3}$, $\frac{1}{3} \times \frac{2}{3}$, $\frac{1}{3} \times \frac{1}{3}$) produce the following four terms in

$$E[\tau_1^{(n)} \tau_3^{(n)}] = \frac{2}{9} E[(U_{KLM_n}^{(n)})^2] + \frac{4}{9} E[U_{LM_n}^{(n)} U_{KLM_n}^{(n)}] + \frac{2}{9} E[U_{M_n}^{(n)} U_{KLM_n}^{(n)}] + \frac{1}{9} E[U_{M_n}^{(n)} U_{LM_n}^{(n)}].$$

It follows,

$$E[\tau_1^{(n)} \tau_3^{(n)}] = E[(U_{M_n}^{(n)})^2] + \frac{2}{9} (U_{KLM_n}^{(n)})^2 + \frac{10}{9} U_{M_n}^{(n)} U_{KLM_n}^{(n)} + \frac{4}{9} U_{LM_n}^{(n)} U_{KLM_n}^{(n)} + \frac{2}{9} U_{M_n}^{(n)} U_{LM_n}^{(n)}].$$

Using the representation for $E[\tau_1^{(n)} \tau_2^{(n)}]$,

$$\begin{aligned} \frac{1}{3} E[(U_{KLM_n}^{(n)})^2] + \frac{2}{3} E[U_{KLM_n}^{(n)} U_{LM_n}^{(n)}] \\ = E\left[H_{M_n}^2 - H_{M_n} \frac{2H_{LM_n} + 4H_{KLM_n} + \bar{H}_{M_n}}{3} + \bar{H}_{M_n} + \frac{2H_{LM_n}H_{KLM_n} + H_{KLM_n}^2 - 2\bar{H}_{LM_n} - \bar{H}_{KLM_n}}{3}\right], \end{aligned}$$

we can write

$$\begin{aligned} E[\tau_1^{(n)} \tau_3^{(n)}] &= H_n^2 - E[2H_n H_{M_n} + \bar{H}_{M_n} - H_{M_n}^2] + \bar{H}_n \\ &\quad + \frac{2}{3} E\left[H_{M_n}^2 - H_{M_n} \frac{2H_{LM_n} + 4H_{KLM_n} + \bar{H}_{M_n}}{3}\right] \\ &\quad + \frac{2}{3} E\left[\frac{2H_{LM_n}H_{KLM_n} + H_{KLM_n}^2 - 2\bar{H}_{LM_n} - \bar{H}_{KLM_n}}{3}\right] \\ &\quad + \frac{5}{9} E[(H_n - H_{M_n})(H_{M_n} - H_{LM_n})] + \frac{10}{9} E[(H_n - H_{M_n})(H_{M_n} - H_{KLM_n})], \end{aligned}$$

which after a rearrangement gives the last statement. \square

Lemma 4.4. We have as $n \rightarrow \infty$

$$\begin{aligned} E[H_{K_n}] &= 2 + O(n^{-1} \log n), \quad E[H_{L_n}] = 3 + O(n^{-1} \log n), \quad E[H_{M_n}] \\ &= \frac{11}{3} + O(n^{-1} \log n), \\ E[H_{KL_n}] &= \frac{3}{2} + O(n^{-1} \log n), \quad E[H_{LM_n}] = \frac{7}{3} + O(n^{-1} \log n), \\ E[H_{KLM_n}] &= \frac{4}{3} + O(n^{-1} \log n). \end{aligned}$$

Proof. The first three stated relations are obtained using Lemma 3.1 and Eq. (9). Equalities

$$\begin{aligned} E[H_{K_n}] &= \frac{n+1}{n-1} \sum_{k=1}^{n-1} \frac{2H_k}{(k+1)(k+2)} = \frac{2(n-H_n)}{n-1}, \\ E[H_{L_n}] &= \frac{(n+1)(n+2)}{(n-1)(n-2)} \sum_{k=2}^{n-1} \frac{6(k-1)H_k}{(k+1)(k+2)(k+3)} \\ &= \frac{6(n+1)(n+2)}{(n-1)(n-2)} \sum_{k=1}^{n-1} \left(\frac{2H_k}{(k+2)(k+3)} - \frac{H_k}{(k+1)(k+2)} \right) \\ &= \frac{3n(n+1) - 6nH_n}{(n-1)(n-2)} \end{aligned}$$

