

Interim Report

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Adaptive Dynamics as a Mathematical Tool for Studying the Ecology of Speciation Processes

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3	Adaptive dynamics as a mathematical tool for studying the ecology of
4	speciation processes
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7	
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16 After Ernst Mayr published his seminal book in 1963 (Mayr 1963), the issue of speciation 17 appeared to be settled: according to the established dogma, biological diversification occurred in allopatry due to the accumulation of genetic differences in geographically 18 19 isolated populations. Despite repeated challenges, this view still prevails today, although 20 perhaps less dominantly than before. The earliest rigorous theoretical challenge was 21 provided by Maynard Smith (1966), who produced the first models of speciation in 22 sympatry. These models were based on very simple ecological and genetic assumptions, 23 with two resource types (or niches) and two loci, one for ecological performance and one 24 for mate choice. Despite its simplicity, this type of model has formed the conceptual basis 25 for most of the theory of sympatric speciation that has been developed since then 26 (Kawecki 2004).

27

28 For sympatric speciation to occur in sexual populations, two processes must unfold. First, 29 frequency-dependent interactions must generate disruptive selection. Second, a lineage 30 split in sexual populations requires the evolution of assortative mating mechanisms. 31 Skepticism towards the feasibility of both these processes has led to a dismissal of 32 sympatric speciation as a plausible mode of diversification. For example, based on 33 Felsenstein's (1981) seminal paper, it has long been thought that recombination between 34 traits under disruptive selection and mating traits responsible for assortativeness can be a 35 significant hindrance to the evolution of reproductive isolation between diverging 36 lineages. Similarly, one of the main reasons why the theoretical developments following 37 in the footsteps of Maynard Smith's model failed to convince speciation researchers was 38 that these models seemed to rely on rather particular ecological circumstances, such as

39	host race formation (Diehl and Bush 1989), and that the ecological conditions for the
40	emergence of disruptive selection in these models were rather restrictive (Kassen 2002,
41	Kawecki 2004).
42	
43	However, there is another line of thinking about the ecology of speciation that already
44	started – how else could it be? – with Darwin, who concluded:
45	
46	"Consequently, I cannot doubt that in the course of many thousands of
47	generations, the most distinct varieties of any one species [] would always have
48	the best chance of succeeding and of increasing in numbers, and thus of
49	supplanting the less distinct varieties; and varieties, when rendered very distinct
50	from each other, take the rank of species." (Darwin 1859, p. 155)
51	
52	According to this view, and in modern parlance, frequency-dependent competition
53	between similar ecological types can lead to disruptive selection and diversification. This
54	perspective was embodied in the concept of competitive speciation by Rosenzweig
55	(1978) and further studied by Seger (1985), who presented the first mathematical model
56	showing that frequency-dependent competition for occupation of a niche continuum can
57	induce sympatric speciation under certain conditions. More generally, it was argued by
58	Kondrashov (1986) that frequency-dependent selection on a continuous character can
59	induce bimodal splits in the character distribution, with the two modes representing
60	emerging species. In Kondrashov's models, the disruptive selection regime giving rise to
61	bimodality is simply a consequence of the a priori assumption that the fitness of common

62	types is low, while that of rare types is high. It is difficult to assess the generality of these
63	models, because it is not clear under what conditions ecological interactions would
64	generate such a frequency-dependent selection regime. In fact, it is known that both
65	competitive interactions (Christiansen 1991) and predator-prey interactions (Abrams et
66	al. 1993) can generate evolutionary scenarios in which the population mean of a
67	continuous trait (such as body size) evolves to a state in which selection becomes
68	disruptive. However, somewhat surprisingly, these results were never put into the
69	common context of speciation, perhaps because these studies used the framework of
70	quantitative genetics and thus assumed Gaussian phenotype distributions with constant
71	variances (and hence implicitly assumed random mating).
72	
73	Overall, it thus remained questionable whether the emergence of disruptive selection due
74	to frequency-dependent interactions would be a general and plausible ecological scenario.
75	In fact, it still seems to be the common wisdom that the origin and maintenance of
76	diversity due to frequency-dependent selection regimes requires a delicate balance of
77	different ecological factors (e.g., Kassen 2002), and that, consequently, most biological
78	diversification occurs in allopatry.

