- Analytical results for directional and quadratic selection
- gradients for log-linear models of fitness functions
- 3 Michael B. Morrissey¹ and I. B. J. Goudie²
- 4 February 22, 2016
- ⁵ School of Biology, University of St Andrews
 - contact

email: michael.morrissey@st-andrews.ac.uk

phone: +44 (0) 1334 463738 fax: +44 (0) 1334 463366 post: Dyers Brae House

School of Biology, University of St Andrews

St Andrews, Fife, UK, KY16 9TH

7 ²School of Mathematics and Statistics, University of St Andrews

contact

email: ig@st-andrews.ac.uk phone: +44 (0) 1334 463705 fax: +44 (0) 1334 463748

post: School of Mathematics and Statistics, University of St Andrews

St Andrews, Fife, UK, KY16 9SS

- 9 Keywords: natural selection, selection gradients, fitness, generalised linear model, capture-
- 10 mark-recapture, survival analysis

Morrissey and Goudie, log-scale fitness models and selection gradients

Abstract

- 1. Established methods for inference about selection gradients involve least-squares regression
- of fitness on phenotype. While these methods are simple and may generally be quite robust,
- they do not account well for distributions of fitness.
- 2. Some progress has previously been made in relating inferences about trait-fitness rela-
- tionships from generalised linear models to selection gradients in the formal quantitative
- 17 genetic sense. These approaches involve numerical calculation of average derivatives of
- relative fitness with respect to phenotype.
- 19 3. We present analytical results expressing selection gradients as functions of the coefficients
- 20 of generalised linear models for fitness in terms of traits. The analytical results allow
- 21 calculation of univariate and multivariate directional, quadratic, and correlational selection
- 22 gradients from log-linear and log-quadratic models.
- 4. The results should be quite generally applicable in selection analysis. They apply to any
- 24 generalised linear model with a log link function. Furthermore, we show how they apply to
- some situations including inference of selection from (molecular) paternity data, capture-
- 26 mark-recapture analysis, and survival analysis. Finally, the results may bridge some gaps
- between typical approaches in empirical and theoretical studies of natural selection.

28 1 Introduction

29 The characterisation of natural selection, especially in the wild, has long been a major research

30 theme in evolutionary ecology and evolutionary quantitative genetics (Endler, 1986; Kingsolver

31 et al., 2001; Lande & Arnold, 1983; Manly, 1985; Weldon, 1901). In recent decades, regression-

32 based approaches have been used to obtain direct selection gradients (especially following Lande

33 & Arnold 1983), which represent the direct effects of traits on fitness. These, and related,

34 measures of selection have an explicit justification in quantitative genetic theory (Lande, 1979;

35 Lande & Arnold, 1983), which provides the basis for comparison among traits, taxa, etc.,

36 and ultimately allows meta-analysis (e.g., Kingsolver et al. 2001). Selection gradients can

37 characterise both directional selection and aspects of non-linear selection, and so are a very

38 powerful concept in evolutionary quantitative genetics.

Formally, the selection gradient is the vector of partial derivatives of relative fitness with

40 respect to phenotype, averaged over the distribution of phenotype observed in a population.

41 Given an arbitrary function $W(\mathbf{z})$ for expected fitness of a (multivariate) phenotype \mathbf{z} , a general

42 expression for the directional selection gradient $\boldsymbol{\beta}$ is

$$\boldsymbol{\beta} = \bar{W}^{-1} \int \frac{\partial W(\mathbf{z})}{\partial z} p(\mathbf{z}) d\mathbf{z}$$
 (1)

3

43 where $p(\mathbf{z})$ is the probability density function of phenotype, and \bar{W} is mean fitness. Mean fitness

44 can itself be obtained by $\int W(\mathbf{z})p(\mathbf{z})d\mathbf{z}$. A quadratic selection gradient can also be defined as the

45 average curvature (similarly standardised), rather than the average slope, of the relative fitness

46 function,

$$\gamma = \bar{W}^{-1} \int \frac{\partial^2 W(\mathbf{z})}{\partial z^2} p(\mathbf{z}) d\mathbf{z}. \tag{2}$$

47 The directional selection gradient has a direct relationship to evolutionary change, assuming

48 that breeding values (the additive genetic component of individual phenotype, Falconer 1960)

49 are multivariate normally-distributed, following the Lande (1979) equation

$$\Delta \bar{\mathbf{z}} = \mathbf{G}\boldsymbol{\beta} \tag{3}$$

Morrissey and Goudie, log-scale fitness models and selection gradients

where $\Delta \bar{\mathbf{z}}$ is per-generation evolutionary change, and \mathbf{G} is the additive genetic covariance matrix, 50 i.e., the (co)variances among individuals of breeding values. The quadratic selection gradient 51 matrix has direct relationships to the change in the distribution of breeding values due to 52 selection, but not with such simple relationships between generations as for the directional 53 selection gradient and the change in the mean (Lande & Arnold, 1983). 54 55 The primary method for obtaining selection gradient estimates has been a simple and robust approach justified in Lande & Arnold (1983). The method involves least-squares multiple 56 regression of relative fitness, i.e., absolute fitness divided by the mean observed in any comparable 57 58 group of individuals over a specific period of the life cycle, potentially the entire life cycle, on measures of phenotype. Fitness, or any component of fitness, will typically have highly non-59 normal residuals in such a regression. Nonetheless, the simple least-squares methods are unbiased 60 61 (see Gever & Shaw 2010). However, methods that account for distributions of residuals that arise in regressions involving fitness as a response variable may provide better precision and 62 63 more reliable statements about uncertainty (i.e., standard errors, p-values, etc.). Some progress has been made at developing generalised regression model methods for 64 inference of selection gradients. Janzen & Stern (1998) proposed a method for binomial responses 65 (e.g., per-interval survival, mated vs. not mated). The Janzen & Stern (1998) method provides 66 estimates of β , and requires fitting a logistic model with linear terms only, calculating the 67 average derivatives at each phenotypic value observed in a sample, and then standardising 68 to the relative fitness scale. Morrissey & Sakrejda (2013) expanded Janzen & Stern's (1998) 69 basic approach to arbitrary fitness functions (i.e., not necessarily linear) and arbitrary response 70 71 variable distributions, retaining the basic idea of numerically averaging the slope (and curvature) 72 of the fitness function over the distribution of observed phenotype. Shaw & Geyer (2010) developed a framework for characterising the distributions of fitness (and fitness residuals) that 73 74arise in complex life cycles, and also showed how the method could be applied to estimate selection gradients by averaging the slope or curvature of the fitness function over the observed 75 values of phenotype in a sample. 76 77 Of the many forms regression analyses of trait-fitness relationships might take, log-linear 78 or log-quadratic models of the relationship between traits and expected absolute fitness may

