

**Analytical Expressions for the Eigenvalues and Confidence Intervals  
Arising from a 3-Stage Wildlife Population Matrix**

A Thesis

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by

Brenda J. Hanley

Major Professor: Brian Dennis, Ph.D.

Committee Members: Michelle Wiest, Ph.D., Ryan Long, Ph.D.

Department Administrator: Chris Williams, Ph.D.

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### Authorization to Submit Thesis

This thesis of Brenda J. Hanley, submitted for the degree of Master of Science with a major in Statistical Science and titled “Analytical Expressions for the Eigenvalues and Confidence Intervals Arising from a 3-Stage Wildlife Population Matrix,” has been reviewed in final form. Permission, as indicated by the signatures and dates below, is now granted to submit final copies to the College of Graduate Studies for approval.

Major Professor: \_\_\_\_\_ Date: \_\_\_\_\_  
Brian Dennis, Ph.D.

Committee Members: \_\_\_\_\_ Date: \_\_\_\_\_  
Michelle Wiest, Ph.D.

\_\_\_\_\_ Date: \_\_\_\_\_  
Ryan Long, Ph.D.

Department Administrator: \_\_\_\_\_ Date: \_\_\_\_\_  
Chris Williams, Ph.D.

## Abstract

We used the well-known symbolic solution for the roots of a cubic polynomial to derive expressions for the dominant and subdominant eigenvalues of a 3-stage population projection matrix. The resulting expressions were used in conjunction with the delta method to obtain symbolic asymptotic confidence limits for the eigenvalues to aid in understanding how errors in the demographic rates are propagated into population growth and volatility. The projection matrix corresponds to a generic life history of many wildlife populations containing juvenile, subadult, and adult stages. In the formulas, the four demographic parameters (three stage survival probabilities and the adult fecundity) collapse into two superparameters (adult recruitment and survival). This paper shows that the eigenvalues and their uncertainties can be calculated using two superparameters only. If growth rate estimation is the goal of a data collection effort, field ecologists can collect data on two parameters instead of four. The eigenvalue results presented here will be useful in population viability analysis, population recovery planning, translocation planning, and hunting/harvest management.

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## Introduction

The population matrix model is one of the most widely used mathematical models in wildlife ecology (Morris et al. 2002). Inputs for the matrix model are the “vital rates,” which include age or stage class survival probabilities and fecundities (Caswell 2001, Morris et al 2002, Gotelli et al 2004). Together with an organism’s life history structure, these vital rates can be used to construct a projection matrix that represents any species (Caswell 2001, Kot 2001). Outputs of the matrix model include the eigenvalues, eigenvectors, and damping ratio, which represent the asymptotic growth rate, stable stage distribution and non-equilibrium population oscillations (respectively) (Caswell 2001, Kot 2001, Morris et al 2002, Gotelli et al 2004).

The dominant eigenvalue of the population matrix model is an important demographic parameter in wildlife management, having been used to guide numerous local, state, and national wildlife management strategies (Caswell 2001, Fryxell et al. 2014). By Perron-Frobenius theorem, each projection matrix has one real eigenvalue with magnitude greater than or equal to the magnitudes of the other eigenvalues. This “dominant eigenvalue” summarizes the function and effects of the vital rates on overall population trajectory. The dominant eigenvalue is interpreted as the long term finite population growth rate (Caswell 2001, Kot 2001, Morris et al 2002, Gotelli et al 2004, Monte 2012). Additionally, sensitivity analysis techniques have been used to determine which vital rate has the largest influence on the dominant eigenvalue (Caswell 2001, Kot 2001, Morris et al 2002, Gotelli et al 2004). With the guidance of sensitivity analysis, wildlife managers can focus their efforts on the cohorts that will most efficiently influence population trajectory. Not only do eigenvalues help inform management strategy, they have been used as supporting evidence in significant

federal policy developments. For instance, the long term finite population growth rate has been cited in listing designations under the Endangered Species Act (Skalski et al. 2007).

Despite the importance placed on the dominant eigenvalue, ecologists have acknowledged that projection matrix eigenvalues are calculated using vital rates estimated from uncertain sample data (Picard et al. 2009). The degree of precision of the eigenvalue must therefore reflect the precision of the vital rates (Skalski et al. 2007). Over the past three decades, research has been conducted to develop appropriate measures of uncertainty for dominant eigenvalues given variation in the vital rates.

Meyer, et al. (1986) proposed simulation approaches to estimate confidence limits for the dominant eigenvalue. Since then, bootstrapping, (Regehr et al. 2010, Devenish Nelson et al. 2010), Monte Carlo (Caswell et al. 1998), or jackknife approaches (Meyer et al. 1986) have been implemented (Skalski et al. 2007).

Lande (1988), Alvarez-Buylla et al. (1993) and Picard et al. (2009) used a Taylor Series expansion approach to obtain confidence intervals for the dominant eigenvalue without the need for computer simulation. Lande (1988), used implicit partial differentiation of the matrix characteristic equation in conjunction with the delta method to estimate the standard error of the dominant eigenvalue. Skalski et al. (2007) published *Mathematica* instructions to implement confidence limits for the dominant eigenvalue, thereby providing managers a convenient tool for estimating the finite growth rate in their own systems. Picard et al. (2009) showed that an influence curve function can be used with the delta method to estimate dominant eigenvalue variation, and remarked that the delta method can be used in conjunction with any function that adequately maps the vital rates to the eigenvalues.

Here, we employed a well-known symbolic solution for the roots of a cubic polynomial to derive expressions that represent the eigenvalues of a generic 3-stage population matrix in terms of the vital rates. The solution is a standard entry in mathematics reference books (e.g. Beyer 1978, Hazewinkel 2001); its publication by Cardano in 1545 triggered a long and bitter argument over scientific priority (Waters 1898). Given a species with the life history of juveniles, non-reproductive subadults, and reproductive adults, the resulting population matrix has a characteristic equation in the form of a cubic polynomial, whose roots are the eigenvalues of the matrix (Cull et al. 1973). We used the symbolic eigenvalue expressions in conjunction with the delta method to derive symbolic approximate confidence limits for each eigenvalue.

Although population matrix models contain as many eigenvalues as the dimensionality of the matrix, subdominant eigenvalues have received much less attention than dominant eigenvalues. Despite decades of focus on the dominant eigenvalues, ecological interest in subdominant eigenvalues has been largely limited to their contribution in the population damping ratio (Caswell 2001). Caswell (2001), Yearsley (2003), and Xu et al. (2009) however, have noted that subdominant eigenvalues play a substantial role of non-equilibrium behavior dynamics, and that research into this arena will be valuable to understanding non-equilibrium population dynamics. However, studies of propagating uncertainty in vital rates to subdominant eigenvalues are lacking. This paper uses the cubic solution to provide symbolic formulas for the subdominant eigenvalues and their confidence limits.

By mathematical corollary, confidence limits for the first two eigenvalues give confidence limits for the non-equilibrium damping ratio. Caswell (2001) states that the ratio between the dominant eigenvalue and the modulus of the subdominant eigenvalue yields the

magnitude of oscillation change in non-equilibrium population trajectory. Confidence limits around the magnitude of oscillation change can help managers further understand the near term risks to their species of extinction.

## Methods

### *Symbolic Expressions for Eigenvalues*

A common wildlife life history consists of three stages: juvenile, subadult, and adult (Figure 1). Further common characteristics of this life table are; (a) the time intervals an individual spends in the juvenile and subadult stages are approximately equal, and (b) subadult reproduction is negligible. By taking these characteristics as model assumptions, a generic wildlife population can be described with a matrix projection model (Keyfitz et al. 2005, Dennis 2013). We denote the number of juveniles, subadults and adults at time  $t$  respectively by  $J_t$ ,  $S_t$  and  $A_t$ , and we denote adult fecundity, juvenile survival, sub adult survival, and adult survival vital rates by  $f$ ,  $p_1$ ,  $p_2$ , and  $p_3$  (respectively). Juveniles move to subadults with probability  $p_1$ , subadults move to adults with probability  $p_2$ , and adults remain adults with probability  $p_3$ . Adults reproduce with fecundity  $f$ .