We believe that the advent of adaptive dynamics, and in particular the discovery of the
phenomenon of evolutionary branching, will change this perspective fundamentally
(Dieckmann et al. 2004). Adaptive dynamics is a general framework for studying
evolution of quantitative characters due to frequency-dependent interactions. Within this
framework, evolutionary branching points represent potential springboards for sympatric

85 speciation: even though such points are attractors for the adaptive dynamics of a 86 unimodal quantitative trait, populations that have converged on such a point experience frequency-dependent disruptive selection for adaptive and sympatric diversification. 87 88 Technically speaking, evolutionary branching points are singular points of the adaptive 89 dynamics that satisfy certain general mathematical conditions. The existence and location 90 of such points can readily be investigated in any adaptive dynamics model, following 91 simple and general procedures. Therefore, the concept of evolutionary branching points 92 serves as a unifying principle for investigating the ecological conditions for adaptive 93 diversification and speciation. Using the tools of adaptive dynamics theory, any 94 ecological scenario can be investigated as to its potential for giving rise to diversification, 95 thus rendering obsolete the conceptually isolated and often idiosyncratic analysis of 96 different ecological scenarios.

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98 In fact, it has become clear from numerous studies over the past few years that 99 evolutionary branching points are a robust feature of many different adaptive dynamics 100 models (e.g., Metz et al. 1996, Doebeli and Ruxton 1997, Meszéna et al. 1997, Geritz et 101 al. 1998, Kisdi 1999, Dieckmann and Doebeli 1999, Kisdi and Geritz 1999, Parvinen 102 1999, Doebeli and Dieckmann 2000, Law et al. 2001, Maire et al. 2001, Van Doorn et al. 103 2001, Doebeli 2002, Claessen and Dieckmann 2002, Mizera and Meszéna 2003, Doebeli 104 and Dieckmann 2003, Bowers et al. 2003, Van Doorn et al. 2004; for a much more 105 exhaustive list of models of evolutionary branching, readers might wish to consult the 106 following website: www.helsinki.fi/~mgyllenb/addyn.htm). Thus, condensing the 107 ecological conditions for sympatric speciation in the concept of evolutionary branching

108 points supports the insight that the emergence of disruptive selection due to frequency-109 dependent interactions is an entirely plausible, and in fact ubiquitously applicable 110 evolutionary scenario. To us, this appears to be an important development, which 111 Waxman and Gavrilets (2005) ignored in their discussion of adaptive dynamics in the 112 context of sympatric speciation, thereby essentially claiming that no new advances over 113 previous models can be gained from the unifying perspective of evolutionary branching. 114 This is hard to understand in view of the fact that it is always a goal of the scientific 115 enterprise to find general principles of which any particular scenarios can be seen as 116 special cases.

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118 Instead of recognizing the potentially fruitful role that adaptive dynamics theory can play 119 in providing a general framework for studying the ecological conditions required for 120 sympatric speciation, Waxman and Gavrilets criticize those aspects of recent speciation 121 models that go beyond the clonal theory of adaptive dynamics by addressing the genetic 122 splitting of initially randomly mating sexual populations. As mentioned above, the 123 evolution of assortative mating mechanisms is of course a crucial component of any 124 model of sympatric speciation. In general, one envisages two different scenarios 125 (Kirkpatrick and Ravigne 2002, Dieckmann and Doebeli 2004): with direct assortative 126 mating, assortative mating is based on the character that is under disruptive selection; 127 with indirect assortative mating, assortative mating is based on some ecologically neutral 128 marker traits. In both cases, the degree of assortativeness may be assumed to be either 129 fixed, or may itself be an evolving trait.

