

Before-After Control-Impact (BACI) Power Analysis For Several Related Populations

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Summary

Effectiveness monitoring in the Columbia Basin has precipitated the need for power analysis tools used to design monitoring programs that can detect important changes in salmon survival. One design considered for effectiveness monitoring is the before-after-control-impact (BACI) design in which there is a Before period of no treatment followed by an After period where some populations are treated and others are not. An *a priori* power analysis was developed for this design using idealized assumptions including (among others) known variance-covariance matrix and measurement error variance and no serial dependence of survival observations. The resulting power analysis yields an estimate of the minimum survival change that can be reasonably detected in an effectiveness monitoring program. The methods were applied using input parameters based on 1992-2006 par-to-smolt survival data from 30 populations in the Snake River Spring Summer chinook Evolutionarily Significant Unit. It was found that detecting a survival change in the range of 1-5% was impossible even when 20 populations were employed over 30 years (assuming equal numbers of treatment and control groups and equal numbers of Before and After years). Survival changes of 30% or more were detectable with one treatment and one control population over 20 years or more. As the number of years and number of populations increase, power also increases and smaller changes in survival may be detected. With the possible exception of a correlation near zero, power to detect significant changes in survival will tend to be greater as correlation between populations increases.

Introduction

Currently there are many watershed projects underway in the Columbia Basin to determine the effects of various management actions on salmon survival. For example, there are a series of intensively monitored watersheds (IMWs) established for the purpose of better understanding how salmon respond to approaches to restore habitat. These projects stand the best chance to identify the effectiveness of restoration and other management actions if they are run as experiments with a planned design. To design such an experiment, it is useful to conduct an *a priori* power analysis that will tell the planners how long the experiment should run and how many populations should be used to detect a significant survival change. The framework for the power analysis given here, although developed with salmon in mind, fits into the framework of the Before-After-Control-Impact (BACI) experiment. Such BACI-type experiments find application beyond Columbia River salmon survival (Osenberg and Schmitt 1996).

The BACI-type experiment analyzed here is aimed at estimating a common change in survival for several populations. The experiment includes a Before period where all populations receive no treatment followed by an After period where only the treatment populations receive treatment. This is a generalization of the BACI-type experiment where the control population and impact population are sampled one time before and one time after the treatment (Green 1979, Osenberg and Schmitt 1996). It is assumed that the variance-covariance matrix is known, measurement error variance is known, and, in the absence of treatment, all populations have a common mean log survival (Table 1). These are idealized assumptions that may not hold in practice. However, the analysis is useful because it will yield an estimate of the maximum power one can reasonably expect from a BACI-type experiment, and the minimum changes in survival that may be reliably detected.

The main goal of this work is to derive the power of a BACI experiment aimed at estimating a treatment effect on survival and demonstrate its use in an application to salmon survival. This goal is accomplished by describing the experiment in a statistically rigorous way: setting up a likelihood function and using maximum likelihood theory to derive an estimator of the treatment effect and its variance. From the asymptotic theory, it is then possible to estimate power to detect a significant change in survival. Power is the probability of rejecting the null hypothesis of “no treatment effect.” The website www.onefishtwofish.net contains a web-based tool that implements this power analysis with the added assumptions that the variances in $\log(\text{survival})$ are equal for all populations and the correlations in $\log(\text{survival})$ are equal for each pair of populations, resulting in an intraclass covariance matrix (Fisher 1925). The R code for implementing this power analysis may be found in Appendix A (R Development Core Team 2009). The use of this code is demonstrated in an application to salmon survival using a range of assumptions about the design and the joint distribution of $\log(\text{survival})$ for several populations.

Table 1. Assumptions used in power analysis.¹

A1	The observations of $\log(\text{survival})$ follow a multivariate normal distribution.
A2	There is no serial dependence.
A3	All populations have a common mean $\log(\text{survival})$ before treatment.
A4	After treatment, the control populations continue to have the same common mean as exhibited in the Before years, and the treatment populations also have a common mean, but shifted by an amount (the effect size) that is the same for all treatment populations.
A5	The measurement errors in $\log(\text{survival})$ follow a multivariate normal distribution and the errors are independent of the error due to actual year-to-year environmental variability.
A6	The estimator of the treatment effect is a maximum likelihood estimate.
A7	The variance-covariance matrix describing the year-to-year variability in $\log(\text{survival})$ is known.

¹These are assumptions for an idealized experiment. For a specific application, a more accurate experimental design may require changing these assumptions and the underlying equations. Therefore this analysis should be treated as a rough guide to power.

Methods

To derive the estimator and its variance for the power analysis, maximum likelihood is used (Mood et al. 1974). It is assumed that mean $\log(\text{survival})$ before treatment, denoted by μ_1 , is the same for each population. After treatment, the mean $\log(\text{survival})$ of the treatment populations shifts by the amount δ to the value of μ_2 , while the control populations continue to have a mean $\log(\text{survival})$ of μ_1 . The goal is to obtain the maximum likelihood estimator (MLE) of δ and its variance. It is assumed that year-to-year random fluctuations in $\log(\text{survival})$ and measurement error follow multivariate normal distributions. Thus the total variance matrix is $\Sigma = \Sigma_y + \Sigma_m$, where Σ_y is the variance-covariance matrix of true $\log(\text{survival})$, and Σ_m represents the variance-covariance matrix of the measurement error of $\log(\text{survival})$.

Under these assumptions, the log-likelihood function may be written as

$$l(\boldsymbol{\mu}) = C - (1/2) \sum_{t=1}^{n_1} (\mathbf{x}_t - [\mathbf{E} \quad \mathbf{0}] \boldsymbol{\mu})' \Sigma^{-1} (\mathbf{x}_t - [\mathbf{E} \quad \mathbf{0}] \boldsymbol{\mu}) - (1/2) \sum_{t=n_1+1}^n (\mathbf{x}_t - \begin{bmatrix} \mathbf{E}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{E}_2 \end{bmatrix} \boldsymbol{\mu})' \Sigma^{-1} (\mathbf{x}_t - \begin{bmatrix} \mathbf{E}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{E}_2 \end{bmatrix} \boldsymbol{\mu}) \quad (1)$$

where $l(\boldsymbol{\mu})$ is the log-likelihood function with vector argument $\boldsymbol{\mu} = [\mu_1 \quad \mu_2]'$ with entries representing the control and treatment means, respectively; C is a constant that does not

depend on the parameters; n_1 is the number of years prior to treatment; n is the total number of years of the experiment; \mathbf{x}_t is a k -vector of observed survivals in year t ; k is the number of populations (treatment + control) used in the experiment; \mathbf{E} is a k -vector of 1s; \mathbf{E}_1 is a k_1 -vector of 1s, where k_1 represents the number of control populations; \mathbf{E}_2 is a k_2 -vector of 1s, where k_2 represents the number of treatment populations. The vector \mathbf{x}_t is arranged so that the k_1 control populations precede the k_2 treatment populations.