give the first and the second stated relations, and the third one follows from

$$\begin{aligned} E[H_{M_n}] &= \frac{(n+1)(n+2)(n+3)}{(n-1)(n-2)(n-3)} \sum_{k=3}^{n-1} \frac{12(k-1)(k-2)H_k}{(k+1)(k+2)(k+3)(k+4)} \\ &= \frac{12(n+1)(n+2)(n+3)}{(n-1)(n-2)(n-3)} \sum_{k=1}^{n-1} \left(\frac{H_k}{(k+1)(k+2)} - \frac{5H_k}{(k+2)(k+3)} \right. \\ &\quad \left. + \frac{5H_k}{(k+3)(k+4)} \right) \\ &= \frac{\frac{11}{3}n^3 + 30n^2 + \frac{391}{3}n - 20 - 12(n^2 + 1)H_n}{(n-1)(n-2)(n-3)}. \end{aligned}$$

The second three stated relations are obtained similarly using

Lemma 3.2 and Eq. (9). Indeed,

$$\begin{aligned} E[H_{KL_n}] &= \frac{(n+1)(n+2)}{(n-1)(n-2)} \sum_{k=1}^{n-1} \frac{12H_k}{(k+1)(k+2)(k+3)} - \frac{n+1}{(n-1)(n-2)} \sum_{k=1}^{n-1} \frac{12H_k}{(k+1)(k+2)} \\ &= \frac{6(n+1)(n+2)}{(n-1)(n-2)} \left(\sum_{k=1}^{n-1} \frac{H_k}{(k+1)(k+2)} - \sum_{k=1}^{n-1} \frac{H_k}{(k+2)(k+3)} \right) - \frac{12(n-H_n)}{(n-1)(n-2)} \\ &= \frac{6n(n-H_n)}{(n-1)(n-2)} - \frac{6(3n^2 + 5n - 4(n+1)H_n)}{4(n-1)(n-2)} = \frac{6H_n}{(n-1)(n-2)} + \frac{3n(n-5)}{2(n-1)(n-2)}, \end{aligned}$$

implying $E[H_{KL_n}] = \frac{3}{2} + O(n^{-1} \log n)$. Furthermore,

$$E[H_{LM_n}] = \sum_{k=2}^{\infty} \frac{72(k-1)H_k}{(k+1)(k+2)(k+3)(k+4)} + O(n^{-1} \log n) = \frac{7}{3} + O(n^{-1} \log n),$$

$$E[H_{KLM_n}] = \sum_{k=1}^{\infty} \frac{72H_k}{(k+1)(k+2)(k+3)(k+4)} + O(n^{-1} \log n) = \frac{4}{3} + O(n^{-1} \log n). \quad \square$$

Lemma 4.5. Let $a_n \Rightarrow a$ stand for $a_n = a + O(n^{-1} \log^2 n)$ as $n \rightarrow \infty$. Then

$$\begin{aligned} E[H_{K_n}^2] &\Rightarrow \frac{\pi^2}{3} + 2, \quad E[H_{L_n}^2] \Rightarrow \frac{21}{2}, \quad E[H_{M_n}^2] \Rightarrow \frac{\pi^2}{3} + \frac{211}{18}, \\ E[\bar{H}_{K_n}] &\Rightarrow \frac{\pi^2}{3} - 2, \quad E[\bar{H}_{L_n}] \Rightarrow \frac{3}{2}, \quad E[\bar{H}_{M_n}] \Rightarrow \frac{\pi^2}{3} - \frac{31}{18}, \end{aligned}$$

and

$$\begin{aligned} E[H_{KL_n}^2] &\Rightarrow \frac{\pi^2}{2} - \frac{9}{4}, \quad E[H_{LM_n}^2] \Rightarrow \frac{167}{18} - \frac{\pi^2}{3}, \quad E[H_{KLM_n}^2] \Rightarrow \frac{2\pi^2}{3} - \frac{41}{9}, \\ E[\bar{H}_{KL_n}] &\Rightarrow \frac{\pi^2}{2} - \frac{15}{4}, \quad E[\bar{H}_{LM_n}] \Rightarrow \frac{85}{18} - \frac{\pi^2}{3}, \quad E[\bar{H}_{KLM_n}] \Rightarrow \frac{2\pi^2}{3} - \frac{49}{9}, \end{aligned}$$