be particularly useful. In generalised linear models, the log link function is often useful and 79 pragmatic. Fitness is a necessarily non-negative quantity, and expected fitness will typically best 80 be modelled as a strictly positive quantity. This will indeed be the case if expected fitness is an 81 exponential function of the sum of the predictors of the regression model, or, equivalently, a log 82 link is used. Also, a log link function is compatible with generalised linear models with various 83 distributions that could be useful for modelling fitness or fitness components. For example, 84 it can be used with the Poisson distribution (counts, e.g., number of mates or offspring), 85 86 the negative binomial distribution (for counts that are overdispersed relative to the Poisson distribution, potentially including lifetime production of offspring), and the exponential and 87 geometric distributions (e.g., for continuous and discrete measures of longevity). The purpose 88 of this short paper is to investigate the relationships between log-linear and log-quadratic models 89 90 of fitness functions, and selection gradients.

⁹¹ 2 Log-linear and log-quadratic fitness functions, and se-

92 lection gradients

- 93 Selection gradients turn out to have very simple relationships to the coefficients of log-
- 94 linear regression models predicting expected fitness from (potentially multivariate) phenotype.
- 95 Suppose that there are k traits in the analysis and that the absolute fitness function, $W(\mathbf{z})$ takes
- 96 the form

$$W(\mathbf{z}) = e^{a+b_1 z_1 + b_2 z_2 + \dots + b_k z_k} \tag{4}$$

5

where a is a log-scale intercept, and the b_i are log-scale regression coefficients relating the traits

98 (z_i) to expected fitness. The equation for the directional selection gradient (equation 1) can then

be simplified. Focusing on the selection gradient for a specific trait, i, in a log-linear model of

100 $W(\mathbf{z})$,

$$\frac{\partial W}{\partial z_i} = b_i W(\mathbf{z})$$

101 and hence

$$\beta_{i} = \frac{\int b_{i}W(\mathbf{z})p(\mathbf{z})d\mathbf{z}}{\int W(\mathbf{z})p(\mathbf{z})d\mathbf{z}}$$

$$= \frac{b_{i}\int W(\mathbf{z})p(\mathbf{z})d\mathbf{z}}{\int W(\mathbf{z})p(\mathbf{z})d\mathbf{z}}$$

$$= b_{i}.$$
(5)

6

102 This result could be quite useful. In any log-linear model regressing expected absolute fitness,

103 or a component of fitness, on trait values, the linear predictor-scale regression coefficients are

104 the directional selection gradients.

The situation is a little bit more complicated if a log-quadratic model is fitted. If $W(\mathbf{z})$ takes

106 the form

114

$$W(\mathbf{z}) = e^{a + \sum_{i} b_{i} z_{i} + \sum_{i} g_{i}(\frac{1}{2} z_{i}^{2}) + \sum_{i=1}^{k-1} \sum_{j=i+1}^{k} g_{ij}(z_{i} z_{j})},$$
(6)

107 i.e., of a log-scale regression model with linear and quadratic terms, plus first-order interactions,

then the b_i coefficients are not necessarily the directional selection gradients, nor are the g_i and

 g_{ij} coefficients the quadratic and correlational selection gradients, as they would be in a least

110 squares analysis following Lande & Arnold (1983). However, we can use the log-scale quadratic

111 fitness function with the general definitions of selection gradients (equations 1 and 2) to obtain

112 analytical solutions for β and γ .

The factor of $\frac{1}{2}$ associated with the quadratic terms in equation 6 is a potential source of

confusion, analogous to that surrounding a similar factor in Lande & Arnold's (1983) paper (see

115 Stinchcombe et al. 2008). In order to obtain the correct values of the g_i coefficients, the covariate

116 values for quadratic terms should be (1) mean-centred, then (2) squared, and then (3) halved.

117 An alternative analysis is possible, where the squared covariate values are not halved, but the

118 estimated coefficient estimates are doubled (analogous to procedures discussed by Stinchcombe

119 et al. 2008). However, this alternative analysis leads to an additional, and potentially confusing,

120 step in the calculation of standard errors (detailed in the appendix).

Define a vector $\mathbf{b} = (b_1, \dots, b_k)'$ containing the coefficients of the linear terms in the exponent

of the model in equation 6, and a matrix $\mathbf{g} = (g_{ij})$ containing the coefficients of the corresponding quadratic form. We can then write the fitness function more conveniently in matrix form

$$W(\mathbf{z}) = e^{f(\mathbf{z})} \tag{7a}$$

7

124

$$f(\mathbf{z}) = a + \mathbf{b}'\mathbf{z} + \frac{1}{2}\mathbf{z}'\mathbf{g}\mathbf{z}.$$
 (7b)

125 Let **d** be a vector of the expectations of the first order partial derivatives of W(z) and let **H** be

the matrix of expectations of the second order partial derivatives of $W(\mathbf{z})$. Thus the elements of \mathbf{d}

127 are $d_i = E\left[\frac{\partial W(\mathbf{z})}{\partial z_i}\right]$ and the elements of **H** are $H_{ij} = E\left[\frac{\partial^2 W(\mathbf{z})}{\partial z_i \partial z_j}\right]$. We can now rewrite the expressions

128 for directional and quadratic selection gradients as

$$\beta = \frac{\mathbf{d}}{E[W(\mathbf{z})]} \tag{8}$$

129 and

$$\gamma = \frac{\mathbf{H}}{E[W(\mathbf{z})]}.\tag{9}$$

Differentiating equation 7 gives

$$\frac{\partial W(\mathbf{z})}{\partial \mathbf{z}'} = (\mathbf{b} + \mathbf{g}\mathbf{z}) e^{f(\mathbf{z})},\tag{10}$$

131 and

$$\frac{\partial^2 W(\mathbf{z})}{\partial \mathbf{z} \partial \mathbf{z}'} = (\mathbf{g} + (\mathbf{b} + \mathbf{g}\mathbf{z})(\mathbf{b} + \mathbf{g}\mathbf{z})') e^{f(\mathbf{z})}.$$
 (11)

Assume that the phenotype **z** is multivariate normal, with mean μ and covariance matrix Σ ,

and denote its probability density by $p_{\mu\Sigma}(\mathbf{z})$. Provided $e^{f(\mathbf{z})}$ has a finite expectation, the function

$$K(\mathbf{z}) = \left(E\left[e^{f(\mathbf{z})}\right]\right)^{-1} e^{f(\mathbf{z})} p_{\mu,\Sigma}(\mathbf{z})$$
(12)

is a probability density function. Define the matrix $\Omega^{-1} = \Sigma^{-1} - \mathbf{g}$ and the vector $\mathbf{v} = \boldsymbol{\mu} + \Omega(\mathbf{b} + \mathbf{g}\boldsymbol{\mu})$.

