

# 1 Supplemental Text: Four Implementations of the Fisher

## 2 Process

### 3 A Population Genetics Model of the Fisher Process

4 **Genetic assumptions.** The model of Kirkpatrick (1982) works with two haploid diallelic loci, of  
5 which  $P$  is the preference locus, with alleles  $P_0$  (no preference) and  $P_1$  (preference for  
6 ornamented males) and  $T$  the ornament locus, with alleles  $T_0$  (no ornamentation) and  $T_1$   
7 (ornamentation). The evolutionary dynamics can be described by keeping track of the changes of  
8 the relative frequencies  $x_{ij}$  of the haploid genotypes ('haplotypes')  $P_iT_j$ . It is often more  
9 convenient to describe the dynamics in terms of allele frequencies, that is the frequencies  
10  $p = x_{10} + x_{11}$  of the preference allele  $P_1$  and  $t = x_{01} + x_{11}$  of the ornament allele  $T_1$ . For a complete  
11 description, one also has to keep track of linkage disequilibrium  $D = x_{00}x_{11} - x_{01}x_{10}$ . In fact, the  
12 four haplotype frequencies  $x_{ij}$  can be recovered from  $p$ ,  $t$  and  $D$ . In statistical terms, linkage  
13 disequilibrium corresponds to the covariance of the alleles with identical subscripts:  $D$  is positive  
14 if  $P_1$  and  $T_1$  or  $P_0$  and  $T_0$  co-occur more often in the same individual than to be expected on basis  
15 of the allele frequencies  $p$  and  $t$ . The build-up of a positive association between  $P_1$  and  $T_1$  (a  
16 positive  $D$ ) is *the* key ingredient of the Fisher process. To derive the evolutionary dynamics of  $p$ ,  
17  $t$  and  $D$ , we closely follow Bulmer (1989).

18 **Viability selection.** The costs of expressing an ornament are assumed to be incurred during a  
19 period of viability selection, which precedes the mating stage. Ornamented males have a relative  
20 survival probability of  $v_1 = 1 - s$  ( $0 < s < 1$ ) in comparison to the viability  $v_0 = 1$  of males without  
21 ornamentation. Since ornaments are sex-limited, only males incur costs (see Seger & Trivers  
22 1986, Albert & Otto 2005, where this assumption is relaxed). Costs of female preference are not  
23 considered in Kirkpatrick's (1982) model. Viability selection changes the frequency of  
24 ornamented males from  $t$  to  $t_m = t \cdot v_1 / \bar{v}$ , where  $\bar{v} = (1 - t)v_0 + tv_1 = 1 - st$  is the mean viability of

25 males.

26 **Mating stage.** We define  $U_{ij}$  as the probability that a female with allele  $P_i$  mates with a male  
27 carrying allele  $T_j$ .  $P_0$  females mate at random, so that the probability of mating with  $T_0$  and  $T_1$   
28 males is identical to their respective frequency in the population,  $U_{00} = 1 - t_m$  and  $U_{01} = t_m$ . In  
29 contrast, for females carrying the  $P_1$  allele the odds are  $a > 1$  that she prefers a  $T_1$  male over a  $T_0$   
30 male, so that  $U_{11} : U_{10} = at_m : (1 - t_m)$ . This way of exerting mate choice is known as ‘fixed  
31 relative preferences.’ It corresponds, for example, to a situation where females encounter males  
32 one at a time in a random sequence, until they accept a male for mating (Maynard Smith 1985).  
33 Other mechanisms of mate choice can lead to very different outcomes (e.g., the ‘best-of- $N$ ’  
34 model, Seger 1985, or the ‘absolute preference’ model, Takahasi 1997). Kirpatrick’s model also  
35 assumes that all choosy females will eventually mate ( $U_{11} + U_{10} = 1$ ). Together with the above  
36 condition on  $U_{11} : U_{10}$  this yields  $U_{10} = (1 - t_m) / (1 - t_m + at_m)$  and  $U_{11} = at_m / (1 - t_m + at_m)$ .

37 **Evolutionary dynamics.** Once the frequency distribution of the various types of mating are  
38 known, the distribution of offspring genotypes can be derived in a standard way (taking into  
39 account recombination and Mendelian segregation). As shown in Bulmer (1989), this leads to the  
40 following system of difference equations describing how the allele frequencies  $p$  and  $t$  and the  
41 linkage disequilibrium  $D$  change from one generation to the next:

$$\begin{aligned}
 \Delta t &= \frac{1}{2} t(1-t)A \\
 \Delta p &= \frac{1}{2} DA \\
 \Delta D &= D \left( (1-r)A \left( \frac{1}{2} - t \right) - \frac{1}{4} A^2 t(1-t) - r \right) + \frac{1}{2} rB \left( D^2 + p(1-p)t(1-t) \right)
 \end{aligned} \tag{A1}$$

