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Highlights

- Certain Indefinite Integrals
- Hyperbolic Cosymplectic Manifold
- Augmented Dickey-Fuller Test
- Nonlinear Advection Equations

Discovering Thoughts, Inventing Future

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Contact Normal Generic Submanifolds of a Nearly Hyperbolic Cosymplectic Manifold

By Saadet DOĞAN & Müge KARADAĞ
Inonu University, Turkey

Abstract- We introduce and study contact normal generic submanifolds of a nearly hyperbolic cosymplectic manifold. We deal with the integrability conditions of the distributions of such manifolds. In addition to these, we study geometry of the leaves of distributions.

Keywords: contact normal generic submanifolds, nearly hyperbolic cosymplectic manifold, integrability condition, leaves of distributions, totally geodesic.

GJSFR-F Classification : MSC 2010: 32Q45, 58J45

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Contact Normal Generic Submanifolds of a Nearly Hyperbolic Cosymplectic Manifold

Saadet DOĞAN[α] & Müge KARADAĞ[σ]

Abstract- We introduce and study contact normal generic submanifolds of a nearly hyperbolic cosymplectic manifold. We deal with the integrability conditions of the distributions of such manifolds. In addition to these, we study geometry of the leaves of distributions.

Keywords: *contact normal generic submanifolds, nearly hyperbolic cosymplectic manifold, integrability condition, leaves of distributions, totally geodesic.*
MSC 2010: 53C15, 53C25, 53D15

I. Introduction

Almost hyperbolic (φ,ξ,η,g)-structure was defined and studied by Upadhyay and Dube [8]. Uddin S, Wong BR and Mustafa AA studied warped product pseudo slant submanifolds of a nearly cosymplectic manifold [7]. The notion of semi invariant submanifolds and CR- submanifolds of nearly hyperbolic cosymplectic manifold was introduced by Ahmad M and Ali K [1,2]. In addition to these, Dogan S and Karadag M studied slant submanifolds of an almost hyperbolic contact metric manifolds[4] and pseudo-slant submanifolds of nearly hyperbolic cosymplectic manifolds[5]. M. Kobayashi study contact normal submanifolds and contact generic normal submanifolds in Kenmotsu manifolds [6]. U.C. De and A.K. Sengupta deal with generic submanifolds of Lorentzian Para-Sasakian manifold [3].

In this paper, we introduce contact generic normal submanifolds of a nearly hyperbolic cosymplectic manifold.

II. Preliminaries

Let M be an n-dimensional almost hyperbolic contact metric manifold with almost hyperbolic contact metric structure(φ,ξ,η,g), where a tensor φ of type (1,1), a vector field η called structure vector field and ξ , the dual 1-form of ξ satisfying the followings

$$\varphi^2 X = X + \eta(X)\xi \tag{2.1}$$

$$g(X,\xi) = \eta(X), \quad \eta(\xi) = -1 \tag{2.2}$$

Author α σ : The University of Inonu, Faculty of Arts and Science, Departments of Mathematics Malatya/TURKIYE.
e-mails: saadetdoganmat@gmail.com, muge.karadag@inonu.edu.tr

$$\varphi\xi = 0, \quad \eta \circ \varphi = 0 \tag{2.3}$$

$$g(\varphi X, \varphi Y) = g(X,Y) - \eta(X)\eta(Y) \tag{2.4}$$

for any vector fields *X* and *Y* in *TM* [4]. In this case,

$$g(\varphi X, Y) = -g(X, \varphi Y) \tag{2.5}$$

X and *Y* in *TM*

An almost hyperbolic contact metric manifold with almost hyperbolic contact metric structure (φ, ξ, η, g) is said to be nearly hyperbolic cosymplectic manifold [4] if

$$(\overline{\nabla}_X \varphi)Y + \varphi(\overline{\nabla}_Y X) = 0 \tag{2.6}$$

$$\overline{\nabla}_X \xi = 0 \tag{2.7}$$

for all *X,Y* tangent to *M*.

Let *M* be submanifold of a nearly hyperbolic cosymplectic manifold *M* with induced metric *g* and if ∇ and $\nabla^{\perp}$ are the induced connections on the tangent bundle *TM* and the normal bundle $TM^{\perp}$ of *M*, respectively, then Gauss and Weingarten formulae are given by

$$\overline{\nabla}_X Y = \nabla_X Y + h(X,Y) \tag{2.8}$$

$$\overline{\nabla}_X N = -A_N X + \nabla_X{}^{\perp} N \tag{2.9}$$

for each *X,Y* in *TM* and N$\in TM^{\perp}$, where *h* and $A_{\mathcal{N}}$ are the second fundamental form and the shape operator, respectively, for the immersion of *M* into $\overline{M}$. They are related as

$$g(h(X,Y),N) = g(A_N X, Y) \tag{2.10}$$

where *g* denotes the Riemannian metric on $\overline{M}$ as well as induced on *M*. For any vector field *X* in *TM*,

$$\varphi X = PX + FX \tag{2.11}$$

where *PX* is the tangential component and *FX* is the normal component of φX . Similarly for any $N \in TM^{\perp}$,

$$\varphi N = tN + fN \tag{2.12}$$

where *tN* is the tangential component and *fN* is the normal component of φN.

A submanifold M of a nearly hyperbolic cosymplectic manifold $\overline{M}$ is said to be a contact generic normal submanifold if the structure vector field ξ is normal to *M* and if there exists a differentiable distribution *D* on *M* such that:

$$TM = D \oplus D^{\perp}, \quad \varphi D = D, \quad \varphi D^{\perp} \subseteq TM^{\perp} \tag{2.13}$$

where $D^{\perp}$ is the complementary distribution of *D* in *TM* [6].

M is called to be a contact generic normal submanifold in $\overline{M}$ if the structure vector field ξ is normal to *M* and

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4. Dogan S, Karadag M. : Slant Submanifolds of an Almost Hyperbolic Contact Metric Manifolds.J Math Syst Sci 4 , 285-288, (2014).

$$\varphi(TM^{\perp}) \subset TM \tag{2.14}$$

holds [6].

The leaves of a distribution D on a manifold M are totally geodesic in M if and only if $\nabla_X Y \in D$ for all *X,Y* in *D*. Which is equivalent to the conditions

$$\nabla_X W \in D^{\perp} \tag{2.15}$$

for all $X \in D$ and $W \in D^{\perp}$. Similarly for the totally geodesicness of the leaves of $D^{\perp}$, the conditions

$$\nabla_Z W \in D^{\perp} \tag{2.16}$$

and

$$\nabla_Z X \in D \tag{2.17}$$

for all $X \in D$ and Z, $W \in D^{\perp}$ are equivalent [3].

III. Integrability of Distributions

a) ***Theorem:*** *Let M be a contact generic normal submanifolds of a nearly hyperbolic cosymplectic manifold $\overline{M}$. Then $D^{\perp}$ is integrable if and only if M is mixed geodesic.*

Proof: Let M be a mixed geodesic contact generic normal submanifolds of a nearly hyperbolic cosymplectic manifold $\overline{M}$. From (2.6), we get

$$\begin{aligned} &(\overline{\nabla}_X \varphi)Y + \varphi\overline{\nabla}_Y X = 0 \\ &\overline{\nabla}_X \varphi Y - \varphi\overline{\nabla}_X Y + \varphi\overline{\nabla}_Y X = 0 \\ &\overline{\nabla}_X \varphi Y = \varphi[X,Y] \end{aligned} \tag{3.1}$$

for any vector fields X ,*Y* in $D^{\perp}$. For all X ,*Y* in $D^{\perp}$ and *Z* in *D.* From (3.1), we get

$$\begin{aligned} g([X,Y],\varphi Z) &= -g(\overline{\nabla}_X \varphi Y, Z) \\ &= g(A_{\varphi Y} X, Z) - g(\nabla^{\perp}_X \varphi Y, Z) \\ &= g(h(X,Z), \varphi Y) = 0 \end{aligned}$$

for any X ,*Y* in $D^{\perp}$ and *Z* in *D*. Then $D^{\perp}$ is integrable.

Contrary to this, let $D^{\perp}$ be integrable. That is ; $[X,Y] \in D^{\perp}$ for all *X,Y* in $D^{\perp}$. Then $\varphi[X,Y]$ in $TM^{\perp}$. In this case, from (3.1)

$$\begin{aligned} \varphi[X,Y] &= \overline{\nabla}_X \varphi Y \\ \varphi[X,Y] &= -A_{\varphi Y} X + \nabla_X{}^{\perp} \varphi Y \end{aligned} \tag{3.2}$$

for all vector fields *X,Y* in $D^{\perp}$. If we take the inner product of (3.2) with *Z* in *D,* we find

$$g(\varphi[X,Y],Z) = -g(A_{\varphi Y} X, Z) + g(\nabla^{\perp}_X \varphi Y, Z)$$

Ref

6. Kobayashi M. : Contact Normal Submanifolds and Contact Generic Submanifolds in Kenmotsu Manifolds, Revista Mathematica 4, (1991).

$$g(A_{\varphi Y}X,Z) = 0$$
$$g(h(X,Z),\varphi Y) = 0$$

for all X,Y in $D^{\perp}$ and Z in D. Then M is mixed geodesic.

b) ***Theorem:*** *Let M be a contact generic normal submanifolds of a nearly hyperbolic cosymplectic manifold $\overline{M}$. Then D is integrable if and only if M is D-geodesic.*

Proof: Let M be a mixed geodesic contact generic normal submanifolds of a nearly hyperbolic cosymplectic manifold $\overline{M}$. From (2.6), we get

$$\begin{aligned}(\overline{\nabla}_X\varphi)Y+\varphi\overline{\nabla}_Y X=0\\ \overline{\nabla}_X\varphi Y-\varphi\overline{\nabla}_X Y+\varphi\overline{\nabla}_Y X=0\\ \overline{\nabla}_X PY+\overline{\nabla}_X FY-\varphi\nabla_X Y-\varphi h(X,Y)+\varphi\nabla_Y X+\varphi h(Y,X)=0\end{aligned} \tag{3.3}$$

for all vector fields X,Y in TM. If we use Gauss and Weingarten equations in (3.3) and we consider tangential and normal component, we have

$$(\nabla_X P)Y = A_{FY}X - P\nabla_Y X \tag{3.4}$$

$$(\nabla_X F)Y = -h(X,PY) - F\nabla_Y X \tag{3.5}$$

for all vector fields X,Y in TM. If we take X,Y in D, we find

$$(\nabla_X F)Y = -F\nabla_X Y \tag{3.6}$$

and

$$(\nabla_X F)Y = -h(X,PY) - F\nabla_Y X \tag{3.7}$$

for all vector fields X,Y in TM. From (3.6) and (3.7), we get that D is integrable if and only if M is D-geodesic.

IV. Geometry of Leaves of Distributions

a) ***Theorem:*** *Let M be a contact generic normal submanifolds of a nearly hyperbolic cosymplectic manifold $\overline{M}$. D is integrable and the leaves of D are totally geodesic in M if and only if $A_{XP}X = P\nabla_Z X$ for all X in D and Z in $D^{\perp}$.*

Proof: Let the leaves of D be totally geodesic in M. That is; $\nabla_X Y \in D$ for all X,Y in D. From (3.4), we find

$$\begin{aligned}(\nabla_X P)Z = A_{FZ}X - P\nabla_Z X\\ \nabla_X PZ - P\nabla_X Z = A_{FZ}X - P\nabla_Z X\end{aligned} \tag{4.1}$$

for all X in D and Z in $D^{\perp}$. If we take the inner product of (4.1) with Y in D, we get

$$g(A_{FZ}X,Y) - g(P\nabla_Z X,Y) = 0$$

for all X in D and Z in $D^{\perp}$. Then we get

$$A_{FZ}X = P\nabla_Z X$$

Notes

for any vector fields X in D and Z in $D^{\perp}$. Now, we suppose that

$$A_{FZ}X = P\nabla_Z X$$

for any vector fields X in D and Z in $D^{\perp}$. From (3.4), we get

$$\nabla_X PZ - P\nabla_X Z = A_{FZ}X - P\nabla_Z X \tag{4.2}$$

Notes

for all vector fields X,Y in D, Z in $D^{\perp}$. From (4.2), we find $P\nabla_X Z = 0$ X for any vector fields X in D and Z in $D^{\perp}$.

Then $\nabla_X Z \in D^{\perp}$. In addition to this, we find

$$(\nabla_X g)(\varphi Y, Z) = \nabla_X g(\varphi Y, Z) - g(\nabla_X \varphi Y, Z) - g(\varphi Y, \nabla_X Z)$$
$$0 = -g(\nabla_X \varphi Y, Z) - g(\varphi Y, \nabla_X Z)$$
$$g(\nabla_X \varphi Y, Z) = -g(\varphi Y, \nabla_X Z) \tag{4.3}$$

for all vector fields X,Y in D, Z in $D^{\perp}$. In this case,

$$g(\varphi[X,Y], Z) = -g(\varphi Y, \nabla_X Z) = 0$$

for all vector fields X,Y in D, Z in $D^{\perp}$. Then $[X,Y] \in D$. That is; D is integrable.

b) ***Theorem:*** *Let M be a contact generic normal submanifolds of a nearly hyperbolic cosymplectic manifold $\overline{M}$ .Let $D^{\perp}$ be integrable and the leaves of $D^{\perp}$ be totally geodesic in M. Then $A_{FV}U = 0$, for all vector fields U,V in $D^{\perp}$.*

Proof: $D^{\perp}$ be integrable and the leaves of $D^{\perp}$ be totally geodesic in M. From (3.4), we get

$$(\nabla_U P)V = A_{FV}U - P\nabla_V U$$
$$\nabla_U PV - P\nabla_U V = A_{FV}U - P\nabla_V U$$
$$0 = A_{FV}U$$

for all vector field U,V in $D^{\perp}$.

Now, we suppose that $A_{FV}U = 0$ FV for all vector field U,V in $D^{\perp}$. We will show that $D^{\perp}$ is integrable and the leaves of $D^{\perp}$ are totally geodesic in M. From (3.4), we find

$$(\nabla_U P)V = -P\nabla_V U \tag{4.4}$$

for all vector field U,V in $D^{\perp}$. Then we get

$$\nabla_U PV - P\nabla_U V = -P\nabla_V U$$
$$P[U,V] = 0$$

for all vector fields U,V in $D^{\perp}$. In this case; $[U,V] \in D^{\perp}$. That is; $D^{\perp}$ is integrable. From (3.4), we get

$$P\nabla_U V = P\nabla_V U$$

for any vector fields U,V in $D^{\perp}$. Then $\nabla_V U \in D^{\perp}$ and $\nabla_U V \in D^{\perp}$. In this case; the proof is complete.

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Notes

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Estimating Effects and Variance Components in Models of Quantitative Genetics in an Era of Sequenced Genomes

By Charles J. Mode
Drexel University, United States

Abstract- As in many other areas of research in genetics, the availability of sequenced genomes in samples of individuals has revolutionized the study of quantitative traits, because researches have developed statistical evidence regarding the lo- cations of genomic regions, loci, that have been implicated with the expression of a quantitative trait or traits. Therefore, in cases in which it is possible to develop operational definitions of at least two alleles at each locus, genomic regions, it becomes possible to identify the genotype of each individual with re- spect to a set of loci that have been shown in other experiments to influence the expression of a quantitative trait. As will be shown in this paper, by knowing the genotype of each individual in a sample with respect to a set of identified loci, it is now possible to directly estimate effects that are measures of not only intra-allelic interactions at each locus under consideration but also various types of epistatic effects that are measures of interactions among alleles at different loci, governing the inheritance of a quantitative trait.

Keywords: genomic regions implicated with a quantitative trait, loci,locus and alleles, known genotypes, effects as measures of intra-allelic and epistatic interactions, direct estimates of effects, phenotypic, genetic and environmental variance components, partitioning the genetic variance into additive, intra-allelic interaction and epistatic components of variance

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Estimating Effects and Variance Components in Models of Quantitative Genetics in an Era of Sequenced Genomes

Charles J. Mode

Abstract- As in many other areas of research in genetics, the availability of sequenced genomes in samples of individuals has revolutionized the study of quantitative traits, because researches have developed statistical evidence regarding the lo- cations of genomic regions, loci, that have been implicated with the expression of a quantitative trait or traits. Therefore, in cases in which it is possible to develop operational definitions of at least two alleles at each locus, genomic regions, it becomes possible to identify the genotype of each individual with re- spect to a set of loci that have been shown in other experiments to influence the expression of a quantitative trait. As will be shown in this paper, by knowing the genotype of each individual in a sample with respect to a set of identified loci, it is now possible to directly estimate effects that are measures of not only intra-allelic interactions at each locus under consideration but also various types of epistatic effects that are measures of interactions among alleles at different loci, governing the inheritance of a quantitative trait. These straight forward methods of estimation differ from those used in classical quantitative genetics, because such effects and corresponding variance components could be estimated indirectly, using analysis of variance procedures or some version of general lin- ear models that have been and are widely in statistical genetics. The direct method of estimation described in this paper, show promise towards shifting the working paradigm that has been used in classical models of the genetics of quantitative traits involving the estimation of variance components to a more direct approach and simpler approach.

Keywords: genomic regions implicated with a quantitative trait, loci,locus and alleles, known genotypes, effects as measures of intra-allelic and epistatic interactions, direct estimates of effects, phenotypic, genetic and environmental variance components, partitioning the genetic variance into additive, intra-allelic interaction and epistatic components of variance.

I. Introduction

In an interesting review paper by Stranger et al. (2010) [21], the impact of genome wide associations studies on the genetics of complex traits is discussed in depth. Among these complex traits are Alzheimer's disease (AD) and immune-mediated diseases such as rheumatoid arthritis. For the case of AD, in a recent paper Raj et al. (2012) [19] have reported that 11 regions of the human genome are involved in susceptibility to this disease, and, moreover, there is evidence that four of these regions form a protein network that is under natural selection. Similarly, in paper by Rossin et al. (2011) [20], it has been found that proteins encoded in genomic regions associated with immune-mediated disease physically interact and this interaction may also suggest some basic biological mechanisms underlying such diseases.

Author: Professor Emeritus, Department of Mathematics, Drexel University, Philadelphia, USA. e-mail: cjmode@comcast.net

There is also another technological development, the sequencing of entire genomes of individuals, that may lead to a deeper understanding of the relationships of phenotypes to genotypes. Suppose, for example, that a sample of individuals with symptoms of a disease, such as AD, is available and that genome of each individual in the sample has been sequenced. Furthermore, suppose that some quantitative measurement is made on each individual in the sample. These measurements will vary among individuals and let W denote a random variable characterizing this variation. Given that the genome of each individual in the sample has been sequenced, the genotype of each individual in the sample can, in principle, be identified with respect to the 11 loci under consideration for the case of AD. It will also be supposed that at each locus at least two alleles can be identified.

In classical quantitative genetics, the loci and alleles at each locus were treated abstractly, because an investigator did not, in general, know the location of the hypothesized loci in the genome of a species or the number of alleles at each locus. However for the case of AD cited above, the genotype of each individual in the sample can be identified with respect to each of the 11 loci, and in some cases it may be known with respect to combinations of the 11 loci or even all 11 loci. Such technological developments provide opportunities to extend some of the ideas of classical quantitative genetics into the age of sequenced genomes. Moreover, as will be demonstrated in subsequent sections of this paper, when the genotype of each individual in a sample is known, the estimation of parameters of the model may be carried out in a relatively simple and straight forward manner based on elementary methods of statistical estimation.

As is recognized among many who have worked in the field of quantitative genetics, the subject known as components of variance analysis began with the publication of a paper on correlations among relatives on the supposition of Mendelian inheritance by R. A. Fisher (1918) [7]. In his paper, Fisher attempted to reconcile existing biometrical theories with Mendelian genetics that led him to describe genetic variation in terms of components of variance. During the 1950s, other investigators published papers that were motivated by the paper by Fisher. Among these investigators was Kempthorne (1954) [10], who introduced an approach to components of variance analysis based on effects defined in terms of expectations of genetics values with respect to the genotypic distribution under the assumption that the population was in a Hardy-Weinberg equilibrium. An alternative approach was introduced by Cockerham (1954) [5] is also of historical interest, because it contains an extensions of Fisher's ideas to accommodate epistatic effects in terms of ideas depending on the concept of orthogonality. If a reader is interested in further details and development of the ideas of Fisher and other workers, it is suggested that the book Kempthorne (1957) [11] be consulted, where many of the themes of statistical genetics as they existed during the 1950s were summarized and extended.

The techniques introduced in these papers have also been applied in the current genomic era. Examples of the ideas introduced by Cockerham have been applied in the paper Kao et al. (2002) [9], and those of Kempthorne have been applied and extended in the paper Mao et al. (2006) [15]. The ideas of Kempthorne were also used and extended in the paper of Mode and Robinson (1959) [16] as well as in unpublished lecture notes by the author written and presented during the period 1960 to 1966. Furthermore, the roots of the ideas presented in this paper are extensions of the some of the unpublished material in the lecture notes complied by the author during the period 1960 to 1966.

During the years following Fisher's seminal work, an extensive literature on quantitative genetics has evolved. It is beyond the scope of this paper to review this literature and in what follows a few books on the subject will be cited. A book that has been very popular with quantitative geneticists is that

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[10] Kempthorne, O. (1954) The Correlations Between Relatives in a Random Mating Population. Proc. Royal Soc. London, B 143: 103-113.

[6] Falconer, D. and MacKay, T. F. C. (1996) Introduction to Quantitative Genetics. Longman, New York.

of Falconer and MacKay (1996) [6] as well as earlier editions. Another book of interest on quantitative genetics is that of Bulmer (1980) [4]. Both of these books contain extensive lists of references on quantitative genetics. A more recent book on genetics and analysis of quantitative traits is that of Lynch and Walsh (1998) [14]. This influential tome consists of over 900 pages and contains what seems to be the most extensive treatment of the subject of quantitative genetics published in the 20-th century. The principal focus of this book is a biological and evolutionary point of view along with an extensive use of applied statistical methods. There is also an extensive list of papers on quantitative genetics that a reader, who is interested in quantitative genetics, may wish to peruse. The book by Liu [13] on statistical genetics focuses on statistical genetics along with linkage, mapping and quantitative trait linkage (QTL) analysis. Two recent books on statistical genetics are those of Laird and Lange [7] and Wu, Ma and Casella (2010) [22].

Historically, procedures for estimating components of the genetic and environmental variances have been based on experimental designs or observational data involving various types of relatives. If a reader is interested in an account of such experimental designs, it is suggested that chapter 6 of Bulmer (1980) [4] be consulted. An in depth account of estimation procedures in various genetic settings may be found in section III of the book by Lynch and Walsh (1998) [14]. In this paper, however, it will be shown that when the genotype of each individual in a sample is known at the DNA level, then it is possible to estimate various types of genetic parameters directly, including variance components, using elementary statistical ideas. It should also be mentioned that the ideas presented in this paper are extensions of techniques from unpublished notes on quantitative genetics written by the author during the period 1960 to 1966. In these notes, it was assumed that for the one locus case the population was in a Hardy-Weinberg equilibrium, and for the case of multiple loci, it was assumed that the population was in linkage equilibrium. In this paper, however, these assumptions have been relaxed.

When two or more quantitative traits are under consideration several measurements are taken on each individual. In this case, it is assumed that the autosomal loci under consideration may influence the expression of alleles for two or more traits. In classical genetics, such joint expressions of alleles for quatitative or qualitative traits is referred to pleiotropism. In a recent paper, Mode (2014) [17] this case has been worked out in detail.

II. The Case of One Locus with Multiple Alleles

Let $\mathbb{A}$ denote a finite set of alleles at some autosomal locus in a diploid species such as man. Elements of $\mathbb{A}$ will be denoted by the symbols x and y, and the genotype of an individual with respect to the locus will be denoted by (x, y), where $x \in \mathbb{A}$ and $y \in \mathbb{A}$ denote, respectively, the alleles contributed the maternal and paternal parent of the individual under consideration. As the technology underlying the sequencing of DNA evolves, it seems likely that it will be possible to distinguish the DNA contributed by each parent to an offspring. More precisely, let $\mathbb{A} \times \mathbb{A}$ denote the Cartesian product of the set $\mathbb{A}$ with itself. Then $\mathbb{G} = \mathbb{A} \times \mathbb{A}$ is the set of all possible genotypes at the locus under consideration and $(x, y) \in \mathbb{G}$ for every genotype $(x.y)$.

One of the objectives in formulating models in quantitative genetics is to provide a framework such that phenotypic measurements on a population of individuals may formally be connected with the genotype of each individual. For many decades it has been observed that phenotypic measurements among individuals with the same genotype in a given environment may vary. But, it has also been observed that in populations consisting of several genotypes responses of the genotypes to a given environment may also vary. Let W denote a random variable that takes values in the set $\mathbb{R}_W$ of real numbers that constitute the

set of possible phenotypic measurements of individuals in the population. In general, by assumption, the numbers in the set $\mathbb{R}_W$ will depend on the genotype of a homogeneous set of individuals.

Given a genotype $(x,y) \in \mathbb{G}$, let $f(w \mid (x,y))$ denote the conditional probability density function of the random variable W. Then,

$$E[W \mid (x,y)] = \mu(x,y) = \int_{\mathbb{R}_W} w f(w \mid (x,y))\, dw \tag{2.1}$$

is the conditional expectation of the random variable W, given the genotype (x,y). It will be assumed that $\mu(x,y)$ is finite for all genotypes $(x,y) \in \mathbb{G}$. Let $p(x,y)$ denote the probability, frequency, that an individual chosen at random from the population is of genotype (x,y). Then, the unconditional expectation of the random variable W is, by definition,

$$\mu = E[W] = \sum_{(x,y)} p(x,y) E[W \mid (x,y)] = \sum_{(x,y)} p(x,y) \mu(x,y). \tag{2.2}$$

It is assumed that $p(x,y) \geq 0$ for all $(x,y) \in \mathbb{G}$ and

$$\sum_{(x,y)} p(x,y) = 1. \tag{2.3}$$

In what follows, it will also be helpful to observe that the joint distribution of a random genotype (x,y) and the phenotypic random variable W is $g((x,y),w) = p(x,y) f(w \mid (x,y))$ for all $(x,y) \in \mathbb{G}$ and $w \in \mathbb{R}_W$.

Next observe that the equation

$$W = \mu + (\mu(x,y) - \mu) + (W - \mu(x,y)) \tag{2.4}$$

is valid and provides a linear relationship connecting an observed phenotypic measurements W with the expectation μ, a measurement of a genetic effect expressed by the deviation $(\mu(x,y) - \mu)$ and the term $(Z - \mu(x,y))$, which may be interpreted as a measure of deviation of the phenotypic measure W from $\mu(x,y)$ due to environmental conditions. By definition, the total phenotypic variance in the population is

$$var_P[W] = E\left[(W-\mu)^2\right]. \tag{2.5}$$

A widely used technique in quantitative genetics is to partition the total phenotypic variance into a genotypic variance measuring the variation among genotypes in their responses to environmental conditions and an environmental variance measuring the variation of the phenotypic measure W around the genotypic values $\mu(x,y)$ for every $(x,y) \in \mathbb{G}$. From equation (2.4), it follows that

$$(W-\mu)^2 = (\mu(x,y) - \mu)^2 + (W - \mu(x,y))^2 + 2(\mu(x,y) - \mu)(W - \mu(x,y)). \tag{2.6}$$

Therefore,

$$\begin{aligned} E\left[(W-\mu)^2 \mid (x,y)\right] &= (\mu(x,y) - \mu)^2 + (W - \mu(x,y))^2 \\ &\quad + 2(\mu(x,y) - \mu) E[(W - \mu(x,y)) \mid (x,y)]. \end{aligned} \tag{2.7}$$

But,

$$E[(W - \mu(x,y)) \mid (x,y)] = 0. \tag{2.8}$$

Therefore,

$$E\left[(W-\mu)^2 \mid (x,y)\right] = (\mu(x,y) - \mu)^2 + (W - \mu(x,y))^2. \tag{2.9}$$

In deriving equation (2.9), some well known properties of conditional expectations have been used. Namely, for any function $f(x)$ with domain a subset of $\mathbb{R}$, the set of real numbers, and range a subset of $\mathbb{R}$, it follows from well

known properties of conditional expectations that $E[f(X) \mid X] = f(X)$. It is also well known that if two random variables X and Y with range $\mathbb{R}$ are under consideration, then $E[XY \mid X] = XE[Y \mid X]$.

An equivalent representation of the phenotypic variance in equation (2.5) is

$$var_P[W] = \sum_{(x,y)} p(x,y) E\left[(W-\mu)^2 \mid (x,y)\right]. \tag{2.10}$$

Given (2.9), it seems reasonable to define and genetic variance due to genetic effects in the population as

$$var_G[W] = \sum_{(x,y)} p(x,y) (\mu(x,y) - \mu)^2. \tag{2.11}$$

Similarly, the variance due to environmental effects is, by definition,

$$var_E[W] = \sum_{(x,y)} p(x,y) E[(W - \mu(x,y))^2 \mid (x,y)]. \tag{2.12}$$

From equation (2.9) it follows, therefore, that

$$var_P[W] = var_G[W] + var_E[W]. \tag{2.13}$$

At this point in the development of the contents of this paper, it should be mentioned that equation (2.13) is not new to quantitative genetics, but its derivation is a departure from derivations that appeared in some papers and books on the subject. For example, in some formulations the effects $(\mu(x,y) - \mu)$ and $(W - \mu(x,y))$ are treated as abstract uncorrelated random variables and sometimes it is assumed that genetic and environmental effects are independent. But, it follows from the use of conditional expectations that these types of assumptions are not necessary in the derivation of (2.13).

From equation (2.13), it can be seen that the total phenotypic variance may be partitioned into two component variances; namely the genetic and environmental variance. If both sides of equation (2.13) are divided by the phenotypic variance, then it is easy to see that

$$1 = F_G + F_E,$$

where

$$F_G = \frac{var_G[Z]}{var_P[Z]}$$

and

$$F_E = \frac{var_E[Z]}{var_P[Z]}. \tag{2.14}$$

Some authors refer to F_G as a measure of the heritability of quantitative trait. In what follows, F_G will be denoted by H_G and referred to as a measure of heritability.

This latter ratio has been given various names by authors of books on quantitative genetics. For example, in the book by Falconer and Mackay (1996) [6] on page 123 an expression similar to the ratio H_G is called the degree of genetic determination. Other authors such as Wu et al. (2010) [22] refer to this ratio as heritability in the broad sense and provide an example in which this parameter may be estimated by an analysis of variance procedure based on a designed breeding experiment, see page 178. If a reader is interested in pursuing the subject of heritability further, it is suggested that the book by Liu (1998) [13] be consulted, in particular see pages 34 and 35. A more in depth treatment of the concept of heritability may be found in the book by Lynch and Walsh (1998) [14], see pages 170 to 175 and elsewhere in that book.

Several recent papers have also been devoted to applications of the concept of heritability. Among these papers is that of Zaitlen et al. (2013) [24], who use

Ref

[14] Lynch, M. and Walsh, B. (1998) Genetics and the Analysis of Quantitative Traits. Sinauer Associates, Inc. Sunderland, MA, 01375.

extended genealogies to estimate components of heritability for 23 quantitative and dichotomous traits, using closely and distantly related relatives. In an interesting paper Price et al. (2011 [11] estimated variance components using single tissue data on cross-tissue heritability gene expression on individuals related by descent and also unrelated individuals. In a paper by Yang et al. (2010) [23] the heritability of human height is studied. These authors show that by considering all common $SNPs$ simultaneously, 45% of the phenotypic variance in human height can be attributed to genetic variation. It should be mentioned, however, that quantitative model or models used by these authors were not as comprehensive as the structure that will be developed in subsequent sections of this paper.