To obtain the maximum likelihood estimate of the treatment effect, the first partial derivatives are arranged in a vector called the gradient and set to zero. The gradient vector is given by

$$\nabla l(\boldsymbol{\mu}) = - \left(n_1 [\mathbf{E} \ \mathbf{0}]' \Sigma^{-1} [\mathbf{E} \ \mathbf{0}] + n_2 \begin{bmatrix} \mathbf{E}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{E}_2 \end{bmatrix}' \Sigma^{-1} \begin{bmatrix} \mathbf{E}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{E}_2 \end{bmatrix} \right) \boldsymbol{\mu} + n_1 [\mathbf{E} \ \mathbf{0}]' \Sigma^{-1} \bar{\mathbf{x}}_1 + n_2 \begin{bmatrix} \mathbf{E}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{E}_2 \end{bmatrix}' \Sigma^{-1} \bar{\mathbf{x}}_2 \quad (2)$$

where $\bar{\mathbf{x}}_1$ represents the sample mean of log(survival) in the Before period, and $\bar{\mathbf{x}}_2$ represents the sample mean of log(survival) observation in the After period. To estimate the treatment effect, this equation is set to zero and solved for the maximum likelihood estimate $\hat{\boldsymbol{\mu}}$. The MLE of the treatment effect is $\hat{\boldsymbol{\delta}} = [-1 \ 1] \hat{\boldsymbol{\mu}}$, which yields

$$\hat{\boldsymbol{\delta}} = \frac{(\mathbf{E}' \Sigma^{-1} \mathbf{E}) \begin{pmatrix} \begin{bmatrix} \mathbf{0} \\ \mathbf{E}_2 \end{bmatrix}' \Sigma^{-1} \bar{\mathbf{x}}_2 \\ \begin{bmatrix} \mathbf{0} \\ \mathbf{E}_2 \end{bmatrix}' \Sigma^{-1} \mathbf{E} \end{pmatrix} - \begin{pmatrix} \begin{bmatrix} \mathbf{0} \\ \mathbf{E}_2 \end{bmatrix}' \Sigma^{-1} \mathbf{E} \end{pmatrix} (\mathbf{E}' \Sigma^{-1} \bar{\mathbf{x}})}{(\mathbf{E}' \Sigma^{-1} \mathbf{E}) \begin{pmatrix} \begin{bmatrix} \mathbf{0} \\ \mathbf{E}_2 \end{bmatrix}' \Sigma^{-1} \begin{bmatrix} \mathbf{0} \\ \mathbf{E}_2 \end{bmatrix} \\ \begin{bmatrix} \mathbf{0} \\ \mathbf{E}_2 \end{bmatrix}' \Sigma^{-1} \mathbf{E} \end{pmatrix} - \left(\frac{n_2}{n} \right) \left(\begin{bmatrix} \mathbf{0} \\ \mathbf{E}_2 \end{bmatrix}' \Sigma^{-1} \mathbf{E} \right)^2} \quad (3)$$

where $\bar{\mathbf{x}}$ represents the vector of sample means over the entire duration of the experiment.

To determine the variance of the estimators, the information matrix is derived. By maximum likelihood theory, the variance matrix of the estimators is the negative inverse information matrix, which is the matrix of second partial derivatives of the log-likelihood function. The information matrix is

$$\mathbf{I}(\boldsymbol{\mu}) = - \left(n_1 [\mathbf{E} \ \mathbf{0}]' \Sigma^{-1} [\mathbf{E} \ \mathbf{0}] + n_2 \begin{bmatrix} \mathbf{E}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{E}_2 \end{bmatrix}' \Sigma^{-1} \begin{bmatrix} \mathbf{E}_1 & \mathbf{0} \\ \mathbf{0} & \mathbf{E}_2 \end{bmatrix} \right) \quad (4)$$

Notice that since the variance-covariance matrix is assumed known, the information matrix does not depend on the parameters $\boldsymbol{\mu}$ or the log(survival) observations: it is a function of the variance-covariance matrix and the number of Before and After years and the number of treatment and control populations. For convenience, the matrix $\boldsymbol{\Sigma}^{-1}$ is expressed as a partitioned matrix containing four submatrices as follows:

$$\boldsymbol{\Sigma}^{-1} = \begin{bmatrix} \boldsymbol{\Sigma}_{11}^{-1} & \boldsymbol{\Sigma}_{12}^{-1} \\ \boldsymbol{\Sigma}_{21}^{-1} & \boldsymbol{\Sigma}_{22}^{-1} \end{bmatrix} \quad (5)$$

where $\boldsymbol{\Sigma}_{11}^{-1}$ is a $k_1 \times k_1$ matrix representing the upper left-hand corner entries of $\boldsymbol{\Sigma}^{-1}$, $\boldsymbol{\Sigma}_{12}^{-1}$ is the $k_1 \times k_2$ matrix representing the upper right-hand corner entries, $\boldsymbol{\Sigma}_{21}^{-1}$ is a $k_2 \times k_1$ matrix representing the lower left-hand corner entries, and $\boldsymbol{\Sigma}_{22}^{-1}$ is a $k_2 \times k_2$ matrix representing the lower right-hand entries of $\boldsymbol{\Sigma}^{-1}$.

The variance matrix is calculated as the negative inverse of the information matrix, which yields

$$\text{var}(\hat{\boldsymbol{\mu}}) = \frac{\begin{bmatrix} n_2 \mathbf{E}'_2 \boldsymbol{\Sigma}_{22}^{-1} \mathbf{E}_2 & -n_2 \mathbf{E}'_2 \boldsymbol{\Sigma}_{21}^{-1} \mathbf{E}_1 \\ -n_2 \mathbf{E}'_1 \boldsymbol{\Sigma}_{12}^{-1} \mathbf{E}_2 & n_1 \mathbf{E}'_1 \boldsymbol{\Sigma}^{-1} \mathbf{E} + n_2 \mathbf{E}'_1 \boldsymbol{\Sigma}_{11}^{-1} \mathbf{E}_1 \end{bmatrix}}{(n_1 \mathbf{E}'_1 \boldsymbol{\Sigma}^{-1} \mathbf{E} + n_2 \mathbf{E}'_1 \boldsymbol{\Sigma}_{11}^{-1} \mathbf{E}_1) n_2 \mathbf{E}'_2 \boldsymbol{\Sigma}_{22}^{-1} \mathbf{E}_2 - n_2^2 (\mathbf{E}'_1 \boldsymbol{\Sigma}_{12}^{-1} \mathbf{E}_2)^2} \quad (6)$$

Since the treatment effect is a simple function of the control and treatment means, namely, $\hat{\delta} = [-1 \ 1] \hat{\boldsymbol{\mu}}$, the following identity may be used:

$$\text{var}(\hat{\delta}) = [-1 \ 1] \text{var}(\hat{\boldsymbol{\mu}}) \begin{bmatrix} -1 \\ 1 \end{bmatrix} = \frac{(n_1 + n_2) \mathbf{E}' \boldsymbol{\Sigma}^{-1} \mathbf{E}}{(n_1 \mathbf{E}'_1 \boldsymbol{\Sigma}^{-1} \mathbf{E} + n_2 \mathbf{E}'_1 \boldsymbol{\Sigma}_{11}^{-1} \mathbf{E}_1) n_2 \mathbf{E}'_2 \boldsymbol{\Sigma}_{22}^{-1} \mathbf{E}_2 - n_2^2 (\mathbf{E}'_1 \boldsymbol{\Sigma}_{12}^{-1} \mathbf{E}_2)^2} \quad (7)$$