43 where  $r$  is the recombination rate between the trait and the preference locus and  $A$  and  $B$  are  
44 defined as:

$$A = \frac{p(U_{11} - U_{01}) - (t - t_m)}{t(1-t)}, \quad B = \frac{U_{11} - U_{01}}{t(1-t)}. \tag{A2}$$

46 The factor  $\frac{1}{2}$  in the first two equations of (A1) reflects the fact that preference and ornament are  
47 only expressed in one sex. The first equation of (A1) shows that there is direct selection on the

48 ornament, which is characterized by the term  $A$ . This term includes two parts, corresponding to  
49 the mating advantage  $p(U_{11} - U_{01})$  of ornamented males and the decline  $t - t_m$  in ornament  
50 frequency in males due to natural selection. The second equation of (A1) shows that the  
51 preference allele changes in frequency as a correlated response to selection on the ornament  
52 allele: once there is a positive linkage disequilibrium  $D$ ,  $p$  changes in the same direction as  $t$ .  
53 Hence, (A1) captures the essential features of the Fisher process.

54 **Equilibria.** Solving for the equilibria by setting  $\Delta t = 0$  and  $\Delta p = 0$ , one finds a set of boundary  
55 equilibria that constitute either loss of the ornament ( $t=0$ ), or fixation of the ornament ( $t=1$ ).  
56 Internal equilibria have to satisfy  $A = 0$ . A straightforward calculation yields:

$$57 \quad A = pB - \frac{s}{1-st}, \quad B = \frac{1-s}{1-st} \cdot \frac{a-1}{1-t+a(1-s)t} \quad (\text{A3})$$

58 This implies that the equation  $A = 0$  is equivalent to

$$59 \quad p = s \frac{1+(a(1-s)-1)t}{(1-s)(a-1)} \quad (\text{A4})$$

60 and that the internal equilibria constitute a line with a slope determined by the interplay of  
61 natural and sexual selection. For a given combination  $(p, t)$  on this line of equilibria, the  
62 equilibrium value of  $D$  can be obtained by solving  $\Delta D = 0$ , a quadratic equation in  $D$ . Since  
63  $A = 0$ , this equation can be simplified considerably. It turns out that the solution of  $\Delta D = 0$  does  
64 not depend on the recombination rate  $r$ . In other words, at equilibrium the statistical association  
65 between preference and ornament alleles does not depend on physical linkage.

66 Figure 2a in the main text depicts the line of equilibria and the dynamic behavior of  
67 Kirkpatrick's model. As predicted by Fisher (1915) the preference allele  $P_1$  has to be sufficiently  
68 common initially to give rise to nonzero frequencies of the ornament allele  $T_1$  (although this  
69 depends on the preference function, Takahashi 1997). Once  $P_1$  is sufficiently common it either  
70 gives rise to polymorphism in which both  $T_0$  and  $T_1$  alleles coexist or to fixation of the  $T_1$  allele.  
71 Notice that the approach to the set of equilibria is roughly linear. The slope of the 'lines of

72 approach' is affected by the 'genetic' parameter  $r$ . In contrast, the line of equilibria itself only  
73 depends on the 'fitness' parameters  $s$  and  $a$ .

74 **Costly preferences.** As already noted by Kirkpatrick (1982) and further investigated by  
75 Pomiankowski (1987) and Bulmer (1989), the line of equilibria in Figure 2a is extremely  
76 sensitive to small deviations in the model assumptions. For example, the addition of the slightest  
77 costs of a female preference leads to a breakdown of the line of equilibria to a single equilibrium  
78 point in which mate choice is absent ( $p = 0, t = 0$ ). Additional assumptions (like mutation bias)  
79 are then needed to explain the evolution of costly ornaments and preferences (see Figure 3 in the  
80 main text).

## 81 **A quantitative genetics model of the Fisher process**

82 Lande's (1981) quantitative genetics implementation of the Fisher process assumes that the  
83 female preference  $p$  and the male ornament  $t$  are continuous, normally distributed characters.

84 **Viability selection.** As in the population genetics model considered above, the costs of  
85 expressing an ornament are assumed to be incurred during a period of viability selection. The  
86 survival probability  $v(t)$  of a male carrying an ornament  $t$  is given by a Gaussian function

$$87 \quad v(t) = \exp \left[ -\frac{1}{2} \left( \frac{t - \theta}{\omega} \right)^2 \right]. \quad (\text{A5})$$

88 Hence selection is stabilizing, and each deviation from the optimal ornament value  $\theta$  (with  
89 respect to viability selection) leads to a decrease in survival. The smaller the term  $\omega$  the stronger  
90 deviations from  $\theta$  are punished by natural selection. Hence  $1/\omega$  reflects the strength of viability  
91 selection against exaggerated ornaments. Exponential fitness functions like the Gaussian above  
92 are popular in quantitative genetics models, since the distribution of traits (here: male ornaments)  
93 after selection is again normal. Like Kirkpatrick's model, Lande's model does not consider costs  
94 of female choosiness.

