Coupled fast and slow feedbacks lead to continual evolution: A general modeling approach

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Abstract

The Red Queen Hypothesis, which suggests that continual evolution can result from solely biotic interactions, has been studied in macroevolutionary and microevolutionary contexts. While the latter has been effective in describing examples in which evolution does not cease, describing which properties lead to continual evolution or to stasis remains a major challenge. In many contexts it is unclear which assumptions are necessary for continual evolution, and whether described behavior is robust under perturbations. Our aim here is to prove continual evolution under minimal conditions and in a general framework, thus automatically obtaining robustness. We show that the combination of a fast positive and a slow negative feedback causes continual evolution with a single evolving trait, provided the ecological timescale is sufficiently separated from the timescales of mutations and negative feedback. Our approach and results form a next step towards a deeper understanding of the evolutionary dynamics resulting from biotic interactions.

1 Introduction

Species typically live in complex ecosystems with many interactions among them and external drivers. The evolutionary dynamics of a species in a complex ecosystem can be caused by the properties of the species, by the interaction with the coexisting species or by external drivers. To better understand to what extent the emerging ecological and evolutionary dynamics is caused by intrinsic properties of the species or biotic interactions (within- and between species interaction) we need to ignore abiotic drivers. Such an abiotically unchanging environment may lead to a static adaptive landscape, where the adaptation will follow a path towards a peak in that landscape—reachable or not[1]. Since the major part of any individual's environment typically is composed of other (evolving) species, any species' environment will in general change even without external abiotic variation, both through ecological and evolutionary changes. Hence, the adaptive landscape will be dynamic, which can lead to continual co-evolutionary dynamics, where traits over evolutionary time are fluctuating, escalating or chasing each other[2].

Of particular interest to us is the emergence of the so-called Red Queen Dynamics[3], a concept that has had a major influence on micro- and macroevolutionary theory. Stenseth and Maynard Smith[4] and others[5,6,7] have analyzed a macro-evolutionary model aiming at understanding under what conditions continual Red Queen dynamics and stasis results from within-system biotic interactions: Stenseth and Maynard Smith demonstrated that both could result depending upon the nature of the within system biotic interactions — without being able translated into ecological terms what these conditions were. Nordbotten and Stenseth[8] found that symmetric competitive interactions are more likely to lead to stasis. Another approach is studying interactions of a few species in more mechanistic detail, microevolutionary Red Queen (RQ) dynamics[2].

Theoretical studies of micro-evolutionary RQ dynamics mostly use methods based on adaptive dynamics and quantitative genetics[9,10,11,12,13,14]. The adaptive dynamics approach assumes the ecological dynamics have reached an equilibrium and studies the invasion of individuals with a slightly deviating phenotype of the

adaptive trait. The advantage of this approach is that it allows for a rigid theoretical analysis of the system. The quantitative genetics approach does not assume the ecological dynamics to be in equilibrium, but has a timescale separation between the evolutionary adaptation and the ecological dynamics. If the evolutionary rate of change is very slow, the quantitative genetics approach becomes similar to the adaptive dynamics approach. Both methods assume that adaptive traits evolve along a fitness gradient. Studies focussing on predator-prey and host-parasite systems have been able to reach conclusions about conditions that increase or decrease the chance of RQ dynamics in a specific setting (e.g. fast adaptation is less likely to lead to RQ dynamics[10] and RQ dynamics requires an intermediate harvesting efficiency of the prey[9]).

Most of the above mentioned studies use specific functional forms for their analysis, hampering the generalisation of the obtained results. Meta-analysis (such as the one by Abrams[15]) can provide some more general insights, but the conclusions are still limited, especially since many studies use similar equations. To obtain general results and therefore a broad understanding of what ecological interactions can cause certain evolutionary patterns, such as continual evolution, we need as general models as possible. With this contribution we aim at extending the theoretical understanding of under which conditions continual evolution and stasis will result. For this purpose we use a very general model with few assumptions regarding the form of the model functions. With such a general approach (making a minimum of assumption on the functional forms and the parameters) we increase the robustness of the obtained results. We find that a system with slow and fast feedback interactions exhibits continual Red Queen type of dynamics depending on the timescales. Moreover we allow for a polymorphic population, not constraining the distribution of phenotypes that may be present in the population, and mutations of small and large effects.

2 Model description and the emerging eco-evolutionary dynamics

2.1 Model description

In order to focus our argument, we use a general model of an evolving trait for a single species, which can be extended to multiple species:

$$\begin{aligned} \frac{du}{dt} &= u \cdot f(u, \varphi) + \epsilon_m \cdot g(u) \\ \frac{d\varphi}{dt} &= \epsilon_e \cdot h(u, \varphi). \end{aligned} \tag{1}$$

Here u represents the population density distribution over the trait space. In the general case the evolving trait is not specified and therefore its trait space could be anything. The external factors (abiotic factors, species without evolving traits) are captured in φ. The function $f(u, \varphi)$ describes the growth of the population (which can depend on the distribution in trait space u as well as the external factors φ). The function $g(u)$ describes the change in the trait due to mutations. The function g does not incorporate how well these phenotypes perform (the change due to mutations is modeled in an unbiased manor), the change of the trait to more fit individuals comes from the modelling of the growth of all phenotypes. The function $h(u, \varphi)$ describes the change in external factors, which can depend on the phenotype densities u. Time scale differences between growth, external factors and mutations are captured in ϵ_e and ϵ_m.