This formula shows how the variance of the treatment effect estimate depends on the values of k_1, k_2, n_1, n_2 and the entries of the variance-covariance matrix $\boldsymbol{\Sigma}$. Using this formula, it is then simple to calculate the standard error of the treatment effect estimate,

$$\text{se}(\hat{\delta}) = \sqrt{\text{var}(\hat{\delta})} \quad (8)$$

The coefficient of variation is

$$CV(\hat{\delta}) = se(\hat{\delta}) / \delta \quad (9)$$

The standard error of the treatment effect is now used to derive power: the probability of rejecting the null hypothesis of “no treatment” effect when the actual treatment effect is δ . Power is a function of the true treatment effect, the probability of a type I error (usually called the significance level and denoted by α), and the standard error of the estimator. By maximum likelihood theory, the estimator of the treatment effect is asymptotically normally distributed, but in this case, the estimator is normally distributed regardless of the sample size. This occurs because the variance-covariance matrix is assumed known and the estimator is a linear combination of random variables x_t that are known to follow a multivariate normal distribution. A linear combination of normal random variables is also normally distributed. Therefore, $\hat{\delta}$ is normally distributed. Thus, power is

$$\Pi(\delta) = \Phi(-z_{\alpha/2} - \delta / se(\hat{\delta})) + 1 - \Phi(z_{\alpha/2} - \delta / se(\hat{\delta})) \quad (10)$$

where $\Phi(z)$ is the cumulative distribution function of the standard normal random variable, and $z_{\alpha/2}$ is the critical value such that $\alpha/2$ probability lies to the right of the value $z_{\alpha/2}$ in a standard normal distribution. For example, when $\alpha = 0.05$, the critical value is equal to 1.96. Experimenters often choose a design such that power of 0.8 is achieved.

Application

To determine the size of treatment effects that may be detected using actual data, I conducted an *a priori* power analysis that used a range of input parameters roughly equal to those found in the parr-to-smolt survival analysis of Paulsen and Fisher (2005) updated with data through 2006. For convenience, an intra-class covariance matrix was assumed. In this structure, variances are equal for all populations under study and covariances between all pairs of populations are also equal (Fisher 1925).²

² Although this is an unrealistic assumption in practice, the standard error of the treatment effect estimate is the main quantity of interest and whatever the true variances and covariances, the assumed common covariances and variances may always be chosen so that the true standard error is achieved.

The year-to-year variance term (excluding measurement error) was allowed to change from 0.1 to 1.0, correlation was $\rho = 0.50$, and the number of years of the experiment ranged from 10 years to 30 with equal numbers of Before and After years. The total number of populations ranged from 2 to 20 with half of the populations being used as control populations and the other half as treatment populations. Log measurement error followed a normal distribution with mean zero and variance that was equal for all populations and measurement error correlation was assumed to be equal to zero for each pair of populations. The standard deviation of log measurement error was assumed to be $\log(1.10)=0.095$. The correlation of 0.5, variance range of 0.1 to 1.0, and measurement error standard deviation of $\log(1.10)$ based on parr-to-smolt survival data from 30 spring-summer chinook populations in the Snake River Basin. Figures 1 and 2 illustrate the estimated variances and distribution of correlations for those populations, respectively.

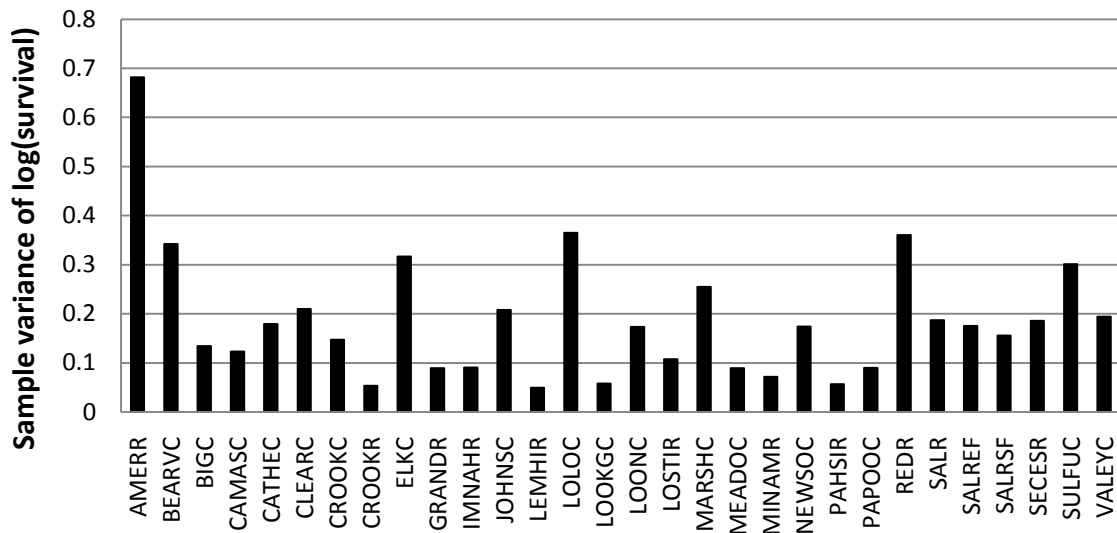


Figure 1. Sample variances for log(survival) calculated from data used in Paulsen and Fisher (2005) with data updates through 2006. Each vertical bar represents a sample variance for a different population.

The results are focused on the percent change in survival that may be reliably detected. When the type I error is $\alpha = 0.05$, power of 0.80 is achieved when CV is about 0.357 (see Eq. 10). Accordingly, the percent change in survival required to achieve power of 0.80 was calculated according to the formula $100 \times (\exp(\text{se}(\hat{\delta})/0.357) - 1)$.

In a sensitivity analysis, the effect of correlation on power was also considered. Correlation was varied from 0.0 to 0.9 assuming a fixed variance at 0.1 and measurement error standard deviation of $\log(1.10)$. Alternative numbers of populations (2 and 10) were used and it was assumed that there were equal numbers of treatment and control populations.

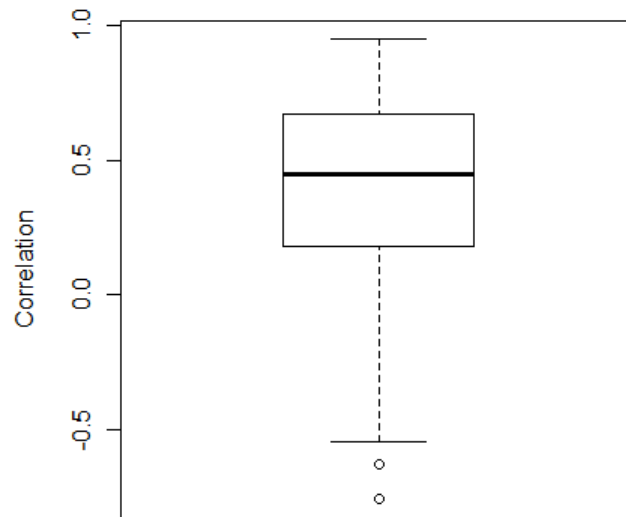


Figure 2. Box and whiskers plot of correlations between the 30 Snake River spring/summer chinook populations. In the plot, the horizontal line within the box indicates the median; the box encompasses 75% sample correlations, and the whiskers are drawn to the nearest value not beyond $1.5 \times \text{IQR}$ from the quartiles, where IQR is the interquartile range.

