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**The Application of Artificial Neural Networks  
to the Detection of Bovine Mastitis**

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March 1998

A thesis submitted to the Faculty of Graduate Studies and Research in partial fulfilment  
of the requirements for the degree of Master of Science

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Short Title: Detecting Mastitis Using Neural Networks

## TABLE OF CONTENTS

Title .....	i
Short Title .....	ii
Table of Contents .....	iii
Abstract .....	vi
Résumé .....	viii
Acknowledgements .....	x
Preface of Thesis .....	xi
List of Tables .....	xiii
List of Figures .....	xiv
List of Abbreviations .....	xv
List of Appendices .....	xvi
 CHAPTER 1 GENERAL INTRODUCTION .....	 1
1.1 INTRODUCTION .....	2
1.2 MASTITIS .....	3
1.3 OVERALL OBJECTIVES OF THIS RESEARCH .....	4
1.4 REFERENCES .....	5
 CONNECTING STATEMENT .....	 6
 CHAPTER 2 LITERATURE REVIEW .....	 7
2.1 IMPORTANCE OF MASTITIS RESEARCH .....	8
2.2 THE PAST AND CURRENT STATUS OF RESEARCH INTO DETECTING BOVINE MASTITIS .....	 9
2.2.1 The Bacteriologic Culture Approach .....	9
2.2.2 Indirect Indicators of Mastitis .....	9
2.2.2.1 The predictability of an electrical conductivity of milk for mastitis .....	 10
2.2.2.2 Somatic cell counts as an indicator of mastitis .....	11

2.2.2.3 Use of NAGase and blood serum albumin as a predictor of mastitis.....	12
2.2.2.4 Conformation traits as predictors of mastitis.....	12
2.2.3 Prediction of Mastitis Occurrence Using Statistical Modelling.....	13
2.2.4 An Emerging New Technology—Artificial Neural Network .....	15
2.3 REFERENCES .....	18
CONNECTING STATEMENT.....	26
CHAPTER 3 NEURAL DETECTION OF MASTITIS FROM DAIRY HERD IMPROVEMENT RECORDS.....	
3.1 ABSTRACT.....	28
3.2 INTRODUCTION .....	29
3.3 MATERIALS AND METHODS.....	31
3.3.1 Artificial neural networks.....	31
3.3.2 Data and variables .....	32
3.3.3 ANN configuration.....	34
3.3.4 Measures to assess the ability of the ANN.....	35
3.3.5 ANN sensitivity to inputs .....	38
3.4 RESULTS .....	39
3.5 DISCUSSION.....	41
3.6 CONCLUSIONS.....	45
3.7 ACKNOWLEDGEMENTS.....	45
3.8 REFERENCES .....	46
CONNECTING STATEMENT.....	58
CHAPTER 4 IDENTIFICATION OF FACTORS INFLUENCING CLINICAL MASTITIS USING TEST-DAY PRODUCTION AND CONFORMATION DATA	

WITH ARTIFICIAL NEURAL NETWORKS .....	59
4.1 ABSTRACT.....	60
4.2 INTRODUCTION .....	61
4.3 MATERIALS AND METHODS.....	62
4.3.1 Artificial Neural Networks .....	62
4.3.2 Data and Variables .....	63
4.3.3 ANN Configuration.....	64
4.3.4 Measures to Assess the Ability of the ANN .....	65
4.4.5 ANN Sensitivity to Inputs .....	66
4.5 RESULT AND DISSCUSSION .....	67
4.6 CONCLUSIONS.....	72
4.7 ACKNOWLEDGMENTS .....	72
4.8 REFERENCES .....	73
CONNECTING STATEMENT.....	92
CHAPTER 5 GENERAL CONCLUSIONS.....	93

## **ABSTRACT**

### **The application of artificial neural networks to the detection of bovine mastitis**

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**(M.Sc., Animal Science)**

The overall objective of this research was to investigate the feasibility of using artificial neural networks to detect the incidence of clinical bovine mastitis and to determine the major factors influencing it. The first part of this research was devoted to a general examination of the learning ability of artificial neural networks by training them with relatively small data sets. These data sets (a total of 460,474 records) contained suspected indicators of mastitis such as milk production, stage of lactation and somatic cell count, and it was hoped that artificial neural networks would be able to detect what statistical modelling had already established elsewhere in the literature. The second part of this research was extended to examine the roles of more information resources such as conformation traits and their genetic values – factors that have not been studied extensively, with either conventional approaches or emerging technologies like artificial neural networks. This study consisted of 1,296,877 records representing 82,807 cows, 4,340 sires in 609 herds covering the period of December 1979 to November 1992. In the process of these investigations, the effects of data preprocessing and neural network architecture were also examined as they relate to quality of prediction. Results of analyses using a "relative operating characteristic" indicated that artificial neural networks could discriminate between mastitic states with an overall accuracy of 86% using conventional information. Conventional 2 x 2 contingency table analyses indicated that a training set with a high proportion of mastitic records yielded a neural network better able to predict presence of the mastitic state and vice versa. The most important production traits were found to be somatic cell count, stage of lactation and test-day milk production. Conformation traits were found to play an almost insignificant role in the prediction of clinical mastitis, especially when compared with test-day production variables. When comparisons were limited to the kinds of conformation data, cow

genetic proofs for conformation traits were found to have a greater influence than either sire genetic proofs or cows' phenotypic scores. However, on an individual basis, the only conformation traits which exhibited any association with the network's ability to predict clinical mastitis were phenotypic scores for rear-teat placement, dairy character and size, cow proof for dairy character, sire reliability for final score and sire proofs for pin-setting (desirability) and loin strength. This research showed that the combined use of "relative operating characteristic" and conventional 2 x 2 contingency table analyses, compared to using only one, could provide a more complete picture of the neural net's ability to discriminate. Sensitivity analysis proved useful in determining the influencing factors for a given prediction network. Results from the preprocessing of data indicated that such a practice may be worth exploring in future research.

## RÉSUMÉ

### L'application des réseaux de neurones artificiels pour la détection de la mammite bovine

**Xingzhu Yang**

**(M.Sc., Sciences Animales)**

L'objectif était d'explorer la possibilité d'utiliser les réseaux de neurones artificiels pour détecter l'incidence de la mammite bovine et déterminer les facteurs l'influençant. La première partie de la recherche a été consacrée à l'analyse de la capacité d'apprentissage des réseaux de neurones à l'aide de fichiers de données relativement petits (i.e., 460,474 observations au total). Ces fichiers contenaient des indicateurs tels le rendement laitier, le stade de lactation et le comptage leucocytaire, et les réseaux de neurones devaient détecter leur relation avec la mammite. Les résultats escomptés devaient être semblables à ceux obtenus par modélisation statistique et présentés dans la littérature. La deuxième partie de la recherche avait comme objectif d'examiner l'apport d'information additionnelle comme les traits de conformation et leurs valeurs génétiques, dont l'impact sur la mammite n'a pas été étudié de façon extensive autant avec les techniques conventionnelles qu'avec de nouvelles techniques. Pour cette étude, le fichier de données comprenait 1,296,877 observations représentant 82,807 vaches réparties dans 609 troupeaux et 4,340 taureaux, et couvrait la période de décembre 1979 à novembre 1992. L'effet du pré-traitement des données et de l'architecture des réseaux sur leur apprentissage a aussi été étudié. Les résultats basés sur l'analyse des caractéristiques relatives d'opération ont indiqué que les réseaux de neurones pouvaient classifier les observations avec une précision de 86% à l'aide des variables conventionnelles. L'analyse de contingence 2 x 2 a démontré qu'un fichier d'apprentissage contenant une plus grande proportion d'observations positives pouvaient mieux prédire la présence de mammite, et vice-versa. Les traits de production les plus importants étaient le comptage leucocytaire, le stade de lactation et le rendement en lait au jour du test. Le rôle des traits de conformation dans la prédiction de la mammite était négligeable comparativement aux données de production. En comparant les différentes données de conformation,

les épreuves génétiques des vaches avaient une plus grande influence que les épreuves génétiques des taureaux ou que les scores phénotypiques des vaches. Toutefois, sur une base individuelle, les seuls traits de conformation pour lequel un impact sur la mammite a été observé ont été le score phénotypique pour la position des trayons arrière, la grosseur et le caractère laitier, l'indice génétique des vaches pour le caractère laitier, la fiabilité de la cote finale du taureau, et les épreuves des taureaux pour la position des ischions la force du rein. Cette recherche a montré que, comparativement à l'utilisation d'une seule méthode d'analyse, l'utilisation combinée des analyses de contingence et des caractéristique relatives d'opération décrivait mieux la capacité discriminante des réseaux de neurones. Il a aussi été observé que les analyses de sensibilité étaient utiles pour déterminer l'influence relative des divers facteurs sur la détection de la mammite. Les résultats de pré-traitement des données ont indiqué que les recherches sur cette pratique valaient la peine d'être poursuivies.

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I thank my wife, Ping, and son, Yangshen, for their love and loyal support throughout this study.

## PREFACE OF THESIS

This thesis is comprised of original papers that have been and will be submitted to appropriate journals for publications. In accordance with part B, section 2 of the "Guideline Concerning Thesis Preparation" from the Faculty of Graduate Studies and Research, McGill University, I quote the entire text that applies to this format:

"Candidates have the option of including, as part of the thesis, the text of one or more papers submitted or to be submitted for publication, or the clearly duplicated text of one or more published papers. These texts must be bound as an integral part of the thesis.

If this option is chosen, **connecting texts that provide logical bridges between the different papers are mandatory**. The thesis must be written in such a way that it is more than a mere collection of manuscripts; in other words, results of a series of papers must be integrated.

The thesis must still conform to all other requirements of the "Guidelines for Thesis Preparation". **The thesis must include:** A Table of Contents, an abstract in English and French, an introduction which clearly states the rationale and objectives of the study, a comprehensive review of the literature, a final conclusion and summary, and a thorough bibliography or reference list.

Additional material must be provided where appropriate (e.g. in appendices) and in sufficient detail to allow a clear and precise judgement to be made of the importance and originality of the research reported in the thesis.

In the case of manuscripts co-authored by the candidate and others, **the candidate is required to make an explicit statement in the thesis as to who contributed to**

**such work and to what extent.** Supervisors must attest to the accuracy of such statements at the doctoral oral defence. Since the task of the examiners is made more difficult in these cases, it is in the candidate's interest to make perfectly clear the responsibilities of all the authors of the co-authored papers.”

This thesis contains a total of two manuscripts to be submitted for publications. Chapter 3 is prepared for Transactions of the ASAE , and has been shaped in accordance with its requirements. Chapter 4 has been in the format of the Canadian Journal of Animal Science for future submission. The two manuscripts are co-authored by myself, René Lacroix and Kevin Wade. The following is a breakdown of the contributions made by the authors towards the preparation of the two manuscripts submitted as part of this thesis.

#### Chapter 3

The candidate was responsible for conducting the research and preparing the manuscript . Assistance was provided by Dr. René Lacroix and Dr. Kevin Wade through their general guidance and editorial input in the preparation of the manuscript.

#### Chapter 4

The candidate was responsible for conducting the research and preparing the manuscript . Assistance was provided by Dr. René Lacroix and Dr. Kevin Wade through their general guidance and editorial input in the preparation of the manuscript.

## LIST OF TABLES

Table 2.1	Comparisons of the accuracy of prediction of mastitis by SCC from different studies .....	23
Table 2.2	Comparisons of predictive ability of logistic models, including a single absolute value, or absolute value plus inter quarter ratio .....	24
Table 2.3	Comparison of sensitivity and specificity of logistic regression models the milking of mastitis observation (T0), the milking before T0 (T12), and the milking 24h before T0 (T24).....	25
Table 3.1	The inputs used in the analyses (traditional or additional variables) And their treatment by the artificial neural network .....	50
Table 3.2	2X2 contingency table for assessing the ability of an artificial neural network .....	51
Table 3.3	Effects of mastitis proportions in training data files on the predictive abilities of the artificial neural networks at a given decision criterion of 0.5.....	52
Table 3.4	Relative importance (RI) of each of the inputs to the predictive abilities of the artificial neural networks that were trained and tested with data files containing a 1:1 ratio of mastitic to non mastitic records.....	53
Table 4.1	The role of each input in the artificial neural network trained with the production data only .....	77
Table 4.2	The role of each input variable in the artificial neural network (106-110-1 architecture) <sup>2</sup> trained with both production and conformation data. ....	79
Table 4.3	The role of each input variable in the artificial neural networks (89-110-1 architecture) trained with the conformation data only. ....	84
Table 4.4	The role of each group of conformation traits in the artificial neural network (106-110-1 architecture) <sup>2</sup> trained with both production and conformation data .....	88
Table 4.5	The effects of different ANN architecture on their performance of an artificial neural network .....	89

## LIST OF FIGURES

Figure 3.1	Three examples of relative operating characteristic curves representing different discrimination capacities where the accuracy indices are 0.75, 0.85, and 0.95. The minimum accuracy index is also shown .....	54
Figure 3.2	Relative operating characteristic analysis for the diagnostic accuracy of the artificial neural network that were trained and tested with traditional plus additional inputs, and a mastitic to non-mastitic ratio of 1:1 The area under the curved line represents the accuracy index of the artificial neural network and, 0.8598 .....	56
Figure 4.1	Diagram of the size, structure and architecture of the various data sets Used in these analyses .....	90
Figure 4.2	A 2x2 contingency table for assessing the ability of an artificial neural networks .....	91

## LIST OF ABBREVIATIONS

ABV	absolute value
AI	artificial intelligence
ANN	artificial neural network
ARTN	adaptive resonance theory network
ATP	adenosine triphosphate
ATRY	antitrypsin
BLUP	best linear unbiased prediction
BSA	bovine serum albumin
CMT	California mastitis test
DHAS	dairy herd analysis service
EC	electrical conductivity
GRNN	general regression neural network
IDF	international dairy federation
IQR	inter quarter ratio
LRM	logistic regression model
LSCC	logarithm of somatic cell count
LSCS	logarithm of somatic cell score
LVQ	learning vector quantization
MSCC	mean somatic cell count for a herd
NAGase	<i>N</i> -acetyl- $\beta$ -glucosaminidase
PATLQ	Programme d'analyse des troupeaux laitiers du Québec
PE	processing element
PNN	probabilistic neural network
ROC	relative operating characteristic
SCC	somatic cell count

## **LIST OF APPENDICES**

Appendix 4.1	The monthly production data consisted of specific test-day variables from the Quebec Dairy Herd Analysis Service. These variables as well as their treatments by the artificial neural network, are shown below.....	97
Appendix 4.2	Further details on the specific conformation information traits as well as the classification procedure.....	98

## **CHAPTER 1**

### **GENERAL INTRODUCTION**

## 1.1 INTRODUCTION

The human society has evolved to a new era -- "the information age". The world has become a global village in terms of world-wide information access, instant information flow and a global share of information resources. This age has been in part shaped by the information related technologies such as E-mail, the World Wide Web, and on-line real time multi-media, i.e. the information super highway. As a result of significant improvements in the area of computer technology (both software and hardware), artificial intelligence (AI), a branch of computer science concerned with designing intelligent computer systems, is emerging from the laboratory and is taking its place in human affairs and assisting in human decision making and reasoning. It is now one of the fastest growing segments of the computer industry. The artificial neural network, for example, is one of the AI technologies that is demonstrating promise for applications in different domains. Its software products have been on the market for a few years, and are becoming more popular and user-friendly. An artificial neural network is defined as a computing system that mimics living nervous systems. This new technology has been developing rapidly in the recent decades. For instance, while neural networks in the 1980s were mainly dedicated to military applications in artificial intelligence, this decade saw the release of commercial professional systems for non-military applications (Hassan and Tohmaz 1995; NeuralWare 1993). Its successful applications have covered wide domains such as the prediction of finances, signal analysis processing, robotics, and clinical diagnosis (NeuralWare 1993). These applications have attracted interest from people working in diverse fields. In recent years interest in artificial neural networks has been extended to applications in agricultural related industries. A number of studies have shown the advantages of artificial neural networks over more conventional approaches. These studies have demonstrated the applicability of the neural networks for modelling natural systems and the possibility of making automated agriculture a reality in the next century (Cook and Wolfe 1994). Although research into its applications for the animal industry is still in a nascent stage, it has been rapidly expanding. Investigations have involved such areas as meat quality control, projection of 305 day milk yields, detection of egg fertility, and diagnosis of mastitis (Lacroix et al. 1995; Yang et al. 1995; Nielen et al. 1994; Brethour 1994). However, compared with the other domains, these validations have been very limited. Where and how to use

artificial neural networks in animal industries still remains to be fully elucidated. This lack of direction forms part of the motivation for this study.

## **1.2 MASTITIS**

Mastitis continues to be a costly disease in modern dairy farming despite considerable efforts dedicated to solving it for the last two centuries. On a global scale, losses from mastitis in the dairy industry account for billions of dollars annually. The recent emphasis placed on mastitis control by the dairy industry has been due not only to its economic consequence, but also due to its association with improvements in production performance. Considerable research has revealed that mastitis has increased along with selection gains in performance (Shook and Schutz 1994; Shook 1989; Schutz 1994; Rogers and Hargrove 1991). These results emphasise the need for further research into mastitis control.