We include a possible polymorphic trait distribution (as is preferable argued by Law et al.[16] and also used in Van Der Laan and Hogeweg[17]). A polymorphic trait distribution arises easily with asexual reproduction or traits that are determined by a few loci, but can also arise when assortive mating develops (see the discussion in Kisdi et al.[18]). We use an approach including genetic variation by modeling the populations with differential equations, which also releases the assumption that mutations have to cause an infinitesimal change in the trait value.

An example of a slow negative feedback is a predator prey interaction, where the generation time of the predator is much slower than that of the prey and the predator predates preferable on prey with a specific phenotype. An example of the specificity of the predator is predators preferring a certain size of prey (e.g. bears preferring large salmon[19] or zooplankton preferring phytoplankton with a certain nitrogen:phosphorus ratio[14]). Other examples besides predator-prey interactions include: a herbivore that changes the vegetation which then becomes less suitable for the herbivore; micro-organisms that produce a compound that inhibits them but is diluted in a large volume (to achieve the feedback being slow); a species with a complex life cycle with a habitat shift (with an evolvable component), if a crowded habitat has a delayed effect on the

habitat quality; or a more complicated response of the whole ecosystem that leads to a negative feedback (e.g. with intransitive cycles as in Bonachela et al. [20]). The last example includes cases where the feedback is caused by human intervention, such as flu vaccinations—common viruses will be vaccinated against during the next season.

The fast positive feedback is an Allee effect on the phenotype. This could be due to for example finding mates (if the trait has effect on suitability of mates), cooperation in defense or in feeding. An example is when the adaptive trait is foraging on a certain vegetation type, the positive feedback could be that the more individuals forage in the same place, the better they are protected against predation. Or in the case of a habitat shift in the life cycle, similar habitat shift will share the second habitat with more individuals, providing mates or protection.

2.2 A single species with two phenotypes shows continual evolutionary dynamics when the negative feedback is sufficiently slow

The best way to understand the system is to reduce it to the simplest version. Therefore we start with an simple version of a trait with only two possible phenotypes, one that is interacting with a external feedback and one that is not (or less strongly) (see Figure 1A). Although the main objective of this simplification is to understand the mechanisms that lead to continual evolution, this representation also reflects a biological system where a trait is either present or not at all, e.g. choosing one host or another. When the trait also affects mate choice (e.g. because they will be located near the same host), the trait has a positive feedback. The slow negative feedback results from the fact that one of the hosts can develop defenses.

We analyse the system where both phenotypes and the feedback change over time. We assume that the phenotypes have a positive feedback effect, i.e. the more individuals with a certain phenotype, the higher the growth rate of that phenotype. To be precise, we study the following system with the interacting phenotype A (the phenotype choosing the host that can develop defenses), the (less) interacting phenotype B (the phenotype choosing the host that cannot develop defenses) and the feedback compound φ (the amount of defense in the host population that can develop defenses in the example):

$$\begin{aligned} \frac{dA}{dt} &= A \cdot f_A(A, B, \varphi) + \epsilon_m \cdot g(A, B) \\ \frac{dB}{dt} &= B \cdot f_B(A, B, \varphi) - \epsilon_m \cdot g(A, B) \\ \frac{d\varphi}{dt} &= \epsilon_e \cdot h(A, B, \varphi). \end{aligned} \tag{2}$$

The growth functions of the phenotypes f_A and f_B include the positive feedback. φ is increased more by A than by B which is incorporated in the function h. Mutations are possible from one phenotype to the other with the mutation function g. ϵ_m and ϵ_e denote the different timescales of the population dynamics (no ϵ), the feedback dynamics (ϵ_e) and the evolutionary dynamics (ϵ_m). We have modeled a positive effect of A on φ and a negative effect of φ on A, but all our results are also valid for the opposite, then we can substitute φ by $-\varphi$.

We prove that, for the system in Figure 1A and Equations (2) and with only slight restrictions on the functions f, g and h, if we can choose ϵ_e and ϵ_m sufficiently small, the system will exhibit continual evolution for almost all initial states. The detailed proof is in the Supplementary Information section 1.1 and 1.2; the reasoning is as follows: First, we prove the case of a constant population size, where we can describe our system by the feedback compound φ and the ratio (R) between the two phenotypes. Observing that the proof for this case does not rely upon knowing the exact value of $\frac{dR}{dt}$ but merely the *sign*, we can extend the proof to systems where the population size is not fixed, by adopting an assumption controlling the sign of $\frac{dR}{dt}$. There are several possibilities but we used the 'unique stable value assumption': when we keep φ fixed and know A there is only one value of B that guarantees a stable state, and likewise when we know B there is only one value of A. The proof only requires knowledge of the sign in a subregion of the domain.

The idea of the proof for a variable population size is illustrated in Figure 2B. The diagrams show an approximation of the dynamics in the (A,B) phase planes. This approximation is without the mutation term, but since mutations are rare (in our case the mutation term is small), the actual phase plane is very similar to the one shown. When at some point the feedback level is intermediate, there are 4 intersections of the lines $\frac{dA}{dt} = 0$ and $\frac{dB}{dt} = 0$ of which one is repelling (the origin), one is a saddle point (the point in the middle)