Results

The results of the application of the *a priori* analysis to parr-to-smolt survival are tabled in Appendix B and Appendix C. Over the range of inputs used, power of 0.80 was not achievable for survival changes in the range of 1% to 5%. Effect sizes of 30% or greater may be detected within 20 years with 2 or more populations, but this result depends on the variance (Figure 3). Power was also influenced by the value of the correlation. When the number of populations was greater than two, there was a nonlinear relationship between power and correlation (Figure 4). Despite this nonlinear relationship, when correlation between populations was sufficiently high, higher correlation resulted in higher power so that smaller effect sizes could be detected.

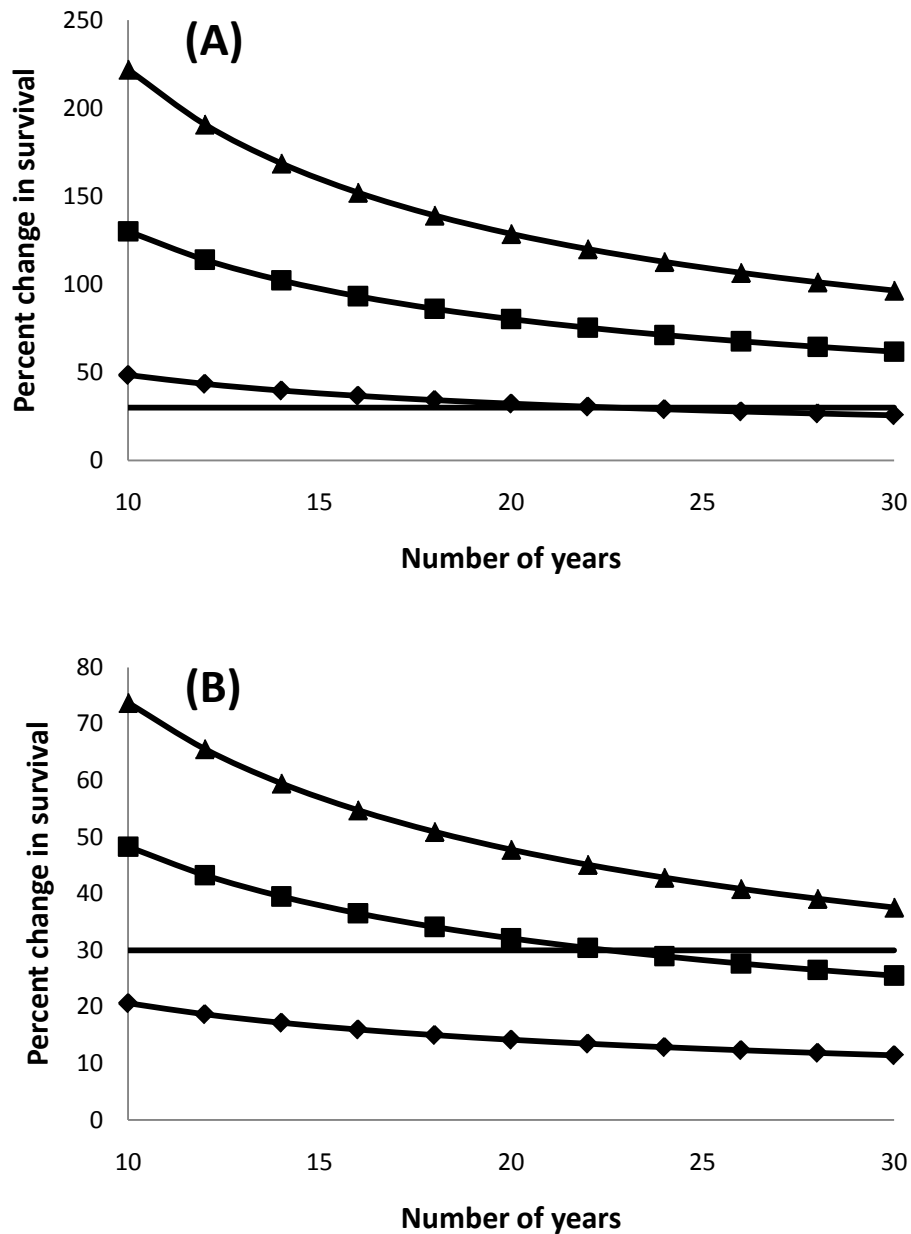


Figure 3. Percent change in survival needed to achieve power of 0.8 varies with the number of years and number of populations used in the experiment. Curves were constructed using a year-to-year variance of 0.1 (diamonds), 0.5 (squares), and 1.0 (triangles). The top panel (A) used 2 populations, and the lower panel (B) used 10 populations. Equal numbers of treatment and control populations and equal numbers of Before and After years were assumed. Measurement error standard deviation was set at $\log(1.10)$. The bolded horizontal line represents a percent change of 30%.

