

1 Mathematical Equivalence of Geometric Mean Fitness with

2 Probabilistic Optimization under Environmental UncertaintyNatural

3 Selection under Environmental Uncertainty: a Canonical Form of

4 Probabilistic Optimization

5 The evolution of prime number intervals in periodical cicadas

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42 **Abstract**

43 Natural selection can be considered as optimising fitness. Because 'mean' fitness is maximized with
44 respect to the genotypes of carriers, traditional theory can be viewed as a statistical theory of natural
45 selection. Probabilistic optimisation is a way to incorporate such uncertainty into optimality analyses
46 of natural selection, where environmental uncertainty is expressed as a probability distribution. Its
47 canonical form is a weighted average of fitness with respect to a given probabilistic distribution.
48 This concept should be applicable to three different levels of uncertainty: (1) behavioural variations
49 of an individual, (2) individual variations within a generation, and (3) temporal change over
50 generations (geometric mean fitness). The former two levels are straightforward with many
51 empirical evidences, but the last category, the geometric mean fitness, has not well understood. Here
52 we studied the geometric mean fitness by taking its logarithm, where the log growth rates become
53 the fitness value. By further transforming the log growth rates, the fitness of log growth rates
54 becomes its linear function. Therefore, a simple average of these distributions becomes the fitness
55 measure across generations and consideration of variance discount or the entire probability
56 distributions becomes unnecessary. We discuss some characteristic features of probabilistic
57 optimization in general. Our view is considered a probabilistic view of natural selection, in contrast
58 with the~~We try to understand what can be viewed as fitness under environmental uncertainty, and~~
59 how and when does the solution change from those expected from the traditional statistical view of

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60 natural selection. Environmental uncertainty can be expressed as a probability distribution.
61 Probabilistic optimisation is a way to incorporate such uncertainty into optimality analyses of natural
62 selection. A canonical form of probabilistic optimization is a weighted average of fitness with
63 respect to a given probabilistic distribution. This concept can be applicable to three different levels
64 of uncertainty: (1) behavioural variations of an individual, (2) individual variations within a
65 generation, and (3) temporal change over generations (geometric mean fitness). Discrepancy
66 between genetic and phenotypic optima often tends to increase with the variance of a probability
67 distribution that is a measure of the degree of uncertainty. For geometric mean fitness, if the
68 probabilistic distribution of generational fitness follows lognormal distribution, its average becomes
69 a measure of fitness, irrespective of its variance.

70
71 Keywords: fitness criteria, weighted average, variable unpredictable environments, geometric mean
72 fitness, probabilistic optimization, ty distribution.

73 **Background: Two hypotheses compete to explain the evolution of prime number**
74 **reproductive intervals (life cycles) among periodical cicadas: the 1) anti-predatory**
75 **hypothesis and 2) hybridization one. The anti-predatory hypothesis claims that**
76 **prime number intervals help to protect cicadas from being overwhelmed by their**
77 **predators. The hybridization hypothesis claims that prime numbers greatly reduce**
78 **the chance of hybridization among cicada broods.**

79 **Goal: To test the hybridization hypothesis using a simulation model.**
80 **Models: A deterministic, discrete population model with three parameters: larval**

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81 survival per year; clutch size; emergence success. Reproductive intervals from ten-
82 years to twenty years compete for survival in the simulations. The model makes
83 three key assumptions: a Mendelian genetic system, and random mating among
84 sympatric or parapatric broods of different life cycle lengths, and integer
85 population sizes. In addition, longer interval phenotypes have larger broods but
86 suffer higher total mortality than shorter interval broods. We keep track of all
87 population sizes of all pure intervals and hybrids with birth year. The life cycle
88 length of hybrids is assumed to be Mendelian inheritance with shorter eye-
89 dominance.
90 Results: Non-prime number reproductive intervals rapidly disappear. Then the
91 19-year phenotype is gradually eliminated by the 13- and 17-year phenotypes. The
92 13- and 17-year phenotypes may coexist. The selection of 13- or 17-year intervals
93 happens only when populations are at the verge of extinction.
94 Keywords: Periodical cicadas, prime number intervals, 13 /17 year, co-emergence,
95 hybridization, extinction threshold, frequency dependence, discrete population model
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97 1. INTRODUCTION

98 Periodical cicadas are among the most remarkable of insects, known for their long,

99 perfectly synchronized life cycles and the explosive emergence of the adults (Marlatt, 1907;

100 Alexander and Moore, 1962; Dybas and Davis, 1962; Lloyd and Dybas, 1966; Simon 1988; Williams and Simon

101 1995). Two types of life cycle are known, 17_ and 13_ year, both prime numbers. The

102 emergence of periodical cicadas is perfectly synchronized in each locality; no little

103 emergence is seen except emergence years (occasional stragglers are seen one or four

104 years early or late Marshall 2001). The periodical cicadas also show very strong site

105 tenacity (Williams and Simon 1995) and a strong tendency for aggregation (Simon et al. 1981).

106 INTRODUCTION

107 Natural selection is often viewed as a statistical process, maximizing the expected or mean

108 reproductive success of individuals carrying a certain gene or genotype (Darwin, 1859; Fisher, 1930).

109 The expected reproductive success is then called 'mean' fitness. In this sense, we can refer to

110 standard theory as a 'statistical' theory of natural selection. In order to analyze the optimality of a

111 phenotypic trait based on mean fitness, most traditional theories of natural selection almost

112 invariably assume constant and predictable environments.

113

114 However, for almost all organisms in the wild, environments are variable and unpredictable

115 (Yoshimura and Clark, 1993). Both abiotic components of environments, such as weather, and biotic

116 components, such as the locations of competitors and predators are always unpredictable to the

117 organisms to some extent. In this sense, environmental uncertainty is an unavoidable factor for all

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118 living systems if they are to persist and evolve through time. Accordingly the *statistical* theory of
119 natural selection needs to incorporate factors and constraints associated with optimization processes
120 (Parker and Maynard Smith, 1990; Williams, 1992). Here environmental uncertainty is one of the
121 most influential and common factors affecting natural selection, as it changes the statistical
122 (mean-fitness) concepts of optimisation (Yoshimura and Shields, 1987; Frank and Slatkin, 1989;
123 Cohen, 1993). However, probabilistic/stochastic ~~models~~~~theories~~ are widely scattered in various
124 fields of ecology and evolution without any generalisation. Many of them are not accessible to
125 empirical researchers because of mathematical ~~difficulty and complexity~~ ~~that is~~ ~~and~~ ~~technical details~~
126 inherent in each specific model. We should also note that the problem of uncertainty is extremely
127 well documented in foraging behaviour both from the theoretical and empirical standpoints (for
128 example, see Stephens and Krebs, 1986; Real and Caraco, 1986). However, the generalization and
129 conceptual developments of the effects of uncertainty in all levels are still lacking.
130
131 In order to understand the basic properties of uncertainty, we need a *probabilistic* perspective for
132 natural selection, a synthetic or integrated view of the effects of uncertainty on natural selection. We
133 can classify environmental uncertainty into three categories based on the level of integration: (1)
134 short-term temporal change experienced by an individual (individual level within a generation), (2)
135 phenotypic variation among individuals (population level within a generation) and (3) population

136 fluctuation across generations due to long-term environmental changes (cross-generation level) First
137 we describe three major categories of uncertainty: (1) the variable daily experience of an individual,
138 (2) variation among individuals and (3) long-term fluctuations across generations (Yoshimura and
139 Shields, 1992; Yoshimura, 1995). It is important to know how these uncertainties can be
140 incorporated into optimality analyses of natural selection. The mathematical Next I will explain the
141 principles of probabilistic optimization in these categories are :-all in how uncertainty can be
142 incorporated into optimality analyses. A canonical form of probabilistic optimization is a some form
143 of simple weighted average with respect to a given probabilistic distribution. It can be considered a
144 canonical form of probabilistic optimization under uncertainty (Yoshimura 1995). The fitness
145 measure across generations (the third category) is the geometric mean fitness (or the expected
146 multiplicative growth rate) (Lewontin and Cohen, 1969). Certainly, by taking the logarithm, the
147 geometric mean fitness becomes a weighted average of the population growth rates (Yoshimura and
148 Clark, 1991). However, the exact mathematical equivalence of geometric mean fitness is not yet well
149 understood.

150
151 This short paper deals with the mathematical nature of geometric mean fitness and its mathematical
152 equivalence with other forms of probabilistic optimization. Here, we first explain in the section of
153 theoretical rationale, the weighted average used for the first two categories of uncertainty at the level

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154 of an individual and a population in a single generation. We then show that the geometric mean
155 fitness can be transformed a simple weighted average of the logarithm of multiplicative growth rates.
156 We further shows that the logarithm of the growth rates becomes an exact value of fitness. The
157 variance discount is not necessary in this logarithmic form of geometric mean fitness. This formula
158 is conceptually true for any type of optimization under uncertainty. Next I describe three major
159 categories of uncertainty: (1) the variable daily experience of an individual, (2) variation among
160 individuals and (3) long term fluctuations across generations. Lastly I discuss briefly the
161 characteristics of the effects of uncertainty on natural selection.

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164 **2. THE THEORETICAL RATIONALE**

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165 **2.1 UNCERTAINTY AT INDIVIDUAL LEVEL**

166 An individual experiences temporal changes in environments. An individual lives in daily changing
167 environments, unstable and unpredictable in many aspects. How an individual behaves, grows and
168 reproduces in such changing environments has often been dealt as a problem of optimisation in
169 behavioral and physiological ecology (Krebs and Davies, 1993; Sibly and Calow, 1986; Mangel and
170 Clark, 1988; Stephens and Krebs, 1986; Real and Caraco, 1986). Here the underlying principle can
171 be illustrated as follows: individual animal forages for varying, and thus unpredictable amounts of

172 food daily. Daily food amounts are then expressed as a probability distribution. The overall fitness of
173 an individual associated with a given phenotype is a weighted sum of all the fitnesses of daily food
174 intake during its life time (Yoshimura and Shields, 1992; Yoshimura, 1995). The optimum based on
175 the overall fitness is a probabilistic optimum that is different from the fitness at the average food
176 intake, a deterministic optimum.

177

178 We first consider the fitness of an individual associated with a phenotype y . Here the notation is
179 listed in Table 1. The fitness $w_i(y)$ of an individual associated with a phenotype y is a weighted sum
180 of all possible environmental fitnesses $f_j(x,y)$ with the distribution of the environments $h_j(x)$, shown
181 in the equation (1) of Table 1.

182

183 For an illustrative example, we consider daily uncertainty in foraging animals (Fig. 1) (Yoshimura,
184 1995). Let x be daily food amounts as an environmental factor, where $x = 0$ in the worst environment
185 and $x = 100$ in the best environment, and $f_j(x,y)$ be the fitness of an individual with a phenotype y in
186 environment x . Naturally $f_j(x,y)$ is an increasing function of x (Fig. 1a). The difference in phenotype
187 y indicates what kind of food environments an individual is adapted for: if $y = 10$, an individual is
188 adapted for bad environments, i.e., fitness is fairly similar for bad and good environments ($10 < x < 50$
189 and $x > 50$). However, if $y = 50$, an individual is adapted for good environments, i.e., fitness is low

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190 (zero) for bad environments ($x < 50$) and extremely high for good environments ($x \gg 50$). The fitness
191 function $f(x, y)$ for phenotypes y in a given environment x is a function with a peak (Fig. 1b).
192
193 Suppose that the probability distribution of daily food abundance $h_i(x)$ is approximated by a
194 distribution with mean $E(x) = 50$ (Fig. 1c). Then the fitness $w_i(y)$ of an individual associated with a
195 phenotype y is an weighted sum of all possible environmental fitnesses $f_i(x, y)$ by their distribution
196 $h_i(x)$ (equation (1) of Table 1). The probabilistic optimum Y_p is then defined on the phenotypic
197 fitness $w_i(y)$ as: $w_i(Y_p) = \max w_i(y)$ (Fig. 1d). In contrast, the deterministic optimum Y_d is the optimal
198 phenotype in the average environment, that is $f_i(M, Y_d) = \max_y f_i(M, y)$, where $M (=50)$ is the
199 expectation of x , i.e., $M = \int h_i(x) dx$ (Fig. 1d). In this case, the probabilistic optimum $Y_p (=30.89)$ is
200 always smaller than the optimum in the average environment $Y_d (=33)$.
201
202 In foraging theories, the concept of risk-sensitivity has been specifically developed to deal with daily
203 uncertainty in food acquisition by animals (Caraco, 1980; Stephens and Krebs, 1986; Real and
204 Caraco, 1986). This body of theory and empirical studies reveal that animals often show sensitivity
205 to the variance and skewness of a temporal distribution of foods (Caraco et al., 1980; Caraco and
206 Chasin, 1984). This demonstrates that not only the mean, but also the entire distribution of food
207 availability is important for the evolution of animal behaviour. The expected utility theory used in

208 risk-sensitive foraging (Caraco, 1980; Real and Caraco, 1986) is a specific form of weighted average,
209 in which the fitness function is an increasing function of the amount of food. In dynamic
210 programming, in every time step of decision-making, the overall fitness of an individual is calculated
211 from the weighted average of individual fitnesses of all possible states (Mangel and Clark, 1988).
212 We should note that the risk-sensitive foraging has been empirically (in fields and laboratories)
213 demonstrated well in many animals, such as the seminal work of yellow-eyed juncos by Caraco and
214 others (Caraco et al., 1980).