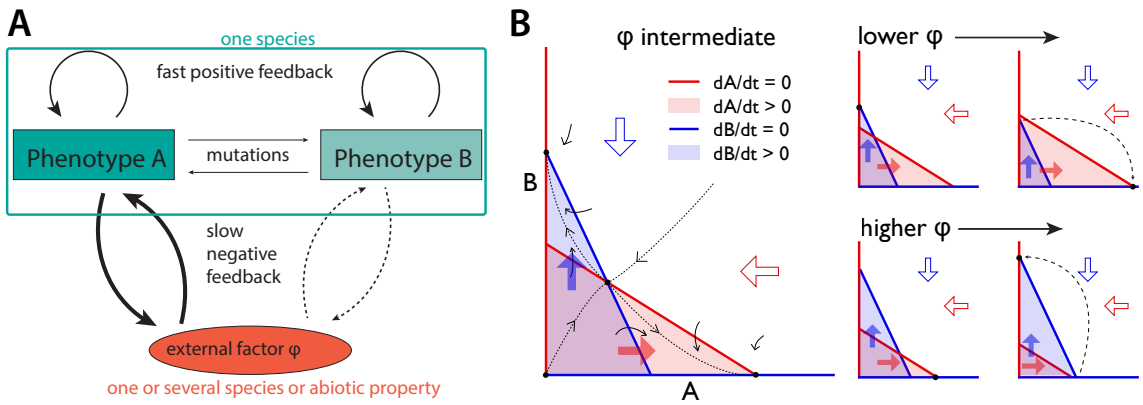

Figure 1: **Continual evolution with two phenotypes.** **A** A species has phenotypes A and B, which both have fast positive feedbacks on their own phenotype. Phenotype A has a strong negative feedback with an external factor φ (e.g. an external compound or other species such as a predator), while phenotype B has no, or a weaker, negative feedback. Mutations are possible between the two phenotypes, although rates are low. **B** The assumptions guarantee that the phase plane for intermediate φ resemble the one shown on the left. The isoclines for $dA/dt = 0$ and $dB/dt = 0$ cross as shown because the fast positive feedback ensures that the growth of phenotype B decreases faster with increasing A than the growth of phenotype A and vice versa. The system will either tend to the intersection of the dA/dt and dB/dt isoclines on the A or the B axis. Near the B axis φ will decrease and as shown on the top right the phase plane diagram will change such that the intersection will become unstable (dA/dt becomes positive) and the system will go to the stable equilibrium at the intersection at the A axis. Similarly, close to the A axis φ will increase, and the intersection near the A axis will become unstable. These properties will lead to continual evolution.

and the other two are attracting (the nature of the equilibria can be seen from the sign of the derivatives). Depending on the initial densities of A and B the system goes to an attracting point near the A-axis or the B-axis. When this is near the A-axis, B will be almost 0 and since A is interacting strongly with the feedback compound, φ will increase. This will in turn change the phase plane diagram and the intersection near the A-axis will become repelling. Then there is only one attracting intersection and that is near the B-axis and the system will approach that state. Since the dynamics in φ are slower than in A and B, the system will come close to the intersection near the B-axis before φ changes significantly. When φ changes we are back to the initial figure for intermediate φ, but now φ will continue to decrease and the intersection near the B-axis will disappear. This will continue indefinitely and therefore will lead to continual evolution.

We only need some restrictions on the functions f, g and h and do not use any functional forms in our proof. Figure 2 illustrates the simulation of an example system. We show continual evolutionary cycles for 2 different initial states if ϵ_e and ϵ_m are chosen sufficiently small. With a high mutation rate and/or a fast feedback a stable equilibrium will be reached (leading to stasis), while lack of mutations causes one of the two phenotypes to go extinct.

2.3 A multi-valued trait

For studying the case of a multi-valued trait, the evolving trait is represented as a range of values, and the external factor is represented by a scalar quantity (normalised between 0 and 1). We can then describe the system with the following set of differential equations:

$$\begin{aligned} \frac{du_i}{dt} &= u_i \cdot f(u, \varphi) + \epsilon_m \cdot g(u) \\ \frac{d\varphi}{dt} &= \epsilon_e \cdot h(u, \varphi). \end{aligned} \tag{3}$$

We split the population in discrete groups u_i with similar trait values. We show that the assumptions of a fast positive feedback and a slow negative feedback on the phenotype in this otherwise general model lead to continual evolution. These assumptions are given by restrictions on the functions f and h. We can extend the reasoning from the previous section to a multi-valued trait. With a multi-valued trait we mean

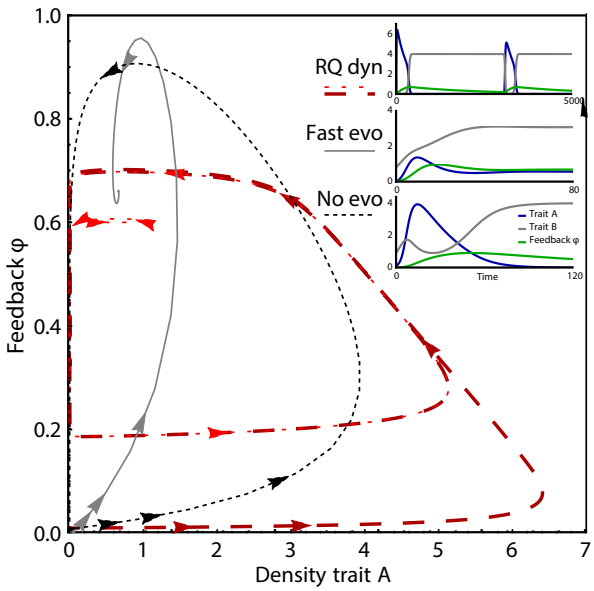

Figure 2: **Example system with two phenotypes.** Behaviour of a system following the outline of Fig 1A. Phase plane diagram of the density of individuals with phenotype A and the feedback φ shows the possible system behaviour depending on the relative timescales of population dynamics, the feedback and mutations. Slow feedback and mutations ($\epsilon_m = 0.00005$ and $\epsilon_e = 0.0005$) leads to continual cyclic evolutionary dynamics (Red Queen dynamics, red lines and top inset), almost independent of initial conditions (2 initial conditions are shown). With fast feedback and mutations ($\epsilon_m = 0.01$ and $\epsilon_e = 0.1$) an equilibrium is reached (gray line and middle inset). No evolution ($\epsilon_m = 0$ and $\epsilon_e = 0.01$) leads to the extinction of one of the traits (black dashed line and bottom inset). Equations are given in the Supplementary Material section 2.3.

