# Using type for improving health of the udder and feet and legs

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## Abstract

Some type traits potentially have value in selection to improve udder health and others may be useful in improving health of feet and legs. Genetic correlations indicate that foot angle and/or the length of foot diagonal may be important for improving hoof health. Selection for straighter rear legs rear , view and for improved hock or bone quality may also have merit, but clear relationships between these traits and health aspects of feet and legs are not well established. The benefits of selection based on subjective composite feet and leg traits and subjective locomotion scores are also not known. Selection for some udder and teat morphological characteristics is likely warranted. Udder depth, fore udder attachment, teat placement, udder cleft, teat length, somatic cell score (SCS) and milk yield were evaluated in an index (sire index with 50 or 100 daughters) to predict clinical mastitis and an aggregate genotype which included clinical mastitis and milking labor. Fore udder attachment, teat placement, and udder cleft were of limited value in an index to predict clinical mastitis when SCS, udder depth, and teat length were available. Somatic cell score is likely the most important component of an udder health index and udder depth is second in importance to SCS. Udder related type traits were more valuable when milking labor was included in the objective. Somatic cell score, udder depth, teat length, and teat placement may all be useful in more comprehensive indexes. Selection for lower somatic cell scores, higher udders, shorter teats, and closer teat placement will reduce clinical mastitis and may reduce labor associated with milking.

#### Introduction

Dairy cattle breeding programs should focus on improving the economic efficiency of dairy cattle. Intense selection for increased yield, especially protein yield, is clearly justified However, strategies for (Rogers, 1994). selection to improve udder health and reduce locomotive diseases are controversial. Some countries such as Norway and Sweden place considerable emphasis on health traits while US and other countries (e.g., many Netherlands) use only indirect measures of the health traits and place much less emphasis on these indirect measures compared to yield traits.

Udder diseases, hoof diseases, and leg

disorders can have large direct costs and can ultimately lead to involuntary culling. Udder disease and hoof diseases also have significant Heritabilities for clinical genetic variation. mastitis in most dairy cattle populations when accurately, consistently, and recorded completely are probably .10 or higher (Lin et al. 1989; Lyons et al., 1991). Heritabilities for hoof diseases are also substantial (Distl et al., 1990; Ral et al., 1995), but estimates of heritabilities for leg disorders (e.g., swollen joints and hock ailments) are not readily available. However, in most countries, the lack of accurate and standardized recording prohibits direct selection for mastitis resistance and hoof diseases. Type traits associated with udder and teat morphology and somatic cell counts (SCC), usually converted to some logarithmic form termed SCS, have been identified as traits that are possibly useful for indirect selection to improve udder health (Emanuelson et al., 1988; Rogers, 1993; Shook, 1989). Type traits associated with feet and legs have been suggested as possible indicator traits useful for selection to reduce hoof diseases and leg disorders (Distl et al., 1990; McDaniel, 1995). The usefulness of these type traits to help improve udder and locomotive health is dependent on heritabilities and correlations among the type traits, their cost of measurement, and their associations with the health traits that they indirectly represent. Type traits should not be part of the actual breeding objective, but should be used as indicator traits for traits included in the breeding objective. The objectives of this paper are to outline and evaluate the traits that potentially could be useful for improving udder diseases, hoof diseases, and leg disorders in dairy cattle.

## Possible traits for improving health of feet and legs

Hoof diseases and leg disorders impact reproductive performance, survival, salable milk, and labor needs. Lameness in cattle was extensively reviewed in recent papers (Boelling and Pollott, 1995; McDaniel, 1995; Ral et al., 1995). Genetic variation in hoof disorders is low to moderate (Distl et al., 1990; Ral et al., 1995). Laminitis, hoof injuries, abnormal claw growth, and skin disorders are the most prevalent problems involving the hoof. Laminitis is perhaps the most important of the disorders and is most frequently associated with lameness. Disorders of the hock are not understood very well, but they could play an important role in the complex issue of locomotive health.

