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

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Abstract

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 (IMW**s**) 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(survival) are equal for all populations and the correlations in log(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 1 (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(survival) for several populations.

Methods

Maximum likelihood estimation. —To derive the estimator and its variance for the power analysis, maximum likelihood is used (Mood et al. 1974). The details of the derivation may be found in Appendix 1. It is assumed that mean log(survival) before treatment, denoted by μ, is the same for each population. After treatment, the mean log(survival) of the treatment populations shifts by the amount δ, while the control populations continue to have a mean log(survival) of μ. 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(survival) and measurement error follow multivariate normal distributions. Thus the total variance matrix is $\mathbf{\Sigma} = \mathbf{\Sigma}_y + \mathbf{\Sigma}_m$, where $\mathbf{\Sigma}_y$ is the variance-covariance matrix of true log(survival), and $\mathbf{\Sigma}_m$ represents the variance-covariance matrix of the measurement error of log(survival).

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 $\mathbf{\Sigma}$. Using this formula, it is then simple to calculate the standard error of the treatment effect estimate,

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

The coefficient of variation is

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

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.

Power analysis. —To determine the size of treatment effects that may be detected in practice, we 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). 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.

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 equation 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.

Application. —To demonstrate the fit of the models to data and the contrast of power between the cases where the variance is estimated and when it is not, we apply the models to data seven populations used in Paulsen and Fisher (2003). We are able to contrast the power results from the baci models developed in this paper with the power results in Paulsen and Fisher (2003). The data used in this application is parr-smolt survival data from eight populations in the Snake River spring chinook evolutionary significant unit (Table 2). The data used may be found in Appendix XX:

Results

The results of the *a priori* analysis to parr-to-smolt survival are tabled in Appendix 2 and Appendix 3. 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.

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.

Acknowledgements

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Tables

Table 1. —Assumptions used in the power analysis.

The observations of log(survival) follow a multivariate normal distribution.
There is no serial dependence.
All populations have a common mean log(survival) before treatment.
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.
The measurement errors in log(survival) follow a multivariate normal distribution and the errors are independent of the error due to actual year-to-year environmental variability.
The estimator of the treatment effect is a maximum likelihood estimate.
The variance-covariance matrix describing the year-to-year variability in log(survival) is known.

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Table 2. — Tagging sites and climatic regions for Snake River populations used in application.

Tagging site	Region
Bear Valley Creek	Middle Fork Salmon River
Elk Creek	Middle Fork Salmon River
Imnaha River	Northeast Oregon
Johnson Creek	South Fork Salmon River
Marsh Creek	Middle Fork Salmon River
Minam River	Northeast Oregon
Poverty Flat	South Fork Salmon River
Sulphur Creek	Middle Fork Salmon River

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Figure captions

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.

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 ×IQR from the quartiles, where IQR is the interquartile range.

Figure 3. —Tagging sites (fish icon) and overwintering areas for the eight passive integrated transponder (PIT) tagged Snake River spring–summer chinook (*Oncorhynchus tshawytscha*) stocks and location of the mainstem hydropower dams where tagged smolts are detected.Degrees latitude and longitude are shown in each corner of the figure. Inset map shows location in the Columbia River basin (northwestern U.S.A.).

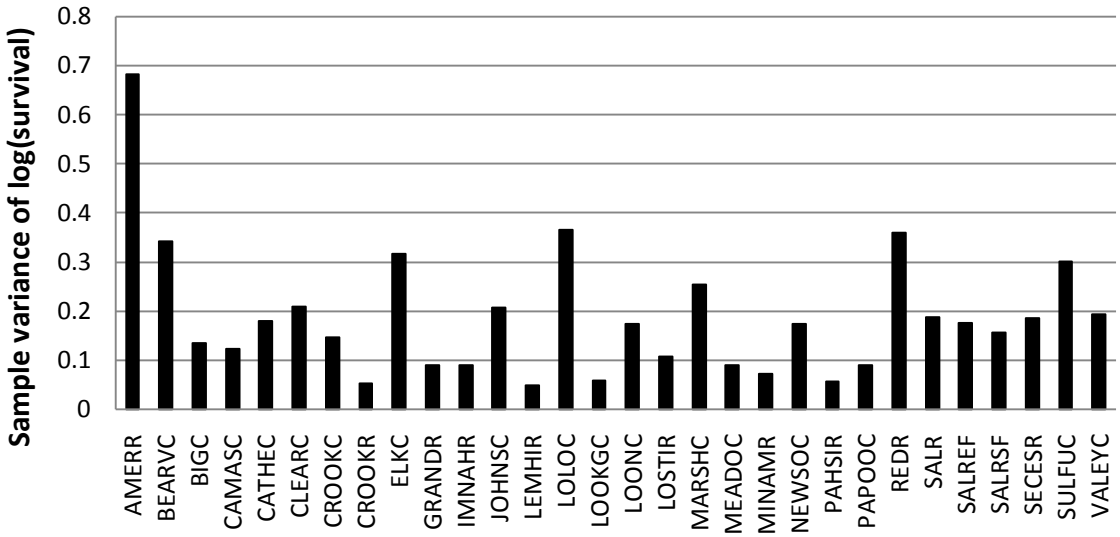
Figure 4. —Percent change in survival needed to achieve power of 0.8 varies with the number of years and number of populations used in the experiment. Curves were constructed using a year-to-year variance of 0.1 (diamonds), 0.5 (squares), and 1.0 (triangles). Equal numbers of treatment and control populations 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 5. —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). 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.

