Application of ANOVA for the Analysis of Temporal and Spatial differences in the Length of pelagic goby preyed on by Cape fur seals in the coasts of Namibia

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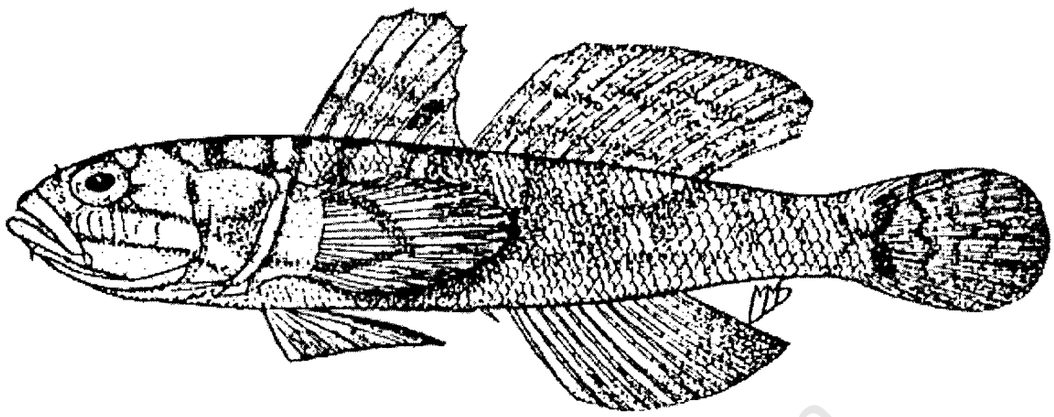
ABSTRACT

The Analysis of variance is a robust technique whereby the total variation present in a set of data is partitioned into two or more components (Wayne, 1999). In this thesis, ANOVA was used to uncover the differences in goby length preyed on by three different colonies of fur seals at the Namibian coast. Moreover, ANOVA was used to investigate temporal differences in lengths of goby preyed on by fur seals in each location of the seal colonies. Results of the analysis are shown in the Analysis and results section, and the findings are discussed in the discussion section. But before these two sections, there are three sections of the thesis. The first section is the general introduction that explains about the general situation and the targets of this thesis. The second section gives a general background on the ANOVA technique. The third section explains the nature of the data and gives background information on gobies.

The following figure of pelagic goby (*Sufflogobius bibarbatus*) is taken (by permission) from the web page www.fishbase.org, picture by Heemstra, Philip C.



CONTENTS

1 GENERAL INTRODUCTION

1. 1 STATEMENT OF THE PROBLEM

Studies on the diets of marine top predators, such as seals and seabirds, have shown that the diet reflects the distribution and abundance of prey species (Berruti & Colclough 1987, Reid 1995, Hunt *et al.*, 1996, North 1996, Crawford 1998, Thompson *et al.*, 1998, Brown *et al.*, 2001, Barlow *et al.*, 2002). Cape fur seals prey on fish such as mackerel and goby. Very little information is available on goby biology; therefore this study should provide some information on goby biology such as changes in fish size and changes in distribution, as well as information on interactions between predator and prey. It is important to determine whether goby length preyed by Cape fur seals vary with season and among different seal colonies in order to find out the changes in fish size and their distribution. Thus, it can contribute towards management of the goby resource if fishing of the species is to commence. Moreover, the possibility of monitoring goby dynamics through scats provides useful information on the availability of goby to predators. If fishing of this resource is to commence, this kind of information would be valuable considering that seabirds in Namibia, such as the endangered African penguin *Spheniscus demersus*, are increasingly relying on goby due to the reduction of the sardine resource (Crawford, 1998).

1. 2 SELECTION OF AN APPROPRIATE STATISTICAL TECHNIQUE

A number of statistical and mathematical techniques are available for analysis of data of different kinds and from different sources. The data to be analyzed could be of practical importance or for experimental purposes. Which technique is appropriate for a particular set of data is

always the most important question to be addressed when one is faced with data to be analyzed. After discovering the right technique for the analysis of specific data, the next important thing is to understand the approaches for the analysis and then correctly interpret the results in order to draw meaningful conclusions. Validity of the results of a statistical analysis clearly depends on the reliability and accuracy of the data used (Keller & Warrack, 1999). Whether one is actually involved in collecting the data, performing a statistical analysis on the data, or simply reviewing the results of such analysis, it is important to realize that the reliability and accuracy of the data depends on the method of collection (Keller & Warrack, 1999).

Among the most widely used descriptive and statistical analysis techniques and models are: Regression Analysis, the Analysis of Variance (ANOVA), Cluster Analysis, Factor Analysis, Principal Component Analysis, Discriminant Analysis, Generalized Linear/Non Linear Models, Survival Analysis, Time Series Analysis/Forecasting, Canonical Analysis, Correspondence Analysis, Multidimensional Scaling, and General Partial Least Squares Models (Wayne, 1999; Iverson & Norpoth, 1987). For this study, ANOVA was chosen to analyze the data. Therefore, it is important to discuss the ANOVA technique and why it is suitable for the analysis of the data of this study.

2 ANALYSIS OF VARIANCE (ANOVA)

2. 1 INTRODUCTION

2. 1. 1 What is ANOVA?

The analysis of variance is a statistical technique for analyzing measurements depending on several kinds of effects operating simultaneously, to decide which of these effects are important and to estimate the effects (Scheffé, 1959). It is a procedure for testing the equality of several 'means' (Montgomery, 1984). In other words, ANOVA is used to test for significant differences between 'means' by comparing variances. More specifically, by partitioning the total variation into different sources associated with the different effects in the design, we are able to compare the variance due to between-groups (or treatments) variability with that of due to the within-group variability (Box *et al.*, 1978). ANOVA is used to uncover the main and interaction effects of categorical explanatory variable(s) called "factors" on an interval response variable (Jaccard, 1998). According to Jaccard (1998) a "main effect" is the direct effect of an explanatory variable on the response variable, while an "interaction effect" is the joint effect of two or more explanatory variables on the response variable. There are also a variety of other ANOVA designs for special purposes: analysis of covariance (ANCOVA) for interval-level control variables, multivariate analysis of variance (MANOVA) for the case of multiple dependent variables, and there is a combination of MANOVA and ANCOVA called MANCOVA (Rutherford, 2001).

2. 1. 2 Assumptions:

The ANOVA model has the following features (John *et al.*, 1988):

A. ANOVA assumes a response variable measured on an interval scale, denoted by y. In its simplest form there are a factor levels (treatments) under study. A probability distribution is associated with each factor level.

B. Homogeneity of Variances ► all probability distributions of y have the same variance, denoted by σ^2. That is, the response variable should have the same variance in each category of the explanatory variables. When there are more than two explanatory variables, there must be homogeneity of variances in the cells formed by the combination of levels of explanatory categorical variables (Iverson & Norpoth, 1987). The reason for this assumption is that the denominator of the F-ratio is the error (within-group) mean square, which is the average of group variances taking group size into account.

C.When groups differ widely in variances, this average is a poor summary measure; however, ANOVA is robust for small and even moderate departures from homogeneity of variances (Box, 1954). A rule of thumb is that the ratio of largest to smallest group variances should be 3.0 or less.(Url: www2.chass.ncsu.edu/garson/pa765/anova.htm, 04/03/2004).

D. Normality ► for each treatment, the probability distribution of the response variable y is normal. For purposes of significance testing, variables follow normality; i.e. the response variable is normally distributed in each category of the explanatory variable(s).

E. ANOVA is robust even for moderate departures from normality (Box *et al.*, 1978).

F. Random Sampling ► for purposes of statistical inference, the subjects in each group need to be randomly sampled.

2. 1. 3 Types of ANOVA Designs

Depending on the number of independent variables (or "factors") involved in the model of the analysis of variance, ANOVA designs are divided into one-way ANOVA, two-way ANOVA, and multi factor n-way ANOVA (Turner & Thayer, 2001; Iverson & Norpoth, 1987).

One-way ANOVA – tests differences in means of a single interval response variable among two, three, or more groups formed by the categories of a single categorical explanatory variable. This method is also known as univariate ANOVA or simple ANOVA or single classification ANOVA or one-factor ANOVA. This design deals with one explanatory variable with categories and one response variable. It tests whether the groups formed by the categories of the explanatory variable are similar; specifically that they have the same pattern of dispersion as measured by comparing estimates of group variances. If the groups seem different then it is concluded that the explanatory variable has an effect on the response. The two-sample t-test may be seen as a special case of one-way ANOVA. The t-test is a test of significance of the difference in the means of a single interval response variable, for the case of two groups formed by a categorical explanatory variable (Levin, 1999).

Two-way ANOVA - analyzes one interval response in terms of the categories formed by combinations of two explanatory variables. Two-way ANOVA tests whether groups formed by the combined categories of the explanatory variables have similar means. There is a set of interaction effects in addition to the effects of the two explanatory variables, in two-way ANOVA.

Two-way ANOVA is less sensitive than one-way ANOVA to moderate violations of the assumption of homogeneity of variances across the

groups. Therefore equal sample sizes for all treatments are recommended for best results in two-way ANOVA (Montgomery, 2001).

Multifactor or n-way ANOVA – To generalize, n-way ANOVA deals with n explanatory variables. It should be noted that as the number of explanatory variables increases, the number of potential interactions proliferates. Two explanatory variables have a single first-order interaction (AB). Three explanatory variables have three first-order interactions (AB, AC, BC) and one-second -order interaction (ABC). Four explanatory variables have six first-order (AB, AC, AD, BC, BD, CD) interactions, three second-order (ABC, ACD, BCD) interactions, and one third-order (ABCD) interaction. As the number of interactions increases, it becomes increasingly difficult to interpret the higher order terms in the model.

According to Turner & Thayer (2001), there are several different types of experimental designs of ANOVA and ANCOVA. These are:

i. Between-groups ANOVA design (a response variable is measured for independent groups of sample members, where each group is exposed to a different condition; the set of conditions is called the between-groups factor).
ii. Completely Randomized design (this is simply a between groups ANOVA design where randomization is an effort to control for all unmeasured factors).
iii. Randomized Complete Block design (this is an experimental design in which the subjects are first matched into blocks on some control variable some times called "nuisance variable" and then within each block randomly allocated to specific treatment groups).

iv. Latin Square designs (which extend the logic of block designs to control for two categorical variables and reduce the number of observations necessary to compute ANOVA).

v. Graeco-Latin Square designs (extend to block designs to control for three categorical variables).

vi. Factorial ANOVA designs (used to assess the relative importance of various combinations of independent variables).

vii. General linear model ANOVA (which is more generalized and supports the use of categorical response variables).

The key test statistic in ANOVA is the F-test for difference of group means, testing if the means of the groups formed by combination of values for multiple explanatory variables are different enough not to have occurred by chance (Box, 1954; Box *et al.*, 1978). The alternative designs affect how the F-ratio is computed in generating the ANOVA table. However, regardless of the designs, the ANOVA table is interpreted similarly (Turner & Thayer, 2001). The statistical significance of the F-ratio indicates the significance of each main and interaction effect (each covariate effect in ANCOVA). If the group means do not differ significantly then it is inferred that the explanatory variable(s) did not have an effect on the response variable. If the F-test shows that over all, the explanatory variable(s) is (are) related to the response variable, then multiple comparison tests of significance are used to explore just which specific groups of the explanatory variable(s) have the most to do with the relationship (Montgomery, 2001).

Like regression, ANOVA is a parametric procedure that assumes normality, which means the response variable has a normal distribution for each combined category of the explanatory variable(s) (Iverson & Norpoth, 1987). But unlike regression, ANOVA does not assume linear relationships and handles interaction effects automatically (Iverson &

Norpoth, 1987). In this thesis only the one-way and two-way fixed effects ANOVA models will be considered, because the data under analysis are suitable for these models, as will be explained later.

2. 2 THE ONE-WAY AND TWO-WAY ANALYSIS OF VARIANCE

2. 2. 1 One-way:

In comparing "a" treatments or "a" levels of a single factor, it is useful to describe the observations by a linear statistical model,

$$y_{ij} = \mu + \tau_i + \varepsilon_{ij} \; ; \quad i = 1,2,....,a \; ; \; j = 1,2,....,n$$

Where y_{ij} is the $(ij)^{th}$ observation (or the j^{th} observation taken under treatment i), μ is a parameter common to all treatments called the overall mean, τ_i is a parameter unique to the i^{th} treatment effect, n is number of observations within each treatment, and ε_{ij} is a random error component (Montgomery, 2001). The total number of observations is na. The objectives will be to test appropriate hypotheses about the treatment effects and to estimate them. For hypotheses testing, the model errors are assumed to be normally and independently distributed random variables with mean of zero and a common variance for all levels of the factor (Montgomery, 2001). In one-way ANOVA, it is relatively acceptable for each treatment to have a different sample size n than in two-way ANOVA, which will be discussed later.

The above model is called the one-way classification analysis of variance, because only one factor is investigated. According to Montgomery (2001), the model describes two different situations with respect to the treatment effects. First, the "a" treatment levels could have been specifically chosen by the experimenter. In this situation there is a need to test hypotheses

about the treatment means, and conclusions will apply only to the factor levels considered in the analysis. The conclusions cannot be extended to similar treatments that were not explicitly considered. Estimation of the model parameters μ, τ_i, and the variance or σ^2 may also be needed. This model is called the fixed effects model (Montgomery, 2001). Alternatively, the "a" treatments could be a random sample from a larger population of treatments. In this situation one should be able to extend the conclusions (which are based on the sample of treatments) to all treatments in the population, whether they were explicitly considered in the analysis or not. Here the τ_i are random variables, and knowledge about the particular ones investigated is relatively less important. Instead, it is important to test hypotheses about the variability of the τ_i and to try to estimate this variability (Montgomery, 1984). This model is called the random effects, or components of variance, model. In our case the fixed effects model will be considered and unequal sizes for each treatment group are permissible.

2. 2. 2 Two-way:

The two-factor design is the simplest type of factorial design, which involves two factors, or sets of treatments (Hicks & Turner, 1999; Montgomery, 2001). There are "a" levels of factor A and "b" levels of factor B. And these are arranged in a factorial design; that is, each replicate of the experiment contains all "ab" treatment combinations. If there are "n" replicates of the experiment, and y_{ijk} represents the observation taken under the i^{th} level of factor A and j^{th} level of factor B in the k^{th} replicate, the observations may be described by a linear statistical model,

$$y_{ijk} = \mu + \tau_i + \beta_j + (\tau\beta)_{ij} + \varepsilon_{ijk} \; ; \; i = 1,2,\ldots,a; \; j = 1,2,\ldots,b; \text{ and } k = 1,2,\ldots,n$$

where μ is the overall mean effect, τ_i is the i^{th} level of the row factor A, β_j is the effect of the j^{th} level of column factor B, $(\tau\beta)_{ij}$ is the effect of the

interaction between τ_i and β_j, and ε_{ijk} is a random error component. Since there are n replicates, there are abn total numbers of observations.