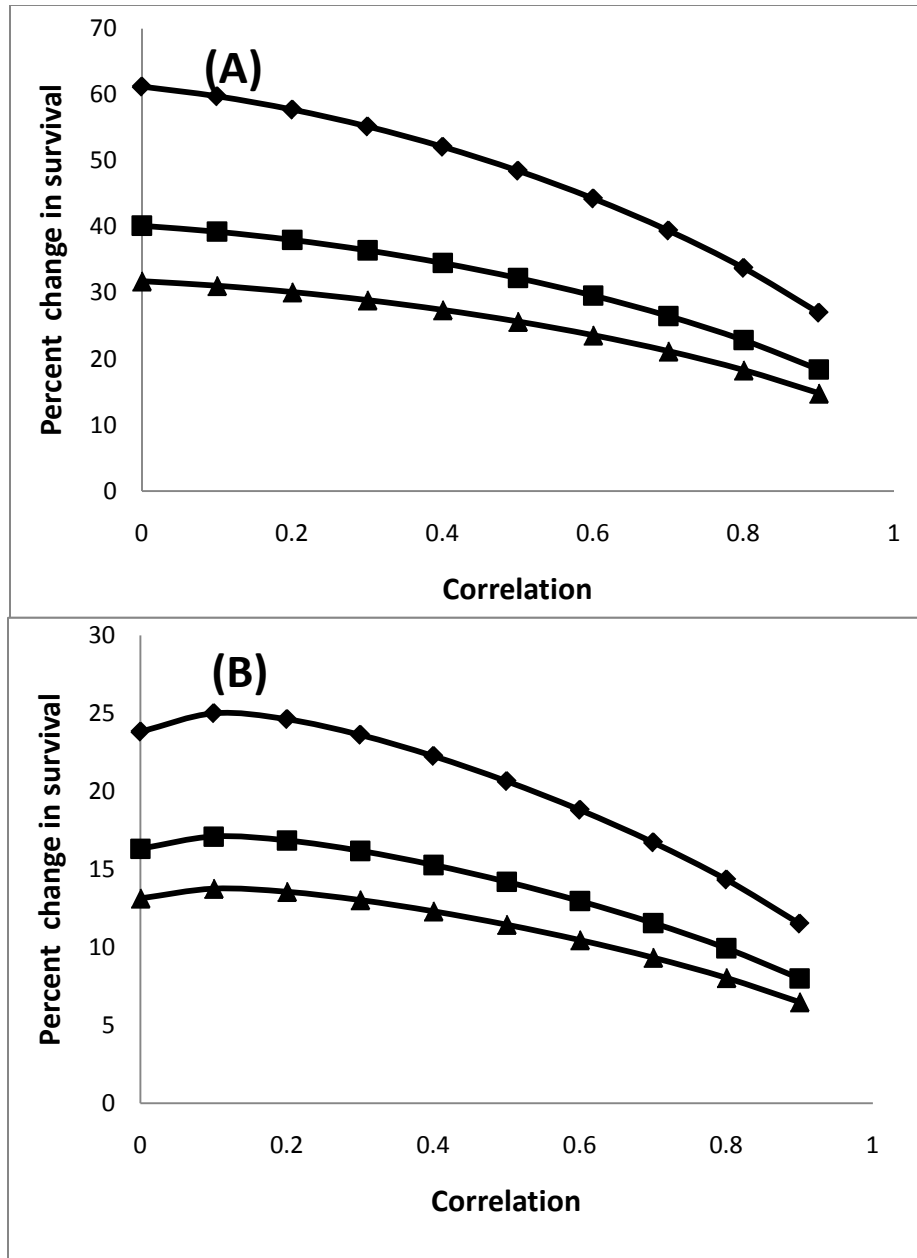


Figure 4. Percent change in survival needed to achieve power of 0.80 varies with the correlation in survival between populations. Curves were constructed using a total number of years of 10 (diamonds), 20 (squares), and 30 (triangles). The top panel (A) used 2 populations, and the lower panel (B) used 10 populations. Equal numbers of treatment and control populations and equal numbers of Before and After years were assumed. Measurement error standard deviation was $\log(1.10)$ and year-to-year variance was 0.1. Notice the nonlinear effect of correlation when 10 populations were used.

Discussion

Despite its many simplifying assumptions, the power analysis of the BACI experiment with several populations proved useful in providing estimates of the very smallest changes in survival that could be reliably detected. Applying the power analysis to salmon from the Snake River Spring/Summer Chinook ESU, it was found that detecting a survival change in the range of 1-5% was impossible even when 20 populations were employed over 30 years (assuming equal numbers of treatment and control groups and equal numbers of Before and After years). Changes of 30% in survival or more were found to be detectable with one treatment and one control population within 20 years. As the number of years and number of populations increase power also increases and small changes in survival may be detected. When correlation is sufficiently greater than zero, population groups with higher correlations in survival will yield greater power (all else being equal). Given these results, experiments on parr-to-smolt survival should be geared toward looking at changes in survival that are 30% or greater. It is expected that similar findings will result when applying the BACI power analysis on any survival data that have variance, correlation, and measurement error values in the same neighborhood as that of the Snake River Spring/Summer Chinook ESU parr-to-smolt data.

There are several future directions to take this power analysis approach that may prove fruitful. Many of the assumptions may be relaxed to make the model applicable to more situations. For example, the variance-covariance matrix may be estimated instead of assumed known, and serial dependence in the survival estimates may be considered in a multivariate time series approach. When these alternative assumptions are included, one would expect power to decrease. Another possibility would be to use a density-dependent survival process so that population abundance also plays a role in the estimate of the treatment effect (Hinrichsen 2001; Bradford et al. 2005). As new tools incorporating these updated assumptions are developed they will be made available for use at www.onefishtwofish.net.

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www.onefishtwofish.net.

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Appendix A. R code used to calculate statistical power for the BACI-type experiment described in this report.¹

```

#Program to estimate standard errors and power in a BACI-type experiment
#s2 is year-to-year variance (assumed equal for all populations)
#rho is the correlation of survivals between each pair of populations
#n1 number of Before years
#n2 number of After years
#k1 number of control populations
#k2 number of treatment populations
#me measurement error
#alpha -- prob. type I error (Probability of rejecting null hypothesis when true.)
#delta -- true treatment effect representing difference in natural log survival ln(Streatment/Scontrol)
baci<-function(s2=1,rho=.9,n1=5,n2=5,k1=1,k2=1,me=log(1.10),alpha=0.05,delta=log(1.50)){
  k<-k1+k2
  SIG2<-matrix(s2*rho,ncol=k,nrow=k)
  diag(SIG2)<-s2+me*me
  INVSIG2<-solve(SIG2)
  e<-rep(1,k)
  se<-(n1+n2)*t(e)%*%INVSIG2%*%e
  e1<-c(rep(1,k1),rep(0,k2))
  e2<-c(rep(0,k1),rep(1,k2))
  det<-n1*t(e)%*%INVSIG2%*%e+n2*t(e1)%*%INVSIG2%*%e1
  det<-det*n2*t(e2)%*%INVSIG2%*%e2-n2*n2*(t(e2)%*%INVSIG2%*%e1)^2
  se<-sqrt(se/det)
  #rule--reject when estimate exceeds 1.96 ses in absolute value (two-sided)
  q<-qnorm(1-alpha/2)
  power<-(1-pnorm(q*se,mean=delta,sd=se))+pnorm(-q*se,mean=delta,sd=se)
  return(list(s2=s2,rho=rho,n1=n1,n2=n2,k1=k1,k2=k2,me=me,
  alpha=alpha,delta=delta,se=se,cv=se/delta,power=power))
}
#outputs
#se -- standard error
#cv -- coefficient of variation
#power -- probability of rejecting the null hypothesis of no effect

```

¹This R code uses the added assumptions of a common variance and common correlation terms. This assumption may be relaxed, however, simply by specifying SIG2 as an input to the function baci in place of the input variables s2 and rho.

Appendix B. The standard error of the estimate of the treatment effect size varies with the number of years of the experiment and the year-to-year variance. Treatment effect size is defined as the change in $\log(\text{survival})$ for a BACI experiment. Equal numbers of treatment and control populations and equal numbers of Before and After years were assumed. The column heading “nyears” represents the total number of years of the experiment. Measurement error standard deviation was $\log(1.10)$ and correlation of survival between populations was 0.50.

k=2 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	0.141	0.193	0.233	0.267	0.298	0.325	0.350	0.374	0.396	0.417
12	0.129	0.176	0.213	0.244	0.272	0.297	0.320	0.342	0.362	0.381
14	0.119	0.163	0.197	0.226	0.251	0.275	0.296	0.316	0.335	0.353
16	0.112	0.152	0.184	0.211	0.235	0.257	0.277	0.296	0.313	0.330
18	0.105	0.144	0.174	0.199	0.222	0.242	0.261	0.279	0.295	0.311
20	0.100	0.136	0.165	0.189	0.210	0.230	0.248	0.265	0.280	0.295
22	0.095	0.130	0.157	0.180	0.201	0.219	0.236	0.252	0.267	0.281
24	0.091	0.124	0.150	0.172	0.192	0.210	0.226	0.241	0.256	0.269
26	0.088	0.119	0.144	0.166	0.185	0.202	0.217	0.232	0.246	0.259
28	0.084	0.115	0.139	0.160	0.178	0.194	0.209	0.224	0.237	0.249
30	0.082	0.111	0.134	0.154	0.172	0.188	0.202	0.216	0.229	0.241
k=4 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	0.103	0.140	0.170	0.195	0.217	0.237	0.255	0.273	0.289	0.304
12	0.094	0.128	0.155	0.178	0.198	0.216	0.233	0.249	0.264	0.278
14	0.087	0.119	0.143	0.165	0.183	0.200	0.216	0.230	0.244	0.257
16	0.081	0.111	0.134	0.154	0.171	0.187	0.202	0.215	0.228	0.240
18	0.077	0.105	0.126	0.145	0.162	0.177	0.190	0.203	0.215	0.227
20	0.073	0.099	0.120	0.138	0.153	0.167	0.181	0.193	0.204	0.215
22	0.069	0.095	0.114	0.131	0.146	0.160	0.172	0.184	0.195	0.205
24	0.066	0.091	0.110	0.126	0.140	0.153	0.165	0.176	0.186	0.196
26	0.064	0.087	0.105	0.121	0.134	0.147	0.158	0.169	0.179	0.189
28	0.062	0.084	0.101	0.116	0.130	0.142	0.153	0.163	0.173	0.182
30	0.059	0.081	0.098	0.112	0.125	0.137	0.147	0.157	0.167	0.176
k=6 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	0.085	0.116	0.140	0.161	0.179	0.196	0.211	0.225	0.239	0.252
12	0.078	0.106	0.128	0.147	0.164	0.179	0.193	0.206	0.218	0.230
14	0.072	0.098	0.119	0.136	0.152	0.166	0.179	0.191	0.202	0.213
16	0.067	0.092	0.111	0.127	0.142	0.155	0.167	0.178	0.189	0.199
18	0.064	0.087	0.105	0.120	0.134	0.146	0.157	0.168	0.178	0.188
20	0.060	0.082	0.099	0.114	0.127	0.139	0.149	0.159	0.169	0.178
22	0.058	0.078	0.095	0.109	0.121	0.132	0.142	0.152	0.161	0.170
24	0.055	0.075	0.091	0.104	0.116	0.126	0.136	0.146	0.154	0.162
26	0.053	0.072	0.087	0.100	0.111	0.122	0.131	0.140	0.148	0.156
28	0.051	0.069	0.084	0.096	0.107	0.117	0.126	0.135	0.143	0.150
30	0.049	0.067	0.081	0.093	0.104	0.113	0.122	0.130	0.138	0.145