The life table in Figure 1 can be represented by a population matrix (Caswell 2001, Kot 2001, Dennis 2013). The matrix of vital rates given by:

$$\mathbf{M} = \begin{bmatrix} 0 & 0 & f \\ p_1 & 0 & 0 \\ 0 & p_2 & p_3 \end{bmatrix} \quad (1)$$

is a form of "Leslie-Lewis matrix" (after Leslie 1942, 1945, Lewis 1941) with an adult stage consisting of breeding adults of any age with a common survival probability  $p_3$ . Letting  $N_t = [J_t \ S_t \ A_t]'$  be the  $3 \times 1$  vector of age classes at time  $t$ , the following recursion projects the age classes one time unit forward:

$$N_{t+1} = \mathbf{M}N_t. \quad (2)$$

The eigenvalues ( $\lambda_j$ ) of the population matrix  $\mathbf{M}$  are scalars that satisfy the matrix equation

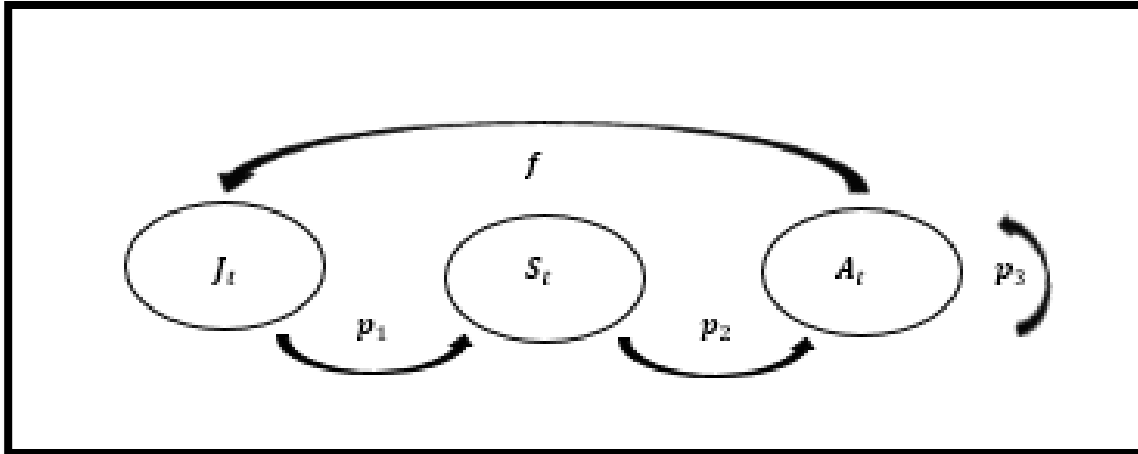
$$\mathbf{M}\mathbf{v}_j = \lambda_j\mathbf{v}_j, \quad (3)$$

where  $j = 1, 2, 3$ . In (3),  $\mathbf{v}_j$  is the  $j$ th eigenvector corresponding to the  $j$ th eigenvalue of  $\mathbf{M}$ .

The dominant right eigenvector ( $\mathbf{v}_1$ ) can be interpreted as the stable age distribution of the population.

The dominant eigenvalue ( $\lambda_1$ ) is the positive, real eigenvalue having the largest magnitude among all the eigenvalues. The magnitude of  $\lambda_1$  determines the trend of the population trajectory (Caswell 2001). An eigenvalue greater than one, less than one, or equal to one means that the population is increasing, decreasing, or stable (respectively) (Caswell 2001). As time increases, the changes in the total population size  $N$  is approximated by discrete time geometric growth, with the dominant eigenvalue representing the finite or discrete per capita growth rate (Caswell 2001). The instantaneous or continuous per capita growth rate is related to the dominant eigenvalue (Caswell 2001) by

$$\frac{1}{N} \frac{dN}{dt} = \log(\lambda_1). \quad (4)$$



**Figure 1. Life history for a 3-stage species.  $J_t, S_t, A_t$  represent the number of juveniles, subadults, and adults present at time  $t$  (respectively). Juveniles move to subadults with probability  $p_1$ , subadults move to adults with probability  $p_2$ , and adults remain adults with probability  $p_3$ . Adults reproduce with fecundity  $f$ .**

The eigenvalues of a matrix are the roots of the characteristic polynomial of the matrix (e.g. Cull et al. 1973). The characteristic polynomial of  $\mathbf{M}$  is

$$\lambda^3 - p_3\lambda^2 - fp_1p_2, \quad (5)$$

so the eigenvalues of  $\mathbf{M}$  are roots of a cubic equation:

$$\lambda^3 - p_3 \lambda^2 - fp_1p_2 = 0. \quad (6)$$

The vital rates in (6) naturally collapse into just two “superparameters”: adult survival ( $p_3$ ) and a combined parameter ( $fp_1p_2$ ) representing adult recruitment. We denote the combined superparameter  $v = fp_1p_2$ . A solution for the roots of a general cubic equation has been known since the 1500s as Cardano's formula (Hazewinkel 2001). Let

$$A = \left\{ \left( \frac{p_3}{3} \right)^3 + \frac{v}{2} + \sqrt{\frac{2}{3} \left( \frac{p_3}{3} \right)^3 \left[ \left( \frac{p_3}{3} \right)^3 + \frac{v}{2} \right]} \right\}^{\frac{1}{3}}, \quad (7)$$

$$B = \left\{ \left( \frac{p_3}{3} \right)^3 + \frac{v}{2} - \sqrt{\frac{2}{3} \left( \frac{p_3}{3} \right)^3 \left[ \left( \frac{p_3}{3} \right)^3 + \frac{v}{2} \right]} \right\}^{\frac{1}{3}}. \quad (8)$$

The expression for the dominant eigenvalue ( $\lambda_1$ ) of  $\mathbf{M}$  is then:

$$\lambda_1 = A + B + \frac{p_3}{3}. \quad (9)$$

And the expression for the subdominant eigenvalues ( $\lambda_2$ ) and ( $\lambda_3$ ) are complex conjugates:

$$\lambda_2 = -\frac{A+B}{2} + \frac{p_3}{3} + i \frac{A-B}{2} \sqrt{3}, \quad (10)$$

$$\lambda_3 = -\frac{A+B}{2} + \frac{p_3}{3} - i \frac{A-B}{2} \sqrt{3}. \quad (11)$$

In (10) and (11),  $i = \sqrt{-1}$ .

Further, using (3), the  $j$ th eigenvector ( $\mathbf{v}_j$ ) is expressed by:

$$\mathbf{v}_j = \begin{bmatrix} \frac{f\lambda_j}{\lambda_j+p_1f+\lambda_j^2} & \frac{fp_1}{\lambda_j+p_1f+\lambda_j^2} & \frac{\lambda_j^2}{\lambda_j+p_1f+\lambda_j^2} \end{bmatrix}. \quad (12)$$

### *Asymptotic Distributions of Eigenvalues*

We used (9), (10) and (11) in conjunction with the delta method (Samaniego 2014) to find the asymptotic distributions of each eigenvalue. We assumed that the two superparameter estimates each contain sampling standard error, and that this error has been estimated by field ecologists. We let  $\mathbf{S}$  be the 2x2 variance covariance matrix for the adult survival and recruitment estimates and acknowledge that the estimates can be either independent or correlated. Letting  $\Phi = \begin{bmatrix} v \\ p_3 \end{bmatrix}$ , under standard estimators of survival and recruitment such as maximum likelihood or moment estimators, the vector  $\hat{\Phi}$  of estimates has an asymptotic multivariate normal distribution:

$$\hat{\Phi} \xrightarrow{d} \text{MVN}(\Phi, \mathbf{S}). \quad (13)$$

Using the delta method, (7), (8), (9), and (13), the asymptotic distribution for the dominant eigenvalue ( $\lambda_1$ ) is normal:

$$\sqrt{n}(\hat{\lambda}_1 - \lambda_1) \xrightarrow{d} \text{N}\left(0, \left[\left(\frac{\partial}{\partial \Phi_j}\right)\left(A + B + \frac{p_3}{3}\right)\right]' \mathbf{S} \left[\left(\frac{\partial}{\partial \Phi_j}\right)\left(A + B + \frac{p_3}{3}\right)\right]\right) \quad (14)$$

where  $j = 1, 2$ . The resulting asymptotic variance in (14) will be a scalar, which can be used to construct a confidence interval around the dominant eigenvalue. R code necessary to numerically calculate the partial derivatives in (14) is furnished in the Supplemental Material. Using (7), (8), (10), and (13), the asymptotic distribution for the second eigenvalue ( $\lambda_2$ ) is multivariate normal:

$$\sqrt{n}(\hat{\lambda}_2 - \lambda_2) \xrightarrow{d} \text{MVN}(0, \mathbf{H}) \quad (15)$$



where  $\mathbf{H} =$

$$\left[ \left( \frac{\partial}{\partial \Phi_j} \right) \left( -\frac{A+B}{2} + \frac{p_3}{3} \right) \quad \left( \frac{\partial}{\partial \Phi_j} \right) \left( i \frac{A-B}{2} \sqrt{3} \right) \right]' \mathbf{S} \left[ \left( \frac{\partial}{\partial \Phi_j} \right) \left( -\frac{A+B}{2} + \frac{p_3}{3} \right) \quad \left( \frac{\partial}{\partial \Phi_j} \right) \left( i \frac{A-B}{2} \sqrt{3} \right) \right],$$