95 **Mating stage.** The female "preference" is any character leading to non-random mating with  
96 respect to the male ornament. The tendency of a female with preference  $p$  to mate with an adult  
97 male with ornament value  $t$  is given by a preference function  $\psi(t|p)$ . Lande (1981) discusses  
98 three different preference functions, but here we focus on one of them:  $\psi(t|p) = \exp(apt)$ . In this  
99 'psychophysical model,' females with  $p \neq 0$  always prefer the most extreme males most; the  
100 sign of  $p$  determines the direction of the preference and the magnitude of  $p$  determines how  
101 strongly a female discriminates between males differing in ornamentation.

102 **Evolutionary dynamics.** It is one of the basic insights of quantitative genetics theory that the  
103 evolution of the mean values of two sex-limited traits in a population with discrete, non-  
104 overlapping generations can be described by the 'multivariate breeder's equation' (Lande &

105 Arnold 1983). There are various version of this equation that differ in their description of  
106 selection and their assumptions on the multivariate distribution of traits (Walsh & Lynch 2012).  
107 Here we follow the approach of Pomiankowski et al. (1991) that is relatively broadly applicable  
108 in case of weak selection:

$$109 \begin{pmatrix} \Delta \bar{t} \\ \Delta \bar{p} \end{pmatrix} = \frac{1}{2} \cdot \begin{pmatrix} G_t & G_{tp} \\ G_{tp} & G_p \end{pmatrix} \begin{pmatrix} \partial \ln(W_m) / \partial t \\ \partial \ln(W_f) / \partial p \end{pmatrix} \Bigg|_{\substack{t=\bar{t} \\ p=\bar{p}}} \quad (\text{A6})$$

110 The matrix in (A6) is the so-called G-matrix, consisting of the additive genetic variances  $G_t$  and  
111  $G_p$  of male traits and female preferences and the additive genetic covariance  $G_{tp}$  describing the  
112 (additive) genetic association between trait and preference. The vector to the right is the gradient  
113 vector of (relative) individual fitness (male fitness  $W_m$  and female fitness  $W_f$ ) with respect to the  
114 individual trait values. The factor  $\frac{1}{2}$  reflects the sex-limited expression of traits and preferences.

115 In Lande's model, the net effect of viability selection and mating preferences on the ornament  
116 trait is given by

$$117 \frac{\partial \ln(W_m)}{\partial t} \Bigg|_{\substack{t=\bar{t} \\ p=\bar{p}}} = a\bar{p} - \frac{\bar{t} - \theta}{\omega^2}. \quad (\text{A7})$$

118 In the absence of direct selection on female preferences (no costs of choosiness),  
119  $\partial \ln(W_f) / \partial p = 0$ , and (A6) can be written as

$$120 \begin{aligned} \Delta \bar{t} &= \frac{1}{2} G_t \left( a\bar{p} - \frac{\bar{t} - \theta}{\omega^2} \right) \\ \Delta \bar{p} &= \frac{1}{2} G_{tp} \left( a\bar{p} - \frac{\bar{t} - \theta}{\omega^2} \right) \end{aligned} \quad (\text{A8})$$

121 Comparing (A8) with (A1) shows a close correspondence between Kirkpatrick's and Lande's  
122 model. If we assign the numerical values 0 and 1 to the alleles  $P_0$  and  $P_1$  and to  $T_0$  and  $T_1$  in  
123 Kirkpatrick's model, the allele frequencies  $p$  and  $t$  in this model correspond to the averages  $\bar{p}$   
124 and  $\bar{t}$  of these numerical values; the term  $t(1-t)$  in the first equation of (A1) corresponds to the  
125 variance ( $G_t$ ) in  $t$ -values; and the linkage disequilibrium  $D$  corresponds to the covariance ( $G_{tp}$ )

126 between  $p$ - and  $t$ -values. Finally, the term  $A$  in (A1) corresponds to  $\partial \ln(W_m)/\partial t$  in Lande's  
127 model.