Appendix B. CONTINUED

k=8 populations

nyears	Year-to-year variance (excluding measurement error)									
	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	0.075	0.101	0.123	0.141	0.157	0.171	0.184	0.197	0.208	0.220
12	0.068	0.093	0.112	0.128	0.143	0.156	0.168	0.180	0.190	0.200
14	0.063	0.086	0.104	0.119	0.132	0.145	0.156	0.166	0.176	0.186
16	0.059	0.080	0.097	0.111	0.124	0.135	0.146	0.156	0.165	0.174
18	0.056	0.076	0.091	0.105	0.117	0.127	0.137	0.147	0.155	0.164
20	0.053	0.072	0.087	0.099	0.111	0.121	0.130	0.139	0.147	0.155
22	0.050	0.068	0.083	0.095	0.106	0.115	0.124	0.133	0.141	0.148
24	0.048	0.065	0.079	0.091	0.101	0.110	0.119	0.127	0.135	0.142
26	0.046	0.063	0.076	0.087	0.097	0.106	0.114	0.122	0.129	0.136
28	0.045	0.061	0.073	0.084	0.094	0.102	0.110	0.118	0.125	0.131
30	0.043	0.059	0.071	0.081	0.090	0.099	0.106	0.114	0.120	0.127

k=10 populations

nyears	Year-to-year variance (excluding measurement error)									
	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	0.067	0.091	0.110	0.126	0.141	0.154	0.166	0.177	0.187	0.197
12	0.061	0.083	0.101	0.115	0.128	0.140	0.151	0.161	0.171	0.180
14	0.057	0.077	0.093	0.107	0.119	0.130	0.140	0.149	0.158	0.167
16	0.053	0.072	0.087	0.100	0.111	0.122	0.131	0.140	0.148	0.156
18	0.050	0.068	0.082	0.094	0.105	0.115	0.123	0.132	0.140	0.147
20	0.047	0.064	0.078	0.089	0.099	0.109	0.117	0.125	0.132	0.140
22	0.045	0.061	0.074	0.085	0.095	0.104	0.112	0.119	0.126	0.133
24	0.043	0.059	0.071	0.082	0.091	0.099	0.107	0.114	0.121	0.127
26	0.042	0.057	0.068	0.078	0.087	0.095	0.103	0.110	0.116	0.122
28	0.040	0.055	0.066	0.076	0.084	0.092	0.099	0.106	0.112	0.118
30	0.039	0.053	0.064	0.073	0.081	0.089	0.096	0.102	0.108	0.114

k=12 populations

nyears	Year-to-year variance (excluding measurement error)									
	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	0.061	0.084	0.101	0.116	0.129	0.141	0.152	0.162	0.172	0.181
12	0.056	0.076	0.092	0.106	0.118	0.129	0.139	0.148	0.157	0.165
14	0.052	0.071	0.085	0.098	0.109	0.119	0.128	0.137	0.145	0.153
16	0.049	0.066	0.080	0.092	0.102	0.111	0.120	0.128	0.136	0.143
18	0.046	0.062	0.075	0.086	0.096	0.105	0.113	0.121	0.128	0.135
20	0.043	0.059	0.071	0.082	0.091	0.100	0.107	0.115	0.121	0.128
22	0.041	0.056	0.068	0.078	0.087	0.095	0.102	0.109	0.116	0.122
24	0.040	0.054	0.065	0.075	0.083	0.091	0.098	0.105	0.111	0.117
26	0.038	0.052	0.063	0.072	0.080	0.087	0.094	0.100	0.106	0.112
28	0.037	0.050	0.060	0.069	0.077	0.084	0.091	0.097	0.103	0.108
30	0.035	0.048	0.058	0.067	0.074	0.081	0.088	0.094	0.099	0.104

Appendix B. CONTINUED

k=14 populations

Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	0.057	0.078	0.094	0.107	0.120	0.131	0.141	0.150	0.159	0.168
12	0.052	0.071	0.086	0.098	0.109	0.119	0.129	0.137	0.145	0.153
14	0.048	0.066	0.079	0.091	0.101	0.110	0.119	0.127	0.135	0.142
16	0.045	0.061	0.074	0.085	0.095	0.103	0.111	0.119	0.126	0.133
18	0.042	0.058	0.070	0.080	0.089	0.097	0.105	0.112	0.119	0.125
20	0.040	0.055	0.066	0.076	0.085	0.092	0.100	0.106	0.113	0.119
22	0.038	0.052	0.063	0.072	0.081	0.088	0.095	0.101	0.107	0.113
24	0.037	0.050	0.060	0.069	0.077	0.084	0.091	0.097	0.103	0.108
26	0.035	0.048	0.058	0.067	0.074	0.081	0.087	0.093	0.099	0.104
28	0.034	0.046	0.056	0.064	0.071	0.078	0.084	0.090	0.095	0.100
30	0.033	0.045	0.054	0.062	0.069	0.075	0.081	0.087	0.092	0.097

k=16 populations

Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	0.053	0.073	0.088	0.101	0.112	0.122	0.132	0.141	0.149	0.157
12	0.049	0.066	0.080	0.092	0.102	0.112	0.121	0.129	0.136	0.144
14	0.045	0.061	0.074	0.085	0.095	0.104	0.112	0.119	0.126	0.133
16	0.042	0.057	0.069	0.080	0.089	0.097	0.104	0.111	0.118	0.124
18	0.040	0.054	0.065	0.075	0.084	0.091	0.098	0.105	0.111	0.117
20	0.038	0.051	0.062	0.071	0.079	0.087	0.093	0.100	0.106	0.111
22	0.036	0.049	0.059	0.068	0.076	0.083	0.089	0.095	0.101	0.106
24	0.034	0.047	0.057	0.065	0.072	0.079	0.085	0.091	0.096	0.101
26	0.033	0.045	0.054	0.062	0.070	0.076	0.082	0.087	0.093	0.097
28	0.032	0.043	0.052	0.060	0.067	0.073	0.079	0.084	0.089	0.094
30	0.031	0.042	0.051	0.058	0.065	0.071	0.076	0.081	0.086	0.091