215

216 **2.2 UNCERTAINTY AT POPULATION LEVEL**

217 Phenotypic variation among individuals of a population is common in many traits, such as body size.
218 Such individual variation arises because environments differ among individuals. Therefore,
219 environmental uncertainty may also appear as phenotypic variation in a population. Most important
220 cases are when phenotypic variation occurs as a result of cumulative effects of past environmental
221 differences.

222

223 Here probabilistic optimization can be stated as follows (Yoshimura and Shields, 1987, 1995).

224 Actual (observed) survivorship and reproduction is determined by the phenotype of an individual for
225 a given environment. Therefore, phenotype is the criterion for realised (observed) fitness. Because of

226 this, we often compare observed mean phenotypes with optimal phenotypes as a measure of
227 achievement of optimality (adaptation) by natural selection (Price and Waser, 1979; Roff, 1981).
228 However, the comparison based on this (deterministic) phenotypic optimum is not valid if there is
229 variation in phenotypes. The evolutionary criterion of fitness is the genotypes that are selected
230 through natural selection. For a given genotype, phenotypic variation is expressed as a probability
231 distribution. The fitness of a genotype is the weighted sum of the fitnesses of all the phenotypes
232 associated with the genotype, the *probabilistic genetic optimum*. We can then compare the observed
233 mean phenotype with this genetic optimum.

234
235 The mathematical expression of the fitness $w_p(z)$ of an individual associated with a genotype is
236 shown in the equation (2) of Table 1. It is the weighted sum of all the phenotypic fitnesses $f_p(y)$
237 multiplied by the distribution of phenotypes $h_p(y, z)$ (equation (2) of Table 1). If the phenotype x is
238 discrete, e.g., clutch size, then $w_p(z)$ becomes the summation (equation (3) of Table 1). This is the
239 weighted average of discrete phenotypes at the population level within a generation.

240
241 An illustrative example is the phenotypic variation in body size (Fig. 2) (Yoshimura, 1995). Let
242 phenotypic fitness f_p be a function of body size y , i.e., $f_p = f_p(y) = w_p(y)$, with a single peak (Fig. 2a:
243 dotted line), and $h_p(y, z)$ be a probability distribution of body size y for a given genotype z (Fig. 2b).

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244 Suppose that genotype z controls the mean body size of a normal distribution with a constant
245 variance (Fig. 2b: three genotypes are shown). We assume here that the mean body size can shift
246 continuously by changing genotypes. Then the fitness of the genotype $w_p(z)$ is the weighted sum of
247 all the phenotypic fitnesses $f_p(y)$ with their distribution $h_p(y, z)$ (Fig. 2a: solid line; equation (2) of
248 Table 1). Here the phenotypic optimum Y_{max} represents the trait that achieves the highest
249 reproductive success in the environment, i.e., $f(Y_{max}) = \max f(y)$. In contrast, the genotypic
250 optimum Z_{max} is the trait selected by natural selection, i.e., $w_p(Z_{max}) = \max w_p(z)$. In general, the two
251 optima differ in their values. In this example, the genetic optimum Z_{max} is always smaller than
252 phenotypic optimum Y_{max} (Fig. 1a).

253

254 The discrepancy between genetic and phenotypic optima can be illustrated as follows: Suppose that
255 2 meters is the optimum height for a man, but that if he is more than 2 meters tall (even slightly) he
256 tends to kill himself by banging into the tops of door frames. A critical point is that genotypes
257 determine the height only *on average*, because their environments vary. We have to consider all the
258 individuals for a given genotype. For people associated with an average 2-meter genotype, nearly
259 half of them become more than 2 meters tall and are knocked out by the door frame. Therefore, the
260 optimal average height (genotype) is actually smaller than 2 meters. For this optimal genotype, most
261 people are suboptimal, but their loss of fitness is much less than killing themselves; and a very few

262 will be lost due to their being >2 meters in height. In other words, the deterministic optimum height
263 lies above the probabilistic genetic optimum.

264

265 More generally, it is well known that there is a discrepancy between phenotypic and genetic optima
266 in most genetic systems because of various genetic constraints, such as segregation, recombination
267 and mutation (Crow and Kimura, 1970), and because of environmental variation (Mountford, 1968;
268 Lalonde, 1991). For example, in quantitative traits like body size, the phenotypes of offspring vary
269 from parental phenotypes. The discrepancies between phenotypic and genetic optima have been
270 observed in the pollen dispersal of a plant (Price and Waser, 1979) and the body size of a fruit fly,
271 Drosophila melanogaster (Roff, 1981; Yoshimura and Shields, 1995).

272

273 The current analyses focus on the uncontrolled phenotypic variation. However, individual variation
274 may be induced as an adaptive response (Pigliucci, 2001; Dewitt and Scheiner, 2004). Phenotypic
275 plasticity may thus increase the fitness of a population (Via and Lande, 1985). In this case, we have
276 diversification of phenotypes with respect to environmental factors. Many individual variations are
277 indeed adaptive variations (Dewitt and Scheiner, 2004). Clutch size variation may be an adaptive
278 plasticity. In the great tit, the variation in clutch size is partly reflecting the parental ability of rearing
279 young (Pettifor et al., 1988). Inducible defence is very common in many organisms (e.g., DeWitt,

280 1998). Probabilistic optimization scheme is also useful in conceptualizing the fitness maximization
281 of such adaptive responses (DeWitt and Yoshimura 1998).

282
283 The body-size example is a case when phenotypic variation appears on the target trait for which we
284 evaluate the optimality. However, it may also appear in correlated traits, which in turn affect the
285 optimality of the target trait. Here phenotypic correlation can be either positive or negative.

286 Allometry (e.g., in body size) is an example of a positive correlation (Schmidt-Nielson, 1984).

287 Negative correlation is often known as a trade-off (Roff, 1992; Stearns, 1992). It is important that
288 phenotypic variation in such correlated traits can affect the optimality of the target traits. For
289 example, if there is a trade-off between current clutch size and future reproduction (via parental
290 survivorship), anticipated variation in future reproduction should be accounted for through the
291 current clutch size (Yoshimura and Shields, 1992; Lalonde, 1991).

292

293

294 **2. THE PRINCIPLE OF OPTIMIZATION**

295 The principle of probabilistic optimisation is a weighted average of fitnesses (or fitness potentials)
296 according to their probability distributions (Yoshimura and Shields, 1992; Cohen, 1993). Suppose
297 that we measure the fitnesses of an individual over some range of temperatures, where temperature

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298 changes over time. Obviously we may just consider the fitness of an individual at the mean
299 temperature. This represents a deterministic optimum, as in the mean fitness concept. However, it
300 does not account for temperatures other than at one point, the mean temperature. Hence the best way
301 to evaluate the fitness of an individual is the weighted average of fitnesses according to the
302 distribution of temperature. This expectation accounts for the entire temperature distribution and
303 gives a correct estimate of the fitness without any error.

304
305 A canonical form of probabilistic optimization is given as follows. Let x and y be individual
306 and collective trait values, respectively. For example, if x is a phenotype value, then y is a
307 genotype value associated with a distribution of phenotype value x . Suppose $f(x, y)$ is the
308 fitness potential function of x given y . Then the canonical form of fitness $w(y)$ is given as:

309 $w(y) = \int f(x, y)h(x, y)dx$ (1)

310 where $f(x, y)$ and $h(x, y)$ are the fitness potential and the probability distribution of
311 trait values x and y , respectively. Depending on the situation given these two functions may be
312 those of a single variable x , such that, $f = f(x)$ and $h = h(x)$.

313
314 In other words, the overall fitness is the expectation (weighted average) of all individual fitnesses (or
315 fitness potentials) associated with each value (probabilistic optimum); this expectation is different

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316 from the fitness for the mean value (deterministic optimum). Weighted averages appear as an
317 underlying concept in any stochastic and probabilistic modelling for uncertainty, not only at the
318 individual level, but also at the population and generation levels. I will discuss how weighted-
319 average fitnesses and mean value fitnesses differ in three different levels later.

320

321 **3. THE LOGARITHMIC FORM OF GOEMETRIC MEAN FITNESS**

322 Fitness varies over generation times. Natural populations often fluctuate widely due to long-term
323 environmental changes in weather and other environmental factors (Andrewartha and Birch, 1954).
324 Similarly, the multiplicative growth rates of a genotype in a population should also vary according to
325 environmental conditions. Here, variation in growth rates might play an important role in the
326 evolution of many phenotypic traits (Philippi and Seger, 1989; Bulmer, 1994; Yoshimura and Clark,
327 1991). In order to assess the effect of the variation in growth rates on natural selection, we have to
328 evaluate the long-term growth rate of a genotype. Here the appropriate concept of fitness is the
329 average (expected) growth rate per generation. This average is called geometric mean fitness,
330 because it is the geometric mean of multiplicative growth rates (Lewontin and Cohen, 1969;
331 Yoshimura and Clark, 1991).

332

333 Mathematically geometric mean fitness can be derived from the population growth as follows.

334 Geometric mean fitness is a specific form of probabilistic optimization, where the fitness function is
 335 a logarithm of population growth rates. Consider the population dynamics of a given genotype (z) for
 336 an organism with discrete generations: $N_z(t+1) = r_z(t) N_z(t)$, for $t = 0, 1, 2, \dots$ where $N_z(t)$ is the
 337 population size and the fitness of a genotype z , $r_z(t)$, is expressed as the population growth rate at
 338 generation t . Then the population size at generation t is given by:

339
$$N_z(t) = r_z(0)r_z(1)\cdots r_z(t-1)N_z(t-1) = \left(\prod_{i=0}^{t-1} r_z(i)\right)N_z(0) \quad (7)$$

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340 The geometric mean fitness is then defined as an average population growth rate per generation:

341
$$G(z) = \prod_{i=0}^{t-1} r_z(i)^{(1/t)}$$
 . Suppose that the population growth rate $r_z(i)$ is randomly drawn from a

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342 probability distribution $h_z(r, z)$ for a given genotype z . Then the geometric mean fitness is expressed
 343 by the probability distribution $h_z(r, z)$ as:

344
$$G(z) = \prod_w w^{h_g(w, z)} \quad (8)$$

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345 Here genotypes with the highest geometric mean fitness ($\max G(z)$) should be selected through
 346 natural selection. Taking logarithm of equation (8), we get the arithmetic form (weighted average) of
 347 the fitness under generational uncertainty (equation (1) of Table 2, Fig. 3), where the notations are
 348 shown in Table 2. Here the probabilistic optimization is a weighted average with the weight $f_g(r) =$
 349 $\log(r)$ (Fig 3a, 3b). This formula is fully equivalent with fitness at the level of an individual and a
 350 population (equations (1) and (2) of Table 1).

351

352 This example indicates that variation in growth rates decreases geometric mean fitness. Because of
353 this, the geometric mean fitness is often approximated with mean and variance using a
354 variance-discount method (Fig. 4) (Frank and Slatkin, 1989; Gillespie, 1977; Yoshimura and Clark,
355 1991). Such approximation clearly depicts the effect of variance. As in the previous calculus
356 example, variance in population growth rate r reduces the geometric mean fitness. Even if the mean
357 r is smaller, if the variance of r is smaller, the geometric mean fitness can be higher (Fig. 4).
358
359 However, ironically such approximation concentrates only on the effects of mean and variance and
360 ignores the entire distribution of growth rates. In addition, the approximation also assumes the
361 normal distribution of growth rate with small variance (Yoshimura and Jansen, 1996). Therefore, it is
362 not applicable to a case when variance is large or when extinction is a prominent possibility. This is
363 evident from the logarithmic function in geometric mean fitness: the weight of negative growth is
364 much higher than the weight of positive growth, because the logarithm drops faster on the negative
365 side, than increases in the positive side. In the limit, if fitness falls to zero in any generation,
366 arithmetic mean fitness will still be positive, but geometric mean fitness will be zero.
367
368 What is the probability distribution best fit to the distribution of population growth rates?
369 Multiplicative population growth rate r is a nonnegative variable. Therefore, normal distribution that

370 can take negative values is not appropriate. In this sense, lognormal distribution is more appropriate
371 or at least applicable. Here we show the geometric mean fitness becomes extremely simple when the
372 lognormal distribution is assumed in population growth rates. Let population growth rate r follows a
373 lognormal distribution such that

374
$$P(r; m_z, \sigma_z) = \left(\frac{1}{r\sqrt{2\pi}\sigma_z} \right) \exp\left(-\frac{(\log(r) - m_z)^2}{2\sigma_z^2} \right) \quad (9)$$

375 Where $P(r) = P(r; m_z, \sigma_z)$ is the probability distribution of r with mean m_z , and variance σ_z for
376 genotype z . Then the logarithmic form of geometric mean fitness (equation (1) of Table 2) can be
377 solved analytically and reduces to the mean of the lognormal distribution m_z , such that (see
378 Appendix for derivation):

379
$$w_g(z) = \log G(z) = \log G(m_z, \sigma_z) = m_z = E_z \{ \log(r) \} \quad (10)$$

380 It has been believed that variance is important in adaptation in stochastic environments. However, it
381 may be an artefact of our use of multiplicative population growth rates.

383 We should note that the current derivation is not necessary for any distribution of log growth rates.

384 The correct measure of the fitness at the generation level is the simple 'arithmetic' mean of

385 logarithmic population growth rates, such that $w_g(z) = E \{ \log(r) \}$. In this measure, variance and the

386 shape of the probability distribution does not affect the overall fitness over generation time.

