

Invasion fitness for gene-culture co-evolution in the family and an application to cumulative culture under vertical transmission

Charles Mullon*, Laurent Lehmann †

Keywords: gene-culture co-evolution, individual learning, social evolution, eco-evolutionary feedback, kin selection, adaptive dynamics, invasion analysis.

Abstract

Human evolution depends on gene-culture co-evolution: genetically determined behavior rules co-evolve with socially learned information. Social transmission of information can occur vertically from parent to child, horizontally from peer to peer, or obliquely from unrelated individuals of different generations. Models for the emergence of cumulative culture have in their majority studied gene-culture co-evolution under random interactions between individuals, which rules out vertical transmission. Yet, vertical transmission is thought to be a primary form of transmission in nature. In order to study gene-culture co-evolution within the family, we derive here the invasion fitness of a mutant allele that influence a deterministic environmental state variable (e.g., amount of knowledge or skill, stock of culture, or any other non-innate environmental feature) to which diploid carriers of the mutant are exposed in subsequent generations. Under the assumption that this environment has a single attractor point, we show that singular strategies and the concomitant environmental state they generate can be evaluated analytically, thereby making gene-culture co-evolution in the family with multigenerational effects mathematically tractable. We then apply our results to model the co-evolution between individual and social learning rules on one hand, and the amount of adaptive information these rules generate on the other. We find that vertical transmission generally favours the accumulation of adaptive information due to kin selection effects, but that when adaptive information is learned as efficiently between family members as between unrelated individuals, this effect is moderate in diploids. We also show that vertical transmission prevents evolutionary branching and therefore can have a qualitative impact on gene-culture co-evolutionary dynamics. More generally, our model is of relevance to study scenarios of niche construction and gene-culture co-evolution within the family, where modifications of the environment by individuals have long-lasting effects on genetic lines of descent.

*Department of Ecology and Evolution, University of Lausanne, Switzerland.

†Department of Ecology and Evolution, University of Lausanne, Switzerland. Corresponding author: Laurent.Lehmann@unil.ch.

Introduction

Cultural evolution, which describes the changes in non-genetically transmitted phenotypes (or information) carried by individuals in a population, is thought to have played a major role in human's ecological success (e.g., Laland et al., 2010; Boyd et al., 2011; van Schaik, 2016). Cultural evolution rests on mechanisms by which individuals learn and communicate, which themselves depend on behavior or cognitive rules that are at least partially genetically determined. Conversely, cultural evolution can significantly affect reproduction and survival, which in turn affects selection on genes determining behavior. Human evolution is therefore influenced by so-called gene-culture co-evolution, whereby genetically determined behaviour rules co-evolve along culturally transmitted information (Feldman and Cavalli-Sforza, 1976; Lumsden and Wilson, 1981; Aoki, 1986; Boyd and Richerson, 1985; Feldman and Laland, 1996; van Schaik, 2016).

It is useful to distinguish between two broad cognitive mechanisms that underly cultural evolution. First, cultural evolution depends on individual learning (IL), which is a generic term for the cognitive processes that lead to the creation of *de novo* non-innate information by an individual and include trial-and-error learning, statistical inference, or insight (Boyd and Richerson, 1985; Rogers, 1988; Dugatkin, 2004; Aoki and Feldman, 2014; Wakano and Miura, 2014). Second, cultural evolution is underlain by social learning (SL), which refers to the cognitive processes that lead to the acquisition of non-innate information from others (Cavalli-Sforza and Feldman, 1981; Boyd and Richerson, 1985; Rogers, 1988; Dugatkin, 2004; Aoki and Feldman, 2014; Wakano and Miura, 2014). If genes are almost always transmitted vertically from parent to offspring, cultural information can be acquired and transmitted in multiple ways via SL. It can be transmitted vertically from parent to offspring, but also horizontally from peer-to-peer, or obliquely between unrelated individuals belonging to different generations (Cavalli-Sforza and Feldman, 1981).

While IL results in the generation of novel information, SL enables the acquisition of skills or information that an individual would be unable to acquire alone by IL over the course of its lifetime. SL thus enables cumulative culture, which is a hallmark of cultural evolution in human populations (e.g., Boyd et al., 2011; van Schaik, 2016). A necessary but not sufficient condition for cumulative culture to occur in a population is that individuals use a composite learning strategy in which SL precedes IL (Boyd and Richerson, 1985; Enquist et al., 2007; Aoki et al., 2012).

Since both IL and SL strategies determine cultural evolution, much theoretical population work on gene-culture co-evolution has been devoted to understand the co-evolution between genetically determined IL and SL learning rules on one hand, and the amount of cultural information these rules generate in evolutionary stable population states on the other. This has led to a rich literature investigating and disentangling the role of various factors, such as the type of cultural information, the regime of environmental change, or the structure of the population for the evolution of IL and SL and their impact on cumulative culture (e.g., Boyd and Richerson,

1985; Feldman et al., 1996; Wakano et al., 2004; Wakano and Aoki, 2006; Enquist et al., 2007; Rendell et al., 2010; Nakahashi, 2010; Aoki et al., 2012; Lehmann et al., 2013; Nakahashi, 2013; Aoki and Feldman, 2014; Wakano and Miura, 2014; Kobayashi et al., 2015).

The vast majority of such theoretical work on gene-culture co-evolution has focused on horizontal and oblique transmission, assuming that information is transmitted independently from genotype via SL (i.e., between randomly sampled individuals in the population, from the same generation for horizontal transmission and different generations for oblique transmission). In this case, the fate of a mutant strategy, here genetically determined IL and SL learning rules, that arises as a single copy in a resident population can be studied under the assumption that the mutant is confronted to a cultural environment determined only by the resident. In other words, SL among mutants is so rare that it can be neglected (no mutant-mutant interactions), which greatly simplifies mathematical analysis (see Metz, 2011 for general consideration on evolutionary invasion analysis and Aoki et al., 2012 for applications to cultural evolution).

By contrast, when information is transmitted vertically via SL, non-random interactions occur between individuals as transmission occurs in a way that is correlated to genotype. As a result, transmission of cultural information among mutants is no longer rare and influences the fate of a mutant strategy. In other words, kin selection occurs, i.e., natural selection when individuals interact with others that are more likely to share a recent common ancestor than individuals sampled randomly from the population (Hamilton, 1964; Michod, 1982; Frank, 1998; Rousset, 2004; van Baalen, 2013). Intuitively, kin selection will favor learning rules that promote the transmission of adaptive information across generations since related individuals preferentially benefit from this information. This should influence cultural information transmission from parent to offspring and hence the selection pressure on IL and SL.

Despite the potential importance of vertical transmission and its prominent role in cultural evolution theory (e.g., Cavalli-Sforza and Feldman, 1981; Feldman and Zhiotovskiy, 1992; McElreath and Strimling, 2008), few studies have investigated the evolution of IL and SL and its effect on cumulative culture under vertical transmission (see Kobayashi et al., 2015 for a notable exception). In fact, there exists no framework to systematically carry out an evolutionary invasion analysis for gene-culture co-evolution under vertical transmission with multigenerational effects. Since a primary form of transmission of information in humans is vertical (Cavalli-Sforza and Feldman, 1981; Guglielmino et al., 1995; Hewlett et al., 2011; Konner, 2010), such a framework would be useful to understand cultural evolution. In particular, it would allow determining how the level of culture generated by evolving IL and SL departs under vertical transmission from oblique and horizontal transmission.

The aim of this paper is therefore two-fold: (1) develop a mathematical model to perform evolutionary invasion analysis for gene-culture co-evolution in a diploid family-structured populations; and (2) study the effects of vertical transmission on the evolution of IL and SL levels and the concomitant level of adaptive information they generate. In the first part of this paper, we derive an expression for invasion fitness of genes in a diploid, family-structured populations,

when each individual carry a general state variable that could represent a stock of knowledge, skill, or any other form of biotic or abiotic capital. The state variable depends deterministically on state variables in the parental generation, and therefore on transmission modes, but also on genes. In turn, state variables influence the reproductive success of individuals, resulting in co-evolutionary feedbacks between genes and state variables. Second, we apply our framework to the evolution of IL and SL levels and concomitant level of adaptive information they generate to study quantitative and qualitative effects of vertical transmission on cumulative culture.

1 Gene-culture co-evolution in the family

1.1 Life-cycle

We consider a diploid monoecious population of large and constant size (large enough to neglect random genetic drift) that is structured into families, each founded by a mated individual. The discrete time life cycle in this population is as follows. (1) Each individual produces offspring and then either survives or dies independently of age so that there is no explicit age-structure. (2) Random mating among juveniles occurs and then each juvenile either survives or dies (possibly according to density-dependent competition) to make it to the next generation of adults.

Each individual is characterized by a state variable \mathcal{E} which is possibly multidimensional and which can represent the total amount of knowledge or skill held by that individual at the stage of reproduction. This state variable can also represent a stock of a biotic or abiotic resource or the size of an artefact (e.g., nest, burrow). We therefore refer to \mathcal{E} as the “environment” of an individual. The environmental state variable \mathcal{E} is influenced by the genetic composition of the population and affects the survival of adults or juveniles, and/or individual fecundity.

1.2 Evolutionary invasion analysis

We assume that only two alleles can segregate in the population, a mutant with type τ and a resident with type θ , which are taken from the set Θ of all possible types. In order to determine the fate—establishment or extinction—of the mutant τ when it arises as a single copy in the population (e.g., Fisher, 1930; Hamilton, 1967; Maynard Smith, 1982; Eshel and Feldman, 1984; Charlesworth, 1994; Metz et al., 1996; Ferrière and Gatto, 1995; Metz, 2011; van Baalen, 2013), we seek an expression for invasion fitness $W(\tau, \theta)$, which is here taken to be the *geometric growth rate* of the mutant τ introduced into the θ population (Cohen, 1979; Tuljapurkar, 1989; Caswell, 2000; Tuljapurkar et al., 2003). Invasion fitness $W(\tau, \theta)$ is the per capita number of mutant copies produced asymptotically over a time step of the reproductive process by the whole mutant lineage descending from the initial mutant (as long as the mutant remains rare), and if $W(\tau, \theta)$ is equal to or less than one the mutant lineage goes extinct with certainty (Lehmann et al., 2016). Therefore

an uninvadable strategy θ ; namely, a strategy resisting invasion by any type satisfies

$$\theta \in \arg \max_{\tau \in \Theta} W(\tau, \theta), \quad (1)$$

i.e., θ maximizes invasion fitness for a resident population at the uninvadable state.

In order to understand gene-culture co-evolution, we aim to derive an expression for invasion fitness $W(\tau, \theta)$ that incorporates how gene (embodied by the segregating alleles) and culture (embodied by the environmental state variable \mathcal{E}) affect the reproductive success of individuals, and how \mathcal{E} depends on alleles in the population. In this task, we first note that we can neglect homozygote mutants since they are rare during invasion and only need to consider mutant individuals that are heterozygotes. Then, we denote by $w(\tau, \theta, \mathcal{E}_t(\tau, \theta))$ the expected number of successful offspring produced by a heterozygote mutant adult individual over one life cycle iteration at demographic time $t = 0, 1, 2, \dots$, since the appearance of the mutant at $t = 0$. This fitness is thus an expression for *individual fitness* as defined in population genetics and social evolution (e.g., Nagylaki, 1992; Frank, 1998; Rousset, 2004). Individual fitness $w(\tau, \theta, \mathcal{E}_t(\tau, \theta))$ depends on both the mutant τ and resident θ types since (i) heterozygotes carry both alleles and (ii) fitness depends on the behavior of individuals in the population at large, who are homozygotes for the resident. Individual fitness $w(\tau, \theta, \mathcal{E}_t(\tau, \theta))$ also depends on the environmental variable $\mathcal{E}_t(\tau, \theta)$ of an individual carrying the mutant at demographic time t , which itself depends on τ and θ .

Since individuals carrying the mutant are all heterozygotes during invasion, there are no fluctuations of allele frequencies within mutant individuals (no stochastic fluctuations between heterozygote and homozygote states owing to segregation). Hence, a heterozygote parent can at most have a heterozygote offspring for the mutant allele, and assuming no exogenous stochastic effects on \mathcal{E} , we can let the sequence of environments $\{\mathcal{E}_t(\tau, \theta)\}_{t=0}^{\infty}$ of a lineage of heterozygote mutants follows a discrete deterministic dynamic:

$$\mathcal{E}_t(\tau, \theta) = F(\tau, \theta, \mathcal{E}_{t-1}(\tau, \theta), \mathcal{E}(\theta, \theta)). \quad (2)$$

Here, F is the environmental map, which transforms the environment $\mathcal{E}_{t-1}(\tau, \theta)$ of a mutant lineage member at time $t - 1$ into a new environment experienced by a lineage member at time t . In addition of depending on $\mathcal{E}_{t-1}(\tau, \theta)$, the environmental map depends on the behavior of a mutant (first argument in F , τ), possibly also on individuals from the resident population (second argument in F , θ) and the equilibrium environment in the resident population (fourth argument in F , $\mathcal{E}(\theta, \theta)$) which satisfies

$$\mathcal{E}(\theta, \theta) = F(\theta, \theta, \mathcal{E}(\theta, \theta), \mathcal{E}(\theta, \theta)), \quad (3)$$

the steady-state version of eq. (2) with $\tau = \theta$.