and

$$\begin{aligned} E[H_{L_n}H_{K_n}] &\Rightarrow \frac{39}{4} - \frac{\pi^2}{2}, \quad E[H_{M_n}H_{LM_n}] \Rightarrow \frac{221}{18} - \frac{\pi^2}{3}, \\ E[H_{M_n}H_{KLM_n}] &\Rightarrow \frac{2\pi^2}{3} - \frac{14}{9}, \quad E[H_{LM_n}H_{KLM_n}] \Rightarrow \frac{148}{9} - \frac{4\pi^2}{3}. \end{aligned}$$

Proof. The stated relations are obtained using Lemmas 3.1, 3.2, and Eq. (9). Firstly,

$$\begin{aligned} E[H_{K_n}^2] &= \frac{n+1}{n-1} \sum_{k=1}^{n-1} \frac{2H_k^2}{(k+1)(k+2)} = \frac{2(n+1)}{n-1} \left(\bar{H}_n + \frac{n-H_n^2-2H_n}{n+1} \right) \\ &= \frac{2(\bar{H}_n(n+1) + n-H_n^2-2H_n)}{n-1} \Rightarrow \frac{\pi^2}{3} + 2. \end{aligned}$$

Similarly, we have

$$\begin{aligned} E[\bar{H}_{K_n}] &= \frac{n+1}{n-1} \sum_{k=1}^{n-1} \frac{2\bar{H}_k}{(k+1)(k+2)} = \frac{2(n+1)}{n-1} \\ &\quad \cdot \frac{n\bar{H}_n - n}{n+1} = \frac{2n\bar{H}_n - 2n}{n-1} \Rightarrow \frac{\pi^2}{3} - 2. \end{aligned}$$

Observe that the limit is $\sum_{k=1}^{\infty} 2\bar{H}_k / ((k+1)(k+2))$. In the same manner we obtain

$$\begin{aligned} E[H_{KL_n}^2] &\Rightarrow \sum_{k=1}^{\infty} \frac{12H_k^2}{(k+1)(k+2)(k+3)} = \sum_{k=1}^{\infty} \frac{6H_k^2}{(k+1)(k+2)} \\ &\quad - \sum_{k=1}^{\infty} \frac{6H_k^2}{(k+2)(k+3)} = \frac{\pi^2}{2} - \frac{9}{4}, \\ E[\bar{H}_{KL_n}] &\Rightarrow \sum_{k=1}^{\infty} \frac{12\bar{H}_k}{(k+1)(k+2)(k+3)} = \sum_{k=1}^{\infty} \frac{6\bar{H}_k}{(k+1)(k+2)} \\ &\quad - \sum_{k=1}^{\infty} \frac{6\bar{H}_k}{(k+2)(k+3)} = \frac{\pi^2}{2} - \frac{15}{4}. \end{aligned}$$

Using partial fraction decomposition we find

$$E[H_{M_n}^2] \Rightarrow \sum_{k=3}^{\infty} \frac{12(k-1)(k-2)H_k^2}{(k+1)(k+2)(k+3)(k+4)} = \frac{\pi^2}{3} + \frac{211}{18},$$

$$E[\bar{H}_{M_n}] \Rightarrow \sum_{k=3}^{\infty} \frac{12(k-1)(k-2)\bar{H}_k}{(k+1)(k+2)(k+3)(k+4)} = \frac{\pi^2}{3} - \frac{31}{18}.$$

Again using partial fraction decomposition we find

$$E[H_{LM_n}^2] \Rightarrow \sum_{k=1}^{\infty} \frac{72(k-1)H_k^2}{(k+1)(k+2)(k+3)(k+4)} = \frac{167}{18} - \frac{\pi^2}{3},$$

$$E[\bar{H}_{LM_n}] \Rightarrow \sum_{k=1}^{\infty} \frac{72(k-1)\bar{H}_k}{(k+1)(k+2)(k+3)(k+4)} = \frac{85}{18} - \frac{\pi^2}{3}$$

and

$$E[H_{KLM_n}^2] \Rightarrow \sum_{k=1}^{\infty} \frac{72H_k^2}{(k+1)(k+2)(k+3)(k+4)} = \frac{2\pi^2}{3} - \frac{41}{9},$$

$$E[\bar{H}_{KLM_n}] \Rightarrow \sum_{k=1}^{\infty} \frac{72\bar{H}_k}{(k+1)(k+2)(k+3)(k+4)} = \frac{2\pi^2}{3} - \frac{49}{9}.$$