In a subsequent section of this paper, procedures for estimating the components of variance just defined will be presented. It is recognized, however, that an investigator may be interested in testing statistical hypotheses as to whether the expectations and variances among the genotypes do indeed differ, but a discussion of tests of hypotheses is beyond the scope of this paper, which will be limited to a presentation of straight forward procedures for estimating the components of variance defined above.

Before preceding to a discussion of estimation procedures, however, it is interesting to note that, even though the rhetoric in this section was confined to the case on one autosomal locus with multiple alleles, the formulas can be easily extended to the case of some finite number of autosomal loci $n \geq 2$ with a finite number of alleles at each locus. For let $(\boldsymbol{x}, \boldsymbol{y})$ denote the genotype of an individual with respect to n loci, where $\boldsymbol{x} = (x_1, x_2, \cdots, x_n)$ and $\boldsymbol{y} = (y_1, y_2, \cdots, y_n)$ denote, respectively, the alleles inherited from the maternal and paternal parent, and suppose $p(\boldsymbol{x}, \boldsymbol{y})$ is the probability of selecting an individual of genotype $(\boldsymbol{x}, \boldsymbol{y})$ at random in the population. Then, it is easy to show that equation (2.13) also holds for some number $n \geq 2$ of autosomal loci, but the details of proving this statement will be left as an exercise of the reader.

Given that it can be shown that equation (2.13) holds for any number of loci $n \geq 2$, it is interesting to note that with respect to AD the total phenotypic variance may be partitioned into the genetic and environmental components for any combination of the 11 loci that have been implicated with this disease. In particular, it would be of interest to estimate the heritability for each of the 11 loci or in combinations of loci in order to gain some insights as to whether heritability would increase as the number of loci under increases.

III. A Partition of the Genetic Variance Into the Additive and Intra-Allelelic Components for the Case of One Autosomal Locus

Again let $p(x, y)$ denote the probability of finding an individual of genotype (x, y) a population. This probability is also known as the frequency of genotype $(x.y)$ in a population. In most past formulations of models in quantitative genetics for the one locus case, it has been assumed that a population was in a Hardy-Weinberg equilibrium and there was no mutation or selection. Mutation and selection will not be considered in this paper, but the condition that a population is in a Hardy-Weinberg equilibrium will be relaxed. Let $p(x)$ and $p(y)$ denote, respectively, the frequencies of alleles x and y in a population. Then, a population is in a Hardy-Weinberg equilibrium if $p(x, y) = p(x)\, p(y)$ for all genotypes $(x, y) \in \mathbb{G}$. In this section, the condition that a population is in a Hardy-Weinberg equilibrium will not be assumed, because in many populations this assumption may not hold. It should be mentioned, however, that an investigator may wish to test whether a sample from a population passes a statistical test or tests for a Hardy-Weinberg equilibrium.

Ref

[11] Kempthorne, O. (1957) An Introduction to Genetic Statistics. John Wiley and Sons, New York.

To relax the assumption that a population is in a Hardy-Weinberg equilibrium, it will be necessary to deal with conditional probabilities and expectations. Let

$$p(x) = \sum_y p(x,y) \tag{3.1}$$

denote that marginal distribution for all maternal alleles $x \in \mathbb{A}$ in a population, and similarly let

$$p(y) = \sum_x p(x,y) \tag{3.2}$$

denote the marginal distribution for all paternal alleles $y \in \mathbb{A}$. Then, if $p(y) \neq 0$

$$p(x \mid y) = \frac{p(x,y)}{p(y)} \tag{3.3}$$

is the conditional distribution of the alleles $x \in \mathbb{A}$, given allele $y \in \mathbb{A}$. Similarly, if $p(x) \neq 0$, then

$$p(y \mid x) = \frac{p(x,y)}{p(x)} \tag{3.4}$$

is the conditional distribution of alleles $y \in \mathbb{A}$, given allele $x \in \mathbb{A}$. The formulas just derived may be summarized in the equation

$$p(x,y) = p(x)\, p(y \mid x) = p(y)\, p(x \mid y) \tag{3.5}$$

for all genotypes $(x,y) \in \mathbb{G}$.

Therefore, the conditional expectation of $\mu(x,y)$, given x is, by definition,

$$\mu(x) = \sum_y p(y \mid x)\, \mu(x,y). \tag{3.6}$$

Therefore, the unconditional expectation of $\mu(x)$ is

$$E[\mu(x)] = \sum_x p(x)\, \mu(x) = \sum_x \sum_y p(x,y)\, \mu(x,y) = \mu. \tag{3.7}$$

For a justification of this equation, see equation (2.5). In particular, if the population is in Hardy-Weinberg equilibrium, then $p(x,y) = p(x)\, p(y)$ for all $(x,y) \in \mathbb{G}$ and equation (3.6) becomes

$$\mu(x) = \sum_y p(y \mid x)\, \mu(x,y) = \sum_y p(y)\, \mu(x,y), \tag{3.8}$$

because in this case $p(y \mid x) = p(y)$. Thus, in formulations in which the assumption that a population is in Hardy-Weinberg equilibrium is in force, (3.8) is the definition of the average value of maternal allele x in a population. Similarly, by using techniques similar to those used in the derivation of a formula for $\mu(x)$, it is straight forward to derive a formula for $\mu(y)$, the average value for paternal allele y in the population that is not in a Hardy-Weinberg equilibrium.

To cast the formulation in terms of an analysis of variance structure, it is useful to define the effects of alleles x and y as the deviations

$$\begin{aligned} \alpha(x) &= \mu(x) - \mu \\ &\text{and} \\ \alpha(y) &= \mu(y) - \mu. \end{aligned} \tag{3.9}$$

Observe that the unconditional expectations of these deviations is $E[\alpha(x)] = E[\alpha(y)] = 0$. The deviation

$$\alpha(x,y) = \mu(x,y) - \mu - \alpha(x) - \alpha(y) \tag{3.10}$$

is a measure of interactions among the maternal and paternal alleles. In this case, it is also easy to see that the unconditional expectation of this deviation is $E[\alpha(x,y)] = 0$. Alternatively, the deviations just described can be written in the form of an analysis of the variance equation

$$\mu(x,y) = \mu + \alpha(x) + \alpha(y) + \alpha(x,y), \tag{3.11}$$

which holds for all genotypes $(x,y) \in \mathbb{G}$. This equation suggests that it seems reasonable to call the terms $\alpha(x)$ and $\alpha(y)$ the additive effects of alleles. With the exception of μ, the terms on the right side of equation (3.11) are known statistically as effects. For if $\alpha(x,y) = 0$ for all genotypes, then

$$\mu(x,y) = \mu + \alpha(x) + \alpha(y) \tag{3.12}$$

for all $(x,y) \in \mathbb{G}$ so that the effects of alleles x and y have an additive effect on the expectation $\mu(x,y)$. But, if $\alpha(x,y) \neq 0$ for all (x,y), then there are interactions among the maternal and paternal alleles.

Having defined additive and intra-allelic interaction effects, the next step in the formulation is to define the additive and intra-allelic interaction variances. The additive genetic variance in the population is defined by

$$var_G(A) = \sum_x p(x)\alpha^2(x) + \sum_y p(y)\alpha^2(y), \tag{3.13}$$

and intra-allelic interaction, IAI, variance is defined by

$$var_G(IAI) = \sum_{(x,y)} p(x,y)\alpha^2(x,y). \tag{3.14}$$

To connect these variances with the total genetic variance in a population write equation (3.11) in the form

$$\mu(x,y) - \mu = \alpha(x) + \alpha(y) + \alpha(x,y)$$

and square both sides. The result is

$$(\mu(x,y) - \mu)^2 = \alpha^2(x) + \alpha^2(y) + \alpha^2(x,y) + R(x,y), \tag{3.15}$$

where

$$R(x,y) = 2\alpha(x)\alpha(y) + 2\alpha(x)\alpha(x,y) + 2\alpha(y)\alpha(x,y). \tag{3.16}$$

By multiplying equation (3.15) by $p(x,y)$ and summing over all genotypes (x,y), it follows that

$$var_G[W] = var_G(A) + var_G(IAI) + E[R(x,y)], \tag{3.17}$$

where

$$E[R(x,y)] = T_1 + T_2 + T_3. \tag{3.18}$$

The explicit forms of the symbols on the right, which involve covariances, are as follows:

$$\begin{aligned} T_1 &= 2\sum_{(x,y)} p(x,y)\alpha(x)\alpha(y) \\ T_2 &= 2\sum_{(x,y)} p(x,y)\alpha(x)\alpha(x,y) \\ &\quad \text{and} \\ T_3 &= 2\sum_{(x,y)} p(x,y)\alpha(y)\alpha(x,y). \end{aligned} \tag{3.19}$$

In general, $E[R(x,y)] \neq 0$, but there is a case when $E[R(x,y)] = 0$. Suppose the population is in a Hardy-Weinberg equilibrium so the $p(x,y) = p(x)p(y)$ for all genotypes $(x,y) \in \mathbb{G}$. Then, T_1 may be written in the form

$$T_1 = 2\left(\sum_x p(x)\alpha(x)\right)\left(\sum_y p(y)\alpha(y)\right). \tag{3.20}$$

But,

$$\sum_x p(x)\alpha(x) = 0,$$

and therefore $T_1 = 0$. Similarly, T_2 may be written in the form

$$T_2 = 2\left(\sum_x p(x)\,\alpha(x)\right)\left(\sum_y p(y)\,\alpha(x,y)\right). \tag{3.21}$$

For every fixed x, consider

$$\begin{aligned}\sum_y p(y)\,\alpha(x,y) &= \sum_y p(y)\left(\mu(x,y) - \mu - \alpha(x) - \alpha(y)\right)\\ &= \alpha(x) - \alpha(x) - \sum_y p(y)\,\alpha(y) = 0\end{aligned} \tag{3.22}$$

for every $x \in \mathbb{A}$. Therefore, $T_2 = 0$, and by a similar argument it can be shown that $T_3 = 0$ so that $E[R(x,y)] = 0$.

Thus, for the case a population is in a Hardy-Weinberg equilibrium at some autosomal locus, it follows that the total genetic variance may be partitioned into the additive and intra-allelic interaction variances. In symbols,

$$var_G[W] = var_G(A) + var_G(IAI). \tag{3.23}$$

It is interesting to observe that when the genotype of each individual may be identified, then each of the component variances on the right may be estimated separately. But, before the age of genomics, in quantitative genetic studies, the genotype of each individual in a population could not be identified. Under such circumstances, experiments could be designed in such a way that components of variance in equation (3.23) could be estimated from mean squares in an analysis of variance table. It should be noted, however, the when the effects $\alpha(x), \alpha(y)$ and $\alpha(x,y)$ can be estimated from the data, then all the covariances terms in $E[R(x,y)]$ could also be estimated. In such cases, one could also estimate the term $E[R(x,y)]$ in equation (3.17), which would be of interest in its own right for the cases in which the population was not in a Hardy-Weinberg equilibrium at the autosomal locus under consideration.

There is a notationally more succinct way to represent the variances and covariances encountered in the above discussion. For each genotype $(x,y) \in \mathbb{G}$ let the

$$\mathbf{\Phi}(x,y) = \begin{pmatrix} \alpha(x) \\ \alpha(y) \\ \alpha(x,y) \end{pmatrix} \tag{3.24}$$

denote a 3×1 matrix whose elements are defined above. The transpose of this matrix is

$$\mathbf{\Phi}^T(x,y) = \begin{pmatrix} \alpha(x) & \alpha(y) & \alpha(x,y) \end{pmatrix}. \tag{3.25}$$

Next observe that

$$\mathbf{\Psi}(x,y) = \mathbf{\Phi}(x,y)\,\mathbf{\Phi}^T(x,y) \tag{3.26}$$

is a 3×3 matrix and the element in position $(1,1)$ is $\alpha^2(x)$, the element in position $(1,2)$ is $\alpha(x)\,\alpha(y)$ and, by proceeding in this way, all nine of the element in the matrix $\mathbf{\Psi}(x,y)$ as squares or products of the elements in the vector $\mathbf{\Phi}(x,y)$. Let $\mathbf{\Psi}_G$ denote the 3×3 genetic variance-covarince matrix for the autosomal locus under consideration. Then,

$$\mathbf{\Psi}_G = \sum_{(x,y)} p(x,y)\,\mathbf{\Psi}(x,y). \tag{3.27}$$

From now on $\mathbf{\Psi}_G$ will be called the genetic covariance matrix for the autosomal locus under consideration. It should be observed that the variance components on the right of equation of equation (3.13) are in the principal diagonal positions $(1,1)$ and $(2,2)$ of the matrix $\mathbf{\Psi}_G$. Moreover, the sum of all elements off the principal diagonal of this matrix is the term $E[R(x,y)]$ in (3.17). Given the genetic matrix $\mathbf{\Psi}_G$, it may be useful to compute the eigenvalues of this matrix as well as its principal components in addition to estimating the components of the matrix $\mathbf{\Psi}_G$. As will be seen in subsequent sections, the matrix approach to computing the genetic covariance matrix described in this section will make it possible to describe the computation of the genetic

Notes

covariance matrix for cases in which more than one autosomal locus is under consideration.

It can be seen from a perusal of books on statistical genetics that the approach used in this section and in subsequent sections of this paper to partition the genetic variance into components differs from that used in some books cited in the introduction. For example, on page 54 of the book Laird and Lange (2011) [12] a phenotypic measurement Y of a quantitative trait is represented as a linear combination of unknown parameters with indicator functions coefficients plus a random error term. Included in these terms are parameters for the additive effects of allele as well as a codominant effect, which appears to be related to the intra-allelic interaction term defined this section. Such models appear to belong to the class of generalized linear models that are widely used in numerous areas of applied statistics. In particular, in the books on statistical genetics cited in the introduction, linear models similar to that cited in Laird and Lange (2011) have been used. As can be seen from the derivations presented in this section, however, the additive and interaction effects of alleles in the case of one autosomal locus are defined in terms of conditional expectations with respect to the genotypic distribution. Moreover, this scheme of using conditional expectations in defining effects when partitioning the total genetic variance into components will be used extensively in subsequent sections of this paper and provides a methodology for estimating effects and corresponding variance components directly from data. Furthermore, as will be shown subsequently, the squared effects making up a component of variance may also be estimated directly from a data set such that the genomes of all individuals in this sample have been sequenced.

IV. Estimating of Parameters and Effects From Data

In this section, a procedure for estimating the parameters defined in the forgoing sections from phenotypic data will be outlined. Suppose in a sample of individuals, $n((x,y)) \geq 2$ individuals of genotype $(x,y) \in \mathbb{G}$ are observed and let the random variables $W_\nu(x,y)$, for $\nu = 1, 2, \cdots, n(x,y)$, denote a sample of phenotypic measurements on the $n((x,y))$ individuals of genotype (x,y) with respect to some quantitative trait. Usually, the set of phenotypic measurements will belong to some set $\mathbb{R}$ of continuous real numbers will also be supposed that these random variable are independently and identically distributed according to common but unknown distribution with a finite expectation and variance. Let

$$n = \sum_{(x,y)} n(x,y) \tag{4.1}$$

denote the total number of individuals in the sample, where the sum runs over all genotypes $(x,y) \in \mathbb{G}$. Then, the random variable

$$\widehat{p}(n(x,y)) = \frac{n(x,y)}{n} \tag{4.2}$$

is an estimator of the frequency $p(x,y)$ of genotype (x,y) in a population or subpopulation from which a sample of individuals was drawn. It is interesting to note that if it is assumed the that the numbers $n(x,y)$ for $(x,y) \in \mathbb{G}$ are viewed as realizations from a multinomial distribution with probabilities $p(x,y)$ for $(x,y) \in \mathbb{G}$ and sample size n, then $E[\widehat{p}(n(x,y))] = np(x,y)/n = p(x,y)$ so that $\widehat{p}(n(x,y))$ is an unbiased estimator of $p(x,y)$ for all $(x,y) \in \mathbb{G}$.

Similarly, the random variable

$$\widehat{\mu}(x,y) = \frac{1}{n(x,y)} \sum_{\nu=1}^{n(x,y)} W_\nu(i,j) \tag{4.3}$$

is an estimator of the parameter $\mu(x,y)$. This estimator is conditionally unbiased, because $\widehat{E}[\widehat{\mu}(x,y) \mid (x,y)] = n(x,y)\mu(x,y)/n(x,y) = \mu(x,y)$ for all genotypes $(x,y) \in \mathbb{G}$. Therefore, the random variable

Ref
[12] Laird, N. M. and Lange, C. (2011) The Fundamentals of Modern Statistical Genetics. DOI 10.1007/978-1-4419-7338-2, Springer New York, Dordrecht, Heidelberg, London.

$$\widehat{\mu} = \sum_{(x,y)} \widehat{p}(n(x,y))\widehat{\mu}(x,y) \tag{4.4}$$

is an estimator of the parameter μ. From these definitions, it follows that the random variable

$$\widehat{var}_G[W] = \sum_{(x,y)} \widehat{p}(x,y)\left(\widehat{\mu}(x,y) - \widehat{\mu}\right)^2 \tag{4.5}$$

is an estimator of the genetic variance in (2.11).

To estimate the environmental variance defined in (2.12), let

$$\sigma^2(x,y) = E\left[\left(W(x,y) - \mu(x,y)\right)^2 \mid (x,y)\right] \tag{4.6}$$

for all genotypes $(x,y) \in \mathbb{G}$. Then

$$\widehat{\sigma}^2(x,y) = \frac{1}{n(x,y)-1} \sum_{\nu=1}^{n(x,y)} \left(W(x,y) - \widehat{\mu}(x,y)\right)^2 \tag{4.7}$$

is a conditionally unbiased estimator of $\sigma^2(x,y)$, given the genotype (x,y). Therefore,

$$\widehat{var}_E[W] = \sum_{(x,y)} \widehat{p}(x,y)\,\widehat{\sigma}^2(x,y) \tag{4.8}$$

is an estimator of the environmental variance defined in (2.12). From (2.13), it follows that an estimator of the phenotypic variance may be obtained by adding the estimators in (4.5) and (4.8), or this variance component could be estimated directly.

Given the estimators $\widehat{\mu}(x,y)$ for all genotypes in the sample, it would be straight forward to derive estimators of the three effects in the column vector $\mathbf{\Phi}(x,j)$ in (3.24) for all genotypes (x,y) in the sample. Let $\widehat{\mathbf{\Phi}}(i,j)$ denote the estimator of the vector $\mathbf{\Phi}(x,j)$ for all genotypes under consideration. Then, let

$$\widehat{\mathbf{\Psi}}(x,y) = \widehat{\mathbf{\Phi}}(x,y)\,\widehat{\mathbf{\Phi}}^T(x,y) \tag{4.9}$$

denote an estimator of the matrix $\mathbf{\Psi}(x,y)$ in (3.26) for all genotypes (x,y). Given these definitions of estimators, it follows that

$$\widehat{\mathbf{\Psi}}_G = \sum_{(x,y)} \widehat{p}(x.y)\,\widehat{\mathbf{\Psi}}(x,y) \tag{4.10}$$

is an estimator of the genetic covariance matrix defined in (3.27). It should also be noted that an investigator would be free to estimate each component of the matrix $\widehat{\mathbf{\Psi}}_G$ separately.

It is also possible to estimate H_G, the measure of heritability defined in section 2. From (2.13), it follows that

$$\widehat{var}_P[W] = \widehat{var}_G[W] + \widehat{var}_E[W] \tag{4.11}$$

is an estimator of the phenotypic variance. Therefore,

$$\widehat{H}_G = \frac{\widehat{var}_G[W]}{\widehat{var}_P[W]} \tag{4.12}$$

is an estimator of H_G, a measure of heritability.

At any step in the development of software to implement the ideas under discussion, one could proceed in a number of directions. Suppose, for example, an investigator was not inclined to estimate the matrix $\widehat{\mathbf{\Psi}}_G$ in (4.10). An alternative approach would be that of considering a remainder estimate $\widehat{R}_G$ which is defined by the equation

$$\widehat{var}_G[W] = \widehat{var}_G(A) + \widehat{var}_G(IAI) + \widehat{R}_G, \tag{4.13}$$

where $\widehat{var}_G(A)$ and $\widehat{var}_G(IAI)$ are estimates of the additive and intra-allelic-interactions variance components defined in (3.13) and (3.14). The remainder

term $\widehat{R}_G$ would be a direct measure of the departure of the population from a Hardy-Weinberg equilibrium when equation (3.23) is valid. Observe that $\widehat{R}_G$ is the sum of all elements in the matrix $\widehat{\mathbf{\Psi}}_G$ off the principal diagonal.

If an investigator were interested in investigating whether the off diagonal elements in this estimator of the covariance matrix would change significantly under the assumption that the population from which the sample was derived was in Hardy-Weinberg equilibrium, the following procedure could be executed. Let $\widehat{p}(x)$ be an estimator of the marginal frequency of maternal alleles $x \in \mathbb{A}$ in the sample, and let the marginal frequency $\widehat{p}(y)$ be defined similarly for paternal alleles $y \in \mathbb{A}$ in the sample. Then, the next step in a computer simulation experiment with a goal of recomputing the estimate of the matrix $\widehat{\mathbf{\Psi}}_G$, under the assumption that the population was in a Hardy-Weinberg equilibrium, would be that of computing the product

$$p^*_{HW}(x,y) = \widehat{p}(x)\,\widehat{p}(y) \tag{4.14}$$

for all genotypes $(x,y) \in \mathbb{G}$ in the sample. Given this trial set of genotypic frequencies, the calculation procedures outlined above could be used to compute an alternative estimate of the covariance matrix $\mathbf{\Psi}_G$, symbolized by $\mathbf{\Psi}_{GHW}$, under the assumption that the population was in a Hardy-Weinberg equilibrium so that one would expect that the remainder term $\widehat{R}_G$ would be zero.

The direct method of estimation described above has many advantages when compared with classical methods of estimating variance components , because the effects defined in section 3 may also be estimated directly from the data. By way of illustrative example, the direct estimator of the conditional expectation $\mu(y)$ is

$$\widehat{\mu}(x) = \textstyle\sum_y \widehat{p}(y \mid x)\,\widehat{\mu}(x,y), \tag{4.15}$$

where

$$\widehat{p}(y \mid x) = \frac{\widehat{p}(x,y)}{\widehat{p}(x)} \tag{4.16}$$

for $\widehat{p}(x) \neq 0$. Therefore, the direct estimator of the additive effect defined in (3.9) is

$$\widehat{\alpha}(x) = \widehat{\mu}(x) - \widehat{\mu} \tag{4.17}$$

for all alleles $x \in \mathbb{A}$. A formula for the direct estimator of the effect $\alpha(y)$ is analogous to that of $\widehat{\alpha}(x)$. Given the estimators $\widehat{\alpha}(x)$ and $\widehat{\alpha}(y)$, a direct estimator of the measure of interaction between alleles x and y defined in (3.10) is

$$\widehat{\alpha}(x,y) = \widehat{\mu}(x,y) - \widehat{\mu} - \widehat{\alpha}(x) - \widehat{\alpha}(y) \tag{4.18}$$

for all genotypes $(x,y) \in \mathbb{G}$.

As can be seen from (3.13) and (3.14), the squares of the estimators of the effects defined above would be terms in the estimators of the additive and intra-allelic interaction components of variance so that if attention was focused only the estimates of these variance components, an investigator may miss detecting the largest of the squared effects which would be of interest in their own right. It is recommended, therefore, that the squares in the sets

$$\left\{\widehat{\alpha}^2(x), \widehat{\alpha}^2(y) \mid x \in \mathbb{A}, y \in \mathbb{A}\right\} \tag{4.19}$$

be calculated and inspected to get an idea as to which allele produces the largest additive effect. Similarly, it is recommended that the set of squares of measures of interaction

$$\left\{\widehat{\alpha}^2(x,y) \mid (x,y) \in \mathbb{G}\right\} \tag{4.20}$$

also be calculated and inspected to get an idea of which genotype has the largest measure of interaction of alleles.

It should also be mentioned that it would be desirable to work out the statistical properties of the estimators defined in this section. Included in these properties of these estimators would be consistent as sample size becomes large and whether an estimator is unbiased. There is also a need for statistical tests to assess whether a particular estimate of a parameter was significantly different from zero. It is recognized that the working out of these statistical properties would be important, but a full response to such statistical issues is beyond the scope of this paper. In this connection, it is interesting to note that computer intensive methods are now being used extensively in judging the statistical significance as to whether some region of a genome is implicated in some quantitative trait. For example, an interested reader may wish consult the papers Raj et al. (2012) [19] and Rossin et al. (2011) [20] in which permutation tests have been used in assessing statistical significance of hypothesized protein and other networks. It should also be mentioned that such computer intensive methods as jack-knifing and boot-strapping could also be used to assess the statistical significance of an estimate of an effect or variance component.

V. The Case of Two Autosomal Loci

Let $\mathbb{A}_1$ and $\mathbb{A}_2$ denote the set of alleles at locus 1 and 2, respectively. It will be assumed that each of these sets contains at least two alleles. In a diploid species with two sexes, such as humans, at every locus there is an allele contributed by the female parent and another allele contributed by the male parent. For the case of two autosomal loci, a genotype will be represented by the symbol (x_1, y_1, x_2, y_2), where (x_1, x_2) denotes the maternal alleles at the two loci and (y_1, y_2) are the corresponding paternal alleles. The set $\mathbb{G}$ all genotypes with respect to the two loci under consideration is the product set

$$\mathbb{G} = \mathbb{A}_1 \times \mathbb{A}_1 \times \mathbb{A}_2 \times \mathbb{A}_2. \tag{5.1}$$

To lighten the notation in what follows, let the vector $\boldsymbol{z} = (x_1, y_1, x_2, y_2)$ denote a genotype $\boldsymbol{z} \in \mathbb{G}$, and let $p(\boldsymbol{z})$ denote the frequency of genotype $\boldsymbol{z} \in \mathbb{G}$ in the population. For some quantitative trait or character under consideration, let the W denote a random variable describing the phenotypic variation with respect to some quantitative measurement among the individuals in a population. Then, given some genotype $\boldsymbol{z} \in \mathbb{G}$, let the conditional expectation

$$\mu(\boldsymbol{z}) = E[W \mid \boldsymbol{z}] \tag{5.2}$$

denote the genetic value for this genotype. Just as in the case of one locus, this conditional expectation will play a basic role in defining measurements of the effects of each allele as well as the interactions among the at the two loci under consideration.

In general, one would not expect that the population under consideration would be in linkage equilibrium; consequently, it will be necessary to define a number of marginal and conditional distributions, that will be derived using the set

$$\mathfrak{D}_G = \{p(\boldsymbol{z}) \mid \boldsymbol{z} \in \mathbb{G}\} \tag{5.3}$$

of genotypic frequencies, which from now on will be called the genotypic distribution. For example, for allele x_1 suppose we wish to derive a formula for the conditional expectation of $\mu(x_1, y_1, x_2, y_2)$, given x_1 with respect to the genotypic distribution. A first step in this derivation, would be to calculate the marginal distribution

$$p(x_1) = \sum_{(y_1, x_2, y_2)} p(x_1, y_1, x_2, y_2) \tag{5.4}$$

for all $x_1 \in \mathbb{A}_1$. By definition, the conditional distribution of $\mu(x_1, y_1, x_2, y_2)$, given x_1 is

[20] Rossin E. J., Lage K., Raychaudhuri S., Xavier R. J., Tatar D, et al. (2011) Proteins Encoded in Genomic Regions Associated with Immune-Mediated Disease Physically Interact and Suggest Underlying Biology. PLoS Genet 7(1): e1001273. doi:10.1371/journal.pgen.1001273

$$p(y_1, x_2, y_2 \mid x_1) = \frac{p(x_1, y_1, x_2, y_2)}{p(x_1)} \tag{5.5}$$

for $p(x_1) \neq 0$. Let $\mu(x_1)$ denote the conditional expectation of $\mu(x_1, y_1, x_2, y_2)$, given x_1. Then, by definition

$$\mu(x_1) = \sum_{(y_1, x_2, y_2)} p(y_1, x_2, y_2 \mid x_1)\, \mu(x_1, y_1, x_2, y_2) \tag{5.6}$$

for all $x_1 \in \mathbb{A}_1$. The unconditional expectation of the $\mu(\boldsymbol{z})$ with respect to the genotypic distribution $\mathfrak{D}_G$, as expressed in a more succinct notation, is

$$\mu = \sum_{\boldsymbol{z} \in \mathbb{G}} p(\boldsymbol{z})\, \mu(\boldsymbol{z}). \tag{5.7}$$

Therefore, in analogy with the case of one allele, the additive effect of allele x_1 in the population will be defined as

$$\alpha(x_1) = \mu(x_1) - \mu \tag{5.8}$$

for all $x_1 \in \mathbb{A}_1$.

An analogous effect could be defined for each of the alleles y_1, x_2, and y_2, by applying the methods described for defining $\alpha(x_1)$. But, as will be demonstrated, for the case of two autosomal loci there are many more interactions terms that need to be defined. For example, for the case of a diploid species, there are four positions to be considered when classifying and defining effects and interactions among alleles. Consider, for example, the set of four alleles in each genotype $\boldsymbol{z} = (x_1, y_1, x_2, y_2) \in \mathbb{G}$, and let $\mathfrak{S} = \{1, 2, 3, 4\}$ denote the set of four positions that need to be considered with respect to two loci with two alleles at each locus that were contributed by the maternal and paternal parent respectively. To provide a framework for describing various types of interactions among the alleles at the two loci under consideration, it will be helpful to consider the class of all subsets of the four positions. Let $\mathfrak{T}$ denote the class of all subsets of $\mathfrak{S}$. Included in the class $\mathfrak{T}$ is the empty set φ as well as subsets containing 1, 2,3 and 4 elements of the set $\mathfrak{S}$. As is well known from combinatorial analysis, the total number of sets in $\mathfrak{T}$ is $2^4 = 16$, and, as is also well known from combinatorics, that the equation

$$\binom{4}{0} + \binom{4}{1} + \binom{4}{2} + \binom{4}{3} + \binom{4}{4} = 2^4 = 16 \tag{5.9}$$

is valid. For $\nu = 0, 1, 2, 3, 4$, let $\mathfrak{T}_\nu$ denote the subclass of sets in $\mathfrak{T}$ that contain ν elements. Then, as can be seen form equation (5.9), each of the subclasses $\mathfrak{T}_0$ and $\mathfrak{T}_4$ contain one set; namely φ and $\mathfrak{S}$, respectively. Similarly, each of the subclasses $\mathfrak{T}_1$ and $\mathfrak{T}_3$ contain 4 sets, and the subclass $\mathfrak{T}_2$ contains 6 sets. Recall that

$$\binom{4}{2} = 6. \tag{5.10}$$

To describe a framework in which to quantify the ideas of intra-allelic interactions and epistatic interactions among alleles at different loci, it will be helpful to enumerate the sets in the subclasses $\mathfrak{T}_1$, $\mathfrak{T}_2$ and $\mathfrak{T}_3$ in terms of elements of the set $\mathfrak{S}$. For example,

$$\mathfrak{T}_1 = (\{1\}, \{2\}, \{3\}, \{4\}) \tag{5.11}$$

is the class of singletons, which are subsets that contain only one element of $\mathfrak{S}$. It is this subclass of sets that was used to define the additive effects mentioned above. The subclass $\mathfrak{T}_2$ of sets has the explicit form

$$\mathfrak{T}_2 = (\{1, 2\}, \{1, 3\}, \{1, 4\}, \{2, 3\}, \{2, 4\}, \{3, 4\}). \tag{5.12}$$

At this point recall that positions 1 and 2 in the set $\mathfrak{S}$ are those for the two alleles at locus 1, and positions 3 and 4 in this set are those for the two alleles at locus 2. Therefore, the two sets of positions in subclass

$$\mathfrak{T}_{2IAI} = (\{1,2\},\{3,4\}) \tag{5.13}$$

will be used to define effects that measure intra-allelic interactions at the two loci under consideration. On the other hand, the pairs of positions in the subclass

$$\mathfrak{T}_{2EPI} = (\{1,3\},\{1,4\},\{2,3\},\{2,4\}) \tag{5.14}$$

represent positions from different loci. Consequently, sets in this class will form a basis for defining effects that measure epistatic interactions among the alleles at the two loci under consideration. The subsets in the subclass $\mathfrak{T}_3$ are as follows

$$\mathfrak{T}_3 = (\{1,2,3\},\{1,2,4\},\{1,3,4\},\{2,3,4\}). \tag{5.15}$$

The sets in this class form a basis for defining effects that measure the effect that an allele at one locus may affect or modify intra-allelic interactions at another locus. For example, the two sets in the subclass

$$\mathfrak{T}_{31EPI} = (\{1,2,3\},\{1,2,4\}) \tag{5.16}$$

would form a basis for defining an effect measuring intra-allelic interactions at locus 1 that may affect the expression of alleles in positions 3 and 4 at locus 2. Similarly, the sets subclass

$$\mathfrak{T}_{32EPI} = (\{1,3,4\},\{2,3,4\}) \tag{5.17}$$

would form a basis for defining an effect measuring intra-allelic interactions at locus 2 that may be affected by alleles at positions 1 and 2 at locus 1.