$j = 1, 2$  and  $i = \sqrt{-1}$ . In (15),  $\mathbf{H}$  is a  $2 \times 2$  variance covariance matrix, where the first diagonal represents the variance in the real dimension, and the second diagonal represents the variance in the imaginary dimension, and the off diagonals represent the covariance between the real and imaginary dimensions. The third root is the complex conjugate of the second root, so the asymptotic distribution for  $(\lambda_3)$  will be:

$$\sqrt{n}(\hat{\lambda}_3 - \lambda_3) \xrightarrow{d} \text{MVN}(0, \mathbf{K}) \quad (16)$$

where  $\mathbf{K} =$

$$\left[ \left( \frac{\partial}{\partial \Phi_j} \right) \left( -\frac{A+B}{2} + \frac{p_3}{3} \right) \quad - \left( \frac{\partial}{\partial \Phi_j} \right) \left( i \frac{A-B}{2} \sqrt{3} \right) \right]' \mathbf{S} \left[ \left( \frac{\partial}{\partial \Phi_j} \right) \left( -\frac{A+B}{2} + \frac{p_3}{3} \right) \quad - \left( \frac{\partial}{\partial \Phi_j} \right) \left( i \frac{A-B}{2} \sqrt{3} \right) \right],$$

$j = 1, 2$  and  $i = \sqrt{-1}$ . Also,  $\mathbf{K}$  is a  $2 \times 2$  variance covariance matrix, with the same interpretation as  $\mathbf{H}$ . The R code necessary to numerically calculate the partial derivatives in (15) and (16) is furnished in the Supplemental Material.

#### *Analytical Delta Method Confidence Interval Coverage Investigation*

We calculated the coverage of the analytical confidence intervals (based on two superparameters) for four realistic case studies, then compared the coverage to those obtained using a four parameter bootstrap method. The assumed distributions of the individualized vital rates and superparameters (Table 1) were selected to illustrate four ecological cases; (1) low adult survival, high recruitment, (2) high adult survival, low recruitment, (3) high adult survival and recruitment and (4) low adult survival and recruitment (Figures 2 – 5). The variance of each vital rate was assumed to be the distribution variance.

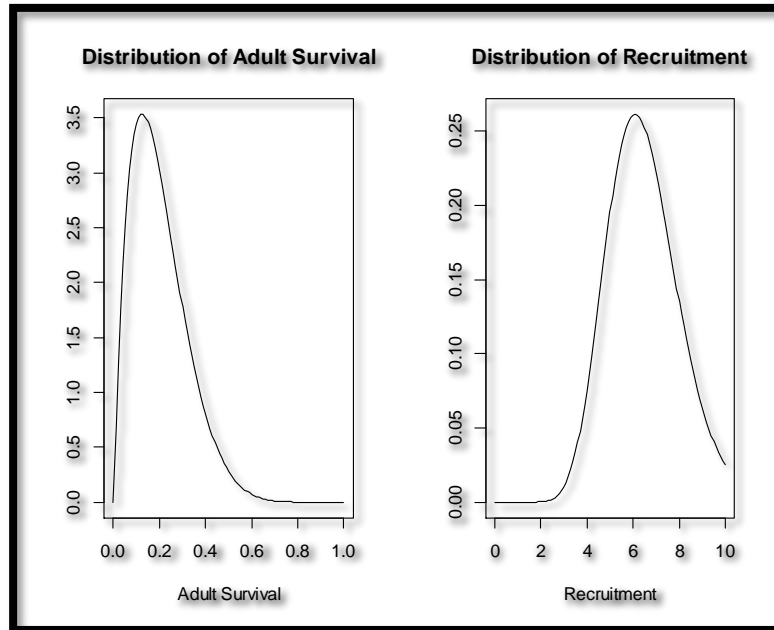
For each case, we used R to sample 1000 point estimates for each vital rate and superparameter. Using equations (1) and (3), four vital rate point estimates, and the “eigen” function in R, we calculated the resulting eigenvalues. After checking for normality, we calculated the 95% confidence limits for the bootstrap approach excluding the extreme most 2.5% observations.

Using equations (7), (8), (9), (10), and (11) we calculated the eigenvalues using the two superparameter point estimates. After checking for normality, we calculated the confidence limits for the eigenvalues using equations (16), (17), (18a), (18b), and (18c).

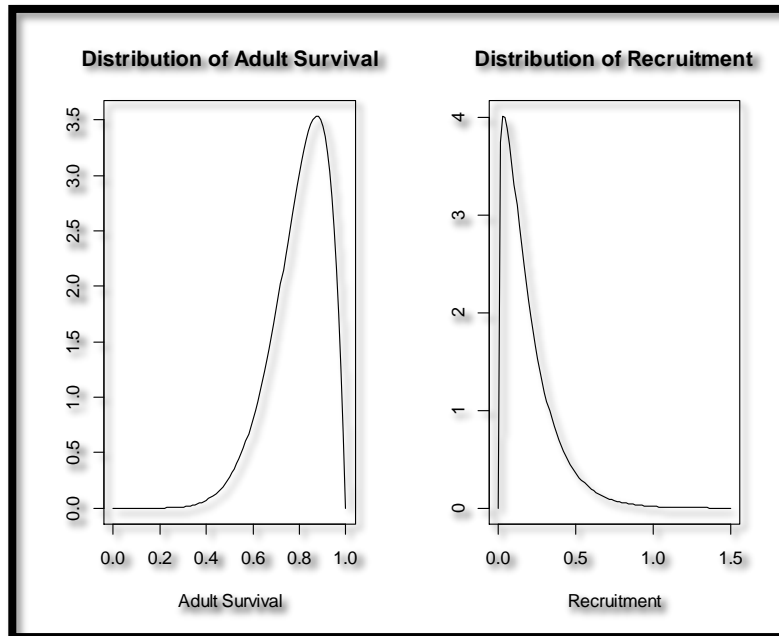
To assess confidence interval coverage, we determined if each of our calculated 95% confidence intervals contained the true eigenvalue. For each case, the true value of the parameter of interest was assumed to be the mean of the 1000 calculated eigenvalues. For both the bootstrap and superparameter approaches, we tabulated the percentage of 95% confidence intervals that captured the true value of the dominant eigenvalue. One simulation was selected at random to compare confidence interval precision amongst the two approaches.

Case	Juvenile Survival	Subadult Survival	Adult Survival	Adult Fecundity	Adult Recruitment
(1)	$p_1 \sim \text{Be}(8,2)$	$p_2 \sim \text{Be}(8,2)$	$p_3 \sim \text{Be}(2,8)$	$f \sim \text{N}(10,1)$	$v \sim \Gamma(17.07, 2.64)$
(2)	$p_1 \sim \text{Be}(2,8)$	$p_2 \sim \text{Be}(2,8)$	$p_3 \sim \text{Be}(8,2)$	$f \sim \text{N}(5,1)$	$v \sim \Gamma(1.24, 6.56)$
(3)	$p_1 \sim \text{Be}(8,2)$	$p_2 \sim \text{Be}(8,2)$	$p_3 \sim \text{Be}(8,2)$	$f \sim \text{N}(10,1)$	$v \sim \Gamma(17.07, 2.64)$
(4)	$p_1 \sim \text{Be}(2,8)$	$p_2 \sim \text{Be}(2,8)$	$p_3 \sim \text{Be}(2,8)$	$f \sim \text{N}(5,1)$	$v \sim \Gamma(1.24, 6.56)$