a trait with more than two phenotypes or an approximation of a continuous trait, such as length or level of toxin production. An overview of the system is shown in Figure 3A, where the trait values are scaled from 0 to 1 according to the strength of their negative feedback. We call these phenotypes i, and the density of individuals with phenotype i is denoted by u_i. The feedback compound is again called φ and can be the same quantities as in the previous section. For the positive feedback we use the population average of the trait, which we call M. We assume that when the level of φ is so low that phenotypes with higher i have higher growth rates for a certain phenotype distribution, growth rates will keep increasing with i when we increase M (and vice versa, if φ is high and growth rates decrease with i, a decrease in M will not change this). We use the assumption that the growth rate is either strictly increasing or strictly decreasing in the trait (therefore one of the extreme traits always has the highest fitness).

Analogous to the system with two phenotypes, we can prove the existence of evolutionary fluctuations under conditions mimicking our earlier assumptions. In the multiple phenotype setting there is one subtle point in the proof, where an additional assumption is needed to guarantee relatively quick changes in phenotypes. One possible additional assumption guaranteeing such rapid fluctuations is the existence of mutations from any trait value to any other trait value. In practical settings this assumptions will not always be applicable. For example, the assumption is more realistic when the trait value describes enzyme levels or levels of toxin production, than when considering length of a species, as we expect length to evolve gradually. An alternative assumption will be discussed later.

The proof that we can choose the timescales to obtain continual evolutionary dynamics is outlined in Fig. 3B, and described in detail in the Supplementary Information section 1.3. Here we provide an outline: We scale φ also between 0 and 1 and without loss of generality may assume that φ tends to M. Then, when for example M is high and φ is low, φ will increase (blue arrows in Fig. 3B) because φ goes to M. At some point φ and M will cross, in which case M must already be declining and will continue to decline. The assumed fast positive feedback ensures that M decreases drastically in a time interval in which φ hardly changes, leading to symmetric conditions and hence continual evolutionary oscillations (green arrows in Fig. 3B).

Again our proof is context free and applies to a wide variety of equations; an example is given in Figure 4. In Figure 4A demonstrates that turning off evolution leads to extinction of all but one phenotype, fast feedback leads to an equilibrium, and slow feedback leads to continual fluctuations. Figure 4B shows the distribution

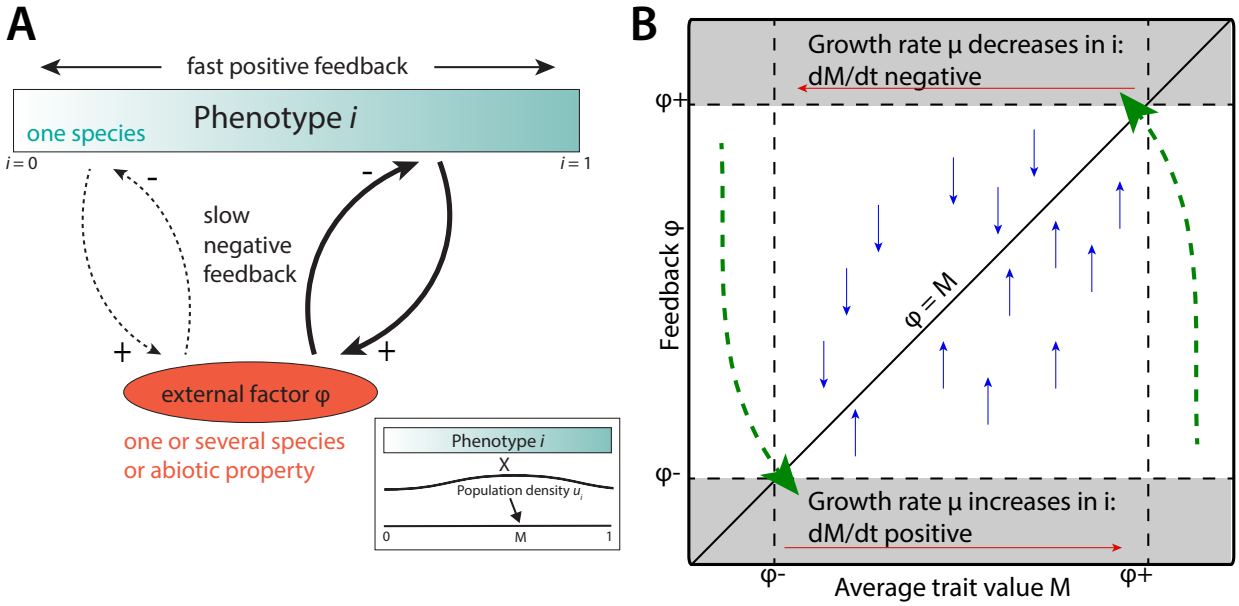

Figure 3: **System with a many-valued trait.** **A** One species has a multi-valued trait, with a phenotype ranging from $i = 0$ to $i = 1$. Higher values of i denote a stronger interaction with the negative feedback φ, which can be a species, an abiotic factor or a property of the ecosystem. The positive feedback is implemented as a high average trait value M leading to higher growth rates for larger trait values. The inset shows that M is calculated by taking the average trait value in the population, thus weighing the trait values by the density of that phenotype. **B** Outline of the proof in the (φ, M) plane. φ always goes to M (blue arrows), while M quickly increases when φ is small and quickly decreases when φ is large (red arrows). The combination of these effects leads to continual oscillating evolutionary dynamics (green arrows).