We assume that the sequence of environments $\{\mathcal{E}_t(\tau, \theta)\}_{t=0}^{\infty}$ converges to a unique fixed point

$\mathcal{E}(\tau, \theta) = \lim_{t \rightarrow \infty} \mathcal{E}_t(\tau, \theta)$, satisfying

$$\mathcal{E}(\tau, \theta) = F(\tau, \theta, \mathcal{E}(\tau, \theta), \mathcal{E}(\theta, \theta)). \quad (4)$$

This is the key simplifying assumption in our analysis and it follows from it (see Appendix A) that invasion fitness is equal to

$$W(\tau, \theta) = w(\tau, \theta, \mathcal{E}(\tau, \theta)), \quad (5)$$

i.e., the individual fitness of a mutant evaluated at the environmental equilibrium of the mutant lineage environmental dynamics (eq. 4).

Invasion fitness $W(\tau, \theta)$ as given by eq. (5) shows that it depends on the equilibrium state of the environment, which is itself a function of the mutant strategy. Hence, even though the mutant is globally rare, individuals carrying the mutant allele affect the environments to which other mutant carriers are exposed in subsequent generations, which result in carry-over effects across generations and influence selection on the mutant.

1.3 Selection gradient and local uninvadability

In order to better understand how carry-over effects across generation influence selection, we assume that the phenotype of an individual consists of a vector of n quantitative traits ($\Theta = \mathbb{R}^n$) and that genes have additive effects on phenotype. We let the vector $\theta = (\theta_1, \theta_2, \dots, \theta_n) \in \mathbb{R}^n$ represent the phenotype of a resident individual (homozygote for the resident allele), $\tau = (\tau_1, \tau_2, \dots, \tau_n) \in \mathbb{R}^n$ the phenotype of a heterozygote individual, and $z = (z_1, z_2, \dots, z_n) \in \mathbb{R}^n$ the phenotype of a homozygote mutant. Owing to additive gene action, the phenotypic trait i of a heterozygote is the mid-value

$$\tau_i = \frac{z_i + \theta_i}{2}. \quad (6)$$

We can therefore write the phenotypic vector of a heterozygote as $\tau(z, \theta)$, which emphasizes that it depends on the two homozygote phenotype. With this notation, invasion fitness (eq. 5) can be written as

$$W(\tau, \theta) = w\left(\tau(z, \theta), \theta, \mathcal{E}(\tau(z, \theta), \theta)\right). \quad (7)$$

It follows from eq. (7) and the linear dependence of τ on z and θ (eq. 6) that

$$\theta \in \arg \max_{z \in \mathbb{R}^n} w\left(\tau(z, \theta), \theta, \mathcal{E}(\tau(z, \theta), \theta)\right) \iff \theta \in \arg \max_{\tau \in \Theta} w(\tau, \theta, \mathcal{E}(\tau, \theta)), \quad (8)$$

i.e., θ is an uninvadable strategy if we cannot find a phenotype z expressed by a homozygote individual that would make a heterozygote individual with phenotype $\tau(z, \theta)$ better off than the

resident homozygote z .

The first-order necessary condition for uninvasibility must therefore satisfy

$$\left. \frac{\partial w(\tau(z, \theta), \theta, \mathcal{E}(\tau(z, \theta), \theta))}{\partial z_i} \right|_{z=\theta} = \frac{1}{2} \left. \frac{\partial w(\tau, \theta, \mathcal{E}(\tau, \theta))}{\partial \tau_i} \right|_{\tau=\theta} = 0 \quad \text{for all } i, \quad (9)$$

using the chain rule and eq. (6). Hence, we can write the first order necessary condition for uninvasibility as

$$s_i(\theta) = 0 \quad \text{for all } i, \quad (10)$$

where

$$s_i(\theta) = \left. \frac{\partial w(\tau, \theta, \mathcal{E}(\tau, \theta))}{\partial \tau_i} \right|_{\tau=\theta} \quad (11)$$

is the selection gradient on trait i , which captures the effect of directional selection on trait i and allows to compute explicitly candidate uninvasible strategies, the so-called singular strategies that satisfy eq. (10) (e.g., Geritz et al., 1998; Rousset, 2004; Leimar, 2009). Eq. (11) shows that under additive gene action (eq. 6), the selection gradient can be expressed in terms of variation in heterozygote effects (the τ_i 's), which has the attractive feature of allowing us to keep simple notations throughout and apply the model to both haploids and diploids with the same notations.

We now disentangle the role of the effects of an individual on its own environment (direct effects) from those it has on downstream generations (indirect effects) for selection. To do so, we re-write the selection gradient by first differentiating eq. (4) on both sides with respect to τ_i using the chain rule, solving for $\partial \mathcal{E}(\tau, \theta) / \partial \tau_i$, and then substituting the result into eq. (11) giving

$$s_i(\theta) = \left. \frac{\partial w(\tau, \theta, \mathcal{E}(\theta, \theta))}{\partial \tau_i} \right|_{\tau=\theta} + \left. \frac{\partial w(\tau, \theta, \mathcal{E})}{\partial \mathcal{E}} \right|_{\tau=\theta} \times \left. \frac{\partial F(\tau, \theta, \mathcal{E}(\theta, \theta), \mathcal{E}(\theta, \theta))}{\partial \tau_i} \right|_{\tau=\theta} \times \frac{1}{1 - \Lambda(\theta)}, \quad (12)$$

where

$$0 \leq \Lambda(\theta) = \left. \frac{\partial F(\tau, \theta, \mathcal{E}, \mathcal{E}(\theta, \theta))}{\partial \mathcal{E}} \right|_{\tau=\theta} < 1 \quad (13)$$

is bounded between zero and one owing to our assumption that environmental dynamics eq. (2) have a single fixed point. Eq. (12) shows that the selection gradient is the sum of two terms. The first term is the change in the fitness of an individual changing its trait i by an infinitesimal amount (that is by switching from the resident to mutant trait expression), which is the standard selection gradient in panmictic populations without class structure or effects on an environmental state variable (e.g., Geritz et al., 1998; Rousset, 2004). The second term in eq. (12) captures the fitness effects of environmental changes, cumulated over the lineage of a focal mutant. These

cumulative effects are equal to the product of (i) the sensitivity of fitness to environmental change ($\partial w(\tau, \theta, \mathcal{E})/\partial \mathcal{E}$), (ii) the sensitivity of current environmental dynamics to a change in trait value in an individual ($\partial F(\tau, \theta, \mathcal{E}(\theta, \theta), \mathcal{E}(\theta, \theta))/\partial \tau_i$), and (iii) the cumulative effects $1/[1 - \Lambda(\theta)]$ on the environment experienced by a focal mutant of a change in environmental dynamics over all individuals in a line of descent connected to the focal mutant.

The cumulative effects can be decomposed between the “direct effect” of a focal mutant on its own environment, and the “indirect cumulated effects” of a lineage of mutants on the environment experienced by its members as follows

$$\frac{1}{1 - \Lambda(\theta)} = \underbrace{1}_{\text{“direct effect”}} + \underbrace{\sum_{t=1}^{\infty} \left(\frac{\partial F}{\partial \mathcal{E}} \Big|_{\tau=\theta} \right)^t}_{\text{“indirect cumulated effects”}}, \quad (14)$$

where $(\partial F/\partial \mathcal{E})^t$ can be interpreted as the effect of the focal mutant on the environment of an individual living $t \geq 1$ generations downstream. Hence, in the absence of any carry-over effects across generations, the selection pressure is given by eq. (14) with $\Lambda(\theta) = 1$. Otherwise, the selection pressure on a trait will depend on its carry-over effects across generations within the family. As such, the selection gradient (eq. 12) can be understood as an inclusive fitness effect of expressing the mutant allele (Hamilton, 1964; Frank, 1998; Rousset, 2004), and the second summand in eq. 14 is conceptually analogous to the carry-over effects that arise in spatially structured populations when individuals affect local environmental dynamics in a deterministic way (Lehmann, 2008, e.g., eq. 17).

When the difference between non-singular resident and mutant phenotypes is small ($\|\tau - \theta\| \ll 1$), the selection gradient is sufficient to determine whether the mutant will go extinct or fix in the population (see Rousset, 2004 for a general argument about this). A singular phenotype θ^* (such that $s_i(\theta^*) = 0$ for all i) will then be approached by gradual evolution, i.e., is convergence stable (Leimar, 2009), if the $n \times n$ Jacobian $\mathbf{J}(\theta^*)$ matrix with (i, j) entry

$$(\mathbf{J}(\theta^*))_{ij} = \frac{\partial s_i(\theta)}{\partial \theta_j} \Big|_{\theta=\theta^*} \quad (15)$$

is negative-definite at θ^* , or equivalently if its eigenvalues all have negative real parts. At a convergence stable singular resident ($s_i(\theta^*) = 0$ for all i), the $n \times n$ Hessian $\mathbf{H}(\theta^*)$ matrix with (i, j) entry

$$(\mathbf{H}(\theta^*))_{ij} = \frac{\partial^2 w(\tau, \theta^*, \mathcal{E}(\tau, \theta^*))}{\partial \tau_i \partial \tau_j} \Big|_{\tau=\theta^*} \quad (16)$$

determines whether the singular is locally uninvadable, which is the case if $\mathbf{H}(\theta^*)$ is negative-definite at θ^* . If this is not the case, then disruptive selection and evolutionary branching can occur. Eqs. (15)–(16) give the standard (multidimensional) convergence stability and local uninvadability conditions for a finite number of quantitative traits (e.g., Lessard, 1990; Leimar,

2009; Mullon et al., 2016).

2 Gene-culture co-evolution and IL and SL levels

2.1 Reproductive assumptions

We now apply our framework to study gene-culture co-evolution through IL and SL. We let \mathcal{E} stand for the amount of adaptive non-innate information (or knowledge or skill) that an individual acquires during its lifespan by IL and SL ($\mathcal{E} \in \mathbb{R}_+$). We are interested in the evolution of resource allocation to IL and SL, and assume that a homozygote individual expressing the resident allele allocates a fraction $\theta_L \in [0, 1]$ of its resources to learning (baseline unit of one), and a fraction $\theta_{IL} \in [0, 1]$ of that effort to IL. Hence, an individual allocates $\theta_L \theta_{IL}$ unit of resources to IL, $\theta_L(1 - \theta_{IL})$ units to SL, and $1 - \theta_L$ to any other function of the organism (e.g., offspring production, maintenance, etc.). With this, a resident homozygote expresses the vector $\theta = (\theta_{IL}, \theta_L) \in [0, 1]^2$ of phenotypes and a heterozygote mutant has trait vector $\tau = (\tau_{IL}, \tau_L) \in [0, 1]^2$.

This formulation of IL and SL learning strategies as levels of learning allow to consider trade-offs between allocating resources to learning and other functions of the organism, and has been endorsed by a number of previous studies (Nakahashi, 2010; Lehmann et al., 2013; Wakano and Miura, 2014; Kobayashi et al., 2015). We aim to assess the role of vertical transmission on the unavoidable learning strategy and concomitant cultural level. In order to do this for a mathematically tractable model, we assume that after IL and SL have been performed, an individual gathers energy according to the amount of adaptive information it has learnt and the resources it has left for reproduction, reproduces using its gathered energy, and then dies (semelparous reproduction). Under these assumptions, which have been made by many previous gene-culture co-evolutionary models (e.g., Lumsden and Wilson, 1981; Boyd and Richerson, 1985; Nakahashi, 2010; Aoki et al., 2012; Lehmann et al., 2013; Wakano and Miura, 2014; Kobayashi et al., 2015), the fitness of a heterozygote mutant can be written as

$$w(\tau, \theta, \mathcal{E}(\tau, \theta)) = \frac{f(\tau_L, \mathcal{E}(\tau, \theta))}{f(\theta_L, \mathcal{E}(\theta, \theta))}, \quad (17)$$

where $f(\tau_L, \mathcal{E}(\tau, \theta))$ is the fecundity (number of offspring produced) of a mutant. We assume that fecundity is monotonically decreasing with the level τ_L of learning (“cost of learning”) and monotonically increasing with the amount of adaptive information \mathcal{E} (“benefit”). The function $f(\theta_L, \mathcal{E}(\theta, \theta))$ is the average fecundity in the population, which is given by the fecundity of a resident in a monomorphic resident population. Eq. (17) shows that in a resident monomorphic population, invasion fitness is equal to one: $w(\theta, \theta, \mathcal{E}(\theta, \theta)) = 1$.