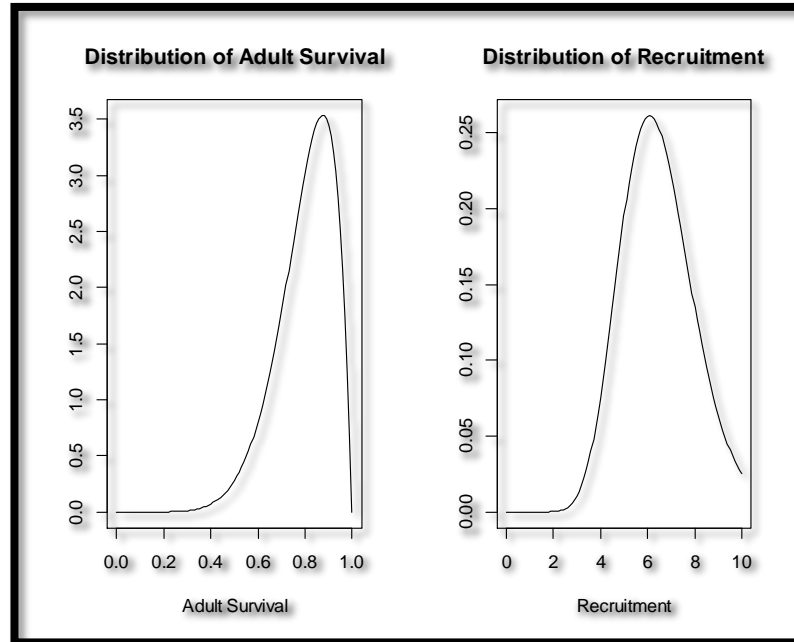
**Table 1. Distributions assumed for each vital rate. The superparameters are highlighted in gray. Case (1) represents low adult survival and high recruitment, case (2) represents high adult survival and low recruitment, case (3) represents high adult survival and recruitment, and case (4) represents low adult survival and recruitment.  $\text{Be}(a, b)$  represents the Beta distribution with shape parameter  $a$  and scale parameter  $b$ .  $\text{N}(c, d)$  represents the Normal distribution with mean  $c$  and standard deviation  $d$ .  $\Gamma(e, f)$  represents the Gamma distribution with shape parameter  $e$  and scale parameter  $f$ .**



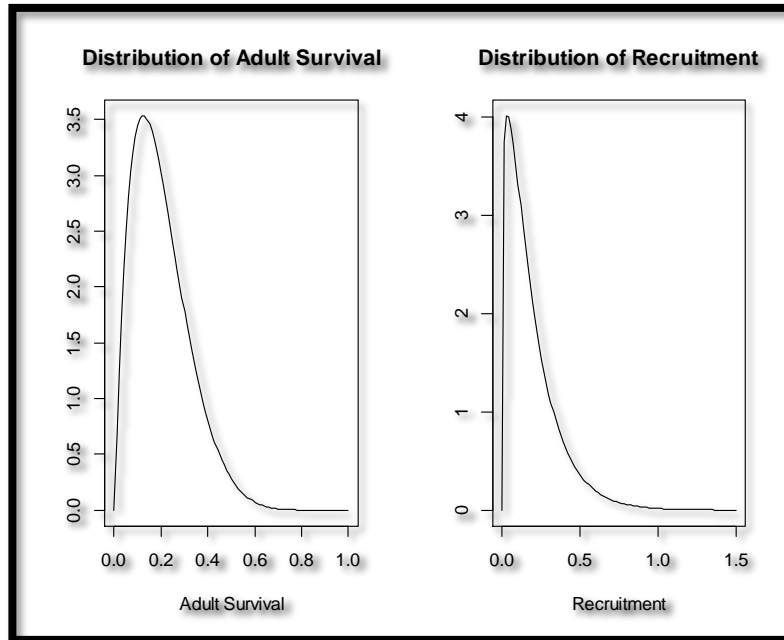
**Figure 2. Superparameter distributions for Case 1. In this case, we have low adult survival and high adult recruitment. We assume that  $p_3 \sim \text{Beta}(2, 8)$ , and  $v \sim \text{Gamma}(17.07, 2.64)$ . The variance of adult survival is 0.013 and the variance of recruitment is .0585**



**Figure 3. Superparameter distributions for Case 2. In this case, we have high adult survival and low adult recruitment. We assume that  $p_3 \sim \text{Beta}(8, 2)$ , and  $v \sim \text{Gamma}(1.24, 6.56)$ . The variance of adult survival is 0.013 and the variance of recruitment is 0.00035**



**Figure 4. Superparameter distributions for Case 3. In this case, we have high adult survival and high adult recruitment. We assume that  $p_3 \sim \text{Beta}(8, 2)$ , and  $v \sim \text{Gamma}(17.07, 2.64)$ . The variance of adult survival is 0.013 and the variance of recruitment is 0.056**



**Figure 5. Superparameter distributions for Case 4. In this case, we have low adult survival and low adult recruitment. We assume that  $p_3 \sim \text{Beta}(2, 8)$ , and  $v \sim \text{Gamma}(1.24, 6.56)$ . The variance of adult survival is 0.013 and the variance of recruitment is 0.0004.**

## Results

### Confidence Intervals for the Eigenvalues of $\mathbf{M}$

Using (13), the 100 (1 -  $\alpha$ ) % asymptotic confidence interval for  $\lambda_1$  is:

$$\hat{\lambda}_1 \pm z_{\frac{\alpha}{2}} \left\{ \sqrt{\left[ \left( \frac{\partial}{\partial \Phi_j} \right) \left( A + B + \frac{p_3}{3} \right) \right]' S \left[ \left( \frac{\partial}{\partial \Phi_j} \right) \left( A + B + \frac{p_3}{3} \right) \right]} \right\}, \quad (17)$$

where  $j = 1, 2$ . The expression in (17) represents a range of plausible dominant eigenvalue magnitudes supported by the data. Given estimates of adult survival, adult recruitment, their variances and covariance, the R code necessary to calculate (17) is in the Supplemental Material.

Similarly, using (14) and (15), the 100 (1 -  $\alpha$ ) % confidence interval for subdominant eigenvalue modulus ( $|\hat{\lambda}_2|$ ) is:

$$|\hat{\lambda}_2| \pm z_{\frac{\alpha}{2}} \sqrt{(h_{11}) + (h_{22}) - 2(h_{12})} \quad (18)$$

where  $h_{ab}$  represents the  $a$ th row and  $b$ th column of  $\mathbf{H}$ . The expression  $(h_{11}) + (h_{22}) - 2(h_{12})$  can be used as the variance of the subdominant eigenvalue modulus in the damping ratio. Given estimates of adult survival, adult recruitment, their variances, and covariance, R code to calculate (18) appears in the Supplemental Material.

The 100 (1 -  $\alpha$ )% confidence ellipse for the second eigenvalue of  $\mathbf{M}$  can be obtained from finding the squared Mahalanobis distance (Rencher 2002):

$$[\hat{\lambda}_2 - \lambda_2]' \mathbf{H}^{-1} [\hat{\lambda}_2 - \lambda_2] = s \quad (19)$$

In (19),  $\hat{\lambda}_2$  is the  $2 \times 1$  vector that represents the estimated real and imaginary components of the second eigenvalue, and  $\mathbf{H}$  is the variance covariance matrix from (15). For a level 100(1 -  $\alpha$ )% confidence region, the constant  $s$  in (19) is the critical value  $\chi_{\alpha}^2$  of a



chisquare(2) distribution (Rencher 2002). For example, if  $\alpha = .05$ ,  $s = 5.991$ , but other confidence levels can be used. When  $h_{11} > h_{22}$ , the semi major axis length for the ellipse given in (19) is

$$2\sqrt{5.991\xi_1}, \quad (20a)$$

where  $\xi_1$  and represent the dominant eigenvalue of  $\mathbf{H}$  (respectively). The semi minor axis length for the ellipse given in (19) is:

$$2\sqrt{5.991\xi_2} \quad (20b)$$

where  $\xi_2$  represents the subdominant eigenvalue of  $\mathbf{H}$  (respectively).

When  $h_{11} < h_{22}$ , half the semi major axis length for the ellipse given in (19) is

$$2\sqrt{5.991\xi_2}, \quad (21a)$$

while the half the semi minor axis length for the ellipse given in (19) is:

$$2\sqrt{5.991\xi_1}, \quad (21b)$$

The inclination of the ellipse in (19) is the angle between the unit dominant eigenvector of  $\mathbf{H}$  ( $\omega_1$ ) and the real axis (Rencher 2002). Letting  $a$  and  $b$  be first and second elements in  $\omega_1$ , the angle of the ellipse is

$$\theta = \arctan\left(\frac{b}{a}\right) \quad (22)$$

Similarly, the 100  $(1 - \alpha)$ % confidence ellipse for the third eigenvalue of  $\mathbf{M}$  can be obtained from finding the squared Mahalanobis distance (Rencher 2002):

$$[\hat{\lambda}_3 - \lambda_3]' \mathbf{K}^{-1} [\hat{\lambda}_3 - \lambda_3] = s \quad (23)$$

In (23),  $\hat{\lambda}_3$  is the  $2 \times 1$  vector that represents the estimated real and imaginary components of the third eigenvalue, and  $\mathbf{K}$  is the variance covariance matrix from (16). Equations (20a), (20b), (21a), (21b) and (22) can be used by calculating  $\xi_1$ ,  $\xi_2$ , and  $\omega_1$  from  $\mathbf{K}$ .