Hoof diseases and leg disorders are not recorded in many populations, but some indirect measures (Boelling and Pollott, 1995; Distl et al., 1990; McDaniel, 1995; Ral et al., 1995; Rogers, 1993) may be helpful for selection. Candidate type traits include those associated with the morphology of the hoof, the structure of the leg, and measures of locomotion and agility. Most traits that reflect structure of feet and legs have low to moderate heritabilities (McDaniel, 1995; Misztal et al., 1992). A number of leg traits are scored in various countries including rear legs side view which is a measure of hock angle, rear legs. rear view, hock quality, and bone quality. Traits related to the hoof which are routinely recorded include foot angle, a foot diagonal measure, and subjective overall measures of Claw lengths, hoof symmetry, the foot. interdigital space, heel depth and various other measures are not routinely recorded in most countries. Measures of mobility and agility usually termed locomotion scores have been proposed, but are not routinely measured in most countries.

Estimates of genetic correlations between leg traits and hoof diseases or leg disorders are not readily available. However, correlations between leg traits and longevity might indicate associations between leg traits and leg Results from longevity studies disorders. should be used cautiously since survival is dependent on producer decisions and these decisions are made based on a large number where factors. Most studies genetic correlations have been estimated indicate that rear legs side view has a very low relationship with longevity. Phenotypic estimates from some studies indicate that cows slightly straighter than mid-range scores might be most desirable (McDaniel, 1995), however, genetic relationships between survival and rear legs side view have not shown this same relationship in many studies (Rogers et al., 1989). Perhaps this difference is due to the smaller range in breeding values compared to phenotypic values. Those studies involving rear legs rear view indicate that straighter legs from the rear might be favorable. In addition, bone quality and hock quality may be favorably associated with longevity (Dekkers et al., 1994). Selection for leg traits may impact joint disorders and improve agility. Directional selection for rear legs side view will likely be of limited value, but selection for straighter

34

4

legs rear view, improved hock quality, and/or improved bone quality may be useful.

Foot angle and foot diagonal appear to be genetically associated with various measures of claw health. Higher foot angles and shorter foot diagonals are favorably associated with laminitis and other diseases of the hoof (Distl et al., 1990). Genetic correlations between foot angle and the foot diagonal measure and hoof diseases may be in the range of .2 to .7 (Distl et al., 1990; Ral et al., 1995). Selection for steeper foot angles and shorter foot diagonals will likely improve hoof health, but selection for leg traits may have little effect on hoof diseases. Correlations between hoof traits and metabolic diseases are unknown, but it is possible that hoof traits could be associated with metabolic diseases.

Little is known about the genetic correlations between locomotion scores and hoof diseases and leg disorders. However, locomotion scores were favorably correlated with hoof diseases in (Groen et al., 1994). Mobility and agility are probably affected by both clinical and subclinical disease. Many countries evaluate subjective composite traits for feet and legs and some of these composite measures may be useful in selection programs. However, the relationship between these composite traits and hoof diseases and leg disorders are unknown.

Most studies have found only low correlations between feet and leg type traits and reproduction (Shapiro and Swanson, 1991), but some exceptions can be found (Choi and McDaniel, 1993). Selection based on feet and leg type traits to improve reproduction will likely be unsuccessful. Direct selection for reproduction would likely be more useful because data on reproduction are collected in most countries in production and management recording programs.

Indexes to predict hoof disease and leg disorders should be developed using parameters supported by the scientific literature. Currently, in most countries, indexes of feet and leg traits have been developed by informal methods.

## Possible traits for improving udder health

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Mastitis is the most costly disease in most dairy cattle populations. Direct measures of clinical mastitis may be useful for selection in populations where direct measurement is feasible (Emanuelson et al., 1988; Lin et al., 1989; Lyons et al., 1991; Shook, 1989). However, in those countries where clinical mastitis is recorded, it is usually only veterinary treated incidents that are recorded which likely results in exclusion of milder clinical episodes from recording. Somatic cell counts are collected extensively in many countries and could be useful to select for reduced mastitis (Rogers, 1993; Shook, 1989; Weller et al., 1992). Somatic cell counts have a moderate to high genetic correlation (.6 or larger) with clinical mastitis (Emanuelson, 1988; Shook, 1989; Weller et al., 1992). Estimates of this genetic correlation involving large data sources likely suffer from incomplete Incomplete recording of clinical mastitis. recording of less severe disease manifestations and the low frequency in some populations may bias estimates toward zero. The genetic correlation between SCS and the trait that should be used to represent mastitis in defining the breeding goal for most countries is likely near .7. Clinical mastitis, as it is recorded in many populations, may not be the best choice for defining udder health in the breeding objective.

