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Abstract— **Losses of nitrogen (N) from dairy cattle farming system cause environmental pollution and impact human health. A number of statistical models for predicting manure N excretion from lactating dairy cows have been developed based on regression analysis. In this study, we proposed a Bayesian network-based approach to modelling relationships among factors influencing manure N excretion of lactating dairy cows using a dataset collated from total diet digestibility studies undertaken at Agri-Food and Biosciences Institute in Northern Ireland. The preliminary results indicate that Bayesian network model can be used to capture relationships among factors that influence N utilization efficiency and can be used to establish causal influence among predictors. These may provide an effective tool for optimizing the management of feed N resource for current dairy production and developing strategies to reduce N excretion in dairy production systems.**

Keywords—milk yield, diets, manure, breed, causal influence

I. INTRODUCTION

Dairy cattle losses a large proportion of consumed nitrogen (N) to environment, causing environment pollution through volatilizing nitrogenous gases (e.g., ammonia, nitrous oxide and nitrogen oxides) to the atmosphere and leaching nitrate, ammonium and organic N to waters sources [1]. In Europe, dairy cattle farming accounts for 47% of ammonia emissions within the agriculture sector [2]. The surplus of anthropogenic N in the ecosystem can cause global warming, acid rain and eutrophication [3]. In addition to the environmental pollution, N-related pollutants are linked to lung diseases, chronic bronchitis and premature mortality [4], [5]. With regard to above concerns, growing interest has been received over the past decades in developing strategies for reducing N excretion in dairy cattle. Among those strategies, improving the efficiency of feed N utilization with less manure N excretion is the most effective approach to reduce N losses from dairy farms [6]. Improving N utilization efficiency of dairy cows can generate various co-benefits, including farm profitability from reduced feed costs (N is the most expensive component of purchased feeds) and environmental improvements from reduced N excretion in manure [7], [8].

It has been well documented that both dietary and animal factors had major influences on N utilization efficiency in dairy cattle [9]-[11]. For example, statistical analysis of a large dataset of 564 lactating dairy cows [12] found that manure N excretion was positively and significantly related to milk yield, diet N content, N intake and animal live weight. Increasing milk yield or decreasing diet N content resulted in decreased manure N excretion per kilogram of milk yield. In addition to the factors mentioned above, previous studies have indicated that dairy cow genotypes (various genetic merits) had significant influence on N utilization efficiency of dairy production [11], [13], [14]. For example, N utilization efficiency of modern Holstein-origin dairy cows utilized consumed N more efficiently than their earlier populations over 30 years ago [11].

Prediction of N excretion by lactating dairy cows are critical for dairy production industries to develop sustainable nutrient management plans for enhancing economic stability and reducing environmental impacts of dairy farming. So far, a number of statistical models have been developed for mitigation of manure N excretion from lactating dairy cows, which are principally based on simple and multiple regression and mixed model analysis [12], [15]-[17]. A range of such prediction models for lactating dairy cows have established using N intake, body weight and milk yield as primary predictors, either alone or combined. These modelling works found that equations had higher prediction accuracy for manure N excretion when using N intake as primary predictor and body weight and milk yield as supporting predictors, whereas, body weight alone is not an accurate predictor [12]. However, N intake is not always available in commercial dairy farms and it's not possible to assess N excretion using models developed using N intake as predicator. An alternative predictor instead of N intake is dietary N content which has been used for evaluating manure N excretion from dairy cows [12]. In recent years, increased computational power and accessible tools have contributed to enhancing the performance of modelling cattle nutrition and energy balance, such as Bayesian Networks (BN) which has been applied to address factors affecting methane emissions from lactating dairy cows and demonstrated that BN had great potential to capture relationships among variables [18]. Therefore, the objective of the current study was to model factors affecting N utilization efficiency of lactating dairy cows using a BN approach and to establish causal influence among predictors. The main contributions are summarized below:

- To our best knowledge, this is the first study that applies Bayesian network-based approach to modelling the nitrogen utilization efficiency of lactating dairy cows.

- Differing from statistical models based on regression analysis which have been developed for prediction of manure N excretion, the approach introduced in this study has the advantage of exploring the dynamic association between factors.

- This study also explored the application of data discretization, learning algorithms, and whitelist

and blacklist function on incorporating domain knowledge in structure learning of BN.