131 With direct assortative mating, a population under frequency-dependent disruptive 132 selection splits into two reproductively isolated subpopulations when the degree of 133 assortativity is (or evolves to be) high enough in the ancestral population. When the 134 degree of assortativeness is an evolving trait, speciation therefore only requires the 135 substitution of one type of alleles, those coding for assortative mating, in the entire 136 population. Models with direct assortative mating thus correspond to the 1-allele models 137 of Felsenstein (1981). It is generally thought that in a population experiencing disruptive 138 selection due to frequency-dependent interactions, speciation will readily ensue with 139 direct assortative mating, because in such populations there is directional selection for 140 higher degrees of direct assortative mating (see also Matessi et al. 2001). With indirect 141 assortative mating, assortativity can only latch on to the ecological trait under disruptive 142 selection if a linkage disequilibrium develops between the ecological trait and the marker 143 trait on which assortative mating is based. Even with a high degree of assortativeness, 144 speciation thus requires the establishment of a polymorphism in the marker trait, and 145 hence the substitution of different alleles in the two emerging subpopulations. Therefore, 146 models with indirect assortative mating correspond to the 2-allele models of Felsenstein 147 (1981). Because of the requirement of a linkage disequilibrium between the marker trait 148 and the ecological trait, it is generally believed that speciation is unlikely to happen with 149 indirect assortative mating.

150

However, as recent work has shown, such skepticism may often be unwarranted. Both
Kondrashov and Kondrashov (1999) and Dieckmann and Doebeli (1999) have
demonstrated that, in fact, sympatric speciation can readily occur also with indirect

154 assortative mating. The modeling approaches in these two studies differ: while 155 Dieckmann and Doebeli (1999) allow for the evolution of the degree of assortative mating, Kondrashov and Kondrashov (1999) do not consider such evolution, but instead 156 157 focus on indirect assortative mating being determined by a preference trait in females and 158 a marker trait in males. Both articles address the basic question of whether indirect 159 assortative mating can lead to speciation in populations experiencing disruptive selection. 160 (Note again that this question is different from the question of how the disruptive 161 selection regime is generated in the first place.) Both papers use models in which all traits 162 involved are determined by many additive loci to show that speciation can, in principle, 163 occur with indirect assortative mating.

164

165 Waxman and Gavrilets do not mention the paper by Kondrashov and Kondrashov (1999), 166 but criticize our model in various ways, albeit without backing up their criticisms with 167 results. For example, they suggest that some of the assumptions in Dieckmann and 168 Doebeli (1999) are biologically unjustified. Waxman and Gavrilets venture that our 169 analysis was, strictly speaking, not about sympatric speciation since initial allele 170 frequencies in the illustrations presented in our article were always chosen at $\frac{1}{2}$. This is 171 far-fetched. First of all, alleles for the ecological trait were not always started at $\frac{1}{2}$ in 172 Dieckmann and Doebeli (1999) (see, e.g., Figure 3 in that paper). Second, for a neutral 173 marker trait the assumption of allele frequencies of $\frac{1}{2}$ in an individual-based model seems 174 actually quite reasonable. Finally, only intermediate values of the assortative mating trait 175 result in random mating, which is a suitable initial condition for studying the evolution of 176 assortative mating. Therefore, allele frequencies of $\frac{1}{2}$ for this trait again seem appropriate

here. Nevertheless, to refute the objection, we have explicitly tested the models of
Dieckmann and Doebeli (1999) by choosing different initial conditions for the allele
frequencies, with the result that, as expected, the evolutionary outcome is just the same
(Figure 1a).