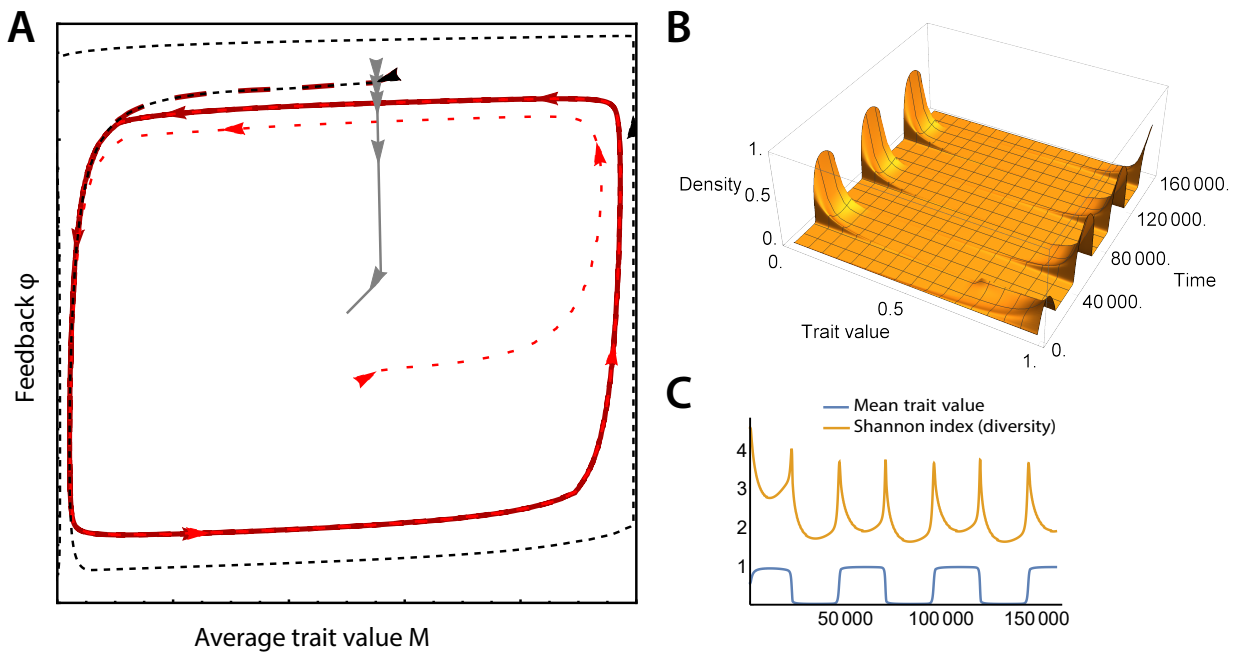

Figure 4: **Dynamics of a system with a multi-valued trait.** Behaviour of a system following the outline of Figure 3. **A** System behaviour for no evolution (thin dashed lines), slow evolution (red and solid dashed lines; RQ dynamics from different intital values) and fast evolution (gray dashed line, leading to an equilibrium). **B** Phenotype abundances from time simulations of the system with RQ dynamics. **C** Mean trait value and Shannon diversity (a diversity measure) show the oscillations. Simulation of 100 phenotypes equally distributed over the range of trait values (40 phenotypes for the phenotype abundances). See Supplementary Information section 2.4 for the equations and parameters.

of phenotypes over time, and in 4C it is shown that the diversity of phenotypes increases at shifts of the mean trait value.

If we do not want to assume the existence of mutations from any phenotype to any other phenotype, we can adopt an alternative assumption, namely that the negative feedback is chosen sufficiently slow *depending on* the rate of mutations. In some circumstances this may even mean that the rate at which φ changes is even slower than the mutation rate. This alternative assumption again may or may not be desirable in practice.

2.4 Extensions to multiple feedbacks

In natural systems, multiple traits determine the fitness in an individual. An extension of our model to more traits will give a more realistic picture of the dynamics we expect in natural populations. We extended the system to a species with two different traits that are both associated with a different negative feedback. The number of possible phenotypes is now the product of the number of phenotypes for each of the traits. In the most simple case, there are four phenotypes in the population: (1) high susceptibility for both feedbacks, (2) low susceptibility for both feedbacks, and (3 and 4) high susceptibility for one and low for the other (Figure 5A). Simulations with this extended system show that this system can also lead to continual adaptation and that the dynamics generally become irregular (Figure 5B). Looking at the change of the diversity index over time, we can conclude that there is no fixed period in the dynamics (Figure 5C). The example with multiple traits shows that we do not expect a natural system to come back to exactly the same state in a regular fashion.