### *Damping Ratio*

The variation of the damping ratio can be obtained by modifying well known variation of a ratio formula (Elandt 1980, Stuart et al. 1998). Letting  $d$  represent the dominant eigenvalue,  $s$  represent the subdominant eigenvalue modulus,  $\sigma_d^2$  and  $\sigma_s^2$  represent the variance of the dominant eigenvalue and subdominant eigenvalue modulus (respectively),  $\mu_d$  and  $\mu_s$  represent the mean of the dominant eigenvalue and subdominant eigenvalue modulus (respectively), and  $\text{Cov}(d, s)$  represent the covariance between the dominant eigenvalue and the subdominant eigenvalue modulus, we found that the expression for the variance of the damping ratio is:

$$\text{Var}\left(\frac{d}{s}\right) \approx \left(\frac{\mu_d^2}{\mu_s^2}\right) \left(\frac{\sigma_d^2}{\mu_d^2}\right) - \left(\frac{2*\text{Cov}(d,s)}{\mu_d*\mu_s}\right) + \left(\frac{\sigma_s^2}{\mu_s^2}\right) \quad (24)$$

To calculate (24),  $\sigma_d^2$  is obtained from equation (14),  $\sigma_s^2$  is calculated as  $h_{11} + h_{22} - 2h_{12}$ ,  $\mu_d$  can be estimated using Equation (9),  $\mu_s$  can be estimated by finding the Euclidean distance between the components in Equation (10), and  $\text{Cov}(d, s)$  is  $h_{12}$ . R code to calculate (24) is in the Supplementary Material.

### *Analytical Delta Method Confidence Interval Coverage*

Table 2 shows the percentage of 95% confidence intervals that captured the true value of the eigenvalue of interest. Notice that in all case scenarios, the superparameter approach had the similar coverage performance as the bootstrap approach, and actually neared the nominal coverage better than the bootstrap approach. Only in case 4 did the analytical method perform below expected. Table 3 shows the width of the confidence intervals from a single exemplary simulation for each case. Notice that in all cases, the analytically derived confidence interval is less precise than the bootstrap intervals.

## Discussion

Population matrix models are central to contemporary wildlife management, as they enhance understanding of the dynamics, structure, and demographic consequences to changes within populations (Caswell 2001, Keyfitz et al. 2005). Population matrix models are built using vital rates that contain variation, and this variation should be reflected in matrix elasticities, eigenvalue variances, demographic inference and subsequent management guidance (Alvarez-Buylla et al. 1994, Devenish Nelson et al. 2010, Cáceres et al. 2013). For this reason, it is widely recognized that estimates of demographic parameters should be reported alongside their inherent uncertainties (Caswell et al. 1998, Devenish Nelson et al. 2010).

Methods to quantify dominant eigenvalue uncertainty using the delta method appear with qualifications in the literature. It has been shown that the delta method is known to yield asymptotic variance estimates that are too narrow (Picard et al. 2009), is unreliable unless sample size is high (Picard et al. 2009), is reliable only if errors on the vital rates remain small (Houllier et al. 1989, Alvarez-Buylla et al. 1993, 1994, Picard et al. 2009), or should be used with caution when the most sensitive entry to the dominant eigenvalue has a high coefficient of variation (Alvarez-Buylla et al. 1993, and Slatkin 1994). Although the delta method approach has been used in practice, sensitivity analysis techniques embedded in asymptotic

Case	Dominant Eigenvalue	
	Bootstrap	Analytical
(1)	100%	95%
(2)	100%	93%
(3)	100%	93%
(4)	100%	88%

**Table 2. The percentage of 95% confidence intervals that captured the true value of the dominant eigenvalue. The percentage displayed for each eigenvalue and each approach was based on the results from 1000 independent calculations. The cases are described in Figures 2-5.**

Case	Dominant Eigenvalue	
	Bootstrap	Analytical
(1)	1.58 2.18	1.37 2.19
(2)	0.68 1.27	-0.04 2.05
(3)	1.81 2.41	1.70 2.53
(4)	0.30 0.96	-1.55 2.54

**Table 3. Example of 95% confidence interval precision for one simulation selected at random. In each cell, the right number represents the lower confidence limit, and the left number represents the upper confidence limit. The headers indicate the parameter of interest and the method used. The cases are described in Figures 2-5.**

variance equations also pose problems. For example, implicit differentiation omits possible covariances between the vital rates, neglects sampling variance caused by spatial and temporal inhomogeneity of the population, and does not take into account possible biases in vital rates (Lande 1988).

Equations (5) - (11) suggest that all eigenvalues of a 3-stage population matrix, along with confidence limits for the eigenvalues, can be estimated using only two superparameters. Individually, these juvenile survival, subadult survival, and adult fecundity form a mathematically “onto” mapping, meaning that multiple combinations of these vital rates map to the same eigenvalue outcome (Gallian 2010). The “onto” nature further means that eigenvalue magnitude is blind to any specific factorization of that product. For this reason, the superparameter (product) is the important parameter, not the individualized vital rates (factors of the product). Equations (5) - (11) show that the relationship between adult survival and eigenvalue magnitude cannot be simplified without losing relationship information, thus adult survival is considered its own superparameter.

Although the literature currently favors the use of bootstrap approaches (Meyer et al. 2013), and cautions the use of the delta method approach for calculating confidence limits for dominant eigenvalues (Bullya- Alvarez et al 1994), our method provides point estimates and confidence limit coverage commensurate with bootstrap methods using less data. The bootstrap method requires the formal construction of a population matrix model, plus individualized estimation of juvenile survival, subadult survival, and adult fecundity. Our method does not mandate a population matrix model to be formally constructed, nor does it depend on individualized estimates of these three parameters. When our approach is used to calculate finite rate of growth, the damping ratio, and their confidence limits, the pooling of

vital rates from four individual vital rates into two superparameters will allow managers to obtain the same estimates, while potentially reducing the cost, time, and resources necessary to conduct data collection.

It has long been known that sampling younger age classes to obtain estimates of survivability can be easy in theory but difficult in practice (Aalto et al. 1980, Doak et al. 1994). Our method alleviates this issue completely, because estimating individualized vital rates for juvenile survival, subadult survival and adult fecundity is simply not necessary. In all four cases, our method adequately calculated eigenvalues and their confidence limits using estimates of adult recruitment, adult survival estimates (and their variances) only. These results can lessen the scientific impact on younger wildlife cohorts, as it is no longer necessary to visit, handle, transmitter, radio collar, pit tag (or any other method used to obtain lower age class survival probabilities) animals of smaller age or size classes. Field efforts aimed at obtaining estimates of adult survival, however, are still necessary.

Despite the adequate confidence interval coverages generated by the analytical method, the obvious savings in field resources by collecting data on two parameters instead of four, and the alleviation of sampling impact on the younger age (or stage classes), mathematical efficiencies can only go so far. Table 3 shows that the bootstrap approach generated narrower confidence intervals than the analytic approach for four simulations chosen at random. However, analysis of the formulas reveal that the precision of the analytical confidence interval will increase as the standard errors of the superparameters decreases. This result places the responsibility of confidence interval precision squarely on the shoulders of data collectors. Resource managers and field technicians should aim to generate the highest quality data possible, coupled with the most appropriate sampling

methodologies for the species at hand. The degree of precision of the confidence intervals is directly related to the standard errors of the estimates from the field. If resource managers can provide precise estimates of adult survivability and recruitment, the analytical results and computer programs reported here can provide the relevant eigenvalue statistics.