For cases in which many alleles can be recognized at each locus, it would be necessary to develop a nomenclature to describe many types of interactions among the alleles at the two autosomal loci under consideration as will be illustrated below. In this connection, an interested reader may wish to consult the pioneering work of Cockerham (1954) [5] that describes a nomenclature for various epistatic effects and components of the genetic variance. For example, effects and variance components corresponding to the sets in the class $\mathfrak{T}_{2IAI}$ would be labeled dominant for either the effects or variance components and would be denoted by the symbol D. Whereas those in the class $\mathfrak{T}_{2EPI}$ would be labeled additive by additive effects or variance components and denoted by the symbol AA. One could proceed in this way to develop a nomenclature of the 15 effects and variance components under consideration. But, this type of nomenclature will, however not be used in this paper and epistasis will be described in terms of sets and effects as well as variance components.

The first step in defining these effects is to derive a formula for the conditional expectation of a genetic value $\mu(\boldsymbol{z})$, given every set A of positions such that

$$A \in E = \bigcup_{\nu=1}^{3} \mathfrak{T}_{\nu}. \tag{5.18}$$

To define these effects, it will be helpful to introduce a succinct notation. For every set A of positions, let A^c denote the complement of this set with respect to the set $\mathfrak{S}$, and let $z(A)$ and $z(A^c)$ denote subsets of alleles in z corresponding to the positions in the sets A and A^c, respectively. In what follows, the symbol $z(A), z(A^c)$ will stand for the union of the positions in the two sets. Given this notation, the marginal distribution $p(z(A))$ is defined by

$$p(z(A)) = \textstyle\sum_{z(A^c)} p(z(A), z(A^c)) \tag{5.19}$$

for every $z(A) \in \mathbb{G}(A)$,where $\mathbb{G}(A)$ is a subset of $\mathbb{G}$ containing only those alleles corresponding to the positions in the set A. Thus, in this succinct notation,

$$p(z(A^c) \mid z(A)) = \frac{p(z(A), z(A^c))}{p(z(A))} \tag{5.20}$$

[5] Cockerham, C. C. (1954) An extension of the concept of partitioning the hereditary variance for analysis of covariance among relatives when epistasis is present. Genetics 39:859-882.

is the conditional distribution of $z(A^c)$, given $z(A)$ for $p(z(A)) \neq 0$. Let $\mu(z(A))$ denote the conditional expectation of $\mu(z)$, given $z(A)$. Then,

$$\mu(z(A)) = \sum_{z(A^c)} p(z(A^c) \mid z(A)) \mu(z(A), z(A^c)) \tag{5.21}$$

for every $A \in E$.

Given formula (5.21), one may proceed systematically through each of the sets in the union E in (5.18) to calculate $\mu(z(A))$ for every $A \in E$. For example, suppose $A = \{1\}$. Then, $\mu(z(A)) = \mu(x_1)$ for all $x_1 \in \mathbb{A}_1$. By continuing in this manner, all the conditional pairs of expectations, $(\mu(x_\nu), \mu(y_\upsilon))$, for $\nu = 1, 2$ could be computed, and formula (5.8) could be used to compute the four effects: $\alpha(x_\nu), \alpha(y_\nu)$ for $\nu = 1, 2$.

Similarly, for every set $A \in \mathfrak{T}_2$, $\mu(z(A))$ would need to be calculated. Suppose, for example, $A = \{1, 2\}$. Then, $\mu(x_1, y_1)$ would need to be calculated for every $(x_1, y_1) \in \mathbb{A}_1 \times \mathbb{A}_1$. Then, as in the case of one locus, the intra-allelic effect $\alpha(x_1, y_1)$ would be defined by

$$\alpha(x_1, y_1) = \mu(x_1, y_1) - \mu - \alpha(x_1) - \alpha(y_1). \tag{5.22}$$

By continuing in this way, an effect $\alpha(z(A))$ could be defined for every subset $A \in \mathfrak{T}_3$. To illustrate how each of these four effects could be defined, consider the case $A = \{1, 2, 3\}$. In this case, $\mu(z(A)) = \mu(x_1, y_1, x_2)$ for all $(x_1, y_1, x_2) \in \mathbb{A}_1 \times \mathbb{A}_1 \times \mathbb{A}_2$. Then, by definition, the effect $\alpha(x_1, y_1, x_2)$ is

$$\begin{aligned} \alpha(x_1, y_1, x_2) \quad = \quad & \mu(x_1, y_1, x_2) - \mu - \alpha(x_1) - \alpha(y_1) - \alpha(x_2) \\ & -\alpha(x_1, y_1) - \alpha(x_1, x_2) - \alpha(y_1, x_2). \end{aligned} \tag{5.23}$$

Altogether, for the subclass $\mathfrak{T}_3$, four effects would need to be computed, using the procedure illustrated in (5.23). Note that all the effects on the right in this equation, were defined for each subset of the set of symbols $\{x_1, y_1, x_2\}$. This procedure may also be used to set down formulas for each of the three remaining subsets in the subclass $\mathfrak{T}_3$. Furthermore, in formulations in which more than two loci were under consideration, the procedure (5.23) used to define the effects for the case of two loci could be extended to defining effects for some number of loci $n \geq 3$. The last step in defining effects for the two loci case is to define the effect $\alpha(z(\mathfrak{S})) = \alpha(x_1, y_1, x_2, y_2)$ for all genotypes $z \in \mathbb{G}$. In this connection let $\alpha(z(\mathfrak{S})) = \alpha(z)$ be such that the equation

$$\mu(z) = \mu + \sum_{A \in \mathfrak{T}_1} \alpha(z(A)) + \sum_{A \in \mathfrak{T}_2} \alpha(z(A)) + \sum_{A \in \mathfrak{T}_3} \alpha(z(A)) + \alpha(z) \tag{5.24}$$

holds for all genotypes $z \in \mathbb{G}$.

Having defined the set of 15 effects for the case of two autosomal loci, the next step is that of defining components of the genetic variance. For example, the additive genetic variance is defined by

$$var_A[W] = \sum_{A \in \mathfrak{T}_1} E_{\mathfrak{D}_G}[\alpha^2(z(A))], \tag{5.25}$$

where the expectation is taken with respect to the genotypic distribution $\mathfrak{D}_G$. The intra-allelic interaction component of the genetic variance is defined by

$$var_{IAI}[W] = \sum_{A \in \mathfrak{T}_{2IAI}} E_{\mathfrak{D}_G}[\alpha^2(z(A))], \tag{5.26}$$

and epistatic component of genetic variance with respect to two loci is defined by

$$var_{EPI}[W] = \sum_{A \in \mathfrak{T}_{2EPI}} E_{\mathfrak{D}_G}[\alpha^2(z(A))] \tag{5.27}$$

For the case of three alleles, the equation

$$var_{IAI1}[W] = \sum_{A \in \mathfrak{T}_{31EPI}} E_{\mathfrak{D}_G}[\alpha^2(z(A))],$$

is the component of variance for intra-allelic interaction at the first locus that may be modified by an alleles at the second locus. Similarly, the component of the genetic variance for intra-allelic interaction at the second locus that may be modified by an allele at the first locus is

$$var_{IAI2}[W] = \sum_{A\in\mathfrak{T}_{32EPI}} E_{\mathfrak{D}_G}[\alpha^2(z(A))]. \tag{5.28}$$

Finally, the component of the genetic epistatic variance as measured by effects $\alpha(z)$ is defined by

$$var_{EPI4}[W] = \sum_{A\in\mathfrak{T}_4} E_{\mathfrak{D}_G}[\alpha^2(z(A))]. \tag{5.29}$$

It should be noted that the set of components of the genetic variance was defined arbitrarily, but a user of the ideas presented in this section may wish to adapt another nomenclature for the set of 15 effects and components of the total genetic variance.

An experimenter could test whether a sample of individuals whose genotypes had been determined with respect to two autosomal loci was in linkage equilibrium, but in any case it would be of interest to compute the genetic covariance matrix for the case under consideration. Let A denote any set of positions in the union

$$A \in \mathfrak{A} = \bigcup_{v=1}^{4} \mathfrak{F}_v \tag{5.30}$$

and let

$$\mathbf{\Phi}(\boldsymbol{z}) = (\alpha(z(A)) \mid A \in \mathfrak{A}) \tag{5.31}$$

denote a 15×1 vector of classes of effects. Observe that within each class of effects corresponding to a set A there would be a collection of effects corresponding the to the number of alleles at each locus. A useful ordering of the effects in this vector would be to let the subset of singletons be the first four elements of the vector, the 6 sets of pairs of positions would be the next 6 element in the vector, the next four elements of the vector would be the four effects corresponding to the sets of triples of positions and lastly the effect for the singleton $\mathfrak{S}$ would be the last 15-th effect in the column vector. As was tacitly used in the definitions of the components of the genetic variance listed above, each effect has the unconditional expectation

$$E_{\mathfrak{D}_G}[\alpha(A(z))] = 0, \tag{5.32}$$

for all $A \in \mathfrak{A}$. Let,

$$\mathbf{\Psi}(z) = \mathbf{\Phi}(z)\mathbf{\Phi}^T(z)$$

denote a 15×15 matrix of products of effects for the genotypes $z \in \mathbb{G}$. Then, by definition, the covariance matrix of the vector $\mathbf{\Phi}(z)$ of effects is

$$\mathbf{\Psi}_G = \sum_{z\in\mathbb{G}} p(z)\mathbf{\Phi}(z)\mathbf{\Phi}^T(z) = E_{\mathfrak{D}_G}[\mathbf{\Psi}(z)]. \tag{5.33}$$

As part of an analysis of data, at this point in the calculations, a data annalist may wish to compute the eigen values and vectors of the symmetric matrix $\mathbf{\Psi}_G$. It would also be of interest to inspect the off-diagonal components of the matrix $\mathbf{\Psi}_G$ to provide an assessment of the impact of effects on the components of the genetic variance when the population is not in linkage equilibrium at the two loci under consideration.

On the other hand, an investigator may not wish to compute and analyze the matrix $\mathbf{\Psi}_G$ in (5.33) and would be content with an estimate of the fraction

$$\frac{var_{EPI}[W] + var_{IAI2}[W] + var_{EPI4}[W]}{var_G[W]}, \tag{5.34}$$

where $var_G[W]$ is the total genetic variance. An estimate of this ratio would be of interest, because it would provide an investigator with some idea of the

significance of the contribution of epistatic effects to the total genetic variance. At the same time, it should be recognized that the estimate in (5.34) under the assumption that the population was not in linkage equilibrium and could be biased by negative covariance terms.

An investigator may, therefore, also wish to carry out a computer simulation experiment under the assumption that the population or sample was in linkage equilibrium. The first step in setting up such a computer experiment would be that of computing the marginal allele probabilities. Let $p_1(x_1)$ and $p_1(y_1)$ denote the marginal probabilities, respectively, for the maternal and paternal alleles at locus 1, and define the marginal $p_2(x_2)$ and $p_2(y_2)$ for locus 2 similarly. Then, the simulated population would be in linkage equilibrium if the genotypic probabilities $p(z)$ satisfied the equation $p(z) = p_1(x_1)\, p_1(y_1)\, p_2(x_2)\, p_2(y_2)$ for all genotypes $z = (x_1, y_1, x_2, y_2) \in \mathbb{G}$. Given these assigned genotypic probabilities, an investigator could carry out a computer simulation experiment under the assumption that the sample or population was in linkage equilibrium.

Just as in the one locus case considered in section 4, it is recommended that an investigator inspect the squares of all effects defined above for the case of two autosomal loci. For example, the set of squares of additive effects is defined by

$$\mathfrak{E}_1 = \left\{\alpha^2(z(A)) \mid A \in \mathfrak{T}_1\right\}. \tag{5.35}$$

It will be tacitly be assumed that the elements in the set $\mathfrak{E}_1$ are estimates of effects so as to simplify the notation. For the case each locus has two alleles, the set $\mathfrak{E}_1$ would contain a small number of elements so that an investigator could easily find the largest one. Similarly, the set of squared effects that are measures of intra-allelic interactions is defined by

$$\mathfrak{E}_{2IAI} = \left\{\alpha^2(z(A)) \mid A \in \mathfrak{T}_{2IAI}\right\}. \tag{5.36}$$

Like set $\mathfrak{E}_1$ for the case of two alleles at each of the two loci under consideration, the set $\mathfrak{E}_{2IAI}$ would contain a small number of estimated squared effects so that an investigator could easily find the largest one. By continuing this way, set of estimated squared effects corresponding to each of the sub-classes of effects defined above for various types of epistatsis could also be defined but the enumeration of these sets will be left as an exercise for an interested reader.

In an interesting paper, Hemani et al. (2013) [8] an evolutionary perspective on epistasis and the missing heritability was the focus of attention. These authors assert that results of genome wide association studies may improved if epistatic effects may be searched for explicitly. It is suggested that the epistatic effects defined in this section may be also be useful in genome wide association studies.

VI. An Overview of the Case of Eleven Autosomal Loci

As mentioned in the introduction, there is an interesting and important case in human genetics pertaining to Alzheimer's disease (AD) in which there is a developing consensus that eleven autosomal regions, loci, of the human genome have been implicated in this disease. It is suggested that an interested reader may wish to consult the paper by Raj et al. (2012) [19] and the literature cited therein for more details regarding these genomic regions. In studies of patients with AD, quantitative measurements are often made on each patient so that AD may be viewed as a quantitative trait in humans. It is, therefore, of interest to provide an overview of an extension of the structure for the case of two autosomal loci developed in section 5 to the case of 11 autosomal loci.

For a diploid species such as humans, two alleles occupy each locus so that for the case of 11 loci, there are $11 \times 2 = 22$ positions to consider in the set

$$\mathfrak{S} = (s \mid s = 1, 2, \cdots, 22) \tag{6.1}$$

of positions. Therefore, in this case the class $\mathfrak{T}$ of all subsets of $\mathfrak{S}$ contains

$$2^{22} = 4,194,304 \tag{6.2}$$

sets. Included in $\mathfrak{T}$ is the empty set φ so, just as for the case of two loci, no effect will be associated with φ. It follows, therefore, that in theory, $2^{22} - 1 = 4,194,303$ effects could be defined for the case of 11 autosomal loci, but it is unlikely that any investigator would attempt to estimate such a large number of effects.

Notes

When dealing 11 or more autosomal loci, it is also important to remember that for the case of many loci, one should keep in mind the caveat that the number of possible genotypes under consideration may be quite large and exceed the sample size that is available to an investigator or investigators. For the case of 11 autosomal loci and two alleles per locus, each vector in the pair $(\boldsymbol{x}, \boldsymbol{y})$ denoting a genotype would contain 11 alleles contributed by the maternal and paternal, respectively. Thus, if it were possible to determine parental source of each allele, one could in principle identify four genotypes per locus. Therefore, if 11 autosomal loci were under consideration, the number of genotypes that could be identified would be

$$4^{11} = 4,194,304. \tag{6.3}$$

Observe that this is the same number as that in (6.2), and, moreover, it in all likelihood exceeds the number of individuals in any sample of individual whose genomes have been sequenced that are presently available to investigators.

Consider, for example, the case of 11 autosomal loci with two alleles at each locus and suppose that an investigator identifies three genotypes per locus; namely two homozygotes and one heterozygote at each locus. In such circumstances, an investigator may not be able to determine whether any alleles was contributed by the maternal or paternal parent. Under this assumption that only three genotypes can be identified per locus, it follows that the total number of "genotypes" that could be identified with respect to 11 autosomal loci would be

$$3^{11} = 177,147. \tag{6.4}$$

A number of this magnitude would in all likelihood exceed the sample size available to present day investigators, particularly if it is required that all individuals in the sample have had their genomes sequenced. If a sample size is considerably smaller than the number in (6.4), then it is recommended that an investigator confine attention to some sub-set $\mathfrak{S}_1$of loci and individuals in a sample such that for each identifiable genotype $(\boldsymbol{x},\boldsymbol{y})$, the number of individuals, $n(\boldsymbol{x},\boldsymbol{y}) \geq 1$, with this genotype is sufficiently large so that one may make reliable and statistically significant genetic inferences based on the available data.

For the case of 11 autosomal loci, a sample available to an investigator may not be sufficiently large to accommodate the set of possible genotypes, because the number of individuals of all genotypes may not be sufficiently large to draw reliable statistical inferences. However, when attention is focused on a sub-set of loci, the number of individuals for each genotype with respect to this sub-set of loci is sufficiently large to draw reliable statistical inferences. By way of an illustrative and hypothetical example, suppose that an investigator was able to find a sufficient sample size for each genotype with respect to six autosomal loci with three distinguishable genotypes at each locus. Let $\mathbb{G}_S$ denote the set of genotypes in the sample and let $n(\boldsymbol{x}, \boldsymbol{y})$ denote the number of individuals in the sample of genotype $(\boldsymbol{x}, \boldsymbol{y}) \in \mathbb{G}_S$. For the case of six autosomal loci, the total number of effects that may be defined is

$$2^{12} - 1 = 4,095. \tag{6.5}$$

It is doubtful that any investigation would have the persistence or interests to estimate $4,095$ effects, but it may be of interest to estimate only first, second

and third order effects. It is easy to see that the number of first order or additive effects would be

$$\binom{12}{1} = 12, \tag{6.6}$$

and as in (5.11) let $\mathfrak{T}_1$ denote the class of subsets of the set $\mathfrak{S} = (1, 2, \cdots, 12)$ of positions containing one position. It is straight forward to enumerate the sets in the class $\mathfrak{T}_1$. For the case of 12 positions, the number of sub-set of $\mathfrak{S}$ containing two positions is

$$\binom{12}{2} = 66. \tag{6.7}$$

Let $\mathfrak{T}_2$ denote the class of sub-sets of $\mathfrak{S}$ containing two positions. Similarly, the number of subsets of $\mathfrak{S}$ containing three positions is

$$\binom{12}{3} = 220. \tag{6.8}$$

Observe that if an investor chose to follow the procedure just outlined, the total number of effects that would need to be defined would be

$$12 + 66 + 220 = 298. \tag{6.9}$$

Let $\mathfrak{T}_3$ denote the class of sub-sets of $\mathfrak{S}$ containing three positions.

It is interesting to note that the enumeration of the sets in the classes $\mathfrak{T}_2$ and $\mathfrak{T}_3$ may be accomplished by using a type of recursive procedure. To describe this recursive procedure, it is helpful if the notation is extended to include the number of loci and positions under consideration. For example, let $\mathfrak{T}_2^{(\nu)}$ denote a class of sub-sets of two positions taken from the sets of positions $\mathfrak{S}_\nu$ for $\nu = 4, 6, \cdots, 12$ sets of positions corresponding to $l = 2, 3, \cdots, 6$ loci. Then, it follows that the containment relations

$$\mathfrak{T}_2^{(4)} \subset \mathfrak{T}_2^{(6)} \subset \mathfrak{T}_2^{(8)} \subset \mathfrak{T}_2^{(10)} \subset \mathfrak{T}_2^{(12)} \tag{6.10}$$

hold. Thus, if an investigator has enumerated the sub-sets in the class $\mathfrak{T}_2^{(4)}$ for the case of two loci, see section 5, then to extend this enumeration to case of 3 loci and 6 positions, one could add positions 5 and 6 to the set $\mathfrak{S}_4$ to obtain the set $\mathfrak{S}_6$ of position for the case of 3 loci. The next step in this recursive process would be that to adding to $\mathfrak{T}_2^{(4)}$ those sets with two positions that include position 5 and 6 to obtain all the sub-sets with two positions from the set $\mathfrak{S}_6$. By continuing in this recursive manner, the set of two positions in the class $\mathfrak{T}_2^{(12)}$ could be enumerated. It also of interest to note that the containments relations

$$\mathfrak{T}_3^{(4)} \subset \mathfrak{T}_3^{(6)} \subset \mathfrak{T}_3^{(8)} \subset \mathfrak{T}_3^{(10)} \subset \mathfrak{T}_3^{(12)} \tag{6.11}$$

for classes of sub-sets containing sets with three positions are also valid. Therefore, the class of sets $\mathfrak{T}_3^{(12)}$ could also be enumerated by using a recursive procedure. It is also highly plausible that a clever computer programmer could write code to accomplish the enumeration of the classes of sets $\mathfrak{T}_2^{(12)}$ and $\mathfrak{T}_3^{(12)}$.

Given the enumerated classes of sub-sets $\mathfrak{T}_1, \mathfrak{T}_2$ and $\mathfrak{T}_3$, the next step in providing an overview of the case of six autosomal loci is that of defining an effects for each set in the three classes of sub-sets. Briefly, the procedures used in defining and setting up algorithms to compute them are given implicitly in equations (5.19) , (5.20) and (5.21) . Let

$$\mathfrak{C}_1 = \{\alpha(z(A)) \mid A \in \mathfrak{T}_1\} \tag{6.12}$$

denote the set of first order effects. Similarly, let

$$\mathfrak{C}_2 = \{\alpha(z(A)) \mid A \in \mathfrak{T}_2\} \tag{6.13}$$

and

$$\mathfrak{C}_3 = \{\alpha(z(A)) \mid A \in \mathfrak{T}_2\} \tag{6.14}$$

denote, respectively, the class of second and third order effects. It should be noted that the formulas for computing the first, second and third order effects are outlined in formulas (5.22) and (5.23) for each combination of alleles.

Just as suggested for the case of two autosomal loci in section 5, it would be of interest to find the largest of the squares of each effects to get some idea as to which effect contributes the most to a variance component under consideration. An explicit form of the squares of first order effects is

$$\mathfrak{D}_1 = \left\{\alpha^2(\nu) \mid \nu \in \mathfrak{S}\right\}, \tag{6.15}$$

where $\mathfrak{S} = (s \mid s = 1, 2, \cdots, 12)$. For the sake of simplicity, suppose there are only two alleles at each the the six loci under consideration. Under this assumption, each of the 12 positions may be occupied by either of the two alleles at each locus. Therefore, the number of squared values in the set $\mathfrak{D}_2$ is 24. Let $\mathfrak{D}_2$ and $\mathfrak{D}_3$ denote, respectively, the set of squared effects from the sets $\mathfrak{C}_2$ and $\mathfrak{C}_3$. Suffice it to say that for the case of two alleles at each of the six loci, the number of squared effects in each of the sets $\mathfrak{D}_\nu$for $\nu = 1, 2, 3$ could be determined, but this exercise will be left to an interested reader.

If an investigator does not have a sufficiently large sample to work with for the case of 6 autosomal loci, then a reduced version of the ideas just outlined could be used to study a smaller number loci such that the number the sample size for each genotype would be sufficiently large to draw reliable statistical inferences. Given the ideas just outlined, a study of cases for 2, 3 or 4 loci may be feasible if there is insufficiently data to study the case of 5 or 6 autosomal loci. It should be noted that for the case that only three genotypes per locus may be identified, the number of effects that an investigator could estimate would significantly smaller than for the case that for in which four genotypes may be identified per locus. It is beyond the scope of this paper to consider the case of only three identifiable genotypes per locus, but the details for this case will be worked out in subsequent papers for one or more autosomal loci.

When one considers of the union of the sets $\mathfrak{D}_1, \mathfrak{D}_2$ and $\mathfrak{D}_3$, it is easy to see that many tests of statistical significance may need to be made if an investigator wishes to assess the statistical significance some chosen number of squared effects. It is beyond the scope of this paper to deal with the problem of making many statistical tests and computing measures of statistical significance, but it is suggested that a reader may wish to consult the literature on this subject. Included among the papers that would be interest to consult are Benjamini et al. (1995) [1], (2001) [2] and (2005) [3].

A version of equation (5.24) may also set down for the case of 6 autosomal loci under consideration and has the form

$$\mu(z) = \mu + \sum_{A\in\mathfrak{T}_1} \alpha(z(A)) + \sum_{A\in\mathfrak{T}_2} \alpha(z(A)) + \sum_{A\in\mathfrak{T}_3} \alpha(z(A)) + \alpha_R(z) \tag{6.16}$$

for all genotypes $z \in \mathbb{G}_S$, where $\alpha_R(z)$ is a remainder effect. In principle, if all the effects on the right hand side of equation have been estimated for all genotypes $z \in \mathbb{G}_S$, then the effect $\alpha_R(z)$ could be estimated for all genotypes $z \in \mathbb{G}_S$. Given these estimates, one could then proceed to estimate the variance component corresponding to the effect $\alpha_R(z)$, by using the formula

$$var_R[W] = \sum_{z\in\mathbb{G}} p(z)\,\alpha_R^2(z) \ . \tag{6.17}$$

Let $\widehat{var}_G[W]$ denote an estimate of the genetic variance defined in equation (2.11) and let $\widehat{var}_R[W]$ denote an estimate of the variance component in (6.17). Then, the ratio

$$\frac{\widehat{var}_R[W]}{\widehat{var}_G[W]} \tag{6.18}$$

[3] Benjamini, Y. and Yekutieli, D. (2005) False discovery rate adjusted multiple confidence intervals for selected parameters. J. Amer. Statist. Assoc. 100:71-93.

may be used as an estimate of the fraction of the total genetic variance that is attributable to the remainder effects $\alpha_R(z)$ for all genotypes $z \in \mathbb{G}_S$.

When interpreting this estimate, an investigator should also be aware of the possibility that the sample of individuals that constitute the data used to estimate all effects and variance components may not be in linkage equilibrium with respect to the 6 autosomal loci under consideration. In this case, it may be worthwhile to compute a version of the genetic covariance $\mathbf{\Psi}_G$ defined in (3.27) for the case of 6 loci. It can be shown that in terms of this matrix, the estimate $\widehat{var}_G[W]$ of the genetic variance may be represented in the form

$$\widehat{var}_G[W] = \mathbf{1}^T \widehat{\mathbf{\Psi}}_G \mathbf{1} \ , \tag{6.19}$$

where $\mathbf{1}$ is column of $1s$, T denotes the transpose of vector or matrix and $\widehat{\mathbf{\Psi}}_G$ is an estimate of $\mathbf{\Psi}_G$. Given this matrix, all variance components associated with equation (6.16) would be on the principal diagonal the the matrix $\mathbf{\Psi}_G$. Therefore, the trace of the matrix, the sum of the elements on the principal diagonal of $\widehat{\mathbf{\Psi}}_G$, is the sum of the variance components corresponding to the effects in equation (6.16). Let $\widehat{trace}\left[\widehat{\mathbf{\Psi}}_G\right]$ denote an estimate of the sum of these variance components. Then, the ratio

$$\frac{\widehat{trace}\left[\widehat{\mathbf{\Psi}}_G\right]}{\widehat{var}_G[W]}, \tag{6.20}$$

is an estimate of the fraction of the total genetic variance that is attributable to the variance components defined in connection with equation (6.16). It would also be of interest to inspect the elements in the matrix $\widehat{\mathbf{\Psi}}_G$ off the principal diagonal to make an assessment as to the affects that non-zero covariance terms contribute to the estimate of the total genetic variance in (6.19).

This ratio may be interpreted as a measure of the genetic variance that is attributable to the effects defined in connection with the construction of equation (6.16) , taking into account these effects may be correlated for the case the sample of individuals is not in linkage equilibrium. If this ratio is equal to one, then the variance components defined in connection with equation (6.16) are sufficient to account for all the genetic variance in the quantitative trait under consideration. But, if this ratio is less than one, then these components of the genetic variance would not be sufficient to account for the total genetic variance. It is also appropriate to mention that the ratio in (6.20) may be computed without computing the matrix $\widehat{\mathbf{\Psi}}_G$, by computing each variance component corresponding to the effects in equation (6.16), using formulas analogous to (6.17).

It is recognized that an investigator who wished to apply the ideas on the estimation of effects and variance components set forth in this paper may also want to test some statistical hypotheses, but it is beyond the scope of this paper to suggest various types of statistical tests of significance in addition to those mentioned briefly above.