We show in the Appendix that Ω is symmetric. Provided it is also positive definite, it is a valid

8

136 covariance matrix, and, by equation A7,

$$K(\mathbf{z}) \propto p_{\nu,\Omega}(\mathbf{z}).$$
 (13)

137 As K is a probability density function this implies,

$$K(\mathbf{z}) = p_{\nu,\Omega}(\mathbf{z}). \tag{14}$$

- Define $\mathbf{Q}^{-1} = \mathbf{\Omega}^{-1} \mathbf{\Sigma} = \mathbf{I}_k \mathbf{g} \mathbf{\Sigma}$. Combining equations 8, 10 and 14 yields $\boldsymbol{\beta} = E[\mathbf{b} + \mathbf{g} \mathbf{z}]$, where
- 139 the expectation is taken with respect to K. This is an expectation of a linear function of \mathbf{z} , and
- 140 so

$$\beta = \mathbf{b} + \mathbf{g}\nu = (\mathbf{b} + \mathbf{g}\mu) + \mathbf{g}\Omega(\mathbf{b} + \mathbf{g}\mu) = (\mathbf{I}_k + \mathbf{g}\Omega)(\mathbf{b} + \mathbf{g}\mu) = \mathbf{Q}(\mathbf{b} + \mathbf{g}\mu), \tag{15}$$

- 141 by use of equation A4.
- 142 Combining equations 9, 11 and 14 yields $\gamma = E[\mathbf{g} + (\mathbf{b} + \mathbf{gz})']$, where the expectation
- 143 is taken with respect to K. Hence

$$\gamma = \mathbf{g} + \text{Var}(\mathbf{b} + \mathbf{gz}) + [\mathbf{E}(\mathbf{b} + \mathbf{gz})][\mathbf{E}(\mathbf{b} + \mathbf{gz})]'$$

$$= \mathbf{g} + \mathbf{g}\Omega\mathbf{g}' + \beta\beta'$$

$$= \beta\beta' + (\mathbf{I}_k + \mathbf{g}\Omega)\mathbf{g}$$

$$= \beta\beta' + \mathbf{Q}\mathbf{g}, \tag{16}$$

- 144 where we have noted that **g** is symmetric and used equation A4.
- In univariate analyses, the matrix machinery necessary for implementing the general formulae
- 146 in equations 15 and 16 can be avoided. If the fitness function is $W(z) = e^{a+bz+g\frac{1}{2}z^2}$ (note, again,
- 147 that the quadratic coefficient is that for centred, then squared, and then halved values of z^1),
- and z has a mean of μ and a variance of σ^2 and then $\beta = \frac{b+g\mu}{1-g\sigma^2}$ and $\gamma = \frac{(b+g\mu)^2+g(1-g\sigma^2)}{(1-g\sigma^2)^2}$. These
- 149 expressions will hold for any univariate analysis, and can be applied to get mean-standardised,

¹This can be accomplished easily in R. Assume that W and z are variables in memory representing absolute fitness and phenotypic data, and that residuals of W are assumed to follow a Poisson distribution. The regression could be implemented by $glm(W^z+I(0.5*(z-mean(z))^2),family=poisson(link="log"))$.

Morrissey and Goudie, log-scale fitness models and selection gradients

variance-standardised, and unstandardised selection gradients, when appropriate values of μ and σ^2 are used, and applied to log-quadratic models of W(z) where the phenotypic records have been correspondingly standardised. For the common case where the trait is mean-centred and (unit) variance standardised, the expressions simplify further to $\beta = \frac{b}{1-g}$ and $\gamma = \frac{b^2 + g(1-g)}{(1-g)^2}$.

The equivalence of the regression coefficients of a log-linear fitness model with directional 154 155 selection gradients (equation 5) of course requires that the regression model provides a reasonable 156 description of the relationship between a trait and expected fitness and makes reasonable assumptions about fitness residuals. Otherwise, the relationship is relatively unburdened by 157 158 assumptions. For example, it does not require any specific distribution of phenotype. The use of selection gradients obtained from log-linear regressions to predict evolution using the Lande 159 equation (equation 3) does assume that breeding values are multivariate normal (see Morrissey 160 161 2014 for a discussion of selection gradients and associated assumptions about multivariate normality of phenotype and breeding values). The expressions for β and γ given a log-quadratic 162163 fitness model (equations 15 and 16) do assume multivariate normality of phenotype. Equations 15 and 16 further require that Ω is positive definite. In univariate analyses, this condition 164 165reduces to $g < \frac{1}{\sigma^2}$, implying that the fitness function should not curve upwards too sharply within the range of observed phenotype. 166

167 A very convenient feature of the expressions for β and γ in equations 5, 15 and 16 is that the 168 model (log) intercept does not influence the selection gradients. This means that the range of 169 modelling techniques that yield selection gradients can be even further expanded. For example, adding fixed and random effects to Lande & Arnold's (1983) least squares analysis will generally 170 result in estimated regression coefficients that are not interpretable as selection gradients. For 171 172 example, it might be desirable to estimate a single selection gradient across two sexes, if data are limited and sex-differences in selection are not anticipated. In such an analysis, it might 173 seem sensible to include an effect of sex, to account for differences in mean fitness between the 174sexes. However, such an analysis would not yield correct selection gradients, because the theory 175 underlying the least squares-based regression analysis of selection requires that mean relative 176 fitness is one, and this would not be the case when different strata within an analysis have 177 different intercepts. On the other hand, adding such an effect to a log-scale model of absolute 178

Morrissey and Goudie, log-scale fitness models and selection gradients

fitness, and then deriving selection gradients using equations 5, 15 and 16 will yield correct selection gradients. Other effects, such as random effects to account for individual heterogeneity in expected fitness, beyond that explained by the traits (or correlated, unmeasured traits), will be usable as well, while still retaining the ability to obtain correct selection gradients.