k=18 populations

Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	0.050	0.069	0.083	0.095	0.106	0.116	0.125	0.133	0.141	0.148
12	0.046	0.063	0.076	0.087	0.097	0.106	0.114	0.121	0.129	0.136
14	0.043	0.058	0.070	0.080	0.089	0.098	0.105	0.112	0.119	0.125
16	0.040	0.054	0.066	0.075	0.084	0.091	0.099	0.105	0.111	0.117
18	0.038	0.051	0.062	0.071	0.079	0.086	0.093	0.099	0.105	0.111
20	0.036	0.049	0.059	0.067	0.075	0.082	0.088	0.094	0.100	0.105
22	0.034	0.046	0.056	0.064	0.071	0.078	0.084	0.090	0.095	0.100
24	0.033	0.044	0.054	0.061	0.068	0.075	0.080	0.086	0.091	0.096
26	0.031	0.043	0.051	0.059	0.066	0.072	0.077	0.083	0.087	0.092
28	0.030	0.041	0.050	0.057	0.063	0.069	0.074	0.080	0.084	0.089
30	0.029	0.040	0.048	0.055	0.061	0.067	0.072	0.077	0.081	0.086

Appendix B. CONTINUED

k=20 populations

Year-to-year variance (excluding measurement error)

nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	0.048	0.065	0.079	0.090	0.101	0.110	0.118	0.126	0.134	0.141
12	0.044	0.060	0.072	0.082	0.092	0.100	0.108	0.115	0.122	0.129
14	0.041	0.055	0.067	0.076	0.085	0.093	0.100	0.107	0.113	0.119
16	0.038	0.052	0.062	0.071	0.080	0.087	0.094	0.100	0.106	0.111
18	0.036	0.049	0.059	0.067	0.075	0.082	0.088	0.094	0.100	0.105
20	0.034	0.046	0.056	0.064	0.071	0.078	0.084	0.089	0.095	0.100
22	0.032	0.044	0.053	0.061	0.068	0.074	0.080	0.085	0.090	0.095
24	0.031	0.042	0.051	0.058	0.065	0.071	0.076	0.082	0.086	0.091
26	0.030	0.040	0.049	0.056	0.062	0.068	0.073	0.078	0.083	0.087
28	0.029	0.039	0.047	0.054	0.060	0.066	0.071	0.076	0.080	0.084
30	0.028	0.038	0.045	0.052	0.058	0.063	0.068	0.073	0.077	0.081

Appendix C. Percent change in survival necessary to deliver a CV of 0.357 (power of 0.80). Equal numbers of treatment and control populations and equal numbers of Before and After years were assumed. The column heading “nyears” represents the total number of years of the experiment. Measurement error standard deviation was $\log(1.10)$ and correlation of survival between populations was 0.50.

k=2 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	48.51	71.51	92.00	111.36	130.12	148.57	166.88	185.17	203.51	221.96
12	43.48	63.63	81.40	98.02	114.00	129.61	145.01	160.29	175.53	190.78
14	39.69	57.76	73.56	88.23	102.26	115.88	129.25	142.46	155.57	168.64
16	36.70	53.18	67.49	80.70	93.26	105.41	117.29	128.98	140.54	152.03
18	34.28	49.49	62.62	74.68	86.12	97.13	107.86	118.38	128.77	139.05
20	32.26	46.44	58.61	69.76	80.28	90.38	100.20	109.80	119.25	128.60
22	30.55	43.86	55.24	65.63	75.40	84.76	93.83	102.69	111.39	119.97
24	29.08	41.65	52.36	62.11	71.25	80.00	88.45	96.68	104.76	112.71
26	27.80	39.73	49.87	59.06	67.68	75.89	83.82	91.53	99.08	106.50
28	26.66	38.04	47.68	56.40	64.55	72.32	79.79	87.06	94.16	101.13
30	25.65	36.54	45.74	54.05	61.80	69.17	76.25	83.13	89.84	96.42
k=4 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	33.44	48.17	60.86	72.51	83.52	94.12	104.43	114.54	124.50	134.35
12	30.13	43.18	54.33	64.50	74.06	83.22	92.08	100.73	109.22	117.59
14	27.61	39.42	49.44	58.54	67.05	75.17	83.00	90.62	98.07	105.40
16	25.62	36.46	45.62	53.89	61.61	68.94	76.00	82.84	89.52	96.07
18	23.99	34.06	42.52	50.14	57.23	63.95	70.40	76.64	82.72	88.66
20	22.63	32.05	39.95	47.04	53.62	59.84	65.80	71.56	77.15	82.61
22	21.47	30.36	37.78	44.43	50.58	56.39	61.95	67.30	72.50	77.57
24	20.47	28.89	35.91	42.19	47.98	53.44	58.66	63.68	68.54	73.28
26	19.59	27.62	34.29	40.24	45.72	50.89	55.81	60.54	65.12	69.58
28	18.82	26.49	32.85	38.52	43.74	48.65	53.32	57.80	62.14	66.36
30	18.12	25.49	31.58	37.00	41.98	46.66	51.11	55.38	59.50	63.51
k=6 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	27.00	38.48	48.21	57.03	65.28	73.13	80.70	88.06	95.26	102.32
12	24.38	34.60	43.21	50.97	58.20	65.05	71.62	77.99	84.20	90.27
14	22.38	31.67	39.45	46.43	52.91	59.03	64.88	70.54	76.04	81.40
16	20.80	29.35	36.49	42.87	48.77	54.33	59.64	64.76	69.72	74.56
18	19.50	27.46	34.08	39.98	45.43	50.55	55.43	60.12	64.67	69.09
20	18.41	25.88	32.08	37.59	42.66	47.42	51.95	56.30	60.50	64.59
22	17.48	24.54	30.38	35.56	40.32	44.78	49.02	53.09	57.01	60.82
24	16.68	23.38	28.91	33.81	38.31	42.52	46.51	50.34	54.02	57.60
26	15.98	22.37	27.64	32.29	36.56	40.55	44.33	47.95	51.43	54.81
28	15.35	21.48	26.51	30.95	35.02	38.82	42.42	45.86	49.17	52.37
30	14.79	20.68	25.50	29.76	33.65	37.29	40.72	44.00	47.16	50.21