If both factors are assumed fixed and there is no interaction effect, the model of a two-factor analysis becomes as follows,

$$y_{ijk} = \mu + \tau_i + \beta_j + \varepsilon_{ijk};\ i = 1,2,\ldots,a;\ j = 1,2,\ldots,b;\ \text{and}\ k = 1,2,\ldots,n$$

Maximum care must be taken in dispensing with the interaction terms, however, because the presence of a significant interaction can have a dramatic impact on the interpretation of the data (Montgomery, 2001). With the two-way ANOVA, it is advisable for a standard analysis to have equal sample sizes n in each of ab cells. But if the situation demands unequal sample size, maximum care must be given to the assumptions of the ANOVA model. The model of such a design with different sample size is called "unbalanced" and the calculations require modifications, as will be discussed later.

2. 3 ANALYSIS OF THE FIXED EFFECTS MODEL

2. 3. 1 One-way:

In the fixed effects model, the treatment effects τ_i are usually defined as deviations from the overall mean, so that

$$\sum_{i=1}^{a} \tau_i = 0$$

If $y_{i.}$ denotes the total of the observations under the i^{th} treatment, then $\bar{y}_{i.}$ denotes the average of the observations under the i^{th} treatment (Montgomery, 2001), and similarly, if $y_{..}$ denotes the grand total of all

observations then $\bar{y}_{..}$ denotes the grand average of all observations, expressed symbolically

$$y_{i.} = \sum_{j=1}^{n} y_{ij} \quad \Rightarrow \quad \bar{y}_{i.} = {}^{y_{i.}}\!/_{n} \; ; \; i = 1,2,\ldots,a$$

and $$y_{..} = \sum_{i=1}^{a} \sum_{j=1}^{n} y_{ij} \quad \Rightarrow \quad \bar{y}_{..} = {}^{y_{..}}\!/_{N}$$

where N is the total number of observations ($N=na$). It is known that the mean of the i^{th} treatment is the expected value of the i^{th} treatment (or $E[y_{ij}]$), which is

$$E[y_{ij}] = \mu_i = \mu + \tau_i \; ; \; i = 1,2,\ldots,a$$

Thus, the mean of the i^{th} treatment consists of the overall mean plus the i^{th} treatment effect. Now, to test the equality of the "a" treatment means, we construct

H_0: $\mu_1 = \mu_2 = \ldots\ldots = \mu_a$

H_1: $\mu_i \neq \mu_j$, for at least one i, j

If H_0 is true, all treatments have a common mean μ.

An equivalent way to write the above hypothesis is in terms of the treatment effects τ_i, as follows

H_0: $\tau_1 = \tau_2 = \ldots\ldots = \tau_a = 0$

H_1: $\tau_i \neq 0$, for at least one i

The appropriate procedure for testing the equality of "a" treatment means (or for testing that the treatment effects τ_i are zero) is the analysis of variance.

2. 3. 2 Two-way:

As in one-way (single factor) ANOVA let $y_{i..}$ denote the total of all observations under the i^{th} level of factor A, $y_{.j.}$ denote the total of all observations under the j^{th} level of factor B, $y_{ij.}$ denote the total of all observations in ij^{th} cell, and $y_{...}$ denote the grand total of all the observations. Similarly, $\bar{y}_{i..}$, $\bar{y}_{.j.}$, $\bar{y}_{ij.}$ and $\bar{y}_{...}$ are defined as the corresponding row, column, cell, and grand averages. Expressed symbolically

$$y_{i..} = \sum_{j=1}^{b}\sum_{k=1}^{n} y_{ijk} \Rightarrow \bar{y}_{i..} = y_{i..}/bn \; ; \; i = 1,2,.....,a$$

$$y_{.j.} = \sum_{i=1}^{a}\sum_{k=1}^{n} y_{ijk} \Rightarrow \bar{y}_{.j.} = y_{.j.}/an \; ; j = 1,2,.....,b$$

$$y_{ij.} = \sum_{k=1}^{n} y_{ijk} \Rightarrow \bar{y}_{ij.} = y_{ij.}/n \; ; \; i = 1,2,....,a; \; j = 1,2,....b$$

$$y_{...} = \sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{n} y_{ijk} \Rightarrow \bar{y}_{...} = y_{...}/abn;$$

If both factors are initially assumed to be fixed, and if the treatment effects are defined as deviations from the overall means, then

$$\sum_{i=1}^{a}\tau_i = 0 \text{ and } \sum_{j=1}^{b}\beta_j = 0$$

Similarly, for the interaction effect, the deviations from the column means and the deviations from the row means are zero:

$$\sum_{i=1}^{a}(\tau\beta)_{ij} = \sum_{j=1}^{b}(\tau\beta)_{ij} = 0$$

In the two-factor design, both row and column factors, A and B, are of equal interest. Hence, the hypotheses of interest are testing for the equality of row treatment effects, say

H_0: $\tau_1 = \tau_2 = \ldots = \tau_a = 0$

H_1: at least one $\tau_i \neq 0$

and the equality of the column treatment effects, say

H_0: $\beta_1 = \beta_2 = \ldots = \beta_b = 0$

H_1: at least one $\beta_j \neq 0$

In addition, to check if row and column treatments interact, we test

H_0: $(\tau\beta)_{ij} = 0$; for all i, j

H_1: at least one $(\tau\beta)_{ij} \neq 0$

Therefore, for the analyses of all the above hypotheses testing, we use the corresponding ANOVA tests (Montgomery, 2001).

However in the two-factor design, the primary interest initially is upon the question of whether or not the two factors interact. This question determines whether or not it is meaningful to simply reduce the discussion of the data to discussion of the row effects and the column effects.

When there is evidence that the two treatment factors interact, the treatment will subsequently focus upon the individual treatment combination means (the cells $\bar{y}_{ij.}$).

When there is very little evidence in favor of interaction, the analysis can be limited to the comparisons of row means $\bar{y}_{i..}$ and the comparisons of column means $\bar{y}_{.j.}$.

2. 4 DECOMPOSITION OF THE TOTAL SUM OF SQUARES

2. 4. 1 One-way:

The total corrected sum of squares is used as a measure of overall variability in data (Rice, 1995; Montgomery, 2001). Montgomery (2001) further stated that intuitively, the above statement is reasonable, because, if one was to divide the total sum of squares (SS_T) by the appropriate number of degrees of freedom (in this case N-1 = an-1), one treats the values as a random sample, and obtains the sample variance of the y's. And the sample variance is, of course, a standard measure of variability.

The total corrected sum of squares (SS_T) may be written as

$$SS_T = \sum_{i=1}^{a}\sum_{j=1}^{n}(y_{ij} - \bar{y}_{..})^2 = \sum_{i=1}^{a}\sum_{j=1}^{n}[(\bar{y}_{i.} - \bar{y}_{..}) + (y_{ij} - \bar{y}_{i.})]^2$$

$$\text{Or } \sum_{i=1}^{a}\sum_{j=1}^{n}(y_{ij} - \bar{y}_{..})^2 = n\sum_{i=1}^{a}(\bar{y}_{i.} - \bar{y}_{..})^2 + \sum_{i=1}^{a}\sum_{j=1}^{n}(y_{ij} - \bar{y}_{i.})^2 + 2\sum_{i=1}^{a}\sum_{j=1}^{n}(\bar{y}_{i.} - \bar{y}_{..})(y_{ij} - \bar{y}_{i.})$$

However, the cross product term in the above equation is zero (Montgomery, 1984; Hicks & Turner, 1999), because

$$\sum_{j=1}^{n}(y_{ij}-\bar{y}_{i.})=y_{i.}-n\bar{y}_{i.}=y_{i.}-n(y_{i.}/n)=0$$

Therefore,

$$\sum_{i=1}^{a}\sum_{j=1}^{n}(y_{ij}-\bar{y}_{..})^2=n\sum_{i=1}^{a}(\bar{y}_{i.}-\bar{y}_{..})^2+\sum_{i=1}^{a}\sum_{j=1}^{n}(y_{ij}-\bar{y}_{i.})^2 \quad \text{.....(Identity equation)}$$

This final equation may be referred to as the fundamental equation of the analysis of variance (Hicks & Turner, 1999). It shows that the total variability in the data, as measured by the total corrected sum of squares, can be partitioned into a sum of squares of differences between treatment averages and the grand averages, plus a sum of squares of differences of observations within treatments from the treatment averages (Hicks & Turner, 1999; Montgomery, 2001). Moreover, the difference between observed treatment averages and the grand average is a measure of differences between treatment means, while the differences of observations within a treatment from the treatment average (for this model) can be due to random error only (Montgomery, 1984). Thus,

$$SS_T = SS_{treatment} + SS_E$$

where $SS_{treatment}$ is called the sum of squares due to treatments (or between treatments), and SS_E is called the sum of squares due to error (or within treatments). There are $N=an$ total number of observations, so SS_T has N-1 degrees of freedom. There are "a" levels of the factor (or "a" treatment means), so $SS_{treatment}$ has a-1 degrees of freedom. Within any treatment there are n replicates providing n-1 degrees of freedom with which to estimate the experimental error. There are "a" treatments, therefore we have $a(n-1) = an-a = N-a$ degrees of freedom for error.

According to Montgomery (1984) it is important to explicitly examine the two terms on the right hand side of the fundamental equation of the analysis of variance. If the error sum of squares is considered first, then

$$SS_E = \sum_{i=1}^{a}\sum_{j=1}^{n}(y_{ij} - \bar{y}_{i.})^2 = \sum_{i=1}^{a}[\ \sum_{j=1}^{n}(y_{ij} - \bar{y}_{i.})^2\ ]$$

In this form it can easily be seen that the term within the brackets, if divided by n-1, is the sample variance S_i^2 in the i^{th} treatment, or

$$S_i^2 = \frac{\sum_{j=1}^{n}(y_{ij} - \bar{y}_{i.})^2}{n-1};\ i = 1, 2, ..., a$$

And the "a" sample variances may be pooled to give one estimate of the common population variance as follows (Montgomery, 1984),

$$\frac{(n-1)S_1^{\ 2} + (n-1)S_2^{\ 2} + ... + (n-1)S_a^{\ 2}}{(n-1) + (n-1) + ... + (n-1)} = \frac{\sum_{i=1}^{a}[\ \sum_{j=1}^{n}(y_{ij} - \bar{y}_{i.})^2\ ]}{\sum_{j=1}^{a}(n-1)} = \frac{SS_E}{(N-a)}$$

Hence, $SS_E/(N-a)$ is an estimate of the common variance within each of the "a" treatments. This estimate is an unbiased estimate of the variance (Hicks, 1993). Similarly, if there were no differences between the "a" treatment means, the variation of the treatment averages from the grand average could be used to estimate σ^2. Specifically, for any value of n,

$$\frac{SS_{treatment}}{(a-1)} = \frac{n\sum_{i=1}^{a}(\bar{y}_{i.} - \bar{y}_{..})^2}{(a-1)},$$

is an estimate of σ^2 if treatment means are equal. The reason for this identity is that the quantity $\sum_{i=1}^{a}(\bar{y}_{i.}-\bar{y}_{..})^2/(a\text{-}1)$ estimates the variance of the treatment averages σ^2/n, so that $n\sum_{i=1}^{a}(\bar{y}_{i.}-\bar{y}_{..})^2/(a\text{-}1)$ must estimate σ^2, when there are no differences in treatment means (Montgomery, 2001; Hicks, 1993). It can be seen that the analysis of variance identity equation provides two estimates of σ^2, one based on the inherent variability within treatments and one based on the variation between treatments (Montgomery, 2001). If there are no differences in treatment means, these two estimates should be very similar, and if they are not, it is suspected that the observed difference must be due to differences in treatment means.

The quantities $MS_{treatment}=\frac{SS_{treatment}}{(a-1)}$ and $MS_E=\frac{SS_E}{(N-a)}$ are called mean squares (Montgomery, 1984). And their expected values are

$E[MS_E] = E[\frac{SS_E}{N-a}] = \sigma^2$; and $E[MS_{treatment}] = \sigma^2+n\frac{\sum_{i=1}^{a}\tau_i^2}{(a-1)}$ (See Montgomery, 1984 for computations).

Therefore, $MS_E = SS_E/N\text{-}a$ estimates σ^2, and if there are no differences in treatment means (which implies that $\tau_i=0$), then $MS_{treatment} = SS_{treatment}/a\text{-}1$ also estimates σ^2. However, when treatment means do differ, the expected value of the treatment mean square is greater than σ^2. Now, it seems clear that comparing $MS_{treatment}$ and MS_E can test the hypothesis of no difference in treatment means. This comparison will be considered later.

2. 4. 2 Two-way:

As in the single factor case, the total corrected sum of squares in the two-factor design can be written as follows (Montgomery, 2001; Hicks & Turner, 1999).

$$\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{n}(y_{ijk}-\bar{y}_{...})^2=\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{n}[(\bar{y}_{i..}-\bar{y}_{...})+(\bar{y}_{.j.}-\bar{y}_{...})+(\bar{y}_{ij.}-\bar{y}_{i..}-\bar{y}_{.j.}+\bar{y}_{...})+(y_{ijk}-\bar{y}_{ij.})\ ]^2$$

Because the six cross products on the right hand side sum to zero (Montgomery, 1984; Hicks & Turner, 1999),

$$\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{n}(y_{ijk}-\bar{y}_{...})^2=bn\sum_{i=1}^{a}(\bar{y}_{i..}-\bar{y}_{...})^2+an\sum_{j=1}^{b}(\bar{y}_{.j.}-\bar{y}_{...})^2+n\sum_{i=1}^{a}\sum_{j=1}^{b}(\bar{y}_{ij.}-\bar{y}_{i..}-\bar{y}_{.j.}+\bar{y}_{...})^2$$

$$+\sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{k=1}^{n}(y_{ijk}-\bar{y}_{ij.})^2$$

The total sum of squares has been partitioned into a sum of squares due to "rows" or factor A (SS_A), a sum of squares due to "columns" or factor B (SS_B), a sum of squares due to the interaction between factor A and factor B (SS_{AB}), and a sum of squares due to error (SS_E). Therefore, the above equation may be written symbolically as (Montgomery, 1984),

$$SS_T = SS_A + SS_B + SS_{AB} + SS_E$$

The number of degrees of freedom associated with each sum of squares is as follows

Effect	Degrees of freedom
A	a-1
B	b-1
AB (interaction)	$(a\text{-}1)(b\text{-}1)$
Error	$ab(n\text{-}1)$
Total	$abn - 1$

The main effects A and B have a and b levels, respectively; therefore, they have a-1 and b-1 degrees of freedom. The interaction degrees of freedom are simply the number of degrees of freedom for cells (which is ab-1) minus the number of degrees of freedom for the two main effects, A and B; that is $ab\text{-}1\text{-}(a\text{-}1)\text{-}(b\text{-}1) = (a\text{-}1)(b\text{-}1)$. Within each of the ab cells there are n-1 degrees of freedom between the n replicates, thus there are $ab(n\text{-}1)$ degrees of freedom for the error (Montgomery, 2001).