183 3 Statistical uncertainty

The expressions for selection gradients, given the parameters of a log-quadratic fitness function 184 (equations 15 and 16) give the selection gradients conditional on the estimated values of **b** and 185 However, \mathbf{b} and \mathbf{g} will not typically be known quantities in empirical studies of natural 186 selection, but rather will be estimates with error. Because equations 15 and 16 are non-linear 187 functions of one or more regression coefficients, unconditional estimators of β and γ would 188 have to be obtained by integrating the expressions for β and γ over the sampling distributions 189 190 of the estimated values of **b** and **g**. Such details are not normally considered in calculations 191 of derived parameters (e.g., heritabilities) in evolutionary studies. Such integration could be achieved using approximations, bootstrapping, or MCMC methods. Alternatively, application 192 193 of equations 15 and 16 directly to estimated values of **b** and **g** may be sufficient in practice. Similarly, while standard errors of the parameters \mathbf{b} and \mathbf{g} are not directly interpretable as 194 standard errors of corresponding values of β and γ , approximations, bootstrapping, and MCMC 195 methods may all potentially be useful in practice. In particular, approximation of standard 196 errors by a first-order Taylor approximation (the "delta method"; Lynch & Walsh 1998) may 197 198 generally be pragmatic. Formulae for approximate standard errors by this method are given in the appendix. For univariate analysis, with phenotype standardised to $\mu = 0$ and $\sigma^2 = 1$, the 199 approximate standard errors of β and γ are given by 200

$$SE[\beta] \approx \sqrt{\frac{\Sigma[b]}{(1-g)^2} + \frac{b^2 \Sigma[g]}{(1-g)^4} + \frac{2b \Sigma[b,g]}{(1-g)^3}},$$
 (17)

201 and

$$SE[\gamma] \approx \sqrt{\frac{4b^2\Sigma[b]}{(1-g)^4} + \frac{(1+2b^2-g)^2\Sigma[g]}{(1-g)^6} + \frac{4b(1+2b^2-g)\Sigma[b,g]}{(1-g)^5}}.$$
 (18)

Morrissey and Goudie, log-scale fitness models and selection gradients

Where $\Sigma[b]$ and $\Sigma[g]$ represent the sampling variances of the estimated b and g terms. These 202 are the squares of their standard errors. $\Sigma[b,g]$ is the sampling covariance of the b and g terms. 203 204 This is not always reported, but can usually be obtained. For example, in R, it can be extracted from a fitted glm object using the function vcov(). 205We performed a small simulation study to assess the extent of any bias in the estimators β 206 207 and γ and the adequacy of their standard errors. We simulated univariate directional selection, with values of b between -0.5 and 0.5, and with g = -0.5, 0 and 0.2. Because β and γ are non-208 linear functions of g, it is not possible to simultaneously investigate ranges of parameter values 209 210 with regular intervals of values of both g and selection gradients. These values of g represent a compromise between investigating a regular range of g and γ . We used a (log) intercept of the 211 fitness function of a = 0. We simulated a sample size of 200 individuals. This sample size reflects 212 213 a very modest-sized study with respect to precision in inference of non-linear selection, and is therefore a useful scenario in which to judge performance of different methods for calculating 214 215 standard errors. Fitness was simulated as a Poisson variable with expectations defined by the ranges of values of b and g, and with phenotypes sampled from a standard normal distribution. 216 217 Firstly we analysed each simulated dataset using the OLS regression described by Lande & Arnold (1983), i.e., $w_i = \mu + \beta z_i + \gamma \left(\frac{1}{2}z_i^2\right) + e_i$, using the R function lm(). For the OLS regressions, we 218 calculated standard errors assuming normality using the standard method implemented in the R 219 220function summary.lm(), and by case-bootstrapping, by generating 1000 bootstrapped datasets 221 by sampling with replacement, running the OLS regression analysis, and calculating the standard deviation of the bootstrapped selection gradient estimates. Secondly we fitted a Poisson glm 222 223 with a linear and quadratic terms, using the R function glm(). We then calculated conditional 224 selection gradient estimates using equations 15 and 16. We obtained standard errors by using a first-order Taylor series approximation (the "delta method"; Lynch & Walsh 1998, appendix 225 A1). For each method of obtaining estimates and standard errors, we calculated the standard 226 deviation of replicate simulated estimates. We could thus evaluate the performance of different 227 methods of obtaining standard errors by their ability to reflect this sampling standard deviation. 228 229 We also calculated mean absolute errors for both estimators of β and γ for all scenarios. Every

simulation scenario and associated analysis of selection gradients was repeated 1000 times.

230

Morrissey and Goudie, log-scale fitness models and selection gradients

Selection gradient estimates obtained by all three methods were essentially unbiased (figure 231 1a,d,g,j,m,p), except for small biases that occurred when the fitness function was very curved. 232 233 Thus, glm-derived values of selection gradients, conditional on estimated values of b and g performed very well as estimators of β and γ in our simulations. 234approximations of standard errors of the glm-derived estimates of β and γ closely reflected the 235 simulated standard deviations of the estimators (figure 1). All methods for obtaining standard 236 errors performed well for estimates of β in the pure log-linear selection simulations (figure 1h,k). 237238 OLS standard errors performed reasonably well under most simulation scenarios, except when g was positive (figure 1n,q); across all scenarios bootstrap standard errors of the OLS estimators 239 outperformed standard OLS standard errors. Mean absolute error of the glm estimators was 240 always smaller than that of the OLS estimators of β and γ . This is unsurprising, as the simulation 241 242scheme corresponded closely to the glm model. These results demonstrate the usefulness of the conditional values of β and γ as estimators, and show that gains in precision and accuracy can 243 be obtained when glm models of fitness functions fit the data well. It remains plausible that 244 the OLS estimators motivated by Lande & Arnold's (1983) work could outperform glm-based 245246 analyses in some scenarios.