II. METHODOLOG

A. Datasets

Data used were collated from total diet digestibility studies with 956 lactating dairy cows undertaken at Agri-Food and Biosciences Institute in Northern Ireland. The information on numbers of experiments, treatments, and cow breeds, and forage types offered are presented in TABLE I. The dataset used in the present study showed a broad range in energy corrected milk yield (5.1 – 40.2 kg/d), diet N content (19.0 – 38.0 g/kg DM), and manure N output as a proportion of N intake (0.495 – 0.893 kg/kg), which represents typical dairy production condition managed within grassland-based dairy systems in UK (TABLE II).

Four main factors were included in this study to model the interaction among them. The main factors are:

- Cow breed: Breed (Categorical variable)

- Energy-corrected milk yield (kg/d): ECMY (Continuous variable)

- Diet N content (g/kg DM): DNC (Continuous variable)

- Manure N output as a proportion of N intake (kg/kg): MN/NI (Continuous variable)

Before processing the Bayesian network, outliers in the database were screened using the interquartile range method. In this study, a factor of 1.5 for extremes was used in constructing markers to identify outliers. As a result, a refined complete dataset (n = 891), containing complete information on breed, ECMY, DNC and MN/NI were used for modelling.

The probability densities of the 3 continuous variables are showed in Fig. 1 and they appear to follow the normal distribution.

B. Bayesian networks

Bayesian networks are graphical representations, representing dependence and independence information [19]. A BN includes two parts: (1) a directed acyclic graph (DAG) that represents dependences and independences in a domain of concern, in which nodes and arcs (edges) denote variables and dependencies, respectively, and arrows represent directions of relationships between variables (nodes), and (2) a joint probability distribution of a set of random variables that is associated with the vertices.

Let X be the node set (random variables) of a BN which is a DAG. The DAG defines a factorization of joint probability distribution of $X = \{X_1, X_2,\ldots, X_n\}$ into a set of local probability distributions, one for each variable. The form of the factorization states that every random variable X_i directly depends only on its parents:

$$P(X_i, \ldots, X_n) = \prod_{i=1}^{n} P(X_i \mid \prod_{X_i}) \qquad (1)$$

TABLE I. INFORMATION ON EXPERIMENT, COW BREED AND FORAGE TYPES IN THE DATASET USED IN THE PRESENT STUDY

	Dataset
Number of experiments	39
Number of treatments	208
Number of individual cow data	891
Cow breeds	
Holstein	736
Holstein Cross	72
Norwegian	57
Swedish Red	16
Forage types	Grass silage, fresh grass, maize silage, whole crop wheat silage

where $\prod_{X_i}$ denotes the set of parents of X_i and $P(X_i \mid \prod_{X_i})$ is the conditional probability of X_i given its parents.

The main process of BN learning consists of structure learning and parameter estimation. The structure learning involves the identification of real dependencies between measurable variables and the algorithms for BN structure learning can be grouped in two categories: constraint-based and score-based algorithms. The parameter estimation aims to find the most probable values for parameters and involves the estimation of conditional probability values.
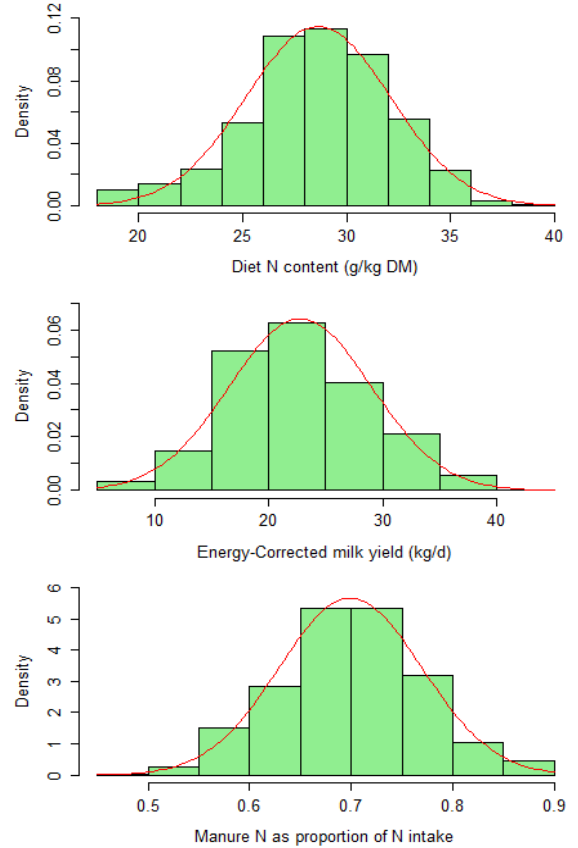

Fig. 1. The probability densities of diet N content, Energy-Corrected milk yield and manure N as proportion of N intake. The red line is the corresponding normal curve.