181

Waxman and Gavrilets also assert that the mutation rates in our models are unrealistic. To 182 183 address this concern, it is helpful to realize that this claim is based on too narrow a 184 perspective on the genetic architecture of ecologically important quantitative traits. 185 Clearly, the view of having, e.g., five independent and freely recombining single loci 186 determining a quantitative trait such as body size is naïve. Instead, in such additive multi-187 locus models, a 'locus' should be understood not as coding for a single protein, but more 188 generally as describing independent stretches of DNA of variable length which affect the 189 trait under consideration additively, and which recombine freely with other such stretches 190 of DNA. In particular, such stretches might be very much longer than a single locus, and 191 hence the mutation rate per such stretch might be quite high. Another way of seeing this is by realizing that with five diploid loci and a mutation rate of 10^{-3} per locus, the chance 192 of having at least one mutation occurring in an offspring is roughly 10⁻². For the 193 194 population sizes that we used in our models, which range between 500 and 1000, this 195 means that we have, on average, 5-10 mutations in the population per generation. If 196 anything, this seems to be a rather small number for mutations of small additive effects on a quantitative trait. With a per locus mutation rate of 10^{-6} that Waxman and Gavrilets 197 regard as realistic, we would obtain one small additive mutation every 100 generations. 198 To us, such a low number would seem to be very unrealistic indeed. 199

201	It is also reassuring that speciation still occurs in the models of Dieckmann and Doebeli
202	(1999) even when the mutation rate is decreased by an order of magnitude (Figure 2). In
203	general, rates of speciation in these models are lower with lower mutation rates,
204	particularly with indirect assortative mating, as in this case speciation relies on the
205	inherently stochastic process of building up a linkage disequilibrium. We note that in
206	principle, this slowing down can be counteracted by any increase in population size,
207	which has to be kept modest in genetically explicit and individual-based numerical
208	explorations for reasons of computational tractability. Based on these considerations, we
209	conclude that the requirements for speciation to occur in these models are not biologically
210	unrealistic.
211	

211

212 Finally, Waxman and Gavrilets note that our models do not include costs of 213 assortativeness, and that such costs would likely impede the speciation process. This 214 point is as correct as it is obvious: of course one must expect large costs of assortative 215 mating to preclude evolution of assortative mating. Consequently, the actual question is 216 not so much whether or not speciation occurs when such costs are present, but rather 217 whether or not the threshold costs predicted by the models are unreasonably low 218 compared with natural settings. By extending the models by Dieckmann and Doebeli 219 (1999) to include costs of assortative mating we can see that the evolution of assortative 220 mating remains possible even when such costs are substantial. There are various ways in 221 which one can introduce these costs into our models, and Figure 3 illustrates two cases. 222

223	In the first case, costs depend on the current distribution of the assortative mating trait in
224	the population, so that the most assortative female in the population has a cost c (incurred
225	as a reduction of her fecundity) compared with the least assortative female. Thus,
226	whenever mating takes place, the chance of reproducing is $1 - c$ for the female with the
227	highest degree of choosiness, while the female with the least degree of choosiness mates
228	with certainty, with the mating chances of other females varying linearly in between. The
229	cost that a particular degree of assortativeness implies therefore depends on how
230	assortative other females in the population are, reflecting a scenario in which it is the
231	relative choosiness of females that determines their chances of producing offspring.
232	
233	Alternatively, costs of assortativeness can be incorporated by granting only a finite
234	number of N sequential mate-choice trials to females that have the opportunity to
235	reproduce (see e.g., Matessi et al. 2001, Arnegard and Kondrashov 2004). In each such
236	trial, a potential mate is first randomly selected from the population and, depending on
237	the female's choosiness and preference, is then either rejected or accepted. In the latter
238	case, the female reproduces. If a female rejects all N potential mates during a given
239	mating opportunity, she cannot reproduce and has to wait until her next opportunity to
240	reproduce comes up at a later moment, at which time she initiates a new round of mate-
241	choice trials. The chance that a female will not accept any of the N potential mates
242	depends on her choosiness, i.e., on her degree of assortativeness, and on the frequency of
243	acceptable mates in the population. Moreover, as the number of allowed mate-choice
244	trials N decreases, the chance increases that females with a given degree of assortativity
245	reject all N males. Hence the cost of assortativeness rises with increasing female

246 choosiness, with a decreasing frequency of acceptable mates, and with a decreasing 247 number of allowed mate-choice trials.