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Notes

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Computation of a Beautiful Summation Formula in Association with Contiguous Relation

By Salahuddin & Shakeeluddin
P.D.M College of Engineering, India

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I. Introduction

Generalized Gaussian Hypergeometric function of one variable is defined by

$$ {}_AF_B\left[\begin{array}{ll} a_1, a_2, \cdots, a_A & ; \\ & \\ b_1, b_2, \cdots, b_B & ; \end{array} \quad z \right] = \sum_{k=0}^{\infty} \frac{(a_1)_k (a_2)_k \cdots (a_A)_k z^k}{(b_1)_k (b_2)_k \cdots (b_B)_k k!} \tag{1} $$

where the parameters $b_1, b_2, \cdots, b_B$ are neither zero nor negative integers and $A,\ B$ are non-negative integers and $\mid z \mid = 1$

Contiguous Relation is defined by

[Andrews p.363(9.16), E. D. p.51(10)]

$$ (a-b)\ {}_2F_1\left[\begin{array}{ll} a,\ b & ; \\ c & ; \end{array} \quad z\right] = a\ {}_2F_1\left[\begin{array}{ll} a+1,\ b & ; \\ c & ; \end{array} \quad z\right] - b\ {}_2F_1\left[\begin{array}{ll} a,\ b+1 & ; \\ c & ; \end{array} \quad z\right] \tag{2} $$

Gauss second summation theorem is defined by [Prudnikov., 491(7.3.7.5)]

$$ {}_2F_1\left[\begin{array}{ll} a,\ b & ; \\ \frac{a+b+1}{2} & ; \end{array} \quad \frac{1}{2}\right] = \frac{\Gamma(\frac{a+b+1}{2})\ \Gamma(\frac{1}{2})}{\Gamma(\frac{a+1}{2})\ \Gamma(\frac{b+1}{2})} \tag{3} $$

$$ = \frac{2^{(b-1)}\ \Gamma(\frac{b}{2})\ \Gamma(\frac{a+b+1}{2})}{\Gamma(b)\ \Gamma(\frac{a+1}{2})} \tag{4} $$

In a monograph of Prudnikov et al., a summation theorem is given in the form [Prudnikov., p.491(7.3.7.8)]

Author α: P.D.M College of Engineering, Bahadurgarh, Haryana, India. e-mail: vsludn@gmail.com
Author σ: AMITY University, Greater Noida, U.P, India.

$$ {}_2F_1\left[\begin{array}{ll} a,\ b & ; \\ \frac{a+b-1}{2} & ; \end{array}\ \frac{1}{2}\right] = \sqrt{\pi}\left[\frac{\Gamma(\frac{a+b+1}{2})}{\Gamma(\frac{a+1}{2})\,\Gamma(\frac{b+1}{2})} + \frac{2\,\Gamma(\frac{a+b-1}{2})}{\Gamma(a)\,\Gamma(b)}\right] \tag{5} $$

Now using Legendre's duplication formula and Recurrence relation for Gamma function, the above theorem can be written in the form

$$ {}_2F_1\left[\begin{array}{ll} a,\ b & ; \\ \frac{a+b-1}{2} & ; \end{array}\ \frac{1}{2}\right] = \frac{2^{(b-1)}\,\Gamma(\frac{a+b-1}{2})}{\Gamma(b)}\left[\frac{\Gamma(\frac{b}{2})}{\Gamma(\frac{a-1}{2})} + \frac{2^{(a-b+1)}\,\Gamma(\frac{a}{2})\,\Gamma(\frac{a+1}{2})}{\{\Gamma(a)\}^2} + \frac{\Gamma(\frac{b+2}{2})}{\Gamma(\frac{a+1}{2})}\right] \tag{6} $$

Recurrence relation is defined by

$$ \Gamma(\zeta+1) = \zeta\,\Gamma(\zeta) \tag{7} $$

II. Main Summation Formula

$$ {}_2F_1\left[\begin{array}{ll} a, & b\ ; \\ \frac{a+b+50}{2} & ; \end{array}\ \frac{1}{2}\right] = \frac{2^b\,\Gamma(\frac{a+b+50}{2})}{(a-b)\,\Gamma(b)\Big[\prod_{\Phi=1}^{24}\{a-b-2\Phi\}\Big]\Big[\prod_{\Omega=1}^{24}\{a-b+2\Omega\}\Big]} $$

$$ \Big[\frac{\Gamma(\frac{b}{2})}{\Gamma(\frac{a}{2})}\Big\{16777216(a^{24}+24a^{23}(-25+49b)+92a^{22}(1850-2450b+2303b^2)+2024a^{21}(-15000+32830b $$
$$ -11515b^2+6909b^3)+3542a^{20}(1078760-1862560b+1862140b^2-296100b^3+127323b^4) $$
$$ +14168a^{19}(-25470000+59043320b-31452400b^2+19575500b^3-1768375b^4+580027b^5) $$
$$ +1748a^{18}(15191158400-29643079200b+30723033320b^2-7949956000b^3+3490772250b^4 $$
$$ -203009450b^5+52782457b^6)+10488a^{17}(-148786880000+357673671040b-232905706320b^2 $$
$$ +148123893400b^3-22677641000b^4+7511349650b^5-304514175b^6+64382997b^7) $$
$$ +7429a^{16}(10023824208640-21069362298880b+22345022210560b^2-7368717121920b^3 $$
$$ +3271593344880b^4-331311422400b^5+86238414360b^6-25753198880b^7+4506809798^8) $$
$$ +6992a^{15}(-417434238672000+1028919146214400b-758185809902080b^2+488413454072320b^3 $$
$$ -97893969213600b^4+32514318327120b^5-2340617754720b^6+491886097080b^7-11267024475b^8) $$
$$ +16524969239^9+1288a^{14}(73498165566150400-162582609590278400b+175048145605518080b^2 $$
$$ -67216907266790400b^3+29982931333152000b^4-4051969321377600b^5+1050250387890480b^6 $$
$$ -56524592337600b^7+9770119794750b^8-177053241750b^9+21954601977b^{10}) $$
$$ +2576a^{13}(-990767756776320000+2486449587901233920b-199607871521267760b^2 $$
$$ +12948027595836748^0b^3-308151278611904000b^4+102121179551686400b^5 $$
$$ -9953696252152800b^6+2070088475301840b^7-86466364971000b^8+12452744669750b^9 $$
$$ -1829550164^75b^{10}+19293438101b^{11})+4a^{12}(14326727885044845429760 $$
$$ -3290588518751035127^80^80b+35774313688848091302400b^2-15286300400532994327040b^3 $$

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$$+6818791881087123508480b^4 - 1110197890899430860800b^5 + 285360756947700062720b^6$$
$$-21034488682299980160b^7 + 35773791502192926000b^8 - 1193565477544440000b^9$$
$$+144512508413273000b^{10} - 1755702867191000b^{11} + 158013258047190b^{12})$$
$$+16a^{11}(-669547155132190072320000 + 1702574806656396147148800b$$
$$-1456597752943573513728000b^2 + 947326460348108910218240b^3 - 254696002292718122456320b^4$$
$$+83889876852140073594880b^5 - 9963924613447640908800b^6 + 2043242878716115614720b^7$$
$$-117990425471551083360b^8 + 16627075164075616240b^9 - 4533830217868952000b^{10}$$
$$+464207838085300400b^{11} - 47403977414157000b^{12} + 3646459801089000b^{13})$$
$$+88a^{10}(1889644037260035979264000-44675008443384303953920000b+4884737551157640234956800b^2$$
$$-226166014583862202257408000b^3 + 10051697310235299233715200b^4 - 1870394856492508155264000b^5$$
$$+475088333910831795481600b^6 - 43073125866540000358400b^7 + 7183206067211035097600b^8$$
$$-333964260828294096000b^9+39344163073960544800b^{10}-8933016188267808000b^{11}+776020667298422000b^{12}$$
$$-67527033353500000b^{13} + 4437490763230000b^{14}) + 176a^9(-12117413105418513408000000$$
$$+3111036718994734998200320000b-279668498932558257249280000b^2+1817332886769069127764992000b^3$$
$$-535941065625167448529920000b^4 + 17485802915445220254080000b^5 - 2395976050800413029312000b^6$$
$$+482844538455392501606400b^7 - 34564912224580914176000b^8 + 4749672227164504640000b^9$$
$$-1817101612701014640000b^{10}+179979159326007496000b^{11}-34557075744573200000b^{12}+2549727638692500000b^{13}$$
$$-191271153587500000b^{14} + 10711184600900000b^{15}) + 7a^8(32036520834224384519962624000$$
$$-774954359718187014052904960000b + 84946482206673031294189568000b^2$$
$$-4189347406236124909795737600000b^3 + 184918660522586233199824896000b^4$$
$$-3810957758982312498094080000000b^5 + 95348706874079672356761600000b^6$$
$$-1005187175780630307379200000b^7 + 16382012261836246649395200000b^8 - 950616408212436725760000000b^9$$
$$+108574252129923740160000000b^{10} - 34796729916906397440000000b^{11} + 2906032975631673888000000b^{12}$$
$$-478072081243680000000b^{13} + 29925033054180000000b^{14} - 1954667788920000000b^{15} + 92846719973700000000b^{16})$$
$$+56a^7(-34149383145217497799065600000 + 882744429988659622361169920000b$$
$$-82581902088381774685929472000b^2 + 53456887855304247968707379200000b^3$$
$$-16965654806439543313050009600000b^4 + 5465855310775186912465305600000b^5$$
$$-836198058114892662239232000000b^6+165051253917006528398745600000b^7-13833130317182886015820800000b^8$$
$$+1846835733004646409625600000b^9 - 88722756599754973696000000b^{10} + 8466696085796543795200000000b^{11}$$
$$-2307335336129992896000000b^{12}+162539717527874400000000b^{13}-23168313446160000000000b^{14}+1226109794868000000000b^{15}$$
$$-70338424222500000000b^{16} + 2813536968900000000b^{17}) + 4a^6(32565504577080501524024524800000$$
$$-802472204014901668373594112000000b + 879424435527365512536732467200000b^2$$
$$-45659572447846766118316802048000000b^3 + 19956317714641264124700557312000000b^4$$
$$-4463337907739548156566159360000000b^5 + 1096352413637740487132606464000000b^6$$

$$-1299462831292472909083607046^7 + 2062091232052339492766361 6b^8$$
$$-1409562354409704470976000b^9+1554394910423122214487046^{10}-629045580880601569484 8b^{11}$$
$$+5026687798293516293126^{12} - 1179746113283793216 0b^{13} + 6995362713692606 40b^{14}$$
$$-872374157430720 0b^{15} + 387986748011310b^{16} - 196947587823 0b^{17} + 65649195941b^{18})$$
$$+8a^5(-867509267057335243741593600 00 + 225253465514342947305019146240b$$
$$-2177913111722105090875431321 60b^2 + 1400399029054055763353765150 72b^3$$
$$-4721329569363322944010780672 0b^4 + 1497151027137515010710192128 0b^5$$
$$-2503637058887526422790021120b^6 + 4822484423113274122084884 48b^7$$
$$-4572742100607843468493824 0b^8 + 5906621910332828686543360b^9$$
$$-3361655919230134900774 40b^{10} + 3075782980051145178214 4b^{11} - 1064027984710141301760b^{12}$$
$$+7115605188580326144 0b^{13} - 1454165064083793600b^{14} + 722307603611092 80b^{15}$$
$$-794816589560280b^{16} + 294356800178 70b^{17} - 133072694475b^{18} + 36419895 33b^{19})$$
$$+2a^4(1403782879734902492948135411712 - 351213672454187301447659421 6960b$$
$$+3838107410321975165361019944960b^2 - 2080638442029282019791360491520b^3$$
$$+8976146061354220713193011937 28b^4 - 214888925778265600487915520 0000b^5$$
$$+5163032157775736503869145088 0b^6 - 6732703340931905058752593920b^7$$
$$+1035802801652608895414433792b^8 - 8057575360120496669921280 0b^9$$
$$+8535593768666229096832000b^{10}-4114690144022022902937 60b^{11}+3127311644339030887065 6b^{12}$$
$$-9365554864560290816 00b^{13} + 5222970518964800000 0b^{14} - 938501032983449440 0b^{15}$$
$$+387399098992508 40b^{16} - 378991033864800b^{17} + 11532966854500b^{18} - 46692173500b^{19}$$
$$+1027227817b^{20}) + 8a^3(-1031945954037245704439385292800$$
$$+2685906915270162634662066782208b - 2670567327357474477691675607040b^2$$
$$+1700586965595271957792400867328b^3 - 6035881079880400983080451440 64b^4$$
$$+1876857135470670244595189678 08b^5 - 3382521151816211965005135872 0b^6$$
$$+6329583335998288659875692544b^7 - 6643720831233511603515678 72b^8$$
$$+8258443868486665899216281 6b^9 - 5379663985242038662410240b^{10}$$
$$+4689237510595873573345 28b^{11} - 1943002203128662595046 4b^{12} + 1224066602288528015360b^{13}$$
$$-3209126665279628800 0b^{14} + 1482193431840486400b^{15} - 23623272446432400b^{16}$$
$$+8006224538499 60b^{17} - 70106590260000b^{18} + 171963858500b^{19} - 626358425b^{20} + 10737573b^{21})$$
$$+28a^2(5880257480757792277297889280 00 - 1489868841591295982965673164800b$$
$$+1619134373497352969398693920 768b^2 - 9111536319898731786989658439 68b^3$$
$$+3865420034621121317370247249 92b^4 - 9813502593717926142277582848 0b^5$$
$$+2295418683500884599863823564 8b^6 - 3246914570925961085847076864b^7$$
$$+4814978609468505913032540 16b^8 - 4171641918834909838331904 0b^9$$

Notes

$$+42155863053774336159068 16b^{10}-233981535209296474349568b^{11}+167721446039900266142 72b^{12}$$
$$-6051622928218092467 20b^{13}+3141674440169714944 0b^{14}-728446051233638400b^{15}$$
$$+275558424414739 20b^{16}-392734168414560b^{17}+10735213609400b^{18}-84659596000b^{19}$$
$$+1627283350b^{20}-5350950b^{21}+68103b^{22})+56a(-350941492603214674211635200000$$
$$+9136781741367615504865296384 00b-9309152567649968772029507174 40b^2$$
$$+5848911132157624907331073474 56b^3-2172469294932871285568647987 20b^4$$
$$+6590998697795561475683647488 0b^5-1268577774911503518631723008 0b^6$$
$$+2291538654085596716282675200b^7-2626486808826365075387187 20b^8$$
$$+3117361521382020743471104 0b^9-2276521650775048577331200b^{10}$$
$$+1872477457468170306252 80b^{11}-8992280885059851724800b^{12}+5274865130755744384 00b^{13}$$
$$-1677386722830932 0960b^{14}+7100927009870387 20b^{15}-147048124096025 60b^{16}$$
$$+447872724172160b^{17}-5753553921360b^{18}+123515535640b^{19}-882312200b^{20}+12723370b^{21}$$
$$-37835b^{22}+329b^{23})+7(14870566932476189219802316800 00$$
$$-3807945612886480201004875776000b+4101124076932069592394419404800b^2$$
$$-2387147616741179381388410880000b^3+9904868702221308856158262394 88b^4$$
$$-2652228413822552777514654105 60b^5+5996050556945672809400500224 0b^6$$
$$-9125628368819773305677441440 0b^7+1292587838978295446849454080b^8$$
$$-1232038867469925870705049 60b^9+1174336127054962551128064 0b^{10}$$
$$-7363444742395662491648 00b^{11}+4909448578700566190080 0b^{12}-2069618165579821301760b^{13}$$
$$+9832113141370655744 0b^{14}-27887407233511936 00b^{15}+946242612455078 40b^{16}$$
$$-1768023172751360b^{17}+42226385098240b^{18}-493112860800b^{19}+7974742160b^{20}-51895360b^{21}$$
$$+521640b^{22}-1400b^{23}+7b^{24}))\Big\}-\frac{\Gamma(\frac{b+1}{2})}{\Gamma(\frac{a+1}{2})}\Big\{16777216(1040939685273333245386162176 0000$$
$$+49a^{24}-1965272358578002175585151 2000000b+1646472094612181837643408998 4000b^2$$
$$-8255567632297965635515082342 400b^3+2807565759469804985896270823424b^4$$
$$-6940074136458681949932748800 00b^5+1302620183083220060960980992 00b^6$$
$$-1912365456132179876747673600 0b^7+2242556458395706916397383680b^8$$
$$-2132664706553658359808000000b^9+1662886752788831661752320 0b^{10}$$
$$-1071275448211504115712000 0b^{11}+5730691154017938171904 0b^{12}-2552217741455800320000b^{13}$$
$$+9466563724920171520 0b^{14}-2918700196794624000b^{15}+744669900459865 60b^{16}$$
$$-15604767974400 00b^{17}+26554144883200b^{18}-3608589600 00b^{19}+3820967920b^{20}$$
$$-30360000b^{21}+170200b^{22}-600b^{23}+b^{24}+392a^{23}(-25+47b)+4508a^{22}(810-470b+423b^2)$$
$$+14168a^{21}(-25640+50290b-10575b^2+6063b^3)+24794a^{20}(2251480-1992800b+1837700b^2$$
$$-202100b^3+82861b^4)+9016a^{19}(-382851600+767177240b-262918000b^2+152585500b^3$$

$$-10357625b^4+3231579b^5)+85652a^{18}(3450995840-3761722080b+3509386600b^2-654804000b^3$$
$$+269298250b^4-12429150b^5+3065857b^6)+171304a^{17}(-72246778880+146411482240b$$
$$-64193227920b^2+37389550920b^3-4424777400b^4+1374663990b^5-45987855b^6+9197571b^7)$$
$$+21413a^{16}(30933070037760-384565215027 20b+360324843955 20b^2-88257684384 00b^3$$
$$+36183542613 60b^4-29694730848 0b^5+72476859480b^6-1839514200b^7+303519843b^8)$$
$$+2576a^{15}(-7578099791715200+154367978475443 20b-791789186123 5200b^2+460308519205 1200b^3$$
$$-72864987032 8800b^4+22431913155 6240b^5-1354618256 8800b^6+266545607 5800b^7-53115972525b^8$$
$$+7318200659b^9)+1288a^{14}(534353975074492160-729298575143883520b+68297270438472 0640b^2$$
$$-19932463759500 80000b^3+81102026692000000b^4-9032081143377600b^5+21724728924511 20b^6$$
$$-100731797592000b^7+16263604920750b^8-2613643092 50b^9+303182598 73b^{10})$$
$$+784a^{13}(-18478733621248404480+376776080768267456 00b-216129390293503302 40b^2$$
$$+12490475533556408320b^3-23891721593266048 00b^4+72608216210003328 0b^5$$
$$-601911282287649 60b^6+116099798234196 00b^7-426850072539000b^8+57238783725750b^9$$
$$-7579564968 25b^{10}+74417546961b^{11})+196a^{12}(1753374492393059353600$$
$$-2569223110017100492800b+23960206577128609448 96b^2-79306212372598473267 2b^3$$
$$+31911343309581947827 2b^4-43429713661638420480b^5+10258546527129625088b^6$$
$$-6592386674657125 6b^7+10378689198684549 6b^8-3103084352573920b^9+348417442460516b^{10}$$
$$-3869712441972b^{11}+322476036831b^{12})+784a^{11}(-6574504234281841510400$$
$$+1337483898191550218752 0b-83564834003320169410 56b^2+47849362353019118095 36b^3$$
$$-10496658530668425772 80b^4+31385540612766787532 8b^5-32094162289826610688 8b^6$$
$$+6047640061283245568b^7-3106850885438071 20b^8+404034847466547 44b^9-100268549051985 6b^{10}$$
$$+947362934867 96b^{11}-895766768975b^{12}+63392725189b^{13})+4312a^{10}(19063898166476664791040$$
$$-2956521624383179970560 0b+27373937047905413090304b^2-99808237203006283161 60b^3$$
$$+39589952544834086720 00b^4-62368384401301204096 0b^5+14419247777579983436 8b^6$$
$$-1152243592204610048 0b^7+17625690280831776 00b^8-741674127633067 20b^9$$
$$+80294210355021 52b^{10}-168231176915360b^{11}+134056130253 50b^{12}-109297802050b^{13}$$
$$+65578681 23b^{14})+112a^9(-770024292168703669190656 0+15586807606910103717355520b$$
$$-1042910479708727459582976 0b^2+58988884774904756422973 44b^3$$
$$-1438852742878660119628800b^4+42190156502377347761 0240b^5-50341512657489445392000b^6$$
$$+9234178665023232048128b^7-59413525513277295360 0b^8+74637706426870787200b^9$$
$$-2624004906508025040b^{10}+23752964520108023 2b^{11}-4262733848373000b^{12}+286413127404250b^{13}$$
$$-20361122801 25b^{14}+10316302219 3b^{15})+7a^8(1292587838978295446849454080$$
$$-2101189447061092060309749760b+19259914437874023652130160 64b^2$$
$$-7592823807124013261160775 68b^3+29594365761503111297555251 2b^4$$
$$-5225990972123249678278656 0b^5+11783378468870511387236352b^6$$

Notes

$$-1106650425374630881265664b^7+16382012261836246649395 2b^8-869060650218034413568 0b^9$$
$$+9030316198779586979 84b^{10}-2696924010778310476 8b^{11}+2044216657268167200b^{12}$$
$$-318196223093280000b^{13}+1797702042234000b^{14}-112541478756 00b^{15}+4783012847 13b^{16})$$
$$+56a^7(-1140703546102471663209676800+229153865408559671628267 5200b$$
$$-1623457285462980542923538432b^2+9042261908568983799822417 92b^3$$
$$-2404536907475680378125926 40b^4+6889263461590391602978406 4b^5$$
$$-9281877366374806493454336b^6+1650512539170065283987456b^7-1256483969725787884224 00b^8$$
$$+1517511406574090719334 4b^9-6768634064742000056 32b^{10}+5837836796331758899 2b^{11}$$
$$-1502463477307141440b^{12}+9522406986388464 0b^{13}-1300065623764800b^{14}+614154926925 60b^{15}$$
$$-341643774795b^{16}+12058015581b^{17})+196a^6(2141446627480597431928750080$$
$$-3624507928318581481804922880b+3279169547858406571234033664b^2$$
$$-1380620878292331414287810560b^3+5268400160995649493744025 60b^4$$
$$-1021892677096949560322457 60b^5+2237453905383143851291033 6b^6$$
$$-2389137308899693320683520b^7+3405310959788559727027 20b^8-2151488698677921903872 0b^9$$
$$+2133049662456795816448b^{10}-8133816010977666048 0b^{11}+5823688917300001280b^{12}$$
$$-130820007885436800b^{13}+690164540613744 0b^{14}-834979558214 40b^{15}+32686998993 90b^{16}$$
$$-16294615650b^{17}+470733341b^{18})+392a^5(-4736122167540272816990453760$$
$$+9415712425422306795480678 40b-7009644709798518673055416320b^2$$
$$+3830320684634020907337121792b^3-1096372070297273471877120000b^4$$
$$+3055410259464316348388147 20b^5-4554426436468926690373632 0b^6$$
$$+7808364729678838446379008b^7-6805281712468415175168 00b^8+7850768655914180522240 0b^9$$
$$-4198845596207671368960b^{10}+3424076606209798922 24b^{11}-1132854990713704960 0b^{12}$$
$$+6710820370539392 00b^{13}-133136134845264 00b^{14}+579949269753120b^{15}-627885856380 0b^{16}$$
$$+2009669263 50b^{17}-905256425b^{18}+20963833b^{19})+98a^4(7074906215872363468 6844731392$$
$$-1241411025675926448896370278 40b+1104405724177463233534356357 12b^2$$
$$-4927249861126857945371797094 4b^3+1831866543133514431263879987 2b^4$$
$$-3854146587235365668580229120b^5+8145435801894393520285941 76b^6$$
$$-9694659889394024750314291 2b^7+1320847575161330237141606 4b^8$$
$$-9625064035717292953190 40b^9+9026013911231697271091 2b^{10}-4158302078248459142144b^{11}$$
$$+2783180359627397350 40b^{12}-8099976466370048000b^{13}+3940613832357120 00b^{14}$$
$$-6984435027974400b^{15}+2480068057052 40b^{16}-242697039600 0b^{17}+6226397850 0b^{18}-255656500b^{19}$$
$$+4601817b^{20})+56a^3(-2983934520926474226735513600 00+5848911132157624907331073474 56b$$
$$-4555768159949365893494829219 84b^2+2429409950850388511132001239 04b^3$$
$$-7430851578676007213540573184 0b^4+2000570041505793947648235929 6b^5$$
$$-3261398031989054722736914432b^6+5345688785530424796870737 92b^7$$

$$-52366842577951561372446720b^8+57116176441313601158328320b^9$$
$$-35540373720321203211878 4b^{10}+27066470295660254577664b^{11}-10918786000380710233 60b^{12}$$
$$+5956092694084904448 0b^{13}-1545988867136179200b^{14}+609819084084582 40b^{15}$$
$$-9775392767632 80b^{16}+27741489178200b^{17}-248152198000b^{18}+4952601500b^{19}-18728325b^{20}$$
$$+249711b^{21})+28a^2(10252810192330173980986048512 00-18618305135299937544059014348 80b$$
$$+16191343734973529693986939207 68b^2-76301923638784985076905017344 0b^3$$
$$+27415052930871251181150142464 0b^4-62226088906345859739298037760b^5$$
$$+12563206221819507321953332096 0b^6-16516380417676354937185894 40b^7$$
$$+21236620551668257823547392 0b^8-17579162790046519027097600b^9$$
$$+15352032303638297881292 80b^{10}-83234157311061343641600b^{11}+51106162412640130432 00b^{12}$$
$$-18363924179956635392 0b^{13}+80522146978538316 80b^{14}-1893298279584051 20b^{15}$$
$$+59286132143660 80b^{16}-87239823138720b^{17}+1917995080120b^{18}-15914914400b^{19}+235560710b^{20}$$
$$-832370b^{21}+7567b^{22})+56a(-47599320161081002512560947 2000$$
$$+91367817413676155048652 96638400b-74493442079564799148283 65824 00b^2$$
$$+38370098789573751923743 8111744b^3-12543345444792403623130693 6320b^4$$
$$+32179066502048992472145 5923 20b^5-57319443143921547740971008 00b^6$$
$$+88274442998865962236 1169920b^7-96869294964773376756613120b^8$$
$$+97775439739834528514867 20b^9-70203584696746763356160 0b^{10}+48644994475897032775680b^{11}$$
$$-23504203705364536627 20b^{12}+11437668104345676032 0b^{13}-37394000205764032 00b^{14}$$
$$+1284679048273408 00b^{15}-2795076652113920b^{16}+669871689619 20b^{17}-92528754360 0b^{18}$$
$$+14937959960b^{19}-117806920b^{20}+1186570b^{21}-4025b^{22}+21b^{23}))\Big\}\Bigg] \qquad (8)$$

III. Derivation of the Summation Formula

Substituting $c=\frac{a+b+50}{2}$ and $z=\frac{1}{2}$ in equation (2), we get

$$(a-b)\ {}_2F_1\left[\begin{matrix}a,\ b\\ \frac{a+b+50}{2}\end{matrix};\quad \frac{1}{2}\right]=a\ {}_2F_1\left[\begin{matrix}a+1,\ b\\ \frac{a+b+50}{2}\end{matrix};\quad \frac{1}{2}\right]-b\ {}_2F_1\left[\begin{matrix}a,\ b+1\\ \frac{a+b+50}{2}\end{matrix};\quad \frac{1}{2}\right]$$

Now involving the derived formula [Salahuddin et. al. p.12-41(8)], the summation formula is obtained.

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Notes

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Certain Indefinite Integrals Involving Harmonic Number

By Salahuddin
P.D.M College of Engineering, India

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GJSFR-F Classification : *MSC 2010: 37A45 , 14K20*

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Certain Indefinite Integrals Involving Harmonic Number

Salahuddin

Abstract- In this paper we have established certain indefinite integrals involving Harmonic Number. The results represent here are assume to be new.

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2010 MSC NO: 33C05, 33C45, 33C15, 33D50, 33D60

I. Introduction and Preliminaries

a) Harmonic Number

The n^{th} harmonic number is the sum of the reciprocals of the first n natural numbers:

$$H_n = \sum_{k=1}^{n} \frac{1}{k} \tag{1.1}$$

Harmonic numbers were studied in antiquity and are important in various branches of number theory. They are sometimes loosely termed harmonic series, are closely related to the Riemann zeta function, and appear in various expressions for various special functions.
An integral representation is given by Euler

$$H_n = \int_0^1 \frac{1-x^n}{1-x} dx \tag{1.2}$$

The equality above is obvious by the simple algebraic identity below

$$\frac{1-x^n}{1-x} = 1 + x + \ldots\ldots + x^n \tag{1.3}$$

An elegant combinatorial expression can be obtained for H_n using the simple integral transform $x = 1 - u$:

$$H_n = \int_0^1 \frac{1-x^n}{1-x} = -\int_1^0 \frac{1-(1-u)^n}{u} du = \int_0^1 \frac{1-(1-u)^n}{u} du$$

$$= \int_0^1 \left[\sum_{k=1}^{n} (-1)^{k-1} \binom{n}{k} u^{k-1} \right] du$$

$$= \sum_{k=1}^{n} (-1)^{k-1} \binom{n}{k} \int_0^1 u^{k-1} du$$

Author: *P.D.M College of Engineering, Bahadurgarh, Haryana, India. e-mails: vsludn@gmail.com, sludn@yahoo.com*

b) Generalized Hypergeometric Functions

A generalized hypergeometric function ${}_pF_q(a_1, ...a_p; b_1, ...b_q; z)$ is a function which can be defined in the form of a hypergeometric series, i.e., a series for which the ratio of successive terms can be written

$$\frac{c_{k+1}}{c_k} = \frac{P(k)}{Q(k)} = \frac{(k+a_1)(k+a_2)...(k+a_p)}{(k+b_1)(K+b_2)...(k+b_q)(k+1)}\ z. \tag{1.5}$$

Where $k+1$ in the denominator is present for historical reasons of notation, and the resulting generalized hypergeometric function is written

$${}_pF_q\left[\begin{array}{ccc} a_1, a_2, \cdots, a_p & ; & \\ & & z \\ b_1, b_2, \cdots, b_q & ; & \end{array}\right] = \sum_{k=0}^{\infty} \frac{(a_1)_k (a_2)_k \cdots (a_p)_k z^k}{(b_1)_k (b_2)_k \cdots (b_q)_k k!} \tag{1.6}$$

or

$${}_pF_q\left[\begin{array}{ccc} (a_p) & ; & \\ & & z \\ (b_q) & ; & \end{array}\right] \equiv {}_pF_q\left[\begin{array}{ccc} (a_j)_{j=1}^{p} & ; & \\ & & z \\ (b_j)_{j=1}^{q} & ; & \end{array}\right] = \sum_{k=0}^{\infty} \frac{((a_p))_k z^k}{((b_q))_k k!} \tag{1.7}$$

where the parameters $b_1, b_2, \cdots, b_q$ are neither zero nor negative integers and $p,\ q$ are non-negative integers.

The ${}_pF_q$ series converges for all finite z if $p \leq q$, converges for $\mid z \mid < 1$ if $p \neq q+1$, diverges for all z , $z \neq 0$ if $p > q+1$.

The ${}_pF_q$ series absolutely converges for $\mid z \mid = 1$ if $R(\zeta) < 0$, conditionally converges for $\mid z \mid = 1, z \neq 0$ if $0 \leq R(\zeta) < 1$, diverges for $\mid z \mid = 1$, if $1 \leq R(\zeta)$, $\zeta = \sum_{i=1}^{p} a_i - \sum_{i=0}^{q} b_i$.

The function ${}_2F_1(a, b; c; z)$ corresponding to $p = 2, q = 1$, is the first hypergeometric function to be studied (and, in general, arises the most frequently in physical problems), and so is frequently known as "the" hypergeometric equation or, more explicitly, Gauss's hypergeometric function (Gauss 1812, Barnes 1908). To confuse matters even more, the term "hypergeometric function" is less commonly used to mean closed form, and "hypergeometric series" is sometimes used to mean hypergeometric function.

The hypergeometric functions are solutions of Gaussian hypergeometric linear differential equation of second order

$$z(1-z)y'' + [c - (a+b+1)z]y' - aby = 0 \tag{1.8}$$

The solution of this equation is

$$y = A_0\Big[1 + \frac{ab}{1!\ c}z + \frac{a(a+1)b(b+1)}{2!\ c(c+1)}z^2 + \cdots\cdots\Big] \tag{1.9}$$

This is the so-called regular solution,denoted

$${}_2F_1(a, b; c; z) = \Big[1 + \frac{ab}{1!\ c}z + \frac{a(a+1)b(b+1)}{2!\ c(c+1)}z^2 + \cdots\cdots\Big] = \sum_{k=0}^{\infty} \frac{(a)_k\ (b)_k z^k}{(c)_k k!} \tag{1.10}$$

which converges if c is not a negative integer for all of $\mid z \mid < 1$ and on the unit circle $\mid z \mid = 1$ if $R(c-a-b) > 0$.

It is known as Gauss hypergeometric function in terms of Pochhammer symbol $(a)_k$ or generalized factorial function.