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388 The current analysis of the geometric mean fitness for a lognormal distribution further implies an
389 important feature of the logarithmic growth rates. Let $R = \log(r)$. Then, the fitness over generation
390 $w_G(z)$ is given by the simple (un-weighted) average of the value R (equation (2) of Table 2), such that
391 $w_G(z) = E\{R\}$ (Fig. 3c and 3d). Thus the generational fitness can be averaged over generation as a
392 simple average if the fitness is measured as the logarithm of the multiplicative growth rates.

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395 **43. DISCUSSION MATHEMATICAL REPRESENTATION AND**
396 **INTERGRATION OF UNCERTAINTY**

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397 We can classify environmental uncertainty into three categories based on the level of integration: (1)
398 short-term temporal change experienced by an individual (individual level within a generation), (2)
399 phenotypic variation among individuals (population level within a generation) and (3) population
400 fluctuation across generations due to long-term environmental changes (cross-generation level). The
401 principle of probabilistic optimisation appears as a form of weighted average (equation (4)) at three
402 levels: individual, population and generation. The fitness at the cross-generation level is the simple
403 average of log growth rates without a weight ($E\{\log(r)\}$ or $E\{R\}$). These uncertainties can be
404 incorporated into the unified fitness at the generation level (Yoshimura and Shields, 1992).

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406 We first consider the fitness of an individual associated with a phenotype.

407 Denote the following variables and functions:

408 y : an environmental factor for an individual

409 x : the phenotype of an individual

410 $f(y|x)$: fitness of an individual with phenotype x in environment y

411 $h_d(y)$: probability distribution of environment y

412 $f(x)$: fitness of an individual with phenotype x

413 Then the fitness $f(x)$ of an individual associated with a phenotype x is a weighted sum of all possible

414 environmental fitnesses $v(y;x)$ with the distribution of the environments $d(y)$:

415
$$f(x) = \int_{y \in D(y|x)} v(y;x) d(y) dy \quad (2)$$

416 where $D(y|x)$ is the domain of environments y for a given phenotype x . This is a weighted average

417 of fitness measures at the individual level.

418

419 Next we consider the fitness of an individual associated with a genotype from the fitness of

420 phenotypes $f(x)$. Denote the following variable and functions:

421 z : a genotype

422 $h(x;z)$: probability distribution of phenotypes x for a given genotype z

423 $w(z)$: fitness of a genotype z (within a generation)

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424 The fitness of a genotype $w(z)$ is then the weighted sum of all the phenotypic fitnesses $f(x)$.

425 multiplied by the distribution of phenotypes $h(x;z)$:

426
$$w(z) = \int_{x \in H(x;z)} f(x)h(x;z)dx \quad (3)$$

427 where $H(x;z)$ is the domain of phenotypes x for a given phenotype z . If the phenotype x is discrete,

428 e.g., clutch size, then $w(z)$ becomes the summation:

429
$$w(z) = \sum_{x \in H(x;z)} f(x)h(x;z) \quad (4)$$

430 This is the weighted average of discrete phenotypes at the population level within a generation.

431

432 Lastly we consider geometric mean fitness as the long-term fitness of a genotype across generations.

433 Denote the following variable and functions:

434 w : fitness per generation measured as multiplicative growth rates

435 $p(w; z)$: the probability distribution of fitnesses w for a genotype z

436 $G(z)$: the geometric mean fitness of a genotype z

437 $g(z)$: the logarithm of the geometric mean fitness

438 Then the geometric mean fitness of a genotype is the expected long term growth rate for a given

439 genotype:

440
$$G(z) = \sum_w w^{p(w;z)} \quad (5)$$

441 Here maximizing $G(z)$ is same as maximizing its logarithm $g(z)$ and the latter is equal to the discrete

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442 ~~weighted average of the logarithmic fitnesses $\log(w)$ with their distribution $p(w; z)$:~~

443 ~~$$g(z) = \log G(z) = \sum_w p(w; z) \log(w) = E\{\log(w)\} \tag{6}$$~~

444 ~~This is the weighted average of fitnesses at the generation level.~~

445

446 ~~The principle of probabilistic optimisation is a weighted average of fitnesses (or fitness potentials)~~

447 ~~according to their probability distributions (Yoshimura and Shields, 1992; Cohen, 1993). A canonical~~

448 ~~form of probabilistic optimization is then given as follows. Let α and β be individual and~~

449 ~~collective trait values, respectively. For example, if α is a phenotype value, then β is a genotype~~

450 ~~value associated with a distribution of phenotype value α . Suppose $f(\alpha, \beta)$ is the fitness potential~~

451 ~~function of α given β . Then the canonical form of fitness $w(\beta)$ is given as:~~

452 ~~$$w(\beta) = \int f(\alpha, \beta) h(\alpha, \beta) d\alpha \tag{11}$$~~

453 ~~where $f(\alpha, \beta)$ and $h(\alpha, \beta)$ are the fitness potential and the probability distribution of trait values~~

454 ~~α and β , respectively. Depending on the situation given these two functions may be those of a single~~

455 ~~variable α , such that $f = f(\alpha)$ and $h = h(\alpha)$.~~

456

457 ~~In other words, the overall fitness is the expectation (weighted average) of all individual fitnesses (or~~

458 ~~fitness potentials) associated with each value (probabilistic optimum); this expectation is different~~

459 ~~from the fitness for the mean value (deterministic optimum). Weighted averages appear as an~~

460 underlying concept in any stochastic and probabilistic modelling for uncertainty, not only at the
461 individual level, but also at the population and generation levels.

462
463 We should also note that these uncertainties can be incorporated into the unified fitness at the
464 generation level (Yoshimura and Shields, 1992). The integration of the individual-level fitness into
465 the population-level fitness is given by $f_p(y) = w_p(y)$, in equations (1) and (2) of Table 1. The fitness
466 measure at the population level $w_p(z)$ should be transformed into the multiplicative population
467 growth rate r for each generation. For example, if $w_p(z)$ is defined as the growth rate per individual
468 adult, then simply, $r = w_p(z)$. However, if it is measured as a number of offspring/adult individual, as
469 is often seen, then $r = \{w_p(z) * (\text{number of adult}) + (\text{number of surviving adult})\} / (\text{number of adult})$ at
470 a generation.

471
472 We can also estimate the effect of uncertainty on the outcome of natural selection. How 4. LEVELS
473 OF UNCERTAINTY.

474 4.1 UNCERTAINTY AT INDIVIDUAL LEVEL

475 An individual experiences temporal changes in environments. An individual lives in daily changing
476 environments, unstable and unpredictable in many aspects. How an individual behaves, grows and
477 reproduces in such changing environments has often been dealt as a problem of optimisation in

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478 behavioral and physiological ecology (Krebs and Davies, 1993; Sibly and Calow, 1986; Mangel and
479 Clark, 1988; Stephens and Krebs, 1986; Real and Caraco, 1986). Here the underlying principle can
480 be illustrated as follows: individual animal forages for varying, and thus unpredictable amounts of
481 food daily. Daily food amounts are then expressed as a probability distribution. The overall fitness of
482 an individual associated with a given phenotype is a weighted sum of all the fitnesses of daily food
483 intake during its life time (Yoshimura and Shields, 1992). The optimum based on the overall fitness
484 is a probabilistic optimum that is different from the fitness at the average food intake, a deterministic
485 optimum.
486
487 Daily uncertainty in foraging animals can be mathematically expressed as follows (Fig. 1). Let y be
488 daily food amounts as an environmental factor, where $y = 0$ in the worst environment and $y = 100$ in
489 the best environment, and $v(y, x)$ be the fitness of an individual with a phenotype x in environment y .
490 Naturally $v(y, x)$ is an increasing function of y (Fig. 1a). The difference in phenotype x indicates what
491 kind of food environments an individual is adapted for: if $x = 10$, an individual is adapted for bad
492 environments, i.e., fitness is fairly similar for bad and good environments ($10 < y < 50$ and $y > 50$).
493 However, if $x = 50$, an individual is adapted for good environments, i.e., fitness is low (zero) for bad
494 environments ($y < 50$) and extremely high for good environments ($y >> 50$). The fitness function $v(y, x)$
495 for phenotypes x in a given environment y is a function with a peak (Fig. 1b).

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Suppose that the probability distribution of daily food abundance $d(y)$ is approximated by a distribution with mean $E(y) = 50$ (Fig. 1c). Then the fitness $f(x)$ of an individual associated with a phenotype x is an weighted sum of all possible environmental fitnesses $v(y, x)$ by their distribution $d(y)$ (equation (2)). The probabilistic optimum x_p is then defined on the phenotypic fitness $f(x)$ as: $f(x_p) = \max f(x)$ (Fig. 1d). In contrast, the deterministic optimum x_d is the optimal phenotype in the average environment, that is $f(M, x_d) = \max_x f(M, x)$, where $M (=50)$ is the expectation of y , i.e., $M = \int d(y) dy$ (Fig. 1d). In this case, the probabilistic optimum $x_p (=30.89)$ is always smaller than the optimum in the average environment $x_d (=33)$.

In foraging theories, the concept of risk sensitivity has been specifically developed to deal with daily uncertainty in food acquisition by animals (Stephens and krebs, 1986; Real and Caraco, 1986). This body of theory reveals that animals often show sensitivity to the variance and skewness of a temporal distribution of foods. This demonstrates that not only the mean, but also the entire distribution of food availability is important for the evolution of animal behaviour. The expected utility theory used in risk sensitive foraging (Real and Caraco, 1986) is a specific form of weighted average, in which the fitness function is an increasing function of the amount of food. In dynamic programming, in every time step of decision making, the overall fitness of an individual is calculated

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532 distribution. The fitness of a genotype is the weighted sum of the fitnesses of all the phenotypes
533 associated with the genotype, the probabilistic genetic optimum (equation (3)). We can then compare
534 the observed mean phenotype with this genetic optimum,
535
536 Phenotypic variation in body size is mathematically expressed as follows (Fig. 2). Let phenotypic
537 fitness f be a function of body size x , i.e., $f = f(x)$, with a single peak (Fig. 2a: dotted line), and
538 $h(x; z)$ be a probability distribution of body size x for a given genotype z . Suppose that genotype z
539 controls the mean body size of a normal distribution with a constant variance (Fig. 2b: three
540 genotypes are shown). We assume here that the mean body size can shift continuously by changing
541 genotypes. Then the fitness of the genotype $w(z)$ is the weighted sum of all the phenotypic fitnesses
542 $f(x)$ with their distribution $h(x; z)$ (Fig. 2a: solid line) (equation (3)). Here the phenotypic optimum
543 x_{max} represents the trait that achieves the highest reproductive success in the environment, i.e.,
544 $f(x_{max}) = \max f(x)$. In contrast, the genotypic optimum z_{max} is the trait selected by natural selection,
545 i.e., $w(z_{max}) = \max w(z)$. In general, the two optima differ in their values. In this example, the genetic
546 optimum z_{max} is always smaller than phenotypic optimum x_{max} (Fig. 1a).
547
548 The discrepancy between genetic and phenotypic optima can be illustrated as follows: Suppose that
549 2 meters is the optimum height for a man, but that if he is more than 2 meters tall (even slightly) he

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550 tends to kill himself by banging into the tops of door frames. A critical point is that genotypes
551 determine the height only on average, because their environments vary. We have to consider all the
552 individuals for a given genotype. For people associated with an average 2-meter genotype, nearly
553 half of them become more than 2 meters tall and are knocked out by the door frame. Therefore, the
554 optimal average height (genotype) is actually smaller than 2 meters. For this optimal genotype, most
555 people are suboptimal, but their loss of fitness is much less than killing themselves; and a very few
556 will be lost due to their being >2 meters in height. In other words, the deterministic optimum height
557 lies above the probabilistic genetic optimum.

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558
559 More generally, it is well known that there is a discrepancy between phenotypic and genetic optima

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560 in most genetic systems because of various genetic constraints, such as segregation, recombination
561 and mutation (Crow and Kimura, 1970), and because of environmental variation (Mountford, 1968;
562 Lalonde, 1991). For example, in quantitative traits like body size, the phenotypes of offspring vary
563 from parental phenotypes.

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564
565 The body size example is a case when phenotypic variation appears on the target trait for which we
566 evaluate the optimality. However, it may also appear in correlated traits, which in turn affect the
567 optimality of the target trait. Here phenotypic correlation can be either positive or negative.

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568 Allometry (e.g. in body size) is an example of a positive correlation (Schmidt-Nielsen, 1984).

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569 Negative correlation is often known as a trade-off (Roff, 1992; Stearns, 1992). It is important that

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570 phenotypic variation in such correlated traits can affect the optimality of the target traits. For

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571 example, if there is a trade-off between current clutch size and future reproduction (via parental

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572 survivorship), anticipated variation in future reproduction should be accounted for through the

573 current clutch size (Yoshimura and Shields, 1992; Lalonde, 1991).

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575 4.3 UNCERTAINTY AT GENERATION LEVEL

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576 Fitness varies over generation times. Natural populations often fluctuate widely due to long-term

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577 environmental changes in weather and other environmental factors (Andrewartha and Birch, 1954).

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578 Similarly, the multiplicative growth rates of a genotype in a population should also vary according to

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579 environmental conditions. Here, variation in growth rates might play an important role in the

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580 evolution of many phenotypic traits (Philippi and Seger, 1989; Bulmer, 1994; Yoshimura and Clark,

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581 1991). In order to assess the effect of the variation in growth rates on natural selection, we have to

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582 evaluate the long-term growth rate of a genotype. Here the appropriate concept of fitness is the

583 average (expected) growth rate per generation. This average is called geometric mean fitness,

584 because it is the geometric mean of multiplicative growth rates (Yoshimura and Clark, 1991;

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585 Lewontin and Cohen, 1969).

