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The Randomized Block Theorem for statistical designs

The Foos Coefficient of Covariance for Replicated Data Sets

First Fundamental Contribution to Statistical Science in the 21st Century

There are three kinds of degrees. There are paper ones which convey a false impression of mastery over a certain subject area. These are not difficult to find. Then there are real degrees consisting of the proven ability to accurately recite the content of a particular body of information and demonstrate the mastery of certain skills, usually computational. Then there are true degrees, the ultimate objective of a quality university, where advanced mastery of subject material in several disciplines is merged to give the holder a far deeper understanding than the holder of the ordinary degree is capable of. The holder of a true degree has the ability to study any complex problem in depth and explain the inner workings of it in a way that nobody else can. Only true degrees reflect an advanced education. They are not usually won in the space afforded by a baccalaureate or even with a PhD, and even then such ability requires extreme personal sacrifice. A true degree and a real education is what I achieved in my eight years of university study in science and mathematics, without a shred of outside support and while enduring severe hardships owing to poverty and overwork. You wouldn't let your child fly United if the pilot was untrained. I paid dearly for the ability to give you also the key to advanced insight, having earned the right to know as well as the unusual ability to impart to you the very rare ability to understand.

Dedication

The Randomized Block Theorem, better termed the Foos coefficient of covariance (to distinguish it from other parameters using the same term) for replicated data sets, is dedicated to those desiring to improve on legitimate scientific research of any kind. The derived coefficient of covariance parameter enables improved methods for both design and analysis phases in scientific research. The formulas and concepts for the coefficient of covariance for replicated data sets of any number, not restricted to blocks in an ANOVA design, copyrighted by Alan R. Foos, inclusive of all intermediate formulas involved in the derivation, were originally produced independently and only by Alan R. Foos between 1978 and 2007. No use of the formulas or concepts used herein, except for the existing combination formula and textbook sums of squares, may be made without permission or proper credit given, including comparable expressions with the same meaning but using substituted symbols.

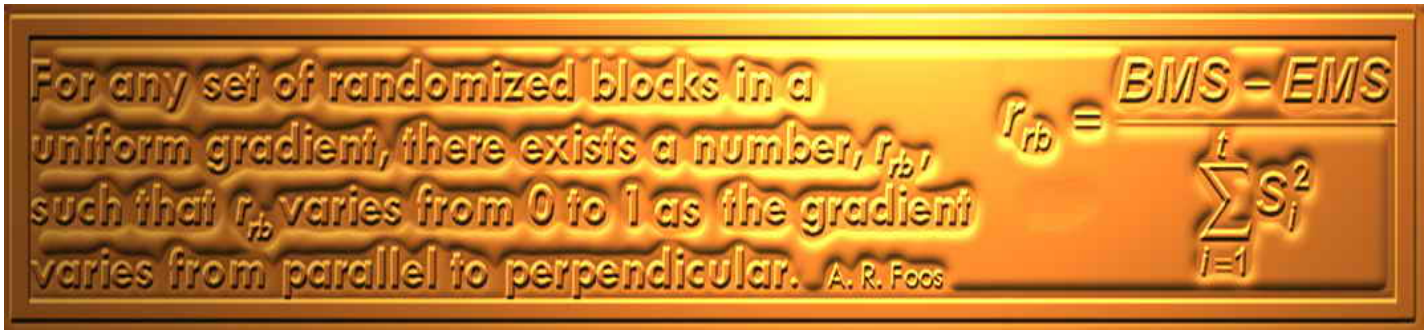
Acknowledgements

Gratitude is owed to special people whose unselfish dedication inspired me to do prove the theorem and make it useful. The Randomized Block Theorem introduces a new and universally valuable parameter , the Foos coefficient of covariance, or r value, for replicated data sets. This is helpful in optimizing the design and analysis of statistical trials for the social, physical.and biological sciences which in turn enable a practical, elegant and accurate reflection of reality with mathematics. It is not the same as the correlation coefficient, infrequently also called an r value.

I'd like to express a big thank you to my faculty advisers, the dept.head Dr. Earl Skogley , a dignified and organized professor , committed researcher, and world class soil scientist. Earl helped design my thesis iield plot while forgiving me for calling him the Duke of Potassium. He gave me everything needed as I worked.up to 36 hours a stretch without food or sleep in the lab for two years on the plant and soil analysis for my thesis. He also offered me the PhD before I left, which I regretted having declined. Unfortunately, Dr. Skogley is no longer with us .

There is really no way I could express enough admiration and appreciation for Dr. Charles Caughlin, a physical chemist whose insight and proficiency could not possibly be matched anywhere.in the world. He was a slave driver in the classroom and yet generously devoted many hours each week transmitting his amaziing and accurate insights privately. Dr. Kelly Mills, feared by all, also imparted a remarkable and exhaustive grasp of physiology both in depth and breadth. Dr. Raymond Ditterline of the Agronomy Department was of indispensable support and inspiration on my thesis work.

Special mention must be made and thanks extended to Dr. Richard Lund of the MSU Mathematics Department for helping me set up the mainframe so that I could program the ANOVA for my thesis data in FORTRAN. Dr. Lund also gave me a workable formula for the p(F) function so that I could use my HP calculator to match exact probabilities to regression results instead of fumbling with textbook tables. Despite all the information on the internet these many years hence, a good algorithm is still not to be found, and I've been unable to duplicate Dr. Lund's. Dr. Lund was the mathematician of mathematicians, extremely capable, always ready with enthusiastic help.



Problem and Postulate.

For any set of randomized blocks in a uniform gradient, there exists a number r such that r varies from zero to one as the gradient varies from parallel to perpendicular through a set of blocks, or in simplest terms, between two replicated data sets.

This can be called the Foos coefficient of covariance (for any replicated data set), the fraction (percent) of cross-block treatment variation that is accounted for by covariance among treatment pairs across blocks. It has long been proper for randomized block designs to orient each replication perpendicular to an external gradient, otherwise the design suffers from bias. The r value (not the well known correlation coefficient, r, between two data sets, which is sometimes called an r value) is specifically the average covariation of all treatment combinations divided by the average variance of single treatments across blocks.

The Foos coefficient of covariance, FCC, or r value for replicated data sets, is a measure of the degree, zero to 100%, of linear correlation of all combinations of cells (treatments in the RB design) from replication to replication. The FCC may also be called the Cat's Cradle, since the lines across "blocks" would form that design. Unlike the limited concepts of r and r squared, and not restricted only to rrandomized blocks, the Foos coefficient of covariance represents the overall degree of linear consistency among replicatations and can be applied to any multiple sets of data, even treatment effects and nested factorials. I first discovered this relationship in 1978 when working on the field plot for my thesis at Montana State University , but without a computer editor, the lengthy derivation could only be tackled with pencil. The first typed version was finished in 1992 with Mathcad, and the actual r ratio was not put into written form until 2007 using Ventura Publisher, While the proof in this paper centers on the r value for blocks in a randomized block design, the same concept may also be used to calculate a Foos coefficient of covariance for treatment effects (including separate members of factorials and both rows and columns in a Latin square, or for any other data replications. The r value represents an improvement in the design and interpretation of results for ANOVA strategies in particular, where the design and analysis of blocks may benefit from a more thorough approach.

An initial distinction between this r value and the conventional coefficient of correlation, r, (or r squared, the coefficient of determination) should be made. The r value defined in this paper can be defined as the ratio of the average covariance among treatment pairs from block to block to the average variance of treatments themselves (taken one at a time across blocks), and also as the fraction or percent of variance accounted for by covariance among all combinations of treatment pairs, i.e., ratio of average covariance among treatment pairs to average variance of single treatments across replications. It

pairs, i.e., ratio of average covariance among treatment pairs to average variance of single treatments across replications. It is also the block mean square reduced by the error mean square divided by the sum of treatment variances across replications. The conventional r, however, also known as Pearson's correlation, is the ratio of covariance between two data pairs to the product of their standard deviations. With some algebraic manipulation, r squared can also be shown to be the ratio of the sum of squares for one variable after reduction by residual error to the original sum of squares. In practice, r squared is usually used for measuring the goodness of fit between a calculated set representing the best fitting model and the original data set, thus is the amount of variation of the independent set explained by the predicting model; that is, the dependent variable. The chosen model for the dependent variable (predictor) usually has the lowest p(F) and highest r squared value from among numerous combinations of variables or transformed data sets.

If there were only two data sets (treatments), then the "r value" would be identical to both the coefficient of correlation and determination if the standard deviations of both were the same (slopes equal, therefore r =1). Both the r value and r (squared) are measures of linear correlation, but the concepts and formulas are different, where the r value is the percentage of linear association among all combinations of any number of data sets as explained by the average covariance of pairs to the average variance taken one at a time. If there is zero sampling error, the r value will be one for a set of blocks intersecting a perpendicular gradient and zero if the blocks have no particular orientation. The major advantage to the r value derived in this paper is that it provides a means of optimizing block orientation in randomized block designs, thereby eliminating bias in treatment effects. It then also permits the measurement of interactions or other distortion. It gives a more sensible estimation of either block or treatment effect than F value since it varies from zero to one (100%) as F varies from one to infinity (and p(F) from 100% to 0%) for the same data set.

Beyond these valuable contributions, however, is that the r value expresses more information than F. Like F, it contains the mean square value of interest and the error mean square, but it also includes cross block treatment (or cross treatment across blocks, or between any replicated sample sets, depending on the type of r value) variances. This has the effect of removing bias from parameters from which a conclusion of significance may be drawn. The F value is simply the ratio of the mean square of interest to the error mean square, while the r value (correlation of covariance) first subtracts the error mean square from the mean square of interest, then divides by the sum of individual cross block (treatment) variances, thus the r value represents the percentage of cross block variance that can be attributed to true gradient effects as manifested in the correlation of effects from one replication to another. The F value does not necessarily reflect those differences properly because any sampling errors isolated in one block that do not affect other cells in the block can produce a larger block mean square without correction for any failure of that effect to be equally distributed throughout any one replication affected.

It is also possible to calculate an r value for treatments in a randomized block design using an analogous, but legitimate, rationale. The advantage of this is that instead of assuming a uniform gradient across treatments, treatment effects (or transformations of) are assumed to be linear as is the traditional assumption for ANOVA designs, and the treatment r value, sans sampling errors, provides a pooled goodness of fit for that assumption with respect to the overall experiment. Non linear effects can be identified with precision by data transformations and appropriate coefficients for treatment factors calculated by stepwise regression techniques for inclusion in prediction models. In addition, the case where an r value for blocks is equal to or greater than the r value for treatments in a given experiment provides a firm rationale for including the extraneous (block) variable as one of the independent variables included in multiple regression procedures for predicting treatment effects.

We start with the observation that any significant variation among replications (blocks) in a randomized block ANOVA design must derive from positive covariance among replicated treatments. This must also be reflected in covariance of treatment pairs from replication to replication. Mathematical derivations will be used to define exactly what the relationship between covariance and replication significance is and understand how block to block treatment variation is useful in reducing sum of squares and increasing experimental precision. An r value is calculated that represents the fraction of (average) covariance for all combinations of treatment pairs across blocks to the total (average) block to block variance. If not intimately acquainted with these concepts, please review Weisstein's definition (Weisstein, Eric W .) of variance and covariance with appropriate mathematical formulas. Though randomized block designs may be the most common experimental design, they are usually conducted without strict regard for how they are oriented with respect to the extraneous variables they are intended to filter. As a result, both block and treatment effects are vulnerable to distortion and the effects of extraneous variables, including treatment interactions, customarily but often needlessly excluded from results. This paper provides a remedy for these shortcomings and allows extraneous variables to be included in multiple regression analysis where appropriate.