2.2 Cultural information assumptions

2.2.1 Cultural dynamics and resident cultural equilibrium

We now introduce the dynamics of adaptive information $\mathcal{E}_t(\tau, \theta)$ held by a heterozygote mutant in demographic time period t at the time of reproduction (after SL and IL occurred). Individuals acquire adaptive information by performing SL from the parental generation by way of vertical transmission with probability v and oblique transmission with probability $1 - v$, but we assume that the efficiency of SL is independent of transmission mode. The main dynamic assumption we make about adaptive information is that it satisfies the recursion

$$\mathcal{E}_{t+1}(\tau, \theta) = F(\tau, \theta, \mathcal{E}_t(\tau, \theta), \mathcal{E}(\theta, \theta)) = a_{\text{IL}}(\tau) + p_{\text{SL}}(\tau) \left(v \left(\frac{\mathcal{E}_t(\tau, \theta) + \mathcal{E}(\theta, \theta)}{2} \right) + (1 - v)\mathcal{E}(\theta, \theta) \right), \quad (18)$$

which depends on two terms. First, it depends on the information $a_{\text{IL}}(\tau)$ an individual can obtain by performing IL alone. This is assumed to be equal to zero in the absence of effort $\theta_{\text{L}}\theta_{\text{IL}}$ devoted to IL, to increase and eventually saturate with effort $\theta_{\text{L}}\theta_{\text{IL}}$. Hence, $a_{\text{IL}}(\cdot)$ is a function of a single argument: $a_{\text{IL}}(\tau) = a_{\text{IL}}(\tau_{\text{L}}\tau_{\text{IL}})$, but we write it in terms of τ for ease of presentation. Second, adaptive information depends on the fraction $p_{\text{SL}}(\tau)$ of information an individual obtains by SL from the parental generation. This is assumed to increase monotonically with the effort $\tau_{\text{L}}(1 - \tau_{\text{IL}})$ allocated to SL. Hence, $p_{\text{SL}}(\cdot)$ is also a function of a single argument: $p_{\text{SL}}(\tau) = p_{\text{SL}}(\tau_{\text{L}}(1 - \tau_{\text{IL}}))$.

The information obtained from the parental generation depends on the type of exemplar individual from which information is obtained. The interpretation of eq. (18) is that with probability v the cultural parent of the mutant is one of its two genetic parent, in which case with probability $1/2$ the exemplar is a heterozygote mutant who carries information level $\mathcal{E}_t(\tau, \theta)$ and with probability $1/2$, a homozygote for the resident who carries resident information level $\mathcal{E}(\theta, \theta)$. With probability $1 - v$ the mutant performs oblique transmission, in which case the exemplar is a resident with the information level $\mathcal{E}(\theta, \theta)$. The equilibrium resident level of information satisfies

$$\mathcal{E}(\theta, \theta) = a_{\text{IL}}(\theta) + p_{\text{SL}}(\theta)\mathcal{E}(\theta, \theta) \quad (19)$$

(by setting $\tau = \theta$ in eq. 18 and letting $\mathcal{E}(\theta, \theta) = \lim_{t \rightarrow \infty} \mathcal{E}_t(\theta, \theta)$), or

$$\mathcal{E}(\theta, \theta) = \frac{a_{\text{IL}}(\theta)}{1 - p_{\text{SL}}(\theta)}. \quad (20)$$

The way of incorporating vertical transmission in eq. (18) is a diploid version of the model of Kobayashi et al. (2015, p. 81) and our formulation of information dynamics in terms of IL and SL components ($a_{\text{IL}}(\tau)$ and $p_{\text{SL}}(\tau)$) allows us to capture a variety of learning models that have previously been considered in the gene-culture co-evolution literature. For instance,

eq. (18) allows to capture cultural processes as those described in the classical models of IL and SL learning, where \mathcal{E} represents the probability of expressing the “correct” (or “optimal”) learned phenotype (e.g., light a fire), when an individual can express two alternative behaviors: the “correct” or the “wrong” phenotype (e.g., Rogers, 1988; Enquist et al., 2007; Kobayashi and Wakano, 2012; Aoki and Feldman, 2014; Wakano and Miura, 2014 and see section 2.3.2 for a concrete example). Equation (18) also allows to captures situations where the amount of information represents the total stock of knowledge or skill of an individual (e.g., Nakahashi, 2010; Aoki et al., 2012; Kobayashi and Aoki, 2012; Lehmann et al., 2013; Wakano and Miura, 2014; Kobayashi et al., 2015). Regardless of the precise cultural trait followed, eq. (18) embodies the feature that an individual can add up information by SL to that acquired by IL, which can result in a larger amount of cultural information at steady state, i.e., SL increases the amount of adaptive information by a factor $1/(1 - p_{\text{SL}}((1 - \theta_{\text{IL}})\theta_{\text{L}}))$ (eq. (20)). Hence, cumulative cultural evolution can occur.

2.2.2 Mutant cultural equilibrium

From eq. (18), the equilibrium level of cultural information is

$$\mathcal{E}(\tau, \theta) = \lim_{t \rightarrow \infty} \mathcal{E}_t(\tau, \theta) = \left(\frac{1}{1 - vp_{\text{SL}}(\tau)/2} \right) a_{\text{IL}}(\tau) + \left(\frac{1 - v/2}{1 - vp_{\text{SL}}(\tau)/2} \right) p_{\text{SL}}(\tau) \mathcal{E}(\theta, \theta). \quad (21)$$

Comparing eq. (21) to eq. (19) shows that for a mutant, vertical transmission ($v > 0$) increases both the level of individually and socially learnt information relative to the baselines of $a_{\text{IL}}(\theta)$ and $p_{\text{SL}}(\theta) \mathcal{E}(\theta, \theta)$ obtained by a resident individual (eq. 19). Hence, vertical transmission can be thought as increasing the effective amount of IL and SL under selection.

2.3 Co-evolutionary equilibrium

We substitute the mutant information equilibrium (eq. 21) into the fitness function (eq. 17) to compute the selection gradients on the two evolving traits,

$$s_{\text{L}}(\theta) = \left. \frac{\partial w(\tau, \theta, \mathcal{E}(\tau, \theta))}{\partial \tau_{\text{L}}} \right|_{\tau=\theta} \quad \text{and} \quad s_{\text{IL}}(\theta) = \left. \frac{\partial w(\tau, \theta, \mathcal{E}(\tau, \theta))}{\partial \tau_{\text{IL}}} \right|_{\tau=\theta}, \quad (22)$$

which describe the adaptive dynamics of learning rules. A necessary first-order condition for the learning rules to be locally uninvadable is then that $s_{\text{L}}(\theta^*) = 0$ and $s_{\text{IL}}(\theta^*) = 0$, where the associated cultural information $\mathcal{E}(\theta^*, \theta^*)$ satisfies eq. (20). Whether the so-obtained singular strategies θ^* are convergence stable and locally uninvadable can be determined using the Jacobian and Hessian matrices eqs. (15)–(16) (see Appendix B).

We find that the selection gradient on learning can be expressed as

$$s_L(\theta) = k(\theta) \left(\underbrace{\theta_{IL} \frac{da_{IL}(x)}{dx} \Big|_{x=\theta_{IL}\theta_L} + (1 - \theta_{IL})\mathcal{E}(\theta, \theta) \frac{dp_{SL}(y)}{dy} \Big|_{y=(1-\theta_{IL})\theta_L}}_{\partial F(\tau, \theta, \mathcal{E}(\theta, \theta), \mathcal{E}(\theta, \theta)) / \partial \tau_L} - [1 - \Lambda(\theta)]C_e(\theta) \right), \quad (23)$$

where

$$k(\theta) = \frac{1}{(1 - \Lambda(\theta))f(\theta_L, \mathcal{E}(\theta))} \frac{df(\theta_L, \mathcal{E})}{d\mathcal{E}} > 0, \quad (24)$$

is a proportionality factor that does not affect the direction of selection,

$$\Lambda(\theta) = vp_{SL}(\theta)/2 \quad (25)$$

captures the cumulative effects that relatives have on the information \mathcal{E} carried by a focal individual (eq. 14), and

$$C_e(\theta) = - \frac{df(\tau_L, \mathcal{E}(\theta, \theta))}{d\tau_L} \Big|_{\tau_L=\theta_L} / \frac{df(\theta_L, \mathcal{E})}{d\mathcal{E}} \quad (26)$$

is the ratio of the marginal cost of learning to the marginal benefit of adaptive information on fecundity. This can be thought of as a marginal rate of substitution (Pindyck and Rubinfeld, 2001), i.e., how much an individual is ready to invest in learning in exchange for obtaining adaptive information while maintaining the same level of fecundity. Eq. (23) shows that the selection pressure on learning θ_L depends on (1) the marginal gain in information obtained by learning ($\partial F(\tau, \theta, \mathcal{E}(\theta, \theta), \mathcal{E}(\theta, \theta)) / \partial \tau_L$), which is the average information gain over the components of IL (weighted by θ_{IL}) and SL (weighted by $1 - \theta_{IL}$); (2) the effective cost $C_e(\theta)$ of a unit of information, which is discounted by a factor $\Lambda(\theta)$ that captures intergenerational effects.

Meanwhile, we find that the selection gradient on IL (θ_{IL}),

$$s_{IL}(\theta) = \theta_L k(\theta) \left(\frac{da_{IL}(x)}{dx} \Big|_{x=\theta_{IL}\theta_L} - \mathcal{E}(\theta, \theta) \frac{dp_{SL}(y)}{dy} \Big|_{y=(1-\theta_{IL})\theta_L} \right) \quad (27)$$

balances the marginal benefit of IL ($da_{IL}(x)/dx$) and the marginal cost ($-dp_{SL}(y)/dy$) of allocating less resources to SL. Interestingly, vertical transmission does not directly influence the direction of selection on IL. Its influence may however be indirect through its effects on θ_L and therefore on the marginal benefits and cost of IL.

The selection gradients (eqs. 27–23) show that vertical transmission reduces the effective cost of learning by increasing the discount rate (eq. 25). In other words, when adaptive information

is transmitted vertically, selection is less sensitive to the individual cost of gathering adaptive information because information will later preferentially benefit relatives. Since $p_{\text{SL}}(y) < 1$, vertical transmission can cut the effective cost by at most a half in this model (when $v = 1$, eq. 25). This moderate impact of vertical transmission, which can be seen from the derivative of the discount factor $d\Lambda(\theta)/dv = p_{\text{SL}}(y)/2$ with respect to v , is due to the assumptions underlying information dynamics (eq. 18): individuals are diploids, vertical transmission is equally likely to occur between a mutant offspring and its mutant and resident parents, and vertical transmission has no effect on the efficiency of transmission. As a result of these assumptions, information transformation eq. (18) depends linearly on vertical transmission rate v and only by a factor of $1/2$, which limits the discounting effect of vertical transmission.

More generally, the effect of vertical transmission on the discount rate is given by

$$\frac{d\Lambda(\theta)}{dv} = \frac{d}{dv} \left. \frac{\partial F(\tau, \theta, \mathcal{E}, \mathcal{E}(\theta, \theta))}{\partial \mathcal{E}} \right|_{\tau=\theta}, \quad (28)$$

namely, the effect of v on how the mutant environment affect its own dynamic. Eq. (28) reveals that if vertical information has a large effect on environmental dynamic, then it can have a large impact on the discount rate $\Lambda(\theta)$, and thus have a significant influence on the evolution of learning strategies (eq. 11) and cumulative culture. This will occur for instance if for the same effort allocated to SL, the fraction of information p_{SL} obtained socially from an exemplar depends linearly on whether the exemplar is related or not, or if \mathcal{E} depends non-linearly on v (e.g., if offspring first learn from their genetic parent and then learn obliquely at a different rate). The assumptions of our model (eq. 18) are therefore conservative for the effect of vertical transmission on cumulative culture. We endorsed them because they allow for direct comparison to models in the literature, to obtain manageable analytical expression, and conveniently check the validity of our results with individual-based simulations, three endeavours to which we next turn.

2.4 Evolution of learning to obtain the “correct” phenotype

In order to fully work out a concrete application of our approach, we now make some further assumptions about the dynamics of cultural information, and let \mathcal{E} be the probability that at the stage of reproduction an individual expresses the “correct” phenotype in its environment (e.g., Rogers, 1988; Enquist et al., 2007; Aoki and Feldman, 2014; Wakano and Miura, 2014). We assume that the level of information obtained by an individual under IL and SL can be written in the form

$$a_{\text{IL}}(\tau) = 1 - \exp(-\alpha\tau_{\text{IL}}\tau_{\text{L}}) \quad \text{and} \quad p_{\text{SL}}(\tau) = \exp(-\alpha\tau_{\text{IL}}\tau_{\text{L}}) [1 - \exp(-\beta(1 - \tau_{\text{IL}})\tau_{\text{L}})], \quad (29)$$

where α can be thought of as the rate of IL and $1 - \exp(-\alpha\tau_{\text{IL}}\tau_{\text{L}})$ is the probability of acquiring the “correct” phenotype by IL, which decelerates with the resources $\tau_{\text{IL}}\tau_{\text{L}}$ allocated to IL. Similarly,

β can be thought of as the rate of SL, and $[1 - \exp(-\beta(1 - \tau_{\text{IL}})\tau_{\text{L}})]$ is the probability of acquiring the “correct” phenotype by SL conditional on not acquiring it by IL, which decelerates with the resources $(1 - \tau_{\text{IL}})\tau_{\text{L}}$ allocated to SL.