Other analyses that correspond to log-linear fitness functions

In addition to generalised linear models with log link functions, there may be other cases where models of trait-fitness relationships may correspond to log-linear or log-quadratic fitness functions. In paternity inference, some methods have been proposed wherein the probability that candidate father i is the father of a given offspring is modelled according to

$$W(\mathbf{z}) \propto e^{f(\mathbf{z})}$$
,

and where realised paternities of a given offspring array are then modelled according to a multinomial distribution, potentially integrating over uncertainty in paternity assignments based

Morrissey and Goudie, log-scale fitness models and selection gradients

on molecular data (Hadfield et al., 2006; Smouse et al., 1999). When f(z) is a linear function, Smouse, Meagher & Korbak (1999; T. Meagher, personal communication) interpreted the analysis as analogous to Lande and Arnold's 1983, but not necessarily identical. For a linear $f(\mathbf{z})$, this analysis does in fact yield estimates of $\boldsymbol{\beta}$, and for a quadratic function, directional and quadratic selection gradients can be obtained using equations 15 and 16. This can be seen by noting that expected fitness, given phenotype, of candidate fathers for any given offspring array will be, in the log-linear case,

$$W(\mathbf{z}) = ce^{a+b\mathbf{z}},$$

where c is a constant. In application of the expressions yielding equation 5, c appears in both the numerator and the denominator, yielding $\beta = \mathbf{b}$.

Another case where our formulae may be applicable pertains to inferences of survival rate. 264 265 Often, data about trait-dependent survival rates may be assessed over discrete intervals. While the experimental unit of time may be an interval (e.g., a day or a year), the biologically-relevant 266 aspect of variation in survival may be longevity, i.e., for how many intervals an individual 267 survives. One such situation arises when per-interval survival rate is assessed via a logistic 268 269 regression analysis, and trait-dependent survival rates are (or may be assumed to be) constant across intervals. A common case of logistic regression analysis that satisfies this first condition 270 is often implemented in capture-mark-recapture procedures. Suppose that per-interval survival 271 272 rate, given phenotype, may be assumed to be constant, and that fitness is defined to be the 273 expected survival time. Then fitness will be given by the mean of a geometric distribution where death in a particular interval of an individual with phenotype \mathbf{z} occurs with probability 274 275 $\rho(\mathbf{z}),$

$$W(\mathbf{z}) = \frac{1 - \rho(\mathbf{z})}{\rho(\mathbf{z})}.$$

If trait-dependent per-interval survival probability is denoted $\phi(\mathbf{z})$ (ϕ being the standard symbol for survival rate in capture-mark-recapture analyses; Lebreton *et al.* 1992), then the fitness function in terms of expected number of intervals lived is $W(\mathbf{z}) = \frac{1-(1-\phi(\mathbf{z}))}{1-\phi(\mathbf{z})} = \frac{\phi(\mathbf{z})}{1-\phi(\mathbf{z})}$. If per-interval

Morrissey and Goudie, log-scale fitness models and selection gradients

279 survival rate has been modelled as a logistic regression, i.e.,

282

$$\phi(\mathbf{z}) = \frac{e^{f(\mathbf{z})}}{1 + e^{f(\mathbf{z})}}$$

where $\phi(\mathbf{z})$ denotes the per-interval fitness function, and $f(\mathbf{z})$ is the fitness function on the logistic scale, then the fitness function on the discrete longevity scale is

$$W(\mathbf{z}) = \frac{\frac{e^{f(\mathbf{z})}}{1 + e^{f(\mathbf{z})}}}{1 - \frac{e^{f(\mathbf{z})}}{1 + e^{f(\mathbf{z})}}} = e^{f(\mathbf{z})}.$$

Therefore, if $f(\mathbf{z})$ is a linear function, then its terms are the directional selection gradients on

the discrete-longevity scale. If f(z) is a quadratic function, then the corresponding directional 283 and quadratic selection gradients, again if the relevant aspect of fitness is the number of 284 285 intervals survived, can be obtained using equations 15 and 16. Waller and Svensson (2016; this issue) takes advantage of these relationships to compare inference of trait-dependent survival 286 in capture-mark-recpature models to classical inference using Lande & Arnold's (1983) least-287 288 squares regression analysis where fitness is assessed as the number of intervals that individuals survive. 289 290 It must be stressed that these results do not justify interpretation of logistic regression coefficients of survival probability as selection gradients in a general way. Such coefficients 291 differ from selection gradients for three reasons: (1) they pertain to a linear predictor scale, and 292natural selection plays out on the data scale, (2) they directly model absolute fitness, not relative 293 294 fitness, and (3) they pertain to per-interval survival, which may not necessarily be the aspect 295 of survival that best reflects fitness in any given study. It is only when the number of intervals 296 survived is of interest (and mean survival can be assumed to be constant across intervals) that these three different aspects of scale cancel out such that the parameters of a logistic regression 297 298 are selection gradients. 299 Finally, another situation where an important analysis for understanding trait-fitness 300 relationships that has an immediate – but not necessarily immediately apparent – relationship to selection gradients, arises in survival analysis. In a proportional hazards model (Cox, 1972), 301 the instantaneous probability of mortality experienced by live individuals, the hazard $\lambda(t)$, as a

Morrissey and Goudie, log-scale fitness models and selection gradients

303 function of their phenotype could be modelled as

$$\lambda(t) = \lambda_0 e^{f(z)}$$

where λ_0 is the baseline hazard, and the $e^{f(z)}$ part of the function describes individual deviations from this baseline hazard. If the baseline hazard is constant in time, then survival distributions conditional on phenotype are exponential, and have mean λ^{-1} . So, if fitness is taken to be expected longevity (as a continuous variable now, not discrete number of intervals as in the relations given above between logistic models of per-interval survival and selection gradients) then

$$W(z) = \frac{1}{\lambda_0 e^{f(z)}} = \frac{1}{\lambda_0} e^{-f(z)}.$$

In expressions for selection gradients (equations 1 and 2), $\frac{1}{\lambda_0}$ would be a constant in the integrals in both the numerators and denominators, and therefore cancels in calculations of selection gradients. Therefore, if proportional hazards are modelled with f(z) as a linear or quadratic function, then the expressions for selection gradients (equations 5, 15 and 16) hold, but the coefficients of the trait-dependent hazard function must be multiplied by -1.