128 **Equilibria.** The equilibria of Lande's model ( $\Delta \bar{t} = \Delta \bar{p} = 0$ ) are given by

129 
$$\bar{p} = \frac{\bar{t} - \theta}{a\omega^2}. \quad (\text{A9})$$

130 Hence when plotting the mean preference  $\bar{p}$  against the mean trait value  $\bar{t}$  a line of equilibria  
131 results with slope  $1/a\omega^2$  (see Figure 2b in the main text). If  $G_t$  and  $G_p$  are constant, the  
132 evolutionary trajectories are straight lines with slope

133 
$$b_{pt} = \frac{\Delta \bar{p}}{\Delta \bar{t}} = \frac{G_{tp}}{G_t}, \quad (\text{A10})$$

134 corresponding to the (additive) genetic regression coefficient of the preference on the trait. If this  
135 regression is weak (more precisely: if the regression line is less steep than line of equilibria, or  
136  $G_p/G_t < 1/a\omega^2$ ), then evolution will proceed towards the line of equilibria (as in Figure 2b of  
137 the main text). If the genetic regression is strong, any positive selection on  $t$  quickly increases the  
138 level of  $p$  as well. In this case a self-reinforcing runaway process occurs and evolution will  
139 proceed away from the line of equilibria.

140 **Costly preferences.** Any costs of female preferences will strongly change the dynamics of  
141 Lande's model. The line of equilibria collapses to a single equilibrium point, located at the values  
142 maximizing male and female survival (i.e.,  $\bar{p} = \theta_p$ ,  $\bar{t} = \theta_t$ ). As in S1, additional assumptions  
143 (like mutation bias) are needed to explain the evolution of costly ornaments and preferences (see  
144 Figure 3 in the main text).

145

## 146 **An Adaptive Dynamics Model of the Fisher Process**

147 Over the years several sexual selection models have been developed that make use of  
148 evolutionary game theory or adaptive dynamics (Pen & Weissing 2000, Kokko et al. 2002,  
149 McNamara et al. 2003, Fawcett et al. 2011). All these models have in common that they consider  
150 the invasion prospects of a rare mutant phenotype in an otherwise monomorphic ‘resident’  
151 population.

152 Here, we discuss Pen & Weissing’s (2000) model for the Fisher process. This model considers a  
153 class-structured population consisting of females and two types of male: non-ornamented males  
154 ( $\sigma_0$ ) and males expressing an ornament ( $\sigma_1$ ). Evolvable traits are the females’ preference  $p$  for  
155 mating with ornamented males and the tendency  $t$  of a male to develop the ornament, that is, the  
156 probability to develop into a male of type 1. The aim is to find evolutionarily stable values  $p^*$  and  
157  $t^*$  that cannot be invaded by any mutant phenotypes.

158 **Viability selection.** The survival probability of ornamented males is reduced by a factor  $1-s$   
159 when compared to non-ornamented males. Males that express an ornament survive with  
160 probability  $1-c$ , whereas males without an ornament survive with probability 1. Costs of female  
161 preferences are not considered in Pen & Weissing’s model but included in later extensions  
162 (Fawcett et al 2011).

163 **Mating stage.** Females have a certain preference  $p$  for type 1 males, which translates into them  
164 giving a proportion  $\alpha$  of their matings to type 1 males,  $\alpha = \alpha(p)$  being an increasing function  
165 of  $p$ . For mutants and residents alike, the number of matings per type of male depends on the  
166 preference  $p^*$  of the females and on the relative frequency of the two types of (adult) males in  
167 the resident population. This follows from the assumption that mutant females and males are  
168 rare. Let  $u_f^*$ ,  $u_{m0}^*$  and  $u_{m1}^*$  denote the density of females, type 0 males and type 1 males in the  
169 resident population, respectively. Then the per capita number of matings per type of male,  $Q_0^*$   
170 and  $Q_1^*$ , can be derived from the consistency requirements  $Q_0^* u_{m0}^* = (1 - \alpha^*) u_f^*$  and  $Q_1^* u_{m1}^* = \alpha^* u_f^*$ ,



171 where  $\alpha^* = \alpha(p^*)$ :

$$172 \quad Q_0^* = \frac{(1-\alpha^*)u_f^*}{u_{m0}^*}, \quad Q_1^* = \frac{\alpha^* u_f^*}{u_{m1}^*}. \quad (\text{A11})$$

173 **Stage-transition matrix.** Assuming non-overlapping generations and a stationary resident  
174 population producing an even primary sex ratio (i.e., each female producing on average one male  
175 and one female offspring), the transitions between the different classes of mutant individuals  
176 from one generation to the next are summarized by the stage-transition matrix

$$177 \quad \mathbf{A}(p, t | p^*, t^*) = \frac{1}{2} \cdot \begin{bmatrix} 1 & Q_0^* & Q_1^* \\ 1-t & (1-t)Q_0^* & (1-t)Q_1^* \\ (1-s)t & (1-s)tQ_0^* & (1-s)tQ_1^* \end{bmatrix}. \quad (\text{A12})$$