Each of the sums of squares divided by its degrees of freedom is a mean square. And the expected values of the mean squares are (Montgomery, 1984):

$$\mathrm{E}[MS_A] = \mathrm{E}\left[\frac{SS_A}{a-1}\right] = \sigma^2 + \frac{bn\sum_{i=1}^{a}\tau_i^2}{a-1}$$

$$\mathrm{E}[MS_B] = \mathrm{E}\left[\frac{SS_B}{b-1}\right] = \sigma^2 + \frac{an\sum_{j=1}^{b}\beta_j^2}{b-1}$$

$$E[MS_{AB}] = E\left[\frac{SS_{AB}}{(a-1)(b-1}\right] = \sigma^2 + \frac{n\sum_{i=1}^{a}\sum_{j=1}^{b}(\tau\beta)_{ij}}{(a-1)(b-1)}$$

$$E[MS_E] = E\left[\frac{SS_E}{ab(n-1)}\right] = \sigma^2$$

If the null hypotheses of no row treatment effects, no column treatment effects, and no interaction are true, then MS_A, MS_B, and MS_E are all estimates of σ^2 (Montgomery, 2001). However, if there are differences between row treatment effects, then MS_A will be larger than MS_E. Similarly, if there are column treatment effects or interactions present, then the corresponding mean squares will be larger than MS_E. Therefore, to test the significance of either main effects or their interaction, the corresponding mean square is divided by the error mean square (MS_E). Large values of these ratios imply that the data do not support the corresponding null hypotheses (Montgomery, 2001).

2. 5 STATISTICAL ANALYSIS

2. 5. 1 F-test:

A formal test of the hypotheses of no difference in the treatment means (H_0: $\mu_1=\mu_2=\ldots=\mu_a$, or H_0: $\tau_1=\tau_2=\ldots=\tau_a=0$) can be performed. From the assumptions that the errors ε_{ij} are normally and independently distributed with mean zero and variance σ^2 or NID (0, σ^2), the observations y_{ij} are normally and independently distributed with mean $\mu+\tau_i$ and variance σ^2 (Hicks & Turner, 1999; Montgomery, 2001). If H_0 is true, each term of the sum of squares on the right hand side of the identity equation divided by its respective degrees of freedom will yield two independent Chi-square distributed unbiased estimates of σ^2; and if two such unbiased estimates of the same variance are compared, their

ratio can be shown to be distributed as F with a-1, N-a degrees of freedom (Hicks, 1993). Hicks (1993) and Montgomery (2001) further explained that SS_T is a sum of squares in normally distributed random variables and, consequently, it can be shown that SS_T/σ^2 is distributed as Chi-square with N-1 degrees of freedom. Furthermore, it is shown that SS_E/σ^2 is a Chi-square with N-a degrees of freedom, and $SS_{treatment}/\sigma^2$ is a Chi-square with a-1 degrees of freedom if the null hypothesis H_0: $\tau_i = 0$ is true. However, while $SS_{treatment}$ and SS_E are statistically independent the three sums of squares are not all independent, because $SS_{treatment}$ and SS_E add to SS_T. The ratio of two independent Chi-squares over their degrees of freedom is F (Hicks & Turner, 1999). Thus,

$$F = \left(\frac{SS_{treatment}}{a-1}\right) \div \left(\frac{SS_E}{N-a}\right)$$

Cochran`s Theorem is useful in establishing the independence of SS_E and $SS_{treatment}$.

2. 5. 2 Cochran`s Theorem:

Let Z_i be NID(0,1) for i = 1,2,...,υ and

$$\sum_{i=1}^{\upsilon} Z_i^{\,2} = Q_1 + Q_2 + \ldots + Q_S$$

Where S≤ υ and Q_i has υ_i degrees of freedom (i=1,2,...,s). Then the Q_1, Q_2,...,Q_S are independent Chi-square random variables with υ_1,υ_2,..., υ_s degrees of freedom, respectively, if and only if $\upsilon = \upsilon_1 + \upsilon_2 + \ldots + \upsilon_s$.

Because the degrees of freedom for $SS_{treatments}$ and SS_E add to N-1, the total number of degrees of freedom, Cochran`s Theorem implies that $SS_{treatment}/\sigma^2$ are independently distributed Chi-square random variables (Montgomery, 1984).

Therefore, if the null hypothesis of no difference in treatment means is true, the ratio

$$F_0 = \frac{SS_{treatment} / (a-1)}{SS_E / (N-a)} = \frac{MS_{treatment}}{MS_E}$$

is distributed as F with a-1 and N-a degrees of freedom (Montgomery, 2001). Hence, $\frac{MS_{treatment}}{MS_E}$ is the test statistic for the hypothesis of no differences in the treatment means.

From the expected mean squares it can be seen that, in general, MS_E is an unbiased estimator of σ^2. However, if the null hypothesis is false, then the expected value of $MS_{treatment}$ is greater than σ^2. Therefore, under the alternative hypothesis the expected value of the numerator of the test statistic is greater than the expected value of the denominator, and hence H_0 is rejected on values of the test statistic, which are too large to leave Ho unchallenged (Montgomery, 1984). This argument implies an upper tail, one tail critical region. H_0 is rejected if

$$F_0 > F_{\alpha,a-1,N-a} \text{ ; where Fo } = \frac{MS_{treatment}}{MS_E}$$

Letting f denote the observed value of F, the p value is $P(F(a-1, N-a) \geq f)$. If this p value is less than or equal to α, we infer we have strong evidence that there is a non zero difference in treatment means ($\mu_1=\mu_2=\ldots=\mu_a$) and that H_0 should be rejected (Hicks & Turner, 1999).

However, this test simply means that statistical evidence exists in the data, not necessarily that the inference differences are important in the

context from which the data arose, that judgement must be made by subject experts.

In the case of a two factor model, if the model is adequate and the error terms ε_{ijk} are normally and independently distributed with constant variance σ^2, then each of the ratios of the mean squares MS_A/MS_E, MS_B/MS_E, and MS_{AB}/MS_E are distributed as F with a-1, b-1, and $(a-1)(b-1)$ numerator degrees of freedom respectively and $ab(n-1)$ denominator degree of freedom. The critical region would be the upper tail of the F-distribution (Hicks, 1993).

The structure of the two-factor design and test involves a partition of $SS_{treatments}$ and $MS_{treatments}$, instead of testing

$F_o = \left(\frac{SS_{treatments}}{ab-1}\right) \div \left(\frac{SS_E}{N-ab}\right)$ as the single F-test, the statistics

$F_{o\alpha} = \frac{SS_A}{(a-1)} \div \frac{SS_E}{(N-ab)}$, $F_{ob} = \frac{SS_B}{(b-1)} \div \frac{SS_E}{(N-ab)}$ and $F_{oab} = \frac{SS_{AB}}{(a-1)(b-1)} \div \frac{SS_E}{(N-ab)}$

are used to make separate tests.

The separate tests allow us to be more specific about our inferences. Instead of simply concluding that some of the ab treatment combinations have different means from the overall average, we can detect if those differences are dominated by either the row factor, or the column factor, or both acting separately, or both in combination (Hicks & Turner, 1999).

In balanced two factor designs the three F-statistics are guaranteed by Cochran's Theorem extensions to be statistically independent (Montgomery, 2001).

2. 6 THE UNBALANCED CASE

The number of observations taken within each treatment may be different in some situations. In the case of the data of this study, the number of observations (i.e. number of samples of fish) differed between months. The design of such experimental analyses of treatments with different number of observations is called an unbalanced design (Montgomery, 2001). And the analysis of variance for such data is used with slight modifications. Let n_i observations be taken under a particular treatment i (i=1,2,...,a) and define $N = \sum_{i=1}^{a} n_i$; the computational formulae for SS_T and $SS_{treatment}$ become

$$SS_T = \sum_{i=1}^{a}\sum_{j=1}^{n_i} y_{ij}^{\ 2} - \frac{y_{..}^{\ 2}}{N} \quad \text{and} \quad SS_{treatment} = \sum_{i=1}^{a} \frac{y_{i.}^{\ 2}}{n_i} - \frac{y_{..}^{\ 2}}{N}$$

and no other changes are required in the analysis of variance (Montgomery, 2001).

There are two advantages in choosing a balanced design: first, the test statistic is relatively insensitive to small departures from the assumption of equal variance of the "a" treatments if the sample sizes are unequal; second, the power of the test is maximized if the samples are of equal size (Montgomery, 2001). However, in the case of this study, it was impossible to avoid unequal sample sizes in different months because the data were collected from phenomena that had already occurred. Goby fish preyed on by Cape fur seals were identified by the structure of their otoliths from the seal scats, and then the total lengths of the goby were calculated by converting otolith diameters using conversion techniques (Mecenero *et al.*, submitted). Therefore, the unbalanced design for the analysis of variance was chosen for investigating trends in fish lengths over a 12 month period.

Adjustments for unbalanced designs can be extended to two-factor designs. However, the corresponding F-statistics obtained from

$$SS_T = \sum_{i=1}^{a}\sum_{j=1}^{b}\sum_{n=1}^{n_{ij}}(y_{ijk} - \frac{y_{...}}{N})^2$$

$$SS_{AB} = \sum_{i=1}^{a}\sum_{j=1}^{b}\frac{y_{ij.}^{\ 2}}{n_{ij}} - \frac{y_{...}^{\ 2}}{N}$$

$$SS_A = \sum_{i=1}^{a}\frac{y_{i..}^{\ 2}}{n_{i..}} - \frac{y_{...}^{\ 2}}{N}$$

$$SS_B = \sum_{j=1}^{b}\frac{y_{.j.}^{\ 2}}{n.j.} - \frac{y_{...}^{\ 2}}{N}$$

$SS_E = SS_T - SS_{AB}$ are not statistically independent. The interpretation of the interaction component,

$\frac{SS_{AB} - SS_A - SS_B}{(a-1)(b-1)}$ amounts to a multiple regression approach: checking if two-factor interactions fitted after row factor and column factor effects can be justified for the data (Box & Hunter, 1978).

2. 7 VIOLATION OF NORMALITY AND COMMON VARIANCE

The conventional ANOVA is built upon F-statistics derived from the assumptions of normal error terms. If the error terms are not strictly normal, then the strict interpretations of F-statistics and their statistical significance may be misleading.

However, if the error terms are assumed to have zero means, then the two-factor cell means derived from independent observations will have to be more normal shaped distributions. For large n_{ij}, the central limit

theorem applies to the cell means. Similar arguments can be applied to row means when there are no column-factor effects, and to column means when there are no row-factor effects.

Thus, use of the two-factor design to detect interaction of row and column factors, and when there is no evidence of interactions, to detect row-factor effects or column-factor effects, can be justified as an intuitive set of indicator rather than a strict-testing procedure.

To ensure that this extended use still produces robust inferences, the precautionary methods of model-checking assumptions are adopted. These precautions involve checking that two-factor cell variances are roughly comparable, and the production of normal probability plots for estimated error terms, to highlight at least some of the anomalous observations (Box & Hunter, 1978).

3 DATA AND DATA EXPLORATION

3. 1 THE BIOLOGY OF PELAGIC GOBIES

3. 1. 1 General

Pelagic gobies (*Sufflogobius bibarbatus*) are demersal marine fish that reach a maximum length of 17 cm and mature after four years (Bianchi *et al.*, 1999). They form shoals, although not discrete shoals (Bianchi *et al.*, 1993). Juveniles are epipelagic, sub adults occur in mesopelagic layers and adults migrate to deeper waters (Hewitson & Cruickshank, 1993); large adults are only recorded from demersal trawls (Bianchi *et al.*, 1993). Studies by O'Toole (1976) indicated that the seasonal distribution and size composition of pelagic goby larvae suggest a continuous spawning time from July to March. Gobies have minor commercial importance but they play a great role in the ecology of the Benguela ecosystem (Cruickshank, 1982). They are preyed on by fish, Jackass penguins(*Spheniscus demersus*), Cape cormorants(*Phalacrocorax capensis*), Bank cormorants(*Phalacrocorax neglectus*), Cape gannets, and Cape fur seals(*Arctocephalus pusillus pusillus*) (Crawford *et. al.*, 1985; Bianchi *et al.*, 1993). The diet of gobies is found to contain phytoplankton (mostly diatoms), zooplankton (copepods) and small protozoan species (Crawford *et al.*, 1985; Hewitson & Cruickshank, 1993; O'Toole, 1976).

Goby, in general, are not attractive to the fishing industry due to the fact that they have low oil content (Cruickshank, 1982). The decline in the pilchard fishery off Namibia has focused attention on the possibility of utilizing abundant species such as pelagic goby and lantern fish, which are less exploited fish species (Cruickshank, 1982). Gobies can provide protein bulk to catches of small fish as evidenced by the switch in fish

diet from pilchard to anchovy to gobies by some of the colonial bird species occurring in large numbers off the Namibian coast (Cruickshank, 1982).

3. 1. 2 Distribution

Pelagic gobies have a wide distribution in the Benguela ecosystem. Studies by Cruickshank (1982), O`Toole (1978) and Cruickshank *et al.* (1980) showed that pelagic gobies occur primarily between Lüderitz (27°S) and Walvis Bay (24°), extending northwards to Cape Cross, and are found on average 35 miles offshore (Fig. 1). Some patchy goby stocks are also reported by these studies, at Palgrave Point (20° 20' S), Cape Frio (19° S), Cunene River (17° 40' S), Orange River (28° S) and Cape Town (34° S).