The natural question that follows from the results of our study is how to estimate adult recruitment? One method we suggest arises from the population matrix model itself. For instance, if cohort population numbers are known at two consecutive time periods (commensurate in time unit with the model assumptions), mathematical manipulation of the recursive matrix equations generates an expression that represents recruitment. Letting  $J_t$  represent female juvenile population at time  $t$ ,  $S_t$  represent female subadult population at time  $t$ , and  $A_t$  represent female adult population at time  $t$ , the recursive equations that specify population trajectory (Dennis 2013) are

$$J_{t+1} = fA_t \quad (25)$$

$$S_{t+1} = p_1J_t \quad (26)$$

$$A_{t+1} = p_2S_t + p_3A_t \quad (27)$$

Rearranging and substituting (25), (26), and (27), adult recruitment can be estimated as

$$v = \frac{J_{t+1}S_{t+1}A_{t+1} - p_3J_{t+1}S_{t+1}A_t}{(J_tS_tA_t)} \quad (28)$$

Other ways of estimating recruitment besides the relationship in (28) are possible, including adapting (28) to time series observations of age class abundances. Given the importance of the recruitment superparameter  $v$  to the eigenvalues, the estimation of  $v$  deserves further research attention. Regardless of the estimation process, the R code in the Supplementary Material can be used for the eigenvalue estimation given any appropriate estimates of recruitment and adult survival.



Provided managers can (1) defend that their wildlife systems adequately meet the 3-stage life history, (2) defend that the model assumptions are met, (3) precisely estimate adult survival and its standard error, and (4) precisely estimate adult recruitment and its standard error, the results of this research provide a new tool that can potentially reduce field cost and reduce scientific impact on sensitive cohorts, yet still obtain eigenvalues and their confidence intervals for management guidance and policy.

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**Supplemental Material: R Code**

```
#####  
  
#PARAMETERS FROM FIELD DATA#  
  
#####  
  
#Enter the recruitment rate  
  
recruitment=  
  
#Enter the adult survival rate  
  
adult.survival=  
  
#Enter the recruitment variance  
  
recruitment.variance=  
  
#Enter the adult survival variance  
  
adult.survival.variance=  
  
#Enter the covariation between recruitment and adult survival  
  
covariation.between.recruitment.and.survival=  
  
#####  
  
#THEORETICAL (DELTA METHOD) CODE - DO NOT MODIFY THIS CODE#  
  
#####  
  
#POPULATE THE SUPERPARAMETER VARIANCE COVARIANCE MATRIX
```

v.v.r.one.hat=recruitment.variance;v.v.r.two.hat=adult.survival.variance

sigma.corr=matrix(0,2,2);

sigma.corr[1,1]=v.v.r.one.hat;sigma.corr[2,2]=v.v.r.two.hat;

sigma.corr[1,2]=covariation.between.recruitment.and.survival;

sigma.corr[2,1]=covariation.between.recruitment.and.survival

#GETTING ROOT ONE AND DERIVATIVES FOR ROOT ONE CALCULATION

v.r.one.hat=recruitment

v.r.two.hat=adult.survival

vrhat1=v.r.one.hat

vrhat2=v.r.two.hat

A={(((vrhat2/3)^3)+(vrhat1/2)+(sqrt((2/3)\*((vrhat2/3)^3)\*(((vrhat2/3)^3)+(vrhat1/2))))})^(1/3)

B={(((vrhat2/3)^3)+(vrhat1/2)-(sqrt((2/3)\*((vrhat2/3)^3)\*(((vrhat2/3)^3)+(vrhat1/2))))})^(1/3)

ROOT.ONE=A+B+(v.r.two.hat/3)

two.real=-((A+B)/2)+(v.r.two.hat/3)

two.imaginary=((A-B)/2)\*sqrt(3)

three.real=-((A+B)/2)+(v.r.two.hat/3)

three.imaginary=(-1)\*((A-B)/2)\*sqrt(3)



```

deriv(~
(((vrhat2/3)^3)+(vrhat1/2)+(sqrt((2/3)*((vrhat2/3)^3)*(((vrhat2/3)^3)+(vrhat1/2))))^(1/3))+
(((vrhat2/3)^3)+(vrhat1/2)-
(sqrt((2/3)*((vrhat2/3)^3)*(((vrhat2/3)^3)+(vrhat1/2))))^(1/3))+vrhat2/3, "vrhat1").expr1 <-
vrhat2/3

.expr2 <- .expr1^3

.expr4 <- .expr2 + vrhat1/2

.expr6 <- 2/3 * .expr2

.expr7 <- .expr6 * .expr4

.expr8 <- sqrt(.expr7)

.expr9 <- .expr4 + .expr8

.expr10 <- 1/3

.expr12 <- .expr4 - .expr8

.expr16 <- .expr10 - 1

.expr18 <- 1/2

.expr22 <- 0.5 * (.expr6 * .expr18 * .expr7^-0.5)

.value <- .expr9^.expr10 + .expr12^.expr10 + .expr1

.grad <- array(0, c(length(.value), 1L), list(NULL, c("vrhat1")))

derivative.vrhat1= .expr9^.expr16 * (.expr10 * (.expr18 +

```

```
.expr22)) + .expr12^.expr16 * (.expr10 * (.expr18 - .expr22))
```

```
deriv(~
```

```
((((vrhat2/3)^3)+(vrhat1/2)+(sqrt((2/3)*((vrhat2/3)^3)*(((vrhat2/3)^3)+(vrhat1/2))))))^(1/3))+
```

```
((vrhat2/3)^3)+(vrhat1/2)-
```

```
(sqrt((2/3)*((vrhat2/3)^3)*(((vrhat2/3)^3)+(vrhat1/2))))^(1/3))+vrhat2/3, "vrhat2")
```

```
.expr1 <- vrhat2/3
```

```
.expr2 <- .expr1^3
```

```
.expr4 <- .expr2 + vrhat1/2
```

```
.expr5 <- 2/3
```

```
.expr6 <- .expr5 * .expr2
```

```
.expr7 <- .expr6 * .expr4
```

```
.expr8 <- sqrt(.expr7)
```

```
.expr9 <- .expr4 + .expr8
```

```
.expr10 <- 1/3
```

```
.expr12 <- .expr4 - .expr8
```

```
.expr16 <- .expr10 - 1
```

```
.expr20 <- 3 * (.expr10 * .expr1^2)
```

```
.expr27 <- 0.5 * ((.expr5 * .expr20 * .expr4 + .expr6 * .expr20) *
```

```
.expr7^-0.5)
```

```

.value <- .expr9^.expr10 + .expr12^.expr10 + .expr1

.grad <- array(0, c(length(.value), 1L), list(NULL, c("vrhat2")))

derivative.vrhat2=.expr9^.expr16 * (.expr10 * (.expr20 +
.expr27)) + .expr12^.expr16 * (.expr10 * (.expr20 - .expr27)) +
.expr10

#collect these derivatives into a vector

derivative.vector.root.one=matrix(0,2,1)

derivative.vector.root.one[1,1]=derivative.vrhat1

derivative.vector.root.one[2,1]=derivative.vrhat2

#GETTING THE DERIVATIVES FOR THE ROOT TWO CALCULATION

derivative.matrix=matrix(0,2,2)

#this is for the real part of the matrix (first column)

deriv(~ (-
1*(((vrhat2/3)^3)+(vrhat1/2)+(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+(vrhat1/2))))^(1/3)
+(((vrhat2/3)^3)+(vrhat1/2)-
(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+(vrhat1/2))))^(1/3))/2)+(vrhat2/3), "vrhat1")

.expr2 <- vrhat2/3

.expr3 <- .expr2^3

.expr5 <- .expr3 + vrhat1/2

```

```

.expr7 <- 2/3 * .expr3

.expr8 <- .expr7 * .expr5

.expr9 <- sqrt(.expr8)

.expr10 <- .expr5 + .expr9

.expr11 <- 1/3

.expr13 <- .expr5 - .expr9

.expr19 <- .expr11 - 1

.expr21 <- 1/2

.expr25 <- 0.5 * (.expr7 * .expr21 * .expr8^-0.5)

.value <- -1 * ((.expr10^.expr11 + .expr13^.expr11)/2) +

.expr2

.grad <- array(0, c(length(.value), 1L), list(NULL, c("vrhat1")))

derivative.matrix[1,1]= -((.expr10^.expr19 * (.expr11 * (.expr21 +
.expr25)) + .expr13^.expr19 * (.expr11 * (.expr21 - .expr25)))/2)

deriv(~ (-1*(((vrhat2/3)^3)+(vrhat1/2)+(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+
(vrhat1/2))))^(1/3)+(((vrhat2/3)^3)+(vrhat1/2)-(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+
(vrhat1/2))))^(1/3))/2)+(vrhat2/3), "vrhat2")

.expr2 <- vrhat2/3