178 This matrix should be interpreted as follows. The first column characterizes the per capita  
179 contribution of a mutant female to female mutants, type 0 male mutants and type 1 male mutants  
180 in the next generation, respectively. The first element is equal to 1, since a female produces on  
181 average one (surviving) female offspring. In addition, the female also produces on average one  
182 male offspring. With probability  $1-t$  this male will be of type 0 (no ornamentation) and survive  
183 to adulthood. With probability  $t$ , the male will be of type 1 and survive with probability  $1-s$  to  
184 adulthood. The other two columns correspond to the contributions of type 0 and type 1 mutant  
185 males to the various types of mutants in the next generation. These columns correspond to  
186 column 1 multiplied by the per capita number of matings ( $Q_0^*$  and  $Q_1^*$ ) of the two types of male.  
187 The factor  $\frac{1}{2}$  in (A12) reflects the fact that each individual has one father and one mother and  
188 prevents double counting of offspring. Notice that the matrix elements do not depend on  $p$ , and  
189 that the dependence on  $p^*$  and  $t^*$  is indirect (via  $Q_0^*$  and  $Q_1^*$ ).

190 **Invasion fitness.** The dominant eigenvalue  $W(p, t | p^*, t^*)$  of the stage transition matrix  $\mathbf{A}$   
191 corresponds to the ‘invasion fitness’ of the rare mutant. For the resident population, the dominant  
192 eigenvalue is equal to one (reflecting the fact that this population is stationary). If  $W > 1$ , the

193 mutant will increase in relative frequency, while it will go extinct if  $W < 1$ .

194 To determine the properties of the invasion fitness function, we first have to investigate the stage  
195 transition matrix  $\mathbf{A}_{res} = \mathbf{A}(p^*, t^* | p^*, t^*)$  of the resident population. The right eigenvector of the  
196 dominant eigenvalue 1 gives the stable distribution of the three types of individuals in the  
197 resident population (which via (A11) affect  $Q_0^*$  and  $Q_1^*$ ):

$$198 \quad u_f^* : u_{m0}^* : u_{m1}^* = 1 : (1-t^*) : (1-s)t^*. \quad (\text{A13})$$

199 The left eigenvector of  $\mathbf{A}_{res}$  corresponds to the reproductive values of the three types:

$$200 \quad v_f^* : v_{m0}^* : v_{m1}^* = 1 : Q_0^* : Q_1^*. \quad (\text{A14})$$

201 Using a standard result of life history theory (Taylor 1996), the dependence of  $W(p, t | p^*, t^*)$  on  
202  $p$  and  $t$  can now be determined without actually calculating invasion fitness (which can be quite  
203 tedious). In fact, the partial derivatives of  $W$  at  $(p^*, t^*)$  are of the form:

$$204 \quad \frac{\partial W(t, p | t^*, p^*)}{\partial t} = \mathbf{v}^{*\top} \frac{\partial \mathbf{A}}{\partial t} \mathbf{u}^* / \mathbf{v}^{*\top} \mathbf{u}^*. \quad (\text{A15})$$

205 Inserting (A13), (A14) and the partial derivatives of (A12) into this equation yields:

$$206 \quad \left. \frac{\partial W}{\partial t} \right|_{t=t^*} = (1-s)Q_1^* - Q_0^*, \quad \left. \frac{\partial W}{\partial p} \right|_{p=p^*} = 0. \quad (\text{A16})$$

207 The total selection differentials are then given by:

$$208 \quad \left. \frac{dW}{dt} \right|_{t=t^*} = \left( \frac{\partial W}{\partial t} + b_{tp} \frac{\partial W}{\partial p} \right)_{t=t^*} = (1-s)Q_1^* - Q_0^* \quad (\text{A17})$$

$$\left. \frac{dW}{dp} \right|_{p=p^*} = \left( \frac{\partial W}{\partial p} + b_{pt} \frac{\partial W}{\partial t} \right)_{t=t^*} = b_{pt} ((1-s)Q_1^* - Q_0^*)$$

209 where  $b_{yx}$  is the statistical regression coefficient of  $y$  on  $x$  (Taylor & Frank 1996), which is  
210 assumed to be a positive parameter.

211 **Evolutionarily singular strategies.** At an internal ‘equilibrium’ both selection differentials in

212 (A17) have to be zero, leading to the condition  $(1-s)Q_1^* = Q_0^*$ , which can be simplified to  
213  $t^* = \alpha(p^*)$ . Once again, this condition describes a whole set of equilibria. For many preferences,  
214 this set is again a straight line. Assume, for example, that females have ‘fixed relative  
215 preferences’ as in Kirkpatrick’s model with probability  $p^*$  while they mate at random with  
216 probability  $1-p^*$ . Then  $\alpha(p^*)$  is given by

$$217 \quad \alpha(p^*) = p^* \frac{au_{m1}^*}{u_{m0}^* + au_{m1}^*} + (1-p^*) \frac{u_{m1}^*}{u_{m0}^* + u_{m1}^*}. \quad (\text{A18})$$

218 Equating this expression with  $t^*$  yields the same line of equilibria as in Kirkpatrick’s model (see  
219 Figure 2c in the main text). The approach to equilibrium (via a sequence of gene substitution  
220 events), which is also indicated in Figure 2c, can be derived from the canonical equation of  
221 adaptive dynamics theory (Geritz et al 1998).