Figures

Figure 1.



267 Figure 2.

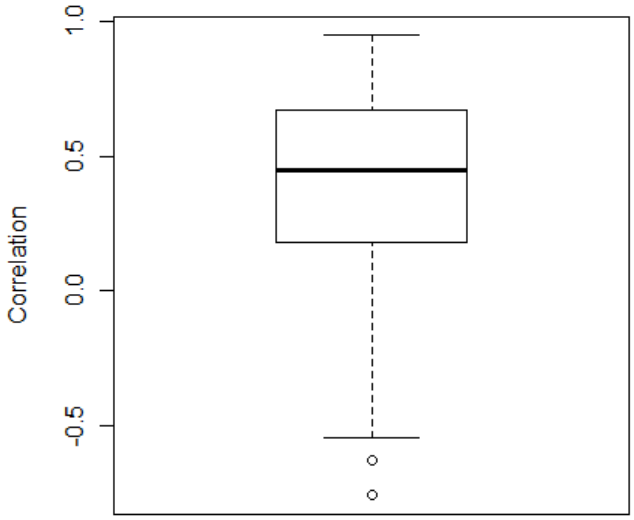


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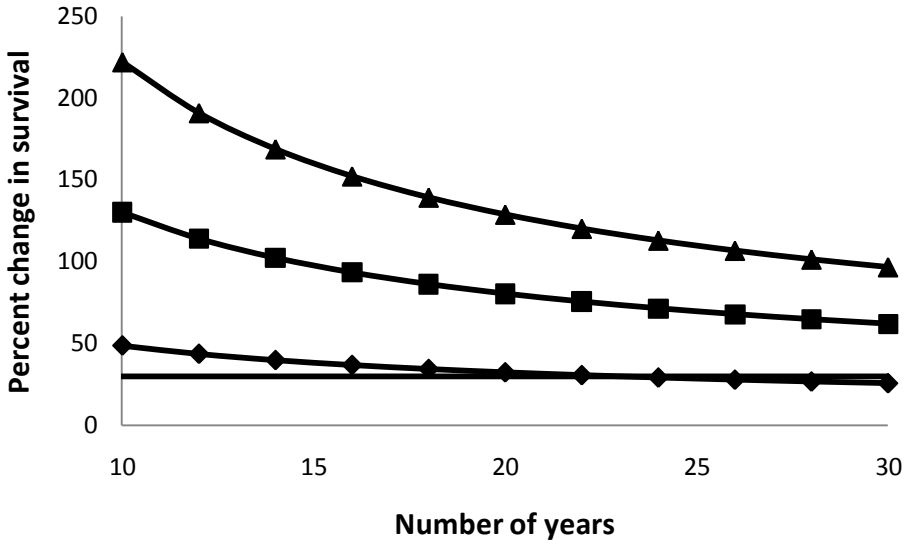
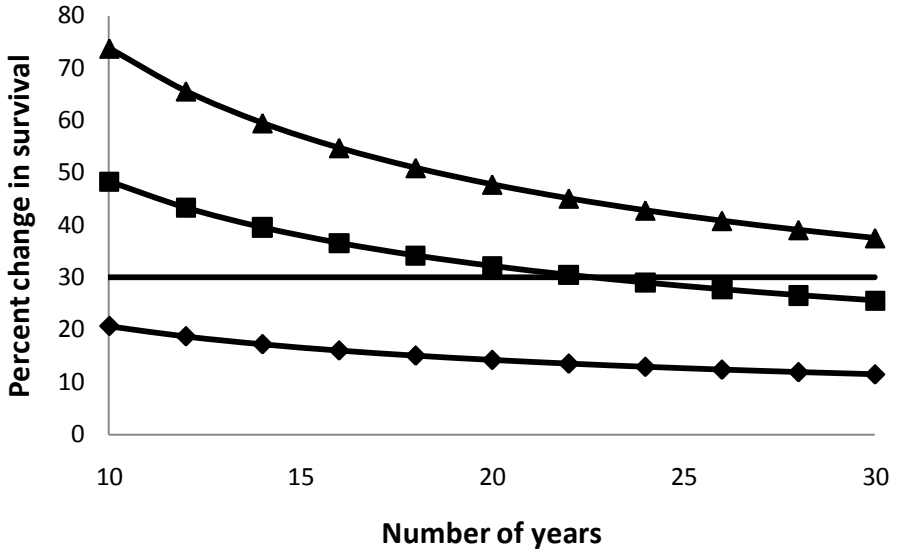
Figure 3