315 **5** Conclusion

We have provided analytical expressions for selection gradients, given the parameters of log-316 linear and log-quadratic functions describing expected fitness. These functions can be applied 317 in conjunction with a range of generalised linear model approaches, specific situations in capture-318 mark-recapture analysis, and relate to fitness functions used in theoretical studies. The general 319 320 relationship of selection gradients to the coefficients of log-linear and log-quadratic models, in particular, various generalised linear models, are probably the most generally useful feature of 321 our results. In empirical applications, our preliminary simulation results indicate that, given 322 323 an appropriate model of a log-scale fitness function, inference using log-linear and log-quadratic 324 models may be very robust, and could provide more reliable statements about uncertainty (e.g., reasonable standard errors) than the main methods used to date. Furthermore, the relationships 325

given here between log-quadratic fitness functions and selection gradients could lead to better 326 integration between empirical and theoretical strategies for modelling selection. In theoretical 327 328 studies, Gaussian fitness functions are often used. These are simply log-quadratic functions that 329 are parameterised in terms of a location parameter (phenotype of maximum fitness), and a width parameter. A relationship between the parameters of a Gaussian fitness function and directional 330 selection gradients (Lande 1979; the expression we give for β is an alternative formulation) is 331 already widely used in the theoretical literature. For any given distribution of phenotype, these 332333 parameters correspond directly to linear and quadratic (log-scale) regression parameters, and so can be directly related to selection gradients in empirical studies. 334

Acknowledgements

- 336 We thank Andy Gardner, Graeme Ruxton, and Kerry Johnson for discussions, comments, and
- 337 advice. Peter Jupp provided particular insights that improved this paper. MBM is supported
- 338 by a Royal Society (London) University Research Fellowship.

339 References

- 340 Cox, D.R. (1972) Regression models and life-tables. Journal of the Royal Statistical Society
- 341 Series B, **34**, 187–220.
- 342 Endler, J.A. (1986) Natural selection in the wild. Princeton University Press.
- 343 Falconer, D.S. (1960) Introduction to Quantitative Genetics. Oliver and Boyd.
- 344 Geyer, C.J. & Shaw, R.G. (2010) Aster models and the Lande-Arnold beta. Technical report,
- 345 University of Minnesota.
- 346 Hadfield, J.D., Richardson, D.S. & Burke, T. (2006) Towards unbiased parentage assignment:
- 347 combining genetic, behavioural and spatial data in a Bayesian framework. Molecular Ecology,
- 348 **15**, 3715–3731.
- 349 Janzen, F.J. & Stern, H.S. (1998) Logistic regression for empirical studies of multivariate
- selection. Evolution, pp. 1564–1571.
- 351 Kingsolver, J.G., Hoekstra, H.E., Hoekstra, J.M., Vignieri, C., Berrigan, D., Hill, E., Hoang, A.,
- 352 Gilbert, P. & Beerli, P. (2001) The strength of phenotypic selection in natural populations.

16

- 353 The American Naturalist, **157**, 245–261.
- 354 Lande, R. (1979) Quantitative genetic analysis of multivariate evolution, applied to brain:body
- size allometry. Evolution, **33**, 402–416.
- 356 Lande, R. & Arnold, S.J. (1983) The measurement of selection on correlated characters.
- 357 Evolution, **37**, 1210–1226.
- 358 Lebreton, J.D., Burnham, K.P., Colbert, J. & Anderson, D.R. (1992) Modeling survival and
- 359 testing biological hypotheses using marked animals: a unified approach with case studies.
- 360 Ecological Monographs, **62**, 67–118.
- 361 Lynch, M. & Walsh, B. (1998) Genetics and analysis of quantitative traits. Sinauer, Sunderland,
- 362 MA.
- 363 Manly, B.F.J. (1985) The statistics of natural selection. Chapman and Hall, New York.
- 364 Morrissey, M.B. (2014) In search of the best methods for multivariate selection analysis. Methods
- 365 in Ecology and Evolution, **5**, 1095–1109.
- 366 Morrissey, M.B. & Sakrejda, K. (2013) Unification of regression-based approaches to the analysis
- of natural selection. Evolution, 67, 2094–2100.
- 368 Shaw, R.G. & Geyer, C.J. (2010) Inferring fitness landscapes. Evolution, 64, 2510–2520.
- 369 Smouse, P.E., Meagher, T.R. & Kobak, C.J. (1999) Parentage analysis in Chamaelirium luteum
- 370 (L.) gray (Liliaceae): why do some males have higher reproductive contributions? Journal of
- 371 Evolutionary Biology, **12**, 1069–1077.
- 372 Stinchcombe, J.R., Agrawal, A.F., Hohenlohe, P.A., Arnold, S.J. & Blows, M.W. (2008)
- 373 Estimating nonlinear selection gradients using quadratic regression coefficients: Dougle or
- 374 nothing? Evolution, **62**, 2435–2440.
- 375 Waller, J. & Svensson, E. (2016) The measurement of selection when detection is imperfect:
- 376 how good are naïve methods? Methods in Ecology and Evolution.
- 377 Weldon, W.F.R. (1901) A first study of natural selection in Clausilia italica (von martens).
- 378 Biometrika, 1, 109–124.

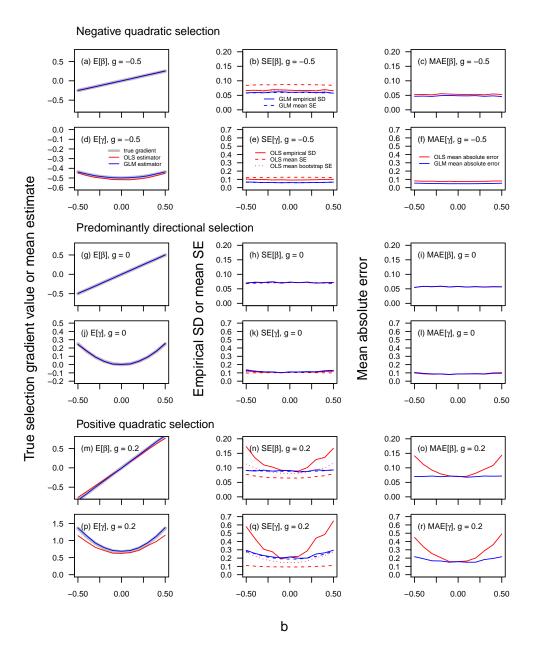


Figure 1: Simulation results for the performance of Lande & Arnold's (1983) least squares-based (OLS) estimators (red lines), and log-quadratic (GLM) estimators (blue lines), of directional and quadratic selection gradients. The first column shows bias in estimates of β and γ , where departure from the grey line (the simulated truth) indicates bias. The middle column shows the performance of OLS standard errors (red dashed lines), bootstrap standard errors (red dotted lines), and first-order approximations (blue dashed lines) of the standard errors of the GLM estimators. Ideally, all values of estimated mean standard errors would fall on the simulated standard deviation of their associated estimators, shown as solid lines. The right column shows the mean absolute errors of the OLS and GLM estimators.