Eq. (29) entails that acquiring the correct phenotype by IL and SL are mutually exclusive events. Eq. (29) can be derived from a mechanistic model of learning, assuming that learning occurs on a fast time scale that is embedded in a single demographic time period (see Appendix C). In this mechanistic model, individuals first perform SL from the parental generation for $(1 - \tau_{\text{IL}})\tau_{\text{L}}$ units of time (on the fast time scale) at rate β , proportionally to the distance between the probabilities \mathcal{E} of the exemplar and target individuals. In other words, only if an individual invests all resources into SL ($(1 - \tau_{\text{IL}})\tau_{\text{L}} = 1$), its probability \mathcal{E} is equal to its exemplar’s after SL. Individuals then perform IL for $\tau_{\text{IL}}\tau_{\text{L}}$ units of time at a rate α proportionally to the distance between its current probability \mathcal{E} and the upper bound 1. Eq. (29) equivalently implements the so-called critical social learning strategy, where an individual first learns from the parental generation by SL and then, if it has not acquired the correct phenotype, performs IL (Enquist et al., 2007; Rendell et al., 2010, see also eq. (C-6) in Appendix C for the interpretation of eq.(29) in terms of the critical social learner strategy).

Finally, we assume that fecundity depends on whether the correct phenotype is acquired, and write it as

$$f(\tau_{\text{L}}, \mathcal{E}(\tau, \theta)) = 1 + \mathcal{E}(\tau, \theta)(1 - \tau_{\text{L}})^{1-\gamma_1} + \lambda [1 - \mathcal{E}(\tau, \theta)] (1 - \tau_{\text{L}})^{\gamma_2}, \quad (30)$$

where “1” is the baseline reproductive unit and the rest can be understood as follows. A mutant has $(1 - \tau_{\text{L}})$ units of resources left to invest into reproduction and the effect of this investment on fecundity depends on whether a mutant expresses the correct phenotype. When the mutant has the “correct” phenotype (with probability $\mathcal{E}(\tau, \theta)$), returns on investment are controlled by the parameter γ_1 and we assume that $0 < \gamma_1 < 1$ so that returns rise sharply with initial investment (Fig. 1). When the mutant has the “wrong” phenotype (with probability $1 - \mathcal{E}(\tau, \theta)$), returns are tuned by γ_2 and we assume that $\gamma_2 > 1$ so that returns increase slowly with initial investment. Finally, the parameter $0 \leq \lambda \leq 1$ bounds the fecundity of an individual with the wrong phenotype (Fig. 1). For example, an individual with the wrong phenotype who invests all resources into reproduction ($\tau_{\text{L}} = 0$) has a fecundity $1 + \lambda$.

2.4.1 Effect of vertical transmission on cumulative culture

We first work out the case where expressing the wrong phenotype results in zero effects on fitness ($\lambda = 0$, the usual case in the literature, Rogers, 1988; Enquist et al., 2007; Kobayashi and Wakano, 2012; Wakano and Miura, 2014; Aoki and Feldman, 2014), for which singular learning strategies ($\theta_{\text{L}}^*, \theta_{\text{IL}}^*$) and the corresponding levels of information \mathcal{E}^* they generate can be determined analytically. Substituting eqs. (29)–(30) into eq. (27), we find that solving for θ_{IL}^*

such that $s_{\text{IL}}(\theta_{\text{L}}^*, \theta_{\text{IL}}^*) = 0$ there is a unique IL singular strategy

$$\theta_{\text{IL}}^* = \frac{1}{\theta_{\text{L}}^* \alpha} \log \left(\frac{\beta}{\beta - \alpha} \right), \quad (31)$$

which rapidly (hyperbolically) decreases with the resources θ_{L}^* allocated to learning, but is otherwise independent of the rate of vertical transmission (as predicted by eq. 27). Eq. (31) also shows that for individuals to evolve a composite learning strategy ($0 < \theta_{\text{IL}}^* < 1$) that mixes SL and IL, it is necessary (but not sufficient) that the rate of SL is greater than the rate of IL ($\beta > \alpha$), otherwise SL cannot be a singular strategy ($\theta_{\text{IL}}^* = 1$).

Substituting eqs. (29)–(31) into eq. (23) with $\lambda = 0$, we find that learning increase from zero (when $\theta_{\text{L}} = 0$ and $\theta_{\text{IL}} = 1$) when $\alpha > 0$ (i.e., $s_{\text{L}}(0, 1) > 0$ when $\alpha > 0$). Then, solving $s_{\text{L}}(\theta_{\text{L}}^*, \theta_{\text{IL}}^*)$ for θ_{L}^* such that $s_{\text{L}}(\theta_{\text{L}}^*, \theta_{\text{IL}}^*) = 0$ by using eq. (31), we find that there is a unique singular level of learning that is given by

$$\theta_{\text{L}}^* = 1 - \frac{1}{\beta} \left(W(x) + \frac{v(1 - \gamma_1)}{2} \right), \quad (32)$$

where $W(x)$ is the principal solution of the Lambert function (the solution for y in $x = ye^y$) with argument

$$x = \frac{(1 - \gamma_1)[\alpha v + \beta(2 - v)]}{2\beta} \left(\frac{\beta}{\beta - \alpha} \right)^{1 - \frac{\beta}{\alpha}} \exp \left(\beta - \frac{v(1 - \gamma_1)}{2} \right). \quad (33)$$

Then, by substituting the singular strategies eqs. (31)–(32) into eq. (20), we find that the singular interior learning strategy generate a level

$$\mathcal{E}^* = \frac{2\alpha W(x)}{2\alpha W(x) + (1 - \gamma_1)(2\beta + v(\alpha - \beta))} \quad (34)$$

of adaptive information.

A numerical inspection of the singular learning strategies $(\theta_{\text{L}}^*, \theta_{\text{IL}}^*)$ and the corresponding amount of adaptive information \mathcal{E}^* they generate shows that while vertical transmission v increases the amount of time invested into learning and adaptive information, its effect is moderate (Fig. 2). In fact, from eq. (34), we see that under pure oblique transmission ($v = 0$), the level of information converges asymptotically to

$$\mathcal{E}^* = \frac{\alpha}{\alpha + (1 - \gamma_1)}, \quad (35)$$

as $\beta \rightarrow \infty$, while under pure vertical transmission ($v = 1$), it converges to

$$\mathcal{E}^* = \frac{2\alpha}{2\alpha + (1 - \gamma_1)}, \quad (36)$$

which shows that vertical transmission cannot more than double the amount of information. This is in line with our result that when vertical transmission has no effect on the efficiency of transmission and the dynamic dependence of \mathcal{E} is linear in v (eq. 25), transmission has a moderate effect on cumulative cultural evolution. This is also consistent with the results of Kobayashi et al. (2015), who considered a model with haploid reproduction in which vertical transmission also has no effect on the efficiency of transmission (see Appendix D for an application of our framework to Kobayashi et al. (2015)'s model and a rederivation of their results). A comparison with Kobayashi et al. (2015)'s results allows us to evaluate the role of diploidy on cumulative culture. If Kobayashi et al. (2015)'s model showed a limited effect of intermediate vertical transmission ($0 < v < 1$), it showed that pure vertical transmission ($v = 1$) could have a strong positive influence on learning when adaptive information is interpreted as the total stock of knowledge held by an individual at the stage of reproduction. This strong effect arises because when $v = 1$, the discount rate can approach one and hence costs can to be totally discounted (see eq. D-8 in Appendix D). By contrast, the effect of pure vertical transmission ($v = 1$) remains moderate in diploids because relatedness between a focal individual and its exemplar is half of that under haploid reproduction and so the discount $\Lambda(\theta)$ on the cost of learning is at most $1/2$ (eqs. 23 and 25).

The other parameters of the model also affect the singular learning strategies $(\theta_L^*, \theta_{IL}^*)$ and therefore the level of adaptive information \mathcal{E}^* at equilibrium. The rate of β SL has a negative effect on the level of IL θ_{IL}^* , and hence positive effect on SL, but only a moderate effect on adaptive information \mathcal{E}^* (Fig. 2). Meanwhile, the returns of investment into reproduction γ_1 significantly increase the investment into learning θ_L^* and adaptive information \mathcal{E}^* . For all parameter values displayed in Fig. 2, we checked numerically (by applying eqs. 15–16, see Appendix B) that singular learning strategy $(\theta_L^*, \theta_{IL}^*)$ defined by eqs. (31)–(34) is convergence stable (Fig. 3) and locally uninvadable. Our analytical approach is confirmed by individual based simulations (Fig. 4).

2.4.2 Effect of vertical transmission on evolutionary branching

We now turn to the case in which individuals with the wrong phenotype can obtain returns on investment in fecundity, $\lambda > 0$, and consider that an individual with the correct phenotype does not need to invest much into reproduction to obtain a fecundity gain (concave returns, $\gamma_1 < 1$), while an individual with the wrong phenotype needs to invest significantly more into reproduction to have a fecundity gains (convex returns, $\gamma_2 > 1$, see Fig. 1).

We find that the singular strategy for individual learning θ_{IL} is the same as when $\lambda = 0$ (eq. 31), but we are unable to obtain a general analytical solution for singular strategies for investment into learning (θ_L) . The model is therefore studied numerically and the main qualitative outcomes are as follows (see Appendix F for details on the numerical approach). By contrast to our results with $\lambda = 0$, it is more difficult for learning (θ_L) to evolve from zero and the evolutionary dynamics to converge to an interior equilibrium $(\theta_L \in (0, 1), \theta_{IL}^* \in (0, 1))$. This is because when individuals with the wrong phenotype obtain a significant fecundity benefit when

all resources are invested into reproduction ($\theta_L = 0$), a mutant that invests only a little into learning cannot compete with a resident who invests all into reproduction. Only passed a critical threshold of learning does extra investment into learning become beneficial compared to the cost of diverting resources from reproduction, in which case both learning and SL can be favored (see Fig. 5)

When a mixed convergence stable interior strategy exists ($\theta_L^* \in (0, 1), \theta_{IL}^* \in (0, 1)$), our analysis suggests that it is usually uninvadable. We found nevertheless parameter values for which convergence stable interior equilibria are locally invadable (i.e., disruptive selection occurs), so that evolutionary branching (Geritz et al., 1997, 1998) can occur at these. Holding everything else constant, we find that vertical transmission inhibits disruptive selection. This is in line with the finding that a reduction in migration (which increases relatedness) inhibits disruptive selection in spatially structured populations (Ajar, 2003; Mullon et al., 2016). We performed individual based simulations that confirmed our predictions of disruptive selection obtained from the Hessian matrix (eq. 16 and eq. B-2), further validating our fitness measure. In addition, simulations showed that when it occurs, disruptive selection leads to evolutionary branching and the emergence of two morphs, one that does less IL than the equilibrium who selfishly exploits the other that does more IL than the convergence stable equilibrium (Fig. 6).

3 Discussion

In spite of the evidence that cultural transmission often occurs between parent and offspring (Cavalli-Sforza and Feldman, 1981; Guglielmino et al., 1995; Hewlett et al., 2011; Konner, 2010), the bulk of theoretical work on gene-culture co-evolution for cumulative culture has focused on oblique or horizontal transmission (e.g., Boyd and Richerson, 1985; Rogers, 1988; Enquist et al., 2007; Rendell et al., 2010; Nakahashi, 2010; Aoki et al., 2012; Lehmann et al., 2013; Nakahashi, 2013; Aoki and Feldman, 2014; Wakano and Miura, 2014). In this paper, we derived the invasion fitness of a mutant allele that co-evolves with cumulative cultural information under vertical transmission. We showed that when cultural dynamics are deterministic and have a single attractor equilibrium, invasion fitness is equal to the *individual fitness* of a mutant when the dynamic of cultural information is at equilibrium (eq. 5). This result allows for an analytically tractable study of gene-culture co-evolutionary adaptive dynamics in the family. Our invasion fitness measure (eq. 5) can also be applied to cases where population size varies, following a deterministic dynamic with a single attractor point (in which case fitness is evaluated at this attractor for the resident population, e.g., Ferrière and Gatto, 1995; Caswell, 2000; Metz, 2011).