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~~The principle of probabilistic optimisation (equation (1)) appears in the concept of geometric mean fitness, as follows: Variation in growth rates is expressed as a probability distribution, and geometric mean fitness is a specific form of weighted sum of all growth rates within the distribution (equation (5)). This becomes evident when we take the logarithm of the geometric mean fitness, which is the usual arithmetic mean of logarithmic growth rates (equation (6)).~~

~~Mathematically geometric mean fitness can be derived from the population growth as follows: Geometric mean fitness is a specific form of probabilistic optimization, where the fitness function is a logarithm of population growth rates. Consider the population dynamics of a given genotype (z) for an organism with discrete generations: $N_z(t+1) = w_z(t) N_z(t)$, for $t = 0, 1, 2, \dots$, where $N_z(t)$ is the population size and the fitness of a genotype z , $w_z(t)$, is expressed as the population growth rate at generation t . Then the population size at generation t is given by:~~

$$N_z(t) = w_z(0)w_z(1)\dots w_z(t-1)N_z(0) = \left(\prod_{i=0}^{t-1} w_z(i)\right)N_z(0) \quad (7)$$

~~The geometric mean fitness is then defined as an average population growth rate per generation:~~

$$G(z) = \prod_{i=0}^{t-1} w_z(i)^{(1/t)}$$

~~Suppose that the population growth rate $w_z(i)$ is randomly drawn from a probability distribution $p(w, z)$ for a given genotype z . Then the geometric mean fitness is expressed by the probability distribution $p(w, z)$ as:~~

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604 $G(z) = \prod_w w^{p(w;z)} \tag{8}$

605 Here genotypes with the highest geometric mean fitness (max $G(z)$) should be selected through
 606 natural selection. Taking logarithm of equation (8), we get:

607 $\log G(z) = \int p(w; z) \log(w) dw \tag{9}$

608 Here the probabilistic optimization (equation (1)) is a weighted average with the weight $f(w) = \log$
 609 (w) .

611 As in the previous examples, geometric mean fitnesses lie below arithmetic mean fitnesses in
 612 variable environments. The difference between geometric mean and arithmetic mean fitnesses
 613 increases when environments fluctuates strongly, because variation in growth rates increases.

614 Suppose that an organism produces two offspring on average in a generation. In stable environments,
 615 after three generations, we expect $2 \times 2 \times 2 = 8$ offspring. However, in changing environments we may
 616 expect, say, $2 \times 1 \times 3 = 6$ offspring. In both environments, the mean fitness is same (i.e.,

617 $(2+2+2)/3 = (2+1+3)/3 = 2$). But the geometric mean fitness is lower ($(2 \times 1 \times 3)^{1/3} = 1.82$) in the variable

618 environment, than in the constant environment ($(2 \times 2 \times 2)^{1/3} = 2$). Since the population reaches only 6

619 individuals after three generations, the average growth rate of 1.82 individual/generation is a correct

620 measure of fitness. To reiterate, the probabilistic optimum is based on geometric mean fitness, and

621 the deterministic optimum is based on arithmetic mean fitness.

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This example indicates that variation in growth rates decreases geometric mean fitness. Because of this, the geometric mean fitness is often approximated with mean and variance using a variance discount method (Fig. 3) (Frank and Slatkin, 1989; Gillespie, 1977; Yoshimura and Clark, 1991). Such approximation clearly depicts the effect of variance. As in the previous calculus example, variance in population growth rate w reduces the geometric mean fitness. Even if the mean w is smaller, if the variance of w is smaller, the geometric mean fitness can be higher (Fig. 3).

However, ironically such approximation concentrates only on the effects of mean and variance and ignores the entire distribution of growth rates. In addition, the approximation also assumes the normal distribution of growth rate with small variance (Yoshimura and Jansen, 1996). Therefore, it is not applicable to a case when variance is large or when extinction is a prominent possibility. This is evident from the logarithmic function in geometric mean fitness: the weight of negative growth is much higher than the weight of positive growth, because the logarithm drops faster on the negative side, than increases in the positive side. In the limit, if fitness falls to zero in any generation, arithmetic mean fitness will still be positive, but geometric mean fitness will be zero.

What is the probability distribution best fit to the distribution of population growth rates? Growth

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640 rate w is a nonnegative variable. Therefore, normal distribution that can take negative values is not

641 appropriate. In this sense, lognormal distribution is more appropriate or at least applicable. Here we

642 show the geometric mean fitness becomes extremely simple when the lognormal distribution is

643 assumed in population growth rates. Let population growth rate w follows a lognormal distribution

644 such that

$$645 \quad P(w; m_z, \sigma_z) = \left(\frac{1}{w\sqrt{2\pi}\sigma_z} \right) \exp\left(-\frac{(\log(w) - m_z)^2}{2\sigma_z^2} \right) \quad (10)$$

646 Where $P(w) = P(w; m_z, \sigma_z)$ is the probability distribution of w with mean m_z and variance σ_z for

647 genotype z . Then the logarithmic form of geometric mean fitness (equation (9)) can be solved

648 analytically and reduces to the mean of the lognormal distribution m_z such that (see Appendix for

649 derivation):

$$650 \quad \log G(z) = \log G(m_z, \sigma_z) = m_z = E_z(\log(w)) \quad (11)$$

651 It has been believed that variance is important in adaptation in stochastic environments. However, it

652 may be an artefact of our use of multiplicative population growth rates. The correct measure may be

653 the logarithmic population growth rates. The simple 'arithmetic' mean of the logarithmic growth

654 rates is the fitness over generation time. In this measure, variance and the shape of the probability

655 distribution does not affect the overall fitness over generation time.

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657 5. EFFECTS OF UNCERTAINTY

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658 How strong is the effect of uncertainty on natural selection? How large is the discrepancy between
659 the deterministic and probabilistic optima for phenotypes, genotypes in a generation or genotypes
660 across generations? This depends on two factors: (1) the fitness response to phenotypes or
661 environmental conditions (the shape of functions v and f and the logarithm of geometric mean
662 fitness) and (2) the degree of uncertainty (the shape of probability distributions ~~$d-h(\alpha, \beta)h$~~ and
663 ~~$p(w; z)$~~ , e.g., variance and skew; see equations in Tables 1 and 2 ~~equations (1-6)~~). Even though exact
664 quantitative differences depend on the exact shape of individual fitness and probability distributions,
665 in general, we can state that sharp fitness responses (steep functions) and large degrees of
666 uncertainty (flat distributions) tends to lead to a large discrepancy between the deterministic and
667 probabilistic optima (Yoshimura and Shields, 1995).
668
669 The variance-discount method is often used to estimate the discrepancy quantitatively, e.g., the
670 Z-score model (Stephens and Krebs, 1986) in risk-sensitive foraging. However, we need to be aware
671 that this approximation ignores the higher order terms of central tendency in probability distributions
672 and may result in a large discrepancy from true probabilistic optima, as in the usual mean fitness
673 approaches. As is discussed in the previous section, the limitation of variance-discount methods
674 becomes clear when we apply them to geometric mean fitness.
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676 Reinforcing and extending earlier generalisations, we should also note here that which direction the
677 probabilistic optimum shifts from the deterministic optimum can be simply identified (Figs. 1-3).
678 In the case of geometric mean fitness, it is always smaller than the arithmetic mean fitness (Figs. 3
679 and 4). Mathematically, this directionality can be often characterised by Jensen's inequality which
680 compares the expectation of values (here, probabilistic optimum) and the value of an expected factor
681 (here, deterministic optimum) (Karlin and Taylor, 1975).

683 Equation (10) has an important meaning for the strategy of species (see also equations (1) and (2) of
684 Table 2). As a thought experiment, we consider two typical species A and B. The reproduction rates
685 during three generations are assumed as follows:

686 Species A: $r(1) = r(2) = r(3) = 1$.

687 Species B: $r(1) = 1$, $r(2) = 0.001$, $r(3) = 1000$.

688 Species A has a safer strategy such as mammals, while species B takes a risky strategy like fish and
689 plankton. For both cases, equation (10) leads to $w_g(z) = E_z\{\log(r)\} = 0$, so that the geometric
690 mean fitness takes the same value; the population size of each species is unchanged after three
691 generations. In contrast, the mean fitness for both species largely differs. The arithmetic mean fitness
692 for species B is much larger than that of species A. Most fish must release a huge amount of eggs to
693 cope with variable environments.

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The empirical studies of geometric mean fitness is extremely difficult, because severe stochastic events are rare and not measurable (Yoshimura and Clark, 1991). This situation is also reflected in the empirical studies. Only few trial attempts are seen for the effects at the level across generations, e.g., the cabbage butterfly (Root and Kareiva, 1984) and the Great Tit (Boyce and Perrins, 1987). However, these attempts are not inconclusive. In contrast, the effects of uncertainty is well documented at the level of an individual (for many empirical studies, see Stephens and Krebs, 1986; Real and Caraco, 1986) and few good examples are reported at the level of a population (e.g., Price and Waser, 1979; Yoshimura and Shields, 1995). The current analyses of geometric mean fitness may help empiricists to measure the effects of cross-generational uncertainty on natural selection.

As in Monod's famous essay (Monod, 1971) "Chance and necessity," chance (or uncertainty) may be equally as important in evolution as necessity (causality). **6. RESULT**

~~Chance and necessity governs the evolution of organisms (Monod, 1971). The traditional statistical theory of natural selection has been developed based mostly on mean fitness, one central tendency, and it describes the causal "necessity" of evolution. Only in a few case, variance, the second order measure, is included as a variance discount. In contrast, the current probabilistic theory covers an entire probability distribution of fitness and it elucidates the intertwining features of "chance"~~

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712 ~~(uncertainty) and “necessity” in evolution. As I showed, this basic principle applies to problems of~~
713 ~~uncertainty in all three major categories of uncertainty: (1) behavioural decision making of an~~
714 ~~individual (individual level: e.g., risk sensitive foraging and dynamic behaviour), (2) phenotypic~~
715 ~~adaptation of life history and behavioral traits (population level: e.g., body size, dispersal strategy),~~
716 ~~and (3) population dynamics and evolution (cross-generation level: e.g., risk spreading,~~
717 ~~bet hedging).~~

718

719 ~~As in Monod's famous essay (Monod, 1971) "Chance and necessity," chance (or uncertainty) may be~~
720 ~~equally as important in evolution as necessity (causality). It has been shown that environmental~~
721 ~~uncertainty often relates to many other issues in evolution and ecology (Yoshimura and Clark, 1993;~~
722 ~~Bulmer, 1994), e.g., game theory (Ellner, 1985), kin selection (McNamara, 1995), and community~~
723 ~~diversity (Chesson and Warner, 1981). However, we still have a very limited knowledge about the~~
724 ~~importance of uncertainty in the evolution of organisms. For example, we have only just started to~~
725 ~~characterise the basic property of randomness in fluctuating environments, such as 1/f-noise (Halley,~~
726 ~~1996). I hope that this synthesis will promote better understanding of the probabilistic nature of~~
727 ~~natural selection.~~

728

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733 ↓これを入れないとダメらしいです↓

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734 Acknowledgements

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735 Please include, at the end of the acknowledgements, a declaration that the experiments
736 comply with the current laws of the country in which they were performed.

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847 **APPENDIX**

848 We solve the logarithmic form of geometric mean fitness (equation (8) to derive equation (10) when

849 $P(r) = P(r; m_z, \sigma_z)$ is a lognormal distribution (equation (9)):

$$850 \log G(r; m_z, \sigma_z) = \int_0^{\infty} \log(r) \left(\frac{1}{r\sqrt{2\pi}\sigma_z} \right) \exp\left(-\frac{(\log(r) - m_z)^2}{2\sigma_z^2}\right) dr \quad (A1)$$

851 Let $\log(r) = y$, $r: 0 \rightarrow \infty$. Then, $dr = rdy$, $y: -\infty \rightarrow +\infty$ and we get

$$852 \log G(r; m_z, \sigma_z) = \int_{-\infty}^{\infty} y \left(\frac{1}{\sqrt{2\pi}\sigma_z} \right) \exp\left(-\frac{(y - m_z)^2}{2\sigma_z^2}\right) dy \quad (A2)$$

853 Then, let $y - m_z = x$, $\frac{1}{\sqrt{2\pi}\sigma_z} = a$, $\frac{1}{2\sigma_z^2} = b$.equation (A2) becomes

$$854 \log G(r; m_z, \sigma_z) = a \left\{ \int_{-\infty}^{\infty} x \exp(-bx^2) dx + m_z \left(\int_{-\infty}^{\infty} \exp(-bx^2) dx \right) \right\} \quad (A3)$$

855 Here let $F(x) = \exp(-bx^2)$. Then we get $\frac{dF}{dx} = -2bx \exp(-bx^2)$, which is transformed to

$$856 \underline{-xF(x) = -\frac{1}{2b} \frac{dF}{dx}}. \text{ Therefore, we get } \int xF(x) dx = \left[-\frac{1}{2b} F(x) \right].$$

857 The right-hand side of Equation (A3) is now calculated as follows.

$$858 \int_{-\infty}^{\infty} x \exp(-bx^2) dx = \left[-\frac{1}{2b} \exp(-bx^2) \right]_{-\infty}^{\infty} = 0$$

859 And from $\int_0^{\infty} \exp(-bx^2) dx = \frac{\sqrt{\pi}}{2\sqrt{b}}$, we get

$$860 \int_{-\infty}^{\infty} \exp(-bx^2) dx = 2 \int_0^{\infty} \exp(-bx^2) dx = \frac{\sqrt{\pi}}{\sqrt{b}}$$

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861 Equation (A3) is then rewritten as

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$$\log G(r; m_z, \sigma_z) = a \left\{ 0 + m_z \times \frac{\sqrt{\pi}}{\sqrt{b}} \right\} = \frac{1}{\sqrt{2\pi}\sigma} \times m_z \times \sqrt{2\pi}\sigma = m_z$$

863 Thus equation (10) is derived.

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866 Table 1. Terms and equations for the fitness at the levels of an individual and a population.