Since $E[H_{K_n}] = 2(n - H_n)/(n - 1)$, we have

$$\begin{aligned} E[H_{L_n}H_{K_{L_n}}] &\Rightarrow \sum_{m=2}^{\infty} \frac{6(m-1)H_m}{(m+1)(m+2)(m+3)} \frac{2(m-H_m)}{m-1} \\ &= \sum_{m=1}^{\infty} \frac{12mH_m}{(m+1)(m+2)(m+3)} - \sum_{m=1}^{\infty} \frac{12H_m^2}{(m+1)(m+2)(m+3)} \\ &= \frac{15}{2} - \left(\frac{\pi^2}{2} - \frac{9}{4}\right) = \frac{39}{4} - \frac{\pi^2}{2}, \end{aligned}$$

where we use the following corollary of Eq. (9)

$$\begin{aligned} \sum_{m=1}^{\infty} \frac{2mH_m}{(m+1)(m+2)(m+3)} &= \sum_{m=1}^{\infty} \frac{3H_m}{(m+2)(m+3)} \\ &\quad - \sum_{m=1}^{\infty} \frac{H_m}{(m+1)(m+2)} = \frac{5}{4}. \end{aligned}$$

Similarly,

$$\begin{aligned} E[H_{LM_n}H_{KLM_n}] &\Rightarrow \sum_{m=2}^{\infty} \frac{72(m-1)H_m}{(m+1)(m+2)(m+3)(m+4)} \frac{2(m-H_m)}{m-1} \\ &= \sum_{m=1}^{\infty} \frac{144mH_m}{(m+1)(m+2)(m+3)(m+4)} \\ &\quad - \sum_{m=1}^{\infty} \frac{144H_m^2}{(m+1)(m+2)(m+3)(m+4)}, \end{aligned}$$

where

$$\begin{aligned} \sum_{k=1}^{\infty} \frac{144kH_k}{(k+1)(k+2)(k+3)(k+4)} &= 24(-1 + 15/4 - 22/9) = \frac{22}{3}, \\ \sum_{k=1}^{\infty} \frac{144H_k^2}{(k+1)(k+2)(k+3)(k+4)} &= \frac{4\pi^2}{3} - \frac{82}{9}, \end{aligned}$$

so that $E[H_{LM_n}H_{KLM_n}] \Rightarrow \frac{148}{9} - (4\pi^2/3)$.

Further, in view of $E[H_{L_n}] = (3n(n+1) - 6nH_n)/(n-1)(n-2)$, the limit for $E[H_{M_n}H_{LM_n}]$ can be computed as

$$\begin{aligned} E[H_{M_n}H_{LM_n}] &\Rightarrow \sum_{m=1}^{\infty} \frac{12(m-1)(m-2)H_m}{(m+1)(m+2)(m+3)(m+4)} \frac{3m(m+1) - 6mH_m}{(m-1)(m-2)} \\ &= \sum_{m=1}^{\infty} \frac{36mH_m}{(m+2)(m+3)(m+4)} \\ &\quad - \sum_{m=1}^{\infty} \frac{72mH_m^2}{(m+1)(m+2)(m+3)(m+4)}, \end{aligned}$$

where

$$\begin{aligned} \sum_{m=1}^{\infty} \frac{6mH_m^2}{(m+1)(m+2)(m+3)(m+4)} &= \frac{\pi^2}{36} + \frac{85}{216}, \\ \sum_{m=1}^{\infty} \frac{mH_m}{(m+2)(m+3)(m+4)} &= \sum_{m=1}^{\infty} \frac{2H_m}{(m+3)(m+4)} \end{aligned}$$

$$- \sum_{m=1}^{\infty} \frac{H_m}{(m+2)(m+3)} = \frac{17}{36},$$

yielding $E[H_{M_n}H_{LM_n}] \Rightarrow \frac{221}{18} - (\pi^2/3)$. Finally, from