Our analysis of the selection gradient revealed that cultural evolution (or environmental dynamics) results in carry-over effects across generations, which feedback on the selection pressure of traits affecting cultural dynamics (see eq. 12). This feedback arises from kin selection, since an individual modifying cultural information as a results of expressing a mutant allele will change the environment to which descendants living in the next or more distant generations are exposed

(and that possibly also carry the mutant allele). These indirect fitness effects depend on the magnitude of how altering trait values affect cultural information dynamics and how the resulting change in dynamics affects individuals in downstream generations (eq. 12). From the perspective of a recipient of these effects, its fitness will depend on a multitude of individuals in past generations (all those from the ancestral lineage of an individual carrying a mutation). These intergenerational effects accumulate in a geometric progression over the lineage of a mutant and can therefore potentially be large (see eq. 14). Our approach thus allows for a clear separation between direct and indirect effects on fitness and can be readily extended to cover more realistic demographic scenario such as aged-structured populations with senescence.

We applied our framework to a generic model in which individual learning (IL) and social learning (SL) rules co-evolve with the adaptive information they generate (eq. 18), and which covers many previous scenarios for the co-evolution of IL and SL (Rogers, 1988; Enquist et al., 2007; Aoki and Feldman, 2014; Wakano and Miura, 2014; Nakahashi, 2010; Aoki et al., 2012; Lehmann et al., 2013; Wakano and Miura, 2014; Kobayashi et al., 2015). The analysis of the selection gradient showed that the impact of vertical transmission, which increases interactions between relatives and thus kin selection effects, can be viewed as a discounting (or reduction) of the cost of learning (eqs. 23 and 25). Vertical transmission therefore favour greater levels of learning and hence cumulative culture. But when transmission is as efficient between relatives than between unrelated individuals, learning costs cannot be discounted by more than a half in diploids (eq. 25). In the case of haploidy Kobayashi et al. (2015) or when transmission is only among heterozygotic mutant parents and offspring (Appendix D), costs can be totally discounted under pure vertical transmission ($v = 1$). Carry-over effects impacting relatives are therefore diluted in the presence of diploidy, and this is because diploidy decreases the correlation between genetic and cultural transmission pathways so that over generations, mutant alleles also benefit resident ones.

In order to illustrate our results, we analyzed in detail a specific scenario of the evolution of IL and SL where adaptive information determines the acquisition of a binary trait describing “correct” and “wrong” phenotype to be expressed in a given environment (e.g., light a fire, see eq. (29) and Rogers, 1988; Wakano et al., 2004; Wakano and Aoki, 2006; Enquist et al., 2007; Rendell et al., 2010; Kobayashi and Wakano, 2012; Wakano and Miura, 2014). In line with our predictions, we found that in this standard model, vertical transmission has a positive yet moderate quantitative impact on the amount of cultural information accumulated by individuals in uninhabitable populations (Fig. 2). By contrast, the parameters shaping the cost of learning can have a significant quantitative influence on the uninhabitable level of adaptive information and affect cumulative culture by an order of magnitude (Fig. 2). However, in the absence of any empirical quantification of learning costs and benefits, it is difficult to make any conclusion about their role relative to vertical transmission on cultural evolution in natural populations. The quantification of these costs and benefits across the lifespan of individuals unfortunately remains a neglected topic in cultural evolution (Dempis et al., 2012).

To conclude, our model shows that vertical transmission favours cumulative culture through kin selection effects, but moderately so when the effect of learning on adaptive information is independent from whether learning occurs between family members or between unrelated individuals (or more generally, when environmental dynamic depends linearly on vertical transmission rate v , eq. 18). We expect that if vertical transmission interacts with cultural dynamics, for example if offspring learn better from relatives, then vertical transmission may have a large influence on cumulative culture (eqs. 12 and 28). Such a scenario would be relevant to investigate in future research, and also raises the question of the evolution of vertical transmission itself. In addition, our finding that vertical transmission inhibits disruptive selection suggests that it can play a qualitative role in the evolution of IL and SL learning strategies themselves (e.g., conformist transmission, payoff biased transmission, teaching), whose evolution under vertical transmission have not been much investigated. Our approach can be readily accommodated to study all these specific questions, and more broadly, questions on niche construction and gene-culture co-evolution within the family where the modified rates of cultural transmission have long-lasting effects on future generations.

Acknowledgments

We thank Yutaka Kobayashi for useful discussion about cultural evolution.

Appendix

Appendix A: invasion fitness

Given the definition of individual fitness $w(\tau, \theta, \mathcal{E}_t(\tau, \theta))$ in the main text and the associated dynamics for the environmental state variable $\mathcal{E}_t(\tau, \theta)$ (eq. 2), our modelling assumptions entail that invasion fitness is given by the geometric growth rate

$$\log(W(\tau, \theta)) = \lim_{h \rightarrow \infty} \frac{1}{h} \log \left(\prod_{t=0}^{h-1} w(\tau, \theta, \mathcal{E}_t(\tau, \theta)) \right) \quad (\text{A-1})$$

(Cohen, 1979; Tuljapurkar, 1989; Charlesworth, 1994; Ferrière and Gatto, 1995; Caswell, 2000; van Baalen, 2013). It is in general challenging to evaluate eq. (A-2) explicitly under an arbitrary dynamics of $\mathcal{E}_t(\tau, \theta)$ (Tuljapurkar, 1989)). But since we assume that the sequence of environments $\{\mathcal{E}_t(\tau, \theta)\}_{t=0}^{\infty}$ converges to a unique fixed point $\mathcal{E}(\tau, \theta)$ (satisfying eq. 4), the limit of eq. (A-2) converges to

$$\lim_{h \rightarrow \infty} \frac{1}{h} \log \left(\prod_{t=0}^{h-1} w(\tau, \theta, \mathcal{E}_t(\tau, \theta)) \right) = \log(w(\tau, \theta, \mathcal{E}(\tau, \theta))) \quad (\text{A-2})$$

(see also Ferrière and Gatto, 1995), and so invasion fitness is given by

$$W(\tau, \theta) = w(\tau, \theta, \mathcal{E}(\tau, \theta)). \quad (\text{A-3})$$

Appendix B: second-order conditions

From eq. (15) we can evaluate the condition of convergence stability for a singular point $\theta^* = (\theta_{\text{IL}}^*, \theta_{\text{L}}^*)$ satisfying eq. (10). This requires that the Jacobian matrix

$$\mathbf{J}(\theta^*) = \begin{bmatrix} \left. \frac{s_{\text{IL}}(\theta)}{\partial \theta_{\text{IL}}} \right|_{\theta=\theta^*} & \left. \frac{\partial s_{\text{IL}}(\theta)}{\partial \theta_{\text{L}}} \right|_{\theta=\theta^*} \\ \left. \frac{\partial s_{\text{L}}(\theta)}{\partial \theta_{\text{IL}}} \right|_{\theta=\theta^*} & \left. \frac{\partial s_{\text{L}}(\theta)}{\partial \theta_{\text{L}}} \right|_{\theta=\theta^*} \end{bmatrix} \quad (\text{B-1})$$

is negative-definite, or equivalently that both its eigenvalues have negative real parts (e.g., Lessard, 1990; Leimar, 2009; Mullon et al., 2016). Meanwhile, a singular point $\theta^* = (\theta_{\text{IL}}^*, \theta_{\text{L}}^*)$ is uninvadable when the Hessian matrix

$$\mathbf{H}(\theta^*) = \begin{bmatrix} \left. \frac{\partial^2 w(\tau, \theta^*, \mathcal{E}(\tau, \theta^*))}{\partial \tau_{\text{IL}}^2} \right|_{\tau=\theta^*} & \left. \frac{\partial^2 w(\tau, \theta^*, \mathcal{E}(\tau, \theta^*))}{\partial \tau_{\text{IL}} \partial \tau_{\text{L}}} \right|_{\tau=\theta^*} \\ \left. \frac{\partial^2 w(\tau, \theta^*, \mathcal{E}(\tau, \theta^*))}{\partial \tau_{\text{IL}} \partial \tau_{\text{L}}} \right|_{\tau=\theta^*} & \left. \frac{\partial^2 w(\tau, \theta^*, \mathcal{E}(\tau, \theta^*))}{\partial \tau_{\text{L}}^2} \right|_{\tau=\theta^*} \end{bmatrix} \quad (\text{B-2})$$

is negative-definite, or equivalently that both its eigenvalues are negative (note that since $\mathbf{H}(\theta^*)$ has real entries and is symmetric, its eigenvalues are necessarily real, e.g., Lessard, 1990; Leimar, 2009; Mullon et al., 2016).

Appendix C: information dynamics

We derive here eq. (29) by assuming a fast time scale of learning within a single demographic time period and setting the total time length of learning to unity. This approach is equivalent to previous models of cultural information (Aoki et al., 2012; Lehmann et al., 2013; Wakano and Miura, 2014; Kobayashi et al., 2015).

We start by assuming that the resident population is at its equilibrium for cultural dynamics (satisfying eq. 3). Then, an individual first learns from the parental generation (either vertically or obliquely) at rate β per unit time and assume that the rate of change of the adaptive information $\mathcal{E}(h)$ held at time h of the fast time scale of an individual is

$$\frac{d\mathcal{E}(h)}{dh} = \beta [\mathcal{E}_{\text{T}} - \mathcal{E}(h)], \quad (\text{C-1})$$

which for a mutant holds for $h \in [0, (1 - \tau_{\text{IL}})\tau_{\text{L}}]$ (i.e., $(1 - \tau_{\text{IL}})\tau_{\text{L}}$ is the time spent performing SL) and where \mathcal{E}_{T} is the cultural information of the exemplar individual (or cultural parent) and

the initial condition is given by $\mathcal{E}(0) = 0$. Eq. C-1 entails that an individual acquires the correct phenotype proportionally to β and the difference between the probability that the focal and the exemplar individual has the correct phenotype. The solution of eq. C-1 is

$$\mathcal{E}(h) = [1 - \exp(-\beta h)] \mathcal{E}_T \quad \text{for } h \in [0, (1 - \tau_{\text{IL}})\tau_L]. \quad (\text{C-2})$$

After SL has been performed, the individual performs IL and the rate of change in adaptive information $\mathcal{E}(h)$ during IL is given by

$$\frac{d\mathcal{E}(h)}{dh} = \alpha [1 - \mathcal{E}(h)], \quad (\text{C-3})$$

which for a mutant holds for $h \in [(1 - \tau_{\text{IL}})\tau_L, \tau_L]$ (i.e., $\tau_{\text{IL}}\tau_L$ is the time spent performing IL) with initial condition $\mathcal{E}((1 - \tau_{\text{IL}})\tau_L)$ (given by eq. C-2). According to eq. (C-3), the individual acquires the correct phenotype by IL proportionally to α and its current distance to the “target” which is 1. This formulation implements standard reinforcement learning (Bush and Mosteller, 1951). The solution to eq. (C-3) is

$$\mathcal{E}(h) = 1 - \exp(-\alpha h) + \exp(-\alpha h)\mathcal{E}((1 - \tau_{\text{IL}})\tau_L) \quad \text{for } h \in ((1 - \tau_{\text{IL}})\tau_L, \tau_L]. \quad (\text{C-4})$$

Combining eq. (C-2) and eq. (C-4) yields that at the final time of the learning period ($h = \tau_L$), say at generation t , the amount of adaptive information held by a mutant is

$$\mathcal{E}_t(\tau, \theta) = \underbrace{1 - \exp(-\alpha\tau_{\text{IL}}\tau_L)}_{a_{\text{IL}}(\tau)} + \underbrace{\exp(-\alpha\tau_{\text{IL}}\tau_L) [1 - \exp(-\beta(1 - \tau_{\text{IL}})\tau_L)]}_{p_{\text{SL}}(\tau)} \mathcal{E}_T, \quad (\text{C-5})$$

which yields the components of eq. (29) of the main text and where \mathcal{E}_T is equal to the average cultural information of the cases when the individual performs vertical transmission ($(\mathcal{E}_{t-1}(\tau, \theta) + \mathcal{E}(\theta, \theta))/2$) and when it performs oblique transmission ($\mathcal{E}(\theta, \theta)$).

Interestingly, the right hand side of eq. (C-5) can be equivalently written as

$$\mathcal{E}_t(\tau, \theta) = [1 - \exp(-\beta(1 - \tau_{\text{IL}})\tau_L)] \mathcal{E}_T + \left(1 - [1 - \exp(-\beta(1 - \tau_{\text{IL}})\tau_L)] \mathcal{E}_T\right) [1 - \exp(-\alpha\tau_{\text{IL}}\tau_L)], \quad (\text{C-6})$$

which shows that we can interpret this model in terms of an individual first attempting to learn the “correct” solution by SL, and if it is unsuccessful, it tries to acquire the correct phenotype by IL. This is equivalent to the learning strategy called *critical SL* (Enquist et al., 2007; Rendell et al., 2010).