Mastitis is a multifactor disease, and as such its control has to be made from different perspectives. To date, herd management is one of most effective tools for reducing mastitis related costs, although some have proposed that selection for genetic resistance to mastitis would be promising as well. It was found that an early diagnosis of mastitis could reduce production losses and shorten the duration of antibiotic treatments, which in turn reduce other related costs. Conventional methods for the identification of mastitis employ indirect indicators such as somatic cell counts, the electrical conductivity of milk, and bovine serum albumin levels. While a number of investigations have shown that a certain degree of predictability can be obtained individually for mastitis by each of the individual indicators, recent studies have implied that statistical modelling of mastitis occurrence with the involvement of more indicators would provide a more accurate prediction (Berning and Shook 1992; Emanuelson et al. 1987). While increasing the number of input variables into a statistical model can enhance a model's predictive ability, such an increase in the number of input variables involved, also increases the required computing capacity. This is especially true for analysing non-or-all traits like a disease incidence and has been highlighted by several authors. It is obvious that a modelling system in which more information can be taken into account would be

preferable. An artificial neural network might be an alternative because the computing capacity is required much less due to its parallel distribution nature compared to a statistical based method, leading to the second motivation for the study into the applications of artificial neural networks in detecting mastitis.

### **1.3 OVERALL OBJECTIVES OF THIS RESEARCH**

This research is intended to examine the general learning ability of Artificial Neural Networks for prediction of the incidence of clinical bovine mastitis. How well ANNs can learn from past data is the first and most important question to be answered in the first part of this project. Successfully proving learning ability of ANNs will lead to our interest in betterment of its predictive ability by exploring more information resources as ANNs have no limitation on number of input variables taken in and facilitate the combination of different input types. This would naturally become our focus in the subsequent research. Identification of those variables having close associations with mastitis incidence has been one of the goals of this studies. In addition, an examination of the advantages and disadvantages of the various methods used in the assessments of learning ability of ANNs will be pursued as well

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## CONNECTING STATEMENT

Chapter 1 has presented a general picture about the information age, indicated some of new technologies that have emerged and shown some of the application potentials of artificial neural networks for a variety of domains. Successful applications of ANNs in other domains have inspired an interest in initialising this form of research in relation to animal industries. The question of where and how to use this ANNs in animal industries has been one of the initial motivations for this project. More specifically, this study intends to validate the potential of applying ANNs to detecting bovine mastitis, which remains an outstanding problem for the dairy industry. Before starting this new research, a full literature review on the advancements in mastitis detection will help understand some important information resources, which might be associated with mastitis. Therefore, the following chapter will be fully devoted to the assessment of past studies related to mastitis detection.

## **CHAPTER 2**

### **LITERATURE REVIEW**

## 2.1 IMPORTANCE OF MASTITIS RESEARCH

Mastitis, defined as an inflammation of udder, has appeared in literature for about two centuries and although considerable research effort has been devoted to solving the disease, it remains a serious problem facing the dairy industry (Morse 1977). Currently, the importance paid by the dairy industry towards the healthy status of a cow's udder is associated with the following: First, the udders themselves are an important organ for milk production with their health status directly determining the value of a cow. Without a healthy udder, a cow is nearly worthless regardless of the breeding value she might have for other traits or the level of milk yield she has had in the past.

Second, from a perspective of genetic improvement, a high occurrence of mastitis would certainly reduce selection intensity for other traits, resulting in a less aggregate genetic progress. Third, mastitis has been widely recognised as one of the most costly diseases in the dairy industry, and has a direct impact on the profit of dairy farms. A study of an experimental herd in Michigan has shown that mastitis was the second most important trait for determining the profit associated with herd life following milk yield. Fourteen percent of profit variance was attributed to mastitis (Andrus and McGilliard 1975). The associated costs include decreased milk yield and its related components, medical treatments, veterinary services, labour costs, nondeliverable milk, involuntary culling and poor milk quality. In addition, the poor milk quality leads to economic loss for the milk-processing sector such as a reduction in cheese yield. It was reported that the cost of mastitis for the dairy industry of New York state alone was nearly \$150 million (U.S.) annually (Miles et al. 1992). For the whole USA such losses were estimated to exceed \$2 billion (National Mastitis Council 1987).

In the United Kingdom the estimate was £100 to £120 million per annum (Booth 1988; Hillerton and Walton 1991). Other economic studies of mastitis costs in U.S., Canada, Sweden, the Netherlands, U.K. and Australia showed similar results that dairy farmers suffered from monetary loss ranging from \$150 to \$250 per year per cow (Dobbins 1977; Gill et al. 1990; Heuven et al 1988; Janzen 1970; Miles et al. 1992; Monardes 1994). Fourth, mastitis incidence does not seem to decrease, but appears to increase along with the genetic improvement in milk production (Shook and Schutz 1994; Shook 1989; Schutz 1994; Rogers and Hargrove 1991). Finally, consumers in current society want animal products produced by healthy animals with minimal use of antibiotics and other

drugs. In short, both economic initiatives and social concern have reflected the necessity and importance of studying the mastitis problem.

## **2.2 THE PAST AND CURRENT STATUS OF RESEARCH INTO DETECTING BOVINE MASTITIS**

Mastitis has been associated with many factors such as herd management, sanitation, milking machines and the genetic resistance of an individual. Correspondingly, work towards solving the mastitis problem has been investigated from all perspectives. Herd management has been widely recognised as one of the most effective ways to reduce mastitis related costs since an early accurate diagnosis of mastitis can reduce production loss and shorten the duration of antibiotic treatments, thus diminishing losses incurred by discarding milk. Additionally, other mastitis related costs can be minimised or eliminated. The methods developed to detect mastitis can be broadly grouped into the following.

### **2.2.1 The Bacteriologic Culture Approach**

The early work was mainly dedicated to seeking the causal agent for mastitis, especially bacteriologic aetiology of bovine mastitis. By the early part of this century when the bacteriologic culture approach to detection of udder infection was available, a mastitis control program was immediately launched (Morse 1977; Dodd et al. 1977). The control program was aimed at reducing new infection rates and reducing the numbers of infected cows. However, it was soon obvious that the bacteriologic test to determine the status of the udder was time consuming and expensive, as well as unsuitable for large scale screening. In particular it proved unsuitable for monitoring herds or implementing the eradication of disease in population. As a result, research was directed to finding a simple and accurate method to identify infected quarters (or udder) from normal quarters.

### **2.2.2 Indirect Indicators of Mastitis**

Numerous investigations into the efficacy of a single indicator of mastitis such as an electrical conductivity of milk, somatic cell count, *N*-acetyl- $\beta$ -D-glucosaminidase (NAGase) activity and bovine serum albumin (BSA) levels, as well as conformation information analyses of individual animals, have been performed. Among these indicators, an electrical conductivity and somatic cell count of milk have been intensively assessed. Although to my knowledge there are few reports on a direct use of conformation information as a predictor of mastitis, some of studies have attempted to determine the association between conformation traits and mastitis status.

#### **2.2.2.1 The predictability of an electrical conductivity of milk for mastitis**

An electrical conductivity (EC) of milk as an indicator of mastitis has been the subject of published research reports since the 1940s (Hillerton and walton 1991) and is based on the fact that mastitis leads to changes in milk composition, especially ion concentrations. Mastitic milk has higher concentrations of sodium and chloride ions than normal milk, whereas the concentrations of lactose and potassium ( $K^+$ ) ions are decreased, causing the EC of mastitic milk to be increased. Based on those findings, a cowside device and an on-line system for detection of clinical and subclinical mastitis have been developed. The cowside device could be a useful advisory/veterinary tool (Hillerton and Walton 1991; Sheldrake and Hoare 1981), but the accuracy for the simple hand-held device was relatively low. An investigation by Sheldrake and Hoare (1981) showed that the mean sensitivity (i.e., correct identification of the occurrence of mastitis, also termed as a conditional probability of a true-positive) and specificity (i.e., correct identification of the absence of mastitis, also termed as a conditional probability of a true-negative) of EC for three herds was on average 49% and 79% respectively. An on-line mastitis detection system was developed to meet the needs of auto-milking systems in the modern dairy industry. To distinguish the changes in EC, several criteria have been investigated such as absolute value (ABV) of EC (referred to running averages of repeated measurements), and inter quarter ratio (IQR) (Nielen et al. 1994). Several studies pointed out that an infected quarter had a higher mean EC than normal (Nielen et al. 1992; Miller 1984; Fernando et al. 1982; Linzell et al. 1974; Sheldrake and Hoare 1981; Hillerton and Walton 1991), leading to the IQR being defined as the ratio between the quarter with the lowest value and

the other quarters of the same cow (Fernando et al. 1982; Gebre-Egziabher and Wood 1979). The assumption for this criterion was that all non-pathological factors influence the EC of all quarters equally. In this way the effects of other factors can be eliminated. Although most studies have proven that the EC of milk is a good indicator of infection (Fernando et al. 1982; Fernando et al. 1985; Gebre-Egziabher and Wood 1979; Nielen et al. 1992; Linzell et al. 1974), the sensitivity and specificity reported in those studies were on average about 70% and 85% respectively. Others found it less accurate (Sheldrake and Hoare 1981; Batra and McAllister 1984; Lansbergen et al. 1994) finding a sensitivity and specificity of below 65% and 75% respectively.

#### **2.2.2.2 Somatic cell counts as an indicator of mastitis**

SCC consists of many types of cells, including neutrophils, macrophages, lymphocytes and various epithelial cell types of the mammary gland (Kehrli and Shuster 1994). In the course of an inflammatory response of the mammary gland, alterations in SCC occur due to the recruitment of neutrophils into the cow's defence mechanisms. Therefore, changes in SCC can illustrate changes the health status of the quarters. SCC has been routinely recorded as an indicator of mastitis and tends to be proposed as an useful selection criterion for dairy cattle breeding programs (Heuven et al. 1988; Kehrli and Shuster 1994; Zhang et al. 1994; Andersson-Eklund and Danell 1993; Shook and Schutz 1994; Dekkers et al. 1994). However, the use of SCC alone to discriminate between normal and infected quarters needs a set of threshold values, which directly affects the usefulness of SCC in the prediction of mastitis. As a consequence, SCC as a decisive indicator of mastitis is still under question (Noordhuizen et al. 1987). The results of the past studies on the identification of mastitis by SCC are presented in Table 2.1. Those results showed that SCC as an indicator of mastitis in general had a low to moderate predictability. Compared with the electrical conductivity, SCC proved less accurate in differentiating between mastitic and normal cows. Also, the different studies outlined in Table 2.1 showed a great deal of variability. This could be attributable to the following factors. a) SCC threshold level, i.e. setting a low level of SCC threshold could result in high sensitivity and reduce the number of cows incorrectly classified as negative (false-negative); whereas setting a high threshold could lead to high specificity reducing the false-positive rate. b)

The prevalence of mastitis in a population, i.e. in a population with low prevalence of mastitis, most of the cows would not have mastitis, thus the probability of classifying healthy cows as infected is high. In these circumstances SCC has a low posterior probability of a true-positive response. In contrast, SCC has a low probability of a true-negative response when a high prevalence of mastitis exists in a population. c) The dilution of SCC, i.e. high SCC milk from infected quarters can be diluted with low SCC from uninfected quarters, which always happens in the bucket milk; d) other factors: milking equipment and time, the age and parity of cows and antibiotic therapy could result in a raised SCC. The disagreements among the findings of past studies, because of the above factors, have made it difficult to establish a fixed baseline for concentration of SCC in distinguishing normal from mastitic quarters. Hence, the International Dairy Federation (IDF) no longer recommends the use of a fixed threshold SCC value to determine the healthy status of quarters (Jensen and Knudsen 1991). In addition to the direct use of the SCC absolute value, other alternatives such as log-transformation of SCC, the inter-quarter ratio (IQR), and the California Mastitis Test (CMT) have also been attempted in order to improve detection of mastitis.

#### **2.2.2.3 Use of NAGase and blood serum albumin (BSA) as a predictor of mastitis**

NAGase activity and BSA levels have been reported to increase in cows with mastitis and are attributable to damaged secretory epithelial cells in mastitic cows. They are seemingly correlated with signs of mastitis, which have led to the possibility of using NAGase activity and BSA levels as rapid tests for determining the severity of clinical mastitis (Wilson et al. 1991). Unfortunately, most reports (Wilson et al. 1991; Fernando et al. 1985; Sheldrake et al. 1983; Emanuelson et al. 1987) have pointed out that the NAGase and BSA can not be used effectively to detect mastitic quarters in a cow. Only 50 % of established mastitic cows can be identified by these mastitic markers (Emanuelson et al. 1987; Sheldrake et al. 1983; Fernando et al. 1985).

#### **2.2.2.4 Conformation traits as predictors of mastitis**

To our knowledge, studies using conformation traits as predictors of mastitis have not been done.

However, some of studies pointed out that there was a low to moderate relationship between some of the conformation traits and mastitis status (or its indicators) (Schutz 1994; Monardes et al. 1990; Rogers 1993; Seykora and McDaniel 1985), suggesting that conformation of individuals plays a minor role in the passive defence mechanism against infection. It seemed reasonable that conformation traits would not be a key indicator of mastitis, but inclusion of conformation traits in a model might improve its predictability for mastitis (Thomas et al. 1984). The use of conformation information to enhance predictability for mastitis has not been extensively studied, attributable to the high computing capacity demand required by a statistical model that simultaneously includes many factors (or variables), especially when modelling a none-or-all trait (Simianer et al. 1991; Emanuelson et al. 1993). Further studies in this area may result in better understanding of which conformation traits play a greater role than others in the detection of mastitis.

### **2.2.3 Prediction of Mastitis Occurrence Using Statistical Modelling**

Less effort has been made in the prediction of bovine mastitis using multiple indicators (Berning and Shook 1992). Reported investigations into this area have involved a combination of one indicator with its transformed value or combination of several different mastitis markers in cows. Using logistic regression, Emanuelson et al. (1987) found that for all indicators like adenosine triphosphate (ATP), SCC, NAGase, BSA, and Antitrypsin (ATRY), but not EC, combinations of absolute values and inter-quarter ratios were no better than predictions based on absolute values alone. Table 2.2 shows the predictive ability of the logistic model. In contrast, a number of studies drew the conclusion that including different indicators of mastitis in a model can enhance a model's ability to correctly classify the health status of a cow's quarters (Berning and Shook 1992; Emanuelson et al. 1987). For example, in the study by Emanuelson et al. (1987), the predictive ability of logistic model combining the two independent factors, log ATP and log EC was .701, which was higher compared to that of .680 for log ATP and .483 for log EC taken separately. The superiority of combining more indicators into a single function to improve predictive ability was supported by Berning et al (1992). In that study they pointed out that the log NAGgase was relatively more effective in identifying major pathogen infections from minor ones, whereas log SCC was better able

to differentiate between infected and uninfected classes. A reasonable explanation was that SCC measures the cellular response to bacterial infection, while NAGase activity reflects secretory cell damage. The study recommended that the final predictors of infection status be herd, log SCC, and log NAGase by stepwise logistic regression of bacterial status on herd, lactation number, milk, log SCC, log NAGase, and stage of lactation.

Statistical modelling of mastitis incidence has been extended to involve the use of electrical conductivity information. Recent studies using an on-line mastitis detection method in the Netherlands, by Nielen et al (1994) found that relevant information on EC appeared at the beginning and the end of the milking process after mapping EC data per quarter per milking. To capture the EC pattern and minimise the number of EC data points per quarter without losing information about the pattern, the measurements of EC of milk were taken for one-minute intervals at the start, middle, and end of each milking, with each quarter being milked sequentially. Four models were developed for three data sets taken during the observation periods defined as: the final period (T0), the milking 12 h before T0 (T-12) and the milking 24 h before T0 (T-24). Clinical mastitis, yes or no, was the dependent variable in all data sets.

model 1)  $MAX^1 + MAX^2 + MAX^3 + SD^1 + SD^2 + SD^3$ ,

model 2) as 1) + RPROD + CTEMP,

model 3)  $MAXS^1 + MAXS^2 + MAXS^3 + SUMD^1 + SUMD^2 + SUMD^3$ ,

model 4) as 3) + RPROD + CTEMP.

Where 1, 2, and 3 are the first, middle and last milking intervals per observation period respectively; MAX is the maximum value of each of three milking intervals; SD is the standard deviation of the 12 points defined in the study; MAXS is the maximum value of the smoothed data from each of the 3 milking intervals; SUMD is referred to the sum of the absolute value of the derivatives; RPROD is the relative milk production per cow per milking calculated as the percentage of the production 24 h before, and CTEMP is the pre-processing milk temperature determined by subtracting the population mean from the per cow observation.