Many of the common mathematical functions can be expressed in terms of the hypergeometric function, or as limiting cases of it. Some typical examples are

$$(1-z)^{-a} = z\ {}_2F_1(1,1;2;-z) \tag{1.11}$$

$$\sin^{-1} z = z\ {}_2F_1(\frac{1}{2},\frac{1}{2};\frac{3}{2};z^2) \tag{1.12}$$

Notes

The special case of (1.3.4) when $a = c$ and $b = 1$, or $a = 1$ and $b = c$, yields the elementary geometric series

$$\sum_{n=0}^{\infty} z^n = 1 + z + z^2 + z^3 + \cdots + z^n + \cdots \tag{1.13}$$

Hence the term "Hypergeometric" is given. The term hypergeometric was first used by Wallis in his work "Arithmetrica Infinitorum". Hypergeometric series or more precisely Gauss series is due to Carl Friedrich Gauss(1777-1855) who in year 1812 introduced and studied this series in his thesis presented at Gottingen and gave the F-notation for it.

Here z is a real or complex variable. If c is zero or negative integer, the series (1.10) does not exist and hence the function ${}_2F_1(a,b;\ c;\ z)$ is not defined unless one of the parameters a or b is also a negative integer such that $-c < -a$. If either of the parameters a or b is a negative integer, say $-m$ then in this case (1.10) reduce to the hypergeometric polynomial defined as

$${}_2F_1(-m,b;\ c;\ z) = \sum_{n=0}^{m} \frac{(-m)_n (b)_n\, z^n}{(c)_n\, n!} \tag{1.14}$$

c) Hypergeometric Function of Second Kind

$$G(a,b;\ c;\ z) = \frac{\Gamma(1-c)}{\Gamma(a-c+1)\,\Gamma(b-c+1)} \times {}_2F_1\left[\begin{array}{ccc} a,\ b & ; & \\ & & z \\ c & ; & \end{array}\right] + \\ + \frac{\Gamma(c-1)\, z^{(1-c)}}{\Gamma(a)\,\Gamma(b)} \times {}_2F_1\left[\begin{array}{ccc} 1+a-c,\ 1+b-c & ; & \\ & & z \\ 2-c & ; & \end{array}\right] \tag{1.15}$$

where $c \neq 0, \pm 1, \pm 2, \ldots$

$$G(a,b;\ c;\ z) = z^{(1-c)}\, G(1+a-c, 1+b-c;\ 2-c;\ z) \tag{1.16}$$

Each of the following functions is a solution of differential equation (1.8).

A system of two linearly independent solutions of differential equation (1.8) in

the vicinity of the singular point $z = 0, 1$ and ∞ are given by

$$w_1^{(0)}(z) = {}_2F_1\left[\begin{array}{ccc} a,\ b & ; & \\ & & z \\ c & ; & \end{array}\right]$$

$$w_1^{(1)}(z) = {}_2F_1\left[\begin{array}{ccc} a,\ b & ; & \\ & & 1-z \\ 1+a+b-c & ; & \end{array}\right] \tag{1.17}$$

$$w_2^{(0)}(z) = z^{(1-c)}\,{}_2F_1\left[\begin{array}{ccc} 1+a-c,\,1+b-c & ; & \\ & & z \\ 2-c & ; & \end{array}\right]$$

$$w_2^{(1)}(z) = (1-z)^{(c-a-b)}\,{}_2F_1\left[\begin{array}{ccc} c-a,\,c-b & ; & \\ & & 1-z \\ 1+c-a-b & ; & \end{array}\right] \tag{1.18}$$

$$w_1^{(\infty)}(z) = (-z)^{-a}\,{}_2F_1\left[\begin{array}{ccc} a,\,1+a-c & ; & \\ & & \frac{1}{z} \\ 1+a-b & ; & \end{array}\right]$$

$$w_2^{(\infty)}(z) = (-z)^{-b}\,{}_2F_1\left[\begin{array}{ccc} 1+b-c,\,b & ; & \\ & & \frac{1}{z} \\ 1+b-a & ; & \end{array}\right] \tag{1.19}$$

where $c \neq 0, \pm1, \pm2, \ldots$; $(c-a-b)$ and $(a-b)$ are not integers.

The equation (1.8) is also denoted by

$${}_2F_1\left[\begin{array}{ccc} a,\,b & ; & \\ & & z \\ c & ; & \end{array}\right] = \sum_{m=0}^{\infty} \frac{(a)_m (b)_m\, z^m}{(c)_m\, m!}$$

$$= 1 + \frac{a\,b\,z}{c} + \frac{a\,(a+1)\,b\,(b+1)\,z^2}{c\,(c+1)\,2!} +$$

$$+ \frac{a\,(a+1)\,(a+2)\,b\,(b+1)\,(b+2)\,z^3}{c\,(c+1)\,(c+2)\,3!} + \cdots + \text{ad inf.} \tag{1.20}$$

It is convergent for $|z| < 1$.

Note:

$${}_2F_1\left[\begin{array}{ccc} a,\,b & ; & \\ & & 0 \\ c & ; & \end{array}\right] = {}_2F_1\left[\begin{array}{ccc} 0,\,b & ; & \\ & & z \\ c & ; & \end{array}\right] = 1 \tag{1.21}$$

$$(1-z)^{-a} = \sum_{r=0}^{\infty} \frac{(a)_r\, z^r}{r!} = {}_1F_0\left[\begin{array}{ccc} a & ; & \\ & & z \\ \text{—} & ; & \end{array}\right];\ |z| < 1 \tag{1.22}$$

d) Generalized Ordinary Hypergeometric Function of One Variable

The generalized Gaussian hypergeometric function of one variable is defined as follows

$${}_AF_B\left[\begin{array}{ccc} a_1,\,a_2,\,a_3,\ldots,a_A & ; & \\ & & z \\ b_1,\,b_2,\,b_3,\ldots,b_B & ; & \end{array}\right] = \sum_{n=0}^{\infty} \frac{(a_1)_n\,(a_2)_n\,(a_3)_n \cdots (a_A)_n\, z^n}{(b_1)_n\,(b_2)_n\,(b_3)_n \cdots (b_B)_n\, n!} \tag{1.23}$$

$$\text{or,} \qquad {}_AF_B\left[\begin{array}{ccc} (a_A) & ; & \\ & & z \\ (b_B) & ; & \end{array}\right] = \sum_{n=0}^{\infty} \frac{[(a_A)]_n\, z^n}{[(b_B)]_n\, n!} \tag{1.24}$$

where for the sake of convenience (in the contracted notation), (a_A) denotes thearray of "A" number of parameters given by $a_1, a_2, a_3, \ldots, a_A$. The denominatorparameters are neither zero nor negative integers. The numerator parameters may be zero and negative integers. A and

B are positive integers or zero. Empty sum is to be interpreted as zero and empty product as unity.

$$\sum_{n=a}^{b} \text{ and } \prod_{n=a}^{b} \text{ are empty if } b < a.$$

$$[(a_A)]_{-n} = \frac{(-1)^{nA}}{[1-(a_A)]_n} \tag{1.25}$$

$$[(a_A)]_n = (a_1)_n(a_2)_n(a_3)_n \cdots (a_A)_n = \prod_{m=1}^{A} (a_m)_n = \prod_{m=1}^{A} \frac{\Gamma(a_m+n)}{\Gamma(a_m)} \tag{1.26}$$

where a_1, a_2, a_3, …, a_A; b_1, b_2, b_3, …, b_B and z may be real and complex numbers.

$$ {}_3F_2\left[\begin{array}{ccc} a,\, b,\, 1 & ; & \\ & & z \\ c,\, 2 & ; & \end{array}\right] = \frac{(c-1)}{(a-1)(b-1)\,z} \times$$

$$\times\left\{ {}_2F_1\left[\begin{array}{ccc} a-1,\, b-1 & ; & \\ & & z \\ c-1 & ; & \end{array}\right] - 1\right\} \tag{1.27}$$

The convergence conditions of ${}_AF_B$ are given below

Suppose that numerator parameters are neither zero nor negative integers (otherwise question of convergence will not arise).

(i) If $A \leq B$, then series ${}_AF_B$ is always convergent for all finite values of z(real or complex) i.e., $|z| < \infty$.

(ii) If $A = B+1$ and $|z| < 1$, then series ${}_AF_B$ is convergent.

(iii) If $A = B+1$ and $|z| > 1$, then series ${}_AF_B$ is divergent.

(iv) If $A = B+1$ and $|z| = 1$, then series ${}_AF_B$ is absolutely convergent, when

$$\mathrm{Re}\left\{\sum_{m=1}^{B} b_m - \sum_{n=1}^{A} a_n\right\} > 0$$

(v) If $A = B+1$ and $z = 1$, then series ${}_AF_B$ is convergent, when

$$\mathrm{Re}\left\{\sum_{m=1}^{B} b_m - \sum_{n=1}^{A} a_n\right\} > 0$$

(vi) If $A = B+1$ and $z = 1$, then series ${}_AF_B$ is divergent, when

$$\mathrm{Re}\left\{\sum_{m=1}^{B} b_m - \sum_{n=1}^{A} a_n\right\} \leq 0$$

(vii) If $A = B+1$ and $z = -1$, then series ${}_AF_B$ is convergent, when

$$\mathrm{Re}\left\{\sum_{m=1}^{B} b_m - \sum_{n=1}^{A} a_n\right\} > -1$$

(viii) If $A = B+1$ and $|z| = 1$, but $z \neq 1$, then series ${}_AF_B$ is conditionally convergent, when

$$-1 < \mathrm{Re}\Big\{\sum_{m=1}^{B} b_m - \sum_{n=1}^{A} a_n\Big\} \leq 0$$

(ix) If $A > B+1$, then series ${}_AF_B$ is convergent, when $z = 0$.

(x) If $A = B+1$ and $|z| \geq 1$, then it is defined as an analytic continuation of this series.

(xi) If $A = B+1$ and $|z| = 1$, then series ${}_AF_B$ is divergent, when

$$\mathrm{Re}\Big\{\sum_{m=1}^{B} b_m - \sum_{n=1}^{A} a_n\Big\} \leq -1$$

(xii) If $A > B+1$, then a meaningful independent attempts were made to define MacRobert's E-function, Meijer's G-function, Fox's H-function and its related functions.

(xiii) If one or more of the numerator parameters are zero or negative integers, then series ${}_AF_B$ terminates for all finite values of z i.e., ${}_AF_B$ will be a hypergeometric polynomial and the question of convergence does not enter the discussion.

II. Main Indefinite Integrals

$$\int \frac{\cosh x\ H_1^{(x)}}{\sqrt{1-\sin x}}\,\mathrm{dx} = \frac{1}{\sqrt{1-\sin x}}\Big(\frac{3}{5}-\frac{\iota}{5}\Big)\Big(\cos\frac{x}{2}-\sin\frac{x}{2}\Big)\Big\{\cosh\Big(1+\frac{\iota}{2}\Big)x-\sinh\Big(1+\frac{\iota}{2}\Big)x\Big\}\times$$
$$\times\Big[(\sin x-\iota\cos x)\ {}_2F_1\Big(\frac{1}{2}+\iota,1;\frac{3}{2}+\iota;\sin x-\iota\cos x\Big)-\Big(\sinh(2x)+\cosh(2x)\Big)\times$$
$$\times{}_2F_1\Big(-\frac{1}{2}-\iota,1;\frac{1}{2}-\iota;\sin x-\iota\cos x\Big)+\Big(\sinh(2x)+\cosh(2x)\Big)\Big]+Constant \tag{2.1}$$

$$\int \frac{\sinh x\ H_1^{(x)}}{\sqrt{1-\sin x}}\,\mathrm{dx} = \frac{1}{\sqrt{1-\sin x}}\Big(\frac{3}{5}-\frac{\iota}{5}\Big)\Big(\cos\frac{x}{2}-\sin\frac{x}{2}\Big)\Big\{\cosh\Big(1+\frac{\iota}{2}\Big)x-\sinh\Big(1+\frac{\iota}{2}\Big)x\Big\}\times$$
$$\times\Big[(\iota\sin x+\iota\cos x)\ {}_2F_1\Big(\frac{1}{2}+\iota,1;\frac{3}{2}+\iota;\sin x-\iota\cos x\Big)-\Big(\sinh(2x)+\cosh(2x)\Big)\times$$
$$\times{}_2F_1\Big(-\frac{1}{2}-\iota,1;\frac{1}{2}-\iota;\sin x-\iota\cos x\Big)+\Big(\sinh(2x)+\cosh(2x)\Big)\Big]+Constant \tag{2.2}$$

$$\int \frac{\sinh x\ H_1^{(x)}}{\sqrt{1-\cos x}}\,\mathrm{dx} = -\frac{1}{5\sqrt{1-\cos x}}\ 2\ e^{(-1+\frac{\iota}{2})x}\Big[(1+2\iota)e^{2x}{}_2F_1\Big(\frac{1}{2}-\iota,1;\frac{3}{2}-\iota;e^{\iota x}\Big)-$$
$$-(1-2\iota){}_2F_1\Big(\frac{1}{2}+\iota,1;\frac{3}{2}+\iota;e^{\iota x}\Big)\Big]\sin\frac{x}{2}+Constant \tag{2.3}$$

$$\int \frac{\cosh x\ H_1^{(x)}}{\sqrt{1-\cos x}}\,\mathrm{dx} = -\frac{1}{5\sqrt{1-\cos x}}\ 2\ e^{(-1+\frac{\iota}{2})x}\Big[(1+2\iota)e^{2x}{}_2F_1\Big(\frac{1}{2}-\iota,1;\frac{3}{2}-\iota;e^{\iota x}\Big)+$$
$$+(1-2\iota){}_2F_1\Big(\frac{1}{2}+\iota,1;\frac{3}{2}+\iota;e^{\iota x}\Big)\Big]\sin\frac{x}{2}+Constant \tag{2.4}$$

$$\int \frac{\cos x\ H_1^{(x)}}{\sqrt{1-\cosh x}}\,\mathrm{dx} = -\frac{1}{5\sqrt{1-\cosh x}}\ e^{-\iota x}(e^x-1)\Big[(1+2\iota){}_2F_1\Big(\frac{1}{2}-\iota,1;\frac{3}{2}-\iota;e^x\Big)+$$
$$+(1-2\iota)e^{2\iota x}{}_2F_1\Big(\frac{1}{2}+\iota,1;\frac{3}{2}+\iota;e^x\Big)\Big]+Constant \tag{2.5}$$

Notes

$$\int \frac{\sin x\ H_1^{(x)}}{\sqrt{1-\cosh x}}\,\mathrm{dx} = \frac{1}{5\sqrt{1-\cosh x}}\ e^{-\iota x}(e^x-1)\Bigg[(2-\iota){}_2F_1\left(\frac{1}{2}-\iota,1;\frac{3}{2}-\iota;e^x\right)+$$
$$+(2+\iota)e^{2\iota x}{}_2F_1\left(\frac{1}{2}+\iota,1;\frac{3}{2}+\iota;e^x\right)\Bigg]+Constant \tag{2.6}$$

$$\int \frac{\sin x\ H_2^{(x)}}{\sqrt{1-\cosh x}}\,\mathrm{dx} = \frac{1}{(25+5\log^2 4-10\log 4)\sqrt{1-\cosh x}}\times$$
$$\times\Bigg[2^{-x}e^{-\iota x}(e^x-1)\Bigg\{(2-\iota)2^x(5+4\log^2 2-4\log 2){}_2F_1\left(\frac{1}{2}-\iota,1;\frac{3}{2}-\iota;e^x\right)+$$
$$+(2+\iota)\Bigg(2^x e^{2\iota x}(5+4\log^2 2-4\log 2){}_2F_1\left(\frac{1}{2}+\iota,1;\frac{3}{2}+\iota;e^x\right)-$$
$$-(1+2\iota)e^{2\iota x}(\log 4-1+2\iota){}_2F_1\left(1,\left(\frac{1}{2}+\iota\right)-\log 2;\left(\frac{3}{2}+\iota\right)-\log 2;e^x\right)+$$
$$+\Big((3-4\iota)+(2+4\iota)\log 2\Big){}_2F_1\left(1,\left(\frac{1}{2}-\iota\right)-\log 2;\left(\frac{3}{2}-\iota\right)-\log 2;e^x\right)\Bigg)\Bigg\}\Bigg]+Constant \tag{2.7}$$

$$\int \frac{\sin x\ H_3^{(x)}}{\sqrt{1-\cosh x}}\,\mathrm{dx} = -\frac{1}{5(2^x+3^x+6^x)\sqrt{1-\cosh x}}\Bigg[\iota 2^{x+1}3^x(2^{-x}+3^{-x}+1)\sinh\left(\frac{x}{2}\right)\times$$
$$\times\Bigg\{\frac{1}{(\log 9+(-1+2\iota))}\ \Bigg((1+2\iota)e^{(\frac{1}{2}-\iota)x}{}_2F_1\left(\frac{1}{2}-\iota,1;\frac{3}{2}-\iota;e^x\right)-$$
$$-(1-2\iota)e^{(\frac{1}{2}+\iota)x}{}_2F_1\left(\frac{1}{2}+\iota,1;\frac{3}{2}+\iota;e^x\right)-\Bigg(5e^{-\frac{1}{2}x(\log 9+(-1+2\iota)}\times$$
$$\times{}_2F_1\left(1,\left(\frac{1}{2}-\iota\right)-\log 3;\left(\frac{3}{2}-\iota\right)-\log 3;e^x\right)\Bigg)\Bigg)+$$
$$+\frac{5\times 3^{-x}e^{(\frac{1}{2}+\iota)}x{}_2F_1\left(1,\left(\frac{1}{2}+\iota\right)-\log 3;\left(\frac{3}{2}+\iota\right)-\log 3;e^x\right)}{(\log 9+(-1-2\iota))}-$$
$$-\frac{5e^{-\frac{1}{2}x(\log 4+(-1+2\iota))}{}_2F_1\left(1,\left(\frac{1}{2}-\iota\right)-\log 2;\left(\frac{3}{2}-\iota\right)-\log 2;e^x\right)}{(\log 4+(-1+2\iota))}+$$
$$+\frac{5\times 2^{-x}e^{(\frac{1}{2}+\iota)}x{}_2F_1\left(1,\left(\frac{1}{2}+\iota\right)-\log 2;\left(\frac{3}{2}+\iota\right)-\log 2;e^x\right)}{(\log 4+(-1-2\iota))}\Bigg\}\Bigg]+Constant \tag{2.8}$$

$$\int \frac{\cos x\ H_2^{(x)}}{\sqrt{1-\cosh x}}\,\mathrm{dx} = \frac{1}{(25+5\log^2 4-10\log 4)\sqrt{1-\cosh x}}\times$$
$$\times\Bigg[2^{1-x}e^{(\frac{1}{2}-\iota)x}\sinh\frac{x}{2}\Bigg\{(1+2\iota)2^x(5+4\log^2 2-4\log 2){}_2F_1\left(\frac{1}{2}-\iota,1;\frac{3}{2}-\iota;e^x\right)+$$
$$+(1-2\iota)2^x e^{2\iota x}(5+4\log^2 2-4\log 2){}_2F_1\left(\frac{1}{2}+\iota,1;\frac{3}{2}+\iota;e^x\right)-$$

$$-5(\log 4 - 1 - 2\iota)_2F_1\left(1, \left(\frac{1}{2} - \iota\right) - \log 2; \left(\frac{3}{2} - \iota\right) - \log 2; e^x\right) +$$

$$+e^{2\iota x}(\log 4 - 1 + 2\iota)_2F_1\left(1, \left(\frac{1}{2} + \iota\right) - \log 2; \left(\frac{3}{2} + \iota\right) - \log 2; e^x\right)\Bigg\}\Bigg] + Constant \qquad (2.9)$$

III. Derivation of the Integrals

Involving the same parallel method of ref[4] , one can derive the integrals.

IV. Applications

The integrals which are presented here are very special integrals.These are applied in the field of engineering and other allied sciences.

V. Conclusion

In our work we have established certain indefinite integrals involving Harmonic Number and Hypergeometric function . However, one can establish such type of integrals which are very useful for different field of engineering and sciences by involving these integrals.Thus we can only hope that the development presented in this work will stimulate further interest and research in this important area of classical special functions.

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Notes

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Study of Viscous Flow through Permeable Walls with Expanding or Contracting Gaps using Laplace Transform and HPM

By Vivek Kumar Sharma & Aisha Rafi
Jagan Nath University, India

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Keywords: permeation reynolds number, homotopy perturbation method (HPM), differential transformation method (DTM), optimal homotopy analysis method (OHAM).

I. Introduction

Studies of fluid transport in biological organisms often concern the flow of a particular fluid inside an expanding or contracting vessel with permeable walls. For a valve vessel exhibiting deformable boundaries, alternating wall contractions produce the effect of a physiological pump. The possibility of emulating peristaltic motion by successive wall contractions and expansions is described by Uchida and Aoki (1977) and Goto and Uchida (1990). Since fluctuating stresses can influence the responsiveness of endothelial cells (Nerem and Levesque, 1987), their accurate determination in a pulsating environment may be appropriate of a number of investigations concerned with the characterization of atherosclerosis (see Dewey et al., 1981; Levesque and Nerem, 1985; Levesque et al., 1989). Considering that abnormalities in fluctuating stresses have been associated with this disease (Sprague et al., 1987), identification of the role of flow dynamics can be meaningful in predicting pulsatory flow attributes. Such results could be used toward a proper characterization of mechanically assisted respiration (Drazen et al., 1984), hemodialysis in artificial kidneys (Wang, 1971) and peristaltic transport (Fung and Yih, 1968). Majdalani and Zhou studied moderate to large injection and suction driven channel flows with expanding or contracting walls. Using perturbations in cross-flow Reynolds number Re, the resulting equation is solved both numerically and analytically. Boutros *et al.* (2003) studied the solution of the Navier-Stokes equations which described the unsteady incompressible laminar flow in a semi-infinite porous circular pipe with injection or suction through the pipe wall whose radius varies with time. Boutros, Y.Z. and M.B. Abd-el-Malek, N.A.Badran and H.S. Hassan,(2006). Lie-group method for unsteady flows in a semi-infinite expanding or contracting pipe with injection or suction through a porous wall. J. Comput. Appl. Math. Ganji, D.D., H.R. Ashory Nezhad and A. Hasanpour,(2011). Effect of variable viscosity and viscous dissipation on the Hagen-Poiseuille flow and entropy generation. Numerical Methods for Partial Differential Equations.

The equations of continuity, momentum are transformed into ordinary differential equations using Similarity transformation and solved using Laplace transform and Homotopy Perturbation Method.

Author α σ : Department of Mathematics, Jagan Nath University, Jaipur. e-mail: aisharafi.math@udml.ac.in

II. Formulation of the Problem

Consider the laminar, isothermal and incompressible flow between two permeable walls that enable the fluid to enter or exit during successive expansions or contractions. One side of the cross section, representing the distance between the walls is taken to be smaller than the other two. Both walls are assumed to have equal permeability and to expand uniformly at a time dependent rate a^*. Furthermore, the origin $x^* = 0$ is assumed to be the center of the channel. This enables us to assume flow symmetry about $x^* = 0$. Under these assumptions, the equations for continuity and motion become

$$\frac{\partial u^*}{\partial x^*} + \frac{\partial v^*}{\partial y^*} = 0, \tag{1}$$

$$\frac{\partial u^*}{\partial t} + u^* \frac{\partial u^*}{\partial x^*} + v^* \frac{\partial u^*}{\partial y^*} = -\frac{1}{\rho}\frac{\partial p^*}{\partial x^*} + \upsilon\left(\frac{\partial^2 u^*}{\partial x^{*2}} + \frac{\partial^2 u^*}{\partial y^{*2}}\right), \tag{2}$$

$$\frac{\partial v^*}{\partial t} + u^* \frac{\partial v^*}{\partial x^*} + v^* \frac{\partial v^*}{\partial y^*} = -\frac{1}{\rho}\frac{\partial p^*}{\partial y^*} + \upsilon\left(\frac{\partial^2 v^*}{\partial x^{*2}} + \frac{\partial^2 v^*}{\partial y^{*2}}\right), \tag{3}$$

where u^*=velocity component in x^* direction, v^*=velocity component in y^* direction, p^*=dimensional pressure, ρ =density, υ=kinematic viscosity, t=time. The boundary conditions are:

$$\begin{aligned} &y^* = a(t): u^* = 0, v^* = -V_w = -\frac{a^*}{c}, \\ &y^* = 0: \quad \frac{\partial u^*}{\partial y^*} = 0, \qquad v^* = 0, \\ &x^* = 0: \qquad u^* = 0. \end{aligned} \tag{4}$$

The streams functions and mean flow can be introduced by putting:

$$\psi^* = \frac{\upsilon x^* f^*(y,t)}{a}, u^* = \frac{\upsilon x^* f_y^*}{a^2}, v^* = \frac{-\upsilon f^*(y,t)}{a}, y = \frac{y^*}{a}, f_y^* = \frac{\partial f^*}{\partial y}. \tag{5}$$

Substitution equation (15) into (14):

$$u_{y\cdot t}^* + u^* u_{y\cdot x\cdot}^* + v^* u_{y\cdot y\cdot}^* = \upsilon u_{y\cdot y\cdot y\cdot}^* \tag{6}$$

In order to solve equation (16) by chain rule:

$$f_{yyyy}^* + \alpha\left(y f_{yyy}^* + 3 f_{yy}^*\right) + f^* f_{yyy}^* - f_y^* f_{yy}^* - a^2 \upsilon^{-1} f_{yyt}^* = 0, \tag{7}$$

where $\alpha(t) = \frac{a^* a}{y}$ is the non dimensional wall dilation rate defined positive for expansion.

From we have

$$f_{yyy}^* + \alpha\left(y f_{yy}^* + 2 f_y^*\right) + f^* f_{yy}^* - f_y^* f_y^* - a^2 \upsilon^{-1} f_{yt}^* = \lambda, \qquad \lambda \neq \lambda(y).$$

Boundary conditions given by equation (14) transformed into

$$f_{yy}^*(0) = 0, \qquad f^*(0) = 0, \qquad f^*(1) = Re, \qquad f_y^*(1) = 0,$$

where Re is the permeation Reynolds number defined by $Re \equiv \frac{a v_w}{\upsilon} > 0$ for injection. This number happens to be a small quantity in many biological applications

$$\begin{aligned} &\text{at } y = 0: f^* = 0, \ f_{yy}^* = 0, \\ &\text{at } y = 1: f^* = Re, \ f_y^* = 0. \end{aligned} \tag{8}$$

Equation (16),(17),(18) can be normalized by putting:

$$\psi = \frac{\varphi^*}{aa\cdot}, u = \frac{u^*}{a\cdot}, v = \frac{v^*}{a}, f = \frac{f^*}{Re},$$
$$\psi = \frac{xf}{c}, u = \frac{xf'}{c}, v = \frac{-f}{c}, c = \frac{\alpha}{Re}. \tag{9}$$

And so:

$$f'''' + \alpha(yf''' + 3f'') + Reff''' - Ref'f'' = 0 \tag{10}$$

Notes

The boundary conditions are:

$$\begin{aligned} &\text{at} \quad y = 0: \quad f = 0, f'' = 0, \\ &\text{at} \quad y = 1: \quad f = 1, f' = 0. \end{aligned} \tag{11}$$

The resulting Equation (20) is the classic Berman's formula , with $\alpha = 0$ The governing boundary layer and thermal boundary layer equations (15) with the boundary conditions (21) are solved using Laplace transformation & Homotopy Perturbation Method. An equation (20) is non-linear coupled differential equation. To solve this equation we use the following Laplace transformation.

$$L[f(y)] = L(f'''' + \alpha(yf''' + 3f'') + Reff''' - Ref'f''), \tag{12}$$

$$L[f(y)] = \frac{a}{s^2} + \frac{b}{s^4} - \frac{1}{s^4}L[\alpha(yf''' + 3f'') + Re(f'f''' - f'f'')], \tag{13}$$

The inverse Laplace transform

$$f(y) = ay + \frac{by^3}{6} - L^{-1}\left[\frac{1}{s^4}L[\alpha(yf''' + 3f'') + Re(f'f''' - f'f'')]\right]. \tag{14}$$

Now applying the HPM

$$D(f,p) = (1-p)[L(f) - L(f_I)] + p\left[ay + \frac{by^3}{6} - L^{-1}\left[\frac{1}{s^4}L[\alpha(yf''' + 3f'') + Re(f'f''' - f'f'')]\right]\right] = 0, \tag{15}$$

With the following assumption

$$f = f_0 + pf_1 + p^2f_2 + \ldots \tag{16}$$

Using equation (26) into equation (25) and comparing the like powers of p, we get the zeoth order equation,

$$f_0 = ay + b\frac{y^3}{6}, \tag{17}$$

with the corresponding boundary conditions are of zeroth order equations are:

$$\begin{aligned} &\text{at} \quad y = 0: \quad f_0 = 0, f_0'' = 0, \\ &\text{at} \quad y = 1: \quad f_0 = 1, f_0' = 0. \end{aligned} \tag{18}$$

And first order equations are:

$$f_1 = -L^{-1}\left[\frac{1}{s^4}L[\alpha(yf_0''' + 3f_0'') + Re(f_0'f_0''' - f_0'f_0'')]\right], \tag{19}$$

With the corresponding boundary conditions are of first order equations are:

$$\begin{aligned} &\text{at} \quad y = 0: \quad f_1 = 0, f_1'' = 0, \\ &\text{at} \quad y = 1: \quad f_1 = 0, f_1' = 0. \end{aligned} \tag{20}$$

And second order equations are:

$$f_2 = -L^{-1}\left[\frac{1}{s^4}L[\alpha(yf_1''' + 3f_1'') + Re(f_1'f_1''' - f_1'f_1'')]\right], \tag{21}$$

With the corresponding boundary conditions are of first order equations are:

$$\begin{aligned} &\text{at} \quad y = 0: \quad f_2 = 0, f_2'' = 0, \\ &\text{at} \quad y = 1: \quad f_2 = 0, f_2' = 0. \end{aligned} \tag{22}$$

Solving equations with corresponding boundary conditions, the following functions can be obtained successively, by summing up the results, and $p \to 1$ we write the f($\boldsymbol{\eta}$) profile as:

$$f(y) = ay + b\frac{y^3}{6} - \left(\frac{b\alpha y^5}{120} + \frac{Re\ aby^4}{24} + \frac{Re\ b^2y^6}{720} - \frac{aby^5}{120} - \frac{b^2y^7}{1680}\right) + Re\ ab\alpha\left(\frac{y^6}{144} - \frac{y^7}{840}\right) + Re\ b^2\alpha\left(\frac{y^8}{5760} - \frac{y^9}{15120}\right) + \frac{b\alpha^2y^7}{210} + Re\left[Re^2a^2b^2\left(\frac{y^{11}}{1140480} - \frac{y^{10}}{72576} + \frac{5y^9}{72576} - \frac{y^8}{10080}\right) + Re^2ab^3\left(\frac{y^{13}}{9884160} - \frac{y^{12}}{712800} + \frac{29y^{11}}{57024} - \frac{y^{10}}{604800}\right) - Re\ ab^2\alpha\left(\frac{y^{11}}{142560} - \frac{y^{10}}{181440} - \frac{y^9}{6048}\right) + Re^2b^4\left(\frac{y^{15}}{314496000} - \frac{y^{14}}{5000000} + \frac{y^{13}}{8236800} - \frac{y^{12}}{8553600}\right) - Re\ b^3\alpha\left(\frac{y^{13}}{2471040} + \frac{y^{12}}{2851200} - \frac{y^{11}}{178200}\right) + b^2\alpha^2\left(\frac{y^{11}}{71280} - \frac{y^{10}}{15120}\right) - \frac{Re\ ab^3y^{10}}{181440}\right]. \tag{23}$$

III. Numerical Discussion and Conclusion

It is observed from Table 1 that the numerical values of f ′(y) in the present paper when α = 0, Re = 1 are in good agreement with results obtained by HPM, DTM and OHAM method. It is noted from Table 2 that the numerical values of f ′(y) in the present paper when α = 1, Re = 2 are in good agreement with results obtained by HPM, DTM and OHAM method.