Udder related type traits may also be useful for selection to improve udder health. Udder related type traits are measured in many dairy cattle populations and are moderately to highly heritable (Misztal et al., 1992; Seykora and McDaniel, 1986; Short et al., 1991). Genetic correlations between udder related type traits and mastitis or other measures of udder health are variable and depend on the type trait involved as well as the study (Rogers et al., and McDaniel, 1986). Seykora 1991: However, most studies involving a large number of observations indicate that udder depth and fore udder attachment are the two traits most closely associated (genetically) with

udder health. Unpublished data from Sweden (Eriksson, personal communication, 1995; Rogers, 1996) support this contention. Teat placement, teat length, and udder cleft also may have small genetic correlations with udder health. Rear udder height and width appear to have little correlation with udder health.

4

Most developed countries include udder traits in their major selection indexes either directly or through the prediction of another Currently, some countries are trait. considering mastitis resistance indexes that combine SCS and udder traits (de Jong, personal communication, 1995). These indexes could be published separately and included as the mastitis component of the major selection indexes within those countries. Udder linear traits may be useful for predicting mastitis especially in those countries where clinical mastitis is not recorded routinely.

Udder traits may be valuable in selecting to improve milking labor efficiency and suitability of the udder to mechanized An index strictly for mastitis milking. resistance may under evaluate the importance of some udder traits in a total merit index. It may not be appropriate to ignore milking labor (labor involved with cow preparation, machine adjustment, and postmilking cow attention) or associated with milking machine traits suitability (independent of machine time) in defining the role of udder traits in total merit Milking labor is also likely indexes. genetically correlated with udder health because mastitis requires attention during the milking process. Milking speed could also be useful for selection, but the value of reduced machine time may be completely offset by increased susceptibility to mastitis. Selection for increased milking speed is probably not be warranted in most populations, but mating to avoid extremes might be reasonable (Groen, personal communication, 1995).

Production traits could also be useful for inclusion in a mastitis resistance index. Genetic evaluations are widely available for production traits and the genetic correlations between yield traits and mastitis are in the range of .2 to .3 (unfavorable). Inclusion of yield traits in a mastitis resistance index will likely depend on how the mastitis resistance index is to be used in a total merit index and in the country's breeding program. Likewise, measures of longevity could be included in a mastitis resistance index. However, longevity evaluations for bulls with new first crop daughter information are primarily based on pedigree information.

## Indexes for selection

Selection index methodology assuming a sire index with information from either 50 or 100 daughters was used to calculate indexes predicting either clinical mastitis or a multiple trait objective that included clinical mastitis and milking labor. The multiple trait objective was included to more accurately represent the importance of the indicator traits in predicting the entire complex of udder health and labor associated with milking. Udder related linear traits, SCS, and milk yield were included in the Accuracies of prediction, the indexes. contribution of traits to the index, and standardized index coefficients were calculated. Reduced indexes were calculated after the traits that contributed the least were sequentially removed and not allowed to re-enter until only one trait remained. Indexes with all the traits considered are included in the results for reference, but other indexes including traits that contributed less than one percent to the standard deviation of the index are not Standardized index coefficients, reported. expressed relative to SCS (SCS equal to 1.0), indicate the weights that should be applied to the traits in the index.

In the US, single trait evaluations are available for SCS, but multiple trait evaluations are available for the type traits. When genetic evaluations used in indexes are calculated from multiple trait evaluation models, index weights are simple to calculate (Rogers, 1994; Schneeberger et al., 1992), and standard selection index weights are not appropriate. Selection index methods were used because

SCS was expected to be very important in the index due to its high genetic correlation with mastitis.