271 Figure 4



4a. —A total of 2 populations were used.



4b. —A total of 10 populations were used.

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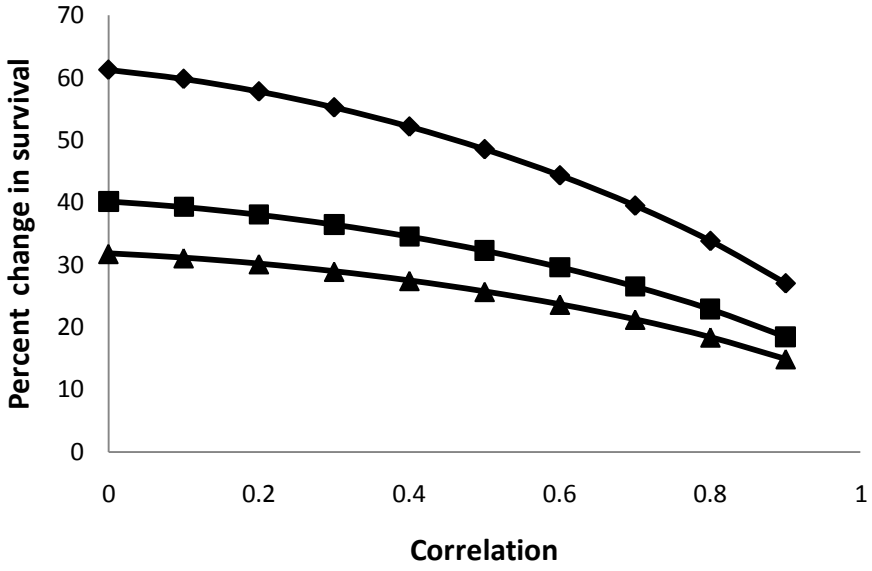
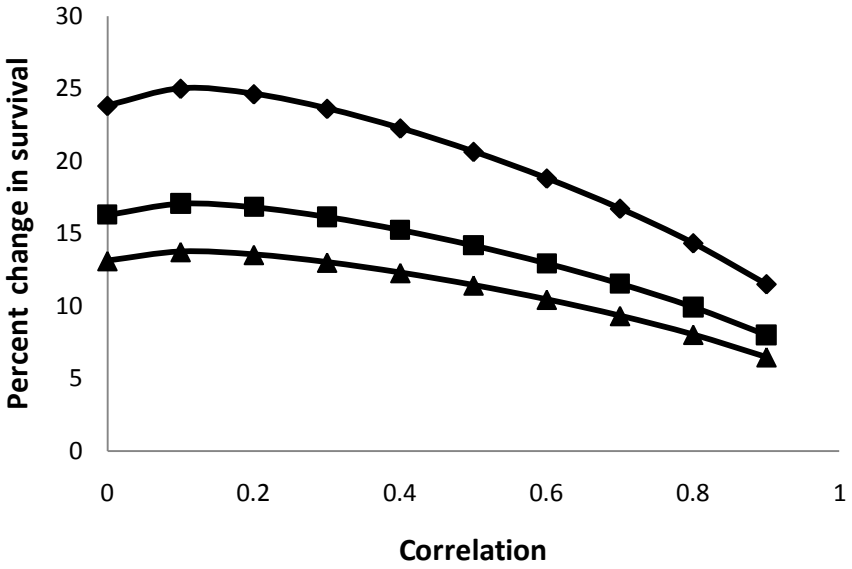
273 Figure 5.