Appendix C. CONTINUED

k=8 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	23.21	32.86	40.97	48.26	55.03	61.44	67.59	73.52	79.30	84.95
12	20.99	29.62	36.82	43.26	49.22	54.84	60.21	65.39	70.41	75.30
14	19.29	27.14	33.67	39.49	44.86	49.90	54.71	59.33	63.80	68.15
16	17.94	25.19	31.19	36.53	41.43	46.03	50.41	54.61	58.66	62.60
18	16.83	23.59	29.17	34.12	38.66	42.91	46.94	50.80	54.53	58.14
20	15.90	22.25	27.48	32.11	36.35	40.31	44.07	47.66	51.12	54.46
22	15.11	21.12	26.05	30.41	34.40	38.12	41.64	45.00	48.24	51.37
24	14.42	20.13	24.81	28.94	32.72	36.23	39.56	42.73	45.78	48.72
26	13.82	19.27	23.73	27.66	31.25	34.59	37.74	40.75	43.64	46.42
28	13.28	18.51	22.78	26.54	29.96	33.14	36.15	39.01	41.76	44.41
30	12.81	17.83	21.93	25.53	28.81	31.86	34.73	37.47	40.09	42.62
k=10 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	20.65	29.11	36.16	42.47	48.31	53.81	59.06	64.11	69.01	73.79
12	18.69	26.26	32.55	38.15	43.30	48.14	52.75	57.18	61.46	65.62
14	17.19	24.10	29.81	34.88	39.53	43.89	48.03	51.99	55.82	59.53
16	16.00	22.38	27.64	32.29	36.56	40.55	44.32	47.94	51.42	54.79
18	15.02	20.97	25.87	30.19	34.15	37.84	41.33	44.66	47.87	50.97
20	14.19	19.80	24.39	28.44	32.14	35.59	38.84	41.95	44.93	47.82
22	13.49	18.80	23.14	26.96	30.44	33.68	36.74	39.65	42.45	45.15
24	12.88	17.93	22.05	25.67	28.97	32.04	34.93	37.68	40.32	42.87
26	12.34	17.17	21.10	24.55	27.69	30.60	33.35	35.96	38.47	40.88
28	11.87	16.49	20.26	23.56	26.56	29.34	31.96	34.45	36.84	39.14
30	11.44	15.89	19.51	22.68	25.55	28.22	30.73	33.11	35.39	37.59
k=12 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	18.77	26.37	32.68	38.30	43.48	48.35	52.98	57.42	61.72	65.90
12	17.00	23.82	29.45	34.45	39.04	43.33	47.41	51.32	55.09	58.74
14	15.65	21.87	27.00	31.53	35.68	39.56	43.23	46.74	50.12	53.39
16	14.56	20.33	25.05	29.22	33.03	36.59	39.94	43.15	46.23	49.21
18	13.68	19.06	23.46	27.34	30.88	34.17	37.28	40.24	43.09	45.84
20	12.93	18.00	22.14	25.77	29.08	32.16	35.07	37.83	40.48	43.04
22	12.29	17.09	21.00	24.44	27.56	30.46	33.19	35.79	38.28	40.68
24	11.74	16.31	20.03	23.28	26.24	28.99	31.57	34.03	36.38	38.65
26	11.26	15.62	19.17	22.28	25.09	27.71	30.17	32.50	34.73	36.88
28	10.83	15.01	18.41	21.38	24.08	26.58	28.92	31.15	33.28	35.33
30	10.44	14.47	17.74	20.59	23.18	25.57	27.82	29.95	31.99	33.95

Appendix C. CONTINUED

k=14 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	17.31	24.27	30.02	35.12	39.81	44.20	48.37	52.37	56.23	59.98
12	15.69	21.94	27.08	31.62	35.79	39.68	43.36	46.88	50.28	53.56
14	14.45	20.16	24.84	28.97	32.74	36.26	39.58	42.75	45.80	48.75
16	13.46	18.74	23.06	26.87	30.33	33.56	36.61	39.51	42.30	44.98
18	12.64	17.58	21.61	25.15	28.37	31.37	34.19	36.88	39.45	41.94
20	11.95	16.61	20.40	23.72	26.74	29.54	32.18	34.69	37.09	39.41
22	11.37	15.77	19.36	22.50	25.35	27.99	30.48	32.84	35.10	37.27
24	10.86	15.06	18.46	21.44	24.15	26.65	29.01	31.24	33.38	35.43
26	10.41	14.42	17.68	20.52	23.10	25.48	27.72	29.85	31.88	33.83
28	10.01	13.86	16.98	19.71	22.17	24.45	26.59	28.62	30.56	32.42
30	9.66	13.36	16.36	18.98	21.35	23.53	25.58	27.53	29.38	31.16
k=16 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	16.15	22.59	27.89	32.59	36.90	40.93	44.74	48.40	51.92	55.33
12	14.64	20.43	25.18	29.37	33.20	36.78	40.16	43.38	46.48	49.48
14	13.49	18.78	23.11	26.93	30.40	33.64	36.69	39.60	42.39	45.09
16	12.56	17.47	21.47	24.99	28.18	31.16	33.96	36.62	39.18	41.64
18	11.80	16.39	20.13	23.40	26.38	29.14	31.74	34.21	36.57	38.85
20	11.17	15.49	19.00	22.08	24.87	27.45	29.89	32.20	34.41	36.53
22	10.62	14.72	18.04	20.95	23.58	26.02	28.32	30.49	32.57	34.57
24	10.15	14.05	17.21	19.97	22.47	24.79	26.96	29.02	30.99	32.88
26	9.73	13.46	16.48	19.12	21.50	23.71	25.78	27.74	29.61	31.40
28	9.36	12.94	15.84	18.36	20.65	22.76	24.73	26.60	28.39	30.10
30	9.03	12.48	15.26	17.69	19.88	21.91	23.80	25.60	27.31	28.95
k=18 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	15.19	21.20	26.15	30.52	34.52	38.26	41.79	45.17	48.42	51.56
12	13.78	19.19	23.62	27.53	31.09	34.41	37.54	40.53	43.40	46.17
14	12.69	17.65	21.70	25.25	28.49	31.49	34.33	37.03	39.61	42.11
16	11.83	16.42	20.16	23.44	26.42	29.19	31.79	34.27	36.64	38.92
18	11.11	15.41	18.91	21.96	24.74	27.31	29.73	32.02	34.22	36.33
20	10.51	14.57	17.85	20.73	23.33	25.74	28.01	30.15	32.21	34.18
22	10.00	13.84	16.96	19.67	22.13	24.41	26.54	28.57	30.50	32.36
24	9.56	13.22	16.18	18.76	21.10	23.26	25.28	27.20	29.03	30.79
26	9.16	12.67	15.50	17.96	20.19	22.25	24.18	26.01	27.75	29.42
28	8.82	12.18	14.89	17.26	19.39	21.36	23.21	24.95	26.61	28.21
30	8.50	11.74	14.35	16.63	18.68	20.57	22.34	24.01	25.60	27.13

Appendix C. CONTINUED

k=20 populations										
Year-to-year variance (excluding measurement error)										
nyears	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
10	14.38	20.04	24.69	28.79	32.54	36.03	39.33	42.48	45.51	48.43
12	13.04	18.15	22.32	25.99	29.33	32.43	35.36	38.15	40.83	43.41
14	12.02	16.70	20.50	23.84	26.88	29.70	32.36	34.88	37.30	39.63
16	11.20	15.54	19.06	22.15	24.95	27.54	29.98	32.30	34.52	36.65
18	10.53	14.59	17.88	20.76	23.36	25.78	28.05	30.20	32.25	34.23
20	9.96	13.79	16.89	19.59	22.04	24.31	26.43	28.45	30.37	32.22
22	9.48	13.11	16.04	18.60	20.92	23.05	25.06	26.96	28.77	30.51
24	9.06	12.52	15.31	17.74	19.94	21.97	23.87	25.68	27.39	29.04
26	8.69	12.00	14.67	16.99	19.09	21.03	22.84	24.55	26.19	27.76
28	8.36	11.54	14.10	16.33	18.34	20.19	21.92	23.56	25.12	26.62
30	8.06	11.12	13.59	15.73	17.66	19.44	21.11	22.68	24.18	25.61