C. Implementations

A constraint-based structure learning algorithm, Growth-Shrink, was used to implement structure learning by using R package bnlearn [20]. Both knowledge-driven and data-driven were incorporated as the processing of structure learning. Function of whitelists and blacklists was used to pre-define the arcs and its directions according to domain knowledge. Visualisation and inference of BN were performed using GeNIe Modeler (https://www.bayesfusion.com/) developed by BayesFusion LLC (Pittsburgh, USA).

The strength of influence was calculated from the conditional probability table of the child node and essentially expresses as distance between the various conditional probability distributions over the child node conditional on the stats of the parent node [21]. The metric Euclidean was used as measure of distance between distributions. The strength of influence between the nodes that they connected in the BN was presented by the thickness of arc.

The continuous variable of ECMY was discretized into 3 categories (i.e. lower than 20.0, between 20.0 and 30.0, higher than 30.0 kg/d) supported by the domain knowledge [18]. The other two continuous variables, DNC and MN/NI, were discretized by Hartemink's Information-preserving Discretization function [22]. It relies on minimizing the loss of pairwise mutual information between each two real-valued vectors (variables). The mutual information between two random variables X and Y with joint distribution $p(X,Y)$ and marginal distributions $p(x)$ and $p(y)$ is defined as:

$$I(X;Y) = \sum_x \sum_y p(x,y) log \frac{p(x,y)}{p(x)p(y)} \qquad (2)$$

The ranges of discretization are as follows:

- DNC (g/kg DM): 3 categories, Low (19.0, 25.3]; Medium (25.3, 29.9]; and High (29.9, 38.0].

- MN/NI: 3 categories, Low (0.495, 0.637]; Medium (0.637, 0.745]; and High (0.745, 0.893].

III. RESULTS

A. Bayesian networks constructed

The structure of BN was learned by the Grow-Shrink algorithm using the R package bnlearn and the nodes were presented by rectangles (Fig. 2). The bar chart displayed in each rectangle represents the corresponding probability distribution values of the node. The causal influence between variables is denoted by arrows and the thickness of arrow reflects the strength of influence one node has on the other. The thicker arrow means a greater influence.

B. Causal influence between nodes

The network showed in Fig. 2 demonstrates that:

- The MN/NI was influenced directly by DNC, ECMY and cow Breed. The DNC and Breed had influences on MN/NI and ECMY.

- The DNC has a strongest influence on MN/NI, irrespective of measures used. Meanwhile, both Breed and ECMY also show a strong influence on MN/NI. For ECMY, DNC has a stronger influence than Breed. All of these relationships were consistent with previous studies showing that manure N excretion rates and efficiency of conversion of dietary N into milk are affected by DNC [7]-[10], [23].

- The impact of DNC. The DNC has a clear and positive influence on ECMY. The higher N consumed the more milk produced by lactating dairy cattle, which is consistent with previous studies [6], [12], [15]. In this study, when cows were fed at high DNC levels, the probability of ECMY less than 20 kg/d drops from 46% to 29% while the probability of

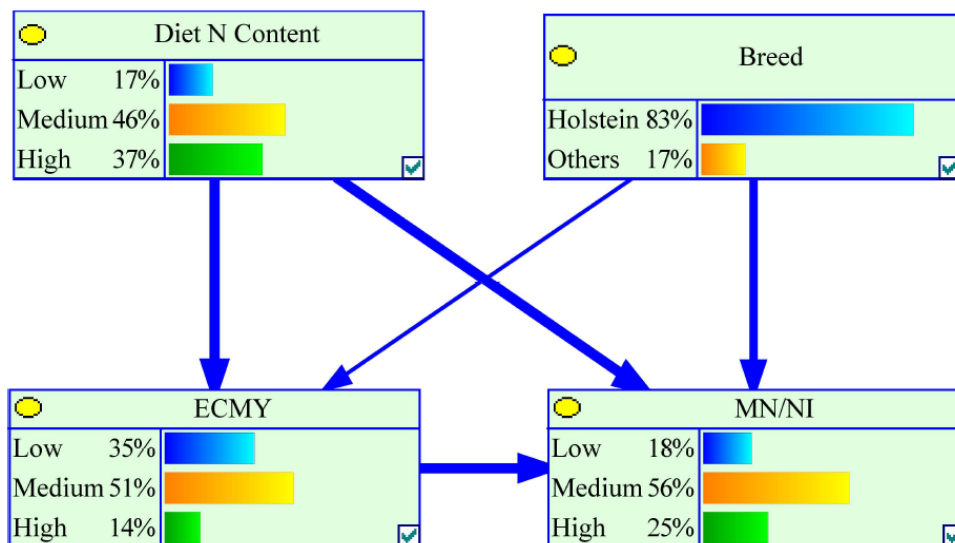Fig. 2. Bayesian network constructed based on the discretization of the dataset. Nodes are presented by rectangles. The bar chart displayed in each rectangle represents the corresponding probability distribution values of the node. Arrows denote causal influence from one feature to another. The thickness of arrow reflects the amount of influence one node has on the other. The thicker arrow indicates a greater influence.