248

249 Figure 3 shows scenarios in which speciation occurs despite these two types of costs, 250 both for direct and indirect assortative mating. Again, as expected, costs are more 251 effective in preventing speciation under indirect assortative mating. Yet, it is difficult to 252 assess what constitutes large costs. For example, N = 200 used in Figure 3d might seem a 253 rather large number of mate-choice trials, and hence to represent a small cost. However, 254 in natural populations mate-choice trials may actually be based on very brief and fleeting 255 encounters (involving e.g., only visual inspection). Thus, N = 200 may actually be rather 256 small, representing a substantial cost. For instance, in a band of chimpanzees, as well as 257 in humans of certain age classes, individuals may have hundreds of mate-choice trials, 258 evaluating the suitability of potential mates before reproducing. It should also be borne in 259 mind that individuals in many species are bound to reduce their choosiness when 260 encountering a low frequency of suitable mates. Such plasticity reduces the costs of 261 assortative mating and thus facilitates speciation in the models considered here. After all, 262 fully random mating appears to be rare in nature, which suggests that costs of 263 assortativeness are not typically very large.

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267

265 Of course, the issues discussed above will still benefit from a more systematic analysis.

For example, Doebeli (2005) investigates the effects of costs of assortative mating in a 266

variant of the models used here. The examples given in Figure 3 already show that in the

models of Dieckmann and Doebeli (1999), speciation is robust to introducing costs of 268

269 assortative mating as long as these costs are not too large. The flip side of this statement, 270 that mating costs can be increased to levels at which the evolution of assortative mating is 271 obstructed, seems to be a truism. It is also intuitively clear that costs of assortative mating 272 are bound to slow down the speciation process, as has already been noted by Kirkpatrick 273 and Nuismer (2004) and by Bolnick (2004). Bolnick (2004), whose models are based on 274 Dieckmann and Doebeli (1999) (see also Bolnick and Doebeli 2003), strikes a rather 275 cautionary note, but it is clear from Figures 2 and 3 in his paper that speciation still 276 occurs within reasonable time frames for a large range of model parameters. We certainly 277 agree with Bolnick (2004) that it will be fruitful to investigate relevant parameter regions 278 in natural systems.

279

280 The assortative mating models of Dieckmann and Doebeli (1999), as well as those of 281 Kondrashov and Kondrashov (1999), must by no means be perceived as being the last 282 word on the topic. We recommend that these models should rather be viewed as a starting 283 point for re-evaluating the view that recombination between ecological traits under 284 disruptive selection and mating traits responsible for reproductive isolation prevents 285 sympatric speciation. To proceed with this re-evaluation, different mating models need to 286 be considered, e.g., models that investigate the evolution of the degree of assortative 287 mating when mating is determined by a preference trait in females and a marker trait in 288 males. In this case, speciation is hindered not only by recombination between ecological 289 traits and mating traits, but also by recombination among mating traits, i.e., between loci 290 coding for the female preference and the male marker trait. Doebeli (2005) reports that 291 speciation is still feasible in such models, a result that holds even when there are costs of

292 assortative mating. In addition, it is important to consider models that explore the 293 possibility of sympatric speciation being driven by sexual selection alone, i.e., by 294 selection resulting from differential mating success (see Van Doorn et al. 2004 and 295 Arnegard and Kondrashov 2004 for two recent studies on this topic). We agree with 296 Waxman and Gavrilets that there is quite some room for exploring effects of costs of 297 assortative mating on the dynamics of speciation models. However, it is already clear 298 from the models available to date that the evolution of assortative mating mechanisms 299 can, in theory and under biologically reasonable assumptions, lead to reproductive 300 isolation between subpopulations emerging in an ancestral population under disruptive 301 selection, even in the presence of such costs. It is also clear that requirements for 302 speciation are more stringent with indirect assortative mating than with direct assortative 303 mating, but even with indirect assortative mating speciation does not seem to be a 304 theoretically unlikely process.