Since this newly derived r value represents the ratio of two variances, it is similar to the conventional correlation counterparts, r and r squared, the "coefficient of covariance" terminology is appropriate. They are not the same concept exactly, but the Foos coefficient of covariance can be correctly interpreted as the overall (or average) strength of linear association of all combinations of data sets taken two at a time across any set of blocks. Because there are other parameters called the coefficient of covariance, the term Foos coefficient of covariance may be required to distinguish between the two. This is also referred to here as the r value, which represents the average linear correlation among treatment pairs from block to block. Again, this r value is distinctive. Additionally, the Foos r value is a ratio that falls within the scope of F probability distributions. Basic formulas for BMS and F ratio in a randomized block design using the conventional ANOVA table are illustrated by StatsDir ect Limited (includes basic statistical definitions including the null hypothesis). For designs using the approach presented in this paper, the extended use of multiple regression analysis using transformed data sets for predictors, including measurable extraneous variables, is now allowable under conditions where an optimum r value can be demonstrated.

While reading this paper, keep in mind that a new and very useful concept is herein developed that extends the functionality of the most common experimental designs and holds existing statistical procedures to a new standard of accountability. Since this endeavor has been a solitary one, it is bound to be blind in some respects, so feedback of any kind is very desirable. Not only may there be errors that need correcting, but a foundation has been established for an important expansion of statistical science. On one hand, the concept and its derivation should be intuitively obvious to any good mathematician, but it has been the habit of science to overlook simple relationships which later turn out to have extremely important applications. The discovery of the calculus by Isaac Newton is no doubt the best example, the importance of which could not possibly be matched.

Ideally, assuming the direction of one variable gradient or vector sum of several across blocks is uniform, the r value of treatment pairs would indicate the deviation from right angles that it intersects replications, the r value (not the same as the conventional correlation coefficient) of 1 corresponding to a perpendicular intersection, and an r value of zero meaning an intersection of zero angle (blocks are parallel to the gradient). Such information could then be used to increase precision in subsequent experimental designs. If the extraneous variable can be identified and measured, the magnitude and direction of

intersection of zero angle (blocks are parallel to the gradient). Such information could then be used to increase precision in subsequent experimental designs. If the extraneous variable can be identified and measured, the magnitude and direction of the gradient can also be estimated and used with other regression variables for predicting outcomes with better precision irrespective of whether an extraneous variable is included in the final regression. It is important for the reader to understand that this theorem represents a fundamental and original insight into the established principles of statistical design, so that any reliance on recent developments in the field is neither necessary nor relevant. Supporting citations are dated according to the approximate time that the theorem was first developed, and the scientific principals have not been otherwise subject to change.

CAUTION: If a set of parallel blocks is intersected by any uniform gradient, and subsequently rotated as a unit around a common center, an oblique angle could be measured as a perpendicular intersection (if for example a line representing a secondary vector intersecting a block at midpoint also intersects all blocks at midpoint - this will result in an r value of one where all points of intersection vary by the same amount between blocks). It is the lack of uniformity from block to block that produces covariance and r values less than a perfect one. If there is no error term, i.e., some background noise, then any uniformly measurable differences in blocks produced by the same angle of incidence other than zero will produce misleading r values since all cells may be affected to a more or less consistent degree, thus masking distortion in treatment effects. To avoid distortion among treatment effects it is necessary to ensure that the primary vector of intersection is perpendicular to all blocks. Not only will an oblique angle cause distortion in treatment effects, but it will reduce the block mean square and mask block differences (BMS). This idea is equivalent to the cautionary comments cited later on, but emphasizes the need to identify the primary gradient. It should also be stressed that any lack of uniformity among cells from block to block, and only such, with or without treatment interactions from gradient effects, will produce r values less than one (with a corresponding increase in random error, EMS). The later section on the Equivalence Principle and Gradient wheel (Gradius) demonstrates a method of identifying a primary gradient as a prerequisite to careful experimental design.

The "candy bar" (representing a set of blocks lengthwise) near the end of this paper may also help visualize this concept using a lighting gradient. The strongest light is towards the upper right. It is not parallel because it is strongest between top and bottom, not side to side. But it is not quite perpendicular, either, because it also varies from side to side. Not only that, but it is not quite uniform, because it is strongest along a clearly visible axis of origin. As a result, the optimum value of r will be less than one for a set of blocks so affected. But there is clearly a definite origin to the light source, such that there is an r value less than one which represents optimum orientation. Let us assume that optimum value for r is 0.8, meaning that we can expect some distortion in any experimental results because of the lack of gradient uniformity, but we can minimize that by optimum orientation (perpendicular). Under such conditions of a non-uniform gradient, including the extraneous variable would be questionable, but identifying it beforehand also presents awareness that treatment affects may be subject to distortion where randomized within a limited number of blocks.

If we were to calculate the precise r value, it would be somewhat less than the optimum of 0.8, perhaps 0.7, because the light source does not intersect the top of the block in the exact center. The only way to know the optimum r value would be to measure the gradient before the experiment is conducted, precisely at points across a set of blocks, and inspect the results to see if the balance from end to end of the blocks is uneven (average treatment variances across blocks are not equal even though covariance is more than zero). If so, then there is clearly an origin to the gradient and blocks can be adjusted to achieve optimum balance. Since there is an obvious origin (light source) to the gradient, the optimum r value will also be slightly less. If the existence of an intersecting variable is not known, the value and direction of r indicating consistent block

slightly less. If the existence of an intersecting variable is not known, the value and direction of r indicating consistent block to block effects could reveal its presence, degree of or lack of uniformity and suggest improvement in block orientation. The use of two sets of blocks arranged at varying angles could also be helpful in verifying the direction, origin and magnitude (if not identity) of a gradient variable.

It may also be helpful to view the following chart which represents the plot layout in my 1976-1979 thesis work at the Plant and Soils Department, Montana State University, Bozeman. Each pink or blue strip is a block of treatments. Part of the experiment was also a comparison between two forages, the pink strip is sainfoin and the blue is alfalfa. The treatments for both were identical and included two factorial sets for N, P and K fertilizer treatments and several micronutrient paired comparisons. The cell numbers in the upper right corners refer to the treatment number after randomizing. The chart just below that is how the matching field plot appeared after planting. My concerns over gradient effects first led to the development of the randomized block theorem in 1978, but the equations were difficult to present without computer assistance. Several versions were written after that until the last in 2007. The layout of these field plots is probably somewhat fixed, such that much flexibility in orientation is not allowable.

North

8' x 16'

22	13	18	20	11	10	7	4	21	16	3	8	5	14	15	9	6	1	19	25	2	12	24	23	17
176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200
24	9	12	1	2	25	22	19	11	20	21	18	3	16	23	4	8	14	15	6	10	13	5	17	7
151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175
4	21	16	11	24	5	14	3	25	9	15	12	8	17	18	10	13	20	22	19	6	1	7	2	23
126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150
14	25	9	15	10	17	4	5	8	12	11	21	23	2	20	1	13	7	6	16	3	24	19	22	18
101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
15	10	5	12	22	13	21	18	6	3	4	19	25	11	17	16	1	23	7	20	2	8	24	14	9
51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75
13	19	1	24	17	11	20	22	10	16	8	18	14	5	7	3	2	6	9	23	21	15	12	4	25
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
2	17	8	21	14	12	9	13	1	23	7	20	15	4	19	24	10	11	18	5	22	3	25	6	16
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Alfalfa - Sainfoin Fertility Trial

Section 2. Introduction: Randomized Block Designs.

The proposal is based on the fact that if a gradient (or trend) exists among replications in a randomized block design (the assumption usually made for randomized block experiments), that all treatments are affected equally (i.e., exposed equally in each separate block) from one replication to another. This is the ideal case only, in which each set of replications must be oriented at the same right angle to the gradient. This ideal is seldom realized in practice, but provides opportunity in certain cases for measuring extraneous variables of interest. This trend can be demonstrated as covariance among treatments, and an r value (zero to one) calculated to estimate the degree of efficiency in terms of the angle of gradient intersection (90 degrees to zero). Two ANOVA models are in common practice. The first model is what is called a CR (completely randomized) and the second is called an RB (randomized block), where TMTs (treatments) are randomized within each replication. Each replication then comprises a set of randomized blocks, where the treatments within the block are randomized so that none are preferentially exposed to extraneous influence. This proof provides a method for measuring gradients, optimizing design layout, and measuring block orientation.

In a CR, completely randomized, design, the more replications are used, the more precision is obtained as reflected in smaller ESS (error sums of squares). This is not directly measurable since replication variance does not enter into the ANOVA table; thus, completely randomized replications do not increase experimental precision under controlled circumstances designed to directly filter it, but only average background distortion or sampling error. The CR is also called a one-way design. In the RB, or two way, design, the overall SS (sum of squares) is reduced by both treatment sum of squares (TSS) and block sum of squares (BSS). The ratio of mean squares obtained by dividing by degrees of freedom (number of treatments or blocks less one) is called F, and corresponds to the probability that the differences are caused by chance (the null hypothesis). The required probability for rejecting the null hypothesis, p(F), may be read from a table or an exact p(F)

calculated for the F value. Precision is not always gained by putting replications into discrete blocks - it can even be

calculated for the F value. Precision is not always gained by putting replications into discrete blocks - it can even be reduced; hence, there may be no point in blocking. While it would not seem meaningful to treat separate replications as blocks, especially where not physically separate, the Foos coefficient of covariance is not a difficult check to perform for hidden effects.

How can that be when variation is always positive? For several reasons, one being that the amount of variation is a measure of significance only when divided by remaining degrees of freedom, so the TMT F ratio may actually be decreased by introducing blocks that reduce both degrees of freedom and error SS. In fact, that must be the case unless there is an extraneous variable intersecting blocks that causes true differences among them (this implies TMT covariance from block to block). The variable may be known or unknown, and the gradient may or may not (as in agricultural field plots) be perfectly uniform. Another problem is that even if TMT precision is gained, the results can be erroneous if the extraneous variable is not independent of TMT variation. This can happen even if the variable itself would not interact normally, but does so anyway because the gradient intersects a small number of blocks at less than 90 but more than 0 degrees, thus affecting some treatments more than others.

Even if the interaction is zero, to the extent to which blocks are not arranged perpendicular to the extraneous or intersecting variable, any reduction in the SS will be lost because block differences will be reduced (and treatment effects likely distorted as well) and will thus not reduce the EMS (error mean square). Snedecor and Cochran, page 256, point out by means of an example that the blocking will improve "accuracy" if the mean square is twice the residual mean square, and that there are "real" differences between replication means. This implies that if no real differences among replications (as blocks) exist, then there was no point in going to the trouble of blocking, even though there may be plenty of reasons to have that many replications in a CR design. Generally, more random replications can be used to match any precision gained by using blocks, but if the block design shows no differences, it may be possible to gain precision by treating the experiment as CR in the final analysis. It may also be possible to use the gradient wheel method described later using final results for exposing unanticipated bias and for making adjustments to layout in the next field plot, if possible to make them.

Mendenhall, page 653, states that blocks may represent temporal, spatial or other differences in experimental replications. They state that if several treatments are compared where a trend occurs, a part of the variation can be removed by blocking. Actually, this really means that extraneous variables that would otherwise obscure true treatment effects are instead isolated between replications instead of being contained within them where they will contribute to sampling error and contaminate results. But then if we can safely assume that effects of the extraneous variable are evenly distributed, no difference in conclusions can be expected, only that an extraneous gradient is at work. It isn't that the variation is actually removed from the experiment, only that it is prevented from having an arbitrary or uncontrolled influence on treatment effects, and this effect should be of interest. The blocked variable has an effect on treatments, but ideally, its effect influences all treatments within a single replication evenly in accord with the fact that design has distributed the strength of that variable equally from block to block. It may also have an interaction with treatments,and its effect be justifiably regarded as a separate treatment and included with others in a stepwise regression for predictor variables. This is, in fact, the preferred approach when possible. Of course, not all blocks may be represented by quantity, but this will not prevent study of any effects or interactions that blocks may have on treatments. Nor is it absolutely necessary to regard such replications as blocks for the study of Foos coefficient of covariance r values among replicated data sets. The tapping of conventional designs for covariance coefficient analyses may reveal many hidden variables of interest.