A comparison on the accuracy of the models is shown in Table 2.3. These results generally showed

that statistical modelling that included more information on the electrical conductivity of milk offered better predictability in terms of the sensitivity and specificity. The limited results from statistical modelling of mastitis incidence using a multiple factor statistical approach revealed some enhancements in predictability compared with using only single factors, indicating a promising approach for the detection of mastitis. However, more investigations in this area are required.

#### **2.2.4 An Emerging New Technology -- Artificial Neural Networks**

An artificial neural network (ANN) --a computer-based simulation of living nervous systems resulting from research into artificial intelligence (AI), is a relatively new technology and is an important branch of artificial intelligence (NeuralWare 1993; Zurada 1992). Its applications have developed rapidly in last fifteen years, especially in areas such as signal processing, the prediction of finances, robotics, detection of explosives in checked airline baggage and clinical diagnoses (NeuralWare 1993; Hassan and Tohmaz 1995). These successes have inspired research initiatives in other domains. For example, researchers on the Human Genome Project at the Los Alamos National Laboratory in Los Alamos, N. M. have applied neural network algorithms to the problems of DNA sequence analysis (Kestelyn 1993). A study of a back-propagation neural network to predict average air temperature has pointed out that neural networks have considerable potential for modelling natural systems (Cook and Wolfe 1991).

Additionally, there has recently been a growing interest in applying ANNs to agriculture-related applications. Zhuang and Engel (1990) attempted to use an ANN with the back-propagation technique in order to recommend a herbicide and an appropriate application system for a given field situation. The problem of selecting an appropriate grain marketing alternative was also overcome with a more complex neural network architecture. It was pointed out that ANNs generally worked faster than other systems such as an expert system. The application of an ANN to predict apple quality provided direct evidence for its merit, in that the remaining error unexplained by the linear model was reduced by 5% using multilayer neural networks (5). Guan and Gertner (1991) applied an ANN to modelling and predicting red pine seedling survival. The results indicated that the ANN-

based red pine seedling survival model not only fit the data better than a statistical model, but was also expected to perform better on future data provided that the training data was representative. Dolenko et al (1995) worked on classifying cereal grains using backpropagation and cascade correlation networks and pointed out that in comparison with a Gaussian classification technique, ANNs delivered higher classification accuracy and were more attractive for implementation in automated grain inspection systems. Ding and Dunasekaran (1994) applied an ANN as a multi-index classifier for food quality and concluded that accuracy and speed of classification were greatly improved. Neural network modelling for predicting flowering and physiological maturity of soybean was performed by Elizondo et al (1994) and shown to be promising.

Although most validations of ANN in animal industry are in a nascent stage, there have been some of examples that show promise. For instance, Lacroix et al (1995) predicted 305-day milk, fat and protein production in dairy cows and found that ANNs generally performed at least as well as the model currently used by Canadian milk recording agencies. The use of ANNs for estimating marbling score in live cattle was more accurate than using the same features in a multiple regression model (Brethour 1994). Neural networks were also used to detect fertility of eggs (Das and Evans 1992). Attempts to apply ANNs to detect bovine mastitis has been made in recent years (Nielen et al. 1994; Yang et al. 1995). The results from those studies have shown a slightly better discriminatory ability to distinguish between mastitic and non-mastitic cows using ANNs compared to statistical modelling. However, it was recommended that further improvement in predictability of ANNs should be pursued through exploration of existing information and manipulation of their internal characteristics.

In a broad sense ANNs have been demonstrated to be a very useful tool in various domains. Their applications have covered wide areas. For the macro-world ANNs can be used for tasks from battlefield management to minding the baby and for the micro-world they can be applied to detecting DNA sequences (Kestelyn 1993), protein structures (Salt et al. 1992), as well as identifying micro-organisms (Chun et al. 1993). The reason for the popularity of ANNs is due to their advantages over the traditional approaches. One of the most distinctive advantages is that there is no need to begin

with an a priori model, nor is there a need to identify the required variables beforehand (Lacroix et al. 1995). With ANNs, no assumptions are required with regard to input and output variables. ANNs are able to internalise the implicit relationships existing between inputs and outputs, and are particularly powerful in approximating highly non-linear relationships. In addition, ANNs have no limitation on the number of input variables taken and also facilitate the combination of different input types. All these advantages have made ANNs a powerful tool for handling information sources. On the other hand, ANNs like other methods have some limitations. For example, the relationship between inputs and outputs can not be explicitly explained. But ANNs, as a new technology and a new alternative, provide renewed hope of solving old problems, which have been difficult to be overcome using traditional approaches.

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TABLE 2.1 Comparison of the accuracy of prediction of mastitis by SCC from different studies

Sources	Sample type	Threshold or log-transformation	SS	SP	Comment
(20)	foremilk	6.05	40.8	75	low
	stripping	6.85	40.3	73	low
	bucket	6.28	49.5	71	low
(19)	foremilk		81	92	high
(53)		200,000	88		high
(50)		500,000	75		middle
(58)		500,000	66		low
(45)	bucket	500,000	53		low
(56)	bucket		51		low
(34)	bucket	400,000	41		low

Where the SS represents the sensitivity of SCC for differentiation of mastitis,  
the SP represents the specificity of SCC for differentiation of mastitis.

TABLE 2.2 Comparison of predictive ability of logistic models, including a single absolute value of indicator, or absolute value plus inter quarter ratio

Component	IQR	ABS	IQR + ABS
Log SCC	0.476	0.675	0.683
Log ATP	0.482	0.680	0.655
Log NAGase	0.443	0.596	0.560
Log BSA	0.378	0.507	0.461
Log ATRY	0.237	0.454	0.351
Log EC	0.465	0.483	0.603

Where the IQR and ABS represent inter quarter ratio and absolute value respectively.

TABLE 2.3 Comparison of sensitivity and specificity of logistic regression models (LRM) the milking of mastitis observation (T0), the milking before T0 (T12), and the milking 24 h before T0 (T24)

Time	n	SS (%)	n	SP ( %)
T0				
Model 1	34	76	37	86
Model 2	26	77	32	94
Model 3	32	78	36	83
Model 4	25	84	31	90
T-12				
Model 1	36	67	44	87
Model 2	30	67	38	89
Model 3	34	71	42	90
Model 4	29	76	36	92
T-24				
Model 1	36	67	36	81
Model 2	25	72	33	85
Model 3	32	63	35	86
Model 4	23	70	32	88

Where the SS represents the sensitivity of Logistic Regression Model.

the SP represents the specificity of Logistic Regression Model.

## CONNECTING STATEMENT

The past studies of mastitis detection, reviewed in the previous chapter, have indicated the basic conclusion that individually, each of the indicators for mastitis status was limited in terms of their discriminating ability and pointed to the importance of including different indicators in a model for the prediction of this multi-factor related disease. While statistical modelling of mastitis is able to account for more input variables, it has some limitations as well. For instance, a high computing capacity is required when more input variables are included in a model, especially for an all-or-none trait. In contrast, ANNs has no such a limitation. Also ANNs are able to process information faster due to parallel distributing processing. Moreover, there is no need to begin with an *a priori* model. All these advantages imply that ANNs may be a potential alternative to more traditional approaches, especially for the mastitis problem. The next chapter will focus on the feasibility of using ANNs to detect bovine mastitis using test day milking records available.

## **CHAPTER 3**

### **NEURAL DETECTION OF MASTITIS FROM DAIRY HERD IMPROVEMENT RECORDS**

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### **3.1 ABSTRACT**

A back-propagation artificial neural network was employed to detect clinical mastitis in a file of 460,474 test day records. Two data files were created to train the artificial neural networks, containing a relatively large (1:1) ratio and a relatively small (1:10) ratio in the incidence to non-incidence of clinical mastitis. These ratios were applied to each of two input file designs: one comprised variables that are traditional in the modelling of mastitis (e.g., age, stage of lactation and somatic cell count) and a second included additional variables (e.g., season of calving, milk components and conformation class). Results from analyses of relative operating characteristics indicated that artificial neural networks could discriminate between mastitic states with an overall accuracy of 86%. This discriminatory ability was subject to patterns that existed in the training data files but was not affected by differing proportions of mastitic records. However, conventional analyses with a 2 x 2 contingency table indicated that differing proportions of mastitic records in the training data files had some effect on the particular purpose of the artificial neural network being developed. Results suggested that the relative operating characteristic method and contingency table analyses should be jointly used to assess diagnostic systems. Additional variables had little effect on the prediction accuracy, but this lack of effect needs to be verified for optimal artificial neural network configuration, data preprocessing, and new sources of information.

### **KEYWORDS**

Artificial neural networks; Bovine mastitis; Detection; Test day records.

### 3.2 INTRODUCTION

Mastitis, an inflammation of the udder in cows, is widely recognised as one of the most costly diseases in the dairy industry that directly impacts the profit of dairy farms. A study of an experimental herd in Michigan found that mastitis was the second most important trait, following milk yield, to determine the profit of herd life. Fourteen percent of the variance of profit was attributed to mastitis (Andrus and McGilliard, 1975). Miles et al. (1992) estimated that the cost of mastitis for the New York state dairy industry alone was nearly \$150 million annually. Throughout the US, loss caused by mastitis has been estimated to exceed \$2 billion/yr (National Mastitis Council, 1987), and in the United Kingdom, the cost was estimated to be \$150 to \$200 million/yr (Booth, 1988; Hillerton and Walton, 1991). Other studies of mastitis in the US, Canada, Sweden and The Netherlands have shown that dairy farmers suffered monetary loss ranging from \$125 to \$250/yr per cow (Dobbins, 1977; Gill et al., 1990; Heuven et al., 1988; Janzen, 1970; Miles et al., 1992; Monardes, 1994). Therefore, mastitis continues to be one of the leading disease and management problems afflicting the dairy cattle industry.

Although an early and accurate diagnosis of mastitis has long been sought, no perfect technique exists. Some of the more conventional methods used to identify subclinical mastitis employ indicators such as stage of lactation and somatic cell count (SCC). Somatic cell count is routinely recorded in dairy herd management programs and is often cited as being useful in selection decisions for breeding programs of dairy cattle (Andersson-Eklund and Danell, 1993; Dekkers et al., 1994; Heuven et al., 1988; Shook and Schutz, 1994; Zhang et al., 1994). However, its use as an indicator of mastitis remains inconclusive (Noordhuizen et al., 1987). For example, findings from past research regarding the discriminatory ability of SCC to determine mastitic states vary greatly, suggesting sensitivities (i.e., correct identification of the occurrence of mastitis) and specificities (i.e., correct identification of the absence of mastitis) of SCC in the range of 40 to 70% and 60 to 89%, respectively (Fernando et al., 1982; Fernando et al., 1985; McDermott et al., 1982; Rindsig et al., 1979; Schultz, 1977; Sheldrake et al., 1983). Other approaches to detect mastitis include the use of statistical modelling which produced a 70% accuracy by considering such effects as herd,

lactation number, stage of lactation, milk yield on test day, SCC, and N-acetyl-13-D-glucosaminidase (Emanuelson et al., 1987). Definitive findings by Berning and Shook (Berning and Shook, 1992) and Emanuelson et al. (1987) support the importance of including different indicators in a model so that the ability to distinguish between mastitic and nonmastitic cows is enhanced.

Recent investigations (Allore and Jones., 1995; Allore et al., 1995; Hogeveen et al., 1995a; Hogeveen et al., 1995b; Nielsen et al., 1994) into the problem of the detection of mastitis include the use of expert systems and artificial neural networks (ANN), which promise better diagnostic results through the employment of increasingly more factors. Artificial neural networks, computing systems comprised of simple, highly interconnected processing elements (PE) that mimic the structure of the human nervous system, are gaining recognition as plausible alternatives for solving real world problems. ANN have been successfully applied in such areas as financial prediction, signal analysis processing and robotics, and clinical diagnoses. To date, however, there have been relatively few instances in which ANN have been applied to agriculture and even fewer instances in which ANN have been applied to the animal industry. In agriculture, research into the applications of ANN has encompassed areas such as the prediction of corn yields (Uhrig et al., 1992), herbicide selection (Zhuang and Engel, 1990), apple quality classification (Bochereau et al., 1992), red pine survival rate prediction (Guan, 1991), and the evaluation of potted plant arrangements (Brons et al., 1991). In the animal industry, ANN have been employed less often, although investigation into their use has been rapidly expanding in recent years, and their success rate is, even in a nascent stage, consistent with that of traditional methods. For example, Lacroix et al. (1995a) predicted 305-d milk, fat, and protein yields in dairy cows and found that ANN generally performed at least as well as the model currently used by Canadian milk recording agencies. The use of ANN to predict meat quality in live cattle has also been studied extensively, producing positive results (Brethour, 1994; Park et al., 1993; Whittaker et al., 1991). Although research by Nielsen et al. (1994) has shown that ANN can differentiate between mastitic and non mastitic cows reasonably well, further study into the methodology remains necessary in many areas. One such area is data preprocessing (the treatment of data prior to their presentation to the ANN). Previous studies (Lacroix et al., 1995b; Lacroix et al., 1997; Lawrence, 1991) have shown that the distribution of output data in training data sets can

have a major influence on the learning of ANN. Another area of study is the assessment of the ability of an ANN to perform specific tasks, since applications based on this approach are relatively recent.

The objective of this research was to evaluate the feasibility of predicting the rate in the incidence of clinical mastitis in individual cows with ANN using test day yield and selected conformation data. The specific objectives were 1) to check the ability of an ANN to differentiate between mastitic and nonmastitic cows, 2) to examine the effect of differing proportions of the rate in the incidence of clinical mastitis in training data files on the learning ability and classification accuracy of an ANN, 3) to compare the accuracy of prediction using traditional variables versus an expanded file of variables (traditional plus additional), 4) to detect variables that have large degrees of influence on the prediction of clinical mastitis using sensitivity analyses, and 5) to examine the advantages and disadvantages of the various methods used in the assessments.

### **3.3 MATERIALS AND METHODS**

#### **3.3.1 Artificial neural networks**

Derived from research in artificial intelligence, ANN were designed to mimic the structure of the human nervous system in order to perform certain complex functions of a human brain, such as reasoning and learning. Artificial neural networks consist of PE and interconnections that correspond to neurons and synapses in the human nervous system. Grouped in layers, PE are the basic units of the ANN in which neurocomputing takes place. The PE that receive information from the environment form the input layer and the output layer of PE is responsible for generating output signals. The PE located between the input and the output layers form the hidden layers, and their number depends on the complexity of a given problem. Interconnections, or weights, store and represent the knowledge acquired by the ANN. Through interconnections, PE in one layer can be connected fully, randomly, or correspondingly to those in an adjacent layer. The basic computations of ANN can be outlined as follows. The PE receive input signals from an environment or a previous layer, and an operation of weighted summation takes place over all inputs. Finally, output signals

are generated by transforming the received signal via a transfer function and are transmitted to the next layer. This basic process takes place in every PE.

There are two main phases in a network operation: learning and recall. The former is the process of adapting or modifying the connection weights in response to stimuli that are being presented to the input buffer and, optionally, to the output buffer. In the recall phase, the same kinds of stimuli are presented to the trained network, which generates corresponding output signals for specific purposes (NeuralWare, 1993). A variety of ANN can be constructed based on differences in the arrangement of the layers, the interconnection of the PE, and the learning procedure employed. For this research, a feed-forward, back-propagation method was employed. Back-propagation ANN are believed to be well suited for prediction and classification problems. In the learning process of a back-propagation ANN, pairs of inputs and outputs are fed to ANN and the basic neurocomputing is then carried out in each PE. The difference between the outputs generated by the network and the actual outputs is calculated and taken as a learning signal to be back-propagated into the ANN. All weights in the ANN are then adjusted to reduce this error as much as possible. All inputs and outputs can be presented repeatedly to the ANN, which progressively changes its weights in a gradient-descent fashion. Through this process, the ANN can acquire knowledge from a data file.

### **3.3.2 Data and variables**

The data for this research (individual Holstein test day records from December 1979 to November 1992) were supplied by the Québec Dairy Herd Analysis Service. The original data contained 885,403 records representing 35,824 cows and 147 herds of which 2550 records indicated an incidence of clinical mastitis. This indication of mastitis is reported by the farmer on the day of test and has the effect of flagging the record of that cow for the purposes of official yield projection. In theory, it only refers to incidence of clinical mastitis on the day of test, and its accuracy has sometimes been questioned in the past. However, for the purpose of this study, it was assumed to be accurate. Each record of the data had 75 fields of which, 15 were determined to contain the most valuable information to detect clinical mastitis. These fields were converted into a file of traditional

and a file of traditional plus additional variables that are listed in Table 3.1. Those considered traditional were essentially those variables or factors which have been used in previous research to predict subclinical mastitis, including herd effect, lactation number, SCC, milk yield on test day, and stage of lactation. In this study, herd effect was characterised by mean SCC for a herd and by the number of cows on the test day. The additional variables included, for example, date of test day, calving, and drying off as well as available conformation classes. The final conformation of cows was classified on a six-point scale (1 = excellent, 2 = very good, 3 = good plus, 4 = good, 5 = fair, and 6 = poor). These rankings, assigned by Holstein Canada classifiers, were based on linear combinations of various conformation traits, e.g., general appearance, dairy character, capacity, rump, feet and legs, mammary system, and fore and rear udders. The desired outputs were mastitic states as reported by farmers in test day records.