Gobies are found in the eastern Atlantic subtropical waters with a temperature range of 11°c to 25°c and at depths of 0-340 m (Bianchi *et al.*, 1999). However, the majority is found within temperature ranges of 13°c to 16°c and water depths of about 50 m (Cruickshank, 1982). Temperature is possibly responsible for some limitation in the distribution pattern of gobies (Cruickshank, 1982; O`Toole, 1978). Cruickshank (1982) further reported that these fish are generally inshore species and are easily taken by purse seiners. The neritic waters of Southern Africa, between latitudes 19°S and 24°S, apparently support a large population of juvenile pelagic goby (O'Toole, 1976). O'Toole (1978) gives the temperature range of pelagic goby larvae in the Namibian coasts (17°s to 25°s) as 11°c to 25°c, with 72% occurring between 13.1°c to 18°c, which corresponds with the adult distribution he found in 14.5°c to 17.5°c water temperature.

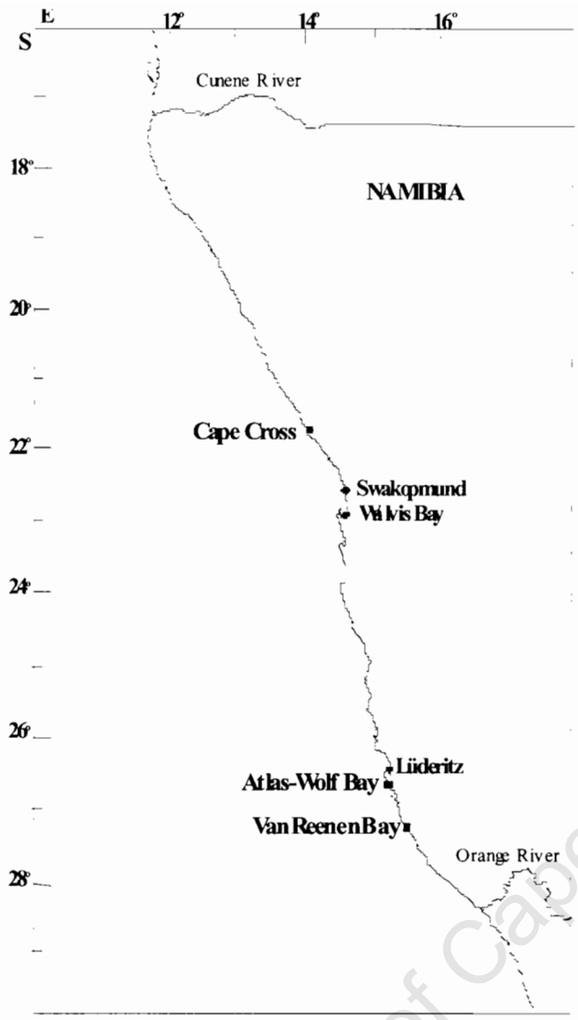


Fig. 1. Map of study area.

3. 2 SCAT COLLECTION AND PROCESSING

Fish lengths of pelagic goby preyed on by Cape fur seals were obtained from a study by Mecenero *et al.* (submitted). Goby otoliths were obtained from Cape fur seal scats using scat analysis techniques. Scats were collected from 1994 to 2001 on a monthly basis (where possible) at three mainland seal colonies in Namibia, namely Atlas-Wolf Bay (26°49'S, 15°08'E), Cape Cross (21°47'S, 13°57'E) and Van Reenen Bay (27°23'S,

15°21'E). The sampling was carried out by staff and researchers of the Ministry of Fisheries and Marine Resources in Namibia. Otolith diameters of sub samples of goby otoliths were measured with a vernier caliper to the closest 0.05 mm. Measurements were corrected for erosion during digestion (Millar *et al.*, In prep.). Corrected otolith diameter lengths were then converted to fish total length, which is the length from the tip of the snout to the tip of the longest caudal ray of the fish, using the otolith diameter-fish total length relationship suggested by Smale *et al.* (1995). Goby counts in monthly samples were corrected for loss in numbers during digestion (Millar *et al.*, In prep.), and the proportion of goby in each sample determined.

3. 2. 1 Data

The data under study consists of monthly goby fish lengths, observation over the years 1994 to 2001. Each data set from the three locations comprises two variables, fish length and month. Length is a continuous response variable and month is a categorical explanatory variable with an underlying cyclical structure. For the temporal length differences within a location, the one-way analysis of variance may be used to test for significant differences among the 12 months. The one-way analysis of variance can be chosen for this analysis when the data exhibit only a single categorical explanatory variable (month). In the case of the spatial length differences, the two-way analysis of variance is the appropriate procedure because a second categorical explanatory variable (factor), location, with three levels is combined with the 12 months. Generally, the analysis of variance is chosen for the analysis of these data sets because it tests for significant differences of the response variable among the different categories of the explanatory variables. It allows for the determination of patterns over time at each location, and where the

patterns are similar over time, combines the data from all locations to estimate a common pattern.

3. 3 DATA EXPLORATION

Length-frequency distributions of the samples of each month show some trends in length of goby with season (Fig. 2). There is some consistency (over the 8 years) in size changes of fish preyed on from one month to the next month. For instance, at Atlas-Wolf Bay, the size of goby in January has a modal class of 7.5 cm, but then in February there are two modal class lengths of 4.5 cm and 7.5 cm (Fig. 2). This feature could possibly be due to the addition of a new cohort of small fish to the older population in that area, but the reason for bimodality in goby lengths is unknown. Again, if we compare February and March, we may infer that the smaller group has reached a size of 5.5 cm and the larger group has attained a size of two modal lengths, 7.5 cm and 8.5 cm. Generally, as we move on from one particular month to the next month, it is evident that there is overall change in goby lengths preyed on by seals (see fig. 2).

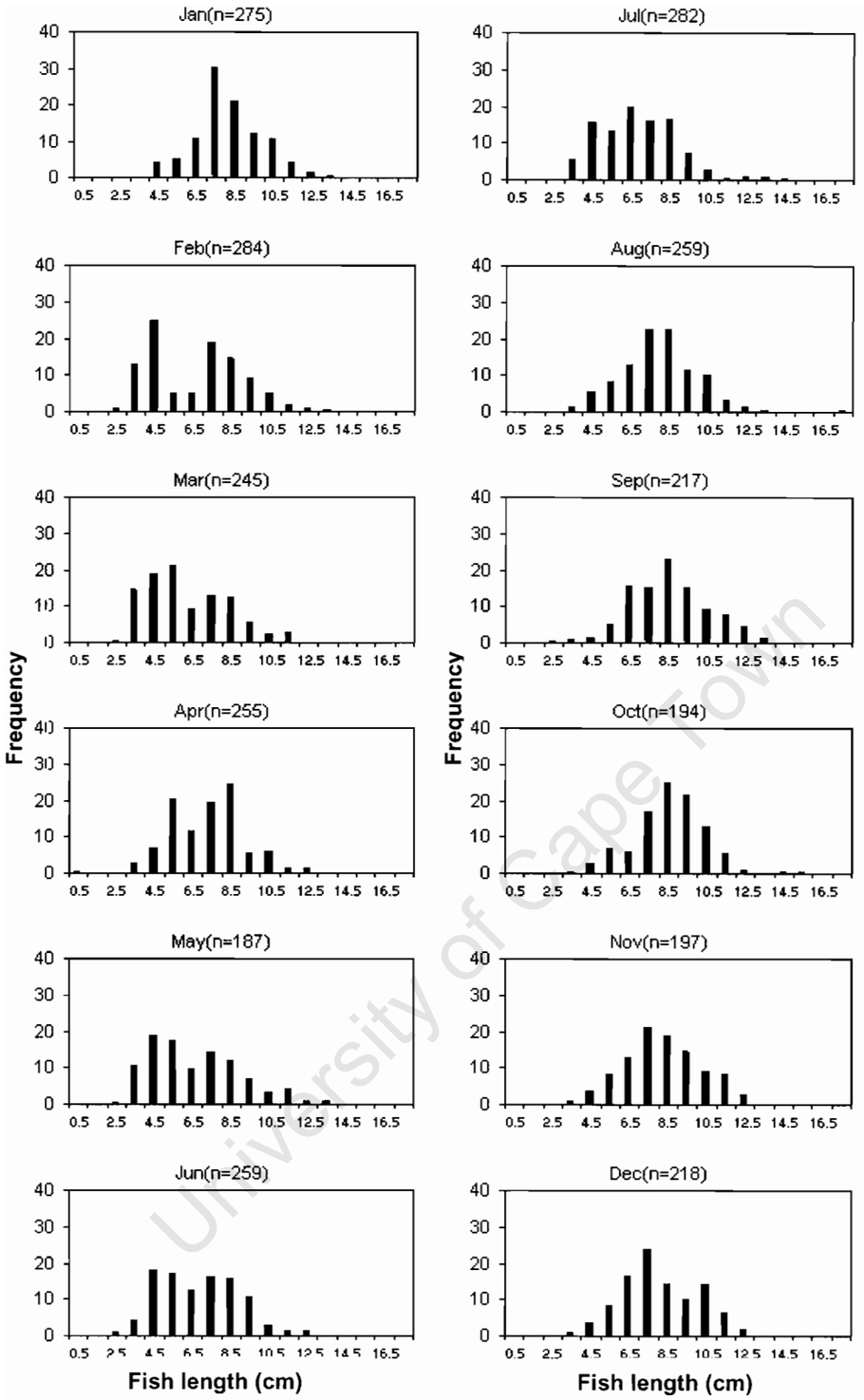


Fig. 2. Length-Frequency distribution of pelagic goby preyed on by Cape fur seals in Atlas-Wolf Bay (1994-2001 combined).

The significance of the mean length differences among months will be tested using the analysis of variance, which will be examined later. But if we follow the trends of the size changes from month to month it can be noticed that two separate groups existed from February till June, but only one group is observed from August to January (see Fig.2). Bimodality may reflect biannual spawning, as is the case with horse mackerel (Kerstan & Leslie, 1994; Kerstan 1995). However, this bimodality may also be caused by varying growth rates within cohorts as a result of size-dependent food availability (Kerstan, 1995). From previous studies (O'Toole, 1976,1978) larger, adult gobies may migrate for spawning from areas of unfavorable environmental conditions to areas of optimum environmental conditions during July to March. This migration may help to explain the size trends in fig 2. Still there is a need to statistically quantify the significance of the differences in mean length within months, using the ANOVA technique.

The data from the other locations, Cape Cross and Van Reenen Bay were explored similarly. Figures 3 and 4 show trends of monthly fish length changes in Cape Cross and Van Reenen Bay, respectively.

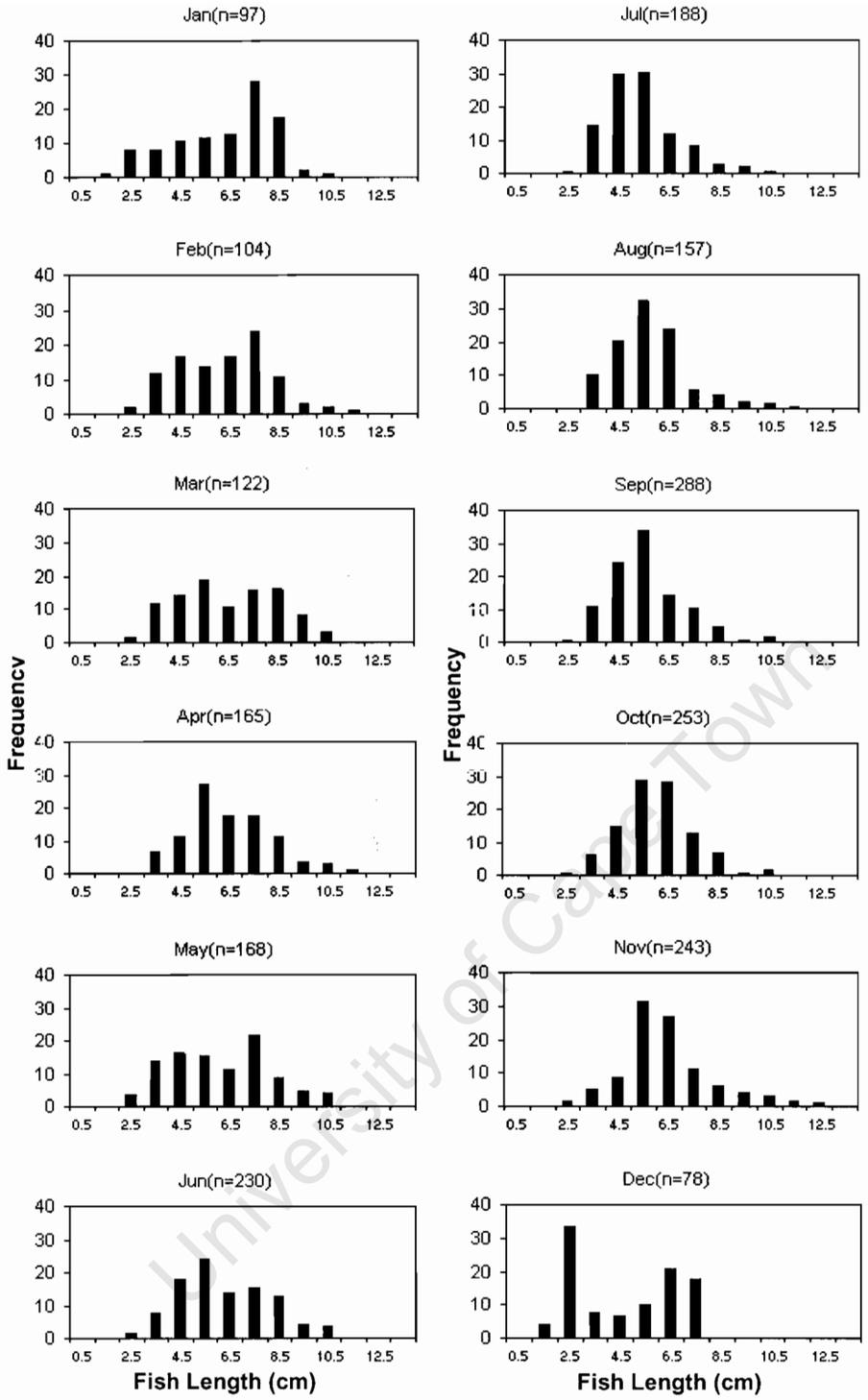


Fig.3. Length-Frequency distribution of pelagic goby preyed on by Cape fur seals in Cape Cross(1994-2001).