867 _____

868 x : an environmental factor for an individual

869 y : the phenotype of an individual

870 z : a genotype

871 H : The domain of a given distribution h

872 $f_i(x,y)$: fitness of an individual with phenotype y in environment x

873 $h_i(x)$: probability distribution of environment x

874 $f_p(y) = w_i(y)$: fitness of an individual with phenotype y

875 $h_p(y,z)$: probability distribution of phenotypes y for a given genotype z

876 $w_p(z)$: fitness of a genotype z (within a generation)

877

878 $w_i(y) = \int_{y \in H_i(x)} f_i(x,y) h_i(x) dx$ _____ (1)

879 $w_p(z) = \int_{y \in H_p(y,z)} f_p(y) h_p(y,z) dy$ _____ (2)

880 $w_p(z) = \sum_{y \in H_p(y,z)} f_p(y) h_p(y,z)$ _____ (3)

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882 Note: the suffix i in equation (1) denotes the individual level

883 (p : population level).

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886 Table 2. Terms and equations for the geometric mean fitness.

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r : fitness per generation measured as multiplicative growth rates

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$f_g(r) = R = \log r$: logarithmic fitness at a generation

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$h_g(r; z)$: probability distribution of fitness r over generations for a given genotype z

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$w_g(z) = w_G(z)$: logarithmic geometric mean fitness of a genotype z

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$H_G(e^R, z)$: probability distribution (or domain) of R for a genotype z in log scale

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$$w_g(z) = \int_{r \in H_g(r, z)} f_g(r) h_g(r, z) dr = \int_{r \in H_g(r, z)} \log(r) h_g(r, z) dr \quad (1)$$

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$$w_G(z) = \int_{e^R \in H_G(e^R, z)} R H_G(e^R, z) e^R dR \quad (2)$$

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899 **Figure Legends**

900 Fig. 1 - Probabilistic optimization of uncertain daily food amounts x^* for a given phenotype y^* . (a)
901 the fitness $f_p(x^*, y^*)$ of an individual with a phenotype y^* in environment x^* . The phenotype $y^* = 10$
902 is adapted for bad environments, $x^* = 30$ for intermediate environments and $y^* = 50$ for good
903 environments. (b) the fitness $f_p(x, y)$ for phenotypes y in a given environment x . The
904 deterministic optimum $Y_{d,1} (=33)$ is the optimal phenotype in the average environment $x_{mm} (=50)$.
905 (c) the (Gaussian) probability distribution of daily food abundance $h_p(x)$ with the mean $E(x) = 50$.
906 (d) The phenotypic fitness of an individual $w_p(y)$. The probabilistic optimum $Y_{p,1} (=30.89)$ is the
907 maximum of $w_p(y)$ for y . The probabilistic optimum $Y_{p,1} (=30.89)$ is different from the
908 deterministic optimum $Y_{d,1} (=33)$.

909
910 Fig. 2 - Probabilistic optimization of body size y^* . (a) $w_p(y)$: the phenotypic fitness of body size
911 (the dotted line); $w_p(z)$: the genotypic fitness of mean body size (the solid line); Y_{max} represents
912 the optimal phenotype (individual body size); and Z_{max} represents the optimal genotype (mean body
913 size). (b) $h_p(y, z)$: probability distributions of body size y for a given genotype z . The normal
914 distributions are assumed with a constant variance and genotypic mean body sizes z (three genotypes
915 are shown). The genetic optimum Z_{max} is different from the phenotypic optimum Y_{max} .

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Fig. 3 - Probabilistic optimization of population growth rates r over cross-generations. (a) $f_G(r) = \log(r)$: the log population growth rate plotted against multiplicative growth rate r . (b) $h_G(r, z)$: probability distributions of multiplicative growth rate r for three genotypes. The log normal distributions are assumed with a constant variance and genotypic mean body sizes z (three genotypes are shown: $z = z_1, z_2$ and z_3). (c) The log-transformed generational fitness $F_G(R) = F_G(\log r) = R$ plotted against $R = \log(r)$. (d) $h_G(r, z)$: probability distributions of log growth rate $\log(r)$ for three genotypes (transformed from (b)).

Fig. 43 - Mean-variance approximation of geometric mean fitness: $G(r^*) \approx \mu - \sigma^2/(2\mu)$, where μ and σ^2 are mean and variance of population growth rates r^* , respectively. -Isoclines indicate several three different level of $G(r^*)$ with grey scale (from top: 1.5, 1 and 0.5). The combination of low mean and low variance (circle) is may be better than that of high mean and high standard deviation (cross). -On an isocline, two genotypes have equal geometric mean fitnesses.

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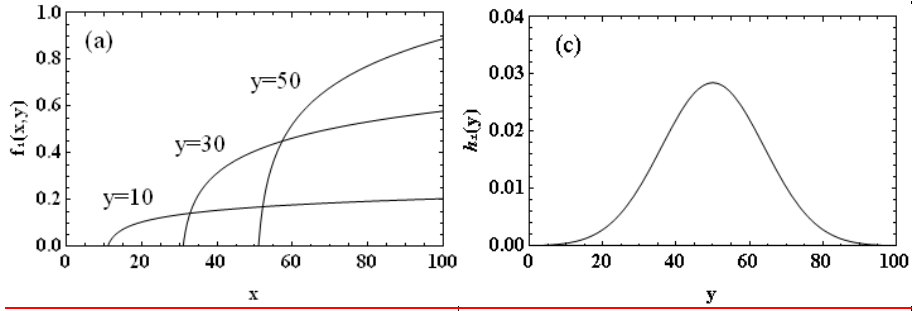
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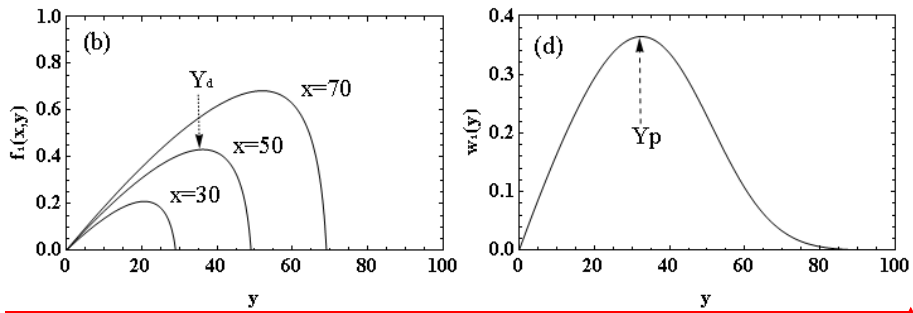
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938 Fig. 1.

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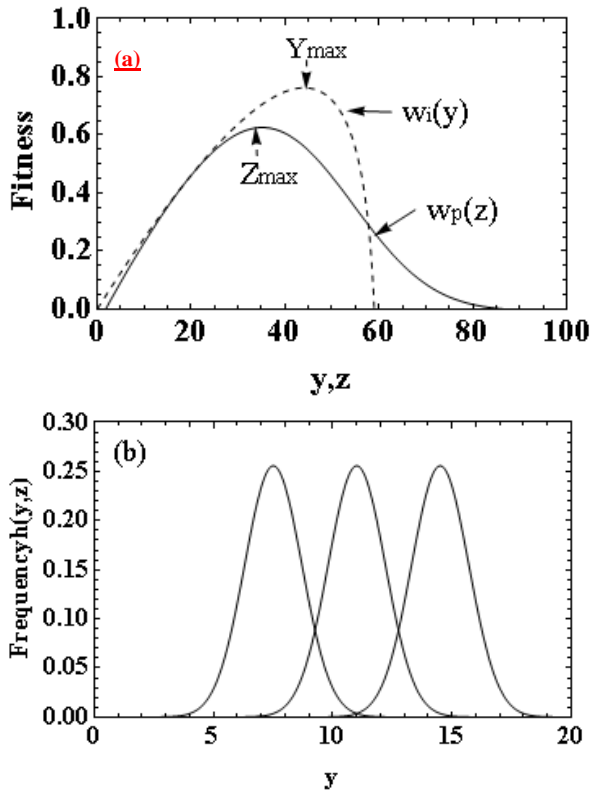
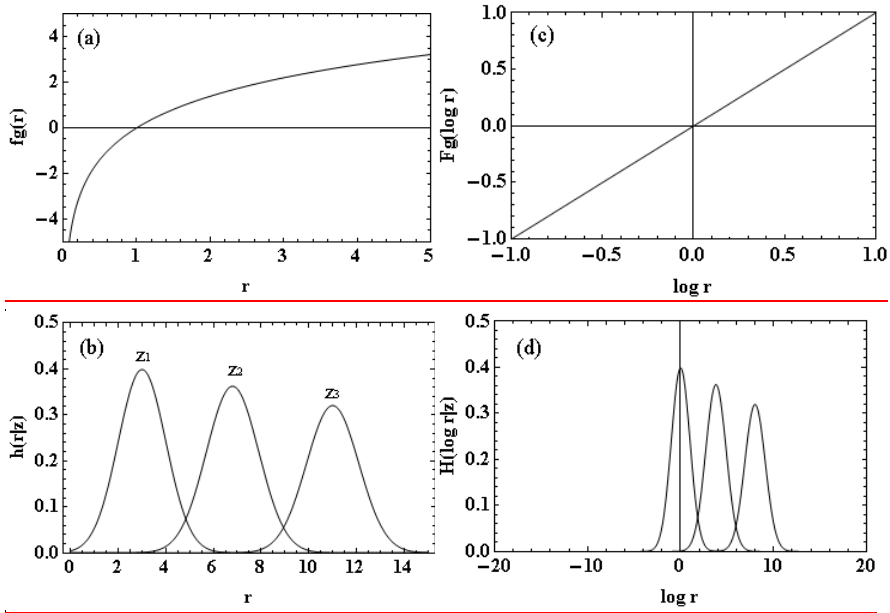