It is fair to restate the conventional approach and say that if there is no block to block gradient or trend, then no variation can be removed. The question may arise as to how much variation is necessary among blocks for there to be success (for a reduction in EMS). This may not be initially easy to grasp. Mendenhall provides a section called Some Cautionary Comments on Blocking, where these points are covered on page 712, essentially that block designs should not be used to investigate the effects of two factors; otherwise a randomized block ANOVA could lead to erroneous conclusions. By this, I think they mean that a blocked variable is not usually suitable for inclusion in the results, as was the case in my thesis, I also think the implication is that it cannot be assumed that the extraneous effects are uniform from block to block. This I do not think is at all true in theory, though common practice in agronomy is to consider the extraneous variable as meaningless in the results, and that this assumption stems in part from being unable to control it. While this may be a practical limitation for most agronomy trials, it is not a theoretical requirement of experimental design, nor should the effects of so called nuisance variables necessarily be ignored.

Thus, a moisture gradient as is often the object in agricultural designs, should (ideally) cause uniform changes in yield for all treatments from block to block (covariance) since otherwise the block - treatment interactions will distort results. Actually, even in the best design, the bias interjected by an extraneous variable cannot be casually dismissed unless it is measured and its effect included in the results just as any other treatment. The most common assumptions in randomized block designs actually are a way of pretending that if the extraneous variable is blocked, then there is no need to consider its influence, yet it may well have biased treatment results by interaction even where properly oriented. This is contradictory to the often stated effect of nitrogen on plant growth in that the effect of nitrogen is compounded by unit additions of moisture. Because such interactions are usually ignored and block orientation not analyzed, the "coefficient of covariance" r value developed in this paper may help remove a serious limitation in RB designs and subsequent regression technique. This can be expressed as follows:

If regression analysis is used to incorporate the block variable, appropriate interactions with all treatment variables may be identified with mathematical precision using routine regression and filtered from the error term as is routinely done for other (intrinsic) treatment factorials, allowing any mixture of intrinsic or extraneous variables which best fit the predictor . Of course, only randomized block designs with measurable gradients will permit this (for example, blocking on gender will not allow regression analysis). It is neither necessary nor desirable to require a linear relationship for gradient effects (with raw data) any more than is customarily required for treatment effects as long as the appropriate data transformations and interactions are selectively identified for goodness of fit under routine multiple regression procedures for inclusion in equations for predicting the dependent variable effects. The results for my thesis indicate that the most appropriate relationships for nutritional responses are invariably quadratic, a sensible conclusion as too much of anything may not be good.

Hence, the question arises as to whether ignoring the nature and effect of a gradient is the most responsible course in certain cases. For many purposes, the effects of a gradient represents uncontrolled conditions which may not be representative of those found in the field, and failure to identify and measure these effects bring the applicability of results into question, even more so if gradient interaction with treatments exists since distortion in results would be omitted under assumptions that they are not present. For example, if a moisture gradient affects yields, the ideal would be to identify and measure the gradient as well as its effects. If moisture does in fact cause an interaction, then treatment effects will be

measure the gradient as well as its effects. If moisture does in fact cause an interaction, then treatment effects will be distorted whether the effects of a block factor are ignored or not; therefore the presence of a gradient should demand thorough measurement of its effects on treatments. Alternatively, it is possible in some cases to incorporate the moisture variable as a potential factor in the experimental design and statistically determine the effect of the gradient variable including interactions with treatments. This can be performed with potentially high precision using standard regression techniques.

In reality, an assumption of non interaction may not be strictly true, but it should be close even if the effect of an extraneous variable is ignored since such distortions will also affect intrinsic variables of interest. Therefore, the RB design is usually used to filter (or average) the effects of nuisance, extraneous variables. These are effects that cannot be precisely controlled or measured and which may cause treatment interactions which are less severe if filtered, and it is reassuring when blocks are significant. It is, however, not always the case that extraneous variables cannot be measured, that these are not sufficiently uniform, or that their interaction with treatments is of any more concern for the extraneous variable than their unseen effect on the treatments under consideration. Additionally, a carefully constructed RB design can be used to great advantage for measuring effects of extraneous variables if experimental controls are sufficient and blocks consistently oriented.

Mendenhall continues in his section on blocking by stating that it is not always beneficial, that it is so only when the between block to block variation is large enough to overcome the smaller degrees of freedom left in the error mean square. This may sound like obscure rattling to most people, but in the ANOVA design, the probability of treatment effects being meaningful depends on the number of observations, and if there is no extraneous variable effect, then blocking may actually mean a lower degree of confidence in the observed results. This is a feature of the F ratio that all statisticians will readily appreciate, so I will not explain it further, other than to say that even if there is no obvious gradient for an extraneous variable, additional replications will generally give better results, yet there is little point in blocking if there is no gradient to block against. There is no harm in making such an attempt, however, and if the attempt exposes no such effect in the results, it is just fine and better not to include the block sum of squares in the ANOVA table. Nevertheless, either the conventional block mean square or the r value developed in this paper may be useful as a test in determining whether or not such an effect does indeed exist, if the blocked ANOVA is preferrable to the non blocked table, and if an extraneous variable can included in the regression whether identified or not.

It is important to note that only to the extent that replications are consistently oriented at right angles to the extraneous variable being filtered can there be a significant block variation. Mathematically, Mendenhall's statements are correct and fairly obvious, but a gain in information only occurs where there is a significant block effect, just as for treatment effects. There is no reason not to use blocks to measure a block effect, as long as the effect is measurable and imposes no external bias on the plot, i.e., the external gradient is directed perpendicular and evenly across replications as much as possible. If the r value, that is, Foos coefficient of covariance for a set of blocks set is as large as the coefficient of covariance for any set of treatments within the same blocks, then you know that the inclusion of block effects and interactions is no less justified as is routinely applied to treatments, and the block variable can also then be included in multiple regression techniques.

Snedecor and Cochran on page 264-5 define the efficiency of blocking as the fraction of sigma squared for a CR design divided by siqma squared for the corresponding RB. The ratio must exceed the value of one for blocking to succeed, and if the experiment was an RB, then the numbers can be inserted to give the comparative value. They provide an example on that page. Substituting sigma squared with ESS/EDF where EDF is error degrees of freedom, and manipulating terms yields the fact that for blocking to succeed, the ratio of SSE for RB to the SSE for CR must be LESS than the ratio of EDF for RB to EDF for CR. This paper introduces a new measure of efficiency in terms of a combined coefficient of covariance for treatment pairs, the ideal r value being 1 for a perpendicular intersection of blocks in a uniform gradient. An r value of less than one suggests the possibility of improving the design by reorienting blocks.

Note that the EDF for the RB is always less than EDF for the CR, since it is equal to the EDF for the CR design less the degrees of freedom (j-1) for blocks. This means that if blocking is to increase precision, the ratio of the ESS for RB to ESS for CR must be less than a value which is less than one; therefore, the reduction in sums of squares by blocking may very possibly decrease experimental precision. This happens where no real (significant) trend (gradient) exists from block to block and the SS for blocks is not large enough to overtake the loss resulting from lesser degrees of freedom. The extent that it is large enough is related to co variation among treatments across blocks, as a zero value for co variation always produces an F ratio equal to one. By substituting the required F ratio for such an experiment into the equation relating F and covariance, the minimum covariance required for any F value (a least significant covariance (LSCOV)) may be derived. Therefore, blocking is meaningless unless a gradient exists due to an extraneous variable or the vector sum resulting from a combination of variables. Covariance and block significance mutually depend on such an extraneous variable exerting an influence on blocks.

A mathematical equivalent for F in terms of covariance is intuitively implied since blocks cannot differ significantly without covariance among treatment pairs. This way of approaching the issue may be more meaningful than the F ratio of two sigmas, since mean square values can be used to calculate covariance effects and r values ranging from zero to one are more informative than F values without upper limits. A trend initially exposed by covariance or calculated r values between two sets of data suggests an extraneous variable is affecting results, and randomized block designs that exploit covariance in such a way can be used to advantage. Since the extraneous variable is not always known (or is a combination / vector sum), r values for treatment pairs in preliminary experiments can be helpful in isolating and eventually identifying unknowns the importance of which were previously overlooked. Results can also help in designing subsequent experiments. Snedecor and Cochran, p255, observe that familiarity with plot technique often gives the experimenter the ability to roughly predict the effects of an experiment. The preliminary use of 2-3 treatment replications set at different angles at random, temporally or spatially, can expose hidden variables and suggest larger RB designs that exploit them for increasing experimental precision. Covariance r values may also, in certain cases, have more practical value than treatment variables in the identification of cause and effect relationships; for example, the etiology of diseases and the identification of preexisting causal links between disease syndromes.

The standard ANOVA for any RB is a shortcut to calculating the combined sum of covariances across blocks. From that, an average covariance or r value for any RB can be readily obtained. The number of degrees of freedom for a randomized block r value depends on the number of treatment pairs in the numerator; that is, the combination of treatments taken two at a time as well as the denominator of t treatments. A function p(r) for the null hypothesis being true should be derivable since p(r=1) would always be zero percent, and p(r=0) would always be 100 percent. In any case, note that p(r) should also be a

function of sine theta, where theta is the angle of incidence to randomized blocks by an intersecting gradient. The following equations for block mean square, (BMS), error mean square, (EMS), F, average covariance and r for covariance ratio, will be proved in the process of establishing the formula for an r value representing the Foos coefficient of covariance for block designs (Sxy refers to the covariance of treatment pairs where x and y is shorthand representing all combinations for any number of treatment pairs). Sigma squared for t treatments also designates the cross block treatment (sample) variance for any treatment, the sum of those forming the denominator of our derived r value in terms of the ratio of covariance to overall variance.

$$EMS = \frac{\left(S^2{}_{x_j} + S^2{}_{y_j} - BMS\right)}{(t-1)}, \quad \text{Treatment variances may be designated } \sum_{i=1}^{t} S_t^2$$

$$BMS = \frac{\sum_{i=1}^{t} S_t^2 (\text{Treatment Variances Across Blocks}) + 2\sum_{n=1}^{C_2{}^t} S_{xy} (\text{Twice Covariances of Treatment Pairs})}{t\ \text{Number Of Treatments}}$$

$$F = \frac{BMS}{EMS} = \frac{(t-1)}{t} \frac{\left(\sum_{i=1}^{t} S_i^2 + 2\sum_{n=1}^{C_2{}^t} S_{xy}\right)}{\sum_{i=1}^{t} S_i^2 - \frac{1}{t}\left(\sum_{i=1}^{t} S_i^2 + 2\sum_{n=1}^{C_2{}^t} S_{xy}\right)}$$

$$\overline{S_{xy}} = \frac{EMS(F-1)}{t}, \text{ also, } \overline{S_{xy}} = \frac{BMS - EMS}{t}$$