Because a zero value existed in one of the 15 fields of interest, 424,929 records were discarded, leaving a final data file of 460,474 records, 1545 of which indicated the presence of clinical mastitis. This final data file was separated into two data files based on the presence or absence of clinical mastitis (1545 and 458,929 records, respectively). Each of these data files was then further split into one third and two thirds by assigning the first record (in each group of three) to the first file and the next two records to the second file. The two training data files were then formed by combining records from both of the larger (2/3) data files. One training data file contained 50% mastitic and 50% nonmastitic records (i.e., a 1:1 ratio) and was thus created by using all 1030 mastitic records and an equal amount of nonmastitic records, assigned randomly from the other data file. This resulted in a data file of 2060 records with a 50% rate in the incidence of clinical mastitis. The second training data file comprised 10 nonmastitic records for every 1 mastitic record and, again, used all 1030 mastitic records and 10,300 randomly assigned nonmastitic records, which resulted in a data file of 11,330 records with a 9.1% rate in the incidence of clinical mastitis (i.e., a 1:10 ratio). The 1:10 ratio was chosen in an effort to model a ratio that is realistic (Batra et al., 1977; Miller, 1984; Wilson et al., 1991), and the 1:1 ratio allowed the ANN to be trained with more mastitic records than normal in order to determine whether an increase in the occurrence changed the ability of the ANN to predict clinical mastitis after training.

The data files that contained one third of the overall data were used to construct two testing data files and the same procedure used to create the training data files was followed. One of the testing files had a 50% rate in the incidence of clinical mastitis (1030 records, 515 mastitic and 515 nonmastitic); the other had a 9.1% rate in the incidence of clinical mastitis (5665 records, 515 mastitic and 5150 nonmastitic). These designs were applied to each of the input files (Table 3.1).

### **3.3.3 ANN configuration**

In order to perform the analyses, an ANN software (NeuralWare, 1993) which facilitates manipulation of the configuration (e.g., type of network, learning rate, momentum, and learning schedule) and architecture (i.e., numbers of hidden layers and numbers of PE in each of the hidden layers to be created) was used. Several architectures of ANN were tested, and the following, which produced good overall results, was employed. Three-layered back-propagation ANN were constructed with 10 PE in the hidden layer. In the first case, two ANN were constructed with 6 PE in the input layer, corresponding to the traditional variables, and trained with the data files containing 50 and 9.1% rates in the incidence of clinical mastitis, respectively. In the second case, two ANN were constructed with 23 PE in the input layer, corresponding to traditional plus additional variables, and were also trained with the corresponding data files. Inputs in this study were coded as continuous variables except for those involving season (i.e., season of calving, dry period and test day) where values, each represented by two binary inputs (00, 01, 10, 11), were used. Although conformation classes were coded as continuous variables, they were not always present, and an extra binary variable (0, 1) was used to indicate the presence or absence of the value for a particular animal. There were, therefore, 17 inputs, 3 of which were coded with 2 binary inputs, and 3 of which needed an additional binary flag to indicate their presence or not, giving the total of 23 (Table 3.1). It should be noted that, except in the case of the conformation variables, no other fields were missing due to initial edits. The ANN were trained with a normalised cumulative delta-rule learning rule and an epoch of 16 records for 100,000 cycles, at which point the classification ability of the ANN was no longer significantly improving. The transfer function in the PE was a hyperbolic tangent function.

Outputs from the ANN, representing predicted mastitic states, consisted of continuous values in the range from 0 to 1. To convert the continuous values into binary states to match the outputs with actual mastitis states, a value had to be artificially determined. This threshold value is analogous to a set level for generating a specific signal in an electronic device. A threshold, or decision criterion, can be any decimal number between 0 and 1, although the value of 0.5 is adopted in most cases. A decision criterion is regarded as an arbitrary value because of its dependence on the prior probability of an event, personal considerations of the values, and the costs associated with correct and incorrect decisions of both kinds (Swets and Pickett, 1982). In this study, various threshold values were used depending on the measuring methods described subsequently.

### **3.3.4 Measures to assess the ability of the ANN**

To evaluate the power of ANN to detect clinical mastitis, a comparison can be made using a 2 x 2 contingency table (Table 3.2). In Table 3.2, the symbols A, B, C and D denote the actual numbers of each observed outcome. The conditional probability for the true-positive response, (TP), is estimated by dividing the number of correctly predicted mastitic states by an ANN (A) by the number of actual incidences (A + C) (Swets and Pickett, 1982) This conditional probability, which is sometimes referred to as sensitivity, is expressed in Eq. (1).

$$P(TP) = \frac{A}{A + C} \quad (1)$$

The other three conditional probabilities of a true-negative (sometimes referred to as specificity), a false-positive, and a false-negative response are denoted as P(TN), P(FP), and P(FN), respectively, and can be obtained similarly (see Eqs. (2), (3), and (4)).

$$P(TN) = \frac{D}{B + D} \quad (2)$$

$$P(\text{FP}) = \frac{B}{B + D} \quad (3)$$

$$P(\text{FN}) = \frac{C}{A + C} \quad (4)$$

These four conditional probabilities measure different facets of the power of ANN to identify mastitic states. It should be noted that  $P(\text{TP}) + P(\text{FN}) = 1$  and  $P(\text{TN}) + P(\text{FP}) = 1$ .

From Table 3.2, two posterior probabilities of a true-positive and a true-negative response can be calculated that measure the reliability of the prediction of clinical mastitis by ANN. A posterior probability of a true-positive response,  $P(\text{PSTP})$ , can be obtained using Eq. (5) (Swets and Pickett, 1982):

$$P(\text{PSTP}) = \frac{A}{A + B} \quad (5)$$

The other posterior probability of a true-negative response,  $P(\text{PSTN})$ , can be similarly obtained using Eq. (6).

$$P(\text{PSTN}) = \frac{D}{C + D} \quad (6)$$

Equations (5) and (6) demonstrate how reliably ANN predict the presence or absence of clinical mastitis for each case and can, therefore, lead to degrees of confidence about certain management practices.

Furthermore, the overall probability of a correct response (i.e., the probability that the response is either true positive or true negative) is an additional measure employed to assess a diagnostic system. That probability,  $P(\text{TTCR})$ , is defined in Eq. (7) (Swets and Pickett, 1982):

$$P(\text{TTCR}) = \frac{A + D}{A + B + C + D} \quad (7)$$

Although equations 1 to 7 represent a certain way of measuring the ability of an ANN, each equation has a common weakness, a natural dependence on the prior probability of an event (e.g., in this study, a prior prevalence of mastitis in a population) and the choice of decision criteria; none of the measures, discussed previously, allows for the comparison of two distinct diagnostic systems in terms of either their screening ability or in terms of their ability to provide an accuracy index ( $A_z$ ). An  $A_z$  for the evaluation of a diagnostic system should reflect only an intrinsic accuracy and should be independent of any external factors (Swets and Pickett, 1982).

For these reasons, a preferred measure of accuracy called a relative operating characteristic (ROC) analysis was recommended by Swets (1988) and Swets and Pickett (1982). In order to construct an  $A_z$ , the ROC method uses the conditional probability of a true-positive response and the conditional probability of a false-positive response because all of the relevant information with regard to accuracy can be captured by these two outcomes. To estimate the single-valued  $A_z$ , outputs from a diagnostic tool are used to plot the conditional probability of a true-positive response against the conditional probability of a false-positive response for various settings of the threshold value. Figure 3.1 shows an ROC graph containing three curves. Each curve has several points which each represents one possible decision criterion; a curve represents the possible location of different points for a particular discrimination capacity. An appropriate nonlinear model is chosen to fit the curve, and the area of the entire graph that lies beneath the empirical curve is calculated. This proportion, relative to the entire graph, is defined as the  $A_z$  value, which has a theoretical range of 0.5 to 1.0. No discrimination exists for  $A_z = 0.5$ , i.e., when the curve is along the diagonal. The diagnostic tool can achieve an  $A_z$  of 0.5 by chance alone; in other words, this diagonal represents a situation in which the diagnostic information is so poor that abnormal and normal cannot be discriminated at a better than chance level. If  $A_z = 1.0$ , discrimination is perfect, illustrating that results from the diagnostic tool are correct regardless of the decision criteria. The solid curves in Fig. 3.1 represent discrimination capacities of diagnostic tools and demonstrate that these conditional probabilities for true-positive responses exceed the conditional probabilities for false-positive responses for every point along the curve. The curve deviation from the major diagonal is attributed to the discrimination capacities rather than to chance alone.

This ROC approach can be applied to ANN. The  $A_z$  value could indicate the real power of an ANN obtained from the training data file. The  $A_z$  would accurately measure the intrinsic capacity of a trained ANN to discriminate between mastitic and nonmastitic cows free of interference from external factors, such as prevalence of mastitis in a population and threshold values. This ROC analysis could be especially useful to compare the abilities of ANN trained with different proportions of mastitic records. In this investigation, the ROC analysis was designed to provide overall assessments of the power of ANN, and the 2 x 2 contingency table analyses were used to show the profiles of ANN or insights into the knowledge that ANN acquired at a given decision criterion of 0.5.

### **3.3.5 ANN sensitivity to inputs**

To examine the importance of each input in the detection of clinical mastitis, a sensitivity analysis was performed using the ANN that was trained with the data file that had a 50% rate in the incidence of clinical mastitis, and that included all inputs. Three sensitivity analysis techniques were proposed and tested by Lacroix et al. (1995a). The method used in this research was to disable individual PE in recall mode. More specifically, the ANN was first trained with all the inputs in the training data file. The PE in the input layer, corresponding to one input variable, was then disabled, and the output value of this PE was set to zero (for input variables with more than one corresponding PE, all PE were disabled). Following this, every record in the testing data file was recalled once. Finally, the results were compared with those from an ANN with no disabled PE. This protocol was applied to each input variable (i.e., 17 times). Results were compared using the criterion of overall probability of a correct response (i.e., probability that the response is either true positive or true negative); prior probability in the testing data file (i.e., 50%) and the decision criterion of 0.5 were the same for each disabling. In order to account for the role of each input, its relative importance (RI) was calculated as defined in Eq. (8).

$$RI = \frac{P(TTCR)_{ds} - P(TTCR)}{P(TTCR)} \times 100 \quad (8)$$

where  $P(TTCR)_{ds}$  is the overall probability of a correct response obtained from the ANN with disabled PE.

### 3.4 RESULTS

Figure 3.2 represents the ROC graph that was created from the output of the ANN with various settings of decision criteria. The ANN was trained and tested with the data file with a 50% rate in the incidence of clinical mastitis, involving traditional plus additional inputs. The empirical curve in Fig. 3.2 accurately reflects a fixed discrimination capacity of the trained ANN. The capacity in terms of  $A_z$  value is approximately 0.8598. Although none of the available research into the detection of clinical mastitis provides an  $A_z$  value and a direct comparison of the accuracy of ANN and conventional methods is near impossible, the accuracy achieved in Fig. 3.2 demonstrates that the ability of the ANN to predict mastitic states is quite good.

In order to examine the effect of differing proportions of clinical mastitis in training data files on the overall discrimination capacity of ANN, the ROC analysis was performed with the output from an ANN that was trained and tested by the data files with a 9.1% rate in the incidence of clinical mastitis. This analysis involved the traditional plus additional inputs. An  $A_z$  value of 0.8631 for the ANN revealed that the proportions of clinical mastitis did not produce obvious differences in the overall accuracy between the two trained ANN. However, results from the conventional 2 x 2 contingency table analyses (Table 3.3) suggested that training with an high proportion of mastitic records yielded an ANN that was favourable for predicting a mastitic state. The conditional probabilities of a true-positive and true-negative response were 0.746 and 0.841, respectively, for the training data files that contained a 50% rate in the incidence of clinical mastitis and 0.25 and 0.99, respectively, for the training data files that contained a 9.1% rate in the incidence of clinical mastitis (conditional probabilities of a false-positive and false-negative response were not included

in the results since they are complementary with the conditional probabilities of a true-negative and true-positive response, respectively (i.e.,  $P(TP) + P(FN) = 1$  and  $P(TN) + P(FP) = 1$ ). The results in Table 3.3 show that the overall probability of a correct response varied from one case to another: for example, the ANN trained and tested with the data files having a 50% rate in the incidence of clinical mastitis had a low overall probability of a correct response of 0.793 compared with 0.923 for the ANN that was trained and tested with the data files having a 9.1% rate in the incidence of clinical mastitis. This difference was due to the proportion, or prevalence, of clinical mastitis in testing data files rather than the intrinsic overall capacity that the ANN acquired.

The ROC and  $2 \times 2$  contingency table analyses were also applied to the files containing only the traditional variables. This allowed the effect of including new sources of information to be examined. Comparing the  $A_z$  values for the ANN that were trained with the data files having 50% and 9.1% rates in the incidence of clinical mastitis (0.8546 and 0.8653, respectively) and involving traditional input variables only, it appeared that additional inputs contributed little to the predictability of the ANN. This conclusion was further supported by the  $2 \times 2$  contingency table analyses with similar values in five corresponding measures between the traditional and the traditional plus additional input files shown in Table 3.3.

Table 3.4 presents the results from the sensitivity analyses for the ANN that was trained and tested with the data files that had a 50% rate in the incidence of mastitic containing traditional plus additional inputs. The first column of Table 3.4 indicates the name of the input variable that corresponds to the PE that were disabled each time. The importance of each of the variables is characterised in terms of the five probabilities that are shown in Table 3.4. The overall probability of a correct response was used as a general measure because all comparisons were made within the same configuration of an ANN and because the decision criterion and testing data file were the same for each disabling. To facilitate visualization, a relative importance was calculated and is listed in the last column. A higher relative importance (in absolute terms) indicates a variable with a greater impact on the accuracy of the prediction.

From the evidence in Table 3.4, input variables can be classified into three groups. The group of inputs including stage of lactation, milk yield on test day, cumulative milk yield, SCC, and mean SCC for a herd has the greatest effect on the prediction of clinical mastitis. Fat percentage on test day and cumulative fat yield compose the second group, and the remaining input variables apparently do not play a significant role. Some variables may even provide a negative effect on the quality of an output, such as drying off, conformation classes for sires and dams, and herd size on test day. As a result, the effect of these latter inputs is not clear. For instance, SCC on test day had a negative influence on the conditional probability of a true-positive response and a positive influence on the conditional probability of a true-negative response and the posterior probability of a true-positive response. In contrast, mean SCC had the reverse effect. Generally speaking, the previous findings were consistent with the results from the ROC analyses, which demonstrates that the use of additional inputs does not significantly enhance the accuracy of ANN over studies employing traditional inputs only.

### **3.5 DISCUSSION**

The ROC analyses indicated that ANN could accurately recognize patterns in test day records to discriminate mastitic states. The success rate of ANN is comparable with other systems used in human clinical practice, such as radionuclide scanning and mammography, and ANN provide a promising alternative for veterinarians in the practice of mastitis diagnosis.

Both the ROC and the conventional 2 x 2 contingency table analyses tended to support each other in the conclusion that the proportion of mastitic records in training data files does not affect the overall capacity of the ANN. However, only the 2 x 2 contingency table has an impact on the specifics of the knowledge. An high proportion of mastitic records in the training data seemed to increase the ability of ANN to recognize the mastitic state (i.e., ANN that were fed more mastitic records could, theoretically, gain more relevant knowledge and, in turn, could more accurately detect mastitic cows). Conversely, low proportions of mastitic records seemed to lead ANN to predict incidence of clinical mastitis less accurately (although the ability to predict nonmastitic states

improved). These results, which confirm results obtained in previous studies (Lacroix et al., 1995b; Lacroix et al., 1997), have a profound implication for the animal industries. For example, in the selection of cows for dry period therapy, the ANN that is trained with a data file containing an high percentage of mastitic records may be applied to the herd in order to reduce the number of cows that are incorrectly classified as negative. This represents an important advantage for ANN over conventional methods and, in essence, permits the end user to determine the goal of the predictive tool.

Regarding the use of traditional and additional variables, small variations existed in the measures resulting from the ROC analyses and the conventional 2 x 2 contingency table. The differences were, however, quite small and did not support the hypothesis that additional inputs make a significant contribution to the predictability of the ANN. Moreover, the results from the sensitivity analysis showed that most of the variables playing important roles (SCC, stage of lactation, and cumulative milk yield), are those having a close biological association with mastitis and are already accounted for in most traditional models. In this sense, the importance of SCC and some of the other variables is not unexpected and no new light is shed on the variables which contribute to clinical mastitis. It is, however, reassuring to see that the ANN was in general agreement with other studies in the literature (Dekkers et al., 1994; Heuven et al., 1988; Shook and Schutz, 1994; Zhang et al., 1994).