## 222 **Individual-Based Simulation Models of the Fisher Process**

223 Individual-based models of sexual selection are the most recent addition to the set of tools to  
224 analyze evolutionary models (Grimm & Railsback 2005); a growing number of sexual selection  
225 models makes use of this versatile technique (e.g., Lorch et al 2003, Gavrilets et al. 2007, Kokko  
226 et al 2007, Fawcett et al 2007). Here, we discuss an individual-based model on Fisherian sexual  
227 selection that is used by Fawcett et al (2007). The source code of this simulation can be found at  
228 <http://www.rug.nl/biol/theobio/fisher.cpp>. A flow diagram of the model is given in Supplemental  
229 Figure 2.

230 **Initialization.** An individual-based simulation starts with a definition of the individuals initially  
231 present and their properties. For sake of comparison to the previous analytical models, we  
232 assume that individuals are genetically characterized by their alleles at two haploid loci, one  
233 coding for a male ornament  $t$  and the other coding for a female preference  $p$ . However, we  
234 emphasize that individual-based simulations easily allow for the implementation of complex  
235 genetic architectures and genotype-phenotype maps (e.g., Ten Tusscher & Hogeweg 2009). The

236 population is initialized by generating a large collection of males and females (say,  $n=2000$   
237 males and  $n=2000$  females) and randomly assigning ornament and preference alleles to each  
238 individual according to some prespecified distribution (e.g. a bivariate normal distribution) (see  
239 Supplemental Figure 2, step 1).

240 **Viability selection.** Subsequently, the population of males enter a procedure that determines their  
241 survival (see Supplemental Figure 2, step 2), whereas all females survive. The simulation  
242 assumes that a male's survival probability  $v$  is given by a Gaussian function  $v(t) = \exp(-ct^2)$ ,  
243 where the parameter  $c$  determines the strength of viability selection. However, in contrast to the  
244 aforementioned deterministic models, survival is implemented in a stochastic fashion (i.e., by  
245 letting a chance process decide whether a given male will die or survive). In Supplemental  
246 Figure 2 (step 2) males with larger ornaments are more likely to die, but individual males may,  
247 by chance, escape mortality.

248 **Mating stage.** The surviving males and all females then enter another procedure, in which  
249 females choose mates. As in the deterministic models, female mate choice can be implemented in  
250 various ways. For example, fixed relative preferences can be implemented by sequentially  
251 assigning randomly drawn males to each female, until one of these males is accepted by the  
252 female for mating. The probability of accepting any given male depends on both, the female's  
253 preference and the male's ornament. Alternatively, each female is confronted with a random  
254 sample of  $N$  males and subsequently mates with the male most closely fitting to her preference  
255 ('best-of- $N$ ' model). A third alternative (implemented by Fawcett et al. 2007) combines the two  
256 approaches above: each female samples  $N$  males and subsequently mates with male  $i$  with a  
257 probability that is proportional to  $i$ 's attractiveness value to the female. Supplemental Figure S2  
258 step 3 shows that large ornamented males are on average more often chosen by females with  
259 high values of the preference, but stochastic variation in mate sampling and mate choice reduces  
260 the strength of assortative mating to a certain extent.

261 **Reproduction and mutation.** After having chosen a mate females reproduce, having their

262 offspring sired by their mate of choice. In the simulation model considered here, all females  
263 contribute effectively two offspring to the next generation, at a 1:1 sex ratio (see Supplemental  
264 Figure 2, step 4). As a consequence, the population size remains constant over the generations.  
265 Upon reproduction, mutation takes place (see Supplemental Figure 2, step 5). The current model  
266 assumes a continuum-of-alleles model of mutation, in which preference and ornament alleles  
267 present in an individual mutate with probabilities  $\mu_p$  and  $\mu_t$  respectively. When mutation takes  
268 place, a deviate from a normal distribution with mean 0 and standard deviation  $\sigma_\mu$  is added to the  
269 current allelic value. The life cycle then repeats itself and males of the next generation enter the  
270 juvenile survival stage.