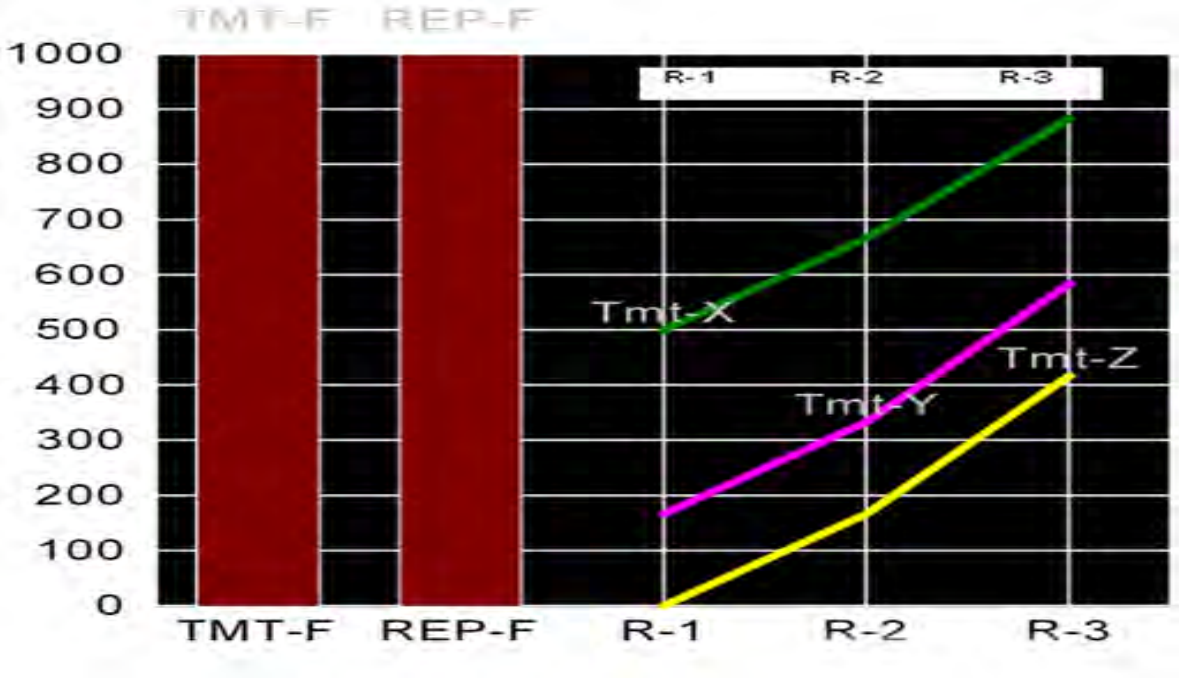
$$r = \frac{\frac{\overline{S_{xy}}}{t}}{\frac{\sum_{i=1}^{t} S_i^2}{t}}$$

$$r_{rb} = \frac{EMS(F-1)}{\sum_{i=1}^{t} S_i^2}$$

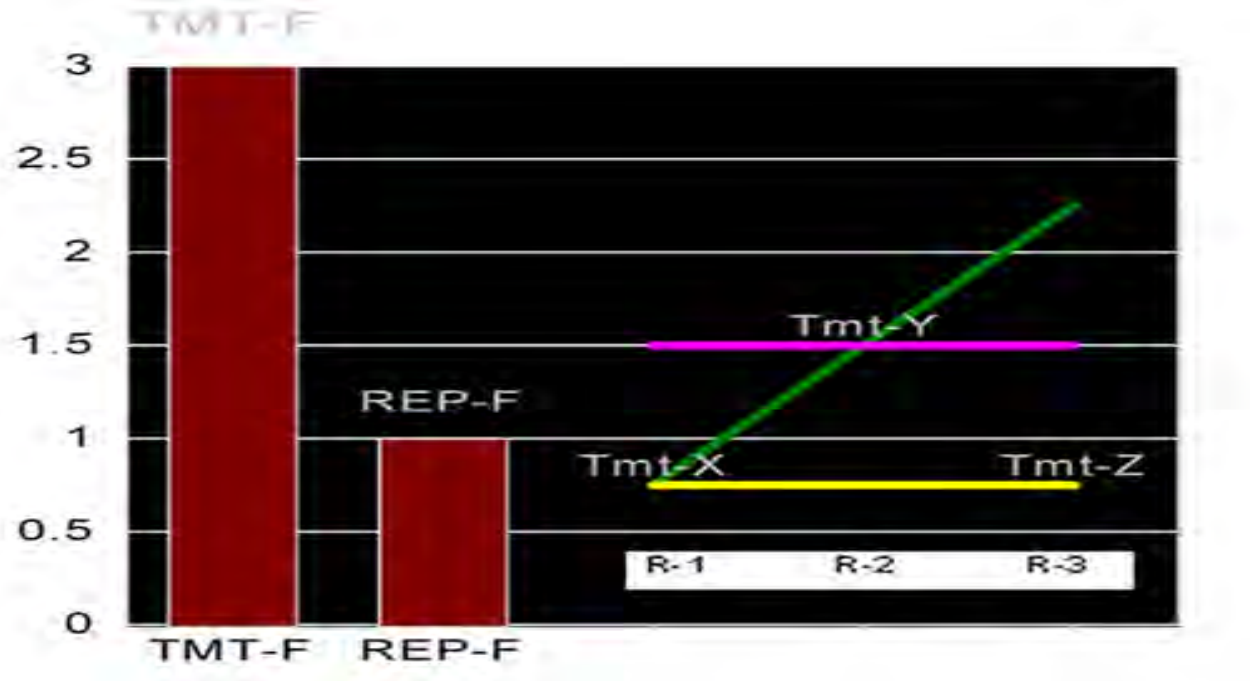
$$r_{rb} = \frac{BMS - EMS}{\sum_{i=1}^{t} s_i^2}$$

Section 3. Discussion Introducing Proof.

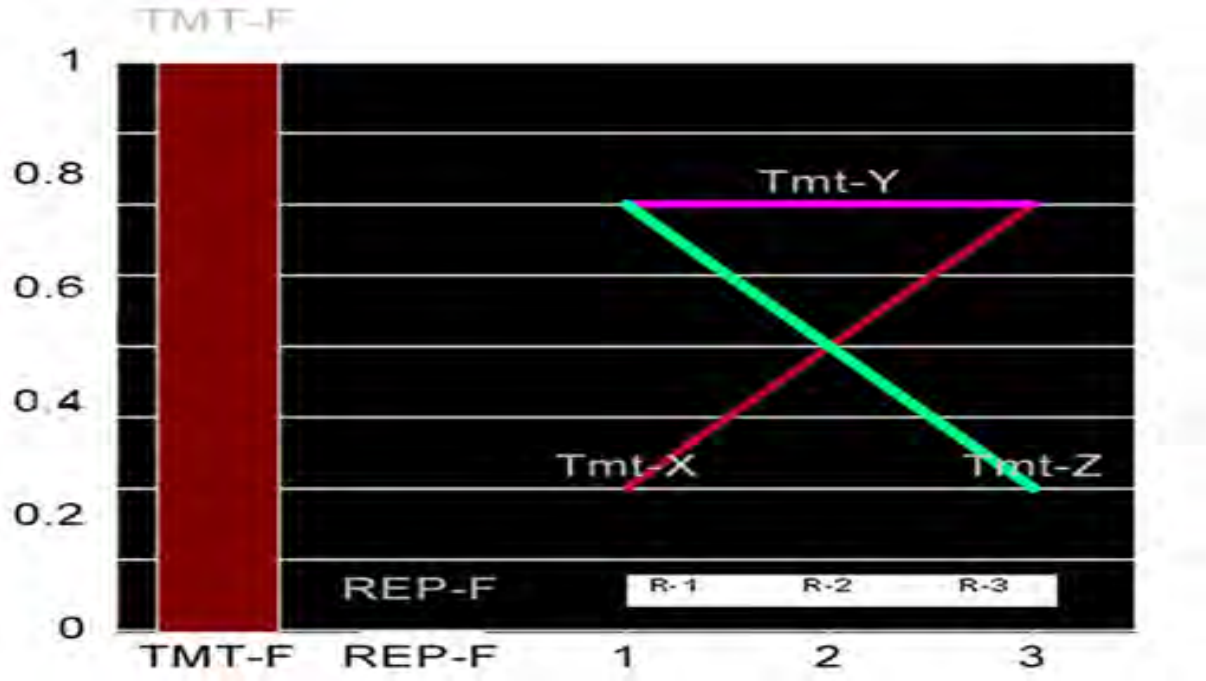
Refer often to the following figures which illustrate the relationship between F values and treatment covariance across blocks)



F-All Treatments Vary Across Blocks. Note that both treatment and block F values are very large and significant differences would be at a very highly significant level, p(F) <0.001. Covariance exists among treatment pairs.



F-One Treatment Varies Across Blocks. Note that treatment F is greater than one and potentially significant, while block F is exactly one and never significant p(F)=1 (100%).



F-Opposing T rends Acr oss Blocks. Note that treatment effects cancel giving an F value of one, and for blocks an F value of zero indicates complete interaction of treatment values with blocks. The case of negative covariance is not suitable for the RB design. In such a case, the ratio of average covariance to variance for t treatments will be negative to a maximum of a negative one.

These relationships will be set in mathematically precise terms and proved in the following sections of this paper. Traditionally, significance for a randomized block design is judged by F, the ratio of variation in a set of observations, the mean square, to the residual variation, the error mean square. An F ratio of only one indicates that the numerator variation is the same as the error term, so no real difference exists, associated probability, p(F), then being 100% that there is no real difference among means (the initial null hypothesis being that there is no difference). Any differences among treatment or replication means would be no greater than that predicted by random variation. For F ratios greater than 1 there is increasingly less than a 100% chance that means differ by chance alone, because the differences are larger than overall variation. It may seem a quirk that an F ratio of zero is obtained when any positive treatment effect in one treatment is offset by the negative effect in another; hence, a negative correlation (covariance) between those two treatments. It is no accident that an F ratio approaching infinity is matched by a Foos coefficient of covariance of one, and that an F value of one represents a coefficient of covariance of zero.

The theorem states that any such differences among replications (an F ratio larger than one) would be accountable only by covariance among treatments from one block to the next. Take the simplest case of two treatments. If treatments in the second replication are consistently greater than in the first, then one should find covariance among treatments associated with a replication F ratio greater than one. For treatments more than two, the covariance is the sum of all possible combinations among them. Perfectly uniform covariance produces F ratios approaching infinity for both replications and treatments. This is because all variation occurs due to these effects, and error mean squares progressively diminished by block differences will approach zero. The proof derives a formula for BMS (block mean square) in such terms by breaking

out the covariance component to show that the F value for BMS is larger than one only for the sum of individual treatment variances across replications that exceed zero. The error term thus excludes covariance effects of treatment pairs from block to block.

Interesting deductions follow from this idea. Random, i.e. inconsistent, variation among replications will produce treatment covariances of zero. Random variation will therefore remain in the error term, so F for replications will be one, the largest F ratio permitted given randomized block assumptions. Obviously, because of the need to combine covariances for all treatment combinations, negative covariance is not workable (this is equivalent to treatment interaction with blocks). This leads to logical errors. An example of negative covariance would be an instance where additions of fertilizer increase yields for some treatments in one replication but decrease them for the next. This is a possibility, but it would violate the assumptions for blocks in an RB design. Good practice foresees such effects and designs a factorial experiment that avoids these kind of trends. Perfectly opposing curvatures across replications, meaning perfectly negative covariance among two treatments, results in replication F ratios of zero and treatment F ratios of one; therefore, such interactions are not appropriate for good experimental results.

In an example, if moisture caused half of the treatments to increase and the other half to decrease, all the variation would be attributed to a significant factorial effect between moisture and fertilizer, and no block differences would result. If the moisture gradient intersected blocks at a zero angle such that only the ends of each block were affected, then the resulting block to block variation would also be zero, and no block efficiency would result (but, possibly, distortion in treatment effects could result). Thirdly, if only random variation occurs between blocks (BMS=EMS or no gradient exists), then again no reduction in the EMS occurs (except by averaging distortion by using repeated random replications), and the practice of blocking is of no value.

The following proof follows standard induction criteria for k treatments =2 and k + 1 treatments = 3. In order to make the concept work, the notation for individual treatments across blocks is retained by giving each treatment a separate designation of x, y, z... rather than the subscript of t ordinarily used to reference treatment values (and where j indicates blocks). Two and then three treatments are used for the proof according to standard induction criteria, the permutation of larger numbers being difficult to work with. By using these designations, mean square formulas can be rearranged to produce individual treatment variances isolated across instead of within replications for rearranging covariance formulas in pairs between them. The result of each case is that replication mean square can be written in terms of the sum of all possible treatment covariance terms (as shorthand here designated as xy) and sum of individual treatment variances throughout replications, the ratio for which varies between zero and one as the orientation of blocks changes from parallel to perpendicular to the gradient. The proof demonstrates that small values of covariance fail to give significance for blocks, and that zero values always give F ratios of 1; therefore, significant variation is entirely derived from covariance between treatment pairs, the value of which can be calculated by subtracting EMS from BMS and dividing the result by the sum of treatment cross block sigmas. This newly introduced parameter of r indicates the fraction of block to block variation attributable to covariance; let p(F) give the associated probability for r.