The fact that some of these additional variables did not have an effect may stem from different reasons. As stated previously, it may have been due to a lack of biological association; however, conformation traits (an amalgamation of other general traits like dairy character, capacity, feet and legs, and mammary system) might have been expected to play a larger role, particularly due to the influence of mammary system, but the effect was negligible. In instances where subgroups of an input are expected to exert a greater influence on the predictive ability, it may be more reasonable to present those subgroups individually; i.e., the coding method for variables of this type might not be appropriate for the ANN to recognize the pattern. Also, data preprocessing (i.e., treatment of the data prior to input) may have a large influence on the results of the ability of an ANN to predict. For example, season of calving, dry period, and test day were classified into four seasons in this research,

but it is possible that converting them into two seasons might have made a difference to recognition of patterns by the ANN.

It is also worth discussing the code in the data for presence or absence of clinical mastitis; this field is used by the milker to report an incidence of clinical mastitis on the day of test, and its accuracy has been questioned in the past. This posed an interesting dilemma in that, presumably, any subsequent interest in a resulting module from this research should ensure a more accurate completion of this field in the future but would also raise some questions as to the reliability of the module, based on the earlier data. Obviously, the ANN assumed that this field was correct and proceeded with its pattern recognition accordingly. The possibility of both false positives and, more frequently, false negatives (no indication of mastitis when, in fact, there was) in the data, as well as their ramifications on the results, cannot be ignored. The ANN may also have been misguided if, for example, certain data were associated with no clinical mastitis on the day of test but the cow showed this symptom the next day or even soon thereafter. The fact that frequently available data were being used to try and generate a useful module for producers meant that their quality was sometimes limited and this should be taken into consideration when judging the results of this research. One can only continue to encourage the accurate coding of data and, assuming the codes were correct, it can be concluded that the ANN was reasonably well able to discriminate between important and unimportant variables when predicting incidence of clinical mastitis on the day of test. However, definitive conclusions as to the usefulness of additional variables are difficult at this time without a better understanding of both the data being used and their optimal manner of presentation to the ANN.

The selection of measures or methods used to evaluate a diagnostic system is an important decision and is a constant subject for discussion. Sensitivity and specificity have traditionally been employed to assess clinical diagnostic tests and the discriminatory ability of a diagnostic system (Fernando et al., 1985; McDermott et al., 1982; Nielen et al., 1994; Rindsig et al., 1979; Schultz, 1977; Sheldrake and Hoare, 1981); however these measures, as diagnostic indexes, have limitations. As a result, a new method, ROC, was recommended and applied to select applications (Brethour, 1994; Swets,

1988). This research supports the view that none of the five measures in conventional contingency table analyses can be used alone as a diagnostic  $A_2$  in the comparison of distinct systems and that  $A_2$  values work quite well in this area. It appears that the overall discrimination capacities, or  $A_2$  values, of ANN are solely dependent on patterns, defined as relationships between inputs and outputs that exist in the training data files and are not subject to proportions of mastitis. The proportions of mastitis, however, have an effect on the learning process of ANN because the more experience ANN can acquire on one perspective, the better the performance. Although the conventional 2 x 2 contingency table analyses had some disadvantages in assessing the power of ANN, it did provide some insights into the knowledge gained by ANN. Hence, we suggest that the joint use of ROC and conventional contingency table analyses provide a more complete picture of the ability of ANN.

This investigation represents merely a first step in the application of ANN to detect clinical mastitis. For ANN to fulfil their potential in this area, continued efforts must be made. First, information resources, specifically the method of coding information and the practice of determining those factors that contribute most to the incidence and detection of clinical mastitis, should be studied. More information resources, such as conformation traits of the udder and veterinary data, should be explored. Second, a better understanding of the internal characteristics of an ANN is in order. Although valuable information is often available, inappropriate architecture design and poor selection of internal characteristics, such as transfer functions and learning schedules, often lead to the failure of a validation. In short, future research in this area should focus on the preprocessing of information for ANN; recent studies concur with this need for future research, stressing the importance of validating the application as well as the optimal configuration of an ANN (Lacroix, 1994; Lawrence, 1991; Stein, 1993). Further understanding of these two aspects is expected to improve the accuracy of predictions of clinical mastitis by ANN. A successful application of ANN in the diagnosis of clinical mastitis should have a great impact on dairy management and disease control. Indeed, a computer that is equipped with such a system may furnish farmers with accurate and efficient means of monitoring the status of mastitis in herds. It may also make automated detection of clinical mastitis possible in the future.

### **3.6 CONCLUSIONS**

This research suggests that ANN are reasonably accurate at detecting mastitic states in dairy herds, using dairy herd improvement records. The proportion of different mastitic states in the training files had little impact on the overall capacity of the ANN to discriminate, but did have significant implications for the intended function of the ANN: a high proportion of mastitic record yielded an ANN that was better able to predict the mastitic state, and a low proportion of mastitic records yielded a less accurate prediction. Furthermore, additional variables had little effect on the results in this study and this may need to be re-examined in terms of data preprocessing or a more accurate gold standard against which to compare the results. Use of more complete data (e.g., historical veterinary data instead of lactation status information) or a change in the way variables are presented to the ANN may yield different results. We also recommend the combination of the ROC method and 2 x 2 contingency table analyses to assess the accuracy of a diagnostic system. Based on these results, further investigation into clinical mastitis detection with a larger data file and better conformation information should be performed and, perhaps, directed toward the study of the more valuable and difficult diagnoses of subclinical mastitis.

### **3.7 ACKNOWLEDGMENTS**

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TABLE 3.1. The inputs used in the analyses (traditional or additional variables) And their treatment by the artificial neural network.

Type of input	Variable	Treatment
Traditional		
	Lactation number	Continuous
	SCC	Continuous
	Milk yield on test day (kilograms)	Continuous
	Stage of lactation (days)	Continuous
	Mean SCC on test day	Continuous
	Herd size on test day	Continuous
Additional		
	Season of calving	2 binary inputs (00, 01, 10, or 11)
	Season of dry period	2 binary inputs (00, 01, 10, or 11)
	Season of test day	2 binary inputs (00, 01, 10, or 11)
	Fat percentage on test day	Continuous
	Protein percentage on test day	Continuous
	Cumulative milk yield	Continuous
	Cumulative fat yield	Continuous
	Cumulative protein yield	Continuous
	Overall conformation class of the cow	Continuous
	Presence of Conformation class of the cow	Binary flag (0 or 1)
	Overall conformation class of the sire	Continuous
	Presence of conformation class of the sire	Binary flag (0 or 1)
	Overall conformation class of the dam	Continuous
	Presence of conformation class of the dam	Binary flag (0 or 1)

TABLE 3.2. 2 x 2 contingency table for assessing the ability of an artificial neural network.

	<u>Observation of mastitis</u>		Total predicted
	Yes	No	
Prediction of mastitis			
Yes	A	B	A + B
No	C	D	C + D
Total Observed	A + C	B + D	A + B + C + D

TABLE 3.3. Effects of mastitis proportions in training data files on the predictive abilities of the artificial neural networks at a given decision criterion of 0.5.

Training ratio	Testing ratio	P(TP)	P(TN)	P(PSTP)	P(PSTN)	P(TTCR)
-----Traditional plus additional variables-----						
1 : 1	1 : 1	0.746	0.841	0.824	0.768	0.793
1 : 10	1 : 10	0.250	0.990	0.717	0.930	0.923
-----Traditional variables only-----						
1 : 1	1 : 1	0.715	0.858	0.834	0.750	0.786
1 : 10	1 : 10	0.239	0.990	0.707	0.929	0.922

TABLE 3.4. Relative importance (RI) of each of the input variables to the predictive abilities of the artificial neural networks that were trained and tested with data files containing a 1 : 1 ratio of mastitic to non mastitic records.

Disabled input	<i>P</i> (TP)	<i>P</i> (TN)	<i>P</i> (PSTP)	<i>P</i> (PSTN)	<i>P</i> (TTCR)	RI
None	0.746	0.841	0.824	0.768	0.793	
Season of test day	0.738	0.845	0.826	0.763	0.791	-0.25
Season of calving	0.755	0.833	0.819	0.773	0.793	0.00
Season of drying off	0.763	0.831	0.819	0.778	0.797	0.50
Lactation number	0.769	0.814	0.805	0.779	0.791	-0.25
Stage of lactation	0.445	0.800	0.690	0.590	0.622	-21.56
Milk yield on test day	0.588	0.852	0.799	0.674	0.720	-9.21
Fat percentage on test day	0.650	0.905	0.872	0.721	0.778	-1.89
Protein percentage on test day	0.755	0.831	0.817	0.773	0.793	0.00
Cumulative milk yield	0.913	0.394	0.601	0.819	0.653	-17.65
Cumulative fat yield	0.728	0.835	0.815	0.754	0.782	-1.39
Cumulative protein yield	0.757	0.819	0.807	0.771	0.788	-0.63
SCC on test day	0.885	0.363	0.582	0.760	0.624	-21.31
Conformation class of the cow	0.701	0.874	0.847	0.745	0.787	-0.76
Conformation class of the sire	0.761	0.835	0.822	0.778	0.798	0.63
Conformation class of the dam	0.750	0.847	0.830	0.772	0.798	0.63
Herd size on test day	0.738	0.856	0.837	0.766	0.797	0.50
Mean SCC	0.322	0.984	0.954	0.592	0.654	-17.65

Figure 3.1. Three examples of relative operating characteristic curves representing different discrimination capacities where the accuracy indices are 0.75 (◆), 0.85 (◻), and 0.95 (▲). The minimum accuracy index is also shown (- - -).

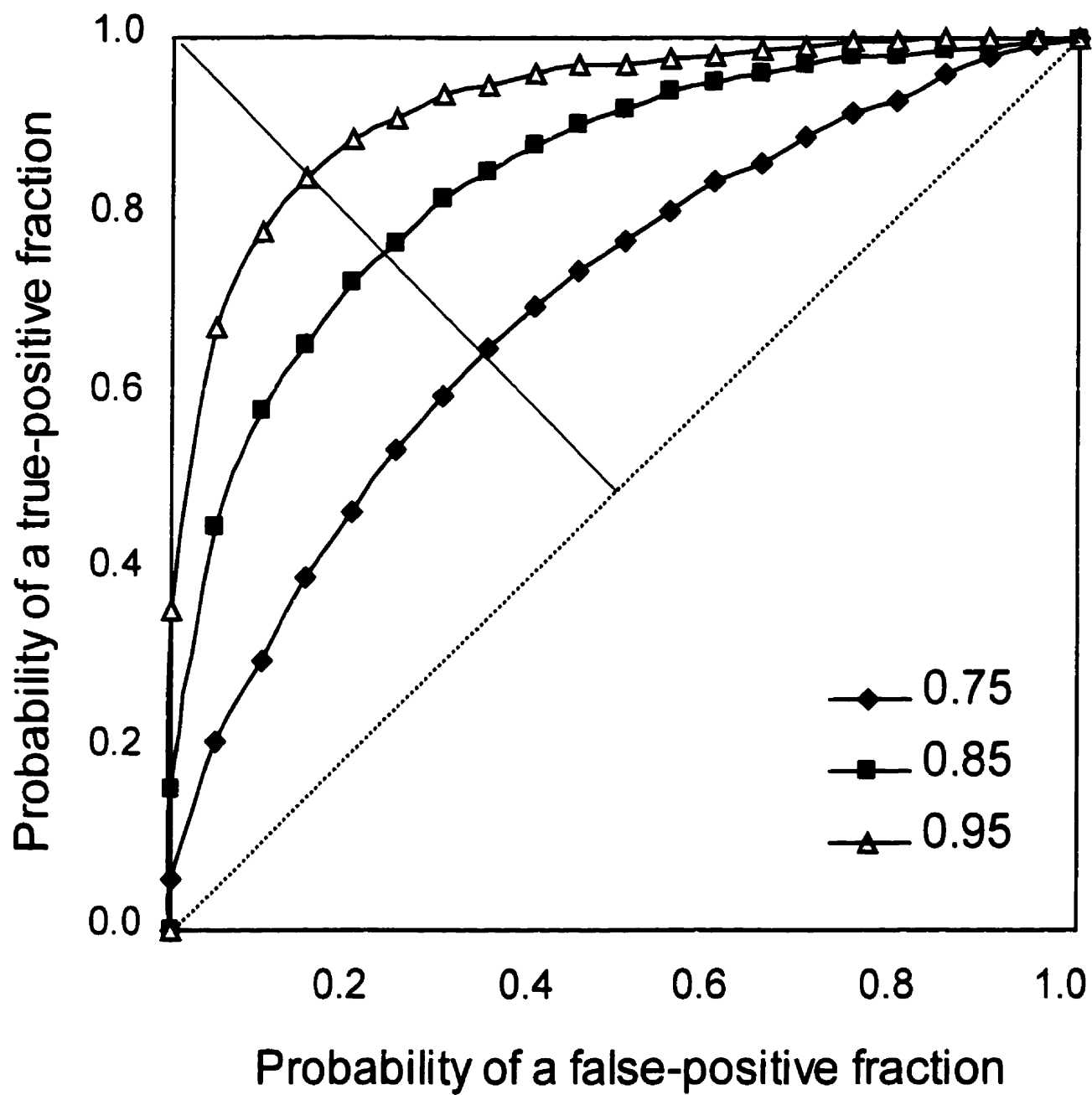
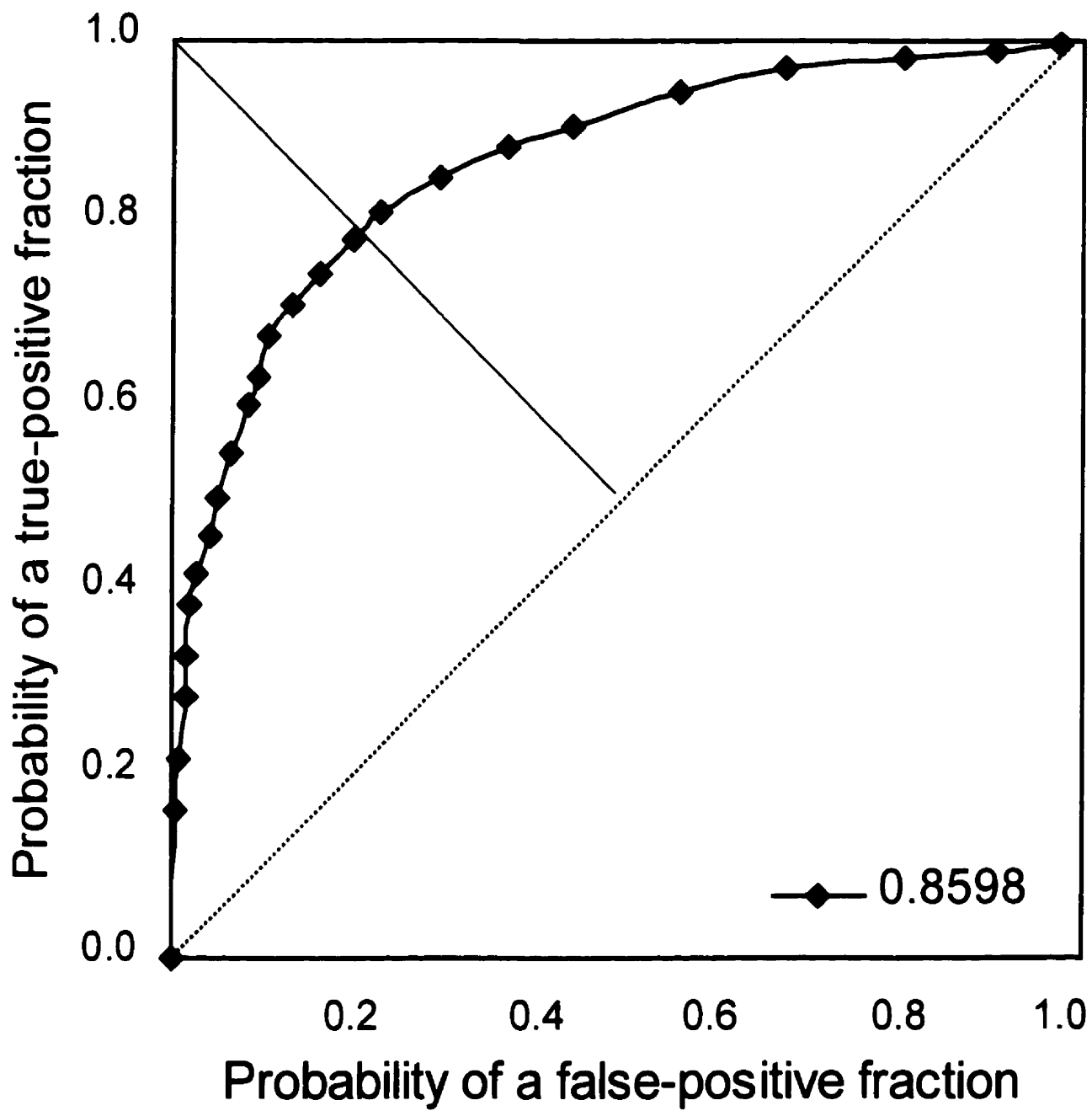


Figure 3.2. Relative operating characteristic analysis for the diagnostic accuracy of the artificial neural network that was trained and tested with traditional plus additional inputs, and a mastitic to nonmastitic ratio of 1:1. The area under the curved line (I) represents the accuracy index of the artificial neural network, 0.8598.