5a. —A total of 2 populations were used.



5b. —A total of 10 populations were used.

Appendix 1: Maximum likelihood estimation

The log-likelihood function may be written as

$$l(\boldsymbol{\theta},\boldsymbol{\Sigma}) = C + (n/2)\ln|\boldsymbol{\Sigma}^{-1}| - (1/2)\sum_{t=1}^{n1}(\mathbf{x}_t - [\mathbf{e} \quad \mathbf{0}]\boldsymbol{\theta})'\boldsymbol{\Sigma}^{-1}(\mathbf{x}_t - [\mathbf{e} \quad \mathbf{0}]\boldsymbol{\theta})) \qquad (A.1)$$

$$-(1/2)\sum_{t=n1+1}^{n}(\mathbf{x}_t - [\mathbf{e} \quad \mathbf{e}_2]\boldsymbol{\theta})'\boldsymbol{\Sigma}^{-1}(\mathbf{x}_t - [\mathbf{e} \quad \mathbf{e}_2]\boldsymbol{\theta});$$

where $l(\boldsymbol{\theta},\boldsymbol{\Sigma})$ is the log-likelihood function with vector argument $\boldsymbol{\theta} = [\mu \quad \delta]'$ with entries representing the control mean and treatment effect, 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; $\mathbf{e}_2$ is a k -vector of k_1 0s followed by k_2 1s, where k_1 represents then number of control populations and 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.

In the most general case, we are interested in maximum likelihood estimate for δ and $\boldsymbol{\Sigma}$. We will consider the case where the variance-covariance matrix is assumed known and when it is assumed to be unknown and needs to be estimated. When it is estimated we consider two cases. In the first case, all populations have the same variance and all pairs of populations have the same covariance. This gives rise to the intraclass covariance matrix structure studied by Fisher (1925) where all diagonal entries are equal and all offdiagonal entries are equal. In the second case, we estimate a general covariance matrix with no restrictions.

Using maximum likelihood theory, we develop estimating equations for both the Before mean and treatment effect and the covariance matrix. In the case of the before mean and treatment effect, we may take advantage of the fact that the maximizing the likelihood function is equivalent to a generalized least squares problem of minimizing

$$SS = \left(\begin{bmatrix} \bar{\mathbf{x}}_1 \\ \bar{\mathbf{x}}_2 \end{bmatrix} - \begin{bmatrix} \mathbf{e} & 0 \\ \mathbf{e} & \mathbf{e}_2 \end{bmatrix} \begin{bmatrix} \mu \\ \delta \end{bmatrix} \right)' \begin{bmatrix} \boldsymbol{\Sigma}^{-1} n_1 & 0 \\ 0 & \boldsymbol{\Sigma}^{-1} n_2 \end{bmatrix} \left(\begin{bmatrix} \bar{\mathbf{x}}_1 \\ \bar{\mathbf{x}}_2 \end{bmatrix} - \begin{bmatrix} \mathbf{e} & 0 \\ \mathbf{e} & \mathbf{e}_2 \end{bmatrix} \begin{bmatrix} \mu \\ \delta \end{bmatrix} \right); \tag{A.2}$$

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.

This generalized sum of squares may be written in the familiar form

$$SS = (\mathbf{y} - \mathbf{B}\boldsymbol{\theta})' \boldsymbol{\Omega}^{-1} (\mathbf{y} - \mathbf{B}\boldsymbol{\theta}); \tag{A.3}$$

where $\mathbf{y}' = [\bar{\mathbf{x}}_1' \quad \bar{\mathbf{x}}_2']$, $\mathbf{B} = \begin{bmatrix} \mathbf{e} & 0 \\ \mathbf{e} & \mathbf{e}_2 \end{bmatrix}$, and $\boldsymbol{\Omega}^{-1} = \begin{bmatrix} \boldsymbol{\Sigma}^{-1} n_1 & 0 \\ 0 & \boldsymbol{\Sigma}^{-1} n_2 \end{bmatrix}$. In this form, the generalized least squares solution, the called the Aitken estimator (Press 2005), is known to be

$$\hat{\boldsymbol{\theta}} = \left(\mathbf{B}^{\mathbf{T}}\boldsymbol{\Omega}^{-1}\mathbf{B}\right)^{-1}\mathbf{B}^{\mathbf{T}}\boldsymbol{\Omega}^{-1}\mathbf{y}\,. \tag{A.4}$$