Let us approach the derivation from the simplest examples. There are three possible ways that treatments can vary in combination across replications (aside from the case in which none of them do). Let us take the case in which only one

treatment varies as shown in the above graph (for these examples, refer carefully to the three matching charts above... in this case where F=1). However this is done for one treatment across blocks, replication differences remain the same as in the error term, F is one, and there is neither significance for replications nor covariance between any two treatment pairs. In fact, because the only increase in replication error (BMS) over error mean square derives from covariance, this is the only possible result. Note that for the purposes of this proof, (sample) "covariance" is defined as the sum of the product of deviations from each across-block treatment mean (sum of squares) divided by the number of replications less one (number of replication degrees of freedom). The average covariance is the total of such combinations as derived then divided by the number of treatment pairs.

Finally, take the case of near uniform trends across replications. Replication mean square is the sum of both single treatment variations and positive covariance. Perfect uniformity cannot be demonstrated adequately with the traditional ANOVA because a positive covariance and an error mean square (EMS) of zero produce significant F ratios approaching infinity. Opposing trends across blocks will violate traditional assumptions for randomized block designs and be difficult to demonstrate for more than two treatments in terms of an r value as results for some pairs would tend to cancel others. This is the instance of negative correlation, significant when approached as a regression problem, but such an effect will be masked in a blocked ANOVA. It may produce non-significant treatment F values between zero and one, but zero F values for blocks. If the effect is exactly opposite to the first treatment, then the two treatment variances are exactly equal to twice their absolute covariance, but the covariance is now negative in sign for F=0 and a randomized block r value of -1 (see equations later).

If you have no formal exposure (coursework) to inferential statistics and advanced algebra, you should not attempt to understand the following proof. For the sake of those who have a non professional background in statistics (meaning upper level coursework with good grades), this brief refresher is offered. The general formula for variance, is the sum of the squared deviations between observations of x and the mean of x divided by n, the number of observations. In practice, we usually have only a sample population, so we use n-1 instead of n in the denominator. This is called the degrees of freedom. The formula is written using summation notation as the sum, as i goes from 1 to n, of the squared differences between each i element of x and the mean of x, divided by n-1 DF. If we have an experiment with r replications or blocks, then we can reference the sum of the ith elements for each jth set, as follows, to represent the grand mean square, GMS. This is usually referred to as the total mean square, but we want to reserve the symbol TMS for treatments. The grand (total) mean square, GMS, is thus the grand sum of squares, GSS divided by rt-1 degrees of freedom:

$$GMS = \frac{\sum_{j=1}^{r}\sum_{i=1}^{t}(\bar{x} - x_{ji})^2}{rt - 1}$$

Pardon my dyslexia, the sum for i elements should come before the j since alphabetical order prevails in the absence of any mathematical meaning. The number of observations is r blocks times t treatments less one for DF in the denominator for a total mean square. Now, it practice this is a tedious calculation. It turns out that the same formula can be represented by the sum of squared observations less the correction factor, CF, which is the square of the sum of all observations divided by the number of them, n, or in this case rt, like this, where the numerator is called the sum of squares, in this case GSS:

$$GMS = \frac{\sum_{j=1}^{r}\sum_{i=1}^{t}(x_{ji})^2 - \frac{\left(\sum_{j=1}^{r}\sum_{i=1}^{t}x_{ji}\right)^2}{rt}}{rt - 1}$$

However, for this proof, we will use BMS, the block mean square. Any replicated set of data within the total set of observations follows the same pattern, whether it be treatment (TMS). The mean square is the sum of squares divided by DF degrees freedom. The sum of squares for replicated sets, here BSS, is the sum of squared sets of observations for all sets, divided by the number of observations in each set, less CF. CF is always the same, the number of all observations squared (divided by the grand total number of observations. It's easier to understand the following algebraic expression. If you can quickly grasp or already know the meaning of the following formula for BMS and can write the counterpart for TMS

(treatment mean square), then you will be able to trace and understand the proof. Note that we only have r-1 degrees freedom for blocks and t-1 for treatments, not rt-1:

$$BMS = \frac{\frac{\sum_{j=1}^{r}\left(\sum_{i=1}^{t} x_{ji}\right)^2}{t} - \frac{\left(\sum_{j=1}^{r}\sum_{i=1}^{t} x_{ji}\right)^2}{rt}}{r-1}$$

Now, we are ready to prove that BMS is only greater than EMS, and statistically different, by virtue of covariance of treatment pairs from replication to replication. We then extract the formula for covariance same can be done for any replicated data set, including TMS for treatments, and should be done. We will explore the reasons for that. It may be a good thing to add that the theory of statistics has flaws, the vague assumptions of randomized blocks being only one of them, though perhaps the most glaring. Nor am I the best statistician with the most comprehensive knowledge. It just turns out that after intensive exposure and use of conventional ANOVA in my MS thesis, that I was able to perceive this important improvement in the procedure that also makes ANOVA in general far easier to understand. Having much practice in the use of mathematics for solving problems grants the ability to labor through the complicated algebra and present it the most understandable fashion. So enjoy.

Section 4. Part 1 of 4: Inductive Mathematical Proof, Block Mean Square Composed of Treatment Covariance Using k=2 T reatments.

Parts 1 and 2 prove that block mean square (BMS) is composed of covariance among treatment pairs and were completed spring, 1978, in pencil. Induction requires proof for k=2 and k=2+1; hence Part 2. Part 3 proves that p(F) is 100% (F=1) when there is no covariance (or that F=<1 applies to negative correlation). Part 4 (Section 7) proves that the ratio of covariance among treatment pairs to the variance of single treatments varies from zero to one as F varies from one to infinity, and that this new parameter discovered as a result of the proof, which may be called the r value or Foos coefficient

of covariance for replicated data sets, depends on block orientation to an extraneous gradient. It may also be used to assess

of covariance for replicated data sets, depends on block orientation to an extraneous gradient. It may also be used to assess sampling error in treatments or separate factors in a factorial design.

Equation 4.1 Block Mean Square Defined Using Sums of Two Treatments.

Equation 4.1 below is a slightly different form of the standard textbook formula for BMS shown above, where t is the number of treatments and r is the number of replications, not to be confused with the FCC, Foos coefficient of covariance, also called an r value, yet to be derived. Treatment cells are usually designated as x (sub ij, meaning the ith treatment and jth block), but here, instead of x observations sub i, each treatment has its own symbol: x, y, etc. instead of x sub i. In the following equation, the sum of r blocks is broken down into the two respective treatments x and y for j to r blocks instead of x sub i to t, so that covariance terms between x, y... treatment pairs can be isolated and rearranged after expansion of the squared expressions. Refer to the prior paragraph if this isn't quickly grasped.

Recall that BMS, block mean square or block variance, is BSS, block sum of squares divided by r-1 degrees of freedom for blocks, where BSS, like any sum of squares, is the sum of squared differences between block means and overall mean. In practice, any SS, sum of squares, is better calculated as the sum of squared observations less the CF, correction factor, CF being the sum of all observations squared divided by the number of observations, n = r*t. For blocks, the BSS is calculated as the sum of squares of block totals divided by t treatment cells less CF, and BMS is BSS divided by r-1 degrees of freedom, as so:

$$BMS = \sum_{j=1}^{r} \frac{(x_j + y_j)^2}{t(r-1)} - \frac{\left(\sum_{j=1}^{r}(x_j + y_j)\right)^2}{rt(r-1)}$$

Equation 4.2 Expansion of First Square.

$$BMS = \frac{1}{t(r-1)}\left[\sum_{j=1}^{r} x_j^2 + 2\sum_{j=1}^{r} x_j y_j + r\sum_{j=1}^{r} y_j^2 - \frac{\left(\sum_{j=1}^{r} x_j + \sum_{j=1}^{r} y_j\right)^2}{r}\right]$$

Equation 4.3 Expansion of Second Square.

$$= \frac{1}{rt(r-1)}\left[r\sum_{j=1}^{r} x_j^2 + 2r\sum_{j=1}^{r} x_j y_j + r\sum_{j=1}^{r} y_j^2\right] - \left[\left(\sum_{j=1}^{r} x_j\right)^2 + \left(\sum_{j=1}^{r} y_j\right)^2 + 2\sum_{j=1}^{r} x_j \sum_{j=1}^{r} y_j\right]$$

Equation 4.4 Group Terms Into Individual Variance and Covariance.

$$= \frac{1}{t}\left[\frac{r\sum_{j=1}^{r} x_j^2 - \left(\sum_{j=1}^{r} x_j\right)^2}{r(r-1)} + \frac{r\sum_{j=1}^{r} y_j^2 - \left(\sum_{j=1}^{r} y_j\right)^2}{r(r-1)} + \frac{2r\sum_{j=1}^{r} x_j y_j - 2\sum_{j=1}^{r} x_j \sum_{j=1}^{r} y_j}{r(r-1)}\right]$$

Equation 4.5 Move r To Numerator As Fraction To Complete Defined Forms. (multiply top and bottom by r)

$$= \frac{1}{t}\left[\frac{\sum_{j=1}^{r} x_j^2 - \frac{\left(\sum_{j=1}^{r} x_j\right)^2}{r}}{(r-1)} + \frac{\sum_{j=1}^{r} y_j^2 - \frac{\left(\sum_{j=1}^{r} y_j\right)^2}{r}}{(r-1)} + 2\frac{\sum_{j=1}^{r} x_j y_j - \frac{\sum_{j=1}^{r} x_j \sum_{j=1}^{r} y_j}{r}}{(r-1)}\right]$$

Equation 4.6 Replace Expressions With Variance and Covariance Symbols.

$$BMS = \frac{\left(S^2 x_j + S^2 y_j + 2S x_j y_j\right)}{t}$$

Equation 4.7 Block Mean Square in T erms of Sum of V ariances for t T reatments and the Sum of Covariances for n=1 to C Combinations of T reatment Pairs. We can use the Binomial Coefficient to calculate the number of treatment pairs from t treatments, and write that as the combination, C, of t treatments taken two at a time, as follows.

$$BMS = \frac{\sum_{i=1}^{t} S_i^2 (\text{Sum Tmt Variances Across Blocks}) + 2\sum_{n=1}^{C_2^t} S_{xy} (\text{Twice Sum Covariances of Tmt Pairs})}{t \text{ Number Of Treatments}}$$

Or...

$$BMS = \frac{\sum_{i=1}^{t} S_i^2 + 2\sum_{n=1}^{C_2{}^t} S_{xy}}{t}$$

Section 5. Part 2 of 2: Inductive Proof, Block Mean Square is Composed of Treatment Covariance When k=2 and k+1=3 T reatments.

Equation 5.1 Block Mean Square (BMS) Defined Using Three Treatments x, y and z for r blocks.