305

306 Thus, perhaps the more fundamental issue – and certainly one of central relevance – is 307 whether regimes of disruptive selection due to frequency-dependent ecological 308 interactions are common or rare in nature. On the theoretical side, the framework of 309 adaptive dynamics is able to provide a clear answer: evolutionary branching points are a 310 common feature of adaptive dynamics models, and this conclusion has been shown to 311 extend to a great variety of different types of ecological scenarios. In general, populations 312 that are attracted by evolutionary branching points remain there until rescued 313 evolutionarily by mechanisms, such as assortative mating, that allow for an escape from 314 the underlying fitness minima. While it remains to be seen whether sympatric speciation

- 315 is indeed much more common in natural systems than was previously believed, adaptive
- 316 dynamics theory has already now provided new perspectives for empirical studies of the
- 317 ecology of speciation, e.g., for investigations of tractably rapid diversification in
- 318 microorganisms (Rainey and Travisano 1998, Travisano and Rainey 2000, Kassen 2002,
- 319 Friesen et al. 2004).

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468 Figure legends

469

Fig. 1 Adaptive speciation in the model of Dieckmann and Doebeli (1999) for different 470 471 initial conditions. (a) Direct assortative mating; (b) Indirect assortative mating. Individual 472 genomes were initialized by assuming that for each trait, the first of 5 diploid loci was 473 fixed for the 1-allele, while the other loci were fixed for the 0 allele. In (a), the lower 474 panel shows the evolution of the degree of assortative mating (mating character). In (b) 475 the lower panels show the evolution of this degree and of the marker character. When 476 speciation occurs with indirect assortative mating, each of the two marker clusters rapidly 477 develops into complete linkage disequilibrium with one of the two ecological clusters. 478 The setup of the shown individual-based simulations is described in Dieckmann and 479 Doebeli (1999). Parameters: $c_{\kappa} = 2.0$, $c_{\alpha} = 0.6$ in (a); $c_{\kappa} = 2.0$, $c_{\alpha} = 0.3$ in (b). 480

481 Fig. 2 Adaptive speciation in the model of Dieckmann and Doebeli (1999) for lower
482 mutation rates. (a) Direct assortative mating; (b) Indirect assortative mating. Panel
483 organization as in Figure 1. The per locus mutation rate was set to 10⁻⁴. Other parameters
484 as in Fig. 1a for (a), and as in Fig. 1b for (b); initial conditions as in Dieckmann and
485 Doebeli (1999).

486

487 **Fig. 3** Adaptive speciation in the model of Dieckmann and Doebeli (1999) with costs of 488 assortative mating. (a) Direct assortative mating with a frequency-dependent cost c =489 0.35, such that whenever mating takes place, the chance of reproducing for the female 490 that encounters the least amount of suitable partners is 1-*c*, while the female that

491	encounters the highest amount of suitable partners mates with certainty. In between,
492	females have intermediate chances of mating and reproducing (obtained through linear
493	interpolation between the two extremal values $1-c$ and 1). (b) Direct assortative mating
494	with finitely many mate-choice trials, $N = 20$. (c) Same as (a), but with indirect
495	assortative mating and $c = 0.15$. (d) Same as (b), but with indirect assortative mating and
496	N = 200. Other parameters as in Fig. 2a for (a) and (b), and as in Fig. 2b for (c) and (d).
497	In all cases, only the time series of the ecological character is shown; if assortative
498	mating is direct, as in (a) and b), the time series of the mating character are similar to
499	those shown in Figures 1a and 2a; if assortative mating is indirect, as in (c) and (d), the
500	time series of the mating characters are similar to those shown in Figures 1b and 2b.
501	