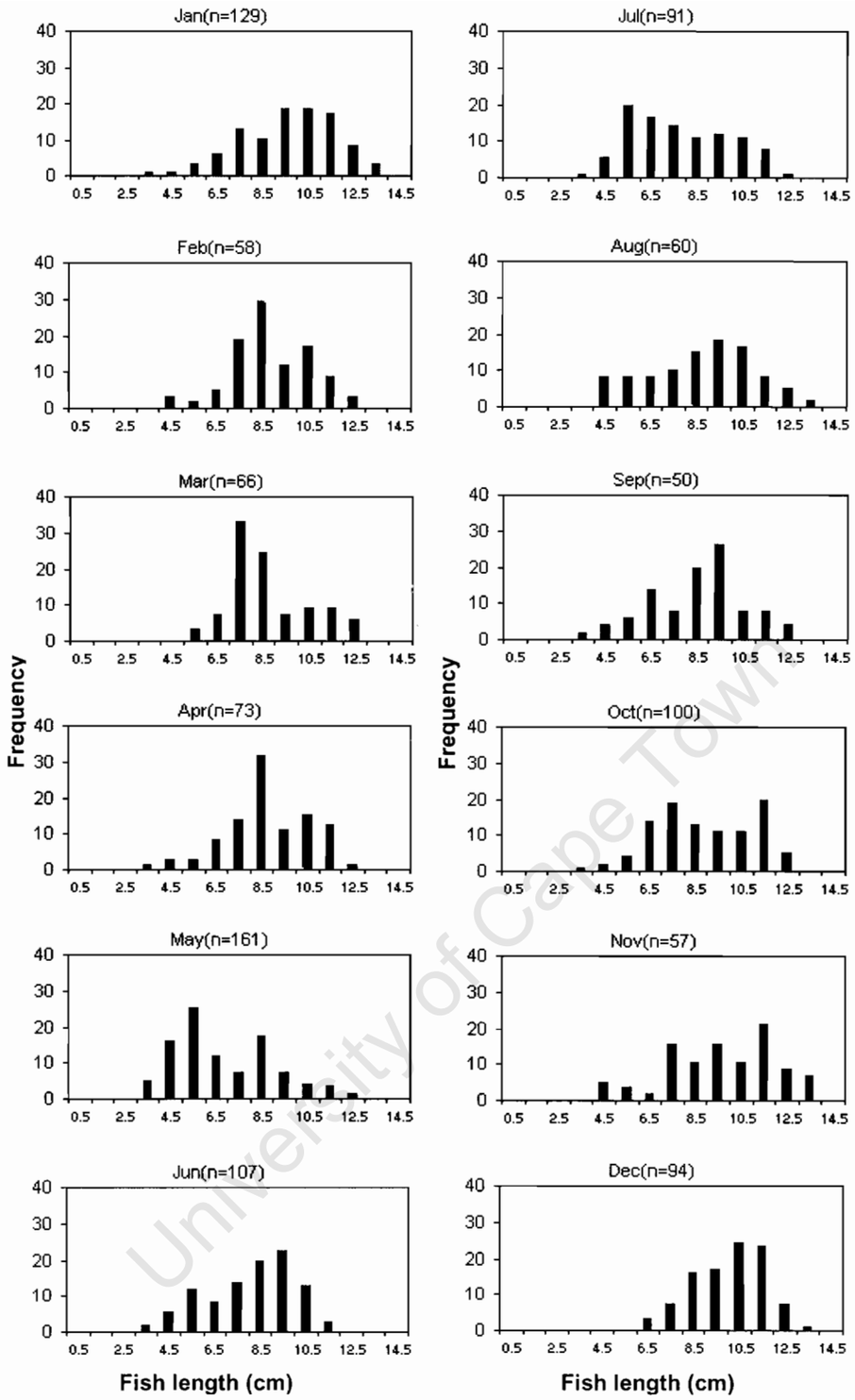


Fig. 4. Length-Frequency distribution of pelagic goby preyed by fur seals in Van Reenen Bay (1994-2001).

These three sets of contrasts of the 12 months amount to an exploration of the interaction of location and time as row and column factors. The number of observations for each cell is very large, with minimum cell frequencies 187, 78 and 50 at Atlas-Wolf Bay, Cape Cross and Van Reenen Bay. The availability of so much data allows that a full set of 36 histograms can be constructed. The bars in the histogram are used to highest visual contrasts that the histogram might obscure.

The histograms would indicate that assumptions of normality within the 36 location-month cells are seldom defensible. Biologically structured bimodality features that alter over time, skew distributions and changing variation (spread) patterns are obvious.

However the data values for length occur over a limited finite range, so that variances over the cells will not differ too much.

The large cell sample "sins" will imply that cell means are subject to central limit theorem effects, so that comparisons of two-factor cell means can be made using standard methods as good approximations.

Two-factor ANOVA will address the questions of the appropriateness of summarizing the data by models with location and month effects alone, with no interaction terms. This analysis may be only a minor part of data interpretations per cell.

In addition, it does not explore fully the cyclical time-structure implicit in the 12 monthly data sets, nor the time-structure in the original 96 months of the data collection.

The idea that the data sets of three locations may be combined into one composite set for analysis presumes comparability. Here biological arguments suggest that combination may be reasonable, but as a precautionary measure data sets were individually explored, by one-

factor analyses at each location. In consequence the combined data set is subject to a two-factor interactive test.

4 ANALYSIS AND RESULTS

4. 1 ANALYSIS OF SPATIAL DIFFERENCES IN FISH LENGTH

For the analysis of spatial differences in fish lengths, the two-way ANOVA technique was used to investigate significant differences in mean fish length due to the pooled effect of differences in month (January to December) and due to differences in location (Atlas-Wolf Bay, Cape Cross and Van Reenen Bay). To carry out a two-way ANOVA test the data from the three locations were combined together. Atlas-Wolf Bay was named location 1, Cape Cross location 2 and Van Reenen Bay location 3. The combined data were checked for the assumptions of the ANOVA model. First the whole data from the three locations were combined and the distribution was found to be significantly different from the normal distribution with tests of Kolmogorov-Smirnov and Lilliefors showing significant results (p-value <0.01), as seen on Fig. 5.

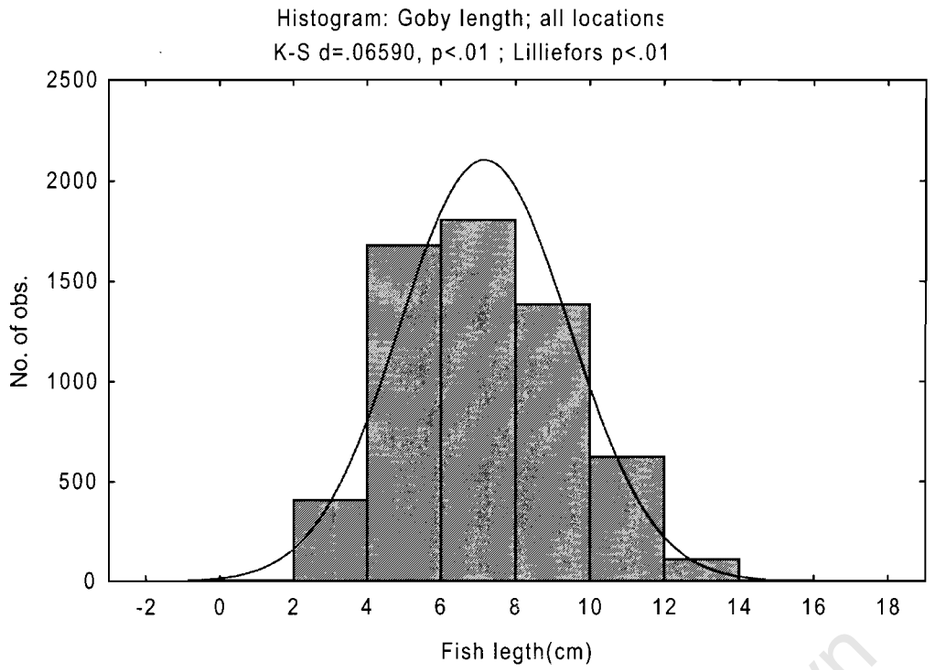


Fig. 5. Distribution of goby lengths consumed by Cape fur seals for the combined data of the three study locations.

These differences may not have serious consequences in the analysis, because the data values are somewhat symmetrically distributed but the right tests for checking of normality must be done for each group defined by the effect variable(s). Large data set sizes will necessarily give greater statistical power so that even minor deviations from normality will be detected by the tests. But the above test is only valid for zero means for location and month. So it was necessary to check for any evident relationship between the mean and variance of each group defined by the effect variable(s) because it is space consuming to show all the individual tests for normality for the 36 combinations of groups formed by the effect variables. Fig. 6 gives an evidence of no clear relationship between mean and variance of each group defined by the effect variable(s).

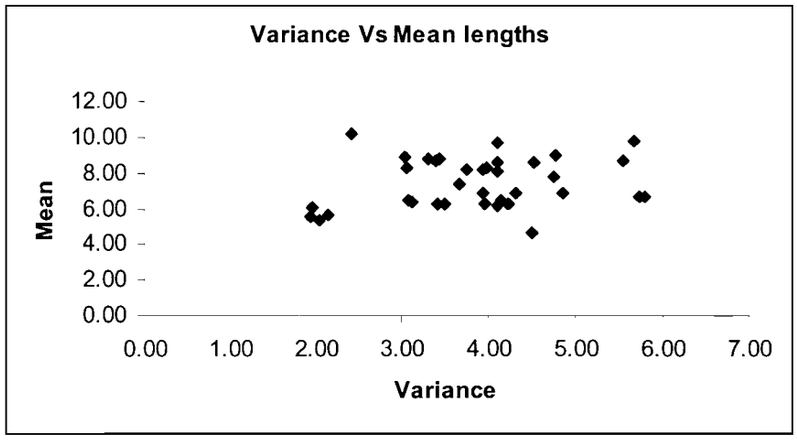


Fig. 6. Relationship between mean length and variance of each group.

Since it is space consuming to show all the individual tests of normality for the 36 combinations, the table of descriptive statistics can be used to describe the summary measurements. The table of descriptive statistics (Table 1) summarizes the interactions of the two explanatory variables, month and location, on fish length.

Table 1. Descriptive Statistics (Goby length; all locations)

Effect	Level of Factor	Level of Factor	N	length Mean	length Std.Dev.	length Std.Err	Lower CI	Upper CI
Total			6011	7.16	2.28	0.03	7.11	7.22
month	jan		501	8.24	2.18	0.10	8.05	8.43
month	feb		446	6.86	2.35	0.11	6.64	7.08
month	mar		433	6.69	2.20	0.11	6.49	6.90
month	apr		493	7.26	1.99	0.09	7.09	7.44
month	may		516	6.55	2.24	0.10	6.36	6.75
month	jun		596	6.84	2.07	0.08	6.67	7.01
month	jul		561	6.49	2.05	0.09	6.32	6.66
month	aug		476	7.33	2.23	0.10	7.13	7.54
month	sep		555	7.00	2.30	0.10	6.81	7.19
month	oct		547	7.48	2.21	0.09	7.30	7.67
month	nov		497	7.51	2.27	0.10	7.31	7.71
month	dec		390	7.93	2.66	0.13	7.66	8.19
location	1		2872	7.50	2.20	0.04	7.42	7.58
location	2		2093	5.98	1.77	0.04	5.90	6.05
location	3		1046	8.62	2.27	0.07	8.48	8.76
month*location	jan	1	275	8.25	1.75	0.11	8.04	8.46
month*location	jan	2	97	6.29	1.99	0.20	5.89	6.69
month*location	jan	3	129	9.69	2.03	0.18	9.34	10.05
month*location	feb	1	284	6.67	2.41	0.14	6.39	6.95
month*location	feb	2	104	6.24	1.87	0.18	5.87	6.60
month*location	feb	3	58	8.90	1.74	0.23	8.45	9.36
month*location	mar	1	245	6.23	2.06	0.13	5.97	6.49
month*location	mar	2	122	6.50	2.04	0.18	6.13	6.86
month*location	mar	3	66	8.78	1.82	0.22	8.33	9.22
month*location	apr	1	255	7.33	1.92	0.12	7.10	7.57
month*location	apr	2	165	6.50	1.75	0.14	6.23	6.77
month*location	apr	3	73	8.74	1.85	0.22	8.31	9.18
month*location	may	1	187	6.70	2.39	0.17	6.35	7.04
month*location	may	2	168	6.11	2.03	0.16	5.80	6.41
month*location	may	3	161	6.85	2.20	0.17	6.51	7.20
month*location	jun	1	259	6.85	2.07	0.13	6.60	7.10
month*location	jun	2	230	6.23	1.85	0.12	5.99	6.47
month*location	jun	3	107	8.13	1.94	0.19	7.75	8.50
month*location	jul	1	282	6.87	1.99	0.12	6.63	7.10
month*location	jul	2	188	5.33	1.43	0.10	5.12	5.53
month*location	jul	3	91	7.75	2.18	0.23	7.30	8.21
month*location	aug	1	259	8.02	2.02	0.13	7.77	8.27
month*location	aug	2	157	5.70	1.46	0.12	5.47	5.93
month*location	aug	3	60	8.67	2.35	0.30	8.06	9.28
month*location	sep	1	217	8.57	2.03	0.14	8.30	8.84
month*location	sep	2	288	5.55	1.39	0.08	5.39	5.71
month*location	sep	3	50	8.55	2.13	0.30	7.94	9.15
month*location	oct	1	194	8.65	1.84	0.13	8.39	8.91
month*location	oct	2	253	6.00	1.40	0.09	5.83	6.18
month*location	oct	3	100	8.96	2.19	0.22	8.53	9.40
month*location	nov	1	197	8.26	1.99	0.14	7.98	8.54
month*location	nov	2	243	6.38	1.77	0.11	6.16	6.60
month*location	nov	3	57	9.76	2.38	0.32	9.13	10.39

month*location	dec	1	218	8.14	1.98	0.13	7.87	8.40
month*location	dec	2	78	4.63	2.12	0.24	4.15	5.11
month*location	dec	3	94	10.17	1.55	0.16	9.86	10.49

Due to the fact that the number of observations pooled together for all three locations is very large (N=6011), there is no fear for violations of normality since the central limit theorem can be applied. To check for the assumption of homogeneity of variances, the Levene's test was used and the result is shown below (Table 2). The results from the Levene's test show that there is significant difference in variances among the 36 combinations of month and location.