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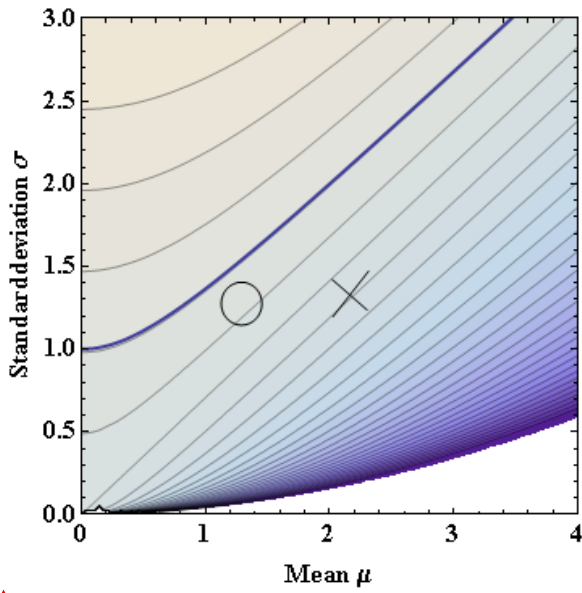
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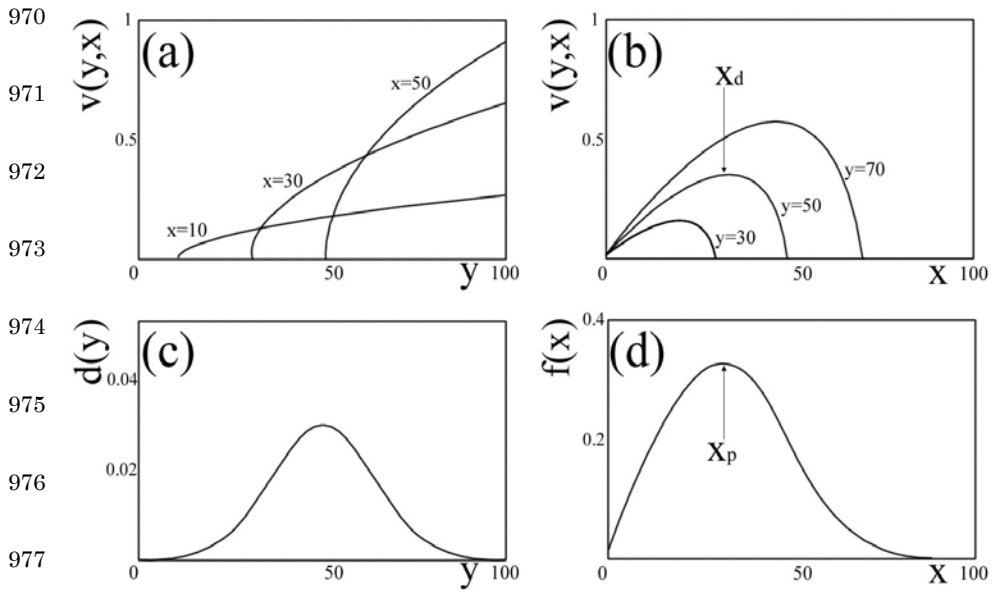
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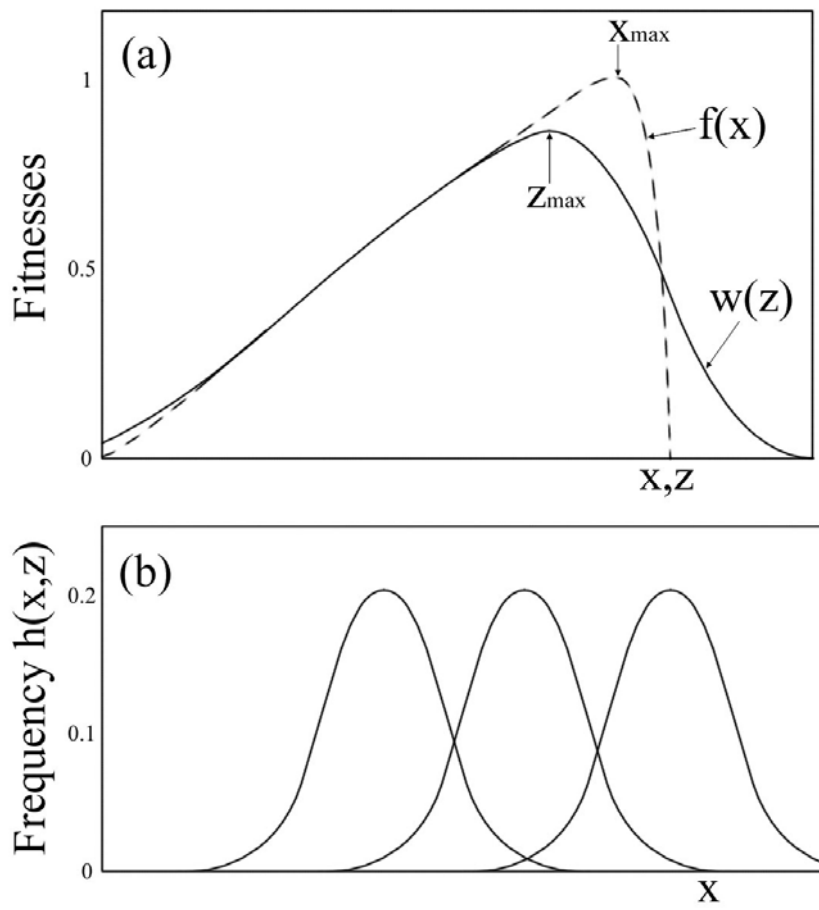
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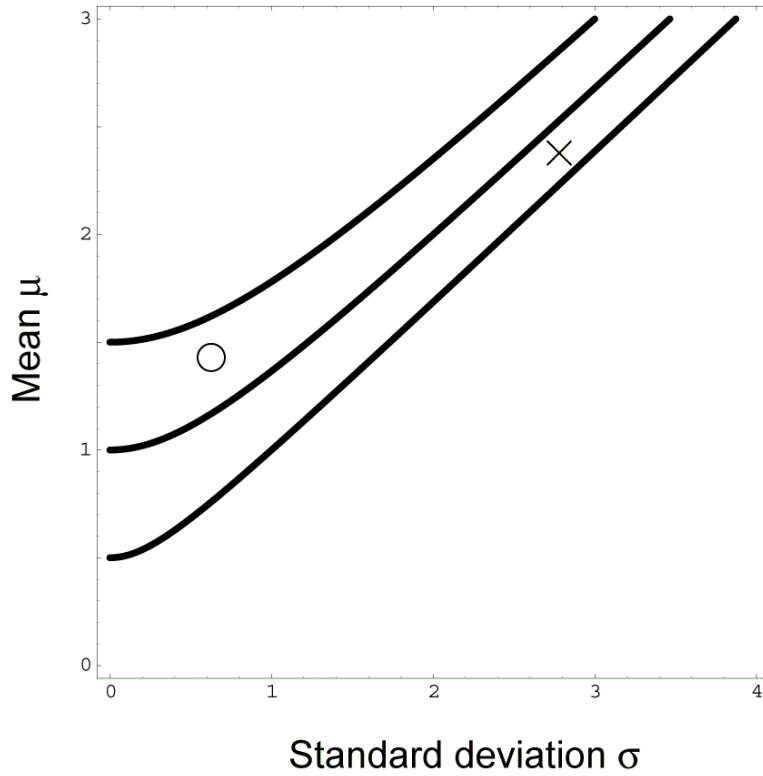
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Fig. 2

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~~Fig. 3 Numerous hypotheses have been advanced to explain the evolution of long perfectly synchronized life cycles, e.g., predator satiation and asynchronization with predator cycles (Lloyd and Dybas, 1966; Hoppensteadt and Keller, 1976), and larval competition (Bulmer, 1977). These arguments are summarized and synthesized in Williams and Simon 1995, Table 1. Two major hypotheses compete to explain the evolution of prime number reproductive intervals (life cycles) among periodical cicadas. The anti-predator hypothesis claims that prime number intervals help to protect cicadas from being overwhelmed by their predators.~~

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~~(Lloyd and Dybas, 1966; Hoppensteadt and Keller, 1976). This hypothesis can explain the origins and maintenance of periodical cycles, but it cannot explain why prime number cycles of periodical cicadas are have originated in the first place (May, 1979). The hybridization hypothesis claims that prime numbers greatly reduce the chance of hybridization among cicada broods (Cox and Carlton, 1988; Cox and Carlton, 1991; Yoshimura, 1997).~~

~~In the hybridization hypothesis, the origin of periodicity is due to environmental cooling during the Pleistocene Ice Ages. Apart from the timing of adult emergence, ancestral periodical cicadas are assumed to be very similar to typical members of the Cicadidae, emerging annually and spending 5-9 years in the larval stages based on the life history of *Okanagana rimosa*, a closely related species. Their determinant of maturation is cumulative temperature because their growth depends on that of the host plants, trees, (Yoshimura, 1997). Periodicity is originally caused by global cooling at the onset of the Pleistocene. Cooling causes a large delay in larval growth and additional mortality before emergence, resulting in a massive decrease in the adult density (Cox and Carlton, 1988; Cox, 1992; Yoshimura, 1997). The synchronization of cycles or periodicity is strongly selected at this stage owing to the adult densities approaching extinction. The~~

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1032 ~~determinant of maturation switches from temperature to time (periodicity).~~
1033
1034 ~~The selection of prime number intervals follows the evolution of periodicity and long~~
1035 ~~intervals (Cox and Carlton, 1988; Yoshimura, 1997). Initially, a variety of incipient periodical~~
1036 ~~cicada brood life-cycle lengths exist. Within a brood, females produce offspring on~~
1037 ~~different lengths. By chance, some broods emerge concurrently; these hybridize~~
1038 ~~randomly. The genetics of hybrids are unknown, but from the current periodical~~
1039 ~~cicadas, it is likely to be Mendelian inheritance with shorter or longer cycle dominance.~~
1040 ~~These hybrids are eliminated because of their small population sizes and lack of~~
1041 ~~coordinated intervals. Such co-emergence is highly disadvantageous and leads to the~~
1042 ~~extinction of broods. Here, the frequency of co-emergence depends on intervals. Note~~
1043 ~~that the lowest common multiplier (L. C. M.) of a prime number is usually large in~~
1044 ~~contrast with those of non-prime numbers. Prime number intervals less frequently~~
1045 ~~co-emerge with other intervals than non-prime number intervals. Non-prime number~~
1046 ~~intervals suffer serious hybridization loss. Once the density of non-prime number~~
1047 ~~broods decreases, selection against hybridization increases exponentially because of~~
1048 ~~frequency-dependent mating between different broods (Yoshimura and Clark, 1994;~~
1049 ~~Yoshimura, 1997). Through frequent hybridization and elimination of non-prime number~~

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1050 ~~intervals, only prime number intervals sustain population densities and all other~~
1051 ~~intervals are wiped out completely.~~
1052
1053 ~~The hybridization hypothesis shows the advantage of prime number intervals in~~
1054 ~~hybridization. However, the hypothesis does not confirm the evolution of prime number~~
1055 ~~intervals, eliminating all other intervals, because this advantage of prime number~~
1056 ~~intervals depends on both population size (density) and frequency of all intervals. The~~
1057 ~~loss of fitness by hybridization varies depending on both population sizes and~~
1058 ~~frequencies. When two cycles co-emerge, the cycle with the larger population size has a~~
1059 ~~small loss of offspring by hybridization, while that with the smaller population size has~~
1060 ~~a large loss, because of frequency dependent hybridization. Thus the evolution of prime~~
1061 ~~number intervals depends on the trade-off between disadvantage of hybridization,~~
1062 ~~population sizes, frequency of intervals and growth conditions which affect the latter~~
1063 ~~two. In this paper, we test the hybridization hypothesis using a deterministic simulation~~
1064 ~~model. We show that prime number intervals persist while all other cycles go extinct~~
1065 ~~under certain conditions, i.e., marginal (near extinction) environmental conditions, as~~
1066 ~~suggested by Yoshimura (Yoshimura, 1997).~~

コメント [CS2]: One problem with this hypothesis that I have noted in the past is that current evidence suggests that periodical cicadas cannot live sympatrically unless separated by at least four years in life cycle due to nymphal competition—but we don't need to mention this here. Perhaps nymphal competition was lower in the past and populations densities not as high as in your model when populations are on the edge of extinction.

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1068 **MODELS**

1069 ~~In our model, we assume identical population sizes of insects with various established~~
1070 ~~cycles (10-20 year cycles). We assume that survival (mortality) rate $S(1-S)$ per year is~~
1071 ~~constant. The larval population size decreases with a constant survival rate S /year~~
1072 ~~(Karban, 1982). This means that the cicadas with longer intervals suffer higher~~
1073 ~~mortalities. The clutch size C of a copulated adult female with interval y is assumed to~~
1074 ~~be an increasing function of interval (growth period) y , such that $C(y) = Ry$, where R is a~~
1075 ~~constant. It is because reproductive output (clutch size) in insects often correlates with~~
1076 ~~effective cumulative temperature (Chapman, 1971). This means that longer intervals~~
1077 ~~(growth period) have larger clutch sizes, but suffer higher mortality per emergence.~~
1078 ~~Note that there is a trade-off between intervals with respect to overall juvenile survival~~
1079 ~~rate and clutch size C per cycle. In contrast, successful emergence rate $E(0 < E < 1)$ is~~
1080 ~~kept constant, assuming emergence failure is independent from intervals. Emergence~~
1081 ~~failure in cicadas is frequently seen in nature.~~

1082

1083

1084

1085

1086 The allele-controlling life cycle follows a single-locus Mendelian inheritance system with
 1087 shorter cycle dominance, such that genotype $[i, j]$ corresponds to phenotype i (years) if $i \leq$
 1088 j . For example, when 12- and 15-year life cycle genotypes co-emerge, all the hybrid
 1089 offspring $[12, 15]$ appear after 12 years (Cox and Carlton, 1991; Lloyd et al., 1983). The
 1090 number of hybrid individuals is assumed to be proportional to the relative population
 1091 sizes of co-emergent broods (Ebert, 1992).

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1092
 1093 We build a discrete population model consisting of three major parameters: survival
 1094 rate S , emergence rate E and clutch size factor R . We keep track the population sizes of
 1095 all the broods with respect to interval genotypes including hybrids and birth year with
 1096 larval and adult stages. For genotype $[i, j]$ of a given birth year, the larval population
 1097 size of a brood at time t ($N_{l,t}$) follows the equation:

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$$N_{l,t}(i, j) = S \times N_{l,t-1}(i, j) \tag{1}$$

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1101 where S ($0 < S < 1$) is survival rate at t (year). S is constant, because all broods occupy the
 1102 same habitat. Adult brood size N_A (only appear in emergence year) is

1103

1104 $N_{A,l}(i,j) = E \times N_{l,r}(i,j)$ (2)

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1106 where $E(0 < E < 1)$ is a constant emergence rate. The offspring (larval) brood size between
 1107 $[i,j]$ and $[m,n]$ is then assumed to be a function of interval (y) , such that:

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1109 Num. offspring := $\frac{1}{2} N_{A,l}(i,j) \times F(N_{A,l}(m,n)) \times C(y)$ (3)

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1111 where F is the frequency of the target brood, such that

1112 $F(N_A(m,n)) = \frac{N_A(m,n)}{\sum N_A}$

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1113 where $\sum N_A$ is the sum of all co-emergent adults for a given year, and C is the clutch
 1114 size and a function of the cycle:

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1116 $C(y) = R \times y$ (4)

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1118 where $R(R > 0)$ is a yearly increase rate of clutch volume.

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1120 The genotype of offspring between $[i,j]$ and $[m,n]$ has 4 pattern: $[i,m]$, $[i,n]$, $[j,m]$ and $[j,n]$.

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1121 So, the offspring brood size at each genotype is determined for the sum of eq.(3). For

1122 example, the offspring brood size of genotype $[i, m]$ follows:

$$1124 \quad N_{i,t}(i, m) = \sum_x \sum_z \left\{ \frac{1}{2} N_{A,t}(i, x) \times F(N_{A,t}(m, z)) \times C(y) \right\} \quad (5)$$

1126 As for the other genotypes, it is similar.

1127 To avoid introducing an advantage to any specific cycle, we keep the initial conditions of
1128 all intervals identical. In the initial settings, we start 11 pure broods with a 10-20 yr
1129 intervals. All the initial brood sizes /cycle are 1000 first-instar larva (the first year). We
1130 will test whether prime number intervals (11,13,17 and 19) are selected for within 10-20
1131 yr intervals and in what conditions.