Parts 1 and 2 to prove that block mean square (BMS) is composed of covariance among treatment pairs were completed spring, 1978, in pencil. Induction requires proof for k=2 and k=2+1. Part 3 proves that p(F) is 100% (F=1) when there is no covariance. Part 4 proves that the ratio of covariance among treatment pairs to the variance of single treatments varies from zero to one as F varies from one to infinity, and that this value, called the Foos r value or coefficient of covariance, depends on block orientation to an extraneous gradient. Thus, BMS is composed of cross replication variance less covariance among treatment pairs for all number of treatments.

$$BMS = \sum_{j=1}^{r} \frac{(x_j + y_j + z_j)^2}{t(r-1)} - \frac{\left[\sum_{j=1}^{r} (x_j + y_j + z_j)\right]^2}{rt(r-1)}$$

Equation 5.2 Expansion of First Square Yields...

$$BMS = \frac{1}{t(r-1)}\left[\sum_{j=1}^{r} x_j^2 + 2\sum_{j=1}^{r} x_j y_j + \sum_{j=1}^{r} y_j^2 + 2\sum_{j=1}^{r} x_j z_j + \sum_{j=1}^{r} z_j^2 + 2\sum_{j=1}^{r} y_j z_j\right] - \left(\frac{\sum_{j=1}^{r} x_j + \sum_{j=1}^{r} y_j + \sum_{j=1}^{r} z_j}{r}\right)^2$$

Equation 5.3 Expansion of Second Square.

$$= \frac{1}{rt(r-1)}\left[r\sum_{j=1}^{r} x_j^2 + 2r\sum_{j=1}^{r} x_j y_j + r\sum_{j=1}^{r} y_j^2 + 2r\sum_{j=1}^{r} x_j z_j + r\sum_{j=1}^{r} z_j^2 + 2r\sum_{j=1}^{r} y_j z_j\right], cont...$$

$$-\left[\left(\sum_{j=1}^{r} x_j\right)^2 + \left(\sum_{j=1}^{r} y_j\right)^2 + \left(\sum_{j=1}^{r} z_j\right)^2 + 2\sum_{j=1}^{r} x_j \sum_{j=1}^{r} y_j + 2\sum_{j=1}^{r} x_j \sum_{j-1}^{r} z_j + 2\sum_{j=1}^{r} y_j \sum_{j=1}^{r} z_j\right]$$

Equation 5.4 Group Terms Into Expressions for Treatment Variances and Covariances.

$$= \frac{1}{rt(r-1)}\left[\left(r\sum_{j=1}^{r} x_j^2 - \left(\sum_{j=1}^{r} x_j\right)^2\right) + \left(r\sum_{j=1}^{r} y_j^2 - \left(\sum_{j=1}^{r} y_j\right)^2\right) + \left(r\sum_{j=1}^{r} z_j^2 - \left(\sum_{j=1}^{r} z_j\right)^2\right)\right], cont\ldots$$

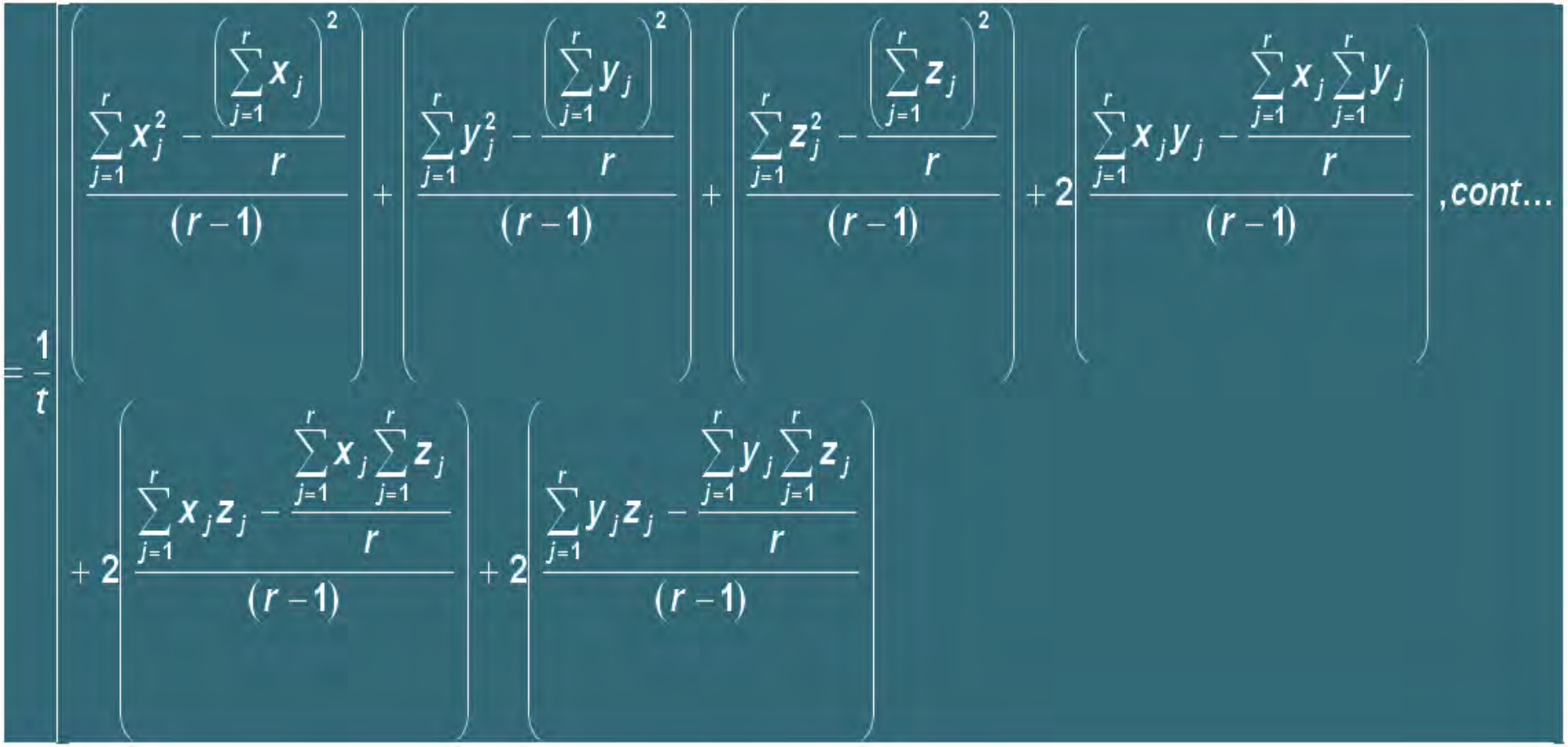
$$- \frac{1}{rt(r-1)}\left[\left(2r\sum_{j=1}^{r} x_j y_j - 2\sum_{j=1}^{r} x_j \sum_{j=1}^{r} y_j\right) + \left(2r\sum_{j=1}^{r} x_j z_j - 2\sum_{j=1}^{r} x_j \sum_{j=1}^{r} z_j\right) + \left(2r\sum_{j=1}^{r} y_j z_j - 2\sum_{j=1}^{r} y_j \sum_{j=1}^{r} z_j\right)\right]$$

Equation 5.5 Move r(r-1) Portion of Denominator to Inner Parentheses (multiply top/bottom by r(r-1)).

$$= \frac{1}{t}\left[\frac{\left(r\sum_{j=1}^{r} x_j^2 - \left(\sum_{j=1}^{r} x_j\right)^2\right)}{r(r-1)} + \frac{\left(r\sum_{j=1}^{r} y_j^2 - \left(\sum_{j=1}^{r} y_j\right)^2\right)}{r(r-1)} + \frac{\left(r\sum_{j=1}^{r} z_j^2 - \left(\sum_{j=1}^{r} z_j\right)^2\right)}{r(r-1)}\right], cont\ldots$$

$$- \frac{1}{t}\left[\frac{\left(2r\sum_{j=1}^{r} x_j y_j - 2\sum_{j=1}^{r} x_j \sum_{j=1}^{r} y_j\right)}{r(r-1)} + \frac{\left(2r\sum_{j=1}^{r} x_j z_j - 2\sum_{j=1}^{r} x_j \sum_{j=1}^{r} z_j\right)}{r(r-1)} + \frac{\left(2r\sum_{j=1}^{r} y_j z_j - 2\sum_{j=1}^{r} y_j \sum_{j=1}^{r} z_j\right)}{r(r-1)}\right]$$

Equation 5.6 Move r From Denominator to Numerator Fraction to Yield Expressions in Terms of Cross Block Treatment V ariance and Covariance (multiply top and bottom).



Equation 5.7 Therefore, Three T reatments Produce the Same Result, BMS Is Composed of Sum of Treatment Variances Plus T wice Sum of Covariance Pairs for Any Value of t.

Note that for treatment numbers greater than two, the generalized terminology is abbreviated to x and y to represent ALL treatments and treatment pairs. In the subscript for covariance S, S sub xy also implies ALL combinations of treatment pairs no matter how many.

$$BMS = \frac{\left(S^2 x_j + S^2 y_j + S^2 z_j\right) + 2\left(Sx_j y_j + Sx_j z_j + Sy_j z_j\right)}{t}$$

Equation 5.8 Therefore, Covariance Between All Combinations of Treatment Pairs Across Replications Is a Component of Block Mean Square for All Values of t. We can use the Binomial Coefficient to calculate the number of treatment pairs from t treatments, and write that as the combination, C, of t treatments taken two at a time, as follows.

$$BMS = \frac{\text{SUM OF TREATMENT VARIANCES} + \text{TWICE COVARIANCE TOTALS}}{\text{NUMBER OF TREATMENTS}}$$

$$BMS = \frac{\sum_{i=1}^{t} S_i^2 + 2\sum_{n=1}^{C_2^t} S_{xy}}{t}$$

Section 6. Derivation of Error Mean Square in Terms of Covariance Among Treatment Pairs, Proof that F=1 when p(F)=100% and Covariance is Zero.

This third of four parts of the overall proof yielding the Foos coefficient of covariance for any replicated data set was completed in 1992 with MathCad. Equations were too lengthy to present in pencil or ink.

EMS (error mean square) can be broken into the above BMS component and sums of variances for treatments across blocks. The derivation from conventional form for three treatments follows the same pattern as the sum of squares and co variation derivations for BMS in the preceding proof. The expression of EMS in terms of treatment covariance across blocks is necessary for deriving an r value that represents the strength of linear correlation across blocks. The sum of all combinations for treatment variance pairs is for the number, n=1 to C treatments taken 2 at a time (number of treatment pairs). Thus, it will be shown in this section that EMS can be written in terms of treatment variance and covariance across blocks as follows:

$$EMS = \frac{\sum_{i=1}^{t} S_i^2 - \frac{\left(\sum_{i=1}^{t} S_i^2 + 2\sum_{n=1}^{C_2^t} S_{xy}\right)}{t}}{(t-1)}$$

$$EMS = \frac{\left(S^2 x_j + S^2 y_j + S^2 z_j\right) - BMS}{t-1}$$

Only two treatments are needed for this illustration, having already proved the BMS component for three treatments designated x, y and z. ESS (error sum of squares) refers to the conventional sum of squares formula where EMS = ESS divided by (r-1)(t-1), the number of residual degrees of freedom.

Equation 6.1 Conventional Calculation For Error Sum of Squares.

$$ESS, errorSS, = \left(SS\ total - SS\ treatments - SS\ blocks\right)$$

Equation 6.2 Break Sums of Squares into Treatment Components.

The following equation may be a bit abrupt. The error sum of squares, ESS, is equal to the total sum of squares less the treatment sum of squares and the block sum of squares. Ordinarily, ESS is just written as the sum of x squared observations over both i treatments and j blocks, but for the theorem we write this as the sum of x squared treatment observations over j blocks plus y squared treatment observations over j blocks. The result is the same value, but using x and y instead of just x, we are able to designate which observation matches which treatment, x or y. In the three major brackets below, the first is the usual SS formula using the correction factor; i.e., sum of squared observations less the correction factor, CF, which is the square of the sum of observations divided by the number of them (usually referred to as n, but here we represent n observations as r blocks times t treatments). The second expression is the block sum of squares, BSS, that being the square of the sum of treatments (here x and y only) divided by t number of treatments per block (in expanded form below), and again less the same CF. Finally, the third expression is treatment sum of squares, TSS, which is the sum of squared sums of treatment x for j blocks and squared sum of treatment y for j blocks, divided by r blocks, and again less CF.