Table 2. Levene's Test for Homogeneity of Variances (Goby length)
Effect: month*location

	MS effect	MS error	F	p
length	13.78191	1.199352	11.49113	0.00

The two-way ANOVA technique was immediately applied after the data was checked for the assumptions of normality and homogeneity of variances despite the violations of the assumptions.

Results from the two-way ANOVA are shown below in Table 3.

Table 3. Univariate Tests of Significance for length (all location)

Effect	SS	Degr. of Freedom	MS	F	p <0.0001
Intercept	248303.8	1	248303.8	66316.75	0.0000
month	1213.2	11	110.3	29.46	0.0000
location	5322.0	2	2661.0	710.70	0.0000
month*location	1797.8	22	81.7	21.83	0.0000
Error	22371.6	5975	3.7		

The above results from the two-way ANOVA show that there are significant differences in goby length preyed on by fur seals at the three different locations (Table 3). Moreover, the interaction effect of the variables month and location on goby length is statistically significant.

This indicates that there is a difference in the effect of months on fish length within the three locations. Therefore, due to the statistical significance of the interaction effect, the effects of month on fish length will be tested separately for each location. And these tests will help to analyze the temporal differences due to month within each location. But the variable month still affects (F= 29.46) fish length regardless of the change in location (Table 3). However, location differences dominate the cell differences (F=710.70). Hence, each location will be analyzed separately using the one-way ANOVA. Multiple comparisons for post hoc tests show which factor levels differ significantly from each other, but the table of results cannot be presented here because it is too large (36 rows by 36 columns), and the practical interpretation is also quite complicated.

4. 2 ANALYSIS OF TEMPORAL DIFFERENCES IN FISH LENGTH

One-way analysis of variance was used to test if significant differences in fish length existed among the 12 months at each of the three study locations. But before the analysis was made it was important to check if the data satisfy the assumptions of analysis of variance. The results of the tests for the assumptions and for significance are presented below for each of the three locations: Atlas-Wolf Bay, Cape Cross and Van Reenen Bay.

4. 2. 1 ATLAS-WOLF BAY

4. 2. 1. 1 Tests for Checking the Assumptions of ANOVA

The histograms of the distributions of goby lengths within groups show that the data from Atlas-Wolf Bay may not satisfy the assumptions of normality. But ANOVA assumes that the response variable is normally distributed in each category of the explanatory variable(s). Because it is

space consuming to present all the graphs of the normality tests, the table of descriptive statistics and the normal probability plot of the residuals is presented to compare the distribution of the data to the normal distribution. From the descriptive statistics (Table 4) it can be seen that the coefficients of skewness and kurtosis lie within the ranges, –0.06 - 0.65, and 2.08 - 4.15, respectively. The normal distribution has a coefficient of skewness equal to zero and a coefficient of kurtosis equal to 3 (Robert & Daniel, 1998). The last two columns of Table 4 show the differences of these coefficients from the normal distribution.

Table 4.Descriptive statistics: Atlas-Wolf Bay

	Valid N	Mean	Lower CI	Upper CI	Minimum	Maximum	Std.Dev.	Skewness	Kurtosis-3
Month									
Jan	275	8.25	8.04	8.46	4.12	13.36	1.75	0.16	-0.04
Feb	284	6.67	6.39	6.95	2.81	13.16	2.41	0.29	-0.92
Mar	245	6.23	5.97	6.49	2.81	11.56	2.06	0.65	-0.46
Apr	255	7.34	7.10	7.57	3.56	12.76	1.92	0.27	-0.33
May	187	6.70	6.35	7.04	2.10	13.36	2.39	0.64	-0.32
Jun	259	6.85	6.60	7.10	2.81	12.96	2.08	0.41	-0.40
Jul	282	6.87	6.63	7.10	3.37	14.17	1.99	0.56	0.37
Aug	259	8.02	7.77	8.27	3.37	17.43	2.03	0.34	1.15
Sep	217	8.57	8.30	8.84	2.10	13.57	2.03	0.08	-0.25
Oct	194	8.65	8.39	8.91	3.93	15.18	1.85	-0.06	0.62
Nov	197	8.26	7.98	8.54	3.93	12.96	1.99	0.08	-0.62
Dec	218	8.14	7.87	8.40	3.93	12.56	1.98	0.09	-0.67

The normal probability plot is also an extremely useful procedure to check the assumption of normality, and the plot of the Atlas-Wolf Bay data, ignoring monthly effects, shows a positive result (Fig. 7). A positive result for the normality test using the normal probability plot occurs when the plot more or less resembles a straight line (Montgomery, 2001). When visualizing the straight line, more emphasis must be placed on the central values of the plot than on the extremes, as Montgomery (2001) further stated.

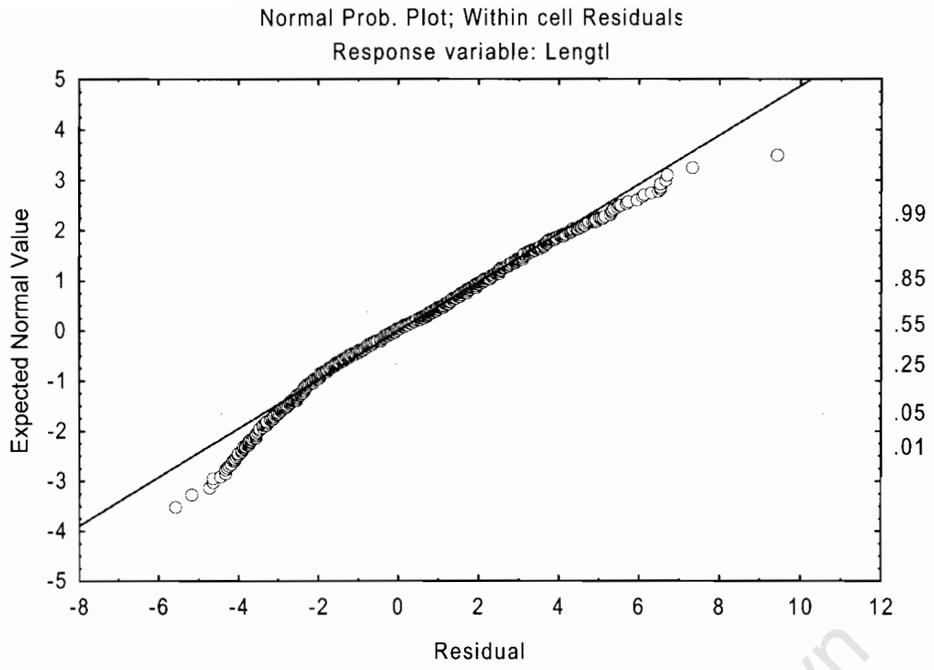


Fig. 7. Normal probability plot of within cell residuals of combined data, Atlas-Wolf Bay.

Normal probability plots for the residuals of each of the months show slightly more deviations from the normal straight line, than the plot from the combined data of the 12 months at Atlas-Wolf Bay does. They are not shown here because they consume large space.

The other important assumption that needs checking is the homogeneity of the variances. ANOVA assumes the response variable should have the same variance in each category of the explanatory variables. A widely used test of equality of variance is the Bartlet's test, however, the fact that Bartlet's test is sensitive to the violations of normality assumption, another robust alternative test, Levene's test, was also used to supplement the result. Results from both Bartlet's and Levene's tests show that there is significant departure from homogeneity of variances in the 12 month samples. However, ANOVA is robust for small and even

moderate departures from the assumption of homogeneity of variance, and thus is still reliable for the analysis of the data.

The significance of Bartlet's and Levene's tests is largely due to the very large sample sizes, which results in even small differences between variances being declared significant. Besides, the ratio of largest to smallest group variances, which is the ratio of the variance in February to the variance in January (5.8081/3.0625), was calculated and is found to be 1.89. Because this ratio is substantially less than 3 (the rule of thumb), as well as the fact that all the monthly sample sizes are large enough , the ANOVA technique is adequate to test for differences between treatment means.

Table 5. Tests of Homogeneity of Variances (Atlas-Wolf Bay)
Effect: month

	Hartley F-max	Cochran C	Bartlett Chi-Sqr.	df	p <0.0001
Length	1.89	0.12	46.31	11	0.0003

Table 6. Levene's Test for Homogeneity of Variances(Atlas-Wolf)
Effect: month
Degrees of freedom for F: 11, 2860

	MS Effect	MS Error	F	p <0.0001
Length	11.41	1.32	8.67	0.000000

4. 2. 1. 2 Tests for significant differences in fish length

The result from the one-way ANOVA shows that differences in fish length analysis within the 12 months at Atlas-Wolf Bay are significant (Table 7).

Table 7. Univariate Tests of Significance for length (Atlas-Wolf Bay)

Effect	SS	Degr. of Freedom	MS	F	p <0.0001
Intercept	160057.0	1	160057.0	38266.03	0.0000
Month	1874.9	11	170.4	40.75	0.0000
Error	11962.6	2860	4.2		
Total	13837.6	2871			

Based on the results in Table 7, the null hypothesis of no difference in treatment means is rejected. To determine which treatment means exactly differ from each other demands pairwise multiple comparison tests. The modified Fisher's Least Significant Difference (LSD) for heterogeneous variances, Tukey-Kramer HSD post hoc testing procedure for unequal sample size, was applied to investigate which treatment means differ from each other (Table 8) (Hochberg & Tamhane, 1987; Montgomery, 2001).

Table 8. Unequal N HSD; Variable length (Atlas-Wolf) Approximate p values for post hoc tests.

Month	Feb **6.6679**	Jan **8.2510**	Mar **6.2292**	Apr **7.3349**	May **6.6954**	Jun **6.8491**	Jul **6.8660**	Aug **8.0187**	Sep **8.5679**	Oct **8.6516**	Nov **8.2602**	Dec **8.1360**
Feb		0.000*	0.424	0.012*	1.000	0.998	0.992	0.000*	0.000*	0.000*	0.000*	0.000*
Jan	0.000*		0.000*	0.000*	0.000*	0.000*	0.000*	0.980	0.904	0.741	1.000	1.000
Mar	0.424	0.000*		0.000*	0.546	0.038*	0.028*	0.000*	0.000*	0.000*	0.000*	0.000*
Apr	0.012*	0.000*	0.000*		0.102	0.235	0.286	0.009*	0.000*	0.000*	0.000*	0.003*
May	1.000	0.000*	0.546	0.102		1.000	1.000	0.000*	0.000*	0.000*	0.000*	0.000*
Jun	0.998	0.000*	0.038*	0.235	1.000		1.000	0.000*	0.000*	0.000*	0.000*	0.000*
Jul	0.992	0.000*	0.028*	0.286	1.000	1.000		0.000*	0.000*	0.000*	0.000*	0.000*
Aug	0.000*	0.980	0.000*	0.009*	0.000*	0.000*	0.000*		0.181	0.095	0.991	1.000
Sep	0.000*	0.904	0.000*	0.000*	0.000*	0.000*	0.000*	0.181		1.000	0.943	0.550
Oct	0.000*	0.741	0.000*	0.000*	0.000*	0.000*	0.000*	0.095	1.000		0.769	0.351
Nov	0.000*	1.000	0.000*	0.000*	0.000*	0.000*	0.000*	0.991	0.943	0.769		1.000
Dec	0.000*	1.000	0.000*	0.003*	0.000*	0.000*	0.000*	1.000	0.550	0.351	1.000	

Values marked by asterisks in Table 8 indicate p-values associated with significant differences between respective treatment means. For instance, there is a significant difference in mean fish length between January (8.25 cm) and February (6.67 cm), January and March (6.23 cm),

January and April (7.34 cm), January and May (6.70 cm), January and June (6.85 cm), and January and July (6.87 cm). There is no significant difference between January and August (8.02 cm), January and September (8.57 cm), January and October (8.65 cm), January and November (8.26 cm), and January and December (8.14 cm). Ranking through the months, the detected changes are Jan-Feb, Feb-April, Mar-April, and July-August.

4. 2. 2 CAPE CROSS

4. 2. 2. 1 Tests for checking the assumptions of ANOVA

Normality tests for the data from Cape Cross show that the data for the 12 months are not normally distributed. The table of descriptive statistics also suggests violation of the normality assumption in this data (Table 9). For ANOVA it is usually more effective to construct a normal probability plot on the residuals to check the normality assumption, rather than on the raw data (Montgomery, 2001). But probability plots constructed on the raw data are also used for checking normality assumptions, especially when using the t-test. Figure 8 shows the normal probability plot of the residuals of the whole data from Cape Cross.

Table 9. Descriptive Statistics (Cape Cross)

Month	Valid N	Mean	Lower CI	Upper CI	Minimum	Maximum	Std.Dev.	Skewness	Kurtosis-3
Jan	97	6.29	5.89	6.69	1.89	10.16	1.99	-0.47	-0.75
Feb	104	6.24	5.87	6.60	2.81	11.76	1.87	0.25	-0.25
Mar	122	6.50	6.13	6.86	2.63	10.96	2.04	0.15	-1.06
Apr	165	6.50	6.23	6.77	3.56	11.36	1.75	0.54	-0.11
May	168	6.11	5.80	6.41	2.07	10.96	2.03	0.30	-0.75
Jun	230	6.23	5.99	6.47	2.07	10.96	1.85	0.50	-0.41
Jul	188	5.33	5.12	5.53	2.63	10.16	1.43	1.09	1.21
Aug	157	5.70	5.47	5.93	3.18	11.96	1.46	1.30	3.03
Sep	288	5.55	5.39	5.71	2.63	10.96	1.39	1.02	1.77
Oct	253	6.01	5.83	6.18	2.81	10.76	1.40	0.52	0.52
Nov	243	6.38	6.16	6.60	2.26	12.16	1.77	0.90	1.23
Dec	78	4.63	4.15	5.11	1.17	7.79	2.12	0.00	-1.63

The values of the coefficients of skewness and kurtosis indicate that little departures from normality exist (Table 9).

Tests for homogeneity of variances show that the hypothesis of equal variances for all treatment groups should be rejected (Tables 10 and 11).