ECMY higher than 30 kg/d is increased 9% to 17% (TABLE III). The DNC had a positive effect on MN/NI. As shown in Table IV, the probability of MN/NI higher than 0.745 kg/kg increases by 20% when DNC change from less than 25.3 g/kg DM to higher than 29.9 g/kg DM.

- The influence of cow breed: The impact of Breed on ECMY and MN/NI is not straightforward (TABLE V, VI), although previous studies have shown that cow breed merits had significant influence on milk yield and N utilization efficiency of lactating dairy cows [11], [13]. This might have been caused by the imbalance in number of cow data in the two breeds in the current dataset (736 Holstein and 145 others).

- Influence of ECMY on MN/NI: The ECMY has significant impact on MN/MI and the higher milk yield the lower MN/NI, which is in line with other researches [12]. For example, when ECMY increased from less than 20 kg/d to more than 30 kg/d, the probability of MN/NI higher than 0.745 kg/kg dropped from 30% to 9% (TABLE VII).

C. The dynamc of the network

- GeNIe is a development environment for building graphical decision-theoretic models and it provides numerous tools. The belief updating is based on the probability distribution of nodes and the constructed structure of the BN model. The posterior probability distribution of a child node over all parent nodes can be performed after setting evidence at this child node.

- In this study, the updated beliefs (Fig. 3) indicates that the probability of producing milk less than 20 kg per day of non-Holstein cows increases sharply (35% vs. 70%) when diets with lower N contents were offered, meanwhile, the probability of MN/NI at medium level (0.637 - 0.745 kg/kg) increases from 56% to 87%. In addition, Holstein cows offered high N content diets (> 29.9 g/kg DM) slightly increases the probability of producing milk more than 20 kg per day but enhances the probability of MN/NI at high level (> 0.745 kg/kg) by 12%. This is in line with previous studies as less N partitions into milk will result in more N excretes from manure [10].

TABLE II.   THE CHARACTERISTICS OF 3 CONTINUOUS VARIABLES

Variable	ECMY	DNC	MN/NI
	kg/d	g/kg DM	kg/kg
Mean	22.8	28.6	0.699
Standard deviation	6.23	3.48	0.0705
Maximum	40.2	38.0	0.893
Minimum	5.10	19.0	0.495

TABLE III.   THE INFLUENCE OF DIET N CONTENT ON MILK YIELD

Diet N content (g/kg DM)	The probability of ECMY		
	Low (<20)	Medium (20-30)	High (>30)
Observation-free	0.35	0.51	0.14
Low (<25.3)	0.46	0.45	0.09
Medium (25.3-29.9)	0.36	0.52	0.12
High (>29.9)	0.29	0.54	0.17

TABLE IV.   THE INFLUENCE OF DIET N CONTENT ON MN/NI

Diet N content (g/kg DM)	The probability of MN/NI		
	Low (<0.637)	Medium (0.637-0.745)	High (>0.745)
Observation-free	0.18	0.56	0.25
Low (<25.3)	0.35	0.51	0.14
Medium (25.3-29.9)	0.15	0.63	0.22
High (>29.9)	0.14	0.52	0.34

TABLE V.   THE INFLUENCE OF COW BREED ON MILK YIELD

Breed	The probability of ECMY		
	Low (<20)	Medium (20-30)	High (>30)
Observation-free	0.35	0.51	0.14
Holstein	0.34	0.51	0.15
Others	0.35	0.53	0.12