Appendix D: haploid reproduction and connection to previous work

We here show that assuming haploid reproduction, we recover with our modeling framework the results about vertical transmission obtained by Kobayashi et al. (2015). As implied by eqs. 1–2 of Kobayashi et al., 2015, the contributions to culture from IL and SL are now given by

$$a_{\text{IL}}(\tau) = \alpha\tau_{\text{IL}}\tau_{\text{L}} \quad \text{and} \quad p_{\text{SL}}(\tau) = 1 - \exp(-\beta(1 - \tau_{\text{IL}})\tau_{\text{L}}). \quad (\text{D-1})$$

Then, to obtain a haploid version of cultural dynamics from our model, we simply drop the factor of diploid reproduction in eq. (18) and write the dynamics of cultural information as

$$\mathcal{E}_{t+1}(\tau, \theta) = a_{\text{IL}}(\tau) + p_{\text{SL}}(\tau, \beta) [v\mathcal{E}_t(\tau, \theta) + (1 - v)\mathcal{E}(\theta, \theta)], \quad (\text{D-2})$$

which at the equilibrium is

$$\mathcal{E}(\tau, \theta) = \frac{a_{\text{IL}}(\tau)}{1 - vp_{\text{SL}}(\tau)} + \frac{(1 - v)p_{\text{SL}}(\tau)}{1 - vp_{\text{SL}}(\tau)} \times \frac{a_{\text{IL}}(\theta)}{(1 - p_{\text{SL}}(\theta))}. \quad (\text{D-3})$$

According to eq. 4 of Kobayashi et al., 2015, fecundity is given by

$$f(\tau_{\text{L}}, \mathcal{E}(\tau, \theta)) = 1 + \mathcal{E}(\tau, \theta)(1 - \tau_{\text{L}}), \quad (\text{D-4})$$

which substituted into fitness (eq. 17) with eqs. (D-1) and (D-3), give that singular strategies are

$$s_{\text{IL}}(\theta) = 0 \quad \implies \quad \theta_{\text{IL}}^* = \frac{1}{\theta_{\text{L}}^*\beta}, \quad (\text{D-5})$$

and

$$s_{\text{L}}(\theta) = 0 \quad \implies \quad \beta(1 - \theta_{\text{L}}^*) - v = (1 - v) \exp(\beta\theta_{\text{L}}^* - 1). \quad (\text{D-6})$$

On substituting eq. (D-5) into the monomorphic equilibrium $\mathcal{E}(\theta, \theta)$ obtained from eq. (D-3) we further have

$$\mathcal{E}^* = \frac{1}{\beta} \exp(\beta\theta_{\text{L}}^* - 1). \quad (\text{D-7})$$

The latter three equations are equivalent, respectively, to eqs. (7a)-(7c) of Kobayashi et al. (2015).

The strong effect of pure vertical transmission observed in Kobayashi et al. (2015)'s study can be seen by considering the discount factor (eq. 25) for their model (using eq. D-2 into eq. 14),

$$\Lambda(\theta) = vp_{\text{SL}}(\theta), \quad (\text{D-8})$$

which is one when $v = 1$ and $p_{\text{SL}}(\theta) = 1$, i.e., costs on learning are completely discounted in the case of pure vertical transmission and complete SL. By contrast, in our model, this discount cannot exceed $1/2$. Note that costs could also be completely discounted in diploids if vertical transmission only occurred between mutants in mutant families so that eq. (D-2) holds.

Appendix E: individual-based simulations

We used Mathematica (Wolfram Research, 2016) to carry out individual-based simulation of the joint evolution of IL and SL in a population with N individuals for our explicit model, see section 2.4 (M-file available on request). Each individual in the population is characterized by an amount of adaptive information and two linked diploid loci that respectively determine additively the level of SL and IL performed by the individual. At the beginning of a generation (taken as stage (1) of the life cycle, see section 1.1), we calculate the fecundity f of each individual according to trait values and environmental variable (eq. (30)). Since we assumed semelparous reproduction (eq. 17) with constant population size, we then apply a Wright-Fisher reproductive process for diploids (Ewens, 2004). Namely, we form N mating pairs by sampling $2N$ individuals from the parental generation proportionally to their fecundity with replacement (hence the number of offspring produced by individual with fecundity f follows a Binomial distribution with parameters N and $f/(\bar{f}N)$ where \bar{f} is the mean fecundity in the population). Each mating pair produces an offspring that inherits a haplotype from each parent (randomly sampled in each parent, i.e., we assume random segregation). Each locus mutates and a mutation has an additive effect sampled from a Normal distribution with mean 0 and standard deviation σ . Quantitative loci values are truncated to remain between 0 and 1. Then we calculate the adaptive information of each offspring according to eq. (18). At the start of a simulation, the population is initially monomorphic for SL, IL and adaptive information value.

In order to produce Fig. 4, we started with a population set for 0.5 at each loci and adaptive information. We set high mutation effects with $\sigma = 0.01$ in order to speed up convergence. After a burn-in period of 5000 generations, we recorded the population average phenotypic values at each generation for a further 5000 generations. The temporal means and standard deviations are displayed in Fig. 4.

To test for evolutionary branching (Figs. 6 and 7), we started with a population at the evolutionary convergence stable singular values for θ_L and θ_{IL} and corresponding equilibrium adaptive information (eq. 20). We set low mutation effects $\sigma = 0.001$ and large population size $N = 10000$ as low population size prevents evolutionary branching (e.g., Wakano and Iwasa, 2013; Débarre and Otto, 2016). The population evolved for 1.5×10^5 generations.

Appendix F: numerical analysis when $\lambda > 0$

We here detail the numerical analyses we performed for the case where $\lambda > 0$ (section 2.4.2). First, we numerically studied which points are convergence stable by holding $\alpha = 2$ and varying

the other parameters by considering all combination of $v = 0, 0.25, 0.5, 0.75, 1$, $\beta = 2, 3, 5, 9, 12$, $\gamma_1 = 0, 0.1, 0.3, 0.7, 0.9$, $\gamma_2 = 1, 1.5, 2, 3, 5$, and $\lambda = 0.1, 0.3, 0.5, 0.7, 1$ (a total of 3125 parameter combinations). To do this, we iterated

$$\begin{aligned}\theta_L(t+1) &= \theta_L(t) + \delta s_L((\theta_L(t), \theta_{IL}(t))) \\ \theta_{IL}(t+1) &= \theta_{IL}(t) + \delta s_{IL}((\theta_L(t), \theta_{IL}(t))),\end{aligned}\tag{F-1}$$

using eqs. (23) and (27) with eqs. (29)–(30) and $\delta = 0.02$ until the euclidean distance between two iterates was less than 10^{-5} , i.e.,

$$\sqrt{(\theta_L(t+1) - \theta_L(t))^2 + (\theta_{IL}(t+1) - \theta_{IL}(t))^2} < 10^{-5},\tag{F-2}$$

or for a maximum of 10^5 steps. We started with 9 different starting values $(\theta_L(0), \theta_{IL}(0))$, with $\theta_L(0) = 0.05, 0.5, 0.95$ and $\theta_{IL}(0) = 0.05, 0.5, 0.95$. For each final values, we computed the eigenvalues of the Hessian matrix to assess local uninviability (Appendix B).

We find four outcomes for the convergence stability of θ_L and θ_{IL} . (1) θ_L always converges to zero, in which case selection on θ_{IL} vanishes (1134 cases). (2) There is a bistability and θ_L converges to either zero or to an interior value $0 < \theta_L^* < 1$, while individual learning θ_{IL} goes to one (i.e., no social learning, 689 cases). (3) There is a bistability and θ_L converges to either zero or both θ_L and θ_{IL} converge to an interior equilibrium $(\theta_L^*, \theta_{IL}^*)$ where θ_{IL} satisfies eq. (31) (1296 cases). (4) In very few cases (6), there are three convergence stable equilibria: either θ_L converges to zero; or θ_L converges to an interior value $0 < \theta_L^* < 1$ while individual learning θ_{IL} goes to one; or both θ_L and θ_{IL} converge to an interior equilibrium $(\theta_L^*, \theta_{IL}^*)$ (where θ_{IL} satisfies eq. (31)).

When we assess the local uninviability (using the eigenvalues of the Hessian matrix, Appendix B) of interior convergence stable equilibria $(\theta_L^*, \theta_{IL}^*) \in (0, 1)^2$, we find that they are also locally uninviability in the majority of cases (1290 out of 1302). In 12 cases (out of 1302), the interior convergence stable equilibria $(\theta_L^*, \theta_{IL}^*) \in (0, 1)^2$ was locally inviable, suggesting that learning undergoes disruptive selection at these equilibria. By looking at the parameter values under which disruptive selection occurs, we find that greater rates of vertical transmission (v) disfavour disruptive selection. For instance, when $\alpha = 2$, $\beta = 12$, $\gamma_1 = 0.7$, $\gamma_2 = 5$, $\lambda = 0.7$, the convergence stable point $(\theta_L^*, \theta_{IL}^*)$ is only uninviability when $v > 0.4$ (Fig. 7). Individual based simulations confirmed our analysis of disruptive selection, and showed that disruptive selection leads to evolutionary branching and the emergence of a polymorphism that can be maintained in the long run in some cases (Fig. 7).

References

Ajar, E. 2003. Analysis of disruptive selection in subdivided populations. *BMC Evolutionary Biology* 3:22.

- Aoki, K. 1986. A stochastic model of gene-culture coevolution suggested by the "culture historical hypothesis" for the evolution of adult lactose. *Proceedings of the National Academy of Sciences of the United States of America* 83:2929–2933.
- Aoki, K. and M. W. Feldman. 2014. Evolution of learning strategies in temporally and spatially variable environments: a review of theory. *Theoretical Population Biology* 91:3–19.
- Aoki, K., J. Y. Wakano, and L. Lehmann. 2012. Evolutionarily stable learning schedules in discrete generation models. *Theoretical Population Biology* 81:300–309.
- Boyd, R. and P. J. Richerson. 1985. *Culture and the Evolutionary Process*. University of Chicago Press, Chicago.
- Boyd, R., P. J. Richerson, and J. Henrich. 2011. The cultural niche: Why social learning is essential for human adaptation. *Proceedings of the National Academy of Sciences of the United States of America* 108:10918–10925.
- Bush, R. and F. Mosteller. 1951. A mathematical model for simple learning. *Psychological Review* 58:313–323.
- Caswell, H. 2000. *Matrix Population Models*. Sinauer Associates, Massachusetts.
- Cavalli-Sforza, L. and M. W. Feldman. 1981. *Cultural Transmission and Evolution*. Princeton University Press, NJ.
- Charlesworth, B. 1994. *Evolution in Age-Structured Populations*. Cambridge University Press, Cambridge, 2th edn.
- Cohen, J. E. 1979. Long-run growth rates of discrete multiplicative processes in Markovian environments. *Journal of Mathematical Analysis and Applications* 69:243–251.
- Débarre, F. and S. P. Otto. 2016. Evolutionary dynamics of a quantitative trait in a finite asexual population. *Theoretical Population Biology* 108:75–88.
- Demps, K., F. Zorondo-Rodríguez, C. García, and V. Reyes-García. 2012. Social learning across the life cycle: cultural knowledge acquisition for honey collection among the Jenu Kuruba India. *Evolution and Human Behavior* 33:460–470.
- Dugatkin, L. A. 2004. *Principles of Animal Behavior*. W. W. Norton and Company, London.
- Enquist, M., K. Eriksson, and S. Ghirlanda. 2007. Critical social learning: a solution to Rogers's paradox of nonadaptive culture. *American Anthropologist* 109:727–734.
- Eshel, I. and M. W. Feldman. 1984. Initial increase of new mutants and some continuity properties of ESS in two-locus systems. *The American Naturalist* 124:631–640.
- Ewens, W. J. 2004. *Mathematical Population Genetics*. Springer-Verlag, New York.

- Feldman, M. W., K. Aoki, and J. Kumm. 1996. Individual versus social learning: evolutionary analysis in a fluctuating environment. *Anthropological Science* 104:209–231.
- Feldman, M. W. and L. L. Cavalli-Sforza. 1976. Cultural and biological evolutionary processes, selection for a trait under complex transmission. *Theoretical Population Biology* 9:238–259.
- Feldman, M. W. and K. L. Laland. 1996. Gene-culture coevolutionary theory. *Trends in Ecology & Evolution* 11:453–457.
- Feldman, M. W. and L. A. Zhivotovsky. 1992. Gene-culture coevolution: toward a general theory of vertical transmission. *Proceedings of the National Academy of Sciences of the United States of America* 89:11935–11938.
- Ferrière, R. and M. Gatto. 1995. Lyapunov exponents and the mathematics of invasion in oscillatory or chaotic populations. *Theoretical Population Biology* 48:126–171.
- Fisher, R. A. 1930. *The Genetical Theory of Natural Selection*. Clarendon Press, Oxford.
- Frank, S. A. 1998. *Foundations of Social Evolution*. Princeton University Press, Princeton, NJ.
- Geritz, S. A. H., E. Kisdi, G. Meszéna, and J. A. J. Metz. 1998. Evolutionarily singular strategies and the adaptive growth and branching of the evolutionary tree. *Evolutionary Ecology* 12:35–57.
- Geritz, S. A. H., J. A. J. Metz, E. Kisdi, and G. Meszéna. 1997. Dynamics of adaptation and evolutionary branching. *Physical Review Letter* 78:2024–2027.
- Guglielmino, C. R., C. Viganotti, B. Hewlett, and L. L. Cavalli-Sforza. 1995. Cultural variation in Africa: role of mechanisms of transmission and adaptation. *Proceedings of the National Academy of Sciences of the United States of America* 92:7585–9.
- Hamilton, W. D. 1964. The genetical evolution of social behaviour, 1. *Journal of Theoretical Biology* 7:1–16.
- Hamilton, W. D. 1967. Extraordinary sex ratios. A sex-ratio theory for sex linkage and inbreeding has new implications in cytogenetics and entomology. *Science* 156:477–88.
- Hewlett, B. S., H. N. Fouts, A. H. Boyette, and B. L. Hewlett. 2011. Social learning among Congo Basin hunter-gatherers. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences* 366:1168–78.
- Kobayashi, Y. and K. Aoki. 2012. Innovativeness, population size and cumulative cultural evolution. *Theoretical Population Biology* 82:38–47.
- Kobayashi, Y. and J. Y. Wakano. 2012. Evolution of social versus individual learning in an infinite island model. *Evolution* 66.