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310 After considerable matrix algebra, we may write

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$$\hat{\boldsymbol{\theta}} = \begin{bmatrix}\hat{\mu}\\ \hat{\delta}\end{bmatrix} = \frac{\begin{bmatrix}\left(\mathbf{e}_2'\Sigma^{-1}\mathbf{e}_2\right)\left(\mathbf{e}'\Sigma^{-1}\bar{\mathbf{x}}\right) - \left(\frac{n_2}{n}\right)\left(\mathbf{e}'\boldsymbol{\Sigma}^{-1}\mathbf{e}_2\right)\left(\mathbf{e}_2'\Sigma^{-1}\bar{\mathbf{x}}_2\right)\\ \left(\mathbf{e}'\boldsymbol{\Sigma}^{-1}\mathbf{e}\right)\left(\mathbf{e}_2'\Sigma^{-1}\bar{\mathbf{x}}_2\right) - \left(\mathbf{e}_2'\Sigma^{-1}\mathbf{e}\right)\left(\mathbf{e}'\Sigma^{-1}\bar{\mathbf{x}}\right)\end{bmatrix}}{\left(\mathbf{e}'\boldsymbol{\Sigma}^{-1}\mathbf{e}\right)\left(\mathbf{e}_2'\Sigma^{-1}\mathbf{e}_2\right) - \left(\frac{n_2}{n}\right)\left(\mathbf{e}_2'\Sigma^{-1}\mathbf{e}\right)^2}; \tag{A.5}$$

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313 where $\bar{\mathbf{x}}$ is a k-vector representing population-specific sample means over the entire
314 duration of the experiment. Furthermore the variance is equal to

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$$\operatorname{var}\hat{\boldsymbol{\theta}} = \operatorname{var}\begin{bmatrix}\hat{\mu}\\ \hat{\delta}\end{bmatrix} = \left(\mathbf{B}^{\mathbf{T}}\boldsymbol{\Omega}^{-1}\mathbf{B}\right)^{-1} = \frac{\begin{bmatrix} n_2\mathbf{e}_2'\Sigma^{-1}\mathbf{e}_2 & -n_2\mathbf{e}_2'\Sigma^{-1}\mathbf{e}\\ -n_2\mathbf{e}_2'\Sigma^{-1}\mathbf{e} & n\mathbf{e}'\boldsymbol{\Sigma}^{-1}\mathbf{e}\end{bmatrix}}{nn_2\left(\mathbf{e}'\boldsymbol{\Sigma}^{-1}\mathbf{e}\right)\left(\mathbf{e}_2'\Sigma^{-1}\mathbf{e}_2\right) - \left(n_2\mathbf{e}_2'\Sigma^{-1}\mathbf{e}\right)^2}\,. \tag{A.6}$$

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317

318 We next turn to the estimating equation for the variance covariance matrix itself. We do
319 this by maximizing the likelihood function with respect to the inverse of the covariance
320 matrix, denoted by $\boldsymbol{\Sigma}^{-1}$. There are two formulas for matrix derivatives, found in Dwyer
321 (1967) that we make use of

$$\frac{\partial \ln|\boldsymbol{\Sigma}^{-1}|}{\partial \boldsymbol{\Sigma}^{-1}} = \boldsymbol{\Sigma} \tag{A.7}$$

and

$$\frac{\partial \mathbf{z}'\boldsymbol{\Sigma}^{-1}\mathbf{z}}{\partial \boldsymbol{\Sigma}^{-1}} = \mathbf{z}\mathbf{z}', \tag{A.8}$$

where $\mathbf{z}$ is any vector of length *k* that does not itself depend on the variance matrix.

We first write the log-likelihood in a more convenient form when conceiving as a function of the variance matrix. Let

$$l(\boldsymbol{\Sigma}) = C + (n/2)\ln|\boldsymbol{\Sigma}^{-1}| - (1/2)\sum_{t=1}^{n}\mathbf{z}_t\boldsymbol{\Sigma}^{-1}\mathbf{z}_t, \tag{A.9}$$

where $\mathbf{z}_t = \mathbf{x}_t - [\mathbf{e} \quad \mathbf{0}]\boldsymbol{\theta}$ when $t \le n_1$ and $\mathbf{z}_t = \mathbf{x}_t - [\mathbf{e} \quad \mathbf{e}_2]\boldsymbol{\theta}$ when $t > n_1$.