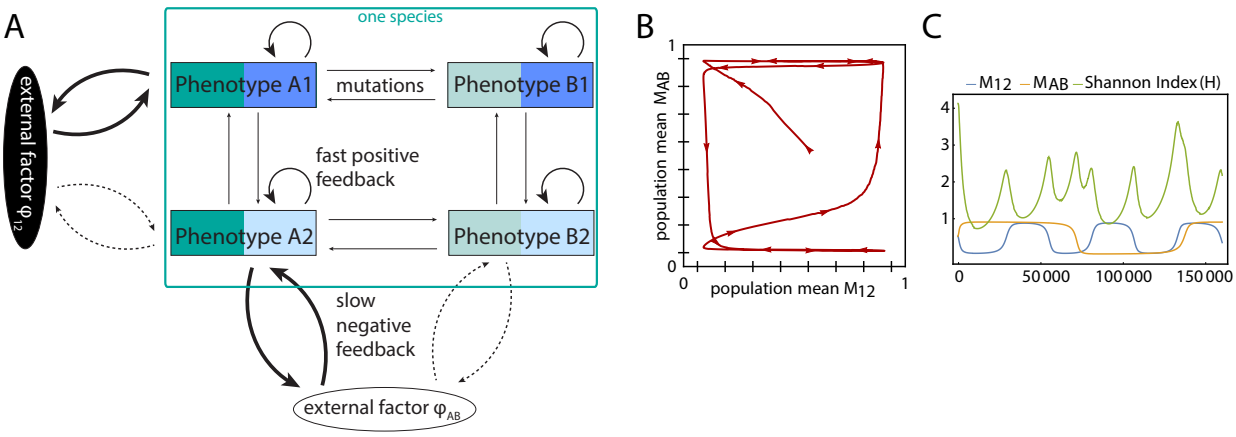

Figure 5: **Species with two traits associated with two different feedbacks.** **A** There are two external feedbacks (φ_1 and φ_A) and in the simplest case two phenotypes associated with each feedback, leading to 4 phenotypes in total. More phenotypes per trait are also possible, leading to a total number of phenotypes as the product of the phenotypes for each trait. **B** The change in mean population phenotype (M) for both traits (i_1 and i_A) in time for an example with more phenotypes per trait. Ticks on the axes show possible individual phenotypes used in the simulation. **C** Mean trait values and diversity over time. With more than one trait periods are not as regular as can be seen from the non-periodic Shannon Index (H). Equations and parameters for the figure are given in the Supplementary Material section 2.5.

3 Discussion

We have shown that a simple motif of fast positive feedback and slow negative feedback leads to continual evolution. Instead of working with a specific model we have shown that continual evolution occurs for other similar models. We allow for phenotypic variation in the population and large effect mutations. We automatically show robustness to model form, because the evolutionary dynamics do not depend on specific equations or parameter values, and also robustness to small fluctuations. Large fluctuations might affect the dynamics, but because our dynamics are reachable from almost all initial conditions, the system will return to continual evolution after a large fluctuation. Previously, it has been shown that continual evolution can be found in specific simple models. In the literature robustness is indicated by showing that a range of parameter values or a different equation will lead to the same result[21,10]. Here we try to avoid the use of

specific equations and parameter values to obtain more general results and stronger robustness. Previous examples of papers not using specific functional forms consider the possibility of the occurrence of evolutionary sliding[21], the conclusion that symmetric interactions are more likely to lead to stasis[8] and the Red Queen evolution in bacterial communities with cyclic inhibition in three species[20], although all of these papers include some restrictions on the models. Dercole et al.[21] focusses only on slow-fast models with separated timescales, Nordbotten and Stenseth[8] only consider bilinear species interactions and Bonachela et al.[20] only consider a fixed set of three species that form a non-transitive cycle with their species interactions.

Our results are accompanied by specific examples, but the results are not restricted to those examples. In all our examples the continual evolutionary dynamics stem from switching between multiple ecological attractors that are steady states (ecogenetically driven Red Queen Dynamics mode B[22]). Our conclusions remain the same when these attractors are limit cycles instead of steady states. An example of this type of dynamics is given in Khibnik and Kondrashov[22] Figure 4 and, interestingly, directly using our assumptions on this example removes the evolutionary oscillations (only ecological cycles remain, with ecologically driven Red Queen Dynamics—that is fluctuations in traits are fast and small and only follow the ecological population density dynamics). However, when we make the negative feedback slower by decreasing the parameters for the predator dynamics tenfold (parameters r4 and γ), we retrieve the ecogenetically driven Red Queen Dynamics (results not shown).

Some of our results are in line with and extend previous conclusions. The dynamics of the continual evolution are very similar to microevolutionary Red Queen dynamics; the difference is that continual evolution does not require co-evolution. Khibnik and Kondrashov[22] mention that Red Queen dynamics with a single evolving trait are possible when the dynamics are ecologically driven (the traits follow ecological dynamics) or ecogenetically driven and switching between two different ecological attractors. Continual evolution of a single trait might be quite prevalent, since examples include predator-prey systems in which the prey evolves but the predator does not (or much slower; as might be relatively common, see e.g. Vermeij[23]). Moreover, our two trait example reproduces the result that fast adaptation is less likely to lead to RQ dynamics[10]. A new observation is that for a multi-valued trait, evolution should not be too slow relative to the negative feedback, and that ecology and evolutionary dynamics can influence each other. The rationale behind this is that the average population trait has to change drastically while the level of the negative feedback variable changes relatively little. If a trait evolved gradually that means that evolution should not be too much slower than the dynamics of the feedback, because then the feedback would 'catch up' with the average population trait while this average is near the equilibrium value. An experimental example of such kind of dynamics is that in cases such as a predator-prey system with a slow predator, the non-optimal predator phenotypes might stay in the population and not go extinct. In that case the species does not need to get a de novo mutations, but can get the new phenotype through selection and recombination. An example is a laboratory system of an algae and a rotifer[24]. This type of RQ dynamics where the traits stay in the population will be more common in higher organisms and is an example of evolutionary rescue. Faster evolutionary change through mutations might also occur when species are regularly exposed to different environments and evolve adaptability[25,26].