$$E[H_{K_{L_m}}] = \frac{6H_m}{(m-1)(m-2)} + \frac{3m(m-5)}{2(m-1)(m-2)}$$

we get

$$\begin{aligned} E[H_{M_n}H_{KLM_n}] &\Rightarrow \sum_{m=1}^{\infty} \frac{12(m-1)(m-2)H_m}{(m+1)(m+2)(m+3)(m+4)} \left(\frac{6H_m}{(m-1)(m-2)} + \frac{3m(m-5)}{2(m-1)(m-2)} \right) \\ &= \sum_{m=1}^{\infty} \frac{72H_m^2}{(m+1)(m+2)(m+3)(m+4)} \\ &\quad + \sum_{m=1}^{\infty} \frac{18m(m-5)H_m}{(m+1)(m+2)(m+3)(m+4)}, \end{aligned}$$

where

$$\sum_{m=1}^{\infty} \frac{72H_m^2}{(m+1)(m+2)(m+3)(m+4)} = \frac{2\pi^2}{3} - \frac{41}{9},$$

$$\sum_{m=1}^{\infty} \frac{m(m-5)H_m}{(m+1)(m+2)(m+3)(m+4)} = \frac{1}{6},$$

so that $E[H_{M_n}H_{KLM_n}] \Rightarrow (2\pi^2/3) - \frac{14}{9}$. \square

Proof of Proposition 4.1. With Lemmas 4.3–4.5 at hand, the proof of Proposition 4.1 is straightforward. The first statement

$$\text{Var}[\tau_1^{(n)}] = E[(\tau_1^{(n)})^2] - (E[\tau_1^{(n)}])^2 = \bar{H}_n + E[H_{K_n}^2 - \bar{H}_{K_n}] - (E[H_{K_n}])^2 \Rightarrow \frac{\pi^2}{6}$$

is obtained applying the classical relation $\bar{H}_n = (\pi^2/6) + O(n^{-1})$. Further, Lemma 4.3 yields

$$\begin{aligned} \text{Cov}[\tau_1^{(n)}, \tau_2^{(n)}] &= E[\tau_1^{(n)}\tau_2^{(n)}] - (E[\tau_1^{(n)}])^2 = H_n E\left[2H_{K_n} - \frac{2H_{L_n} + 4H_{K_{L_n}}}{3}\right] \\ &\quad + \bar{H}_n + \frac{1}{3}E\left[2H_{L_n}H_{K_{L_n}} + H_{K_{L_n}}^2 - 2\bar{H}_{L_n} - \bar{H}_{K_{L_n}}\right] - (E[H_{K_n}])^2, \end{aligned}$$

where according to Lemma 4.4

$$E\left[2H_{K_n} - \frac{2H_{L_n} + 4H_{K_{L_n}}}{3}\right] = O(n^{-1} \log n).$$

Thus, applying Lemma 4.5 we obtain the second statement

$$\begin{aligned} \text{Cov}[\tau_1^{(n)}, \tau_2^{(n)}] &\Rightarrow \frac{\pi^2}{6} + \frac{1}{3} \left(+2 \left(\frac{39}{4} - \frac{\pi^2}{2} \right) + \frac{\pi^2}{2} - \frac{9}{4} - 2 \cdot \frac{3}{2} - \frac{\pi^2}{2} + \frac{15}{4} \right) \\ &\quad - 4 = 2 - \frac{\pi^2}{6}. \end{aligned}$$

Finally, the third statement follows from

$$\begin{aligned} \text{Cov}[\tau_1^{(n)}, \tau_3^{(n)}] &= H_n E\left[2H_{K_n} - \frac{3H_{M_n} + 5H_{LM_n} + 10H_{KLM_n}}{9}\right] + \bar{H}_n \\ &\quad - (E[H_{K_n}])^2 - \frac{1}{3}E[\bar{H}_{M_n}] + \frac{1}{9}E[H_{M_n}H_{LM_n} + 2H_{M_n}H_{KLM_n} \\ &\quad + 4H_{LM_n}H_{KLM_n} + 2H_{KLM_n}^2 - 4\bar{H}_{LM_n} - 2\bar{H}_{KLM_n}]. \end{aligned}$$

Indeed, according to Lemma 4.4

$$E\left[2H_{K_n} - \frac{3H_{M_n} + 5H_{LM_n} + 10H_{KLM_n}}{9}\right] = O(n^{-1} \log n).$$