## **CONNECTING STATEMENT**

The results presented in the previous chapter have shown that the accuracy of the ANNs for differentiating mastitic cows from non-mastitic cows was at least as good as the conventional approaches using the relatively small data sets. This finding encouraged us to carry out further studies in this area with the expanded data sets and more input information sources. The following research is intended to check the role of conformation traits in the prediction of mastitis. In addition, the effects of the data preprocessing and ANNs architectures on the quality of the results were also examined.

## CHAPTER 4

### **Identification of factors influencing clinical mastitis using test-day production and conformation data with artificial neural networks**

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Short Title

### **FACTORS INFLUENCING MASTITIS FOUND WITH ARTIFICIAL NEURAL NETWORKS**

**Key words:** Artificial neural networks, clinical mastitis, production, conformation traits, sensitivity analysis, milk production

**Abbreviations:** ANN, artificial neural network; PE, processing element; SCC, somatic cell count

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## 4.1 ABSTRACT

A data set comprised of 1,296,877 test-day records and covering the period of December 1979 to November 1992 was used to investigate the usefulness of artificial neural networks to detect influential variables in clinical mastitis. These data were complemented with phenotypic and genetic conformation data in an effort to improve the predictive ability of the artificial neural network. The data were analysed using the production data only, the conformation data only, and a combination of the two. Results from a  $2 \times 2$  contingency table analysis indicated that stage of lactation, milk yield on test day, cumulative milk yield and somatic cell count were the major production factors influencing the occurrence of clinical mastitis. Among the conformation traits, such variables as phenotypic scores for rear-teat placement, dairy character and size, cow proof for dairy character, sire reliability for final score and sire proofs for pin-setting (desirability) and loin strength were found to have some influence on the network's predictive ability although they were all very minor in relation to the production variables mentioned. As a group, cow genetic proofs seemed more important than either sire genetic proofs or cow phenotypic scores. Architecture had little impact on the performance of the artificial neural networks in this study but it is felt that future research in this, as well in the area of data preprocessing would be beneficial.

## 4.2 INTRODUCTION

Mastitis continues to be one of the more serious diseases facing the modern dairy industry (Morse 1977) and, despite much research efforts into finding a means to diagnose and prevent it, financial losses do not seem to be reducing drastically over time (Dobbins 1977; Booth 1988; Gill et al. 1990; Miles et al. 1992). In fact, the incidence of mastitis may actually be rising with increased selection pressure for milk production (Shook 1989; Rogers et al. 1991; Schutz 1994; Shook and Schutz 1994). In the absence, therefore, of an effective approach to preventing the occurrence of mastitis, its early and accurate diagnosis (in conjunction with an instant therapy) provides the best means of reducing mastitis-associated costs to farmers. It also follows that the identification of factors that play a role in its occurrence will allow for better subsequent management of dairy cows with regard to this disease.

In the early part of this century the bacteriological culture approach was discovered and used accurately to identify infected mammary glands in cows; it is, however, time consuming and a high labour cost limited its practical application (Dodd et al. 1977; Morse 1977). Research was subsequently directed towards the use of indicators of mastitis such as somatic cell count, bovine serum albumin and electrical conductivity but a single indicator has generally been found to be inadequate since mastitis is caused by many different factors (genetics, management, sanitation, milking techniques, etc.). This is further evidenced by the fact that statistical models in this area generally consider multiple sources of information. They are, however, relatively scarce in the literature, possibly because mastitis is not consistently recorded in most dairy cattle populations (Seykora and McDaniel 1986; Rogers et al. 1991; Kehrl and Shuster 1994; Schutz 1994; Zhang et al. 1994) or because of the heretofore limitation in computing power (Simianer et al. 1991; Emanuelson et al. 1993). Most past research into statistical modelling of mastitis has been limited to some of the performance traits, physiological markers and environmental factors (Emanuelson et al. 1987; Berning and Shook 1992; Lescourret et al. 1995). Although phenotypic and genetic data on conformation traits have long been available, their use as predictors of mastitis has not been

studied extensively, despite a number of studies which showed low to moderate correlations between them and mastitis or SCC (Seykora and McDaniel 1985; Monardes et al. 1990; Rogers et al. 1991; Rogers 1993; Schutz et al. 1993). Those studies suggested that the possibilities of reducing the incidence of mastitis existed through indirect selection for conformation traits (Batra and McAllister 1984; Thomas et al. 1984; Monardes et al. 1990). This also implied that patterns might exist between conformation traits (both phenotypic and genetic) and mastitis.

Artificial neural networks (ANNs) are part of an emerging technology which has many advantages over traditional approaches, one of which is their ability to handle large amounts of information sources simultaneously in a non-sequential process (Freeman 1993). Although applications of ANNs in the agricultural industry are not as common as in other fields, a review of some of the existing cases has proved interesting (Yang et al. Submitted) and there is a growing interest in studies into where and how ANNs can be used. The application of ANNs in the detection of clinical mastitis has already been reported (Nielen et al. 1994; Yang et al. 1995; Yang et al. Submitted). However it may be possible to enhance the ability of these ANNs by exploring additional sources of information such as phenotypic scores and genetic values for conformation traits.

The objectives, therefore, of this study were 1) to investigate the possibility of enhancing the power of ANNs to predict the occurrence of clinical mastitis through the use of phenotypic and genetic information on conformation traits (as opposed to production data only); 2) to examine the relative importance of these (and production) variables on the occurrence of mastitis; and 3) to check the effects of data size and network architecture on the quality of ANN performance.

## **4.4 MATERIALS AND METHODS**

### **4.4.1 Artificial Neural Networks**

Derived from research into artificial intelligence, ANNs were designed as an imitation of the human

nervous system in order to perform complex functions such as reasoning and learning on computers. They consist of processing elements (PEs) – the equivalent of biological neurons – that are grouped into interconnected layers. Each connection possesses a weight, which corresponds to a synapse. Through a learning process, an ANN is able to detect patterns in a data set, i.e., it learns how to map sets of inputs to their corresponding output(s) and, when presented with a specific set of inputs, a trained ANN can then generate the corresponding output(s). Neurocomputing takes place in the PEs, and ANN learning occurs through the adjustment of the connection weights. Detailed descriptions of how ANNs work can be found in the literature (e.g., Freeman 1993, NeuralWare 1993).

A variety of ANNs can be constructed based on differences in the arrangement of the layers, the interconnection of the PEs, and the learning procedure employed. For this research, a feed-forward, back-propagation method was employed. Here, the learning process is said to be supervised: pairs of inputs and outputs are fed to the ANN and the basic neurocomputing is then carried out in each PE. The difference between the outputs generated by the network and the actual outputs is calculated and taken as a learning signal to be back propagated into the ANN. The weights in the ANN are then adjusted to reduce this error as much as possible. All inputs and outputs from a data file can be presented repeatedly to the ANN, which progressively changes its weights in a gradient-descent fashion. Through this process, the ANN learns the relationships existing between the various sets of inputs and their corresponding output(s).

#### **4.4.2 Data and Variables**

The data for this study consisted of individual Holstein test-day records obtained from the Québec Dairy Herd Analysis Service (PATLQ) and conformation information on cows and sires provided by Holstein Canada and the Canadian Dairy Network. The test-day records (3.5 million) were originally retrieved from the data base of PATLQ and fifteen specific fields were chosen for use in this study. Two additional variables – mean SCC and herd size on test day – were constructed from the data as an indication of the herd effect and three “flag” variables that were used to indicate

whether the three conformation variables in the test-day data were present or not. A summary of these variables, as well as their treatment is shown in the Appendix. 4.1 Elimination of records that included a suspect (or absent) value in one of the fifteen fields of interests reduced the data set from 3.5 to 1.9 million. Keeping only those records where matching conformation data existed further reduced this data set. The conformation data included phenotypic scores for cows and genetic proofs for cows and their sires (see the Appendix 4.2 for further details on the specific conformation traits as well as the classification procedure). The final data set comprised 1,296,877 records representing 82,807 cows, 4,340 sires in 609 herds covering the period of December 1979 to November 1992.

To facilitate the construction of training and testing data sets with no duplicate records between them, the following procedures were applied: the final data set was categorised according to presence (4,610) or absence (1,294,116) of the code for clinical mastitis. Each of these two categories was then randomly split into two data sets (i.e., two sets of 2,305 records *with* an indication of clinical mastitis and two sets of 647,058 records *without* an indication of clinical mastitis). The splits were achieved simply by reading every second record. A training data set was subsequently formed by using all records from one of the data sets with mastitis (i.e., 2,305) and by randomly assigning equal numbers of records (2,305) from one of the data sets without mastitis. A testing data set was created in the same way, but using another two data sets. These two data sets had 4,610 records with a mastitis proportion of 50% and no repeated records between them. From these data sets the training and testing files were constructed for 1) production information only; 2) conformation information only; and 3) a combination of the two. In the case of the combination, some summary conformation data that is present in test-day production files was excluded due to the presence of more complete data in the actual conformation file. . A summary of the various data structures is shown in Fig. 4.1.

#### **4.4.3 ANN Configuration**

Artificial neural networks consist of input layers (representing the input variables), an output layer (representing the variable that is being predicted) and a hidden layer. Most of the actual processing

occurs in the hidden layer, and its structure can vary in terms of the number of processing elements therein. In the case of the production data, there were 23 input PEs (i.e., 17 inputs, six of which were coded as binary) and one output PE – namely the prediction of mastitis. Four different architectures were examined with respect to the hidden layer in order to gauge its effect on the training process. Using a notation which refers to the number of PEs in each of the input, hidden and output layers, respectively, the four architectures examined were: 23-2-1, 23-10-1, 23-50-1, and 23-110-1. For example, a 23-2-1 network referred to 23 input PEs, two PEs in a hidden layer, and one output PE. The number of PEs in the hidden layer (i.e., 2, 10, 50 and 110) were chosen arbitrarily but it was felt that the spread was large enough to show any effect. When analysing the production and conformation data combined, the same architectures were applied at the hidden and output layers and there were 106 input PEs. These input PEs contained the 89 conformation variables and seventeen of the production inputs (the three conformation classes in the production data set were omitted along with their respective “flag” indicators). A single network was implemented when analysing the conformation data only; it contained 89 input PE, 110 PEs in the hidden layer and one PE at output layer. A summary of the various architectures is also shown in Fig. 4.1.

The ANNs were trained with a normalized cumulative delta-rule learning rule and an epoch of 16 records for 100,000 cycles, at which point the classification ability of the ANN was no longer significantly improving. The transfer function in the PEs was a hyperbolic tangent function. Since the output PE of these ANNs is a binary “Yes/No” and is represented by a continuous value between 0 and 1, a cutoff point of 0.5 was chosen for determining the outcome.

#### **4.4.4 Measures to Assess the Ability of the ANN**

This research adopted the 2 x 2 contingency table analysis, which has been well documented by Swets et al. (1982), Radostits et al. (1994) and Yang et al. (Submitted). Measures employed in the analyses included the two conditional probabilities for a true-positive and a true-negative response, denoted as  $P(TP)$  and  $P(TN)$ , respectively, and the overall probability of a correct (positive or

negative) response denoted as  $P(\text{TTCR})$ .  $P(\text{TP})$  refers to the percentage of correct identification of the occurrence of mastitis by the ANN given its prevalence.  $P(\text{TN})$  refers to the percentage of correct identification of the absence of mastitis by the ANN given its absence.  $P(\text{TTCR})$  measures the overall predictability of the ANN for mastitis. Since the distribution of true positives to true negatives is 50:50,  $P(\text{TTCR})$  is simply the average of  $P(\text{TP})$  and  $P(\text{TN})$ . These measures, as well as their derivation, are shown in Fig. 2.

#### 4.4.5 ANN Sensitivity to Inputs

Sensitivity analyses were carried out to examine the influence of an individual input or a group of inputs on the occurrence of clinical mastitis as supplied on test-day reports. The method entailed the disabling of certain PEs in recall mode only. A detailed description of this procedure can be found in Lacroix et al. (1995a) and Yang et al. (Submitted). Sensitivity analyses were performed for the production data (using the 23-10-1 architecture), the conformation data (using an 89-110-1 architecture) and the combination of production and conformation data (using the 106-110-1 architecture). A relative importance of each input (or a group of inputs) defined was also calculated. This is simply the percentage change in  $P(\text{TTCR})$  when a specific input is disabled from when no variables are disabled. It was calculated as:

$$\text{RI} = \frac{P(\text{TTCR})_{\text{ds}} - P(\text{TTCR})}{P(\text{TTCR})} \times 100$$

where  $P(\text{TTCR})_{\text{ds}}$  is the overall probability of a correct response from the ANN with a specific processing element disabled. The RI value was used as the main method for evaluating a variable's importance towards the prediction, and a higher absolute value indicated a larger influence. Changes in the measures of  $P(\text{TP})$  and  $P(\text{TN})$  were also considered since their values were different measures of the ability of an ANN.

## 4.5 RESULTS AND DISCUSSION

Table 4.1 contains the results from sensitivity analyses of the ANN trained with the production data only. The values are presented as a comparison of the different networks with disabled inputs to the network with no disabling (first line). The RI values indicate that the input variables of stage of lactation, milk yield on test day, cumulative milk yield and SCC played a major role in the prediction process, while other inputs, including seasons of test day, calving day and drying off, protein %, cumulative fat, cumulative protein, sire conformation score, dam conformation score and herd size seemed to have very little effect on the process at all. At the same time, there were variations in the networks' abilities to predict true positives and true negatives (as evidenced by the  $P(TP)$  and  $P(TN)$ , respectively). In addition it was observed that there were some degree of association between incidence of clinical mastitis and lactation number, fat %, mean SCC and cow conformation score. It should be noted that the conformation variables used in this part of the study refer to those found in the test-day files and are not as complete or extensive as those in the conformation files that were also used.

The results in Table 4.1 are in general agreement with those of Yang et al. (Submitted): those variables with a major contribution to predictability in the previous work also demonstrated a similar role in this study. The more than doubling of the training data size (an increase from 2,060 to 4,610 records) had little effect on the overall ability of the ANN to predict –  $P(TTCR)$  actually dropped from 0.793 to 0.782. It should, however, be noted that some changes emerged. For instance, the roles of SCC and stage of lactation appeared strengthened, while the role of mean SCC and cumulative milk yield appeared weakened to a certain degree. Input variables such as lactation number and cow conformation score, that showed little role in previous work (Yang et al. Submitted), seemed to demonstrate some association with mastitis in this study.

These findings are supported by other work in the literature. For example, Houben et al. (1993) found the risk of clinical infection was influenced by stage of lactation and lactation number and

Berning and Shook (1992) performed logistic regression of bacterial status on herd, lactation number, milk yield, log SCC, logarithm of N-acetyl- $\beta$ -D-glucosaminidase, and stage of lactation. After removing the least significant variables in a stepwise process, final predictors of infection status were found to be herd, log SCC, and logarithm of N-acetyl- $\beta$ -D-glucosaminidase (Berning and Shook 1992). Lescourret et al. (1995) used calving month, production potential and herd effect in a model to predict the occurrence of mastitis. Stage of lactation and milk yield had a role in modelling logarithm of SCC. Heuven et al. (1988) observed that stage of lactation effects for logarithm of SCC disappeared when corrected for milk yield. A similar phenomenon also occurred in this study where the role of mean SCC seemed to diminish with increasing numbers of inputs; previous work (Yang et al. Submitted) categorised the role of mean SCC with an RI value of approximately -17%, while the current study found RI values -2.3% (Table 4.1), and 0% (Table 4.3). It should also be stated that a small RI value for mean SCC does not imply that it is unimportant; in fact  $P(TP)$  and  $P(TN)$  both indicate that it did play some role. Hence, it may be worth considering the idea that the pattern or role of an input is subject to a given set of information, used to train an ANN, and may be modified if new information is included. This phenomenon could be due to that fact that these inputs are overwhelmed by the presence of certain production traits, or due to a redistribution of roles among the inputs.

Table 4.2 shows the results of the sensitivity analyses for each input variable when the ANNs were trained and tested with both the production and the conformation data. As before, those variables seen as exerting the greatest influence on the predictive ability of the ANN included stage of lactation, milk yield on test day, cumulative milk yield and SCC. This time, lactation number was also prominent as an influential factor. Relatively weak associations were observed for season of test day, cow proof for dairy character, cow proof for final score and reliability of sire proof for final score. While the remaining inputs did not seem to have any obvious influence on the overall predictability of the ANNs, the exclusion of many of them (e.g., Mean SCC on test day) resulted in an ANN with different abilities, depending on whether they were attempting to predict true positives or true negatives. The general conclusion from these specific sensitivity analyses was that

conformation traits were relatively unimportant as predictors of clinical mastitis. In fact, only three variables (cow proof for dairy character and final score and reliability of sire proof for final score) had RI values of greater than one.