1133 In order to introduce the selection on small population sizes (Yoshimura 1997), we
1134 measure the abundance of cicada ($N_{i,t}$ and $N_{t,i}$) by the number of individuals (integers).
1135 It leads disadvantages for smaller broods. For example, suppose that survival rate,
1136 $S=0.955$. The brood size of $N_{i,t}=1000$ becomes $N_{t+1,i}=1000 * 0.955 = 955$, whereas that of
1137 $N_{i,t}=100$ becomes $N_{t+1,i}=100 * 0.955 = 95$. This disadvantage of smaller brood sizes
1138 becomes larger when brood sizes decrease. In a small brood, the actual survival rate, S
1139 becomes veris relatively low. In extremity, when equation (3) is less than 4, the number

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1140 of offspring (eq. (5)) is evaluated to zero, because the number of offspring for each
1141 genotype (4 patterns) becomes less than 1 individual. Thus, smaller broods have a
1142 disadvantage when the population size is counted as an integer.

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1143
1144 The hybridization yields a small brood size of mostly hybrids (Yoshimura, 1997). The
1145 hybridization between genotype $[i, j]$ and $[i, j]$ ($i < j$) makes three genotypes (broods): $[i, j]$,
1146 $[i, j]$ and $[i, j]$. In our model, brood $[i, j]$ and brood $[i, j]$ co-emerge at i year. The brood $[i, j]$
1147 reduces its population size considerably, and results in a huge disadvantage. On the
1148 other hand, brood $[i, j]$ and brood $[i, j]$ hybridize and make three genotypes (broods): $[i, j]$,
1149 $[i, j]$ and $[i, j]$. Brood $[i, j]$ and brood $[i, j]$ then also reduce their population sizes.

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1151 RESULTS AND DISCUSSION

1152 We simulate the population dynamics of cicadas from eleven pure broods at 10-20-yr
1153 intervals. Figure 1 shows a case where only prime number cycles survive. All non-prime
1154 number cycles are eliminated within 200 years (Fig. 1A). In contrast to the elimination
1155 process of non-prime number intervals, the subsequent selection among prime numbers
1156 lasts many hundreds of years (Fig. 1B). Furthermore, in some conditions, coexistence is
1157 possible at least within a couple thousand years (Fig. 1C).

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~~Next we evaluate the parameter sensitivity for all three parameters: (1) larval (nymphal) survival rate S , (2) clutch size parameter R , and (3) emergence success E (Fig. 2). Only the prime number cycles survive, but at the edge of survival limits. We find no region in which only non-prime cycles eliminate all other cycles. This suggests that the advantage of prime number cycles prevails specifically at the verge of extinction. In the S - R and S - E phase planes, prime number cycles are aligned along the edge of survival limits; shorter cycles with low S and high R or E and longer cycles show the reverse pattern (Figs. 2A and B). The coexistence regions of two prime numbers are usually located slightly inside of the single prime number regions, forming a shell structure in the R - E phase plane (Fig. 2C). Thus, under a specific combination of the three parameters, S , R and E , we find the dynamics results in the survival of only 13- and/or 17-year cycles (Fig. 2). Furthermore, the density reduction along the environmental (parameter) cline shows that the advantage of prime number appears sporadically (often discontinuously) at the verge of extinction (Fig. 3).~~

~~Disadvantage of small broods is a prerequisite of Yoshimura's hypothesis (Yoshimura, 1997). In reality, a population size is finite and integer. The stability of a small~~

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1176 ~~population is inferior to that of a large population in the same environment. Using the~~
1177 ~~number of individuals (integer) as the abundance of population (brood), we include the~~
1178 ~~innate disadvantage of small populations without additional assumptions. We should~~
1179 ~~note that the Allee effect is expected to be much stronger in the small populations of~~
1180 ~~periodical cicadas during ice ages. The variability in predation pressures and/or mate~~
1181 ~~encounters should lead to an additional huge disadvantage on a small population,~~
1182 ~~resulting in the quick elimination of small broods (see e.g., Tainaka, Hayashi and~~
1183 ~~Yoshimura, 2006). It is important that we did not introduce any additional Allee effect,~~
1184 ~~but the subtle effects of integer are sufficient for the selection of prime numbers.~~
1185 ~~Introduction of additional Allee effects may strengthen the selection of prime numbers,~~
1186 ~~as well as increase the area of convergence (Fig. 2).~~
1187
1188 ~~Our results demonstrate that the hybridization breakdown associated with~~
1189 ~~co-emergence can indeed lead to the selection of prime number cycles. A brood under~~
1190 ~~frequent hybridization tends to suffer reduced population size and this process is~~
1191 ~~accelerated as the population size decreases owing to the frequency dependence of~~
1192 ~~random mating (Fig. 1) (Kuno, 1992; Yoshimura and Clark, 1994). The density profiles also~~
1193 ~~indicate the superiority of prime numbers near the extinction borders (Fig. 3). Almost~~

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1194 ~~all non-prime number cycles disappear when the survival rate is slightly lowered.~~
1195 ~~Interestingly, the lower prime number cycles tend to have a separate density peak at~~
1196 ~~the edge of extinction (Fig. 3B), whereas density profiles are smoothly decreasing in~~
1197 ~~higher prime numbers (Fig. 3A).—~~
1198
1199 ~~Our results also indicate that prime number selection is a very rare event, occurring at~~
1200 ~~the verge of extinction (Figs. 2 and 3). This is probably why the evolution of prime~~
1201 ~~number periodicity was likely only in what is now the central and eastern United States,~~
1202 ~~where glacial advances created many refugia during the Pleistocene glaciation (Deleourt~~
1203 ~~and Deleourt, 1987; Gates, 1993).—~~
1204
1205 ~~Our model is a deterministic simulation model without random numbers. The simulated~~
1206 ~~results are numerical calculations derived from set initial conditions; thus the selection~~
1207 ~~of prime number cycles is numerically shown. We also run simulations with variable~~
1208 ~~initial conditions. The results are almost same with those of identical initial conditions.~~
1209 ~~Which prime number cycles are established depends simply on the combination of three~~
1210 ~~key parameters: larval survival S , clutch size parameter R and emergence rate E .~~
1211 ~~Figure 2 shows that there is a relatively broad range of environmental conditions in~~

1212 ~~which both 13- and 17-year cycles are only fixed. In contrast, the range of 11-year~~
1213 ~~interval is very narrow. The temporal isolation benefit of prime number reduces with~~
1214 ~~shorter intervals. The advantage of shorter reproductive cycles seems to dominate in~~
1215 ~~shorter intervals. Our results also show that 19-year intervals are plausible. We~~
1216 ~~speculate that larva could not survive nineteen years in the soil or host trees cannot~~
1217 ~~survive under such conditions.~~

1218 There is one very important aspect of the biology of periodical cicadas that must be
1219 reconciled with the theory of the origination of prime-numbered life cycles presented in
1220 this paper and elsewhere (Yoshimura 1997; Cox and Carleton 1988, 1991) and that is
1221 the four-year acceleration hypothesis. — There is strong evidence that four-year shifts in
1222 life cycle are common in the evolution of periodical cicadas: — 1) the largest year classes
1223 (broods) of periodical cicadas are separated in time by four years, these are the only
1224 broods that overlap geographically (Lloyd and Dybas 1966, Lloyd and While 1976); 2) in
1225 the large, overlapping 17-year cicada broods, lagging broods seem to be increasing
1226 historically while leading broods, four years later, seem to be diminishing in numbers of
1227 populations (Kritsky 1988); 3) forests seem to be able to support more cicadas if they are
1228 separated into two year classes spaced four years apart (Simon et al. 1981); 4) 17-year
1229 cicadas differ from 13-year cicadas in their nymphal growth patterns in possessing a

コメント [CS3]: I would remove the sentence below because Okanagana synodica might have 19 year cycles in Canada.

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1230 ~~4-year dormaney period in the second instar; if this dormaney period is lost, 17-year~~
1231 ~~cicadas would be transformed into 13-year cicadas (White and Lloyd 1975); 5) Long~~
1232 ~~Island, NY is a microcosm of periodical cicada evolution possessing independently~~
1233 ~~derived populations of cicadas that appear in the same years as broods I, V, IX, and X in~~
1234 ~~addition the native brood XIV (Simon and Lloyd 1982); 5) In the Midwestern US, the~~
1235 ~~northern third of the distribution of 13-year cicadas is recently derived from 17-year~~
1236 ~~cicadas that permanently switched their life cycle to 13 years and joined two different~~
1237 ~~year classes of —pre-existing 13-year cicadas (Martin and Simon 1988, Martin and~~
1238 ~~Simon 1990, Simon et al. 2000, Marshall and Cooley 2000). —Lloyd and Dybas (1966)~~
1239 ~~suggested that 13-year cicadas evolved first and gave rise to 17-year cicadas when they~~
1240 ~~acquired their 4-year dormaney period~~

1241 ~~Our model is relatively simple and the actual evolution of periodical cicadas may have~~
1242 ~~been more complicated. — Selection pressures related to inferior hybrids between~~
1243 ~~different life cycles could have resulted in the formation of 13-year cicadas as described~~
1244 ~~by this model while the 17-year life cycle could have evolved via four-year accelerations~~
1245 ~~from the 13-year cycle later in the Pleistocene when glaciation intensified (Zachos et al.,~~
1246 ~~2001).~~

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コメント [CS4]: Zachos, J., M. Pagani,
L. Sloan, E. Thomas, and K. Billups.
2001. Trends, rhythms, and aberrations
in global climate 65 Ma to present.
Science 292:686-693.

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~~Furthermore, earlier in the Pleistocene, prime number fixation might not be achieved by a single glacial period, but may have extended over a few glacial periods with hybridization taking place during interglacial periods. We should also note that the short year dominance genetic system is not essential for the selection of prime number intervals. The prime number intervals also appear under longer year dominance or a genetic system in which the hybrids are immediately removed (unpublished data). Our results indicate that the disadvantage in hybridization resulting in prime number intervals appears under severe environmental conditions (at the verge of extinction), while coexistence of many intervals with shorter interval dominance appears under good environmental conditions.~~

~~Our model only deals with the origins of periodical cicadas under glacial environmental conditions (Cox and Carlton, 1988; Yoshimura, 1997). The current maintenance of the extremely high densities of cicada populations is a different problem (May, 1979). A newly recognized 13-year brood and 17-year type genotypes in 13-year cicadas are suspected to~~

1266 ~~have arisen from a relatively recent hybridization event after the onset of the most~~
1267 ~~recent interglacial period. (Martin and Simon, 1988; Marshall and Cooley, 2000; Cooley *et al.*,~~
1268 ~~2001; Cooley *et al.*, 2003). Here the complete dominance of 13-year broods is suspected in~~
1269 ~~this hybridization process. Our results demonstrate that the Mendelian genetic system~~
1270 ~~is indeed enough to extinct all non-prime number intervals. Thus we have shown~~
1271 ~~mathematically that co-emergence hybridization is indeed a plausible mechanism for~~
1272 ~~the evolution of prime number intervals. (to Chris: please rewrite the paragraph and~~
1273 ~~add the whole acceleration hypothesis. jin)~~

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1274
1275 ~~The hybridization hypothesis of periodical cicadas is a temporal version of rendezvous~~
1276 ~~habitat selection (Rosenzweig, 1979). Rendezvous habitat selection is niche separation due~~
1277 ~~to the mating at specific host plants. In the case of periodical cicadas, niche separation~~
1278 ~~is achieved by emergent years, thus temporal separation, instead of spatial separation.~~
1279 ~~In both cases, the evolution of this kind of phenomenon is achieved by severe frequency~~
1280 ~~dependence in mating (Rosenzweig, 1979; Kuno, 1992; Yoshimura and Clark, 1994).—~~

コメント [CS5]: We do not believe that the origin of the new 13-year cicadas was a result of hybridization. That is what Cox and Carlton believe and we think that they are wrong as explained in Marshall et al. 2003. However, that is less relevant to this paper.