From figure 1, 2 and 3, we observe that as α and Re increases, value of f(y) also increases. From figure 4,5 and 6 it is observed that when α and Re increase simultaneously, numerical value of f ′(y) decreases.

In this research, the HPM, and Laplace transform were successfully applied to find the analytical solution for two-dimensional viscous flow in a rectangular domain bounded by two moving porous walls. The accuracy of the methods is shown by the figures and tables clearly.

Table 1 : The HPM, DTM, OHAM and present paper solution results for f(y) when α = 0, Re = 1

Y	HPM	DTM	OHAM	Present Paper
0.0	0	0	0	0
0.2	0.337421	0.332018	00.378868	0.327289
0.4	0.628838	00.621875	0.692581	0.652286
0.5	0.746307	0.740259	0.809906	0.7897253
1	1	1	1	1

Table 2 : The HPM, DTM, OHAM and present paper solution results for f(y) when α = 1, Re = 2

Y	HPM	DTM	OHAM	Present Paper
0.0	0	0	0	0
0.2	0.314954	0.311636	0.337174	0.3699881
0.4	0.596412	0.591678	0.630506	0.657786
0.5	0.715375	0.710901	0.749366	0.766599
1	1	1	1	1

Notes

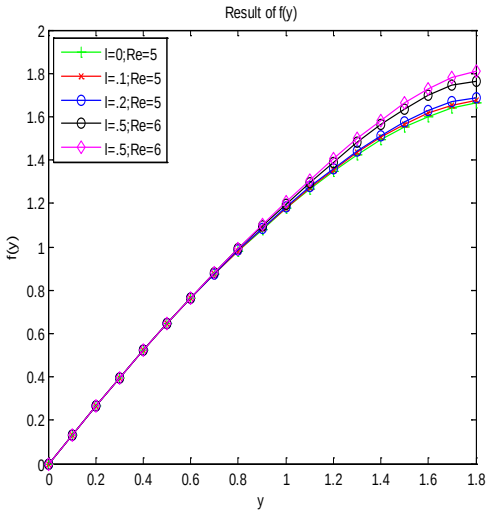

Figure 1

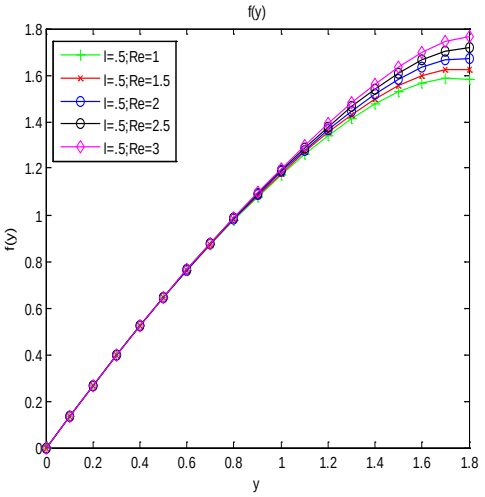

Figure 2

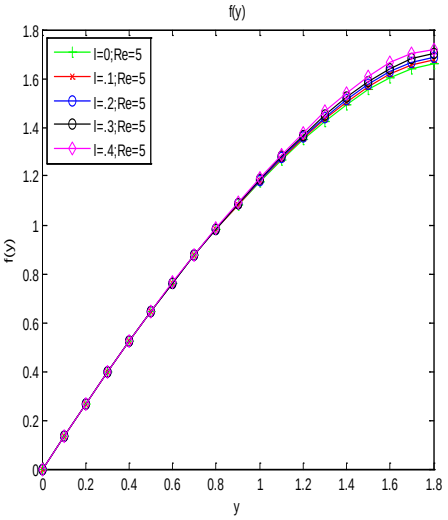

Figure 3

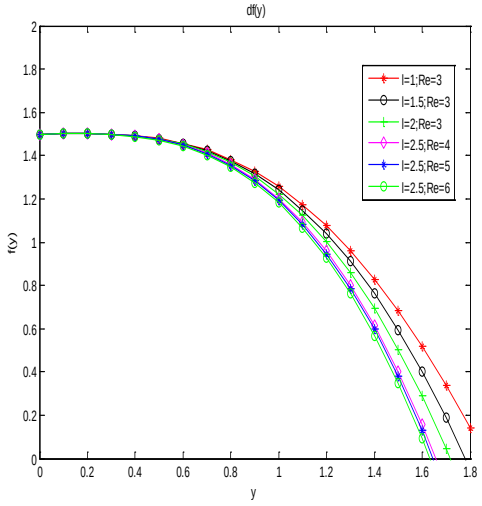

Figure 4

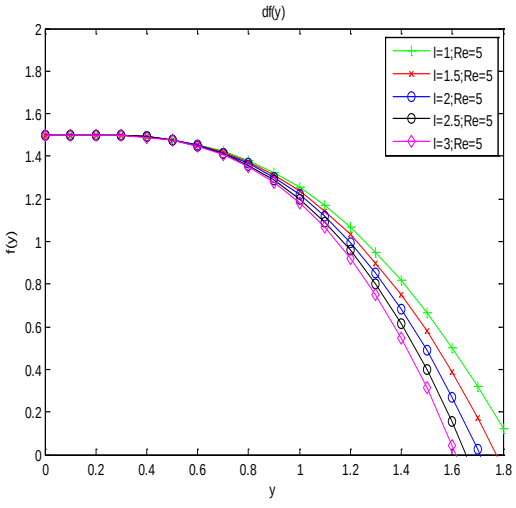

Figure 5

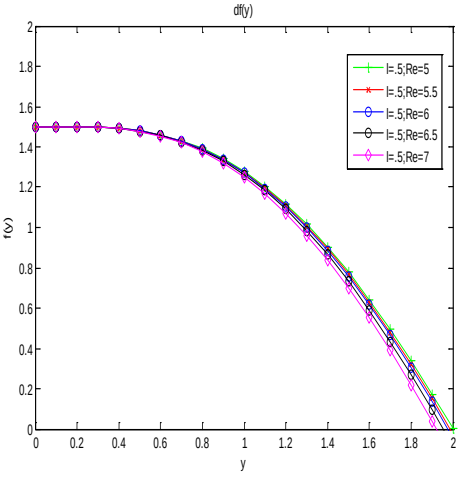

Figure 6

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Notes

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Boundary and Sign Problems of Parameters along with its Solutions of the Augmented Dickey-Fuller Test

By Shayla Naznin, Gowranga Kumar Paul & Ajit Kumar Majumder
Mawlana Bhashani Science and Technology University, Bangladesh

Abstract- Usual test of testing unit root such as Dickey-Fuller (DF), Augmented Dickey-Fuller (ADF), Phillips Perron etc ignores sign and boundary of parameters. In this paper, we demonstrated the ignorance of sign and boundary of parameters and consequences of this ignorance in estimation and testing by Monte Carlo Simulation. Our main objective is to develop a method to capture the non-stationarity keeping in mind the boundary and sign problem and to develop the restricted ADF test based on ESS using the constraint estimate of parameters. We compare the power properties of the usual ADF test and ADF test with restricted error sum of squares using the constraint estimate of parameters by Monte Carlo Simulation and we find that the proposed ADF test gives better result than the usual ADF test in terms of power properties.

Keywords: *stationarity test, simulation, restricted ADF test, power of the test, optimization.*

GJSFR-F Classification : *JEL Code: C12, C13, C15*

Strictly as per the compliance and regulations of :

Boundary and Sign Problems of Parameters along with its Solutions of the Augmented Dickey-Fuller Test

Shayla Naznin [α], Gowranga Kumar Paul [σ] & Ajit Kumar Majumder [ρ]

Abstract- Usual test of testing unit root such as Dickey-Fuller (DF), Augmented Dickey-Fuller (ADF), Phillips Perron etc ignores sign and boundary of parameters. In this paper, we demonstrated the ignorance of sign and boundary of parameters and consequences of this ignorance in estimation and testing by Monte Carlo Simulation. Our main objective is to develop a method to capture the non-stationarity keeping in mind the boundary and sign problem and to develop the restricted ADF test based on ESS using the constraint estimate of parameters. We compare the power properties of the usual ADF test and ADF test with restricted error sum of squares using the constraint estimate of parameters by Monte Carlo Simulation and we find that the proposed ADF test gives better result than the usual ADF test in terms of power properties.

Keywords: stationarity test, simulation, restricted ADF test, power of the test, optimization.

I. Introduction

In modeling time series econometrics, non-stationary test is very essential for analyzing the behavior of time series data and for advance research. Usually this can be tested by Dickey-Fuller, Augmented Dickey-Fuller, Phillips Perron etc. Almost all of the unit root test as well as the estimation of the model suffers from sign and boundary problem of the parameters. According to the assumption or analysis of the Dickey-Fuller test, $|\rho|<1$ or $-2<\delta<0$ of the time series models such as $Y_t=\rho Y_{t-1}+u_t$. Any estimated value of δ less than -2 or greater than 0 may results in invalid model. This invalid model can not be used for making decision regarding non-stationarity. To overcome this situation it is necessary to make suitable restrictions on the parameter. So our aim is to develop a model and estimates its parameters and check stationarity by using unit root test and to develop restricted testing approach based on error sum of square (ESS) of Augmented Dickey-Fuller test.

II. Problems and Motivations

In real world most of the time series data are non-stationary. But for our analysis purpose we assumed them stationary. Most of the financial time series data, such as share index, stock price, exchange rate, inflation rate, etc. often exhibit the phenomenon of non-stationarity. Non-stationary series leads to spurious regression and provides wrong results that misguide us (Brockwell and Davis,1996, Gujarati ,2003).In time series model, it is essential to identify correctly the non-stationarity of a time series with the aid of appropriate statistical tests. If we can not correctly identify the

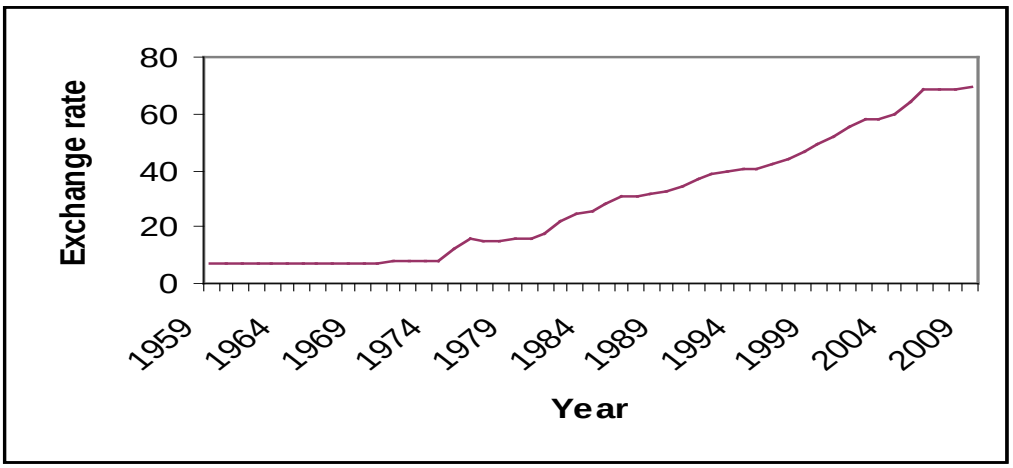
Author α σ : Lecturer, Department of Statistics, Mawlana Bhashani Science and Technology University.
Author ρ : Professor, Department of Statistics, Jahangirnagar University.

stationarity of the series, we will not be able to make better decision. If error terms are correlated, then Augmented Dickey-Fuller test is appropriate. The ADF test consists of estimating the following regression

$$\Delta y_t = \beta_0 + \beta_1 t + \delta y_{t-1} + \sum_{i=1}^{m} \alpha_i \Delta y_{t-i} + \varepsilon_t .$$

None of the tests such as Dickey-Fuller, Augmented Dickey-Fuller, Phillips-Perron unit root test etc can capture non-stationarity problem in all cases. For example, we consider some Bangladeshi time series data such as Exchange rate.

Figure 1 : Time series plot for exchange rate of Bangladesh



From the above graph we see that there is upward trend in exchange rate series. Since with the increase of time, mean Exchange rate is increasing and thus the graph guaranteed that the Exchange rate series is non-stationary.

The Dickey-Fuller test is estimated in three different forms such as random walk, random walk with drift, random walk with drift around a stochastic trend respectively. Consider the following model for Exchange rate series,

$\Delta Ex_t = 0.037741 Ex_{t-1}$ $\Delta Ex_t = 0.535546 + 0.025245 Ex_{t-1}$ $\Delta Ex_t = -0.38666 - 0.079t + 0.1518 Ex_{t-1}$

se =(0.005659) se=(0.331992) (0.00954) se=(0.42723) (0.03490) (0.0491)

τ =(2.6462) τ =(2.6462) τ =(3.091455)

From the above it is shown that the Exchange rate series is stationary. But from the graph we see that it is nonstationary. It happens because of Ignoring sign and boundary problem of parameter. This test suffers from a number of problems such as sign and boundary problem of parameter δ, $-2 < \delta < 0$ (Akter, 2009). Ignoring sign and boundary problem of parameter, the usual two-sided test is likely to be misleading. In this paper we will propose a method of tackle the boundary problem and compare the results with the existing tests in terms of power properties.

III. Objectives

Our main objective is to develop a method to capture the non-stationarity keeping in mind the boundary and sign problem and to develop the restricted ADF test based on ESS using the constraint estimate of parameters.

IV. Methodology

In the first stage we estimate the parameters by usual method such as least square method, maximum likelihood method. In the second stage we compare the power properties of the restricted ADF test based on ESS of constraint estimate of parameters by optimizing under the restriction.

V. Data Generation

Monte Carlo Simulation required from generated observations. In this section we demonstrated how to generate sequence of observations of the model $\Delta y_t = \beta_0 + \beta_1 t + \delta y_{t-1} + \sum_{i=1}^{m} \alpha_i \Delta y_{t-i} + u_t$ and in the same we generated observations of the newly proposed restricted test based on error sum of squares.

Notes

VI. Proposed Augmented Dickey-Fuller Test

There are some problems in usual unit root tests. In some cases, time series may follow strictly upward or downward trend. The responses increase (or decreases) with rate β for every time. In case of β is strictly positive or negative for such case the following model will be more appropriate.

$$\Delta y_t = \beta_0 + \beta_1 t + \delta y_{t-1} + \sum_{i=1}^{m} \alpha_i \Delta y_{t-i} + u_t \quad (1)$$

We impose some restrictions on the parameters. In case of upward or downward trended time series, the coefficient of time series is likely to be positive or negative respectively and ρ (autocorrelation coefficient) is bounded to lie between -1 to +1. Also the boundary problem of autocorrelation arises in testing co-integration. The autocorrelation is bounded, therefore the δ is bounded to be $-2 < \delta < 0$. In order to estimate the model we require constraint optimization subroutine. Appropriate modification is needed to overcome the testing problem. The most used least square method does not consider these restrictions on the parameters. For this reason the usual unrestricted test cannot capture the non-stationary for trend stationary series. We observe that the τ-statistic is positive, which indicate that δ is positive. But since $\delta = \rho - 1$, a positive δ would imply that $\rho > 1$ Hence, there is present uncertain unit root in the residual of two non-stationary series. If we want to estimate the model correctly we have to minimize the error sum of squares (ESS). Using equation (1) we get

Minimizing: ESS= $\sum_{t=0}^{T} \tilde{u}_t = \sum_{t=o}^{T} (\Delta y_t - \beta_0 - \beta_1 t - \delta y_{t-1} - \sum_{i=1}^{m} \alpha_i \Delta y_{t-i})^2$.

Subject to: $-2 < \tilde{\delta} < 0, \beta > 0 \, or \, \beta < 0.$

where, $\beta > 0$ means the series has an upward trend or $\beta < 0$ means the series has a downward trend.

Based on the optimized estimates, our proposed τ statistic is

$$\tilde{\tau} = \frac{\tilde{\delta}}{SE(\tilde{\delta}),}$$

where τ is the optimized τ statistic and $\tilde{\delta}, \tilde{\beta}$ optimized estimate of the parameters. The τ statistic follow the weighted mixture τ-distribution (Majumder, 1999).We expect this approach will give better result than all other methods with efficiency, consistency and in terms of power properties.

Table 1 : Estimated value of restricted parameter

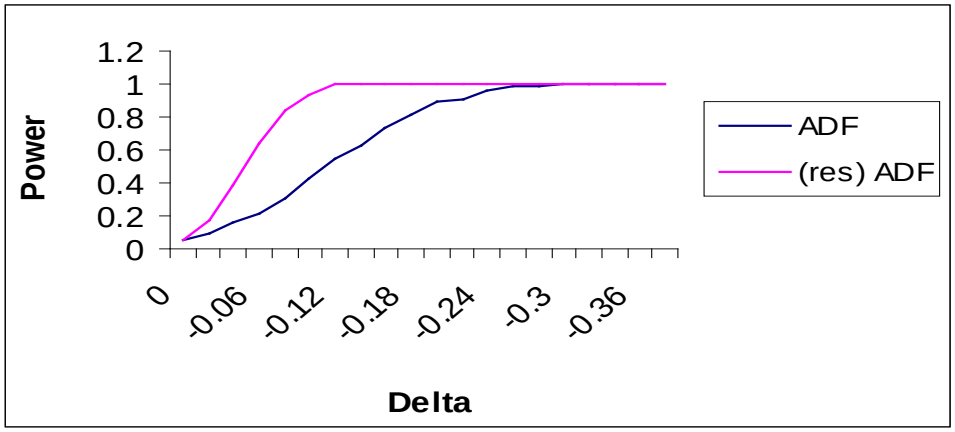
Estimated value (before optimization)	τ -value	True value	Estimated value (after optimization)	τ -value
0.0326	2.2176		-0.0492	-3.5142
0.0591	1.8411		-0.0233	-4.2983
0.0261	2.8681		-0.0457	-3.6560
-0.0342	-2.2352		-0.5917	-43.1898
0.0229	1.4135		-0.2602	-27.6809

In ADF test we test $\delta = 0$. Before optimization the estimated δ coefficient is positive but after optimization the estimated δ coefficient is negative and it is happen because of estimation problem. For overcoming this problem we have to use constraint optimization. The computed τ value should be more negative than the critical τ value. Since in general δ is expected to be negative. A large negative τ value is generally an indication of stationarity and we capture stationarity properly.

VII. Power Comparison

This section compares power of the existing Augmented Dickey-Fuller tests and the newly proposed restricted test based on ESS using the constraint estimate of parameters of Augmented Dickey-Fuller tests.

Figure 2 : Power curve of usual Augmented Dickey-Fuller test and the restricted Augmented Dickey-Fuller test.



From the above figure it is obvious that power of the newly proposed restricted Augmented Dickey-Fuller test based on restricted ESS gives better result than the usual Augmented Dickey-Fuller test.

Table 2 : Estimated parameters of the unconstraint and constraint Augmented Dickey-Fuller test with corresponding standard error.

Unconstraint parameter			Constraint parameter		
β_1	δ	α_1	β_1	δ	α_1
-0.0160	-0.3263	-0.0011	-0.0160	-0.0263	-0.0011
(0.0011)	(0.0147)	(0.0216)	(0.0010)	(0.0124)	(0.0213)
0.0915	-0.1984	0.1102	0.0000	-0.0457	0.0279
(0.0058)	(0.0176)	(0.0368)	(0.0052)	(0.0125)	(0.0361)
0.1187	-0.2459	0.1506	0.0000	0.0000	0.0890
(0.0018)	(0.0104)	(0.0268)	(0.0012)	(0.0106)	(0.0264)
-0.0974	-0.5917	0.4465	-0.0974	-0.5917	0.3455
(0.0017)	(0.0121)	(0.0143)	(0.0007)	(0.0137)	(0.0143)
-0.0494	-0.2611	-0.1153	-0.0510	-0.2602	-0.1158
(0.0003)	(0.0091)	(0.0147)	(0.0002)	(0.0094)	(0.0124)
-0.0292	-0.3808	0.0391	-0.0107	-0.0400	-0.0592
(0.0002)	(0.0053)	(0.0136)	(0.0001)	(0.0088)	(0.0101)
-0.0159	-0.2298	-0.1054	-0.0159	-0.2298	-0.1054
(0.0005)	(0.0062)	(0.0020)	(0.0005)	(0.0062)	(0.0020)
-0.0342	-0.2086	-0.3393	-0.0213	-0.1563	-0.2254
(0.0001)	(0.0042)	(0.0033)	(0.0001)	(0.0039)	(0.0032)
0.0495	-0.1037	-0.2723	0.0000	0.0238	-0.1374
(0.0001)	(0.0025)	(0.0023)	(0.0001)	(0.0020)	(0.0030)

∗ Number of the parenthesis is the Standard Error.

The above table shows the changes of the estimate of parameter of Augmented Dickey-Fuller with their corresponding standard errors when some prior information is given. We observe from the table that the restricted estimates are changed. The changes in the results of the parameters clearly demonstrate the potential of imposing this restriction in estimating parameters. It implies that parameters can be accurately estimated by using the obtained approach and is also proved effective when restriction is given.

Notes

We discuss the new approach of testing unit root for checking non-stationarity of the series considering the restriction on the parameter. We observe that this optimized method based on restricted ESS of Augmented Dickey-Fuller test. We found that this approach gives better result than all other methods with efficiency, consistency and in terms of power properties.

VIII. Applications

Any estimated value of δ less than -2 or greater than 0 may results in different solution. To overcome this situation it is necessary to impose suitable restrictions on the parameter during estimation. Our main focus is boundary problem $(-2 < \delta < 0)$ of the Augmented Dickey-Fuller test. When the value of δ is close to zero then our proposed estimation technique is likely to be appropriate.

IX. Conclusions

Due to boundary condition on parameters, usual estimates can result in different solution. ADF test suffers from such conditions. To overcome this problem we propose a constraint based ADF test based on error sum of squares. Monte Carlo Simulation study indicates that the power of the proposed ADF test gives better result than the usual ADF test.

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On Certain Subclass of Analytic Functions involving Generalized Derivative Operator

By T. Thulasiram, T.V. Sudharsan, K. Suchithra & M.K.Aouf
A.M.Jain College, India

Abstract- In this paper, a new subclass of analytic functions is introduced by means of a generalized derivative operator. Several properties like coefficient inequalities, growth and distortion theorems, convex linear combinations and radii of close-to-convexity, starlikeness and convexity of analytic functions belonging to the subclass are investigated.

Keywords and Phrases: *analytic function, starlike function, generalized derivative operator, coefficient inequalities, extreme points.*

GJSFR-F Classification : *MSC 2010: 11E45*

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[4] M.K. Aouf, H.M. Hossen and A.Y. Lashin, On certain families of analytic functions with negative coefficients, *Indian J. Pure Appl. Math.*, **31**(8) (2000), 999–1015.

On Certain Subclass of Analytic Functions involving Generalized Derivative Operator

T. Thulasiram [α], T.V. Sudharsan [σ], K. Suchithra [ρ] & M.K.Aouf [ω]

Abstract- In this paper, a new subclass of analytic functions is introduced by means of a generalized derivative operator. Several properties like coefficient inequalities, growth and distortion theorems, convex linear combinations and radii of close-to-convexity, starlikeness and convexity of analytic functions belonging to the subclass are investigated.

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AMS Mathematics Subject Classification: 30C45.

I. Introduction

Let $\mathcal{A}(k)$ be the class of functions $f(z)$, analytic in the unit disc $U = \{z : z \in \mathbb{C} \text{ and } |z| < 1\}$ given by

$$f(z) = z + \sum_{j=k+1}^{\infty} a_j z^j, \quad \text{for } k \in \mathbb{N} = \{1, 2, 3, \dots\}. \tag{1.1}$$

Let $\mathcal{S}(k)$ be the subclass of $\mathcal{A}(k)$ consisting of functions that are univalent in U. The class $\mathcal{A}(k)$ was studied by Sekine [8] and Aouf et al. [4].

For $f(z)$,$g(z)$ in $\mathcal{A}(1)$ of the form

$$f(z) = z + \sum_{j=2}^{\infty} a_j z^j, \tag{1.2}$$

and

$$g(z) = z + \sum_{j=2}^{\infty} b_j z^j, \tag{1.3}$$

Aouf et al. [5] considered the subclass $S(g, \lambda, \alpha, \beta)$ which satisfy the analytic characterisation

$$Re\left(\frac{z\,(f*g)'(z)}{(1-\lambda)\,(f*g)(z) + \lambda z\,(f*g)'(z)} - \alpha\right) > \beta \left|\frac{z\,(f*g)'(z)}{(1-\lambda)\,(f*g)(z) + \lambda z\,(f*g)'(z)} - 1\right|,$$

Author α ρ : Department of Mathematics A.M. Jain College, Chennai, India. e-mails: ltthulasiram@gmail.com, suchithravenkat@yahoo.co.in
Author σ : Department of Mathematics S.I.V.E.T College, Chennai, India. e-mail: tvsudharsan@rediffmail.com
Author ω: Mathematics Department, Faculty of Science, Mansoura, Egypt. e-mail: mkaouf127@yahoo.com

where $f*g$ is the Hadamard product of f and g. Further, the class $TS(g,\lambda,\alpha,\beta)$ defined by $TS(g,\lambda,\alpha,\beta) = S(g,\lambda,\alpha,\beta) \cap T$ was also investigated by Aouf et al. [5].

In 1991, Sekine [9] investigated the class $T(\alpha)$ which consists functions of the form

$$f(z) = z - \sum_{j=2}^{\infty} a_j z^j, \quad (e^{i\alpha}a_j \geq 0; |\alpha| < \frac{\pi}{2}), \tag{1.4}$$

analytic in the unit disc U.

Let $T(k,\alpha)$ be the class of analytic functions of the form

$$f(z) = z - \sum_{j=k+1}^{\infty} a_j z^j, \quad (e^{i\alpha}a_j \geq 0; |\alpha| < \frac{\pi}{2}; k \in \mathbb{N} = \{1,2,3,\dots\}). \tag{1.5}$$

The class $T(1,0) = T$ called functions with negative coefficients was introduced and studied by Silverman [10].

The new generalized derivative operator $\mu^{n,m}_{\lambda_1,\lambda_2}$ introduced by Al-Abbadi and Darus [1] is given as follows.

Definition 1.1. *For $f \in \mathcal{A} = \mathcal{A}(1)$, the generalized derivative operator $\mu^{n,m}_{\lambda_1,\lambda_2} : \mathcal{A} \to \mathcal{A}$ is defined by*

$$\mu^{n,m}_{\lambda_1,\lambda_2} f(z) = z + \sum_{j=2}^{\infty} \frac{(1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m} c(n,j) a_j z^j, \quad z \in U \tag{1.6}$$

where $n, m \in \mathbb{N}_0 = \{0,1,2,\dots\}$, $\lambda_2 \geq \lambda_1 \geq 0$, and $c(n,j) = \binom{n+j-1}{n} = (n+1)_{j-1}/(1)_{j-1}$, $(x)_k$ denotes the Pochhammer symbol defined by

$$(a)_n = \frac{\Gamma(a+n)}{\Gamma(a)} = \begin{cases} 1 & \text{for } n = 0 \\ a(a+1)(a+2)\dots(a+n-1) & \text{for } n \in \mathbb{N} = \{1,2,\dots\} \end{cases}. \tag{1.7}$$

Also,

$$\left.\begin{array}{l} \mu^{0,1}_{\lambda_1,0} f(z) = \mu^{0,m}_{0,0} f(z) = \mu^{0,0}_{0.\lambda_2} f(z) = \mu^{1,1}_{\lambda_1,1} f(z) = f(z), \\ \text{and} \\ \mu^{1,1}_{\lambda_1,0} f(z) = \mu^{1,m}_{0,0} f(z) = \mu^{1,0}_{0.\lambda_2} f(z) = \mu^{0,2}_{1,0} f(z) = z f'(z) \end{array}\right\} \tag{1.8}$$

Motivated essentially by the classes studied by Altintas and Owa [3], Mostafa [7], Sivasubramanian et al. [11] and Aouf et al. [5], we define a class $TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$ below by using the generalized derivative operator $\mu^{n,m}_{\lambda_1,\lambda_2}$ as given by (1.6).

Definition 1.2. *A function $f(z) \in T(k,\alpha)$ is in the class $TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$ if and only if*

$$Re\left(\frac{e^{i\alpha} z \left(\mu^{n,m}_{\lambda_1,\lambda_2} f(z)\right)'}{(1-\lambda)\left(\mu^{n,m}_{\lambda_1,\lambda_2} f(z)\right) + \lambda z \left(\mu^{n,m}_{\lambda_1,\lambda_2} f(z)\right)'}\right) > \beta, \tag{1.9}$$

where $|\alpha| < \frac{\pi}{2}, 0 \leq \beta < cos\alpha, 0 \leq \lambda < 1$ and for all $z \in U$.

Ref
[5] M.K. Aouf, A.A.Shamandy, A.O.Mostafa and A.K.Wagdy, Certain subclasses of uniformly starlike and convex functions defined by convolution with negative coefficients, *Math. Bech.*, (2012), (online), 15pp.

Remark 1.1. *(i)* $TM^{n,m}_{\lambda_1,\lambda_2}(k,0,0,\beta) = TH^{n,m}_{\lambda_1,\lambda_2}(k,\beta)$ *studied by Al-Abbadi et al. [2].*

(ii) $TM^{n,m}_{\lambda_1,\lambda_2}(k,0,\lambda,\alpha) = TS\big(z+\sum_{j=2}^{\infty}\frac{(1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)z^j,\lambda,\alpha,0\big)$ *studied by Aouf et al. [5].*

(iii) $TM^{0,0}_{0,\lambda_2}(1,0,0,\beta) = TM^{0,1}_{\lambda_1,0}(1,0,0,\beta) = TM^{0,m}_{0,0}(1,0,0,\beta) = TM^{1,1}_{\lambda_1,1}(1,0,0,\beta) = \mathcal{S}^*_T(\beta)$, *starlike of order β with negative coefficients studied by Silverman [10].*

(iv) $TM^{0,0}_{0,\lambda_2}(k,0,0,\beta) = TM^{0,1}_{\lambda_1,0}(k,0,0,\beta) = TM^{0,m}_{0,0}(k,0,0,\beta) = TM^{1,1}_{\lambda_1,1}(k,0,0,\beta) = \mathcal{S}^*_T(k,\beta)$. *was studied by Chatterjea [6].*

In the present paper, employing the techniques used by Sekine [9] we obtain several properties like coefficient inequalities, growth and distortion theorems, convex linear combinations and radii of close-to-convexity, starlikeness and convexity for functions belonging to the class $TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$.

II. Coefficient Inequalities

In this section, we obtain a necessary and sufficient condition for a function $f(z)$ analytic in U to be in $TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$.

Lemma 2.1. *Let $f(z) \in TM^{n,m}_{\lambda_1,\lambda_2}(1,\alpha,\lambda,\beta)$ be defined by (1.5) for $k=1$. Then $f(z) \in TM^{n,m}_{\lambda_1,\lambda_2}(1,\alpha,\lambda,\beta)$ if and only if*

$$\sum_{j=2}^{\infty}\frac{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_j \le cos\alpha-\beta, \quad (2.1)$$

is satisfied for some $\alpha(|\alpha|<\frac{\pi}{2})$ and $\beta(0\le\beta<cos\alpha)$.