This is standard textbook form except that instead of using x with both i and j subscripts, we omit the i and use separate symbols for each treatment, x and y for two treatments. This should be easily understood.

$$ESS = \left[\sum_{j=1}^{r} x_j^2 + \sum_{j=1}^{r} y_j^2 - \frac{\left(\sum_{j=1}^{r}(x_j + y_j)\right)^2}{rt}\right] - \left[\frac{\sum_{j=1}^{r} x^2 + 2\sum_{j=1}^{r} x_j y_j + \sum_{j=1}^{r} y_j^2}{t} - \frac{\left(\sum_{j=1}^{r} x_j + \sum_{j=1}^{r} y_j\right)^2}{rt}\right], cont...$$

$$- \left[\frac{\left(\sum_{j=1}^{r} x_j\right)^2 + \left(\sum_{j=1}^{r} y_j\right)^2}{r} - \frac{\left(\sum_{j=1}^{r} x_j + \sum_{j=1}^{r} y_j\right)^2}{rt}\right]$$

Equation 6.3 Expand squares.

$$ESS=$$

$$= \sum_{j=1}^{r} x_j^2 + \sum_{j=1}^{r} y_j^2 - \frac{\left(\sum_{j=1}^{r} x_j\right)^2}{rt} - \frac{\left(\sum_{j=1}^{r} y_j\right)^2}{rt} - \frac{2\sum_{j=1}^{r} x_j \sum_{j=1}^{r} y_j}{rt} - \frac{\sum_{j=1}^{r} x_j^2}{t} - \frac{\sum_{j=1}^{r} y_j^2}{t} - \frac{2\sum_{j=1}^{r} x_j y_j}{t} + \frac{\left(\sum_{j=1}^{r} x_j\right)^2}{rt} + \frac{\left(\sum_{j=1}^{r} y_j\right)^2}{rt}, cont.$$

$$+ \frac{2\sum_{j=1}^{r} x_j \sum_{j=1}^{r} y_j}{rt} - \frac{\left(\sum_{j=1}^{r} x_j\right)^2}{r} - \frac{\left(\sum_{j=1}^{r} y_j\right)^2}{r} + \frac{\left(\sum_{j=1}^{r} x_j\right)^2}{rt} + \frac{\left(\sum_{j=1}^{r} y_j\right)^2}{rt} + \frac{\sum_{j=1}^{r} x_j \sum_{j=1}^{r} y_j}{rt}$$

Note that by careful arrangement of these terms, sums of squares in terms of x and y treatments and covariance between them is isolated, as follows:

Equation 6.4 Group Into Variance-Covariance Expressions, Divide Num and Den By (r-1)(t-1) to Obtain Error Mean Square.

$$EMS = \frac{1}{(t-1)}\left(\frac{r\sum_{j=1}^{r}x_j^2 - \frac{\left(\sum_{j=1}^{r}x_j\right)^2}{r}}{(r-1)} + \frac{r\sum_{j=1}^{r}y_j^2 - \frac{\left(\sum_{j=1}^{r}y_j\right)^2}{r}}{(r-1)}\right), \text{cont...}$$

$$- \frac{\left(\frac{\sum_{j=1}^{r}x_j^2}{t} - \frac{\left(\sum_{j=1}^{r}x_j\right)^2}{rt} + \frac{\sum_{j=1}^{r}y_j^2}{t} - \frac{\left(\sum_{j=1}^{r}y_j\right)^2}{rt} + \frac{2\sum_{j=1}^{r}x_jy_j}{t} - \frac{2\sum_{j=1}^{r}x_j\sum_{j=1}^{r}y_j}{rt}\right)}{(r-1)(t-1)}$$

$$= \frac{S^2{}_{x_j} + S^2{}_{y_j}}{(t-1)} - \frac{1}{t(t-1)}\left[\left(\frac{\sum_{j-1}^{r}x_j^2 - \frac{\left(\sum_{j-1}^{r}x_j\right)^2}{r}}{(r-1)}\right) + \left(\frac{\sum_{j-1}^{r}y_j^2 - \frac{\left(\sum_{j-1}^{r}y_j\right)^2}{r}}{(r-1)}\right) + 2\left(\frac{\sum_{j-1}^{r}x_jy_j - \frac{\sum_{j-1}^{r}x_j\sum_{j-1}^{r}y_j}{r}}{(r-1)}\right)\right]$$

$$EMS = \frac{1}{(t-1)}\left(\frac{r\sum_{j=1}^{r} x_j^2 - \frac{\left(\sum_{j=1}^{r} x_j\right)^2}{r}}{(r-1)} + \frac{r\sum_{j=1}^{r} y_j^2 - \frac{\left(\sum_{j=1}^{r} y_j\right)^2}{r}}{(r-1)}\right), \text{cont...}$$

$$- \frac{\left(\frac{\sum_{j=1}^{r} x_j^2}{t} - \frac{\left(\sum_{j=1}^{r} x_j\right)^2}{rt} + \frac{\sum_{j=1}^{r} y_j^2}{t} - \frac{\left(\sum_{j=1}^{r} y_j\right)^2}{rt} + \frac{2\sum_{j=1}^{r} x_j y_j}{t} - \frac{2\sum_{j=1}^{r} x_j \sum_{j=1}^{r} y_j}{rt}\right)}{(r-1)(t-1)}$$

$$= \frac{S^2_{x_j} + S^2_{y_j}}{(t-1)} - \frac{1}{t(t-1)}\left[\left(\frac{\sum_{j-1}^{r} x_j^2 - \frac{\left(\sum_{j-1}^{r} x_j\right)^2}{r}}{(r-1)}\right) + \left(\frac{\sum_{j-1}^{r} y_j^2 - \frac{\left(\sum_{j-1}^{r} y_j\right)^2}{r}}{(r-1)}\right) + 2\left(\frac{\sum_{j-1}^{r} x_j y_j - \frac{\sum_{j-1}^{r} x_j \sum_{j-1}^{r} y_j}{r}}{(r-1)}\right)\right]$$

Equation 6.5 Reduce Expression To Conventional Notation.

Note that for treatment numbers greater than two, the generalized terminology is abbreviated to x and y to represent ALL treatments and treatment pairs. In the subscript for covariance S, S sub xy also implies ALL combinations of treatment pairs no matter how many. If you prefer, replace Sxy with Sxy... .

no matter how many. If you prefer, replace Sxy with Sxy... .

Note that EMS is equal to the sum of cross replication variance less BMS (replication mean square), divided by degrees of freedom for treatments. Do you suspect that it would also be equal to the sum of individual block variances less TMS (treatment mean square) divided by block degrees of freedom? Well worth contemplating during an idle moment.

$$EMS = \frac{S^2_{x_j} + S^2_{y_j} \ldots - \frac{\left(S^2_{x_j} + S^2_{y_j} \ldots + 2Sx_j y_j\right)}{t}}{(t-1)}$$

$$EMS = \frac{\sum_{i=1}^{t} S_i^2 - \frac{\left(\sum_{i=1}^{t} S_i^2 + 2\sum_{n=1}^{C_2{}^t} S_{xy}\right)}{t}}{(t-1)}$$

Equation 6.6 Substituting Equation 8, Section 5 for BMS...

$$EMS = \frac{\sum_{i=1}^{t} S_i^2 - BMS}{(t-1)}$$

To show that without covariance, F for replications cannot be greater than one, rephrase F by substituting these terms for BMS and EMS into the formula:

Equation 6.7 Conclusion: F=1 When Covariance=0.

$$F = \frac{BMS}{EMS} = \frac{(t-1)}{t} \frac{\left(S^2_{x_i} + S^2_{y_i} + 2S_{x_i y_i}\right)}{S^2_{x_i} + S^2_{y_i} - \frac{1}{t}\left(S^2_{x_i} + S^2_{y_i} + 2S_{x_i y_i}\right)}$$

It is seen that the larger covariance is, the greater F will be. But how large can F be whenever covariance is zero? If we allow covariance to approach zero, we find that F approaches a lower limit of one. This is proved by the formula itself. Let covariance be zero, then the above equation becomes:

$$F = \frac{BMS}{EMS} = \frac{(t-1)}{t} \frac{\left(S^2_{x_j} + S^2_{y_j}\right)}{S^2_{x_j} + S^2_{y_j} - \frac{1}{t}\left(S^2_{x_j} + S^2_{y_j}\right)} = \frac{(t-1)\left(S^2_{x_j} + S^2_{y_j}\right)}{t\left(S^2_{x_j} + S^2_{y_j}\right) - \left(S^2_{x_j} + S^2_{y_j}\right)}$$

Factoring yields:

$$F = \frac{(t-1)\left(S^2_{x_j} + S^2_{y_j}\right)}{(t-1)\left(S^2_{x_j} + S^2_{y_j}\right)} = 1$$

Therefore, F is exactly one whenever across-block treatment covariance is zero, whatever across block variance may be. So far, the expression for average covariance across blocks (and r value) is not complete. But the sum of treatment combinations can be represented as the average times t times (t-1) divided by 2. In Section 7 we make this substitution in the standard formula for F to illustrate the dependence of F on average covariance among treatment pairs. Using that relationship, we can then express the Foos r value, or Foos coefficient of covariance, as a simple equation in terms of BMS, EMS and treatment cross block variance.

Section 7. Derivation of Covariance and r value (Foos coefficient of covariance) for Treatment Pairs from Equation 6.7.

The r value (fraction of cross-block variation due to covariance among treatment pairs) was completed in January of 2007 using Ventura Publisher. Recall that Sxy always denotes all combinations of treatment pairs, however many beyond x and y, spanning from j=1 to n treatments through j=r blocks. The r value is the ratio of (average) covariance among treatment pairs to the variance of single treatments across blocks. An r value for treatments or separate members of factorials can also be calculated that represents consistency for treatment effects within replications. These values can be used to evaluate bias introduced by extraneous variables, known or unknown, for any replicated data set.

$$F = \frac{BMS}{EMS} = \frac{(t-1)}{t} \frac{\left(S^2_{x_j} + S^2_{y_j} + 2S_{x_j y_j}\right)}{S^2_{x_j} + S^2_{y_j} - \frac{1}{t}\left(S^2_{x_j} + S^2_{y_j} + 2S_{x_j y_j}\right)}$$

Equation 7.1 Extending Equations Per Proofs for BMS and EMS With More Than Two Treatments...

$$F = \frac{BMS}{EMS} = \frac{(t-1)}{t} \frac{\left(\sum_{i=1}^{t} S_i^2 + 2 \sum_{n=1}^{C_2^t} S_{xy} \right)}{\sum_{i=1}^{t} S_i^2 - \frac{\left(\sum_{i=1}^{t} S_i^2 + 2 \sum_{n=1}^{C_2^t} S_{xy} \right)}{t}}$$

Equation 7.2 Multiplying Numerator and Denominator Expressions

$$F = \frac{t \sum_{i=1}^{t} S_i^2 + 2t \sum_{n=1}^{C_2^t} S_{xy} - \sum_{i=1}^{t} S_i^2 - 2 \sum_{n=1}^{C_2^t} S_{xy}}{t \sum_{i=1}^{t} S_i^2 - \sum_{i=1}^{t} S_i^2 - 2 \sum_{n=1}^{C_2^t} S_{xy}}$$

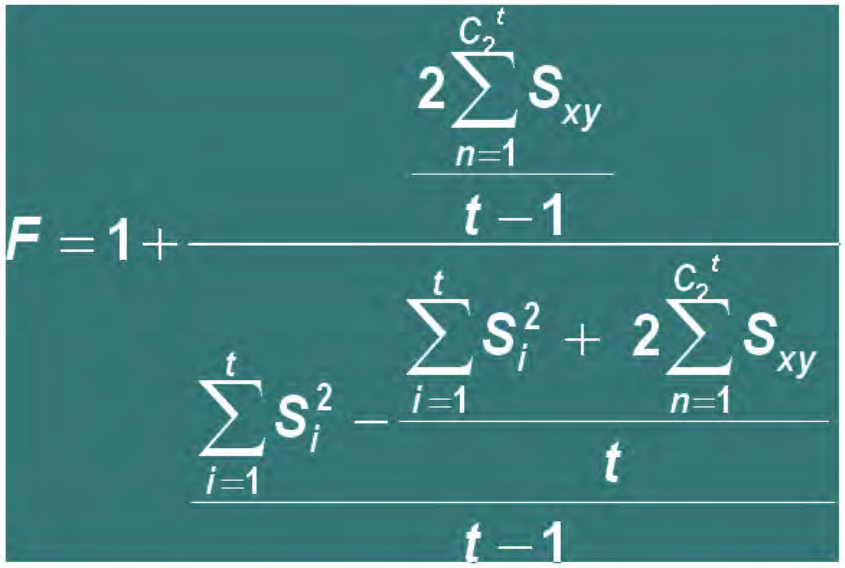
Grouping...