Using these formulas, we may show that

$$\frac{\partial l(\boldsymbol{\Sigma})}{\partial \boldsymbol{\Sigma}^{-1}} = (n/2)\boldsymbol{\Sigma} - (1/2)\sum_{t=1}^{n}\mathbf{z}_t\mathbf{z}_t'. \tag{A.10}$$

Setting this derivative equal to zero and solving for $\boldsymbol{\Sigma}$ yields the estimating equation

$$\hat{\boldsymbol{\Sigma}} = (1/n)\sum_{t=1}^{n}\mathbf{z}_t\mathbf{z}_t'. \tag{A.11}$$

We also consider a special case when the variance matrix has the form of an intraclass covariance matrix, $\boldsymbol{\Sigma}_2$. In such a case we can write

$$\boldsymbol{\Sigma}_2^{-1} = (a-b)\mathbf{I} + b\mathbf{e}\mathbf{e}' . \tag{A.12}$$

343

344 In this case, all of the diagonal entries of the inverse covariance matrix are equal to the
345 scalar quantity *a* all of the off-diagonal entries are equal to the scalar quantity *b*. In this
346 special case, the log-likelihood function may be written as

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$$l(\boldsymbol{\Sigma}_2) = C + (n/2)\ln|\boldsymbol{\Sigma}_2^{-1}| - (1/2)\sum_{t=1}^{n}\mathbf{z}_t\boldsymbol{\Sigma}_2^{-1}\mathbf{z}_t . \tag{A.13}$$

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349 We make use of the following formulas when deriving the derivative of this function

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$$\frac{\partial \ln|\boldsymbol{\Sigma}_2^{-1}|}{\partial a} = k\sigma_{11} \text{ and } \frac{\partial \ln|\boldsymbol{\Sigma}_2^{-1}|}{\partial b} = k(k-1)\sigma_{12} , \tag{A.14}$$

351

352 where σ_{11} is the common variance term in the variance matrix and σ_{12} is the common
353 covariance value. Also used are the formulas

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$$\frac{\partial \mathbf{z}'\boldsymbol{\Sigma}_2^{-1}\mathbf{z}}{\partial a} = \mathbf{z}'\mathbf{z} \text{ and } \frac{\partial \mathbf{z}'\boldsymbol{\Sigma}_2^{-1}\mathbf{z}}{\partial b} = \mathbf{e}'\mathbf{z}\mathbf{z}'\mathbf{e} - \mathbf{z}'\mathbf{z} \tag{A.15}$$

355

356 Armed with these equations, we may show that

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$$\frac{\partial l(\boldsymbol{\Sigma}_2^{-1})}{\partial a} = (n/2)k\sigma_{11} - (1/2)\sum_{t=1}^{n}\mathbf{z}_t'\mathbf{z}_t \tag{A.16}$$

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359 and

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$$\frac{\partial l(\boldsymbol{\Sigma}_2^{-1})}{\partial a} = (n/2)k(k-1)\sigma_{12} - (1/2)\sum_{t=1}^{n}\mathbf{e}'\mathbf{z}_t\mathbf{z}_t'\mathbf{e} - \mathbf{z}_t'\mathbf{z}_t . \tag{A.17}$$

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Setting these partial derivatives equal to zero yields the following estimating equations

$$\hat{\sigma}_{11} = \frac{\sum_{t=1}^{n} \mathbf{z}_t' \mathbf{z}_t}{nk} \tag{A.18}$$

and

$$\hat{\sigma}_{12} = \frac{\sum_{t=1}^{n} \mathbf{e}' \mathbf{z}_t \mathbf{z}_t' \mathbf{e} - \mathbf{z}_t' \mathbf{z}_t}{nk(k-1)}. \tag{A.19}$$

The maximum likelihood estimator for the intraclass covariance matrix is therefore equal to

$$\hat{\boldsymbol{\Sigma}}_2 = (\hat{\sigma}_{11} - \hat{\sigma}_{12})\mathbf{I} + \hat{\sigma}_{12}\mathbf{e}\mathbf{e}'. \tag{A.20}$$

Numerical algorithm.—Armed with the estimating equations for the parameters we are now prepared to derive an algorithm to solve the estimating equations for the unknown estimates of $\hat{\boldsymbol{\theta}}$ and $\hat{\boldsymbol{\Sigma}}$ (or $\hat{\boldsymbol{\Sigma}}_2$ in the case of the intraclass covariance matrix). Note that an iterative procedure is used because the maximum likelihood estimate of $\boldsymbol{\theta}$ depends on the maximum likelihood estimate of $\boldsymbol{\Sigma}$ in equation (A.6). (When the variance matrix is assumed known, no such iterative procedure is required, one simply uses equation (A.6) with the known variance matrix.)