Proof. Assume that the inequality (2.1) holds.
Then we have

$$\left|\frac{e^{i\alpha}z\left(\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)'}{(1-\lambda)\left(\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)+\lambda z\left(\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)'}-1\right| = \left|\frac{e^{i\alpha}(1-\lambda)\left(z\left(\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)'-\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)}{(1-\lambda)\left(\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)+\lambda z\left(\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)'}\right|$$

$$= \left|-\frac{e^{i\alpha}(1-\lambda)\sum_{j=2}^{\infty}\frac{(j-1)(1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_jz^j}{z+\sum_{j=2}^{\infty}\frac{(1-\lambda+\lambda j)(1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_jz^j}\right|, \quad |z|<1,$$

$$\le \frac{e^{i\alpha}(1-\lambda)\sum_{j=2}^{\infty}\frac{(j-1)(1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_j}{1-\sum_{j=2}^{\infty}\frac{(1-\lambda+\lambda j)(1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_j} \quad (2.2)$$

$$\le cos\alpha-\beta \quad (2.3)$$

which implies (1.9). Also we note that the denominator in (2.2) is positive provided that (2.1) holds.

Ref
[9] T. Sekine, On generalized of analytic functions with negative coefficients, *Math. Japonica*, **36**(1) (1991), 13–19.

Thus it follows from this fact that $f(z) \in TM^{n,m}_{\lambda_1,\lambda_2}(1,\alpha,\lambda,\beta)$.

Conversely, assume that the function $f(z)$ is in the class $TM^{n,m}_{\lambda_1,\lambda_2}(1,\alpha,\lambda,\beta)$. Then

$$Re\left(\frac{e^{i\alpha}z\left(\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)'}{(1-\lambda)\left(\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)+\lambda z\left(\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)'}\right)>\beta$$

implies

$$Re\left(\begin{array}{l}\dfrac{e^{i\alpha}(1-\lambda)\sum\limits_{j=2}^{\infty}\dfrac{(j-1)(1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_jz^j}{(1-\lambda)\left(z-\sum\limits_{j=2}^{\infty}\dfrac{(1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_jz^j\right)}\\ \quad+\lambda z\left(z-\sum\limits_{j=2}^{\infty}\dfrac{j(1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_jz^j\right)\end{array}\right)\leq cos\alpha-\beta,\ (z\in U)$$

Choose values of z on the real axis so that $\dfrac{e^{i\alpha}z\left(\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)'}{(1-\lambda)\left(\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)+\lambda z\left(\mu^{n,m}_{\lambda_1,\lambda_2}f(z)\right)'}$ is real. Letting $z\to 1^-$ through real values, we obtain

$$\frac{e^{i\alpha}(1-\lambda)\sum\limits_{j=2}^{\infty}\dfrac{(j-1)(1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_j}{1-\sum\limits_{j=2}^{\infty}\dfrac{(1-\lambda+\lambda j)(1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_j}\leq cos\alpha-\beta$$

which gives (2.1).

The result is sharp with the extremal function $f(z)$ defined by

$$f(z)=z-\frac{(cos\alpha-\beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}c(n,j)}z^j, j\geq k+1. \tag{2.4}$$

With the aid of the Lemma 2.1, we prove the following Theorem.

Theorem 2.1. *Let $f(z)\in TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$ be defined by (1.5) Then $f(z)\in TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$ if and only if*

$$\sum_{j=k+1}^{\infty}\frac{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_j \leq cos\alpha-\beta,\quad k=1,2,\ldots, \tag{2.5}$$

is satisfied for some $\alpha(|\alpha|<\frac{\pi}{2})$ and $\beta(0\leq\beta<cos\alpha)$.

Proof. Putting $a_j=0$ $(j=2,3,4,\ldots,k)$ in Lemma 2.1, we can prove the assertion of Theorem 2.1.

Corollary 2.1. *Let the function $f(z)$ defined by (1.5) be in the class $TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$. Then*

$$|a_j| \leq \frac{(cos\alpha - \beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)((j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}c(n,j)}, \tag{2.6}$$

where $\lambda_2 \geq \lambda_1 \geq 0$, $j \geq k+1$, $k = 1, 2, \ldots$ $|\alpha| < \frac{\pi}{2}$ *and* $0 \leq \beta < cos\alpha$.

Equality in (2.6) is attained for the function given by (2.4) for $j \geq k+1$.

III. Growth and Distortion Theorems

Theorem 3.1. *Let the function* $f(z)$ *defined by (1.5) be in the class* $TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$. *Then for* $0 < |z| = r < 1$,

$$r - \frac{(cos\alpha-\beta)(1+\lambda_2 k)^m}{[(1-\lambda)k+(1+\lambda k)(cos\alpha-\beta)](1+\lambda_1 k)^{m-1}c(n,k+1)}r^{k+1} \leq |f(z)| \leq r + \frac{(cos\alpha-\beta)(1+\lambda_2 k)^m}{[(1-\lambda)k+(1+\lambda k)(cos\alpha-\beta)](1+\lambda_1 k)^{m-1}c(n,k+1)}r^{k+1} \tag{3.1}$$

where $0 \leq \beta < cos\alpha$, $m \in \mathbb{N}_0 = \{0, 1, 2, \ldots\}$, *and* $n \in \mathbb{N} = \{1, 2, \ldots\}$.

Proof. We only prove the right hand side inequality in (3.1), since the other inequality can be justified using similar arguments.
Since $f(z) \in TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$ by Theorem 2.1, we have

$$\sum_{j=k+1}^{\infty} \frac{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_j$$

$$\leq cos\alpha - \beta.$$

Consider

$$\frac{[(1-\lambda)(ke^{i\alpha}+cos\alpha-\beta+\lambda(k+1)(cos\alpha-\beta)](1+\lambda_1 k)^{m-1}}{(1+\lambda_2 k)^m}c(n,k+1)\left(\sum_{j=k+1}^{\infty} a_j\right)$$

$$= \sum_{j=k+1}^{\infty} \frac{[(1-\lambda)(ke^{i\alpha}+cos\alpha-\beta+\lambda(k+1)(cos\alpha-\beta)](1+\lambda_1 k)^{m-1}}{(1+\lambda_2 k)^m}c(n,k+1)a_j$$

$$\leq \sum_{j=k+1}^{\infty} \frac{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_j$$

$$\leq cos\alpha - \beta, \quad k = 1, 2, \ldots.$$

Therefore,

$$\sum_{j=k+1}^{\infty} |a_j| \leq \frac{(cos\alpha-\beta)(1+\lambda_2 k)^m}{[(1-\lambda)(k+cos\alpha-\beta)+\lambda(k+1)(cos\alpha-\beta)](1+\lambda_1 k)^{m-1}c(n,k+1)}, \quad k = 1, 2, \ldots. \tag{3.2}$$

Since

$$f(z) = z - \sum_{j=k+1}^{\infty} a_j z^j, \quad k = 1, 2, \ldots,$$

we have

$$|f(z)| = \left| z - \sum_{j=k+1}^{\infty} a_j z^j \right|.$$

Hence

$$|f(z)| \leq |z| + |z|^{k+1} \sum_{j=k+1}^{\infty} |a_j||z|^{j-(k+1)}$$

$$\leq r + r^{k+1} \sum_{j=k+1}^{\infty} |a_j|.$$

Using the inequality (3.2), we get the right hand side inequality of (3.1). This completes the proof.

Theorem 3.2. *Let the function $f(z)$ given by (1.5) be in the class $TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$. Then for $0 < |z| = r < 1$,*

$$1 - \frac{(k+1)(cos\alpha-\beta)(1+\lambda_2 k)^m}{[(1-\lambda)k+(1+\lambda k)(cos\alpha-\beta)](1+\lambda_1 k)^{m-1}c(n,k+1)} r^k \leq |f'(z)| \leq$$

$$1 + \frac{(k+1)(cos\alpha-\beta)(1+\lambda_2 k)^m}{[(1-\lambda)k+(1+\lambda k)(cos\alpha-\beta)](1+\lambda_1 k)^{m-1}c(n,k+1)} r^k, \quad k = 1,2,\ldots$$

where $0 \leq \beta < cos\alpha$, $\lambda_2 \geq \lambda_1 \geq 0$, $m \in \mathbb{N}_0 = \{0,1,2,\ldots\}$, and $n \in \mathbb{N} = \{1,2,\ldots\}$.

Proof. Since $f(z) \in TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$ by Theorem 2.1, we have

$$\sum_{j=k+1}^{\infty} \frac{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m} c(n,j)a_j \leq cos\alpha-\beta,$$

Now

$$\frac{[(1-\lambda)ke^{i\alpha}+(1+\lambda k)(cos\alpha-\beta)](1+\lambda_1 k)^{m-1}}{(1+\lambda_2 k)^m} c(n,k+1)\left(\sum_{j=k+1}^{\infty} ja_j\right)$$

$$= \sum_{j=k+1}^{\infty} \frac{[(1-\lambda)ke^{i\alpha}+(1+\lambda k)(cos\alpha-\beta)](1+\lambda_1 k)^{m-1}}{(1+\lambda_2 k)^m} c(n,k+1)ja_j$$

$$\leq (k+1)\sum_{j=k+1}^{\infty} \frac{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^{m-1}} c(n,j)a_j$$

$$\leq (k+1)(cos\alpha-\beta).$$

Hence,

$$\sum_{j=k+1}^{\infty} j|a_j| \leq \frac{(k+1)(cos\alpha-\beta)(1+\lambda_2 k)^m}{[(1-\lambda)k+(1+\lambda k)(cos\alpha-\beta)](1+\lambda_1 k)^{m-1}c(n,k+1)}, \quad k = 1,2,\ldots. \tag{3.3}$$

Since,

$$f'(z) = 1 - \sum_{j=k+1}^{\infty} ja_j z^{j-1}, \quad \text{for } k = 1,2,\ldots,$$

we have

$$1-|z|^k\sum_{j=k+1}^{\infty}j|a_j||z|^{j-(k+1)}\leq|f'(z)|\leq 1+|z|^k\sum_{j=k+1}^{\infty}j|a_j||z|^{j-(k+1)}.$$

Therefore

$$1-r^k\sum_{j=k+1}^{\infty}j|a_j|\leq|f'(z)|\leq 1+r^k\sum_{j=k+1}^{\infty}j|a_j|,\quad k=1,2,\ldots. \tag{3.4}$$

By using the inequality (3.3) in (3.4), we get Theorem 3.2. This completes the proof.

IV. Convex Linear Combinations

Theorem 4.1. *Let $\mu_\gamma\geq 0$ for $\gamma=1,2,...,l$ and $\sum_{\gamma=1}^{l}\mu_\gamma\leq 1$. If the functions $f_\gamma(z)$ defined by $f_\gamma(z)=z-\sum_{j=k+1}^{\infty}a_{j,\gamma}z^j,\quad (e^{i\alpha}a_{j,\gamma}\geq 0,\gamma=1,2,...,l)$ are in the class $TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$ for every $\gamma=1,2,...,l$, then the function $f(z)=z-\sum_{j=k+1}^{\infty}(\sum_{\gamma=1}^{l}\mu_\gamma a_{j,\gamma})z^j$ is in the class $TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$.*

Proof. Since $f_\gamma(z)\in TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$, it follows from Theorem 2.1 that

$$\sum_{j=k+1}^{\infty}\frac{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_{j,\gamma}$$
$$\leq cos\alpha-\beta,\quad k=1,2,\ldots,. \tag{4.1}$$

for every $\gamma=1,2,...,l$. Hence

$$\sum_{j=k+1}^{\infty}\frac{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)\left(\sum_{\gamma=1}^{l}\mu_\gamma a_{j,\gamma}\right)$$
$$=\sum_{\gamma=1}^{l}\mu_\gamma\left[\sum_{j=k+1}^{\infty}\frac{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m}c(n,j)a_{j,\gamma}\right]$$
$$\leq(cos\alpha-\beta)\sum_{\gamma=1}^{l}\mu_\gamma\leq(cos\alpha-\beta),$$

which implies $f(z)\in TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$, by virtue of Theorem 2.1.

Corollary 4.1. *The class $TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$ is closed under convex linear combinations.*

Theorem 4.2. *Let $f_k(z)=z$ and*

$$f_j(z)=z-\frac{(cos\alpha-\beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}c(n,j)}z^j, \tag{4.2}$$

where $0\leq\beta<cos\alpha$, $\lambda_2\geq\lambda_1\geq 0$, $n,m\in\mathbb{N}_0=\{0,1,2,\ldots\}$ and $j\geq k+1$, for $k=\{1,2,\ldots\}$. Then $f(z)\in TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$, if and only if it can be expressed in the form

$$f(z) = \sum_{j=k}^{\infty} \delta_j f_j(z) \tag{4.3}$$

where $\delta_j \geq 0$ *and* $\sum_{j=k}^{\infty} \delta_j = 1$.

Proof. Suppose $f(z)$ is expressed as in (4.3).
Then we have

$$\begin{aligned}
f(z) &= \sum_{j=k}^{\infty} \delta_j f_j(z) \\
&= \delta_k f_k(z) + \sum_{j=k+1}^{\infty} \delta_j f_j(z) \\
&= \delta_k f_k(z) + \sum_{j=k+1}^{\infty} \delta_j \left(z - \frac{(cos\alpha - \beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)(e^{i\alpha}(j-1) + cos\alpha - \beta) + \lambda j(cos\alpha - \beta)](1+\lambda_1(j-1))^{m-1} c(n,j)} z^j \right) \\
&= \sum_{j=k}^{\infty} \delta_j z - \sum_{j=k+1}^{\infty} \delta_j \left(\frac{(cos\alpha - \beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)(e^{i\alpha}(j-1) + cos\alpha - \beta) + \lambda j(cos\alpha - \beta)](1+\lambda_1(j-1))^{m-1} c(n,j)} z^j \right) \\
&= z - \sum_{j=k+1}^{\infty} \delta_j \left(\frac{(cos\alpha - \beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)(e^{i\alpha}(j-1) + cos\alpha - \beta) + \lambda j(cos\alpha - \beta)](1+\lambda_1(j-1))^{m-1} c(n,j)} z^j \right).
\end{aligned}$$

Since

$$f(z) = z - \sum_{j=k+1}^{\infty} a_j z^j = z - \sum_{j=k+1}^{\infty} \delta_j \left(\frac{(cos\alpha - \beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)(e^{i\alpha}(j-1) + cos\alpha - \beta) + \lambda j(cos\alpha - \beta)](1+\lambda_1(j-1))^{m-1} c(n,j)} z^j \right)$$

we have

$$|a_j| = \frac{\delta_j (cos\alpha - \beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)((j-1) + cos\alpha - \beta) + \lambda j(cos\alpha - \beta)](1+\lambda_1(j-1))^{m-1} c(n,j)}. \tag{4.4}$$

Now, for $k = 1, 2, \ldots,$

$$\sum_{j=k+1}^{\infty} \delta_j = 1 - \delta_k \leq 1$$

and so

$$\begin{aligned}
\sum_{j=k+1}^{\infty} \delta_j = \sum_{j=k+1}^{\infty} \delta_j &\left(\frac{(cos\alpha - \beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)(e^{i\alpha}(j-1) + cos\alpha - \beta) + \lambda j(cos\alpha - \beta)](1+\lambda_1(j-1))^{m-1} c(n,j)} \right) \\
&\times \left(\frac{[(1-\lambda)(e^{i\alpha}(j-1) + cos\alpha - \beta) + \lambda j(cos\alpha - \beta)](1+\lambda_1(j-1))^{m-1} c(n,j)}{(cos\alpha - \beta)(1+\lambda_2(j-1))^m} \right) \\
&\leq 1,
\end{aligned}$$

which implies

$$\sum_{j=k+1}^{\infty} \frac{[(1-\lambda)(e^{i\alpha}(j-1) + cos\alpha - \beta) + \lambda j(cos\alpha - \beta)](1+\lambda_1(j-1))^{m-1}}{(cos\alpha - \beta)(1+\lambda_2(j-1))^m} c(n,j) a_j \leq 1,$$

by virtue of (4.4).
And therefore,

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$$\sum_{j=k+1}^{\infty} \frac{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(1+\lambda_2(j-1))^m} c(n,j)a_j \leq cos\alpha-\beta.$$

Thus $f(z) \in TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$, in view of Theorem 2.1.

Conversely, let $f(z) \in TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda,\beta)$.

Then

$$a_j \leq \frac{(cos\alpha-\beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}c(n,j)}, \ \ j \geq k+1.$$

That is,

$$\frac{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(cos\alpha-\beta)(1+\lambda_2(j-1))^m} c(n,j)a_j \leq 1, \ \ j \geq k+1.$$

Since $\sum_{j=k}^{\infty} \delta_j = 1$, we see that $\delta_j \leq 1$, for each $j \geq k+1$, $k = 1, 2, \ldots$.

We may take

$$\delta_j = \frac{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(cos\alpha-\beta)(1+\lambda_2(j-1))^m} c(n,j)a_j, \ \ j \geq k+1$$

so that

$$|a_j| = \frac{\delta_j(cos\alpha-\beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}c(n,j)}. \tag{4.5}$$

Then,

$$\begin{aligned}
f(z) &= z - \sum_{j=k+1}^{\infty} a_j z^j \\
&= z - \sum_{j=k+1}^{\infty} \delta_j \left(\frac{(cos\alpha-\beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}c(n,j)} z^j \right) \\
&= z - \sum_{j=k+1}^{\infty} \delta_j (z - f_j(z)) \\
&= z \ \ 1 - \left(\sum_{j=k+1}^{\infty} \delta_j \right) + \sum_{j=k+1}^{\infty} \delta_j f_j(z) \\
&= f_k(z)\delta_k + \sum_{j=k+1}^{\infty} \delta_j f_j(z) \\
&= \sum_{j=k}^{\infty} \delta_j f_j(z),
\end{aligned}$$

which proves (4.3).

Corollary 4.2. *The extreme point of* $TM^{n,m}_{\lambda_1,\lambda_2}(k,\alpha,\lambda)$ *are the functions*

$$f_k(z) = z,$$

$$f_j(z) = z - \frac{(cos\alpha - \beta)(1+\lambda_2(j-1))^m}{[(1-\lambda)(e^{i\alpha}(j-1)+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}c(n,j)} z^j,$$

where $\lambda_2 \geq \lambda_1 \geq 0$, $n, m \in \mathbb{N}_0 = \{0, 1, 2, \dots\}$, *and* $j \geq k+1$, $k = \{1, 2, \dots\}$.

V. Radii of close-to-convexity, Starlikeness and Convexity

Theorem 5.1. *Let the function $f(z)$ defined by (1.5) be in the class $TM^{n,m}_{\lambda_1,\lambda_2}(k, \alpha, \lambda, \beta)$. Then $f(z)$ is close to convex of order ρ $(0 \leq \rho < 1)$ in $|z| < r_1(n, m, \lambda, \alpha, k, \rho)$,*

where

$$r_1 = \inf_j \left[\frac{[(1-\lambda)(j-1+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}(1-\rho)}{(cos\alpha-\beta)(1+\lambda_2(j-1))^m j} c(n,j) \right]^{\frac{1}{j-1}}, \tag{5.1}$$

$j \geq k+1$. *The result is sharp, with extremal function $f(z)$ given by (2.4) for* $j \geq k+1$.

Proof. It is sufficient to show that

$$|f'(z) - 1| \leq 1 - \rho$$

for $|z| < r_1(n, m, \lambda, \alpha, k, \rho)$, where $r_1(n, m, \lambda, \alpha, k, \rho)$ is given by (5.1).
Indeed we find, from (1.5) that

$$|f'(z) - 1| \leq \sum_{j=k+1}^{\infty} j|a_j||z|^{j-1}.$$

Thus

$$|f'(z) - 1| \leq 1 - \rho$$

if

$$\sum_{j=k+1}^{\infty} \left(\frac{j}{1-\rho} \right) |a_j||z|^{j-1} \leq 1. \tag{5.2}$$

But, by Theorem 2.1, (5.2) will be true if

$$\left(\frac{j}{1-\rho} \right) |z|^{j-1} \leq \frac{[(1-\lambda)(j-1+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(cos\alpha-\beta)(1+\lambda_2(j-1))^m} c(n,j)$$

that is, if (for $j \geq k+1$)

$$|z| \leq \left[\frac{[(1-\lambda)(j-1+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}(1-\rho)}{(cos\alpha-\beta)(1+\lambda_2(j-1))^m j} c(n,j) \right]^{\frac{1}{j-1}}. \tag{5.3}$$

Thus the theorem follows from (5.3).

Theorem 5.2. *Let the function $f(z)$ defined by (1.5) be in the class $TM^{n,m}_{\lambda_1,\lambda_2}(k, \alpha, \lambda, \beta)$. Then $f(z)$ is starlike of order ρ $(0 \leq \rho < 1)$ in $|z| < r_2(n, m, \lambda, \alpha, k, \rho)$, where*

$$r_2 = \inf_j \left[\frac{[(1-\lambda)(j-1+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}(1-\rho)}{(cos\alpha-\beta)(1+\lambda_2(j-1))^m (j-\rho)} c(n,j) \right]^{\frac{1}{j-1}}, \tag{5.4}$$

$j \geq k+1$. *The result is sharp, with extremal function $f(z)$ given by (2.4)for* $j \geq k+1$.

Notes

Proof. It is sufficient to show that

$$\left|\frac{zf'(z)}{f(z)} - 1\right| \leq 1 - \rho$$

for $|z| < r_2(n, m, \lambda, \alpha, k, \rho)$, where $r_2(n, m, \lambda, \alpha, k, \rho)$ is given by (5.4). Indeed we find, from (1.5) that

$$\left|\frac{zf'(z)}{f(z)} - 1\right| \leq \frac{\sum_{j=k+1}^{\infty}(j-1)|a_j||z|^{j-1}}{1 - \sum_{j=k+1}^{\infty}|a_j||z|^{j-1}}.$$

Thus

$$\left|\frac{zf'(z)}{f(z)} - 1\right| \leq 1 - \rho$$

if

$$\sum_{j=k+1}^{\infty}\left(\frac{j-\rho}{1-\rho}\right)|a_j||z|^{j-1} \leq 1. \tag{5.5}$$

But, by Theorem 2.1, (5.5) will be true if

$$\left(\frac{j-\rho}{1-\rho}\right)|z|^{j-1} \leq \frac{[(1-\lambda)(j-1+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(cos\alpha-\beta)(1+\lambda_2(j-1))^m}c(n,j)$$

that is, if (for $j \geq k+1$)

$$|z| \leq \left[\frac{[(1-\lambda)(j-1+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}(1-\rho)}{(cos\alpha-\beta)(1+\lambda_2(j-1))^m(j-\rho)}c(n,j)\right]^{\frac{1}{j-1}}. \tag{5.6}$$

Thus the theorem follows from (5.6).

Theorem 5.3. *Let the function $f(z)$ defined by (1.5) be in the class $TM^{n,m}_{\lambda_1,\lambda_2}(k, \alpha, \lambda, \beta)$. Then $f(z)$ is convex of order ρ $(0 \leq \rho < 1)$ in $|z| < r_3(n, m, \lambda, \alpha, k, \rho)$, where*

$$r_3 = \inf_j\left[\frac{[(1-\lambda)(j-1+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}(1-\rho)}{(cos\alpha-\beta)(1+\lambda_2(j-1))^m j(j-\rho)}c(n,j)\right]^{\frac{1}{j-1}}, \tag{5.7}$$

$j \geq k+1$. The result is sharp, with extremal function $f(z)$ given by (2.4)for $j \geq k+1$.

Proof. It is sufficient to show that

$$\left|\frac{zf''(z)}{f'(z)}\right| \leq 1 - \rho$$

for $|z| < r_3(n, m, \lambda, \alpha, k, \rho)$, where $r_3(n, m, \lambda, \alpha, k, \rho)$ is given by (5.7). Indeed we find, from (1.5) that

$$\left|\frac{zf''(z)}{f'(z)}\right| \leq \frac{\sum_{j=k+1}^{\infty} j(j-1)|a_j||z|^{j-1}}{1-\sum_{j=k+1}^{\infty} j|a_j||z|^{j-1}}.$$

Thus

$$\left|\frac{zf''(z)}{f'(z)}\right| \leq 1-\rho$$

if

$$\sum_{j=k+1}^{\infty}\left(\frac{j(j-\rho)}{1-\rho}\right)|a_j||z|^{j-1} \leq 1. \tag{5.8}$$

But, by Theorem 2.1, (5.8) will be true if

$$\left(\frac{j(j-\rho)}{1-\rho}\right)|z|^{j-1} \leq \frac{[(1-\lambda)(j-1+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}}{(cos\alpha-\beta)(1+\lambda_2(j-1))^m}c(n,j)$$

that is, if (for $j \geq k+1$)

$$|z| \leq \left[\frac{[(1-\lambda)(j-1+cos\alpha-\beta)+\lambda j(cos\alpha-\beta)](1+\lambda_1(j-1))^{m-1}(1-\rho)}{(cos\alpha-\beta)(1+\lambda_2(j-1))^m j(j-\rho)}c(n,j)\right]^{\frac{1}{j-1}}. \tag{5.9}$$

Thus the theorem follows from (5.9).

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Further Results on Modified Variational Iteration Method for the Analytical Solution of Nonlinear Advection Equations

By M.O.Olayiwola, K.O.Kareem & A.W.Gbolagade
Osun State University, Nigeria

Abstract- In this paper, the result shows that the method is elegant and reliable with less computational efforts. This method is strongly recommended for the solution of strongly nonlinear partial differential equations and systems of differential equations further to our results in [12] on the solution of nonlinear advection equations, we present a further results on the nonlinear non-homogeneous advection equations using a modified variational iteration method.

Keywords: *lagrange multiplier, non-homogeneous equations, advection equations.*

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Further Results on Modified Variational Iteration Method for the Analytical Solution of Nonlinear Advection Equations

M.O.Olayiwola [α], K.O.Kareem [σ] & A.W.Gbolagade [ρ]

Abstract- In this paper, the result shows that the method is elegant and reliable with less computational efforts. This method is strongly recommended for the solution of strongly nonlinear partial differential equations and systems of differential equations further to our results in [12] on the solution of nonlinear advection equations, we present a further results on the nonlinear non-homogeneous advection equations using a modified variational iteration method.

Keywords: lagrange multiplier, non-homogeneous equations, advection equations.

I. Introduction

A Modified Variational Iteration Method (MVIM) for the solution of nonlinear advection equations is presented. The method is an elegant combination of the Taylor's approximation and the Variational Iteration Method (VIM). The method is seen to be a very reliable alternative to some existing techniques for the nonlinear advection equations.

This paper outlines a reliable method among many others; the method gives rapidly convergent series with specific significant features for the problem.

The nonlinear non-homogeneous partial differential equation problem is of the form:

$$U_t + UU_x = 2x^2t + 2xt^2 + 2x^3t^4 \tag{1}$$

with the initial condition:

$$U(x,0) = 1$$

Many authors have worked on different numerical approaches for the solution of differential equations [1-23]. The nonlinear non-homogeneous advection equations plays a crucial role in applied mathematics and physics. A substantial amount of research work has been directed for the study of the solution of nonlinear non-homogeneous problems and on partial differential equations in particular.

In this paper, further to our results in [12] , a Modified Variational Iteration Method (MVIM) which accurately compute the solution of nonlinear non-homogeneous partial differential equations is presented. The main advantage of this method is that it can be applied directly to partial differential equation without any linearization.

II. Modified Variational Iteration Method

The variational Iteration Method was proposed by He [1-4]. In this paper a Modified Variational Iteration Method (MVIM) proposed by Olayiwola [5-8] is presented for the solution of nonlinear non-homogeneous partial differential equations.

Author α ρ : Department of Mathematical & Physical Sciences, Faculty of Basic Applied Sciences, College of Sciences, Engineering & Technology, Osun State University, Osogbo Nigeria. e-mail: olayiwola.oyedunsi@uniosun.edu.ng
Author α: Information Management & Technology Centre Office of the Vice-Chancellor Osun State University, Osogbo, Nigeria
Author σ: Department of Mathematical Sciences, Faculty of Science, Olabisi Onabanjo University, Ago-Iwoye Nigeria.

We consider the following general nonlinear partial differential equation of the form:

$$LU(x,t)+RU(x,t)+NU(x,t)=g(x,t) \tag{2}$$

Where: L is a linear time derivative operator,
R is a linear operator which has partial derivative with respect to x
N is a nonlinear operator and
g is an inhomogeneous term.

According to Variational Iteration Method (VIM), we can apply the correction functional as follows:

$$U_{n+1}(x,t)=U_n(x,t)+\int_0^t \lambda[LU_n+RU_n+NU_n-g]d\tau \tag{3}$$

Where $\lambda=-1$ is a Lagrange multiplier which can be identified optimally via Variational Iteration Method.