```

```

.expr3 <- .expr2^3

.expr5 <- .expr3 + vrhat1/2

.expr6 <- 2/3

.expr7 <- .expr6 * .expr3

.expr8 <- .expr7 * .expr5

.expr9 <- sqrt(.expr8)

.expr10 <- .expr5 + .expr9

.expr11 <- 1/3

.expr13 <- .expr5 - .expr9

.expr19 <- .expr11 - 1

.expr23 <- 3 * (.expr11 * .expr2^2)

.expr30 <- 0.5 * ((.expr6 * .expr23 * .expr5 + .expr7 * .expr23) *
.expr8^-0.5)

.value <- -1 * ((.expr10^.expr11 + .expr13^.expr11)/2) +

.expr2

.grad <- array(0, c(length(.value), 1L), list(NULL, c("vrhat2")))

derivative.matrix[2,1]= .expr11 - (.expr10^.expr19 * (.expr11 *
(.expr23 + .expr30)) + .expr13^.expr19 * (.expr11 * (.expr23 -

```

```

.expr30))) / 2

#this is for the imaginary part of the matrix (second column)

deriv(~((sqrt(3))*((((vrhat2/3)^3)+(vrhat1/2)+(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+
(vrhat1/2))))))^(1/3)-(((vrhat2/3)^3)+(vrhat1/2)-(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+
(vrhat1/2))))^(1/3))/2), "vrhat1")

.expr1 <- as.complex(sqrt(3))

.expr3 <- as.complex((vrhat2/3)^3)

.expr5 <- as.complex(.expr3 + vrhat1/2)

.expr7 <- as.complex(2/3 * .expr3)

.expr8 <- as.complex(.expr7 * .expr5)

.expr9 <- as.complex(sqrt(.expr8))

.expr10 <- as.complex(.expr5 + .expr9)

.expr11 <- as.complex(1/3)

.expr13 <- as.complex(.expr5 - .expr9)

.expr18 <- as.complex(.expr11 - 1)

.expr20 <- as.complex(1/2)

.expr24 <- as.complex(0.5 * (.expr7 * .expr20 * .expr8^-0.5))

.value <- as.complex(.expr1 * ((.expr10^.expr11 - .expr13^.expr11)/2))

```

```

.grad <- array(0, c(length(.value), 1L), list(NULL, c("vrhat1")))

derivative.matrix[1,2]= as.complex(.expr1 * ((.expr10^.expr18 * (.expr11 *
(.expr20 + .expr24)) - .expr13^.expr18 * (.expr11 * (.expr20 -
.expr24))))/2))

deriv(~((sqrt(3))*((((vrhat2/3)^3)+(vrhat1/2)+(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+
(vrhat1/2))))))^(1/3)-(((vrhat2/3)^3)+(vrhat1/2)-(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+
(vrhat1/2))))^(1/3))/2),"vrhat2")

.expr1 <- sqrt(3)

.expr2 <- as.complex(vrhat2/3)

.expr3 <- as.complex(.expr2^3)

.expr5 <- as.complex(.expr3 + vrhat1/2)

.expr6 <- as.complex(2/3)

.expr7 <- as.complex(.expr6 * .expr3)

.expr8 <- as.complex(.expr7 * .expr5)

.expr9 <- as.complex(sqrt(.expr8))

.expr10 <- as.complex(.expr5 + .expr9)

.expr11 <- as.complex(1/3)

.expr13 <- as.complex(.expr5 - .expr9)

```

```

.expr18 <- as.complex(.expr11 - 1)

.expr22 <- as.complex(3 * (.expr11 * .expr2^2))

.expr29 <- as.complex(0.5 * ((.expr6 * .expr22 * .expr5 + .expr7 * .expr22) *
.expr8^-0.5))

.value <- .expr1 * ((.expr10^.expr11 - .expr13^.expr11)/2)

.grad <- array(0, c(length(.value), 1L), list(NULL, c("vrhat2")))

derivative.matrix[2,2]= .expr1 * ((.expr10^.expr18 * (.expr11 *
(.expr22 + .expr29)) - .expr13^.expr18 * (.expr11 * (.expr22 -
.expr29)))/2)

asymptotic.variance.root.one.corr=t(derivative.vector.root.one)%*%sigma.corr%*%(derivativ
e.vector.root.one)

g=Re(derivative.matrix)

asymptotic.variance.root.two.corr=g%*%(sigma.corr)%*%t(g)

#CONFIDENCE INTERVAL FOR ROOT ONE

upper1=ROOT.ONE+(1.96)*sqrt(asymptotic.variance.root.one.corr)

lower1=ROOT.ONE-(1.96)*sqrt(asymptotic.variance.root.one.corr)

#CONFIDENCE INTERVAL FOR MODULUS OF ROOT TWO

mod=sqrt(two.real^2+two.imaginary^2)

```



```

asymptotic.modulus.var=Re(asymptotic.variance.root.two.corr[1,1]+
asymptotic.variance.root.two.corr[2,2]-asymptotic.variance.root.two.corr[1,2]-
asymptotic.variance.root.two.corr[2,1])
uppermod=mod+(1.96)*sqrt(asymptotic.modulus.var)
lowermod=mod-(1.96)*sqrt(asymptotic.modulus.var)
#CONFIDENCE ELLIPSE FOR ROOT TWO
if (Re(asymptotic.variance.root.two.corr[1,1]) >=
Re(asymptotic.variance.root.two.corr[2,2])){
eigen(asymptotic.variance.root.two.corr)
e1=eigen(asymptotic.variance.root.two.corr)$values[1]
v1=eigen(asymptotic.variance.root.two.corr)$vectors[,1]
e2=eigen(asymptotic.variance.root.two.corr)$values[2]
v2=eigen(asymptotic.variance.root.two.corr)$vectors[,2]
major.axis=Re(sqrt(5.991*e1))
if (e2 < 0){
e2=(-1*e2)
}
minor.axis=Re(sqrt(5.991*e2))

```

```

} else {

eigen(asymptotic.variance.root.two.corr)

e1=eigen(asymptotic.variance.root.two.corr)$values[1]

v1=eigen(asymptotic.variance.root.two.corr)$vectors[,1]

e2=eigen(asymptotic.variance.root.two.corr)$values[2]

v2=eigen(asymptotic.variance.root.two.corr)$vectors[,2]

minor.axis=Re(sqrt(5.991*e1))

if (e2 < 0){

e2=(-1*e2)

}

major.axis=Re(sqrt(5.991*e2))

#this is the angle of inclination for the second root

angle=atan(v1[2]/v1[1])

#THIS IS FOR THE THIRD ROOT

derivative.matrixI=matrix(0,2,2)

#this is for the real part of the matrix (first column)

deriv(~ (-1*(((vrhat2/3)^3)+(vrhat1/2)+(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+

(vrhat1/2))))^(1/3)+(((vrhat2/3)^3)+(vrhat1/2)-(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+

```

```

(vrhat1/2))))))^(1/3))/2)))+(vrhat2/3), "vrhat1")

.expr2 <- vrhat2/3

.expr3 <- .expr2^3

.expr5 <- .expr3 + vrhat1/2

.expr7 <- 2/3 * .expr3

.expr8 <- .expr7 * .expr5

.expr9 <- sqrt(.expr8)

.expr10 <- .expr5 + .expr9

.expr11 <- 1/3

.expr13 <- .expr5 - .expr9

.expr19 <- .expr11 - 1

.expr21 <- 1/2

.expr25 <- 0.5 * (.expr7 * .expr21 * .expr8^-0.5)

.value <- -1 * ((.expr10^.expr11 + .expr13^.expr11)/2) +

.expr2

.grad <- array(0, c(length(.value), 1L), list(NULL, c("vrhat1")))

derivative.matrixI[1,1]= -((.expr10^.expr19 * (.expr11 * (.expr21 +

.expr25)) + .expr13^.expr19 * (.expr11 * (.expr21 - .expr25)))/2)