The genetic standard deviation for clinical mastitis on a non-incidence versus incidence (0 or 1) basis per lactation was assumed to be .15, and the cost per lactation (excluding cost of reduced milk yield) that involves at least one clinical episode was assumed to be \$150 (US) (Rogers, 1993; Rogers, 1994). Milking labor was defined to include only labor involved with cow adjustment, and preparation. machine postmilking cow attention. The phenotypic variance for milking labor over the lactation was from Blake et al. (1979) and a heritability of .10 was assumed. Labor cost was \$9 per hour; this cost included wages and benefits. Milking labor and clinical mastitis were assumed to have a genetic correlation of .20 because milking labor included postmilking labor time which involves time for mastitis therapy.

phenotypic heritabilities, The correlations, and genetic correlations among the traits in the index used in this study are in Table 1. These parameters are for the situation in the US (Misztal et al., 1992; Rogers et al., 1991; Seykora and McDaniel, 1986; Shook, 1989; Short et al., 1991), but they probably are similar in many other populations. Phenotypic and genetic variances for these traits are not index interest because of specifically Genetic standardized. coefficients are correlations among the traits in the index and mastitis and milking labor are in Table 2 (Blake and McDaniel, 1979; Emanuelson et al., 1988; Rogers et al., 1991; Rogers and Spencer, 1991; Seykora and McDaniel, 1986; Weller et al., 1992). Calculations were made assuming the genetic correlation between SCS and mastitis was .7 and .6.

## Results of index calculations

Indexes assuming clinical mastitis as the breeding objective are in Table 3. Teat placement, udder cleft, and fore udder

attachment contribute very little to the accuracy and variation of the index. These traits were removed because they did not contribute one percent to the standard deviation of the index. Fore udder attachment probably contributed very little because it has a high genetic correlation with udder depth which was in the index. When the index was assumed to have information from 50 daughters per sire, SCS, udder depth, teat length, and milk yield all contributed more than one percent to the standard deviation of the index. The standardized index coefficients reflect the importance of the traits in the index. Weights for SCS were largest followed by udder depth, then by milk yield and teat length which had weights of similar magnitude. Sequential removal to get to a one trait index followed this same pattern. Reductions in accuracy with the elimination of these traits were small (2 to 3 percent) until udder depth was eliminated. Somatic cell score is the most important trait in the index, but the improvement in accuracy above SCS with the addition of udder depth was 9 to 15 percent. Weights for udder depth and the other type traits were smaller in magnitude relative to SCS when the genetic correlation between SCS and mastitis was .70 compared to when the genetic correlation was .60. The weight for udder depth was 56 to 78 percent as large as the weight for SCS when only SCS and udder depth were in the index. Large milk price premiums based on SCS would increase the emphasis that should be placed on SCS relative to the udder linear traits in a manner similar to using a higher genetic correlation between SCS and mastitis.

When calculations assumed 100 daughters per sire, only SCS and udder depth contributed more than one percent to the standard deviation of the index. In addition, the pattern for elimination of the traits was slightly different compared to indexes with 50 daughters per sire. Type traits were less important in the index when 100 daughters per sire were assumed compared to 50 daughters per sire. Udder depth and SCS appear to be very useful for predicting mastitis resistance; teat length and milk yield may have limited value for predicting mastitis resistance. Teat placement, udder cleft, and fore udder attachment are probably not valuable for predicting mastitis resistance when SCS, udder depth, teat length, and milk yield are included in the index.

Indexes assuming clinical mastitis and milking labor as the breeding objective are included in Table 4. Indexes constructed in this manner could be used to represent the complete contribution of the udder related traits to total merit indexes. Indexes indicate that udder cleft and fore udder attachment, as well as milk yield (when 100 daughters per sire), contribute very little to the accuracy and variation of the index. Udder cleft and fore udder attachment were removed because they did not contribute one percent to the standard deviation of the index. Milk yield did not contribute one percent to the standard deviation of the index when information from 100 daughters per sire was assumed. Weights for SCS were largest and weights for udder depth were second largest. Weights for teat length and teat placement were similar in magnitude, placement however, teat was always sequentially eliminated from the index before teat length. In some indexes, the contribution from udder depth was nearly equal to the contribution of SCS. The udder traits were more important in the indexes which included milking labor as a component of the objective compared with indexes that included only mastitis in the objective. Somatic cell score, udder depth, teat length, and teat placement may all be useful in most breeding programs.

### Conclusions

4

Selection for steeper foot angles and shorter foot diagonals will likely improve hoof health. Clear recommendations for selection on leg traits are not readily available, but selection for straighter legs rear view, improved hock quality, and/or improved bone quality may be useful.