The subscript n denoted nth approximation, U_n is considered as a restricted variation i:e $\partial U_n=0$. The successive approximation U_{n+1},n≥0 of the solution U will be readily obtained upon using the determined Lagrange multiplier and any selective functionU_0 .Consequently, the solution is given by:

$$U=\lim_{n\to\infty}U_n \tag{4}$$

In a Modified Variational Iteration Method, $U_0(x,t)$ in equation (3) becomes:

$$U_0(x,t)=\sum_{i=0}^{3} g_i(x)t^i \tag{5}$$

Where $g_i(x)=k_i(x)$ can be found by substituting for $U_0(x,t)$ in (2) at $t=0$

III. Numerical Examples

a) Problem 1

$$U_t+UU_x=2x^2t+2xt^2+2x^3t^4, U(x,0)=1 \tag{6}$$

Let

$$U(x,0)=1$$
$$U^+=1+kt$$
$$U^+{}_t=k$$
$$U^+{}_x=0$$

Then

$$U^+(x,t)=1+0(t)=1 \tag{7}$$

$$U^{++}(x,t)=1+kt^2 \tag{8}$$

$$U^{++}{}_t=2kt \tag{9}$$

$$U^{++}{}_x=0$$

Substitute for (9) in (6)

$$U^{++}{}_t+U^{++}U^{++}{}_x=2x^2t+2xt^2+2x^3t^4 \tag{10}$$

$$2kt+(1+kt^2)(0)=2x^2t+2xt^2+2x^3t^4$$

$$2kt = 2x^2t + 2xt^2 + 2x^3t^4$$

$$k = x^2 + xt + x^3t^3$$

When t=0,

$$k = x^2 \tag{11}$$

Notes

Then

$$U^{++}(x,t) = 1 + x^2t^2$$

Let

$$U^{+++}(x,t) = 1 + x^2t^2 + kt^3 \tag{12}$$

$$U^{+++}{}_t = 2x^2t + 3kt^2 \tag{13}$$

$$U^{+++}{}_x = 2xt^2 \tag{14}$$

Substitute for (13) and (14) in (6)

$$U^{+++}{}_t + U^{+++}U^{+++}{}_x = 2x^2t + 2xt^2 + 2x^3t^4 \tag{15}$$

$$(2x^2t + 3kt^2) + (1 + x^2t^2 + kt^3)(2xt^2) = 2x^2t + 2xt^2 + 2x^3t^4$$

$$2x^2t + 3kt^2 + 2xt^2 + 2x^3t^4 + 2kxt^5 = 2x^2t + 2xt^2 + 2x^3t^4$$

$$3kt^2 + 2kxt^5 = 0$$

$$k(3t^2 + 2xt^5) = 0$$

$$k = 0 \tag{16}$$

$$U^{+++}(x,t) = 1 + x^2t^2 + 0(t^3)$$

$$U^{+++}(x,t) = 1 + x^2t^2 \tag{17}$$

Let

$$U^{++++}(x,t) = 1 + x^2t^2 + kt^4 \tag{18}$$

$$U^{++++}{}_t = 2x^2t + 4kt^3 \tag{19}$$

$$U^{++++}{}_x = 2xt^2 \tag{20}$$

Substitute for (19) and (20) in (6)

$$U^{++++}{}_t + U^{++++}U^{++++}{}_x = 2x^2t + 2xt^2 + 2x^3t^4 \tag{21}$$

$$(2x^2t + 4kt^3) + (1 + x^2t^2 + kt^4)(2xt^2) = 2x^2t + 2xt^2 + 2x^3t^4$$

$$2x^2t + 4kt^3 + 2xt^2 + 2x^3t^4 + 2kxt^6 = 2x^2t + 2xt^2 + 2x^3t^4$$

$$4kt^3 + 2kxt^6 = 0$$

$$k(4t^3 + 2xt^6) = 0$$

$$k = 0 - \tag{22}$$

$$U_0^{++++}(x,t)=1+x^2t^2=U_0\ (x,t)=1+x^2t^2 \tag{23}$$

By using Modified Variational Iteration Method(MVIM) Formula:

$$U_{n+1}(x,t)=U^{++++}(x,t)-\int_0^t[\frac{\partial U_n^{++++}(x,t)}{\partial\xi}+U_n(x,\xi)\frac{\partial U_n^{++++}(x,\xi)}{\partial x}-2x^2\xi-2x\xi^2-2x^3\xi^4]d\xi \tag{24}$$

$$U^{++++}{}_1(x,t)=1+x^2t^2$$

$$U^{++++}{}_1(x,t)=1+x^2t^2$$

$$\frac{\partial U^{++++}{}_1(x,\xi)}{\partial\xi}=2x^2\xi$$

$$\frac{\partial U^{++++}{}_1(x,\xi)}{\partial x}=2x\xi^2$$

Substitute for $U^{++++}{}_1(x,t)$, $U^{++++}{}_1(x,\xi)$, $\frac{\partial U^{++++}{}_1(x,t)}{\partial\xi}$ and $\frac{\partial U^{++++}{}_1(x,\xi)}{\partial x}$ in (24)

$$U_1(x,t)=1+x^2t^2-\int_0^t[2x^2\xi+(1+x^2\xi^2)(2x\xi^2)-2x^2\xi-2x\xi^2-2x^3\xi^4]d\xi$$

$$U_1(x,t)=1+x^2t^2-\int_0^t[2x^2\xi+2x\xi^2+2x^3\xi^4-2x^2\xi-2x\xi^2-2x^3\xi^4]d\xi$$

$$U_1(x,t)=1+x^2t^2-\int_0^t(0)d\xi$$

$$U_1(x,t)=1+x^2t^2 \tag{25}$$

This is the exact solution.

b) Problem 2

$$U_t+UU_x=1+tCosx+\frac{1}{2}Sin2x,\ U(x,0)=Sinx \tag{26}$$

Let

$$U(x,0)=Sinx$$

$$U^{+}(x,t)=Sinx+t \tag{27}$$

$$U^{++}(x,t)=Sinx+t+kt^2 \tag{28}$$

Ssubstitute for (27 and 28) in (26)

$$U^{++}{}_t+U^{++}U^{++}{}_x=1+tCosx+\frac{1}{2}Sin2x$$

$$1+2kt+(Sinx+t+kt^2)(Cosx)=1+tCosx+\frac{1}{2}Sin2x$$

$$1+2kt+tCosx+SinxCosx+kt^2Cosx=1+tCosx+\frac{1}{2}Sin2x$$

$$2kt + kt^2 Cosx = \frac{1}{2} Sinx - SinxCosx$$

$$k = \lim_{t=0} \left[\frac{\frac{1}{2} Sinx - SinxCosx}{2t + t^2 Cosx} \right] \tag{29}$$

Let

$$U^{+++}(x,t) = t + Sinx = U^{+}(x,t)$$

For Modified Variational Iteration Method (MVIM)

$$U_{n+1}^{+++}(x,t) = U^{+++}(x,t) - \int_0^t [\frac{\partial U_n^{+++}(x,t)}{\partial \xi} + U_n(x,\xi)\frac{\partial U_n(x,\xi)}{\partial x} - 1 - \xi Cosx - \frac{1}{2} Sin2x] d\xi \tag{30}$$

$$U^{+++}{}_1(x,t) = t + Sinx$$

$$U_1(x,\xi) = \xi + Sinx$$

$$\frac{\partial U_n(x,t)}{\partial \xi} = 1$$

$$\frac{\partial U_n(x,\xi)}{\partial x} = Cosx$$

Substitute for $U^{+++}{}_1(x,t)$, $U^{+++}{}_1(x,\xi)$, $\frac{\partial U^{+++}{}_1(x,t)}{\partial \xi}$ and $\frac{\partial U^{+++}{}_1(x,\xi)}{\partial x}$ in (30)

$$U_1(x,t) = (t + Sinx) - \int_0^t [1 + (\xi + Sinx)(Cosx) - 1 - \xi Cosx - \frac{1}{2} Sin2x] d\xi \tag{31}$$

$$U_1(x,t) = t + Sinx - \int_0^t [1 + \xi Cosx + SinxCosx - 1 - \xi Cosx - \frac{1}{2} Sin2x] d\xi$$

$$U_1(x,t) = t + Sinx - \int_0^t [SinxCosx - \frac{1}{2} Sin2x] d\xi$$

$$U_n{}^{+++}(x,t) = t + Sinx - [\xi SinxCosx - \frac{\xi}{2} Sin2x]_0^t$$

$$U_1(x,t) = t + Sinx \tag{32}$$

This also gives the exact solution.

IV. Conclusion

In this paper, further to our recent results in [12], we presented a Modified Variational Iteration Method proposed in [5-8] to the solution of nonlinear non-homogeneous advection equations. The result shows that the method is elegant and reliable with less computational efforts. This method is strongly recommended for the solution of strongly nonlinear partial differential equations and systems of differential equations.

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The recommended size of original research paper is less than seven thousand words, review papers fewer than seven thousands words also.Preparation of research paper or how to write research paper, are major hurdle, while writing manuscript. The research articles and research letters should be fewer than three thousand words, the structure original research paper; sometime review paper should be as follows:

Papers: These are reports of significant research (typically less than 7000 words equivalent, including tables, figures, references), and comprise:

(a)Title should be relevant and commensurate with the theme of the paper.

(b) A brief Summary, "Abstract" (less than 150 words) containing the major results and conclusions.

(c) Up to ten keywords, that precisely identifies the paper's subject, purpose, and focus.

(d) An Introduction, giving necessary background excluding subheadings; objectives must be clearly declared.

(e) Resources and techniques with sufficient complete experimental details (wherever possible by reference) to permit repetition; sources of information must be given and numerical methods must be specified by reference, unless non-standard.

(f) Results should be presented concisely, by well-designed tables and/or figures; the same data may not be used in both; suitable statistical data should be given. All data must be obtained with attention to numerical detail in the planning stage. As reproduced design has been recognized to be important to experiments for a considerable time, the Editor has decided that any paper that appears not to have adequate numerical treatments of the data will be returned un-refereed;

(g) Discussion should cover the implications and consequences, not just recapitulating the results; conclusions should be summarizing.

(h) Brief Acknowledgements.

(i) References in the proper form.

Authors should very cautiously consider the preparation of papers to ensure that they communicate efficiently. Papers are much more likely to be accepted, if they are cautiously designed and laid out, contain few or no errors, are summarizing, and be conventional to the approach and instructions. They will in addition, be published with much less delays than those that require much technical and editorial correction.

The Editorial Board reserves the right to make literary corrections and to make suggestions to improve briefness.

It is vital, that authors take care in submitting a manuscript that is written in simple language and adheres to published guidelines.

Format

Language: The language of publication is UK English. Authors, for whom English is a second language, must have their manuscript efficiently edited by an English-speaking person before submission to make sure that, the English is of high excellence. It is preferable, that manuscripts should be professionally edited.

Standard Usage, Abbreviations, and Units: Spelling and hyphenation should be conventional to The Concise Oxford English Dictionary. Statistics and measurements should at all times be given in figures, e.g. 16 min, except for when the number begins a sentence. When the number does not refer to a unit of measurement it should be spelt in full unless, it is 160 or greater.

Abbreviations supposed to be used carefully. The abbreviated name or expression is supposed to be cited in full at first usage, followed by the conventional abbreviation in parentheses.

Metric SI units are supposed to generally be used excluding where they conflict with current practice or are confusing. For illustration, 1.4 l rather than 1.4 × 10-3 m3, or 4 mm somewhat than 4 × 10-3 m. Chemical formula and solutions must identify the form used, e.g. anhydrous or hydrated, and the concentration must be in clearly defined units. Common species names should be followed by underlines at the first mention. For following use the generic name should be constricted to a single letter, if it is clear.

Structure

All manuscripts submitted to Global Journals Inc. (US), ought to include:

Title: The title page must carry an instructive title that reflects the content, a running title (less than 45 characters together with spaces), names of the authors and co-authors, and the place(s) wherever the work was carried out. The full postal address in addition with the e-mail address of related author must be given. Up to eleven keywords or very brief phrases have to be given to help data retrieval, mining and indexing.

Abstract, used in Original Papers and Reviews:

Optimizing Abstract for Search Engines

Many researchers searching for information online will use search engines such as Google, Yahoo or similar. By optimizing your paper for search engines, you will amplify the chance of someone finding it. This in turn will make it more likely to be viewed and/or cited in a further work. Global Journals Inc. (US) have compiled these guidelines to facilitate you to maximize the web-friendliness of the most public part of your paper.

Key Words

A major linchpin in research work for the writing research paper is the keyword search, which one will employ to find both library and Internet resources.

One must be persistent and creative in using keywords. An effective keyword search requires a strategy and planning a list of possible keywords and phrases to try.

Search engines for most searches, use Boolean searching, which is somewhat different from Internet searches. The Boolean search uses "operators," words (and, or, not, and near) that enable you to expand or narrow your affords. Tips for research paper while preparing research paper are very helpful guideline of research paper.

Choice of key words is first tool of tips to write research paper. Research paper writing is an art.A few tips for deciding as strategically as possible about keyword search:

- One should start brainstorming lists of possible keywords before even begin searching. Think about the most important concepts related to research work. Ask, "What words would a source have to include to be truly valuable in research paper?" Then consider synonyms for the important words.
- It may take the discovery of only one relevant paper to let steer in the right keyword direction because in most databases, the keywords under which a research paper is abstracted are listed with the paper.
- One should avoid outdated words.

Keywords are the key that opens a door to research work sources. Keyword searching is an art in which researcher's skills are bound to improve with experience and time.

Numerical Methods: Numerical methods used should be clear and, where appropriate, supported by references.

Acknowledgements: Please make these as concise as possible.

References

References follow the Harvard scheme of referencing. References in the text should cite the authors' names followed by the time of their publication, unless there are three or more authors when simply the first author's name is quoted followed by et al. unpublished work has to only be cited where necessary, and only in the text. Copies of references in press in other journals have to be supplied with submitted typescripts. It is necessary that all citations and references be carefully checked before submission, as mistakes or omissions will cause delays.

References to information on the World Wide Web can be given, but only if the information is available without charge to readers on an official site. Wikipedia and Similar websites are not allowed where anyone can change the information. Authors will be asked to make available electronic copies of the cited information for inclusion on the Global Journals Inc. (US) homepage at the judgment of the Editorial Board.

The Editorial Board and Global Journals Inc. (US) recommend that, citation of online-published papers and other material should be done via a DOI (digital object identifier). If an author cites anything, which does not have a DOI, they run the risk of the cited material not being noticeable.

The Editorial Board and Global Journals Inc. (US) recommend the use of a tool such as Reference Manager for reference management and formatting.

Tables, Figures and Figure Legends

Tables: Tables should be few in number, cautiously designed, uncrowned, and include only essential data. Each must have an Arabic number, e.g. Table 4, a self-explanatory caption and be on a separate sheet. Vertical lines should not be used.

Figures: Figures are supposed to be submitted as separate files. Always take in a citation in the text for each figure using Arabic numbers, e.g. Fig. 4. Artwork must be submitted online in electronic form by e-mailing them.

Preparation of Electronic Figures for Publication

Even though low quality images are sufficient for review purposes, print publication requires high quality images to prevent the final product being blurred or fuzzy. Submit (or e-mail) EPS (line art) or TIFF (halftone/photographs) files only. MS PowerPoint and Word Graphics are unsuitable for printed pictures. Do not use pixel-oriented software. Scans (TIFF only) should have a resolution of at least 350 dpi (halftone) or 700 to 1100 dpi (line drawings) in relation to the imitation size. Please give the data for figures in black and white or submit a Color Work Agreement Form. EPS files must be saved with fonts embedded (and with a TIFF preview, if possible).

For scanned images, the scanning resolution (at final image size) ought to be as follows to ensure good reproduction: line art: >650 dpi; halftones (including gel photographs) : >350 dpi; figures containing both halftone and line images: >650 dpi.

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Figure Legends: Self-explanatory legends of all figures should be incorporated separately under the heading 'Legends to Figures'. In the full-text online edition of the journal, figure legends may possibly be truncated in abbreviated links to the full screen version. Therefore, the first 100 characters of any legend should notify the reader, about the key aspects of the figure.

6. AFTER ACCEPTANCE

Upon approval of a paper for publication, the manuscript will be forwarded to the dean, who is responsible for the publication of the Global Journals Inc. (US).

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The corresponding author will receive an e-mail alert containing a link to a website or will be attached. A working e-mail address must therefore be provided for the related author.

Acrobat Reader will be required in order to read this file. This software can be downloaded

(Free of charge) from the following website:

www.adobe.com/products/acrobat/readstep2.html. This will facilitate the file to be opened, read on screen, and printed out in order for any corrections to be added. Further instructions will be sent with the proof.

Proofs must be returned to the dean at dean@globaljournals.org within three days of receipt.

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Before start writing a good quality Computer Science Research Paper, let us first understand what is Computer Science Research Paper? So, Computer Science Research Paper is the paper which is written by professionals or scientists who are associated to Computer Science and Information Technology, or doing research study in these areas. If you are novel to this field then you can consult about this field from your supervisor or guide.

TECHNIQUES FOR WRITING A GOOD QUALITY RESEARCH PAPER:

1. Choosing the topic: In most cases, the topic is searched by the interest of author but it can be also suggested by the guides. You can have several topics and then you can judge that in which topic or subject you are finding yourself most comfortable. This can be done by asking several questions to yourself, like Will I be able to carry our search in this area? Will I find all necessary recourses to accomplish the search? Will I be able to find all information in this field area? If the answer of these types of questions will be "Yes" then you can choose that topic. In most of the cases, you may have to conduct the surveys and have to visit several places because this field is related to Computer Science and Information Technology. Also, you may have to do a lot of work to find all rise and falls regarding the various data of that subject. Sometimes, detailed information plays a vital role, instead of short information.

2. Evaluators are human: First thing to remember that evaluators are also human being. They are not only meant for rejecting a paper. They are here to evaluate your paper. So, present your Best.

3. Think Like Evaluators: If you are in a confusion or getting demotivated that your paper will be accepted by evaluators or not, then think and try to evaluate your paper like an Evaluator. Try to understand that what an evaluator wants in your research paper and automatically you will have your answer.

4. Make blueprints of paper: The outline is the plan or framework that will help you to arrange your thoughts. It will make your paper logical. But remember that all points of your outline must be related to the topic you have chosen.

5. Ask your Guides: If you are having any difficulty in your research, then do not hesitate to share your difficulty to your guide (if you have any). They will surely help you out and resolve your doubts. If you can't clarify what exactly you require for your work then ask the supervisor to help you with the alternative. He might also provide you the list of essential readings.

6. Use of computer is recommended: As you are doing research in the field of Computer Science, then this point is quite obvious.

7. Use right software: Always use good quality software packages. If you are not capable to judge good software then you can lose quality of your paper unknowingly. There are various software programs available to help you, which you can get through Internet.

8. Use the Internet for help: An excellent start for your paper can be by using the Google. It is an excellent search engine, where you can have your doubts resolved. You may also read some answers for the frequent question how to write my research paper or find model research paper. From the internet library you can download books. If you have all required books make important reading selecting and analyzing the specified information. Then put together research paper sketch out.

9. Use and get big pictures: Always use encyclopedias, Wikipedia to get pictures so that you can go into the depth.

10. Bookmarks are useful: When you read any book or magazine, you generally use bookmarks, right! It is a good habit, which helps to not to lose your continuity. You should always use bookmarks while searching on Internet also, which will make your search easier.

11. Revise what you wrote: When you write anything, always read it, summarize it and then finalize it.

12. Make all efforts: Make all efforts to mention what you are going to write in your paper. That means always have a good start. Try to mention everything in introduction, that what is the need of a particular research paper. Polish your work by good skill of writing and always give an evaluator, what he wants.

13. Have backups: When you are going to do any important thing like making research paper, you should always have backup copies of it either in your computer or in paper. This will help you to not to lose any of your important.

14. Produce good diagrams of your own: Always try to include good charts or diagrams in your paper to improve quality. Using several and unnecessary diagrams will degrade the quality of your paper by creating "hotchpotch." So always, try to make and include those diagrams, which are made by your own to improve readability and understandability of your paper.

15. Use of direct quotes: When you do research relevant to literature, history or current affairs then use of quotes become essential but if study is relevant to science then use of quotes is not preferable.

16. Use proper verb tense: Use proper verb tenses in your paper. Use past tense, to present those events that happened. Use present tense to indicate events that are going on. Use future tense to indicate future happening events. Use of improper and wrong tenses will confuse the evaluator. Avoid the sentences that are incomplete.

17. Never use online paper: If you are getting any paper on Internet, then never use it as your research paper because it might be possible that evaluator has already seen it or maybe it is outdated version.

18. Pick a good study spot: To do your research studies always try to pick a spot, which is quiet. Every spot is not for studies. Spot that suits you choose it and proceed further.

19. Know what you know: Always try to know, what you know by making objectives. Else, you will be confused and cannot achieve your target.

20. Use good quality grammar: Always use a good quality grammar and use words that will throw positive impact on evaluator. Use of good quality grammar does not mean to use tough words, that for each word the evaluator has to go through dictionary. Do not start sentence with a conjunction. Do not fragment sentences. Eliminate one-word sentences. Ignore passive voice. Do not ever use a big word when a diminutive one would suffice. Verbs have to be in agreement with their subjects. Prepositions are not expressions to finish sentences with. It is incorrect to ever divide an infinitive. Avoid clichés like the disease. Also, always shun irritating alliteration. Use language that is simple and straight forward. put together a neat summary.

21. Arrangement of information: Each section of the main body should start with an opening sentence and there should be a changeover at the end of the section. Give only valid and powerful arguments to your topic. You may also maintain your arguments with records.

22. Never start in last minute: Always start at right time and give enough time to research work. Leaving everything to the last minute will degrade your paper and spoil your work.

23. Multitasking in research is not good: Doing several things at the same time proves bad habit in case of research activity. Research is an area, where everything has a particular time slot. Divide your research work in parts and do particular part in particular time slot.

24. Never copy others' work: Never copy others' work and give it your name because if evaluator has seen it anywhere you will be in trouble.

25. Take proper rest and food: No matter how many hours you spend for your research activity, if you are not taking care of your health then all your efforts will be in vain. For a quality research, study is must, and this can be done by taking proper rest and food.

26. Go for seminars: Attend seminars if the topic is relevant to your research area. Utilize all your resources.

27. Refresh your mind after intervals: Try to give rest to your mind by listening to soft music or by sleeping in intervals. This will also improve your memory.

28. Make colleagues: Always try to make colleagues. No matter how sharper or intelligent you are, if you make colleagues you can have several ideas, which will be helpful for your research.

29. Think technically: Always think technically. If anything happens, then search its reasons, its benefits, and demerits.

30. Think and then print: When you will go to print your paper, notice that tables are not be split, headings are not detached from their descriptions, and page sequence is maintained.

31. Adding unnecessary information: Do not add unnecessary information, like, I have used MS Excel to draw graph. Do not add irrelevant and inappropriate material. These all will create superfluous. Foreign terminology and phrases are not apropos. One should NEVER take a broad view. Analogy in script is like feathers on a snake. Not at all use a large word when a very small one would be sufficient. Use words properly, regardless of how others use them. Remove quotations. Puns are for kids, not grunt readers. Amplification is a billion times of inferior quality than sarcasm.

32. Never oversimplify everything: To add material in your research paper, never go for oversimplification. This will definitely irritate the evaluator. Be more or less specific. Also too, by no means, ever use rhythmic redundancies. Contractions aren't essential and shouldn't be there used. Comparisons are as terrible as clichés. Give up ampersands and abbreviations, and so on. Remove commas, that are, not necessary. Parenthetical words however should be together with this in commas. Understatement is all the time the complete best way to put onward earth-shaking thoughts. Give a detailed literary review.

33. Report concluded results: Use concluded results. From raw data, filter the results and then conclude your studies based on measurements and observations taken. Significant figures and appropriate number of decimal places should be used. Parenthetical remarks are prohibitive. Proofread carefully at final stage. In the end give outline to your arguments. Spot out perspectives of further study of this subject. Justify your conclusion by at the bottom of them with sufficient justifications and examples.

34. After conclusion: Once you have concluded your research, the next most important step is to present your findings. Presentation is extremely important as it is the definite medium though which your research is going to be in print to the rest of the crowd. Care should be taken to categorize your thoughts well and present them in a logical and neat manner. A good quality research paper format is essential because it serves to highlight your research paper and bring to light all necessary aspects in your research.

Informal Guidelines of Research Paper Writing

Key points to remember:

- Submit all work in its final form.
- Write your paper in the form, which is presented in the guidelines using the template.
- Please note the criterion for grading the final paper by peer-reviewers.

Final Points:

A purpose of organizing a research paper is to let people to interpret your effort selectively. The journal requires the following sections, submitted in the order listed, each section to start on a new page.

The introduction will be compiled from reference matter and will reflect the design processes or outline of basis that direct you to make study. As you will carry out the process of study, the method and process section will be constructed as like that. The result segment will show related statistics in nearly sequential order and will direct the reviewers next to the similar intellectual paths throughout the data that you took to carry out your study. The discussion section will provide understanding of the data and projections as to the implication of the results. The use of good quality references all through the paper will give the effort trustworthiness by representing an alertness of prior workings.

Writing a research paper is not an easy job no matter how trouble-free the actual research or concept. Practice, excellent preparation, and controlled record keeping are the only means to make straightforward the progression.

General style:

Specific editorial column necessities for compliance of a manuscript will always take over from directions in these general guidelines.

To make a paper clear

· Adhere to recommended page limits

Mistakes to evade

- Insertion a title at the foot of a page with the subsequent text on the next page
- Separating a table/chart or figure - impound each figure/table to a single page
- Submitting a manuscript with pages out of sequence

In every sections of your document

· Use standard writing style including articles ("a", "the," etc.)

· Keep on paying attention on the research topic of the paper

· Use paragraphs to split each significant point (excluding for the abstract)

· Align the primary line of each section

· Present your points in sound order

· Use present tense to report well accepted

· Use past tense to describe specific results

· Shun familiar wording, don't address the reviewer directly, and don't use slang, slang language, or superlatives

· Shun use of extra pictures - include only those figures essential to presenting results

Title Page:

Choose a revealing title. It should be short. It should not have non-standard acronyms or abbreviations. It should not exceed two printed lines. It should include the name(s) and address (es) of all authors.

Abstract:

The summary should be two hundred words or less. It should briefly and clearly explain the key findings reported in the manuscript--must have precise statistics. It should not have abnormal acronyms or abbreviations. It should be logical in itself. Shun citing references at this point.

An abstract is a brief distinct paragraph summary of finished work or work in development. In a minute or less a reviewer can be taught the foundation behind the study, common approach to the problem, relevant results, and significant conclusions or new questions.

Write your summary when your paper is completed because how can you write the summary of anything which is not yet written? Wealth of terminology is very essential in abstract. Yet, use comprehensive sentences and do not let go readability for briefness. You can maintain it succinct by phrasing sentences so that they provide more than lone rationale. The author can at this moment go straight to shortening the outcome. Sum up the study, with the subsequent elements in any summary. Try to maintain the initial two items to no more than one ruling each.

- Reason of the study - theory, overall issue, purpose
- Fundamental goal
- To the point depiction of the research
- Consequences, including definite statistics - if the consequences are quantitative in nature, account quantitative data; results of any numerical analysis should be reported
- Significant conclusions or questions that track from the research(es)

Approach:

- Single section, and succinct
- As a outline of job done, it is always written in past tense
- A conceptual should situate on its own, and not submit to any other part of the paper such as a form or table
- Center on shortening results - bound background information to a verdict or two, if completely necessary
- What you account in an conceptual must be regular with what you reported in the manuscript
- Exact spelling, clearness of sentences and phrases, and appropriate reporting of quantities (proper units, important statistics) are just as significant in an abstract as they are anywhere else

Introduction:

The **Introduction** should "introduce" the manuscript. The reviewer should be presented with sufficient background information to be capable to comprehend and calculate the purpose of your study without having to submit to other works. The basis for the study should be offered. Give most important references but shun difficult to make a comprehensive appraisal of the topic. In the introduction, describe the problem visibly. If the problem is not acknowledged in a logical, reasonable way, the reviewer will have no attention in your result. Speak in common terms about techniques used to explain the problem, if needed, but do not present any particulars about the protocols here. Following approach can create a valuable beginning:

- Explain the value (significance) of the study
- Shield the model - why did you employ this particular system or method? What is its compensation? You strength remark on its appropriateness from a abstract point of vision as well as point out sensible reasons for using it.
- Present a justification. Status your particular theory (es) or aim(s), and describe the logic that led you to choose them.
- Very for a short time explain the tentative propose and how it skilled the declared objectives.

Approach:

- Use past tense except for when referring to recognized facts. After all, the manuscript will be submitted after the entire job is done.
- Sort out your thoughts; manufacture one key point with every section. If you make the four points listed above, you will need a least of four paragraphs.

- Present surroundings information only as desirable in order hold up a situation. The reviewer does not desire to read the whole thing you know about a topic.
- Shape the theory/purpose specifically - do not take a broad view.
- As always, give awareness to spelling, simplicity and correctness of sentences and phrases.

Procedures (Methods and Materials):

This part is supposed to be the easiest to carve if you have good skills. A sound written Procedures segment allows a capable scientist to replacement your results. Present precise information about your supplies. The suppliers and clarity of reagents can be helpful bits of information. Present methods in sequential order but linked methodologies can be grouped as a segment. Be concise when relating the protocols. Attempt for the least amount of information that would permit another capable scientist to spare your outcome but be cautious that vital information is integrated. The use of subheadings is suggested and ought to be synchronized with the results section. When a technique is used that has been well described in another object, mention the specific item describing a way but draw the basic principle while stating the situation. The purpose is to text all particular resources and broad procedures, so that another person may use some or all of the methods in one more study or referee the scientific value of your work. It is not to be a step by step report of the whole thing you did, nor is a methods section a set of orders.

Materials:

- Explain materials individually only if the study is so complex that it saves liberty this way.
- Embrace particular materials, and any tools or provisions that are not frequently found in laboratories.
- Do not take in frequently found.
- If use of a definite type of tools.
- Materials may be reported in a part section or else they may be recognized along with your measures.

Methods:

- Report the method (not particulars of each process that engaged the same methodology)
- Describe the method entirely
- To be succinct, present methods under headings dedicated to specific dealings or groups of measures
- Simplify - details how procedures were completed not how they were exclusively performed on a particular day.
- If well known procedures were used, account the procedure by name, possibly with reference, and that's all.

Approach:

- It is embarrassed or not possible to use vigorous voice when documenting methods with no using first person, which would focus the reviewer's interest on the researcher rather than the job. As a result when script up the methods most authors use third person passive voice.
- Use standard style in this and in every other part of the paper - avoid familiar lists, and use full sentences.

What to keep away from

- Resources and methods are not a set of information.
- Skip all descriptive information and surroundings - save it for the argument.
- Leave out information that is immaterial to a third party.

Results:

The principle of a results segment is to present and demonstrate your conclusion. Create this part a entirely objective details of the outcome, and save all understanding for the discussion.

The page length of this segment is set by the sum and types of data to be reported. Carry on to be to the point, by means of statistics and tables, if suitable, to present consequences most efficiently.You must obviously differentiate material that would usually be incorporated in a study editorial from any unprocessed data or additional appendix matter that would not be available. In fact, such matter should not be submitted at all except requested by the instructor.

Content

- Sum up your conclusion in text and demonstrate them, if suitable, with figures and tables.
- In manuscript, explain each of your consequences, point the reader to remarks that are most appropriate.
- Present a background, such as by describing the question that was addressed by creation an exacting study.
- Explain results of control experiments and comprise remarks that are not accessible in a prescribed figure or table, if appropriate.
- Examine your data, then prepare the analyzed (transformed) data in the form of a figure (graph), table, or in manuscript form.

What to stay away from

- Do not discuss or infer your outcome, report surroundings information, or try to explain anything.
- Not at all, take in raw data or intermediate calculations in a research manuscript.
- Do not present the similar data more than once.
- Manuscript should complement any figures or tables, not duplicate the identical information.
- Never confuse figures with tables - there is a difference.

Approach

- As forever, use past tense when you submit to your results, and put the whole thing in a reasonable order.
- Put figures and tables, appropriately numbered, in order at the end of the report
- If you desire, you may place your figures and tables properly within the text of your results part.

Figures and tables

- If you put figures and tables at the end of the details, make certain that they are visibly distinguished from any attach appendix materials, such as raw facts
- Despite of position, each figure must be numbered one after the other and complete with subtitle
- In spite of position, each table must be titled, numbered one after the other and complete with heading
- All figure and table must be adequately complete that it could situate on its own, divide from text

Discussion:

The Discussion is expected the trickiest segment to write and describe. A lot of papers submitted for journal are discarded based on problems with the Discussion. There is no head of state for how long a argument should be. Position your understanding of the outcome visibly to lead the reviewer through your conclusions, and then finish the paper with a summing up of the implication of the study. The purpose here is to offer an understanding of your results and hold up for all of your conclusions, using facts from your research and generally accepted information, if suitable. The implication of result should be visibly described. Infer your data in the conversation in suitable depth. This means that when you clarify an observable fact you must explain mechanisms that may account for the observation. If your results vary from your prospect, make clear why that may have happened. If your results agree, then explain the theory that the proof supported. It is never suitable to just state that the data approved with prospect, and let it drop at that.

- Make a decision if each premise is supported, discarded, or if you cannot make a conclusion with assurance. Do not just dismiss a study or part of a study as "uncertain."
- Research papers are not acknowledged if the work is imperfect. Draw what conclusions you can based upon the results that you have, and take care of the study as a finished work
- You may propose future guidelines, such as how the experiment might be personalized to accomplish a new idea.
- Give details all of your remarks as much as possible, focus on mechanisms.
- Make a decision if the tentative design sufficiently addressed the theory, and whether or not it was correctly restricted.
- Try to present substitute explanations if sensible alternatives be present.
- One research will not counter an overall question, so maintain the large picture in mind, where do you go next? The best studies unlock new avenues of study. What questions remain?
- Recommendations for detailed papers will offer supplementary suggestions.

Approach:

- When you refer to information, differentiate data generated by your own studies from available information
- Submit to work done by specific persons (including you) in past tense.
- Submit to generally acknowledged facts and main beliefs in present tense.

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Result	Well organized, Clear and specific, Correct units with precision, correct data, well structuring of paragraph, no grammar and spelling mistake	Complete and embarrassed text, difficult to comprehend	Irregular format with wrong facts and figures
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References	Complete and correct format, well organized	Beside the point, Incomplete	Wrong format and structuring

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