```

```
deriv(~ (-1*(((vrhat2/3)^3)+(vrhat1/2)+(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+
(vrhat1/2))))^(1/3)+(((vrhat2/3)^3)+(vrhat1/2)-(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+
(vrhat1/2))))^(1/3))/2)+(vrhat2/3), "vrhat2")
```

```
.expr2 <- vrhat2/3
```

```
.expr3 <- .expr2^3
```

```
.expr5 <- .expr3 + vrhat1/2
```

```
.expr6 <- 2/3
```

```
.expr7 <- .expr6 * .expr3
```

```
.expr8 <- .expr7 * .expr5
```

```
.expr9 <- sqrt(.expr8)
```

```
.expr10 <- .expr5 + .expr9
```

```
.expr11 <- 1/3
```

```
.expr13 <- .expr5 - .expr9
```

```
.expr19 <- .expr11 - 1
```

```
.expr23 <- 3 * (.expr11 * .expr2^2)
```

```
.expr30 <- 0.5 * ((.expr6 * .expr23 * .expr5 + .expr7 * .expr23) *
```

```
.expr8^-0.5)
```

```
.value <- -1 * ((.expr10^.expr11 + .expr13^.expr11)/2) +
```

```

.expr2

.grad <- array(0, c(length(.value), 1L), list(NULL, c("vrhat2")))

derivative.matrixI[2,1]= .expr11 - (.expr10^.expr19 * (.expr11 *
(.expr23 + .expr30)) + .expr13^.expr19 * (.expr11 * (.expr23 -
.expr30)))/2

#this is for the imaginary part of the matrix (second column)

deriv(~(-
1)*((sqrt(3))*((((vrhat2/3)^3)+(vrhat1/2)+(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+
(vrhat1/2))))))^(1/3)-((((vrhat2/3)^3)+(vrhat1/2)-(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+
(vrhat1/2))))))^(1/3))/2), "vrhat1")

.expr1 <- -1

.expr2 <- sqrt(3)

.expr4 <- (vrhat2/3)^3

.expr6 <- .expr4 + vrhat1/2

.expr8 <- 2/3 * .expr4

.expr9 <- .expr8 * .expr6

.expr10 <- sqrt(.expr9)

.expr11 <- .expr6 + .expr10

```

```

.expr12 <- 1/3

.expr14 <- .expr6 - .expr10

.expr20 <- .expr12 - 1

.expr22 <- 1/2

.expr26 <- 0.5 * (.expr8 * .expr22 * .expr9^-0.5)

.value <- .expr1 * (.expr2 * ((.expr11^.expr12 - .expr14^.expr12)/2))

.grad <- array(0, c(length(.value), 1L), list(NULL, c("vrhat1")))

derivative.matrixI[1,2]= .expr1 * (.expr2 * ((.expr11^.expr20 *
(.expr12 * (.expr22 + .expr26)) - .expr14^.expr20 * (.expr12 *
(.expr22 - .expr26))))/2))

deriv(~(-
1)*((sqrt(3))*(((vrhat2/3)^3)+(vrhat1/2)+(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+
(vrhat1/2))))))^(1/3)-(((vrhat2/3)^3)+(vrhat1/2)-(sqrt((2/3)*((vrhat2/3)^3)*((vrhat2/3)^3)+
(vrhat1/2))))^(1/3))/2),"vrhat2")

.expr1 <- -1

.expr2 <- sqrt(3)

.expr3 <- vrhat2/3

.expr4 <- .expr3^3

```

```

.expr6 <- .expr4 + vrhat1/2

.expr7 <- 2/3

.expr8 <- .expr7 * .expr4

.expr9 <- .expr8 * .expr6

.expr10 <- sqrt(.expr9)

.expr11 <- .expr6 + .expr10

.expr12 <- 1/3

.expr14 <- .expr6 - .expr10

.expr20 <- .expr12 - 1

.expr24 <- 3 * (.expr12 * .expr3^2)

.expr31 <- 0.5 * ((.expr7 * .expr24 * .expr6 + .expr8 * .expr24) *
.expr9^-0.5)

.value <- .expr1 * (.expr2 * ((.expr11^.expr12 - .expr14^.expr12)/2))

.grad <- array(0, c(length(.value), 1L), list(NULL, c("vrhat2")))

derivative.matrixI[2,2]= .expr1 * (.expr2 * ((.expr11^.expr20 *
(.expr12 * (.expr24 + .expr31)) - .expr14^.expr20 * (.expr12 *
(.expr24 - .expr31))))/2))

```

```
asymptotic.variance.root.one.corr=t(derivative.vector.root.one)% **%sigma.corr%**%(derivativ
e.vector.root.one)
```

```
gI=derivative.matrixI
```

```
asymptotic.variance.root.two.corr=gI%** (sigma.corr)% **%t(gI)
```

```
#CONFIDENCE ELLIPSE FOR ROOT THREE
```

```
if (Re(asymptotic.variance.root.two.corr[1,1]) >=
```

```
Re(asymptotic.variance.root.two.corr[2,2])){
```

```
eigen(asymptotic.variance.root.two.corr)
```

```
e1=eigen(asymptotic.variance.root.two.corr)$values[1]
```

```
v1=eigen(asymptotic.variance.root.two.corr)$vectors[,1]
```

```
e2=eigen(asymptotic.variance.root.two.corr)$values[2]
```

```
v2=eigen(asymptotic.variance.root.two.corr)$vectors[,2]
```

```
major.axis3=Re(sqrt(5.991*e1))
```

```
if (e2 < 0){
```

```
e2=(-1*e2)
```

```
}
```

```
minor.axis3=Re(sqrt(5.991*e2))
```

```
} else {
```

```
eigen(asymptotic.variance.root.two.corr)
```



```

e1=eigen(asymptotic.variance.root.two.corr)$values[1]

v1=eigen(asymptotic.variance.root.two.corr)$vectors[,1]

e2=eigen(asymptotic.variance.root.two.corr)$values[2]

v2=eigen(asymptotic.variance.root.two.corr)$vectors[,2]

minor.axis3=Re(sqrt(5.991*e1))

if (e2 < 0){

e2=(-1*e2)

}

major.axis3=Re(sqrt(5.991*e2))

#this is the angle of inclination for the third root

angle3=atan(v1[2]/v1[1])

#Variance of damping ratio

mds=ROOT.ONE^2

mss=mod^2

md=ROOT.ONE

ms=mod

sds=asymptotic.variance.root.one.corr

sss=asymptotic.modulus.var

```

covds=asymptotic.variance.root.two.corr[1,2]

var.d.r=Re((mds/mss)\*((sds/mds)-((2\*(covds))/(md\*ms))+(sss/mss)))

LOWER1=lower1;UPPER1=upper1;MOD=mod

LOWERM0D=lowermod;UPPERM0D=uppermod

TWOREAL=two.real;TWOIMAGINARY=two.imaginary

MAJOR.AXIS=2\*major.axis;MINOR.AXIS=2\*minor.axis

ANGLE=angle

THREEREAL=three.real;THREEIMAGINARY=three.imaginary

MAJOR.AXIS3=2\*major.axis3;MINOR.AXIS3=2\*minor.axis3

ANGLE3=angle3

DAMPING.RATIO=ROOT.ONE/mod;VARIANCE.DAMPING.RATIO=var.d.r

#####

#HERE ARE YOUR RESULTS#

#####

#Dominant Eigenvalue

ROOT.ONE

#Lower 95% confidence limit for Dominant Eigenvalue

LOWER1

#Upper 95% confidence limit for Dominant Eigenvalue

UPPER1

#Subdominant Eigenvalue Modulus

MOD

#Lower 95% confidence limit for Subdominant Eigenvalue Modulus

LOWERMOD

#Upper 95% confidence limit for Subdominant Eigenvalue Modulus

UPPERMOD

#SECOND ROOT Eigenvalue Real

TWOREAL

#SECOND ROOT Eigenvalue Imaginary

TWOIMAGINARY

#95% SECOND Eigenvalue Ellipse Major Axis

#(Listed as Real dimension, Imaginary dimension)

MAJOR.AXIS

#95% SECOND Eigenvalue Ellipse Minor Axis

#(Listed as Real dimension, Imaginary dimension)

MINOR.AXIS

#Angle of inclination of SECOND Eigenvalue Ellipse (in radians, from the real axis)

ANGLE

#THIRD ROOT Eigenvalue Real

THREEREAL

#THIRD ROOT Eigenvalue Imaginary

THREEIMAGINARY

#95% THIRD Eigenvalue Ellipse Major Axis (Listed as Real dimension, Imaginary dimension)

MAJOR.AXIS3

#95% THIRD Eigenvalue Ellipse Minor Axis

#(Listed as Real dimension, Imaginary dimension)

MINOR.AXIS3

#Angle of inclination of THIRD Eigenvalue Ellipse (in radians, from the real axis)

ANGLE3

#Damping Ratio

DAMPING.RATIO

#Variance of the Damping Ratio

VARIANCE.DAMPING.RATIO