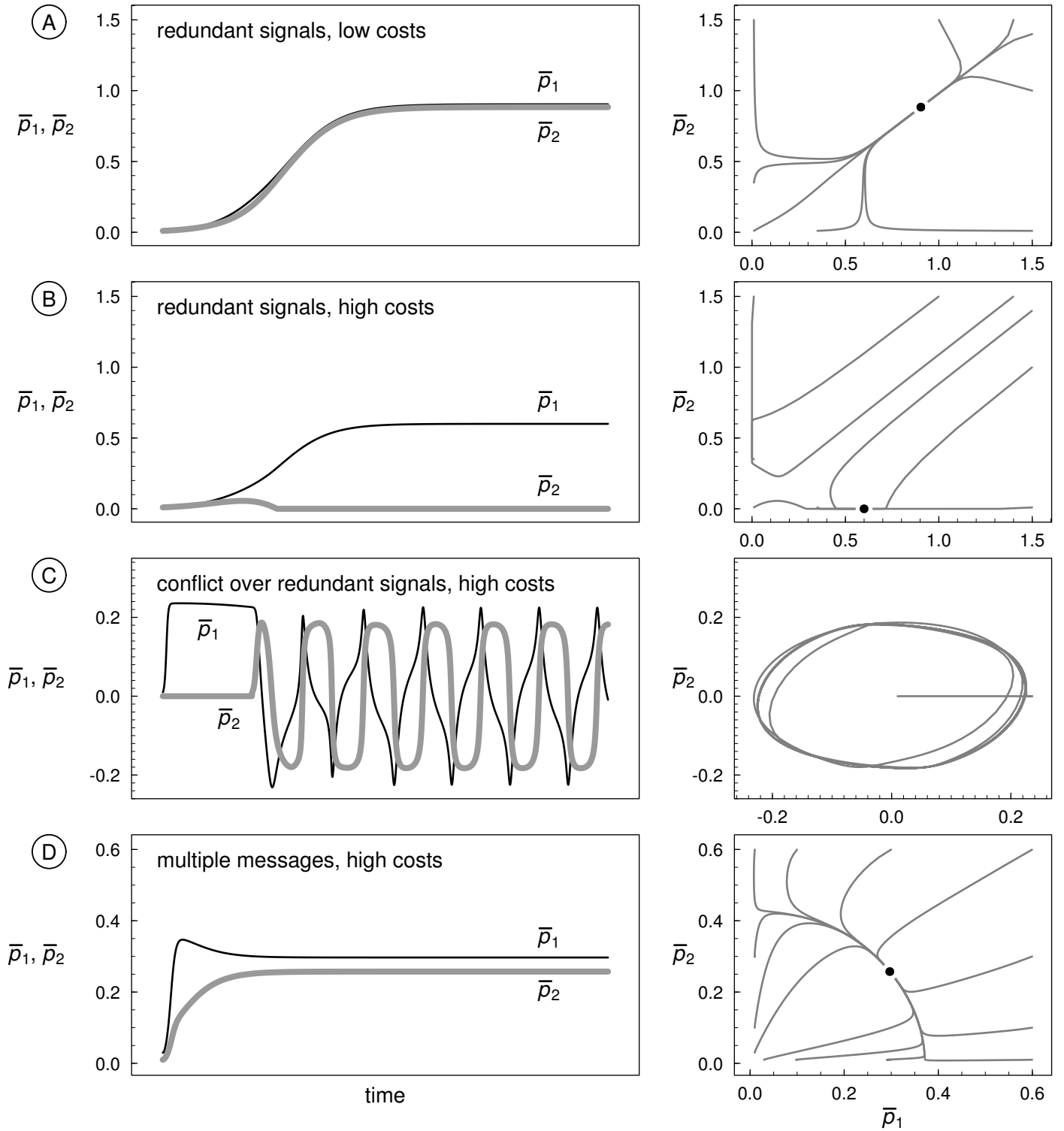
271 **Evolutionary dynamics.** Figure 2*d* in the main text illustrates the course of evolution of an  
272 individual-based simulation. For similar parameter values as in Lande's model (Figure 2*b*), the  
273 system converges to Lande's line of equilibria and subsequently 'drifts' along this line. The  
274 irregularities in the evolutionary trajectory clearly illustrate the stochastic nature of an  
275 individual-based simulation.