Somatic cell score is likely the most

important component of an udder health index and udder depth is second in importance to SCS. Teat length and teat placement will also be useful in comprehensive indexes that include mastitis and husbandry aspects of the udder. Selection for lower somatic cell scores, higher udders, shorter teats, and closer teat placement will reduce clinical mastitis and may reduce labor associated with milking.

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- TABLE 1. Heritabilities (on diagonal), genetic (above diagonal), and phenotypic (below diagonal) correlations among the traits in the index.

	MY	UD	FU	TP	UC	TL	SCS
MY	.25	40	30	.00	.00	.00	.25
UD	20	.28	.75	.40	.40	10	45
FU	10	.40	.29	.65	.50	.00	35
TP	.00	.30	.40	.26	.65	10	20
UC	.00	.30	.30	.50	.24	.00	10
TL	.00	10	.00	20	.00	.26	.15
SCS	10	20	20	10	.00	10	.10

<sup>1</sup> MY = milk yield; UD = udder depth; FU = fore udder attachment; TP = teat placement; UC = udder cleft; TL = teat length; SCS = somatic cell score.

TABLE 2.	Genetic correlations among the tr	aits in the in	ndex and	clinical	mastitis	and	milking
	labor.						.11

		<u> </u>										
_					MY <sup>1</sup>	UD	FU	TP	UC	TL	SCS	
	Clinia	al maint	itie		25	- 45	_ 35	- 20	10	.15	.70 <sup>2</sup>	
	Milkin	a masu 1g lahor	.us		دع. 10	30	20	40	20	.20	.20	
	AVAILANII)		• 									
	MY =	= milk	yield; I	JD =	udder d	epth; F	U = f	ore udd	er attac	hment;	TP = te	at placement
	UC =	udder	cleft: ]	[L ≕ t	eat leng	th; SC	s = so	matic c	ell score	e.		
	Geneti	ic corre	lation	between	n somat	ic cell	score a	nd clini	cal mas	titis of	.60 was	also used.
ΓABL	E 3.	Index	coeffic	ients st	andardi	zed and	presen	ted relat	tive to s	omatic	cell score	and accurac
		for a	sire ind	lex assu	iming c	linical	mastitis	as bre	eding of	bjective	•	
	0.001	Index	Coeffi	cients								
	SC2,	UD	TL	Т <b>Р</b>	UC	FU	MY		Accu	racy		
nder	with Sf	) daugt		e cire.								
nucx	Genet	ic corre	elation	hetwee	n SCS a	and clir	nical ma	stitis of	f .70:			
	-1.0	.43	- 19	.07	11	.11	21		.586			
	-1.0	.47	19	2	•••		21		.584			
	-1.0	.49	rem <sup>3</sup>	•••			20		.578			
	-1.0	.56	rem		•••	•••	rem		.572			
	-1.0	rem	rem	•••	•••	•••	rem		.525			
	Genet	ic corre	elation	betwee	n SCS a	and clir	nical ma	stitis o	f .60:			
	-1.0	.62	25	.10	18	.16	26		.535			
	-1.0	.0/	23	•••	•••	•••	20		.531			
	-1.0	.69	rem	•••	•••	•••	25		524			
		/X	rem		•••	• • •	rem		.218			
	-1.0	.70										
	-1.0	rem	rem	•••	•••	•••	rem		.450			
Index	-1.0 with 10	rem	rem ghters p	er sire	···· : - 505	••••	rem		.450			
Index	-1.0 -1.0 with 10 Genet	rem 00 daug ic corre	rem ghters p elation	 er sire betwee	 : n SCS :	and clin	rem	astitis o	.450 f .70:			
Index	-1.0 -1.0 with 10 Genet -1.0	rem 00 daug ic corre .37	rem ghters p elation 14	 er sire betwee .08	 n SCS : 11	 and clir .06	rem nical ma 14	astitis o	.450 f .70: .638			
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Index	-1.0 with 10 Genet -1.0 -1.0 -1.0	00 daug ic corro .37 .44 rem	rem ghters p elation 14 	er sire betwee .08 	: n SCS : 11 	 and clir .06 	rem nical ma 14 	astitis o	.450 f .70: .638 .628 .594			
Index	-1.0 with 10 Genet -1.0 -1.0 -1.0 Genet	rem 00 daug ic corro .37 .44 rem tic corro	rem ghters p elation 14  elation	er sire betwee .08  betwee	 n SCS : 11  m SCS :	and clir .06  and clir	rem nical ma 14  nical ma	astitis o astitis o	.450 f .70: .638 .628 .594 f .60:			
Index	-1.0 with 10 Genet -1.0 -1.0 -1.0 Genet -1.0	rem 00 daug ic corro .37 .44 rem ic corro .56	rem shters p elation 14  elation 19	 betwee .08  betwee .11	 n SCS : 11  n SCS : 17	and clir .06   and clir .10	rem nical ma 14  nical ma 19	astitis o astitis o	.450 f .70: .638 .628 .594 f .60: .576			
Index	-1.0 with 10 Genet -1.0 -1.0 -1.0 Genet -1.0 -1.0	.70 rem 00 daug ic corro .37 .44 rem ic corro .56 .65	rem shters p elation 14  elation 19 	 betwee .08  betwee .11 	 n SCS 11  n SCS 17	and clir .06  and clir .10 	rem nical ma 14  nical ma 19 	astitis o astitis o	.450 f .70: .638 .628 .594 f .60: .576 .562			