Moreover, from the following three limits

$$\bar{H}_n - (E[H_{K_n}])^2 - \frac{1}{3}E[\bar{H}_{M_n}] \Rightarrow \frac{\pi^2}{18} - \frac{185}{54},$$

$$E[H_{M_n}H_{LM_n} + 2H_{M_n}H_{KLM_n} + 4H_{LM_n}H_{KLM_n}] \Rightarrow \frac{1349}{18} - \frac{13\pi^2}{3},$$

$$E[H_{KLM_n}^2 - 2\bar{H}_{LM_n} - \bar{H}_{KLM_n}] \Rightarrow \frac{2\pi^2}{3} - \frac{77}{9},$$

we get the stated overall limit

$$\frac{\pi^2}{18} - \frac{185}{54} + \frac{1}{9} \left(\frac{1349}{18} - \frac{13\pi^2}{3} \right) + \frac{2}{9} \left(\frac{2\pi^2}{3} - \frac{77}{9} \right) = 3 - \frac{5\pi^2}{18}. \quad \square$$

Acknowledgements

The research of Serik Sagitov was supported by the Swedish Research Council Grant 621-2010-5623. Krzysztof Bartoszek was supported by the Centre for Theoretical Biology at the University of Gothenburg, Svenska Institutets Östersjösamarbete Scholarship nr. 11142/2013, Stiftelsen för Vetenskaplig Forskning och Utbildning i Matematik (Foundation for Scientific Research and Education in Mathematics), Knut and Alice Wallenbergs travel fund, Paul and Marie Berghaus fund, the Royal Swedish Academy of Sciences, and Wilhelm and Martina Lundgrens research fund.

We thank the reviewer whose suggestions helped us to improve the presentation of our proofs.