The  $P(TP)$  values resulting from when SCC – the most significant factor in Tables 1 and 2 – was disabled require some further explanation as they were unity for both the network trained with production data only and the network trained with both production and conformation data. This arose, in essence, from the fact that inputs were disabled by setting the input value to zero which, in the case of a bipolar mode of presentation (all inputs mapped between  $-1$  and  $+1$ ), results in the output value being set to the average of the minimum and the maximum input values. Since SCC values actually ranged from approximately zero to several million, this value – the average of the minimum and the maximum values – was still quite significant and, therefore, *all* animals had a high associated SCC and were all diagnosed as being mastitic. Mathematically, this means that the values C and D (Fig. 4.2) were always equal to zero for this particular sensitivity analysis (i.e.,  $P(TP)$  was always equal to 1.0 and  $P(TN)$  was, therefore, always equal to 0.0). These values of 1.0 and 0.0 are, therefore, a result of the specific technique used, and should not be interpreted as anything other than the fact that SCC played an important variable in the prediction of mastitis from these data sets.

Sensitivity analyses were also performed for ANNs trained and tested with only the conformation data (Table 4.3). This was done in order to exclude the production variables, some of which seemed to be having an overwhelming effect on the predictive process, and to try and spread out the conformation variables more. The results indicate that, despite their low level of influence on the prediction of clinical mastitis, not all variables were equal in their effects. However, of the 89 input variables only six – phenotypic scores for rear-teat placement, dairy character and size, cow proof for dairy character, sire reliability for final score and sire proofs for pin-setting (desirability) and loin strength – had an RI value of greater than one. That being said, the role of many of the other variables (e.g., cow proof for final score) was found to be different depending on whether the network was predicting presence or absence of clinical mastitis [i.e.,  $P(TP)$  versus  $P(TN)$ ].

While the results from Tables 4.2 and 4.3 basically show that conformation data did not exhibit a large role in the prediction of clinical mastitis (as defined in this study), those which did show some influence were not altogether unexpected. For instance, Rogers et al. (1991) and Schutz et al. (1993) found genetic correlations between the logarithm of somatic cell score and udder depth, fore udder attachment, and front teat placement, ranging from -0.35 to -0.2.

The next analysis looked at conformation data on a group, rather than on an individual basis. Variables were grouped according to their natural divisions – cow phenotypic scores, cow proofs and sire proofs. All combinations of group disabling were examined and compared to the network trained with both production and conformation data (i.e., each group was first disabled on its own, then pairs of groups were disabled, and, finally, all three groups were disabled). The results are shown in Table 4 and indicate that each source of conformation traits (or their combinations) played a small but, as expected, unequal role in the prediction of clinical mastitis. For the role of each individual information source, cow proofs seemed to be more influential (RI value of -2.4 %), as a group, than either sire proofs or cow scores. In fact, sire proofs seemed to have somewhat of a reversed role: disabling this group of information resulted in a slight enhancement in the overall predictability (RI value of 1.3%). This trend was also observed when more than one group was disabled: group disabling that involved sire proofs seemed to “improve” the situation while involvement of cow proofs led to a more negative RI value. These results are in support of some work concerning genetic evaluations, indicating that udder conformation traits had higher a genetic (about 0.3) than phenotypic (-0.1) correlation with SCC (Monardes et al. 1990; Rogers et al. 1991; Schutz 1994). In addition, it was concluded that the correlations between sire proofs for somatic cell score and type traits were generally small (Zhang et al. 1994).

With regard to the effect of different architectures (in this study, number of hidden PEs) on the ability of ANNs to predict, Table 4.5 shows the results for both the ANN that was trained with the production data only and the ANN that was trained with the production and conformation data

together. While there was little difference in the results obtained from the production information only, the same overall trend was not observed with both sets of ANNs (i.e., the performance of the ANN trained and tested with both production and conformation information actually seemed to deteriorate with higher numbers of PEs in the hidden layer while the opposite was the case for the ANN trained and tested with only the production data).

This might not be the case for other applications since the number of hidden PEs depend primarily on the nature of data. For example, Dolenko et al. (1995) and Hassan and Tohmaz (1995) found that ANN architectures had quite a large effect on the performance of ANNs. While no general rule seems to exist, a broad guideline for the number of PEs in a hidden layer is presented in the Tutorial for NeuralWorks Professional II/Plus and NeuralWorks Explorer (1993). More specifically, Pizzi and Somorjai (1994) concluded that, for classification problems with two classes, the number of PEs in the hidden layer should be at least twice the number of input variables. On the other hand, Freeman (1993) believed that for networks of a "reasonable" size (hundreds or thousands of inputs), the hidden layer need only be a relatively small fraction of the size of the input layer. It could be argued that the results from this study supported Freeman's theory. Since the primary aim of this research was not one of fine-tuning ANN architectures, extensive investigations were not carried out. The conclusion from this study, however, would seem to be that architecture design is not a key factor. This might not be the case in other applications and much research (both theoretical and practical nature) remains to be carried out.

Although this study has shown a minor role of conformation traits as predictors of mastitis, the authors believe that the discriminatory ability of an ANN can be further enhanced through an exploration of new information resources. Research in other area has exhibited some associations. For instance, the estimated genetic correlations between milk yield and indicators of mastitis suggested that genetic proofs for production traits might be an important source of information for improving an ANN's ability to predict mastitis (Miller 1984; Banos and Shook 1990; Simianer et al. 1991; Schutz 1994). Furthermore, SCC itself has a high genetic correlation with mastitis (0.6 to

0.8) indicating that a pattern may exist (Shook and Schutz 1994). Future research should also look at the creation of new variables using available sources of information (e.g., a log-transformation of SCC, SCC on test day divided by mean SCC for the herd, etc.). This could lead to a better use of information resources and an enhancement in predictability of ANNs at no increased cost. Of course, further efforts should be devoted to data preprocessing as well and the importance of this issue has been addressed in previous studies (Lawrence 1991; Stein 1993; Pizzi and Somorjai 1994; Lacroix et al. 1995b; Lacroix et al. 1995c; Yang et al. Submitted). In order to apply ANNs in this particular field, a final optimal configuration needs to be determined.

#### **4.6 CONCLUSIONS**

The most influential variables associated with clinical mastitis are production traits, specifically, SCC, milk yield and stage of lactation. When compared to that of production traits, the role of conformation traits seemed to be minor. However, some of these variables (e.g., phenotypic scores for rear-teat placement, dairy character and size, cow proof for dairy character, sire reliability for final score and sire proofs for loin strength and pin-setting – desirability) had a higher degree of association than others, and were consistent with other studies from the literature. While relatively important conformation variables were seen across categories, as a group, cow proofs seemed to be more influential than either sire proofs or even cow phenotypic scores. The architecture of the ANN seemed to play very little role in its predictive ability for this application.

#### **4.7 ACKNOWLEDGEMENTS**

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TABLE 4.1. The role of each input variable in the artificial neural network trained with the production data only.

Disabled input variable	$P(TP)^{\ast}$	$P(TN)$	$P(TTCR)$	RI (%)
<b>None</b>	<b>0.713</b>	<b>0.851</b>	<b>0.782</b>	<b>-</b>
Season of test day	0.706	0.855	0.780	-0.3
Season of calving	0.692	0.869	0.780	-0.3
Season of drying off	0.692	0.865	0.778	-0.5
Lactation number	0.772	0.773	0.772	-1.3
Stage of lactation	0.107	0.997	0.552	-29.4
Milk yield on test day	0.537	0.885	0.711	-9.1
Fat percentage on test day	0.639	0.900	0.770	-1.5
Protein percentage on test day	0.726	0.840	0.784	0.3
Cumulative milk yield	0.537	0.885	0.711	-9.3
Cumulative fat yield	0.766	0.799	0.783	0.1
Cumulative protein yield	0.672	0.875	0.778	-0.5
SCC on test day	1.000	0.000	0.500	-36.1
Conformation score of the cow	0.652	0.889	0.770	-1.5
Conformation score of the sire	0.728	0.840	0.782	0.0
Conformation score of the dam	0.723	0.848	0.785	0.4
Herd size on test day	0.721	0.846	0.784	0.3
Mean SCC on test day	0.609	0.920	0.764	-2.3

<sup>\*</sup>  $P(TP)$  = Conditional probability of a true-positive response,  $P(TN)$  = Conditional probability

of a true-negative response,  $P(\text{TTCR})$  = Overall probability of a correct response (i.e., probability that the response is either true-positive or true-negative), and  $\text{RI} =$

$$\frac{P(\text{TTCR})_{\text{ds}} - P(\text{TTCR})}{P(\text{TTCR})} \times 100 \text{ where } P(\text{TTCR})_{\text{ds}} = \text{Overall probability of a correct response}$$

from the artificial neural network with a specific disabled processing element.

TABLE 4.2. The role of each input variable in the artificial neural network (106-110-1 architecture)<sup>2</sup> trained with both production and conformation data.

Disabled input variable	<i>P</i> (TP) <sup>2</sup>	<i>P</i> (TN)	<i>P</i> (TTCR)	RI (%)
None	0.731	0.794	0.762	-
Test day production data				
Season of test day	0.708	0.834	0.771	1.2
Season of calving	0.718	0.815	0.761	0.7
Season of drying off	0.726	0.801	0.764	0.3
Lactation number	0.866	0.555	0.710	-6.8
Stage of lactation	0.114	0.996	0.555	-27.2
Milk yield on test day	0.557	0.852	0.705	-7.5
Fat percentage on test day	0.667	0.867	0.767	0.7
Protein percentage on test day	0.732	0.792	0.762	0.0
Cumulative milk yield	0.871	0.562	0.716	-6.0
Cumulative fat	0.728	0.801	0.764	0.3
Cumulative protein	0.757	0.761	0.759	-0.4
SCC on test day	1.000	0.000	0.500	-34.4
Herd size on test day	0.742	0.777	0.759	-0.4
Mean SCC on test day	0.660	0.865	0.762	0.0
Cow phenotypic scores for conformation				
Conformation	0.714	0.807	0.761	-0.1
Frame / Capacity	0.731	0.794	0.763	0.1
Stature (height at rump)	0.736	0.789	0.763	0.1

Size	0.695	0.834	0.766	0.5
Chest width	0.731	0.795	0.763	0.1
Loin strength	0.724	0.811	0.767	0.7
Rump	0.731	0.795	0.763	0.1
Pin setting	0.731	0.794	0.762	0.0
Pin width	0.718	0.809	0.764	0.3
Feet & legs	0.730	0.795	0.762	0.0
Foot angle	0.730	0.797	0.764	0.3
Bone quality	0.734	0.788	0.761	-0.1
Rear-leg set	0.734	0.794	0.764	0.3
Mammary system	0.731	0.793	0.761	-0.1
Udder texture	0.726	0.804	0.765	0.4
Median suspensory	0.727	0.802	0.764	0.3
Fore udder	0.722	0.806	0.764	0.3
Fore attachment	0.728	0.794	0.761	-0.1
Fore-teat placement	0.734	0.792	0.763	0.1
Rear udder	0.735	0.790	0.763	0.1
Rear-attachment height	0.725	0.803	0.764	0.3
Rear-teat placement	0.716	0.803	0.760	-0.3
Dairy character	0.725	0.797	0.671	-0.1

#### Cow proofs for conformation

Conformation	0.729	0.794	0.762	0.0
Final score	0.557	0.921	0.739	-3.0
Reliability of final score	0.720	0.800	0.764	0.3
Frame / Capacity	0.748	0.785	0.766	0.5
Stature (height at rump)	0.730	0.793	0.762	0.0
Relative height at front end	0.730	0.792	0.761	-0.1

Size	0.738	0.793	0.766	0.5
Chest width	0.730	0.792	0.761	-0.1
Body depth	0.730	0.794	0.762	0.0
Loin strength	0.727	0.795	0.761	-0.1
Rump	0.730	0.795	0.762	0.0
Pin-setting tendency	0.739	0.788	0.764	0.3
Pin-setting desirability	0.721	0.805	0.763	0.1
Pin width	0.730	0.795	0.762	0.0
Feet & legs	0.727	0.793	0.760	-0.3
Foot angle	0.720	0.797	0.763	0.1
Bone quality	0.735	0.782	0.759	-0.4
Rear-leg set tendency	0.724	0.800	0.762	0.0
Rear-leg set desirability	0.731	0.796	0.763	0.1
Mammary system	0.734	0.794	0.764	0.3
Udder depth	0.713	0.811	0.762	0.0
Udder texture	0.715	0.816	0.766	0.5
Median suspensory	0.733	0.789	0.761	-0.1
Fore udder	0.723	0.805	0.764	0.2
Fore attachment	0.740	0.784	0.762	0.0
Fore-teat placement	0.732	0.794	0.763	0.1
Fore-teat length	0.733	0.790	0.761	-0.1
Rear udder	0.729	0.790	0.760	-0.3
Rear-attachment height	0.731	0.796	0.764	0.3
Rear-attachment width	0.738	0.782	0.760	-0.3
Rear-teat placement	0.732	0.795	0.763	0.1
Dairy character	0.739	0.748	0.743	-2.5
Dairy form	0.737	0.790	0.763	0.1

# Sire proofs for conformation

Conformation	0.744	0.777	0.761	-0.1
Final score	0.719	0.805	0.762	0.0
Reliability of final score	0.855	0.606	0.730	-4.2
Frame / Capacity	0.735	0.789	0.762	0.0
Stature (height at rump)	0.721	0.801	0.761	-0.1
Relative height at front end	0.731	0.792	0.761	-0.1
Size	0.734	0.790	0.762	0.0
Chest width	0.740	0.786	0.763	0.1
Body depth	0.715	0.816	0.766	0.5
Loin strength	0.743	0.778	0.761	-0.1
Rump	0.747	0.770	0.758	-0.5
Pin-setting tendency	0.741	0.776	0.758	-0.5
Pin-setting desirability	0.643	0.881	0.762	0.0
Pin width	0.701	0.817	0.759	-0.4
Feet & legs	0.730	0.795	0.762	0.0
Foot angle	0.715	0.812	0.764	0.3
Bone quality	0.723	0.799	0.761	-0.1
Rear-leg set tendency	0.733	0.797	0.765	0.4
Rear-leg set desirability	0.721	0.805	0.763	0.1
Mammary system	0.728	0.798	0.763	0.1
Udder depth	0.708	0.818	0.763	0.1
Udder texture	0.722	0.802	0.762	0.0
Median suspensory	0.731	0.792	0.762	0.0
Fore udder	0.731	0.795	0.763	0.1
Fore attachment	0.731	0.796	0.763	0.1
Fore-teat placement	0.725	0.801	0.763	0.1
Fore-teat length	0.728	0.800	0.764	0.3

Rear udder	0.735	0.791	0.763	0.1
Rear-attachment height	0.716	0.812	0.764	0.3
Rear-attachment width	0.734	0.787	0.760	-0.3
Rear-teat placement	0.723	0.807	0.765	0.4
Dairy character	0.714	0.807	0.760	-0.3
Dairy form	0.731	0.795	0.763	0.1

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- <sup>4</sup> An architecture of 106-110-1 represents 106 input, 110 hidden and 1 output processing element(s), respectively.
- <sup>5</sup>  $P(TP)$  = Conditional probability of a true-positive response,  $P(TN)$  = Conditional probability of a true-negative response,  $P(TTCR)$  = Overall probability of a correct response (i.e., probability that the response is either true-positive or true-negative), and  $RI = \frac{P(TTCR)_{ds} - P(TTCR)}{P(TTCR)} \times 100$  where  $P(TTCR)_{ds}$  = Overall probability of a correct response from the artificial neural network with a specific disabled processing element.

TABLE 4.3. The role of each input variable in the artificial neural network (89-110-1 architecture)<sup>c</sup> trained with the conformation data only.