Appendix

- 380 Denote a vector containing all unique elements of γ by $\tilde{\gamma}$. The following assumes that $\tilde{\gamma}$ is
- 381 composed by vertically stacking the columns of the diagonal and sub-diagonal elements of γ .
- For example, in an analysis with three traits, $\tilde{\boldsymbol{\gamma}} = \left[\gamma_{1,1}, \gamma_{2,1}, \gamma_{3,1}, \gamma_{2,2}, \gamma_{3,2}, \gamma_{3,3}\right]'$. Let $\mathbf{v}()$ denote
- 383 the function mapping the distinct elements of a symmetric matrix \mathbf{r} onto the column vector $\tilde{\mathbf{r}}$.
- 384 The first-order approximation to the sampling covariance matrix of the elements of $\boldsymbol{\beta}$ and
- 385 γ is then given by $\mathbf{J}\tilde{\Sigma}\mathbf{J}'$, where $\tilde{\Sigma}$ is the sampling covariance matrix of a vector containing the
- 386 elements of \mathbf{b} and $\tilde{\mathbf{g}}$, where the latter is a column vector containing the distinct elements of \mathbf{g}
- 387 arranged according to the same scheme that defines $\tilde{\gamma}$. J is the Jacobian, or gradient matrix of
- 388 first order partial derivatives, of $\boldsymbol{\beta}$ and $\tilde{\boldsymbol{\gamma}}$ with respect to **b** and $\tilde{\mathbf{g}}$, i.e.,

$$\mathbf{J} = \begin{bmatrix} \frac{\partial \boldsymbol{\beta}}{\partial \mathbf{b}} & \frac{\partial \boldsymbol{\beta}}{\partial \tilde{\mathbf{g}}} \\ \frac{\partial \tilde{\boldsymbol{\gamma}}}{\partial \mathbf{b}} & \frac{\partial \tilde{\boldsymbol{\gamma}}}{\partial \tilde{\mathbf{g}}} \end{bmatrix},$$

- 389 evaluated at the estimated values of **b** and **g**.
- Note that some users may prefer to fit the model 6 with g_{ii} replaced by $2g_i$, say. The formulae
- 391 for β and γ are readily re-expressed in terms of these variables by making this substitution. If Σ_1
- 392 denotes the covariance matrix obtained when fitting this revised model, the required covariance
- 393 matrix $\tilde{\Sigma}$ can be calculated using $\tilde{\Sigma} = D\Sigma_1 D'$, where **D** is a diagonal matrix with all the diagonal
- 394 elements equal to one, apart from those corresponding to the variables g_{ii} which equal 2.
- 395 The four submatrices of **J** can be treated separately. Noting that $\beta = \mathbf{Q}(\mathbf{b} + \mathbf{g}\mu)$ (equation 396—15),

$$\frac{\partial \boldsymbol{\beta}}{\partial \mathbf{b}} = \mathbf{Q}.\tag{A1}$$

- Let $s = \frac{1}{2}k(k+1)$, where k is the number of traits in the analysis, and let $\mathbf{e}_1, \dots, \mathbf{e}_s$ be the standard basis for an s dimensional space (i.e., $\mathbf{e}_1 = [1, 0, \dots, 0]'$, etc.). Define an indicator
- 399 matrix $\mathbf{C}_m = \mathbf{C}^{(i,j)}$ where $\mathbf{C}^{(i,j)}$ is a k by k matrix in which

400

$$\left[\mathbf{C}^{(i,j)}\right]_{xy} = \begin{cases} 1, & (x,y) = (i,j) \text{ or } (j,i); \\ 0, & \text{otherwise.} \end{cases}$$

Using the standard expression for the derivative of the inverse of a matrix with respect to a

401 scalar, we can obtain $\frac{\partial \boldsymbol{\beta}}{\partial \tilde{\mathbf{g}}}$, i.e., the upper-right sub-matrix of \mathbf{J} .

$$\beta = \Psi^{-1} (\mathbf{b} + \mathbf{g}\mu) \qquad \Rightarrow \frac{\partial \beta}{\partial \tilde{g}_{m}} = \frac{\partial \beta}{\partial g_{ij}} = -\Psi^{-1} \left[\frac{\partial \Psi}{\partial g_{ij}} \right] \Psi^{-1} (\mathbf{b} + \mathbf{g}\mu) + \Psi^{-1} \left[\frac{\partial (\mathbf{b} + \mathbf{g}\mu)}{\partial g_{ij}} \right]$$

$$= -\mathbf{Q} \left[\frac{\partial \mathbf{I}_{k} - \mathbf{g}\Sigma}{\partial g_{ij}} \right] \mathbf{Q} (\mathbf{b} + \mathbf{g}\mu) + \mathbf{Q} \left[\frac{\partial \mathbf{g}}{\partial g_{ij}} \right] \mu$$

$$= \mathbf{Q} \left[\frac{\partial \mathbf{g}}{\partial g_{ij}} \right] [\Sigma \mathbf{Q} (\mathbf{b} + \mathbf{g}\mu)] + \mathbf{Q} \left[\frac{\partial \mathbf{g}}{\partial g_{ij}} \right] \mu$$

$$= \mathbf{Q} \mathbf{C}^{(ij)} (\Sigma \beta + \mu) = \mathbf{Q} \mathbf{C}_{m} (\Sigma \beta + \mu)$$

$$\Rightarrow \frac{\partial \beta}{\partial \tilde{\mathbf{g}}} = \sum_{m=1}^{s} \frac{\partial \beta}{\partial \tilde{g}_{m}} \mathbf{e}'_{m} = \mathbf{Q} \sum_{m=1}^{s} \mathbf{C}_{m} (\Sigma \beta + \mu) \mathbf{e}'_{m}$$
(A2)

Let $\mathbf{Q}_{[u]}$ denote the u^{th} column of \mathbf{Q} . Using the previous relation $\frac{\partial \beta}{\partial \mathbf{b}} = \mathbf{Q}$, we can obtain $\frac{\partial \tilde{\gamma}}{\partial \mathbf{b}}$, 403 i.e., the lower-left sub-matrix of \mathbf{J} .