SCS = somatic cell score; UD = udder depth; TL = teat length; TP = teat placement; UC = udder cleft; FU = fore udder attachment; MY = milk yield.Traits designated ... were sequentially removed and not allowed to re-enter because they contributed less than one percent to the standard deviation of the index.Traits designated rem were sequentially removed and not allowed to re-enter based on their contribution to the index.

	SCS <sup>1</sup>	Index UD	Coeffic TL	cients TP	UC	FU	MY	Accuracy
Index	with 50	) daugh	iters pe	r sire:				
	Genet	ic corre	lation	between	SCS 8	ind clim	ical mas	autis of ./0:
	-1.0	.62	27	.43	17	10	24	.009
	-1.0	.53	29	.29	•••*	•••	25	.607
	-1.0	.63	28	.25	•••	•••	rem	.600
	-1.0	.71	30	rem	•••	•••	rem	.593
	-1.0	.73	rem	rem	•••	•••	rem	.580
	-1.0	rem	rem	rem	•••	•••	rem	.510
	Genet	ic corre	elation	between	SCS a	and clini	ical mas	stitis of .60:
	-1.0	.85	34	.55	25	09	30	.570
	-1.0	.73	36	.37			30	.566
	-1.0	.85	36	.32			rem	.559
	-1.0	.96	38	rem			rem	.551
	-1.0	.98	rem	rem			rem	.537
	-1.0	rem	rem	rem	•••	•••	rem	.445
Index	with 1	M daue	thtere r	er sire.				
mucx	Genet	ic corre	sinces p	hetween	902	and clin	ical mag	stitis of 70.
		52	_ 21		- 17		- 18	659
	-1.0	.50 51	21		17	10	10	651
	-1.0	.51	2.25	.2J	•••	•••	•••	643
	-1.0	.00	2J	rem	•••	•••	•••	.633
	-1.0	.01 Tem	Tem	rem	•••	•••	•••	577
	-1.0	IÇIII	ICIII	ICIII	•••	•••	•••	
	Genet	ic com	elation	between	SCS	and clin	ical mas	stitis of .60:
	-1.0	.81	28	.57	25	20	23	.612
	-1.0	.73	30	.30	•••	•••	•••	.002
	-1.0	.83	32	rem	•••	•••	•••	.293
	-1.0	.84	rem	rem	•••	•••	• • •	.581
	-1.0	rem	rem	rem	•••	•••		.503
	· · ·							

Index coefficients standardized and presented relative to somatic cell score and accuracy for a sire index assuming clinical mastitis and milking labor as breeding objective. TABLE 4.

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1

2

SCS = somatic cell score; UD = udder depth; TL = teat length; TP = teat placement; UC = udder cleft; FU = fore udder attachment; MY = milk yield.Traits designated ... were sequentially removed and not allowed to re-enter because they contributed less than one percent to the standard deviation of the index.Traits designated rem were sequentially removed and not allowed to re-enter based on their contribution to the index.3

 $T=\sum_{i=1}^{n} (1-i) \sum_{i=1}^{n} (1-i) \sum_{i=1}^$ 

1.5