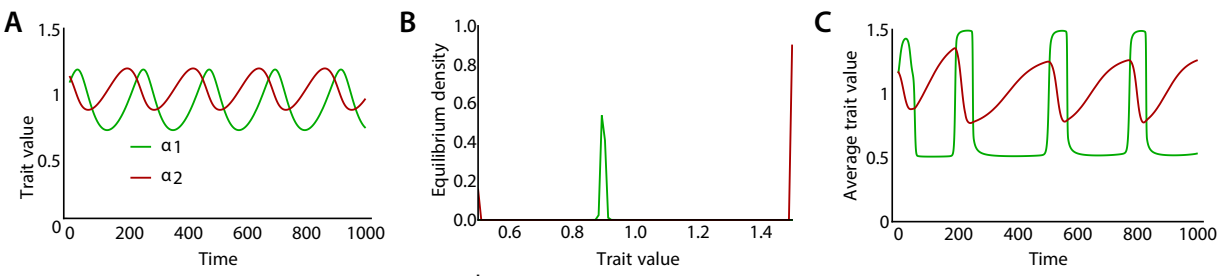

Figure 6: **RQ dynamics disappears when adding polymorphism to a population.** **A** The competitor-competitor model of Khibnik and Kondrashov[22] shows the evolvable trait (α) of the two competitors following each other in a RQ manner (figure replicated from figure 2 in Khibnik and Kondrashov[22]). **B** When we allow for a polymorphic population the system tends to a bimodal distribution for the trait α_2. **C** When we change the timescales (we made the dynamics of competitor two ten times slower), the RQ dynamics return. For equations and parameters see 2.6.

Phenotypic variation is often left out of Red Queen dynamics analysis. Outright restricting phenotypic variation can have a pronounced effect on the results. We have adapted a competitor-competitor model (Figure 6A) with originally an adaptive dynamics approach that previously showed Red Queen Dynamics to an in-

stance with our assumptions (the possibility of a polymorphic trait distribution and larger mutations). As shown in Figures 6B, switching to the modelling approach used in this paper removes the RQ dynamics that were found in the original paper. However, when we change the timescales and make the feedback (competitor species in this example) slower, we retrieve the feedback, in line with the results of this paper (see Figure 6C). In Mougi and Iwasa [10], the RQ dynamics remain with phenotypic variation (data not shown), but there the RQ dynamics are ecologically driven: the adaptation follows the ecological predator-prey cycles. Other methods that do include phenotypic varions are the model by Dieckmann et al. [9], which does contain a polymorphic model which, different from our model, is also stochastic; models of evolutionary branching and extinction using adaptive dynamics (summarized in Kisdi et al. [18]); and Van Der Laan and Hogeweg [17], where a Lotka-Volterra predator-prey model with a polymorphic population similar to our methods shows examples of RQ dynamics.

Collecting evidence of RQ dynamics from natural systems is a difficult task [15] and in experiments the long term of the measurements is a problem. One experiment that shows the effect of evolution on predator-prey dynamics [10] suggests RQ dynamics, but due to the measurement time it cannot be excluded that the cycles will dampen. While there is an increase in long term adaptation experiments these are usually in bacterial systems while most of the modelling has focused on sexually reproducing predator-prey communities. Here we have tried to include these systems by allowing for phenotypic variation and larger mutation effect sizes. In bacterial systems polymorphic populations are common, even under reasonably constant conditions as recently shown in the Long Term Evolution Experiment with *E. coli* [27]. The polymorphic trait distribution might result from density dependent dynamics, as shown theoretically in a chemostat [28]. Therefore our results are an important addition for linking theoretical to experimental observations of evolutionary dynamics.

Although we have tried to keep the modelling in this paper general, our results have some limitations. We show that with some assumptions we can guarantee that continual dynamics will arise with enough time scale separation. Systems that do not follow our assumptions (e.g. fast negative feedbacks, no positive feedback) are more likely to lead to stasis. However we do not prove any conditions that necessarily lead to stasis. Although we tried to keep our equations general, we did not include individual variation within the population. It would be interesting to see if we can combine the methods used in this paper with the polymorphic population and link of the ecological and evolutionary timescales with individual-based models. We limited our results here to only one evolving population, but the feedback we describe could come from another evolving species or be a result of a complex ecosystem. A next step would be to extend this mathematical approach to more than one evolving species. The results in this paper are constrained to micro-evolutionary dynamics, it would be interesting to extend these results to macro-evolutionary phenomena. In this line, there is a nice analogy with the results of Doebeli and Ispolatov [29]. They show that most coevolutionary dynamics are found with intermediate diversity, where not all niches are filled. Here we see that if we get diversification, and therefore more different phenotypes, the co-evolutionary dynamics cease.

Without constraining both the functional forms used in our model and the phenotypic diversity within the system we have demonstrated that a fast positive feedback combined with a slow negative feedback always leads to continual dynamics with the proper timescales. By so doing we have improved the understanding of continual evolution and co-evolution in a large class of models, and may be used to predict evolutionary dynamics without knowledge of the exact equations describing the system.

References

[1] Michael J Wiser, Noah Ribeck, and Richard E Lenski. Long-term dynamics of adaptation in asexual populations. *Science*, 342(6164):1364–1367, 2013.

[2] Michael A Brockhurst, Tracey Chapman, Kayla C King, Judith E Mank, Steve Paterson, and Gregory DD Hurst. Running with the red queen: the role of biotic conflicts in evolution. *Proceedings of the Royal Society of London B: Biological Sciences*, 281(1797):20141382, 2014.