Disabled input variable	<i>P</i> (TP) <sup>y</sup>	<i>P</i> (TN)	<i>P</i> (TTCR)	RI (%)
<b>None</b>	<b>0.436</b>	<b>0.666</b>	<b>0.551</b>	<b>-</b>
Cow phenotypic scores for conformation				
Conformation	0.427	0.672	0.546	-0.9
Frame / Capacity	0.462	0.638	0.550	-0.2
Stature (height at rump)	0.444	0.657	0.551	0.0
Size	0.312	0.777	0.544	-1.3
Chest width	0.428	0.677	0.552	0.2
Loin strength	0.346	0.753	0.549	-0.4
Rump	0.420	0.682	0.551	0.0
Pin setting	0.433	0.663	0.548	-0.5
Pin width	0.402	0.697	0.549	-0.4
Feet & legs	0.450	0.650	0.550	-0.2
Foot angle	0.423	0.678	0.551	0.0
Bone quality	0.479	0.622	0.550	-0.2
Rear-leg set	0.440	0.657	0.549	-0.4
Mammary system	0.492	0.610	0.551	0.0
Udder texture	0.458	0.643	0.551	0.0
Median suspensory	0.413	0.689	0.551	0.0
Fore udder	0.438	0.662	0.550	-0.2
Fore attachment	0.441	0.664	0.552	0.2
Fore-teat placement	0.428	0.671	0.549	-0.4

Rear udder	0.449	0.658	0.554	0.5
Rear-attachment height	0.441	0.662	0.551	0.0
Rear-teat placement	0.305	0.778	0.642	16.5
Dairy character	0.376	0.713	0.545	-1.1

Cow proofs for conformation

Conformation	0.440	0.662	0.551	0.0
Final score	0.389	0.708	0.548	-0.5
Reliability of final score	0.492	0.616	0.554	0.5
Frame / Capacity	0.459	0.647	0.553	0.4
Stature (height at rump)	0.434	0.670	0.552	0.2
Relative size at front end	0.436	0.672	0.554	0.5
Size	0.435	0.667	0.551	0.0
Chest width	0.440	0.665	0.552	0.2
Body depth	0.436	0.668	0.552	0.2
Loin strength	0.433	0.664	0.548	-0.5
Rump	0.439	0.663	0.551	0.0
Pin-setting tendency	0.440	0.660	0.550	-0.2
Pin-setting desirability	0.384	0.714	0.549	0.4
Pin width	0.443	0.663	0.553	0.4
Feet & legs	0.439	0.669	0.554	0.5
Foot angle	0.446	0.659	0.553	0.4
Bone quality	0.433	0.666	0.549	-0.4
Rear-leg set tendency	0.438	0.664	0.551	0.0
Rear-leg set desirability	0.439	0.667	0.553	0.4
Mammary system	0.439	0.655	0.547	-0.7
Udder depth	0.430	0.678	0.554	0.5
Udder texture	0.416	0.680	0.548	-0.5

Median suspensory	0.442	0.663	0.552	0.2
Fore udder	0.423	0.682	0.552	0.2
Fore attachment	0.452	0.652	0.552	0.2
Fore-teat placement	0.429	0.676	0.554	0.5
Fore-teat length	0.443	0.659	0.551	0.0
Rear udder	0.432	0.671	0.552	0.2
Rear-attachment height	0.435	0.664	0.549	-0.4
Rear-attachment width	0.454	0.654	0.549	-0.4
Rear-teat placement	0.440	0.659	0.550	-0.2
Dairy character	0.487	0.592	0.540	-2.0
Dairy form	0.436	0.671	0.553	0.4

#### Sire proofs for conformation

Conformation	0.449	0.656	0.552	0.2
Final score	0.432	0.672	0.552	0.2
Reliability of final score	0.916	0.113	0.516	-6.4
Frame / Capacity	0.436	0.666	0.551	0.0
Stature (height at rump)	0.428	0.673	0.551	0.0
Relative height at front end	0.440	0.659	0.550	-0.2
Size	0.439	0.666	0.552	0.2
Chest width	0.449	0.652	0.550	-0.2
Body depth	0.425	0.674	0.549	-0.4
Loin strength	0.504	0.584	0.544	-1.3
Rump	0.475	0.630	0.552	0.2
Pin-setting tendency	0.482	0.619	0.550	-0.2
Pin-setting desirability	0.305	0.771	0.538	-2.4
Pin width	0.376	0.719	0.547	-0.7
Feet & legs	0.438	0.664	0.551	0.0

Foot angle	0.461	0.640	0.551	0.0
Bone quality	0.443	0.653	0.551	0.0
Rear-leg set tendency	0.452	0.659	0.555	0.7
Rear-leg set desirability	0.426	0.675	0.551	0.0
Mammary system	0.425	0.683	0.554	0.5
Udder depth	0.451	0.653	0.552	0.2
Udder texture	0.431	0.669	0.550	-0.2
Median suspensory	0.439	0.664	0.551	0.0
Fore udder	0.430	0.678	0.554	0.5
Fore attachment	0.443	0.667	0.555	0.7
Fore-teat placement	0.433	0.672	0.553	0.4
Fore-teat length	0.433	0.662	0.548	-0.5
Rear udder	0.447	0.653	0.550	-0.2
Rear-attachment height	0.423	0.683	0.553	0.4
Rear-attachment width	0.440	0.659	0.549	-0.4
Rear-teat placement	0.423	0.669	0.546	-0.9
Dairy character	0.412	0.675	0.543	-1.5
Dairy form	0.426	0.681	0.554	0.5

<sup>4</sup> An architecture of 89-110-1 represents 89 input, 110 hidden and 1 output processing element(s), respectively.

<sup>5</sup>  $P(TP)$  = Conditional probability of a true-positive response,  $P(TN)$  = Conditional probability of a true-negative response,  $P(TTCR)$  = Overall probability of a correct response (i.e., probability that the response is either true-positive or true-negative), and  $RI = \frac{P(TTCR)_{ds} - P(TTCR)}{P(TTCR)} \times 100$  where  $P(TTCR)_{ds}$  = Overall probability of a correct response from the artificial neural network with a specific disabled processing element.

TABLE 4.4. The role of each group of conformation traits in the artificial neural network (106-110-1 architecture)<sup>z</sup> trained with both production and conformation data.

Disabled set of input variables <sup>y</sup>	$P(TP)^x$	$P(TN)$	$P(TTCR)$	RI (%)
<b>None</b>	<b>0.731</b>	<b>0.794</b>	<b>0.762</b>	<b>-</b>
Cow scores	0.643	0.874	0.759	-0.4
Cow proofs	0.587	0.902	0.744	-2.4
Sire proofs	0.718	0.826	0.772	1.3
Cow scores and Cow proofs	0.500	0.945	0.723	-5.1
Cow scores and Sire proofs	0.634	0.897	0.765	0.4
Cow proofs and Sire proofs	0.577	0.922	0.749	-1.7
All scores and proofs	0.484	0.957	0.721	-5.4

<sup>z</sup> An architecture of 106-110-1 represents 106 input, 110 hidden and 1 output processing element(s), respectively.

<sup>y</sup> A = All cow phenotypic scores for conformation, B = All cow proofs for conformation, and C = All sire proofs for conformation.

<sup>x</sup>  $P(TP)$  = Conditional probability of a true-positive response,  $P(TN)$  = Conditional probability of a true-negative response,  $P(TTCR)$  = Overall probability of a correct response (i.e., probability that the response is either true-positive or true-negative), and  $RI = \frac{P(TTCR)_{ds} - P(TTCR)}{P(TTCR)} \times 100$  where  $P(TTCR)_{ds}$  = Overall probability of a correct response from the artificial neural network with a specific disabled processing element.

TABLE 4.5. The effects of different ANN architectures on their performance of an artificial neural network

Architecture <sup>z</sup>	$P(TP)^y$	$P(TN)$	$P(TTCR)$
ANN TRAINED AND TESTED WITH THE PRODUCTION DATA			
23-2-1	0.734	0.841	0.787
23-10-1	0.713	0.851	0.782
23-50-1	0.724	0.849	0.786
23-110-1	0.725	0.856	0.790
ANN TRAINED AND TESTED WITH THE PRODUCTION AND CONFORMATION DATA			
106-2-1	0.751	0.800	0.775
106-10-1	0.738	0.808	0.771
106-50-1	0.748	0.790	0.769
106-110-1	0.731	0.794	0.762

<sup>z</sup> An architectures is denoted in terms of number of input-hidden-output processing elements

<sup>y</sup>  $P(TP)$  = Conditional probability of a true-positive response.  $P(TN)$  = Conditional probability of a true-negative response and  $P(TTCR)$  = Overall probability of a correct response (i.e., probability that the response is either true-positive or true-negative).

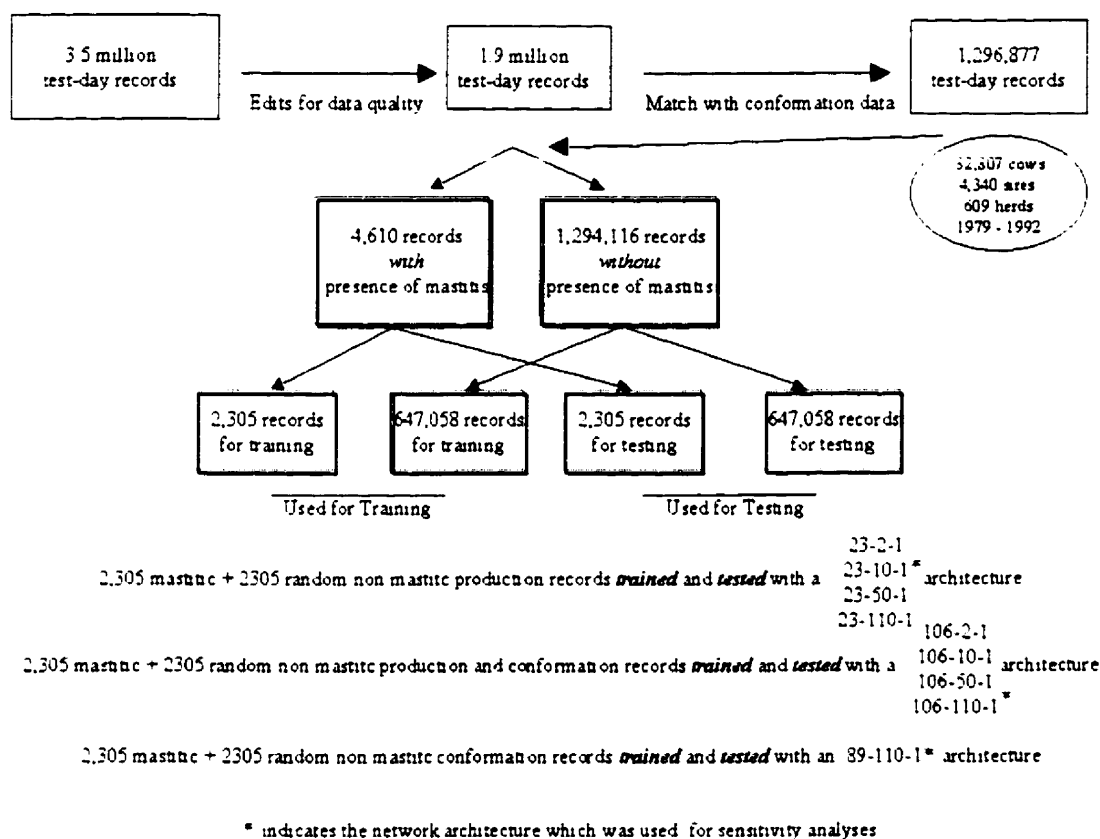


Fig. 4.1 Diagram of the size, structure and architecture of the various data sets used in these analyses.

	YES (Observed)	NO (Observed)	TOTAL (Predicted)
YES (Predicted)	A	B	A + B
NO (Predicted)	C	D	C + D
TOTAL (Observed)	A + C	B + D	A + B + C + D

$$P(\text{TP}) = \frac{A}{A + C}, \quad P(\text{TN}) = \frac{D}{B + D} \quad \text{and} \quad P(\text{TTCR}) = \frac{A + D}{A + B + C + D}$$

Fig. 4.2. A 2 x 2 contingency table for assessing the ability of an artificial neural network.

## **CONNETING STATEMENT**

Major valuable points drawn from these studies are summarised in the following chapter. The limitations of ANNs in detecting bovine mastitis are also presented. Recommendations for the direction of future research in the area of ANNs' application into the detection of bovine mastitis are presented.

## **CHAPTER 5**

### **GENERAL CONCLUSIONS**

This research concluded that ANNs could be used to detect bovine mastitis because ANNs provide a high predictive accuracy of mastitis (about 86%) in terms of  $A_2$ -value. The success rate of ANNs was comparable with other systems used in human clinical practice, such as radionuclide scanning and mammography. Although it was difficult to give a general assessment on the superiority of ANNs over traditional approaches in terms of predictive ability, since the measure of  $A_2$ -value were not employed in the past studies in the prediction and detection of mastitis, the authors judged that the predictability of ANNs was at least as good as that of conventional methods in terms of sensitivity and specificity, the most commonly used criteria in the past research. This general conclusion indeed answered one of the most common questions of interest: is it possible to use ANNs in the animal industry? This study also illustrated an example of how and where ANNs can be applied.

This study not only validated the feasibility of using ANNs to detect mastitis, as set in the research objectives, but also provided sufficient results related to the role of input variables. This research showed that input variables such as lactation stage, milk yield on test day, somatic cell count on test day, played dominant roles in the prediction of mastitis, while the input variables of lactation number, fat % on test day and cumulative fat yield had a small contribution to predictability of ANNs. When production data was compared to conformation traits, as a whole, the conformation traits played a small role. But when the three component groups of the confirmation traits were compared they demonstrated unequal contribution to the prediction of mastitis, with a greater role played by cow proofs than either cow scores or sire proofs. When the individual confirmation traits were compared, conformation traits such as phenotypic scores for rear-teat placement, dairy-character and size, cow proof for dairy character, sire reliability for final score and sire proofs for pin-setting (desirability) and loin strength, had a relatively greater impact on the prediction of mastitis. Sensitivity analyses also indicated that each source of information on conformation traits had different effects, suggesting that cow genetic proofs had a greater role than phenotypic scores and sire genetic proofs in enhancing the predictive ability of ANNs for mastitis. All the results

presented in this study were generally in agreement with those published previously using statistical methodology. However, it should be noted that because of the full interactions involved among the input variables, a small modification in the role of each individual input may take place due to changes in the number of inputs and changes in encoding method. It should be emphasised that the role of each input in these studies was subjected to a given set of input variables in the training data set. The role of each input as reflected by the sensitivity analysis might not be due to its own direct association with mastitis status. Therefore, the relations between input information and mastitis could not be explicitly explained.

Some work was also done with data pre-processing and internal characteristics of ANNs. Primary results from ANNs trained on training data sets with differing proportions of mastitis have shown no effect on the overall discriminatory ability of ANNs through "ROC" analyses. However, conventional 2-by-2 contingency table analyses indicated some effect on the particular purpose of the artificial neural network being developed. While this research has revealed that the architecture and the size of the training data had little impact on performance of an ANN, this conclusion may not be applicable to other applications of ANNs.

In addition, this research was the first to adopt "ROC" analyses in the assessment of predictability for mastitis and proved that  $A_2$ -value was a preferable measure for evaluation of diagnostic systems, especially when the systems are applied to the situations where prevalence of an event differs from one situation to another. It was suggested that joint use of "ROC" and 2-by-2 contingency table analysis would provide a whole picture of the power of a diagnostic system. This study also recommended that the measures of  $P(TP)$ ,  $P(TN)$  and  $P(TTCR)$  should be taken into consideration in evaluation of the role of each input or a group of inputs.

Future research in this area should focus on the pre-processing of information for ANNs, including a creation of new input variables using available input information, such as genetic information for SCC and milk yield, and different coding methods applied to inputs. The pursuit of an optimal

artificial neural network is encouraged. Further research should be directed towards a more valuable but difficult area, i.e. the prediction of subclinical mastitis.

## APPENDIX

Appendix 4.1. The monthly production data consisted of specific test-day variables from the Quebec Dairy Herd Analysis Service. These variables, as well as their treatment by the artificial neural network, are shown below:

Variable	Treatment
Lactation number	Continuous
SCC	Continuous
Milk yield on test day (kilograms)	Continuous
Stage of lactation (days)	Continuous
Season of calving	2 binary inputs (00, 01, 10, or 11)
Season of dry period	2 binary inputs (00, 01, 10, or 11)
Season of test day	2 binary inputs (00, 01, 10, or 11)
Fat percentage on test day	Continuous
Protein percentage on test day	Continuous
Cumulative milk yield	Continuous
Cumulative fat yield	Continuous
Cumulative protein yield	Continuous
Overall conformation class of the cow	Continuous
Presence of Conformation class of the cow	Binary flag (0 or 1)
Overall conformation class of the sire	Continuous
Presence of conformation class of the sire	Binary flag (0 or 1)
Overall conformation class of the dam	Continuous
Presence of conformation class of the dam	Binary flag (0 or 1)
Mean SCC on test day	Continuous
Herd size on test day	Continuous
Total number of inputs	23

#### Appendix 4.2 Further details on the specific conformation traits as well as the classification procedure.

The conformation data consisted of records from Holstein Canada that matched the already existing data set for production. A total of 89 conformation variables were associated with each cow's production record (23 of which were the individual cow's phenotypic scores, 33 of which were that same cow's genetic proofs and 33 of which were the genetic proofs of cow's sire). The fact that there are more proofs than phenotypic observations stems from the fact that, over the period 1979 – 1992, new proofs have been added and, animals were able to receive a proof (through genetic relationships) even though the corresponding phenotypic score was not measured. A brief summary of the collection of conformation data follows.

Type classifications are obtained once every 9 months when a classifier evaluates the animals in a given herd. Traits evaluated on the farm are either given a linear score (1 – 9) and/or measured.

The computer then generates certain composite traits based on these scores/measurements and all the scores are subsequently fed through single-trait BLUP animal model programs to arrive at genetic proofs for both the animals, on which the scores were taken, as well as their sires. The reliability of final score is then calculated, based on the accuracy and size of the data.

For up to date information on the *current* system of classification, the reader is invited to visit Holstein Canada's Web site at:

**<http://www.holstein.ca/>**

All of these 89 variables were treated as continuous by the artificial neural networks.