$$\gamma = \beta \beta' + \mathbf{Q}\mathbf{g} \qquad \Rightarrow \frac{\partial \gamma}{\partial b_{u}} = \beta \left(\frac{\partial \beta}{\partial b_{u}}\right)' + \left(\frac{\partial \beta}{\partial b_{u}}\right) \beta' = \beta \mathbf{Q}'_{[u]} + \mathbf{Q}_{[u]} \beta'
\Rightarrow \frac{\partial \tilde{\gamma}}{\partial b_{u}} = \mathbf{v} \left(\beta \mathbf{Q}'_{[u]} + \mathbf{Q}_{[u]} \beta'\right)
\Rightarrow \frac{\partial \tilde{\gamma}}{\partial \mathbf{b}} = \sum_{u=1}^{k} \mathbf{v} \left(\beta \mathbf{Q}'_{[u]} + \mathbf{Q}_{[u]} \beta'\right) \mathbf{e}'_{u}$$
(A3)

Let $\mathbf{M}^{(m)} = \mathbf{Q}\mathbf{C}_m (\mathbf{\Sigma}\boldsymbol{\beta} + \boldsymbol{\mu})\boldsymbol{\beta}'$. Note that $\mathbf{Q}^{-1} = \mathbf{\Omega}^{-1}\mathbf{\Sigma}$ implies $\mathbf{\Omega} = \mathbf{\Sigma}\mathbf{Q}$. Moreover $\mathbf{\Omega}^{-1} = \mathbf{\Sigma}^{-1} - \mathbf{g}$

405 implies firstly that

$$\mathbf{I}_k + \mathbf{g}\mathbf{\Omega} = \mathbf{\Sigma}^{-1}\mathbf{\Omega} = \mathbf{Q} \tag{A4}$$

20

406 and secondly that Ω is symmetric, since Σ and \mathbf{g} are both symmetric. It follows that

$$\mathbf{Q}' = \mathbf{I}_k + (\mathbf{g}\mathbf{\Omega})' = \mathbf{I}_k + \mathbf{\Omega}\mathbf{g}. \tag{A5}$$

407 The lower-right sub-matrix of **J** can then be derived.

$$\frac{\partial \gamma}{\partial g_{ij}} = \left[\frac{\partial \beta}{\partial g_{ij}}\right] \beta' + \beta \left[\frac{\partial \beta}{\partial g_{ij}}\right]' + \mathbf{Q} \mathbf{C}^{(ij)} + \mathbf{Q} \mathbf{C}^{(ij)} \mathbf{\Sigma} \mathbf{Q} \mathbf{g}$$

$$= \left[\mathbf{Q} \mathbf{C}^{(ij)} \left(\mathbf{\Sigma} \beta + \mu\right)\right] \beta' + \beta \left[\mathbf{Q} \mathbf{C}^{(ij)} \left(\mathbf{\Sigma} \beta + \mu\right)\right]' + \mathbf{Q} \mathbf{C}^{(ij)} + \mathbf{Q} \mathbf{C}^{(ij)} \mathbf{\Omega} \mathbf{g}$$

$$\Rightarrow \frac{\partial \tilde{\gamma}}{\partial g_{ij}} = \mathbf{v} \left[\mathbf{M}^{(m)} + (\mathbf{M}^{(m)})' + \mathbf{Q} \mathbf{C}_{m} (\mathbf{I}_{k} + \mathbf{\Omega} \mathbf{g})\right]$$

$$\Rightarrow \frac{\partial \tilde{\gamma}}{\partial \tilde{\mathbf{g}}} = \sum_{m=1}^{s} \mathbf{v} \left[\mathbf{M}^{(m)} + (\mathbf{M}^{(m)})' + \mathbf{Q} \mathbf{C}_{m} \mathbf{Q}'\right] \mathbf{e}'_{m}, \tag{A6}$$

408 by use of equation A5.

- Finally note that equations A4 and A5 are also relevant to the derivation of formula 13. By
- 410 definition, $f(\mathbf{z}) = a + \mathbf{z}'\mathbf{b} + \frac{1}{2}\mathbf{z}'\mathbf{g}\mathbf{z}$, and we have $\log[p_{\boldsymbol{\mu},\boldsymbol{\Sigma}}(\mathbf{z})] = -\frac{1}{2}\mathbf{z}'\boldsymbol{\Sigma}^{-1}\mathbf{z} + \mathbf{z}'\boldsymbol{\Sigma}^{-1}\boldsymbol{\mu} + \alpha$, where α does
- 411 not depend on **z**. Thus, if $\alpha' = \alpha + a$, it follows that, as a function of **z**,

$$f(\mathbf{z}) + \log[p_{\boldsymbol{\mu},\boldsymbol{\Sigma}}(\mathbf{z})] = -\frac{1}{2}\mathbf{z}'(\boldsymbol{\Sigma}^{-1} - \mathbf{g})\mathbf{z} + \mathbf{z}'(\mathbf{b} + \boldsymbol{\Sigma}^{-1}\boldsymbol{\mu}) + \alpha' = -\frac{1}{2}\mathbf{z}'\boldsymbol{\Omega}^{-1}\mathbf{z} + \mathbf{z}'\boldsymbol{\Omega}^{-1}\left[\boldsymbol{\Omega}(\mathbf{b} + \boldsymbol{\Sigma}^{-1}\boldsymbol{\mu})\right] + \alpha',$$

- 412 Now, by A4 and A5, we have $\Omega(\mathbf{b} + \Sigma^{-1}\mu) = \Omega\mathbf{b} + (\Sigma^{-1}\Omega)'\mu = \Omega\mathbf{b} + \mathbf{Q}'\mu = \Omega\mathbf{b} + (\mathbf{I}_k + \Omega\mathbf{g})\mu = \nu$,
- 413 implying that

$$f(\mathbf{z}) + \log[p_{\boldsymbol{\mu},\boldsymbol{\Sigma}}(\mathbf{z})] = -\frac{1}{2}\mathbf{z}'\boldsymbol{\Omega}^{-1}\mathbf{z} + \mathbf{z}'\boldsymbol{\Omega}^{-1}\boldsymbol{\nu} + \boldsymbol{\alpha}' = -\frac{1}{2}(\mathbf{z} - \boldsymbol{\nu})'\boldsymbol{\Omega}^{-1}(\mathbf{z} - \boldsymbol{\nu}) + \boldsymbol{\alpha}'', \tag{A7}$$

21

- where α'' is constant as a function of **z**. The exponent of $e^{f(\mathbf{z})}p_{\mu,\Sigma}(\mathbf{z})$ is thus identical, as a function
- of **z**, to that of $p_{\nu,\Omega}(\mathbf{z})$. Hence formula 13 holds.