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333

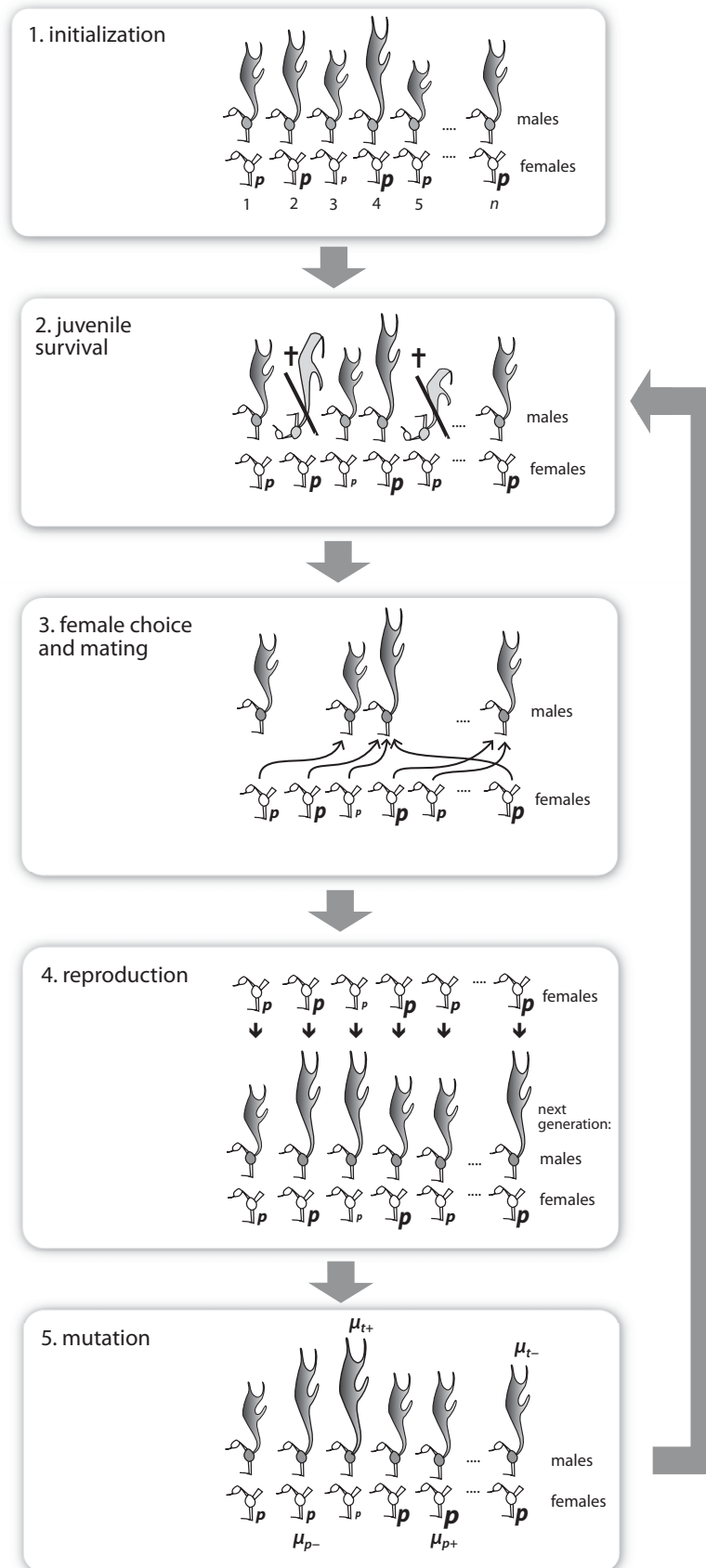
**Supplemental Figure 1**





334 **Supplemental Figure 1.** The evolution of female preferences for multiple indicators of male  
335 quality. *Panel A:* multiple female preferences for redundant signals only evolve to stable levels  
336 when the cost of expressing multiple preferences is sufficiently low (Iwasa & Pomiankowski  
337 1994). *Panel B:* In contrast, when the cost of expressing multiple preferences is higher, the cost  
338 of expressing the first preference ( $\bar{p}_1 > 0$ ) blocks the evolution of any additional preferences  
339 ( $\bar{p}_2 = 0$ ), and the evolution of a particular preference towards nonzero equilibrium levels  
340 depends on initial conditions. *Panel C:* Nonequilibrium dynamics of preferences and ornaments  
341 (for example due to sexual conflict over signaling) can lead to the establishment of multiple  
342 preferences for redundant indicators, even when high costs of female preferences would preclude  
343 the evolution multiple preferences at equilibrium (van Doorn & Weissing 2006). *Panel D:*  
344 multiple female preferences for indicators that each signal distinct components of male quality  
345 (“multiple messages”) can evolve to stable levels, even in the face of high costs (van Doorn &  
346 Weissing 2004).

## Supplemental Figure 2.



347 **Supplemental Figure 2.** Flow diagram of an individual-based simulation, reflecting a  
348 population of Arnold's bird of paradise (Arnold 1985) that experiences the Fisher process. Step  
349 1: the population is initialized by generating a population of  $n$  males (that vary in tail length) and  
350  $n$  females (that vary in their preferences for tail length,  $p$ ). Step 2: male viability selection takes  
351 place, in which males with the smaller ornaments are most likely (but not certain) to survive.  
352 Step 3: female choices takes place based on ornaments and preferences (see Supplement S4) and  
353 the eventual choices are indicated by black arrows. Males with large ornaments are likely (but  
354 not certain) to achieve a high mating rate. Step 4: after fertilization by their male of choice,  
355 females reproduce and give rise to the next generation of males and females. Step 5: mutation  
356 events can take place (indicated by  $\mu$ ) that can either increase or decrease values of ornaments  
357 and preferences (indicated by + or -). After mutation, the next cycle of the program starts again at  
358 step 2.  
359