References

- Adamchik, V., 1997. On Stirling numbers and Euler sums. *J. Comput. Appl. Math.* 79 (1), 119–130.
- Aldous, D., Popovic, L., 2005. A critical branching process model for biodiversity. *Adv. Appl. Probab.* 37 (4), 1094–1115.
- Ané, C., 2008. Analysis of comparative data with hierarchical autocorrelation. *Ann. Appl. Stat.* 2 (3), 1078–1102.
- Ané, C., Ho, L.S.T., Roch, S., 2014. Phase transition on the convergence rate of parameter estimation under an Ornstein–Uhlenbeck diffusion on a tree. *ArXiv e-prints*.
- Bartoszek, K., 2014. Quantifying the effects of anagenetic and cladogenetic evolution. *Math. Biosci.* 254, 42–57.
- Bartoszek, K., Sagitov, S., 2015. Phylogenetic confidence intervals for the optimal trait value. *J. Appl. Probab.* 52 (4).
- Bartoszek, K., Pienaar, J., Mostad, P., Andersson, S., Hansen, T.F., 2012. A phylogenetic comparative method for studying multivariate adaptation. *J. Theor. Biol.* 314, 204–215.
- Bohrnstedt, G.W., Goldberger, A.S., 1969. On the exact covariance of products of random variables. *J. Am. Stat. Assoc.* 64, 1439–1442.
- Butler, M.A., King, A.A., 2004. Phylogenetic comparative analysis: a modelling approach for adaptive evolution. *Am. Nat.* 164 (6), 683–695.
- Crawford, F.W., Suchard, M.A., 2013. Diversity, disparity, and evolutionary rate estimation for unresolved Yule trees. *Syst. Biol.* 62 (3), 439–455.
- Edwards, A.W.F., 1970. Estimation of the branch points of a branching diffusion process. *J. R. Stat. Soc. B* 32 (2), 155–174.
- Feller, W., 1971. *An Introduction to Probability Theory and Its Applications*, vol. II. John Wiley & Sons, New York.
- Felsenstein, J., 1985. Phylogenies and the comparative method. *Am. Nat.* 125 (1), 1–15.
- Felsenstein, J., 1988. Phylogenies and quantitative characters. *Annu. Rev. Ecol. Syst.* 19, 445–471.
- Gascuel, O., Steel, M., 2014. Predicting the ancestral character changes in a tree is typically easier than predicting the root state. *Syst. Biol.* 63 (3), 421–435.
- Gernhard, T., 2008. The conditioned reconstructed process. *J. Theor. Biol.* 253, 769–778.
- Hansen, T.F., 1997. Stabilizing selection and the comparative analysis of adaptation. *Evolution* 51 (5), 1341–1351.
- Hansen, T.F., Bartoszek, K., 2012. Interpreting the evolutionary regression: the interplay between observational and biological errors in phylogenetic comparative studies. *Syst. Biol.* 61 (3), 413–425.
- Hansen, T.F., Pienaar, J., Orzack, S.H., 2008. A comparative method for studying adaptation to a randomly evolving environment. *Evolution* 62, 1965–1977.
- Helgen, K.M., Miguel Pinto, C., Keys, R., Helgen, L.E., Tsuchiya, M.T.N., Quinn, A., Wilson, D.E., Maldonado, J.E., 2013. Taxonomic revision of the olingos (*Bassaricyon*), with description of a new species, the Olinguito. *ZooKeys* 324, 1–83.
- Ho, L.S.T., Ané, C., 2013. Asymptotic theory with hierarchical autocorrelation: Ornstein–Uhlenbeck tree models. *Ann. Stat.* 41 (2), 957–981.
- Ho, L.S.T., Ané, C., 2014a. A linear-time algorithm for Gaussian and non-Gaussian trait evolution models. *Syst. Biol.* 63 (3), 397–408.
- Ho, L.S.T., Ané, C., 2014b. Intrinsic inference difficulties for trait evolution with Ornstein–Uhlenbeck models. *Methods Ecol. Evol.* 5, 1133–1146.
- Jones, K.E., Bielby, J., Cardillo, M., Fritz, S.A., O'Dell, J., Orme, C., David L., Safi, K., Sechrest, W., Boakes, E.H., Carbone, C., Connolly, C., Cuttis, M.J., Foster, J.K., Grenyer, R., Habib, M., Plaster, C.A., Price, S.A., Rigby, E.A., Rist, J., Teacher, A., Binnida-Emonds, O.R.P., Gittleman, J.L., Mace, G.M., Purvis, A., 2009. PanTHERIA: a species-level database of life history, ecology, and geography of extant and recently extinct mammals. *Ecology* 90 (9), 2648.
- Moors, A., Gascuel, O., Stadler, T., Li, H., Steel, M., 2012. Branch lengths on birth–death trees and the expected loss of phylogenetic diversity. *Syst. Biol.* 61 (2), 195–203.
- Mossel, E., Steel, M., 2014. Majority rule has a transition ratio 4 on Yule trees under a 2-state symmetric model. *J. Theor. Biol.* 360, 315–318.
- Mulder, W.H., Crawford, F.W., 2015. On the distribution of interspecies correlation for Markov models of character evolution on Yule trees. *J. Theor. Biol.* 364, 275–283.
- Piwczynski, M., Szpila, K., Grzywacz, A., Pape, T., 2014. A large-scale molecular phylogeny of flesh flies (Diptera: Sarcophagidae). *Syst. Entomol.* 38, 783–799.
- R Core Team, 2013. *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria. URL <http://www.R-project.org>.
- Sagitov, S., Bartoszek, K., 2012. Interspecies correlation for neutrally evolving traits. *J. Theor. Biol.* 309, 11–19.
- Sofo, A., 2011. Harmonic number sums in higher powers. *J. Math. Anal.* 2 (2), 15–22.
- Sofo, A., 2012. New classes of harmonic number identities. *J. Int. Seq.* 15 (Art. 12.7.4).
- Sofo, A., 2013. Finite number sums in higher order powers harmonic numbers. *Bull. Math. Anal. Appl.* 5 (1), 71–79.
- Stadler, T., 2009. On incomplete sampling under birth–death models and connections to the sampling-based coalescent. *J. Theor. Biol.* 261 (1), 58–68.
- Stadler, T., 2011. Simulating trees with a fixed number of extant species. *Syst. Biol.* 60 (5), 676–684.
- Stadler, T., Steel, M., 2012. Distribution of branch lengths and phylogenetic diversity under homogeneous speciation models. *J. Theor. Biol.* 297, 33–40.
- Steel, M., McKenzie, A., 2001. Properties of phylogenetic trees generated by Yule-type speciation models. *Math. Biosci.* 170, 91–112.
- Yule, G.U., 1924. A mathematical theory of evolution: based on the conclusions of Dr. J.C. Willis. *Philos. Trans. R. Soc. B* 213, 21–87.