- Kobayashi, Y., J. Y. Wakano, and H. Ohtsuki. 2015. A paradox of cumulative culture. *Journal of Theoretical Biology* 379:79–88.
- Konner, M. 2010. *The Evolution of Childhood*. Belknap, Harvard.
- Laland, K. L., F. J. Odling-Smee, and S. Myles. 2010. How culture shaped the human genome: bringing genetics and the human sciences. *Nature Reviews Genetics* 11:137–148.
- Lehmann, L. 2008. The adaptive dynamics of niche constructing traits in spatially subdivided populations: evolving posthumous extended phenotypes. *Evolution* 62:549–566.
- Lehmann, L., C. Mullan, E. Akçay, and J. Van Cleve. 2016. Invasion fitness, inclusive fitness, and reproductive numbers in heterogeneous populations. *Evolution* 70:1689–1702.
- Lehmann, L., J. Y. Wakano, and K. Aoki. 2013. On optimal learning schedules and the marginal value of cumulative cultural evolution. *Evolution* 67:1435–1445.
- Leimar, O. 2009. Multidimensional convergence stability. *Evolutionary Ecology Research* 11:191–208.
- Lessard, S. 1990. Evolutionary stability: one concept, several meanings. *Theoretical Population Biology* 37:159–170.
- Lumsden, C. J. and E. O. Wilson. 1981. *Genes, Mind and Culture*. Harvard University Press, MA.
- Maynard Smith, J. 1982. *Evolution and the Theory of Games*. Cambridge University Press, Cambridge.
- McElreath, R. and P. Strimling. 2008. When natural selection favors imitation of parents. *Current Anthropology* 49:307–316.
- Metz, J. A. J. 2011. Thoughts on the geometry of meso-evolution: collecting mathematical elements for a post-modern synthesis. In Chalub, F. A. C. C. and J. Rodrigues (eds.), *The mathematics of Darwin's legacy*, Mathematics and biosciences in interaction, pp. 193–231. Birkhäuser, Basel.
- Metz, J. A. J., S. A. H. Geritz, G. Meszéna, F. J. A. Jacobs, and J. S. van Heerwaarden. 1996. Adaptive dynamics: a geometrical study of the consequences of nearly faithful reproduction. In van Strien, S. J. and S. M. Verduyn Lunel (eds.), *Stochastic and Spatial Structures of Dynamical Systems*, pp. 183–231. North-Holland, Amsterdam.
- Michod, R. E. 1982. The theory of kin selection. *Annual Review of Ecology and Systematics* 13:23–55.
- Mullan, C., L. Keller, and L. Lehmann. 2016. Evolutionary stability of jointly evolving traits in subdivided populations. *American Naturalist* 188:175–195.

- Nagylaki, T. 1992. Introduction to population genetics. Springer-Verlag, Heidelberg.
- Nakahashi, W. 2010. Evolution of learning capacities and learning levels. *Theoretical Population Biology* 78:211–224.
- Nakahashi, W. 2013. Evolution of improvement and cumulative culture. *Theoretical Population Biology* 83:30–38.
- Pindyck, R. S. and D. L. Rubinfeld. 2001. Microeconomics. Prentice Hall, Upper Saddle River, NJ.
- Rendell, L., L. Fogarty, and K. N. Laland. 2010. Rogers' paradox recast and resolved: population structure and the evolution of social learning strategies. *Evolution* 64:534–548.
- Rogers, A. R. 1988. Does biology constrain culture? *American Anthropologist* 90:819–831.
- Rousset, F. 2004. Genetic Structure and Selection in Subdivided Populations. Princeton University Press, Princeton, NJ.
- Tuljapurkar, S. 1989. An uncertain life: demography in random environments. *Theoretical Population Biology* 35:227–94.
- Tuljapurkar, S., C. C. Horvitz, and J. B. Pascarella. 2003. The many growth rates and elasticities of populations in random environments. *American Naturalist* 162:489–502.
- van Baalen, M. 2013. The unit of adaptation, the emergence of individuality, and the loss of evolutionary sovereignty. In Huneman, P. and F. Bouchard (eds.), *From Groups to Individuals. Evolution and Emerging Individuality*, pp. 117–140. MIT Press.
- van Schaik, C. P. 2016. The Primate Origin of Human Behavior. Wiley-Blackwell, New Jersey.
- Wakano, J. Y. and K. Aoki. 2006. A mixed strategy model for the emergence and intensification of social learning in a periodically changing natural environment. *Theoretical Population Biology* 70:486–497.
- Wakano, J. Y., K. Aoki, and M. W. Feldman. 2004. Evolution of social learning: a mathematical analysis. *Theoretical Population Biology* 66:249–258.
- Wakano, J. Y. and Y. Iwasa. 2013. Evolutionary branching in a finite population: deterministic branching vs. stochastic branching. *Genetics* 193:229–241.
- Wakano, J. Y. and C. Miura. 2014. Trade-off between learning and exploitation: The Pareto-optimal versus evolutionarily stable learning schedule in cumulative cultural evolution. *Theoretical Population Biology* 91:37–43.
- Wolfram Research, I. 2016. Mathematica. Wolfram Research, Inc., Champaign, Illinois.

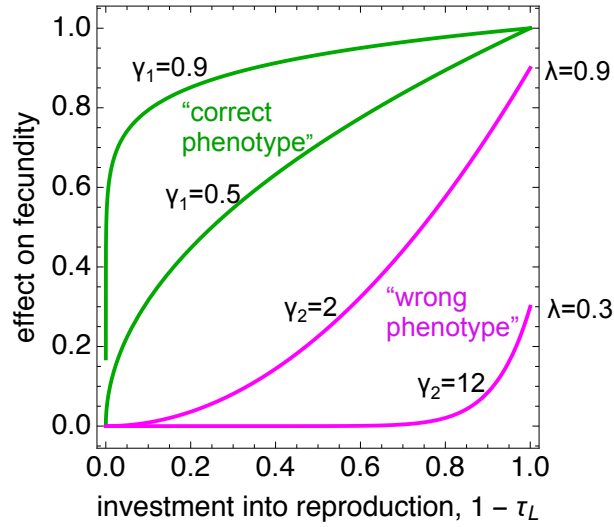


Figure 1: Components of the fecundity function (eq. 30) as a result of expressing the correct or wrong phenotype. When a mutant expresses the correct phenotype, it obtains rapidly rising returns on investment $((1 - \tau_L)^{1-\gamma_1}$ where $0 < \gamma_1 < 1$ tunes the sharpness of the rise, in green). When a mutant expresses the wrong phenotype, it obtains slowly rising returns on investment $(\lambda(1 - \tau_L)^{\gamma_2}$ where $\gamma_2 > 1$ controls how slowly the returns are and $0 \leq \lambda < 1$ bounds the returns, in pink). The total effect on fecundity eq. (30) is then given by the average returns, averaged over the probabilities of expressing the correct $(\mathcal{E}(\tau, \theta))$ and wrong $(1 - \mathcal{E}(\tau, \theta))$ phenotype.

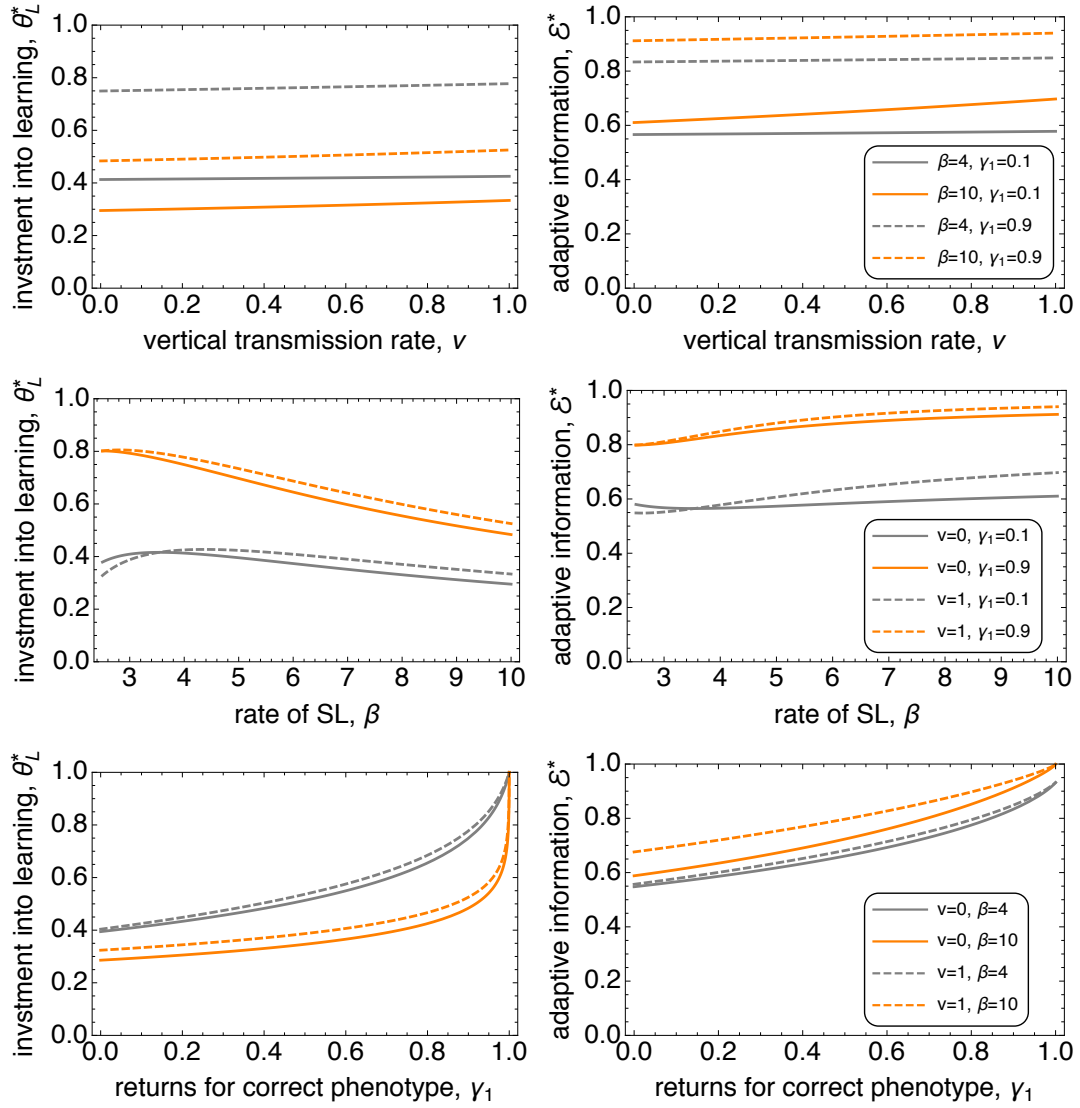


Figure 2: Singular learning strategy θ_L^* and the corresponding level of adaptive information \mathcal{E}^* it generates obtained from eqs. (31)-(34) with $\alpha = 2$ (other parameter values shown on graphs).

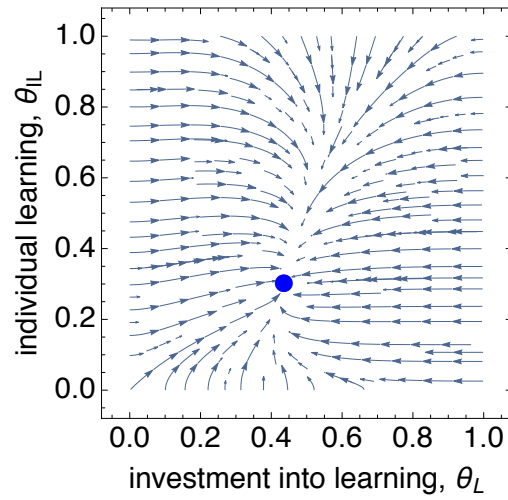


Figure 3: Phase portrait of the co-evolutionary dynamics of θ_L and θ_{IL} given by the selection gradients on each corresponding trait (eqs. 23 and 27 using eqs. 29–30 and $\lambda = 0$, other parameters: $\alpha = 1$, $\beta = 8$, and $\gamma_1 = 0.5$ and $v = 0.75$). The evolutionary dynamics converge to the single interior point shown in blue ($\theta_L^* = 0.436$, $\theta_{IL}^* = 0.306$), which is convergence stable as can be seen from the graph, and which can also be shown to be locally uninvadable (using Appendix B).