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1282 **Acknowledgements**

1283 ~~We thank Donald G. Miller, III, Michael L. Rosenzweig and anonymous referee for~~

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1284 ~~valuable comments. This work was supported by grants-in-aids from the Ministry of~~
1285 ~~Education, Culture, Sports, Science and Technology of Japan.~~

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1356 **Figure legends**

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1358 **Fig. 1. Population dynamics of 11 pure broods, 10-20yr intervals. Parameters are**
1359 **$S=0.948$, $R=1.45$ and $E=0.2$. (A) The first 200 years in the case of only 17-year brood-**
1360 **survival. (B) The continuation of (A) up to 700 years. (C) 600 years in the case of both**
1361 **13- and 17-year co-survival. Parameters are $S=0.943$, $R=1.63$ and $E=0.2$. Thick lines are**
1362 **the populations of prime number broods. Thin lines are those of non-prime numbers.**
1363 **Serrated lines show a decrease in larval to adult stages and an increase by the egg-**
1364 **laying. Irregular serrations are produced by a time lag caused by hybrid mating. All**
1365 **non-prime number broods go to extinct during the first few hundred years.**

1366

1367 **Fig. 2. Thousand-year survival phase planes of prime numbers only (colored), both**
1368 **prime and non-prime numbers (grey) and all extinction (white) for the three main**
1369 **parameters. (A) Plane for larval survival rate S and clutch size parameter R . The other**
1370 **parameter is $E=0.2$. (B) Plane for larval survival rate S and emergence success E . The**
1371 **other parameter is $R=1.8$. (C) Plane for clutch size parameter R and emergence success**
1372 **E . The survival of only prime number broods appears at the edges of extinction. The**
1373 **other parameter is $S=0.94$. The non-prime numbers (grey) means most phenotypes**

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1374 ~~including hybrids and prime number intervals.~~

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1376 ~~Fig.3: Density profiles (log scale) for larval survival rate S , when emergence success is~~

1377 ~~$E=0.2$ and clutch size parameter is (A) $R=1.6$ and (B) $R=1.8$. The density profiles of~~

1378 ~~larger prime number intervals tends to decreasing smoothly near the border of~~

1379 ~~extinction (B), whereas those of smaller primer number intervals tend to have a~~

1380 ~~separate peak near the border of extinction (B). The population sizes are measured at~~

1381 ~~1000 years unless exploded (calculations are terminated, when $S>0.96$).~~

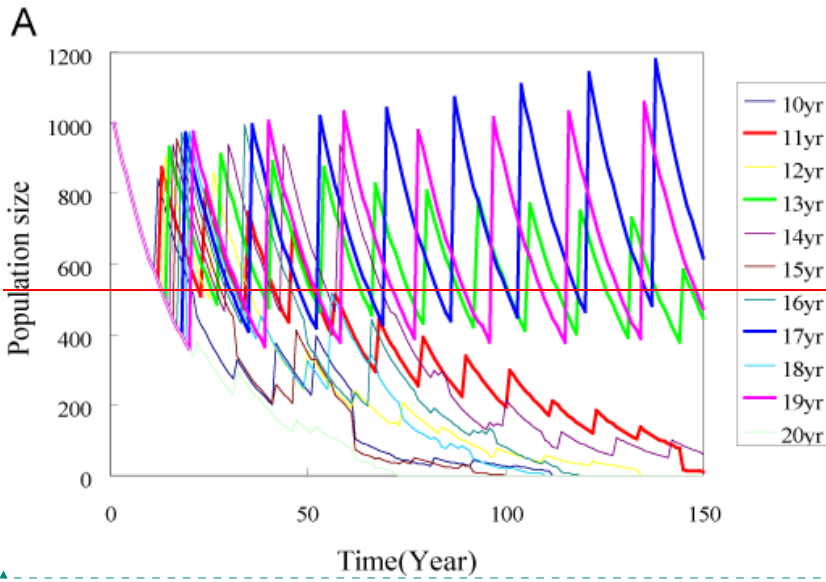
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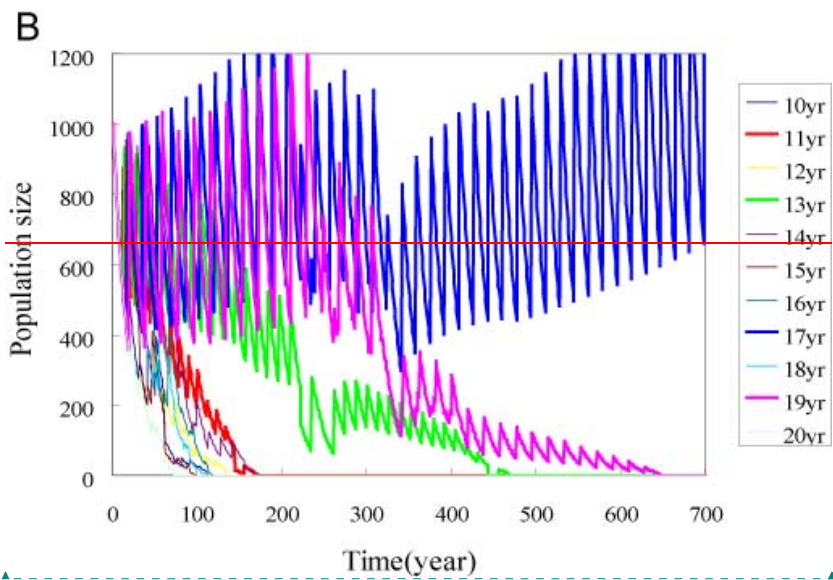
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1387 *Fig. 1A.*

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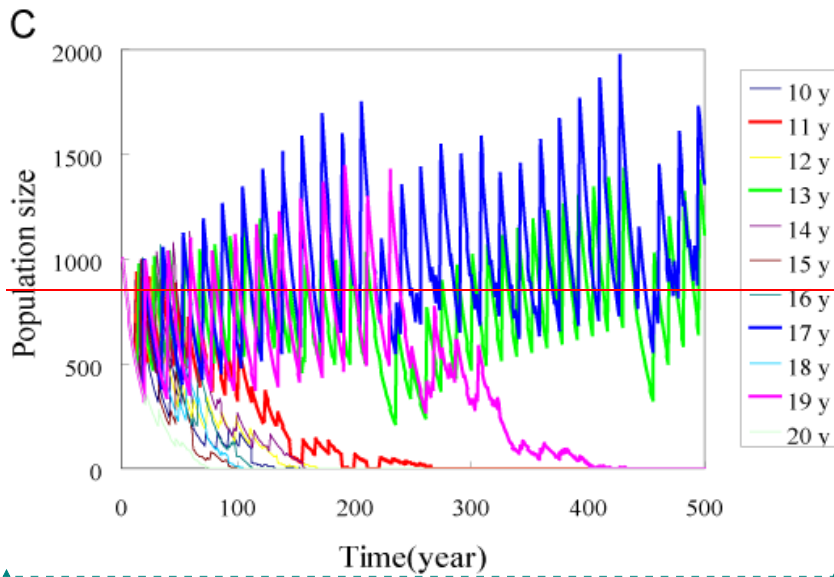
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1390 [Fig. 1B.](#)

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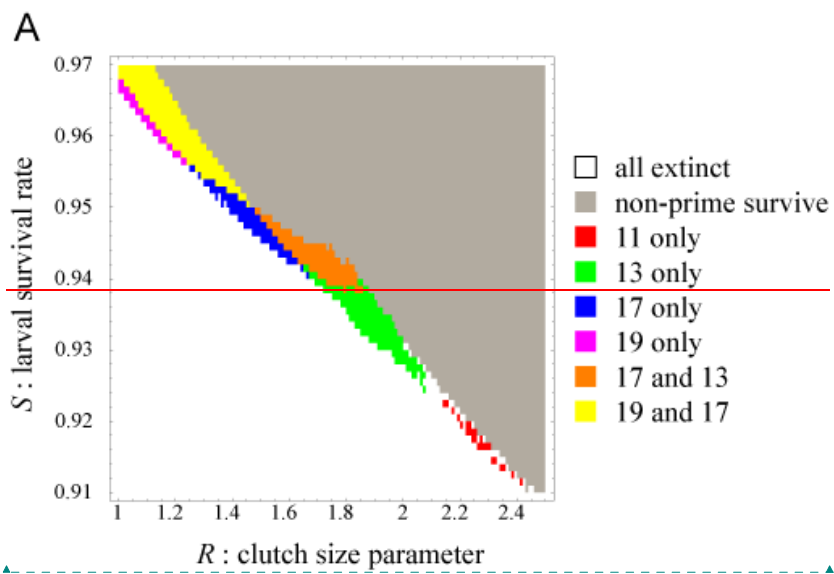
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1393 **Fig. 1C.**

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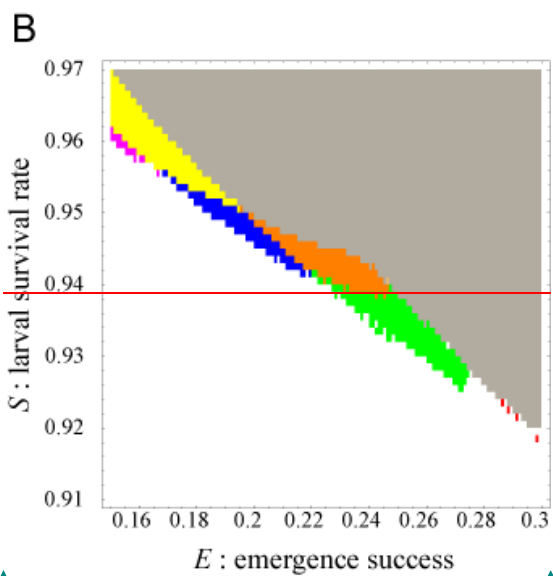
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1396 **Fig. 2A.**

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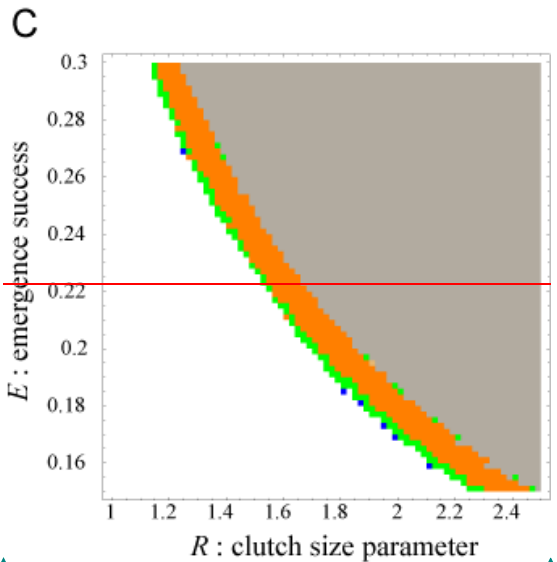
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1400 ~~Fig. 2B.~~

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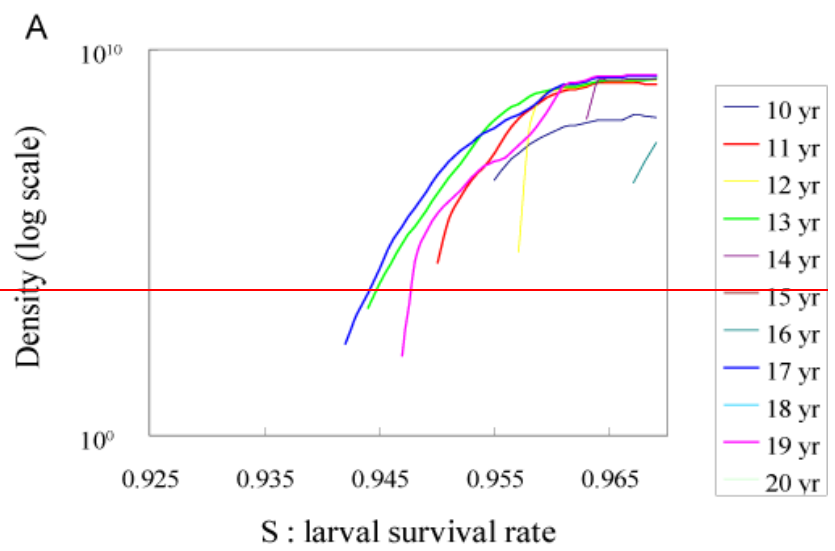
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Fig. 2C.

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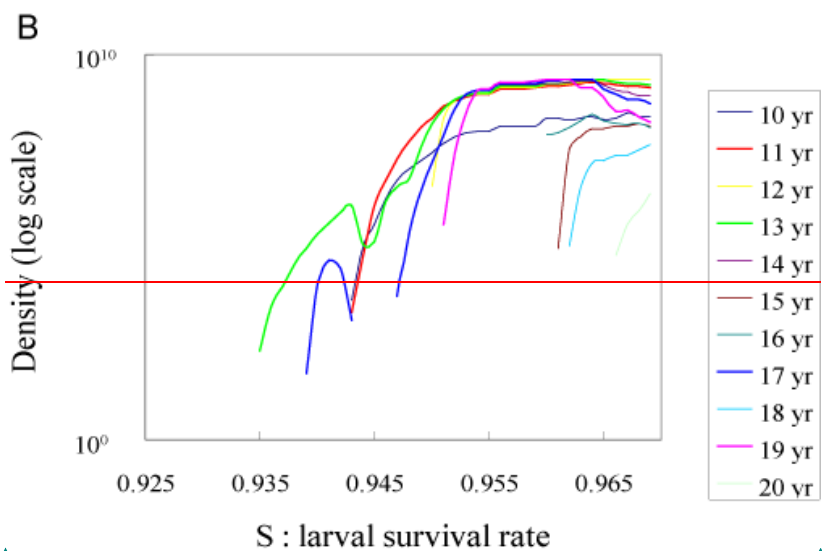
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Fig. 3A.

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1409 ~~Fig. 3B.~~

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フォント : Century, フォントの色 : 赤

ページ 69: [4] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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フォント : Century, フォントの色 : 赤

ページ 69: [4] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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フォント : Century, フォントの色 : 赤

ページ 69: [4] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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フォント : Century, フォントの色 : 赤

ページ 69: [4] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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フォント : Century, フォントの色 : 赤

ページ 69: [4] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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フォント : Century, フォントの色 : 赤

ページ 69: [4] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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フォント : Century, フォントの色 : 赤

ページ 69: [4] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [4] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [4] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [4] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [4] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [4] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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フォント : Century, フォントの色 : 赤

ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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フォント : Century, フォントの色 : 赤

ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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フォント : Century, フォントの色 : 赤

ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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ページ 69: [5] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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フォント : Century, フォントの色 : 赤

ページ 80: [6] 書式変更	Taro HAYASHI	2008/01/21 16:40:00
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フォント : (英) Century, (日) MS 明朝