Table 10. Tests of Homogeneity of Variances (Cape Cross)
Effect: month

	Hartley F-max	Cochran C	Bartlett Chi-Sqr.	df	p <0.0001
Length	2.33	0.12	94.12	11	0.0000

Table 11. Levene's Test for Homogeneity of Variances (Cape Cross)
Effect: month
Degrees of freedom for all F's: 11, 2081

	MS Effect	MS Error	F	p <0.0001
Length	14.70	1.00	14.69	0.0000

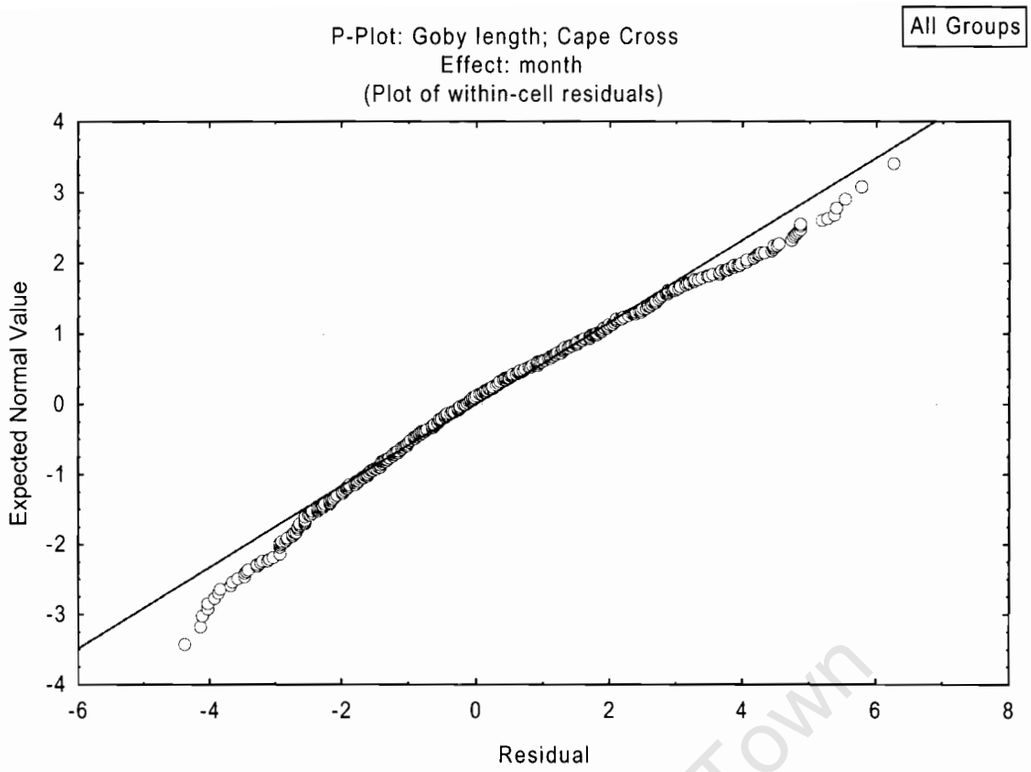


Fig. 8. Normal probability plot of within cell residuals for the 12 months data from Cape Cross.

Due to the fact that ANOVA is robust for small departures of this assumption and that the ratio of largest to smallest group variances is less than 3, use of ANOVA may be considered as an approximate method to test significant difference in treatment means. The ratio of largest to smallest group variances (ratio of the variance in December to variance in September) for the Cape Cross data is calculated to be 2.33.

4. 2. 2. 2 Tests for significant differences in fish length

The one-way ANOVA table for the Cape Cross data shows that there are significant differences in fish lengths within the 12 months (Table 12). The null hypothesis of no difference in treatment means is rejected because the test shows that there are statistically significant differences

in treatment means. Hence, the next procedure is to carry out a multiple comparisons post hoc test.

Table 12. Univariate Tests of Significance for length (Cape Cross)

Effect	SS	Degr. of Freedom	MS	F	p <0.0001
Intercept	63392.17	1	63392.17	21695.97	0.0000
Month	437.73	11	39.79	13.62	0.0000
Error	6080.35	2081	2.92		

The results from the post hoc multiple comparisons procedure show that there are significant differences between January (6.29 cm) and July (5.33 cm), January and December (4.63 cm), February (6.24 cm) and July, February and December, March (6.50 cm) and July, March and August (5.70 cm), March and September (5.55 cm), March and December, and so on (Table 13). The results from the post hoc tests will be explained graphically in the discussion section.

Table 13. Unequal N HSD; variable length (Cape Cross) Approximate p values for Post Hoc Tests

Month	Jan **6.2898**	Feb **6.2372**	Mar **6.4987**	Apr **6.5011**	May **6.1055**	Jun **6.2290**	Jul **5.3282**	Aug **5.6970**	Sep **5.5486**	Oct **6.0046**	Nov **6.3795**	Dec **4.6304**
Jan		1.000	0.999	0.999	1.000	1.000	0.005*	0.396	0.103	0.992	1.000	0.000*
Feb	1.000		0.995	0.994	1.000	1.000	0.007*	0.492	0.139	0.998	1.000	0.000*
Mar	0.999	0.995		1.000	0.820	0.986	0.000*	0.013*	0.001*	0.507	1.000	0.000*
Apr	0.999	0.994	1.000		0.621	0.954	0.000*	0.002*	0.000*	0.258	1.000	0.000*
May	1.000	1.000	0.820	0.621		1.000	0.002*	0.610	0.113	1.000	0.949	0.000*
Jun	1.000	1.000	0.986	0.954	1.000		0.000*	0.199	0.001*	0.962	0.999	0.000*
Jul	0.005*	0.007*	0.000*	0.000*	0.002*	0.000*		0.752	0.985	0.007*	0.000*	0.309
Aug	0.396	0.492	0.013*	0.002*	0.610	0.199	0.752		1.000	0.912	0.021*	0.006*
Sep	0.103	0.139	0.001*	0.000*	0.113	0.001*	0.985	1.000		0.108	0.000*	0.038*
Oct	0.992	0.998	0.507	0.258	1.000	0.962	0.007*	0.912	0.108		0.394	0.000*
Nov	1.000	1.000	1.000	1.000	0.949	0.999	0.000*	0.021*	0.000*	0.394		0.000*
Dec	0.000*	0.000*	0.000*	0.000*	0.000*	0.000*	0.309	0.006*	0.0388	0.000*	0.000*	

4. 2. 3 VAN REENEN BAY

4. 2. 3. 1. Tests for checking the assumptions of ANOVA

The tests for normality for the data from Van Reenen indicate that most of the samples for the 12 months have skewed distributions from the normal distribution. The coefficients of skewness and kurtosis (Table 14) also show the above fact. The descriptive statistics (Table 14) show that the coefficients of skewness and kurtosis lie within the ranges, –0.52 - 0.60, and 2 - 3.25, respectively. Moreover, the normal probability plot of the samples from Van Reenen Bay (Fig. 9) can be visually compared with the ideal normal straight line. Due to the fact that the sample sizes are large enough to apply the central limit theorem, it is possible to assume normal approximations to the data.

Table 14. Descriptive Statistics (Van Reenen Bay)

Month	Valid N	Mean	Lower CI	Upper CI	Minimum	Maximum	Std.Dev.	Skewness	Kurtosis-3
Jan	129	9.69	9.34	10.05	3.93	13.77	2.03	-0.39	-0.34
Feb	58	8.91	8.45	9.36	4.50	12.36	1.75	-0.23	0.25
Mar	66	8.78	8.33	9.22	5.08	12.96	1.82	0.59	-0.19
Apr	73	8.74	8.31	9.18	3.37	12.56	1.86	-0.44	0.11
May	161	6.85	6.51	7.20	3.18	12.96	2.20	0.61	-0.41
Jun	107	8.13	7.75	8.50	3.75	11.56	1.94	-0.48	-0.74
Jul	91	7.76	7.30	8.21	3.37	12.16	2.18	0.27	-1.00
Aug	60	8.67	8.06	9.28	4.12	13.36	2.35	-0.26	-0.74
Sep	50	8.55	7.94	9.15	3.93	12.56	2.12	-0.35	-0.35
Oct	100	8.96	8.53	9.40	3.18	12.96	2.19	-0.19	-0.88
Nov	57	9.76	9.13	10.39	4.12	13.57	2.38	-0.52	-0.31
Dec	94	10.17	9.86	10.49	6.43	13.16	1.55	-0.36	-0.51

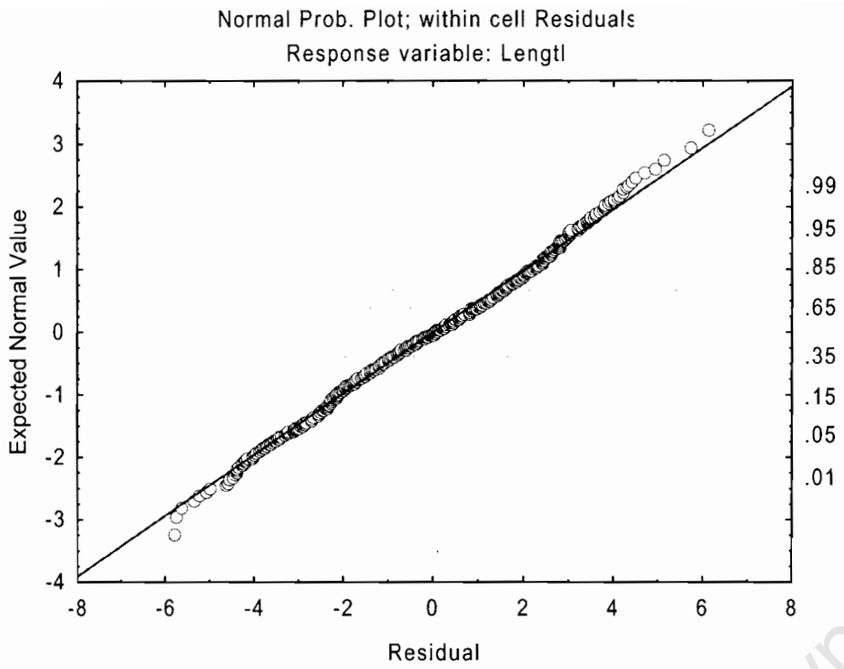


Fig. 9. Normal probability plot of within cell residuals for the 12 months combined data, Van Renen Bay.

Tests for homogeneity of variances for the 12 months reject the hypothesis that the 12 months have equal variances in the size distributions of the fish. Tables 15 and 16 show the results of the Levene's test for homogeneity and the Bartlet's test, respectively.

Table 15. Levene's Test for Homogeneity of Variances (Van Reenen Bay)
Effect: month
Degrees of freedom for F: 11, 1034

	MS Effect	MS Error	F	p <0.0001
Length	4.71	1.28	3.69	0.0000

Table 16. Tests of Homogeneity of Variances (Van Reenen Bay)
Effect: month

	Hartley F-max	Cochran C	Bartlett Chi-Sqr.	df	p <0.0001
Length	2.36	0.11	27.12	11	0.0044

Although the tests for homogeneity of variances reject the hypothesis of equal variances among groups, the ratio of largest to smallest group variances indicates that the ANOVA technique may still be adequate as an approximate procedure. This value for the data from Van Reenen Bay was calculated to be 2.35 (ration of variance in November to variance in December), which is less than 3. And remember that ANOVA is also robust to small departures from the assumption of homogenous variances.

4.2.3.2 Tests for significant differences in fish length

Table 17 shows the ANOVA results for the test of significant differences in fish length at Van Reenen Bay. From the ANOVA table it can be seen that the hypothesis of no difference in treatment means is rejected. This indicates that there are statistically significant differences in mean fish length among the 12 months.

Table 17. Univariate Tests of Significance for length
(Van Reenen Bay)

Effect	SS	Degr. of Freedom	MS	F	p <0.0001
Intercept	70967.05	1	70967.05	16952.16	0.0000
Month	1066.11	11	96.92	23.15	0.0000
Error	4328.65	1034	4.19		

The above result from the ANOVA table motivates for a further investigation of multiple comparison tests among the 12 months. This was done using the Tukey-Kramer post hoc test for unequal sample size (Table 18).

Table 18. Unequal N HSD; variable length (Van Reenen)
Approximate p values for Post Hoc Tests.
Error: Between MS = 4.1863, df = 1034.0

Month	Jan **9.6935**	Feb **8.9046**	Mar **8.7765**	Apr **8.7433**	May **6.8526**	Jun **8.1257**	Jul **7.7546**	Aug **8.6690**	Sep **8.5472**	Oct **8.9631**	Nov **9.7572**	Dec **10.174**
Jan		0.640	0.294	0.177	0.000*	0.000*	0.000*	0.205	0.179	0.324	1.000	0.906
Feb	0.640		1.000	1.000	0.000*	0.659	0.101	1.000	0.999	1.000	0.531	0.040*
Mar	0.294	1.000		1.000	0.000*	0.803	0.152	1.000	1.000	1.000	0.303	0.005*
Apr	0.177	1.000	1.000		0.000*	0.805	0.134	1.000	1.000	1.000	0.254	0.001*
May	0.000*	0.000*	0.000*	0.000*		0.000*	0.116	0.000*	0.002*	0.0008*	0.000*	0.000*
Jun	0.000*	0.659	0.803	0.805	0.000*		0.987	0.952	0.997	0.143	0.001*	0.000*
Jul	0.000*	0.101	0.152	0.134	0.116	0.987		0.373	0.736	0.004*	0.000*	0.000*
Aug	0.205	1.000	1.000	1.000	0.000*	0.952	0.373		1.000	1.000	0.164	0.003*
Sep	0.179	0.999	1.000	1.000	0.002*	0.997	0.736	1.000		0.997	0.121	0.004*
Oct	0.324	1.000	1.000	1.000	0.000*	0.143	0.004*	1.000	0.997		0.643	0.003*
Nov	1.000	0.531	0.303	0.254	0.000*	0.001*	0.000*	0.164	0.121	0.643		0.995
Dec	0.906	0.040*	0.005*	0.001*	0.000*	0.000*	0.000*	0.003*	0.004*	0.003*	0.995	

Table 18 shows that there are significant difference between January (9.69 cm) and May (6.85 cm), January and June (8.13 cm), January and July (7.76 cm), February (8.91 cm) and May, February and December (10.17 cm) and so on. All the values marked by asterisks indicate significant differences among the months. The results of the ANOVA table and the post hoc tests will be explained in the discussion section.

5 DISCUSSION

5. 1 SPATIAL DIFFERENCES IN GOBY LENGTH

The size of goby preyed on by Cape fur seals differed between the three locations. Atlas-Wolf Bay and Van Reenen Bay may have somewhat similar size trends with season, but they exhibit different mean lengths of goby, and appear different from Cape Cross.