The iterative procedure begins by making an initial estimate of the variance matrix, call it $\hat{\boldsymbol{\Sigma}}^{(0)}$. The next step is to make an initial estimate of the $\boldsymbol{\theta}$ vector. This is accomplished by using $\hat{\boldsymbol{\Sigma}}^{(0)}$ in place of $\boldsymbol{\Sigma}$ in equation (A.6) and solve for $\hat{\boldsymbol{\theta}}^{(0)}$. The estimate $\hat{\boldsymbol{\theta}}^{(0)}$ is then used in equation (A.11) to get an updated estimate of the variance matrix, $\hat{\boldsymbol{\Sigma}}^{(1)}$. This entire procedure is repeated with the most recent updates of the parameters until the

likelihood function fails to decrease by some specified tolerance. If the intraclass covariance matrix structure is used, simply use equation (A.20) in place of equation (A.11) in the above algorithm.

Appendix 2: Code to calculate statistical power of a BACI-type experiment with known variance

```
#Program to estimate standard errors and power of a BACI-type experiment
#This 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.
#variables and descriptions
#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 q*se 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
```

Appendix 3: Code for estimation when variance is unknown

```
#Iterate until maximum likelihood estimates are obtained
#solving the estimating equations which were
#determined by setting the partial derivatives of the
#likelihood function to zero.
myoptim2<-function(xmat,s2,rho,me,n1,k1,iform=iform){
 k<-dim(xmat)[1]
 n<-dim(xmat)[2]
 SIG2<-diag(1,k)
 par<-get.pars(xmat,SIG2,n1,k1)
 SIG2<-get.SIG2(par,xmat,n1,k1,iform=iform)
 lf1<-lf(par=par,x=xmat,n1=n1,k1=k1,SIG2)
 etol<-1.e-5
 err<-2.*etol*(abs(lf1)+etol)
 #look for relative function convergence to mles
 iter<-0
 while(err>etol*(abs(lf1)+etol)){
   par<-get.pars(xmat,SIG2,n1,k1)
   SIG2<-get.SIG2(par,xmat,n1,k1,iform=iform)
   lf2<-lf(par=par,x=xmat,n1=n1,k1=k1,SIG2)
   err<-abs(lf2-lf1)
   lf1<-lf2
   iter<-iter+1
   if(iter>100)stop("too many iterations in myoptim2")
 }
 print(iter)
 return(list(par=par,SIG2=SIG2))
 }

#Use estimating equations to solve for parameter values
#Returns control mean (mu) and treatment effect (delta)
get.pars<-function(xmat,SIG2,n1,k1){
 n<-dim(xmat)[2]
 n2<-n-n1
 k<-dim(xmat)[1]
 E<-rep(1,k)
 E1<-c(rep(1,k1),rep(0,k-k1))
 E2<-c(rep(0,k1),rep(1,k-k1))
 xbar2<-apply(xmat[,(n1+1):n],c(1),mean)
 xbar<-apply(xmat,c(1),mean)
 INVSIG2<-solve(SIG2)
```

```
 delta<-(t(E2)%*%INVSIG2%*%xbar2)*(t(E)%*%INVSIG2%*%E)-
t(E)%*%INVSIG2%*%xbar*(t(E2)%*%INVSIG2%*%E)
 den<-(t(E)%*%INVSIG2%*%E)*(t(E2)%*%INVSIG2%*%E2)-
(n2/n)*(t(E2)%*%INVSIG2%*%E)^2
 delta<-delta/den
 mu<-t(E2)%*%INVSIG2%*%xbar2-(t(E2)%*%INVSIG2%*%E2)*delta
 den<-t(E2)%*%INVSIG2%*%E
 mu<-mu/den
 return(c(mu,delta))
 }

#log-likelihood function
lf<-function(par,x,n1,k1,SIG2){
 INVSIG2<-solve(SIG2)
 n<-dim(x)[2]
 k<-dim(x)[1]
 z<-x
 like<--k*.5*n*log(2*pi)-.5*n*log(det(SIG2))
 for(ii in 1:n1){
  z[,ii]<-x[,ii]-rep(par[1],k)
  like<-like-.5*t(z[,ii])%*%INVSIG2%*%z[,ii]
 }
 for(ii in (n1+1):n){
  z[,ii]<-x[,ii]-c(rep(par[1],k1),rep(par[1]+par[2],k-k1))
  like<-like-.5*t(z[,ii])%*%INVSIG2%*%z[,ii]
 }
 return(like)
}

#Get the estimate variance-covariance matrix
#This is based on the esimating equations
#variance is unknown and has the
#form of an intraclass covariance matrix when iform=1
get.SIG2<-function(par,x,n1,k1,iform=1){
 n<-dim(x)[2]
 k<-dim(x)[1]
 z<-x
 SIG2<-matrix(0,ncol=k,nrow=k)
 for(ii in 1:n1){
  z[,ii]<-x[,ii]-rep(par[1],k)
  SIG2<-SIG2+z[,ii]%*%t(z[,ii])/n
 }
 for(ii in (n1+1):n){
  z[,ii]<-x[,ii]-c(rep(par[1],k1),rep(par[1]+par[2],k-k1))
```

```
514       SIG2<-SIG2+z[,ii]%*%t(z[,ii])/n
515      }
516
517      if(iform==1){
518       s2<-mean(diag(SIG2))
519       s12<-(sum(SIG2)-sum(diag(SIG2)))/(k*k-k)
520       SIG2<-matrix(s12,ncol=k,nrow=k)
521       diag(SIG2)<-s2
522      }
523      return(SIG2)
524     }
```