$$F = \frac{\left(t\sum_{i=1}^{t} S_i^2 - \sum_{i=1}^{t} S_i^2 - 2\sum_{n=1}^{C_2^t} S_{xy} \right) + 2t\sum_{n=1}^{C_2^t} S_{xy}}{\left(t\sum_{i=1}^{t} S_i^2 - \sum_{i=1}^{t} S_i^2 - 2\sum_{n=1}^{C_2^t} S_{xy} \right)}$$

By sectioning into separate terms, then dividing numerator and denominator by t...

$$F = 1 + \frac{2\sum_{n=1}^{C_2^t} S_{xy}}{\sum_{i=1}^{t} S_i^2 - \frac{\sum_{i=1}^{t} S_i^2 + 2\sum_{n=1}^{C_2^t} S_{xy}}{t}}$$

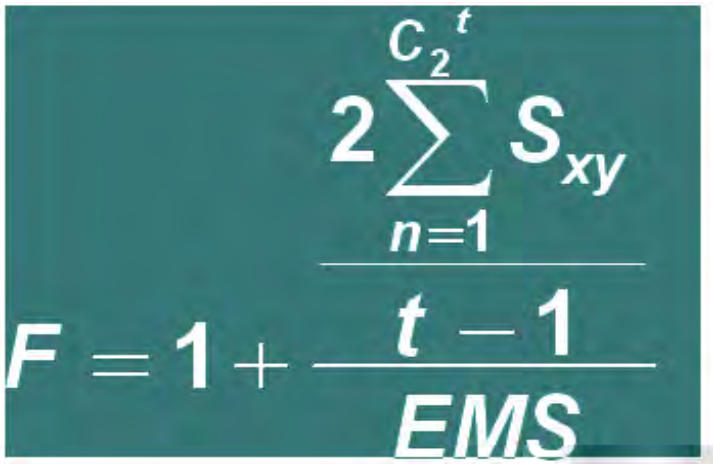
At this point, you are likely asking what the point of this complicated algebraic juggling is. What we are aiming for is a way of expressing block F in terms of the covariance among treatment pairs from block to block, part so that we can verify that the Foos coefficient of covariance contains the same information as F. Ultimately, we wish to find a way of expressing the fraction of cross block treatment variance in BMS that can be attributed to covariance of treatment pairs from block to block, to be designated the FCC, Foos coefficient of covariance. Dividing both numerator and denominator by t-1...



$$F = 1 + \frac{2\sum_{n=1}^{C_2^t} S_{xy}}{t-1} \Bigg/ \frac{\sum_{i=1}^{t} S_i^2 - \frac{\sum_{i=1}^{t} S_i^2 + 2\sum_{n=1}^{C_2^t} S_{xy}}{t}}{t-1}$$

Equation 7.3 Substitute EMS From Equation 6.5 as Denominator in Equation 7.2.

Note from Equation 6.5 that the greater denominator of the second expression is in fact equal to the error mean square, EMS; therefore.



$$F = 1 + \frac{2\sum_{n=1}^{C_2^t} S_{xy}}{t-1} \Big/ EMS$$

Next comes an awkward step for the algebraic transition of our proof to the Foos coefficient of covariance, FCC, or r value for replications. We need to substitute the average covariance for treatment pairs (S bar sub xy), where the numerator of that average is the sum of the covariance pairs divided by the number of those pairs, and where the number of pairs is simply t*(t-1)/2. To replace the sum with the above average, we must we multiply the number of combinations as a factor of

the average in the numerator. If you have trouble with this, refer back to the basic equations for numbers of combinations and how those are expressed symbolically, then work through the problem carefully. The average covariance is the sum divided by the number of combinations; therefore we replace that by the average times the number of pairs t*(t-1)/2,

$$F = 1 + \frac{2t\overline{S_{xy}}(t-1)}{(t-1)2EMS}$$

We can now cancel 2 and (t-1) in the upper fraction...

$$F = 1 + \frac{t\overline{S_{xy}}}{EMS}$$

Equation 7.4 Now, calculate the average covariance for any randomized block design as...

$$\overline{S_{xy}} = \frac{EMS(F-1)}{t}, \text{ also, } \overline{S_{xy}} = \frac{BMS - EMS}{t}$$

To derive the Foos coefficient of covariance for randomized blocks (or any replicated data set), or the r value if you prefer, we start with the following definition. See Statistical Methods, Snedecor and Cochran, Seventh Edition, (1980), page 477, for the possibility of using a probability table for the r value. Note that p(r) should be a function of sine theta where theta is the average angle of intersection of blocks with a gradient. All block to block variation will be comprised of "random" plus co variation among treatments, if any. Note that the randomized block r value is the Foos coefficient of covariance as defined

here for the first time, it is NOT the coefficient of correlation used in linear regression or between two variables, apologies for misunderstandings leading to that conclusion. It is, however, a similar ratio that suits our purposes for describing block to gradient intersection (or a lack of gradient uniformity). The r value for block covariance is the fraction of (total) variation for treatments across blocks accounted for by covariance between (all combinations of) treatment pairs (average covariance divided by variance). The following expression gives us the average fraction of rep to rep variance of cell (treatment) pairs that consists of covariance of all combinations of pairs between them:

$$r = \frac{\overline{S_{xy}}}{\frac{\sum_{i=1}^{t} S_i^2}{t}}$$

Equation 7.5 Finally , the r Value for Correlations Among All Treatment Pairs Across Blocks, the Average Covariance Across Blocks Is:

$$\overline{r_{c_2}}^{t} = \frac{EMS(F-1)}{\sum_{i=1}^{t} S_i^2}$$

The above expression, obtained by substitution from the prior terms for average covariance, is a useful parameter since it tells us that the significance of the F ratio is just as easily expressed in terms of an average coefficient of covariance, not the correlation coefficient between two sets of data, but the average covariance among all combinations of cells for any number

of replications. This concludes and encapsulates the point of the theorem, so we give it the following distinctive form to represent a new parameter for all randomized blocks or other replicated data sets, the r value for blocks designated here as r sub rb. Note that whenever F is one, the r value must be zero, though it isn't necessary or convenient to use the F value in an expression for the r value. Also, it would be better to call the r value r(sub rb) as below to distinguish it from the r value (coefficient of correlation) customarily assigned between only two sets of data (treatments),

$$r_{rb} = \frac{EMS(F-1)}{\sum_{i=1}^{t} S_i^2}$$

Ther efore, in a much mor e elegant and finished form, by substitution of BMS/EMS for F, the r value or FCC (Foos coefficient of covariance for replicated data sets) becomes:

$$r_{rb} = \frac{BMS - EMS}{\sum_{i=1}^{t} S_i^2}$$

Note as a matter of casual interest that BMS-EMS, times t number of treatments, is equivalent to the average covariance among treatment pairs, and TMS-EMS times r number of blocks is the average covariance among block pairs across treatments; i.e., the consistency of change from treatment to treatment which must be one for the treatment values.

Remember, BMS is for purposes of derivation and concept only. The replicated data set could be treatments (TMS, treatment mean square) instead of blocks, irrespective of any number of blocks including one replication, or they could be either P or K treatments within blocks as in P x K factorial, as long as the design is orthogonal; that is, the same levels of P for each level of K, say four levels of P with three levels of K for each for twelve total treatments. We would then replace BMS with PMS and KMS for the r values for each. For PMS, the sum of cross block variances for each treatment must be replaced by the sum of each variance for each level of P, varP1+varP2+varP3+varP4, and for KMS, var K1-K3. Try to think in reverse, with each treatment set as a block. Therefore, for any data set, the Foos coefficient of covariance is a preferred substitution for F, giving a percentage for consistency of change for all cells in a set of data that is replicated for any reason.

Q.E.D.

It wasn't easy getting here, but we now have a very simple expression that tells us the overall goodness of fit for data cells from replication to replication where affected by either extraneous or intrinsic variables, or in the case of randomized blocks, the ideal orientation of those blocks to an extraneous (nuisance) variable where the r value would be equal to 1. We have also devised a very valuable new parameter which measures the best fit for replicated data sets where influenced by either extraneous or intrinsic variables. It is quite easy to reshuffle terms and obtain an FCC, Foos coefficient of covariance or r value, for all treatments, or subsets of treatments in a factorial design, or for all combinations of cell values among replicated data sets of interest, and not just the conventional coefficient of correlation for a single pair of variables. The FCC r value for blocks can be used to measure consistent change in all treatment values from block to block for a completely randomized design.

We can also define an FCC value for treatments, where the r value for a set of treatment effects measures the consistency in change from treatment to treatment within replications. If this is hard to see, imagine that the set of treatments one through four represent four blocks, and each of three replications may be considered a treatment. The calculation is similar for the same experiment, though instead of BMS in the numerator, use TMS, while the denominator is the sum of each separate block variance. Note that any time an r value for blocks is greater than the r value for treatments, it would be permissible to include the extraneous variable in the overall regression equation for treatment effects. The extraneous variable simply transforms a 4x3 factorial design into a 5x3 design. Note that for 4 levels of N over 3 levels of P, separate r values for N and P can also be easily calculated. The r values for each source can tabulated right along with the F values for a far more understandable parameter. Since the r value contains the same information as F, but also includes the variance of separate cells that cross from one replication to another (even if the source is a treatment effect), it is likely that a separate density function for the Foos coefficient of covariance herein discovered will provide more accurate probability values than F.

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Subj. Area	Cat. No.	Course Title	Cr.	Gd.
AUT 1976-77				
BIOL	510	ADV PLT PHYSL	3	B
CHEM	301	ELEM PHYS CH	3	B
MATH	121	CAL ANAL GEOM	0	
P&S	201	SOIL RESOURCE	4	A
P&S	418	AG BIOMETRICS	4	A
QTR		14.0 14.0 50.0		3.57
WTR 1976-77				
BIOL	511	ADV PLT PHYSL	3	B
CHEM	302	ELEM PHYS CH	4	A
MATH	122	CAL ANAL GEOM	4	A
P&S	405	PRIN CRP GROW	4	A
P&S	420	MICROCLIMATOL	3	A
QTR		18.0 18.0 69.0		3.83
SPR 1976-77				
BIOL	512	ADV PLT PHYSL	3	A
CHEM	551	SOIL CHEM	3	B
MATH	123	CAL ANAL GEOM	4	A
P&S	415	SOIL ANALYSIS	4	A
QTR		14.0 14.0 53.0		3.78
SUM 1977-78				
P&S	590	MSTRS THESIS	9	P
QTR		0.0 9.0 0.0		0.00
AUT 1977-78				
P&S	410	SOIL PHYSICS	4	A
P&S	510	SOIL SCI&NUTR	4	A
P&S	590	MSTRS THESIS	3	P
QTR		8.0 11.0 32.0		4.00
WTR 1977-78				
P&S	500	SEMINAR	1	A
P&S	515	SOIL PHYSICS	3	A
P&S	590	MSTRS THESIS	5	P
QTR		4.0 9.0 16.0		4.00
SPR 1977-78				
P&S	412	SOIL CLAS SUR	4	A
P&S	516	FLD PLOT TECH	4	A
P&S	590	MSTRS THESIS	3	P
QTR		8.0 11.0 32.0		4.00
SUM 1978-79				
C S	101	INTR SCI COMP	4	A
P&S	590	MASTRS THESIS	3	P
QTR		4.0 7.0 16.0		4.00
AUT 1978-79				
P&S	500	SEMINAR	1	A
P&S	590	MASTRS THESIS	6	P
QTR		1.0 7.0 4.0		4.00
WTR 1978-79				
P&S	590	MASTRS THESIS	7	P
QTR		0.0 7.0 0.0		0.00
SPR 1978-79				
P&S	590	MASTRS THESIS	3	P
QTR		0.0 3.0 0.0		0.00

G R A D U A T E D
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Randomized Block Theorem