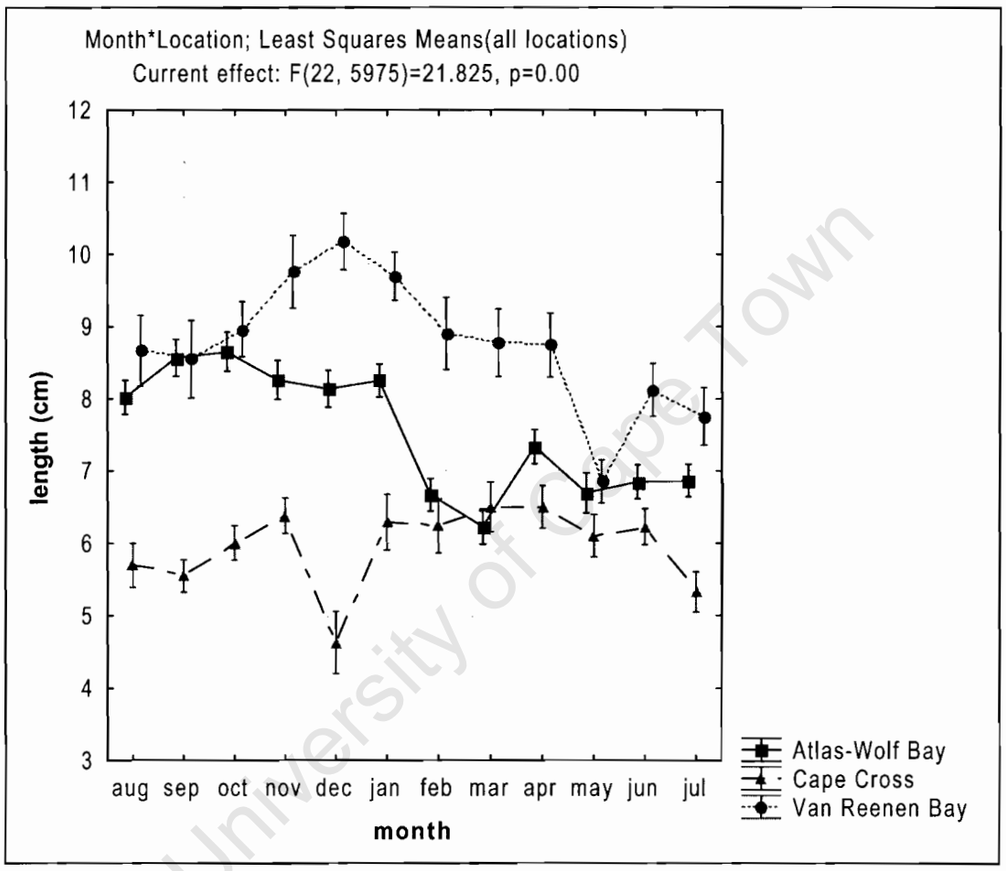


Fig. 10. Seasonal mean lengths of gobies preyed upon by Cape fur seals, all locations (1994-2001).

The descriptive statistics for all locations (Table 1) indicates that mean goby length was 7.50 cm at Atlas-Wolf Bay, 5.98 cm at Cape Cross and

8.62 cm at Van Reenen Bay. The two-way ANOVA result (Table 3) indicates significant difference between the mean lengths of goby at the three locations. Fig. 10 shows graphical comparisons of the size trends of gobies at the three locations.

Generally, there is an increase in goby length as we go from north to south (Fig. 10). The size of goby at Atlas-Wolf Bay (26°49'S) is larger than the size of goby at Cape Cross (21°47'S). And the size of goby at Van Reenen (27°23'S) is larger than the size at Atlas-Wolf Bay.

5. 2 TEMPORAL DIFFERENCES IN GOBY LENGTH

The length of goby fish preyed on by Cape fur seals at Atlas-Wolf Bay, Cape Cross and Van Reenen Bay displayed seasonal variation. The results from the ANOVA tests indicated that there are significant differences in mean goby length among the 12 months.

Generally, distinct differences exist between two groups of months: August to January constitutes the first season and February to July constitutes the second season. But some discrepancies are evident for each location as will be seen below.

5. 2. 1 ATLAS-WOLF BAY

The mean length of goby consumed by seals at Atlas-Wolf Bay can be categorized into two seasons, August to January and February to July. From the post hoc ANOVA results (Table 8), the mean length of goby in the first season (August to January) is significantly higher than the mean length of goby in the second season (February to July). The sampling year beginning on 1 August and ending 31 July the following year, corresponds approximately to sea surface temperature, wind and upwelling cycles in the Benguela ecosystem (Cole & McGlade, 1998; Cole

& Villacastin, 2000). Bailey (1979) also indicated that upwelling peaks in the Benguela ecosystem are seen from September to November. Based on these general environmental cycles in the Benguela ecosystem, it can be seen that there is some plausible correlation of goby length at Atlas-Wolf Bay with these cycles. The mean length of goby preyed on by the seals at Atlas-Wolf Bay was longest during the period when upwelling peaks (September-November), and then decreased to a shorter mean length during the February to July season (Fig. 11).

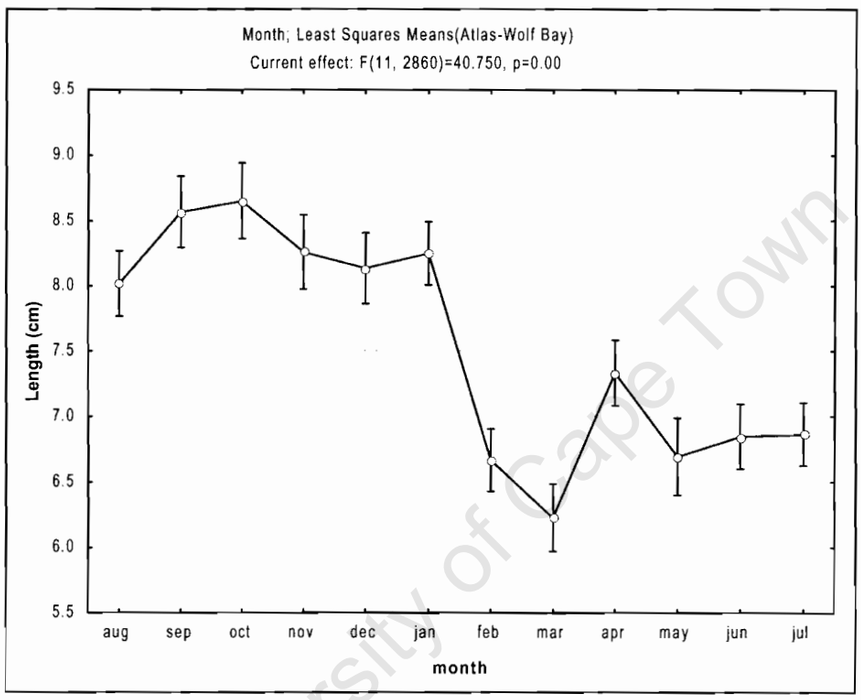


Fig. 11. Monthly mean lengths of gobies preyed upon by Cape fur seals at Atlas-Wolf Bay (1994-2001).

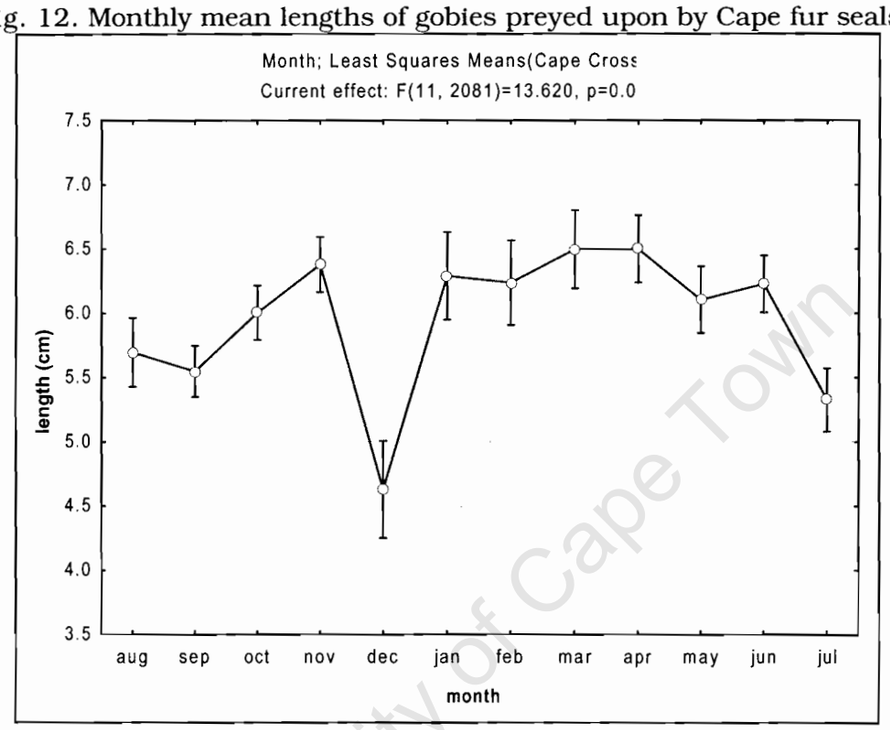
Cape fur seals forage within 200 km from the colony, and 66%-79% of dives are to depth less than 50 m (Kooyman & Gentry, 1986). Large gobies are mainly bottom dwellers, whereas small gobies are more pelagic and thus more accessible to seals (Crawford *et al.*, 1985). This pattern may explain the small size of gobies preyed on by the seals; however, the

seasonal trend in sizes of gobies consumed by seals may very well be representing changes in the structure of the goby population.

5. 2. 2 CAPE CROSS

The mean lengths of goby preyed on by seals at Cape Cross do not show a clear pattern of seasonality (Fig. 12).

Fig. 12. Monthly mean lengths of gobies preyed upon by Cape fur seals at Cape



Cross (1994-2001).

The length differences within months are not statistically significant for most month-by-month comparisons, except for July and December. The lower mean lengths of goby consumed during December and July may be reflective of the fewer number of years when samples were collected during these months, than other months. This is because there were no samples taken for July 98, 99, 2000, and December 94, 97, 98, 99,

2000. In general, seals at Cape Cross consumed gobies of 6.5 cm and less.

Cape Cross might have relatively different environmental conditions from the other two study locations due to the fact that it is geographically distant from them, so that different seasonal trends in mean goby lengths are observed here. Highest densities of goby larvae were found to the south of Walvis Bay (23°S) (O`Toole, 1978). This finding may indicate that gobies migrate towards the south during the spawning season, but there is not enough evidence to decide whether or not gobies migrate for spawning. The fact that there is paucity of information about gobies makes it difficult to understand the patterns observed. Knowledge of the gobies at the study areas and the corresponding environmental conditions would help to provide explanations for the results.

5. 2. 3 VAN REENEN BAY

Trends in lengths of goby preyed on by seals at Van Reenen Bay show similar patterns of seasonality to those at Atlas-Wolf Bay (Fig. 13). This finding is congruent with the annual cycles of upwelling and sea surface temperature as discussed for Atlas-Wolf Bay. However, the means plot do not exactly confirm the same pattern as those for Atlas-Wolf Bay. The mean length of goby at Van Reenen Bay reaches its highest peak (10.17 cm) in December and then starts to decrease in January until it reaches its lowest value (6.85 cm) in May (Fig. 13). This feature indicates some seasonality in mean goby length preyed on by Cape fur seals at Van Reenen Bay. Moreover, as can be seen on the map of the study area (Fig. 1) because Atlas-Wolf Bay and Van Reenen Bay are relatively closer to one another than to Cape Cross, goby in the former areas may experience similar environmental conditions. Thus, the similarity in seasonality of mean goby lengths consumed by seals at Atlas-Wolf Bay and Van Reenen Bay may reflect some effect of environmental factors

such as sea surface temperature and upwelling cycles, on the length of the fish.

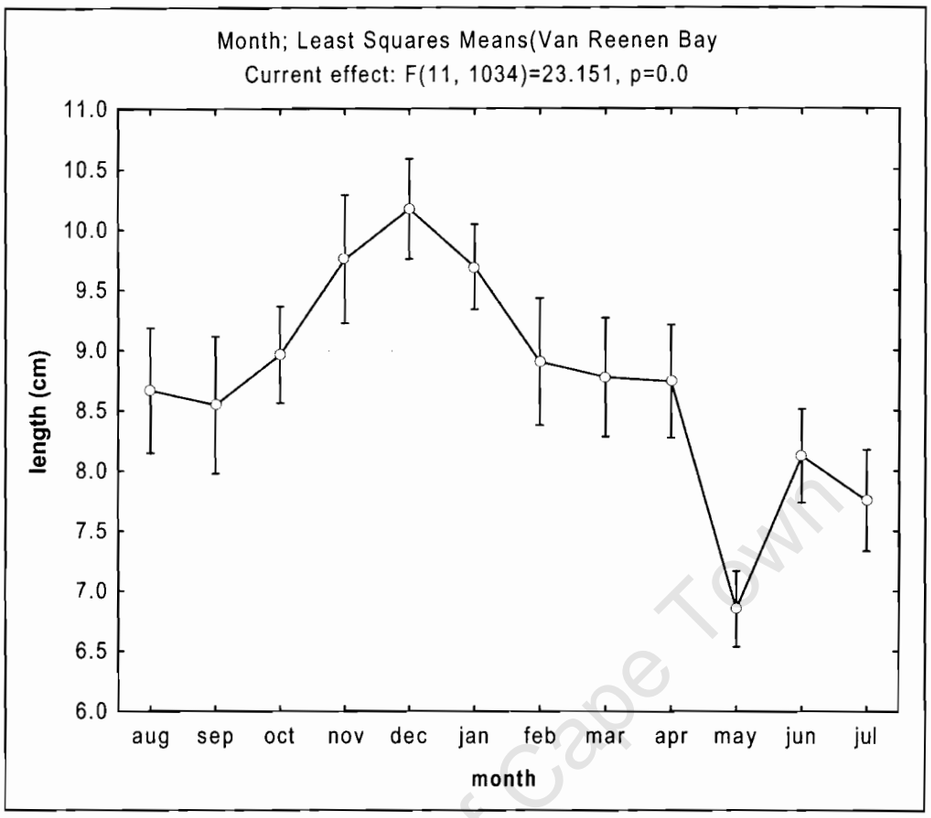


Fig. 13. Monthly mean lengths of gobies preyed upon by Cape fur seals at Van Reenen Bay (1994-2001).

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