Appendix 3: Parr-to-smolt survival data

Table A.1. — Parr-to-smolt survival data for eight Snake River populations used in application.

Tagging site	Tagging year	Parr-to-smolt survival
Bear Valley Creek	1992	0.1708
Bear Valley Creek	1993	0.2290
Bear Valley Creek	1994	0.0824
Bear Valley Creek	1997	0.3517
Bear Valley Creek	1998	0.2101
Bear Valley Creek	1999	0.2000
Bear Valley Creek	2000	0.2240
Bear Valley Creek	2001	0.1454
Elk Creek	1992	0.1260
Elk Creek	1993	0.1622
Elk Creek	1994	0.1032
Elk Creek	1997	0.4732
Elk Creek	1998	0.2221
Elk Creek	1999	0.2201
Elk Creek	2000	0.3125
Elk Creek	2001	0.1369
Imnaha River	1992	0.1492
Imnaha River	1993	0.2271
Imnaha River	1994	0.1701
Imnaha River	1995	0.2849
Imnaha River	1996	0.2911
Imnaha River	1997	0.4788
Imnaha River	1998	0.3058
Imnaha River	1999	0.3024

Imnaha River	2000	0.3194
Imnaha River	2001	0.2538
Johnson Creek	1992	0.1722
Johnson Creek	1993	0.2791
Johnson Creek	1994	0.0703
Johnson Creek	1998	0.2918
Johnson Creek	1999	0.2766
Johnson Creek	2000	0.3131
Johnson Creek	2001	0.2798
Marsh Creek	1992	0.1418
Marsh Creek	1993	0.3045
Marsh Creek	1994	0.2114
Marsh Creek	1995	0.3943
Marsh Creek	1997	0.5774
Marsh Creek	1998	0.3126
Marsh Creek	1999	0.2661
Marsh Creek	2001	0.2778
Minam River	1992	0.1966
Minam River	1993	0.2996
Minam River	1994	0.1568
Minam River	1995	0.2032
Minam River	1996	0.2238
Minam River	1997	0.2307
Minam River	1998	0.1858
Minam River	1999	0.2458
Minam River	2000	0.2780
Minam River	2001	0.1480
Poverty Flat	1992	0.2309
Poverty Flat	1993	0.1925

Poverty Flat	1994	0.1099
Poverty Flat	1995	0.1642
Poverty Flat	1996	0.1488
Poverty Flat	1997	0.2707
Poverty Flat	1998	0.1547
Poverty Flat	1999	0.1931
Poverty Flat	2000	0.1712
Poverty Flat	2001	0.0888
Sulphur Creek	1992	0.1053
Sulphur Creek	1994	0.1840
Sulphur Creek	1998	0.1404
Sulphur Creek	1999	0.2261

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Appendix 3: Standard errors of treatment effect

Table A.1. —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(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

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	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

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	0.067	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

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	0.061	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

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

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

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Appendix 4: Percent change in survival needed to deliver power of 0.80.

Table A.2. —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
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

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
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

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