[3] Leigh Van Valen. A new evolutionary law. *Evolutionary theory*, 1:1–30, 1973.

[4] Nils Chr Stenseth and J Maynard Smith. Coevolution in ecosystems: Red queen evolution or stasis? *Evolution*, 38(4):870–880, 1984.

[5] Geerat J Vermeij and Peter D Roopnarine. Reining in the red queen: the dynamics of adaptation and extinction reexamined. *Paleobiology*, 39(4):560–575, 2013.

[6] Lee Hsiang Liow, Leigh Van Valen, and Nils Chr Stenseth. Red queen: from populations to taxa and communities. *Trends in ecology & evolution*, 26(7):349–358, 2011.

[7] Kjetil L Voje, Øistein H Holen, Lee Hsiang Liow, and Nils Chr Stenseth. The role of biotic forces in driving macroevolution: beyond the red queen. *Proc. R. Soc. B*, 282(1808):20150186, 2015.

[8] Jan Martin Nordbotten and Nils C Stenseth. Asymmetric ecological conditions favor red-queen type of continued evolution over stasis. *Proceedings of the National Academy of Sciences*, 113(7):1847–1852, 2016.

[9] Ulf Dieckmann, Paul Marrow, and Richard Law. Evolutionary cycling in predator-prey interactions: population dynamics and the red queen. *Journal of theoretical biology*, 176(1):91–102, 1995.

[10] Akihiko Mougi and Yoh Iwasa. Evolution towards oscillation or stability in a predator–prey system. *Proceedings of the Royal Society of London B: Biological Sciences*, page rspb20100691, 2010.

[11] Paul Marrow, Richard Law, and C Cannings. The coevolution of predatorprey interactions: Esss and red queen dynamics. *Proc. R. Soc. Lond. B*, 250(1328):133–141, 1992.

[12] Paul Marrow and Chris Cannings. Evolutionary instability in predator-prey systems. *Journal of theoretical biology*, 160(2):135–150, 1993.

[13] Ulf Dieckmann and Richard Law. The dynamical theory of coevolution: a derivation from stochastic ecological processes. *Journal of mathematical biology*, 34(5-6):579–612, 1996.

[14] Pedro Branco, Martijn Egas, James J Elser, and Jef Huisman. Eco-evolutionary dynamics of ecological stoichiometry in plankton communities. *The American Naturalist*, 192(1):E000–E000, 2018.

[15] Peter A Abrams. The evolution of predator-prey interactions: theory and evidence. *Annual Review of Ecology and Systematics*, 31(1):79–105, 2000.

[16] Richard Law, Paul Marrow, and Ulf Dieckmann. On evolution under asymmetric competition. *Evolutionary Ecology*, 11(4):485–501, 1997.

[17] Jan D Van Der Laan and Pauline Hogeweg. Predatorprey coevolution: interactions across different timescales. *Proc. R. Soc. Lond. B*, 259(1354):35–42, 1995.

[18] E Kisdi, FJA Jacobs, and SAH Geritz. Red queen evolution by cycles of evolutionary branching and extinction. *Selection*, 2(1-2):161–176, 2002.

[19] SM Carlson, TP Quinn, and AP Hendry. Eco-evolutionary dynamics in pacific salmon. *Heredity*, 106 (3):438, 2011.

[20] Juan A Bonachela, Meike T Wortel, and Nils Chr Stenseth. Eco-evolutionary red queen dynamics regulate biodiversity in a metabolite-driven microbial system. *Scientific reports*, 7(1):17655, 2017.

[21] F Dercole, R Ferriere, A Gragnani, and S Rinaldi. Coevolution of slow–fast populations: evolutionary sliding, evolutionary pseudo-equilibria and complex red queen dynamics. *Proceedings of the Royal Society of London B: Biological Sciences*, 273(1589):983–990, 2006.

[22] Alexander I Khibnik and Alexey S Kondrashov. Three mechanisms of red queen dynamics. *Proceedings of the Royal Society of London B: Biological Sciences*, 264(1384):1049–1056, 1997.

[23] Geerat J Vermeij. Unsuccessful predation and evolution. *The American Naturalist*, 120(6):701–720, 1982.

[24] Takehito Yoshida, Laura E Jones, Stephen P Ellner, Gregor F Fussmann, and Nelson G Hairston Jr. Rapid evolution drives ecological dynamics in a predator–prey system. *Nature*, 424(6946):303, 2003.

[25] Anton Crombach and Paulien Hogeweg. Chromosome rearrangements and the evolution of genome structuring and adaptability. *Molecular biology and evolution*, 24(5):1130–1139, 2007.

[26] Anton Crombach and Paulien Hogeweg. Evolution of evolvability in gene regulatory networks. *PLoS computational biology*, 4(7):e1000112, 2008.

[27] Benjamin H Good, Michael J McDonald, Jeffrey E Barrick, Richard E Lenski, and Michael M Desai. The dynamics of molecular evolution over 60,000 generations. *Nature*, 551(7678):45, 2017.

[28] Meike T Wortel, Evert Bosdriesz, Bas Teusink, and Frank J Bruggeman. Evolutionary pressures on microbial metabolic strategies in the chemostat. *Scientific reports*, 6:29503, 2016.

[29] Michael Doebeli and Iaroslav Ispolatov. Diversity and coevolutionary dynamics in high-dimensional phenotype spaces. *The American Naturalist*, 189(2):105–120, 2017.