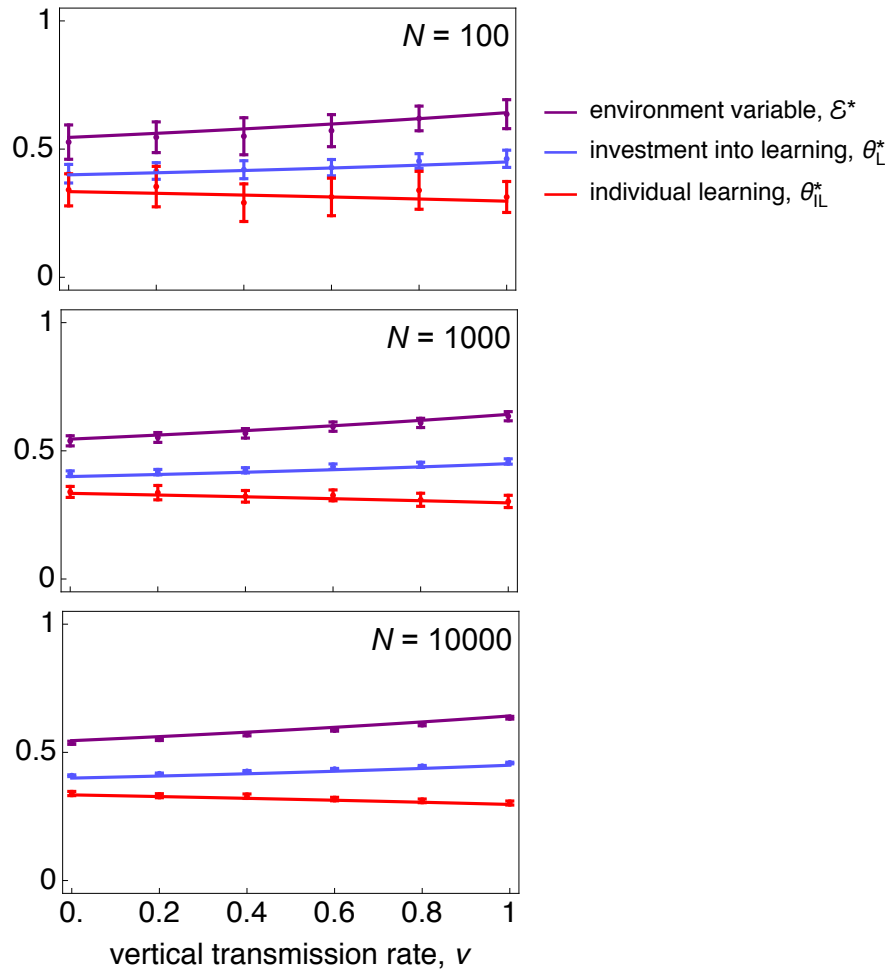


Figure 4: Comparison between analytical results and individual-based simulations. In each panel, analytical equilibria are shown in full lines (θ_L^* in blue, θ_{IL}^* in red, and \mathcal{E}^* in purple given by eqs. 31-34, with $\alpha = 1$, $\beta = 8$, and $\gamma_1 = 0.5$). The results of simulations (described in Appendix E) are given by the temporal population trait averages (points, same colour as lines) and the temporal standard deviation of population trait averages (error bars centred on averages, same colour as lines). The top panel is for a population size of $N = 100$, middle for $N = 1000$, and bottom for $N = 10000$, which show a good agreement between analytical predictions and simulation results, especially for large populations in which genetic drift has little effect and in which deviations between invasion analysis results and exact results for finite population based on fixation probabilities are of the order $1/N$ (Rousset, 2004).

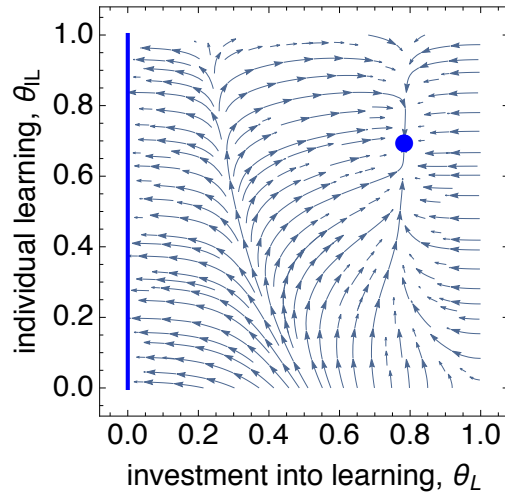


Figure 5: Phase portrait given by the selection gradients on each trait (eqs. 23 and 27 with $v = 0$, $\alpha = 2$, $\beta = 3$, $\gamma_1 = 0.9$, $\gamma_2 = 3$, $\lambda = 0.7$) and evolutionary convergence equilibria shown in blue (blue line for zero, and filled blue circle for convergence stable interior point), which shows that either θ_L converges to zero, or both θ_L and θ_{IL} converge to an interior equilibrium (θ_L^* , θ_{IL}^*) depending on the initial population values. As the graph shows, the co-evolutionary dynamics of θ_L and θ_{IL} exhibit bistability and the population must cross a threshold level of learning in order for selection to favour greater investment into learning.

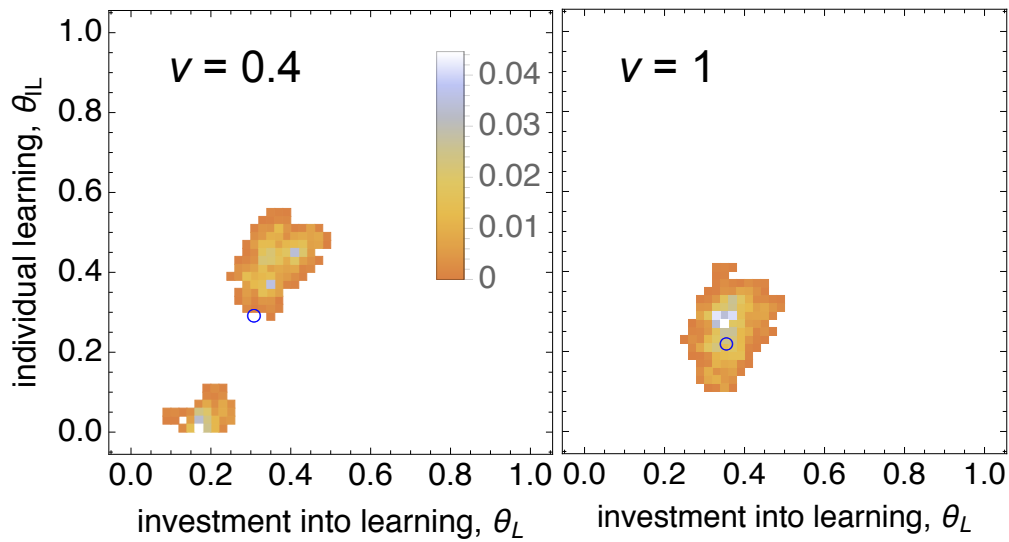


Figure 6: Evolutionary branching and stability. Bivariate distributions of trait values (θ_L and θ_{IL}), depicted as two-dimensional colour histograms with bins of width 0.02 and in which bin colour gives the frequency of individuals within each bin (see figure legend), obtained under individual-based simulations (frequencies averaged over the last 10^3 generations after 9.9×10^4 generations of evolution, parameters: $\alpha = 2$, $\beta = 12$, $\gamma_1 = 0.7$, $\gamma_2 = 5$, $\lambda = 0.7$, Appendix E for details). When $v = 0.4$, the population is split into two morphs around the interior convergence stable equilibrium ($\theta_L^*, \theta_{IL}^*$) (blue empty circle), but when $v = 1$ the population is unimodal, centred around the convergence stable equilibrium (blue empty circle).

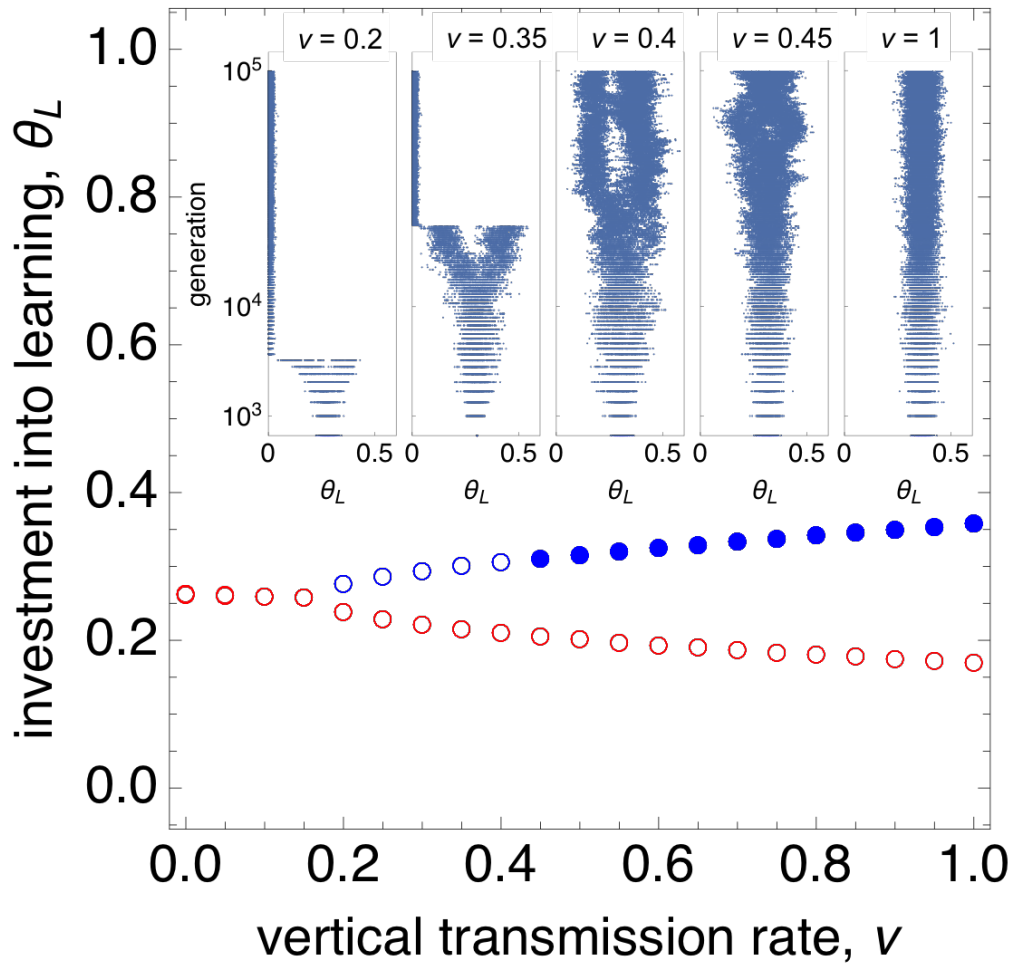


Figure 7: Evolutionary branching and vertical transmission. Outset: Interior singular learning strategies of θ_L according to vertical transmission rate, generated by computing the roots of the selection gradients (eqs. 23 and 27, other parameters: $\alpha = 2$, $\beta = 12$, $\gamma_1 = 0.7$, $\gamma_2 = 5$, $\lambda = 0.7$). For each singular value, we computed their convergence stability and local invadability (Appendix B). Red empty circles indicate singular strategies that are convergence unstable and thus represent threshold values above which learning is favoured by selection. Blue empty circles are convergence stable but invadable (i.e., potential evolutionary branching points), while blue filled circles are convergence stable and uninvadable (i.e., ESSs). Hence, the analytical model predict that for $0.4 \leq v \leq 1$ selection is stabilizing, for $0.2 \leq v \leq 0.4$ selection is disruptive, while for $v < 0.2$ there is no interior convergence stable point. Inset: values of θ_L for each individual in the population for every 500 generations under individual-based simulations started at the convergence stable singular value, where different panels correspond to different v values (Appendix E). As predicted by the model, we see that when $v > 0.4$, the population remains unimodal, when $0.2 \leq v \leq 0.4$, disruptive selection occurs, which results in evolutionary branching whereby the population splits into two morphs. However, when v decreases too much below 0.4, the two morphs are not maintained in the long run and the population converges to zero learning. This is because evolutionary branching causes the population to cross the threshold value of learning, resulting in the collapse of learning.