TABLE VI.   THE INFLUENCE OF COW BREED ON MN/NI

Diet N content (g/kg DM)	The probability of MN/NI		
	Low (<0.637)	Medium (0.637-0.745)	High (>0.745)
Observation-free	0.18	0.56	0.25
Holstein	0.17	0.55	0.28
Others	0.26	0.59	0.15

TABLE VII.   THE INFLUENCE OF MILK YIELD ON MN/NI

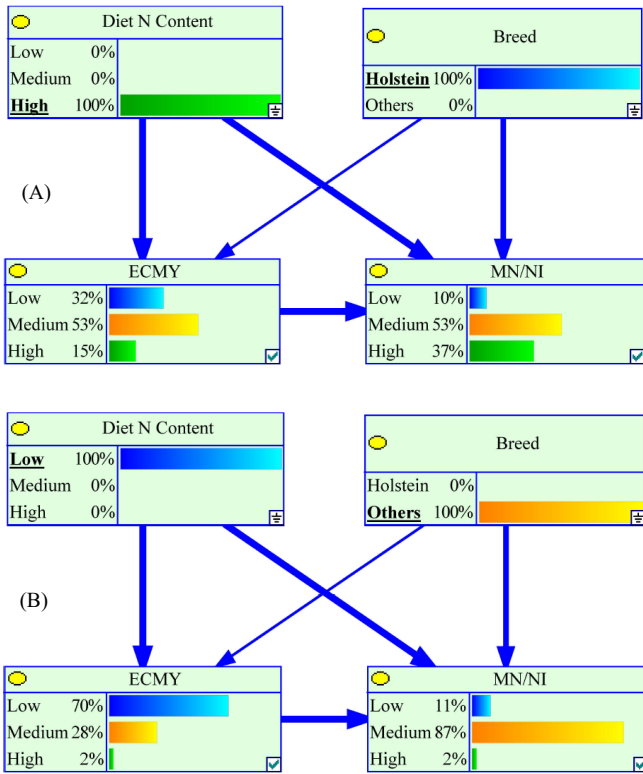| Energy-Corrected Milk Yield (kg/d)	The probability of MN/NI		
	Low (<0.637)	Medium (0.637-0.745)	High (>0.745)
Observation-free	0.18	0.56	0.25
Low (<20)	0.11	0.60	0.30
Medium (20-30)	0.21	0.52	0.26
High (>30)	0.32	0.59	0.09

Fig. 3. The updated beliefs in the Bayesian network for a Holstein cow taking diet with high N content (A) and for a non Holstein cow taking low N content diet (B).

IV. A CORRELATIONAL STUDY

A. The impact of discretization

To test the impact of discretization, we compared the structure and strength of arcs by adjusting interval boundaries of DNC which had the strongest influence on MN/NI and dividing continuous variables DNC and MN/NI into 4 categories. The Akaike information criterion (AIC) was used to measure the strength of arcs with R function *arc.strength*. The strength is measured by the AIC score gain/loss which would be caused by the arc's removal. Negative AIC values correspond to decreases in the network score and positive AIC values correspond to increases in the network score (the stronger the relationship, the more negative the difference).

- Adjusting interval boundaries and different discretization did not alter the structure of BN.

TABLE VIII.   IMPACT OF DICRETIZATION ON MODEL

Arcs		AIC values		
From	*To*	*Old boundary with three categories*	*New boundary*	*Four categories*
DNC	ECMY	-16.2	-15.6	-13.9
DNC	MN/NI	-28.9	-20.8	-13.1
Breed	ECMY	-9.12	-4.17	-4.67
Breed	MN/NI	-9.38	-11.3	-7.98
ECMY	MN/NI	-19.4	-26.0	-20.8

- Compared to previous BN, adjusting interval boundaries only slightly altered the strength of arcs (TABLE VIII) while the classification error was increased by 60% if variables were dividing into 4 categories.

B. The impact of learning algorithms

Two constraint-based, Grow-Shrink and Incremental Association Markov Blankets (IAMB), and two score-based structure learning algorithms, Hill Climbing and Tabu Search, were used to implement structure learning. Two whitelists were incorporated in the structure learning process: Breed → ECMY and ECMY → MN/NI.

- The structure of BN derived based on four kinds of learning algorithms with pure data-driven process are showed in Fig. 4. Under the pure data-driven approach, constrained-based algorithms captured more arcs than that of score-based algorithms. The directed arc between MN/NI and ECMY was reversed with domain knowledge although it was leaned by both constrained- and score-based algorithms. All the algorithms failed to capture information between nodes Breed and ECMY which has been confirmed to be affected by breed of cows.
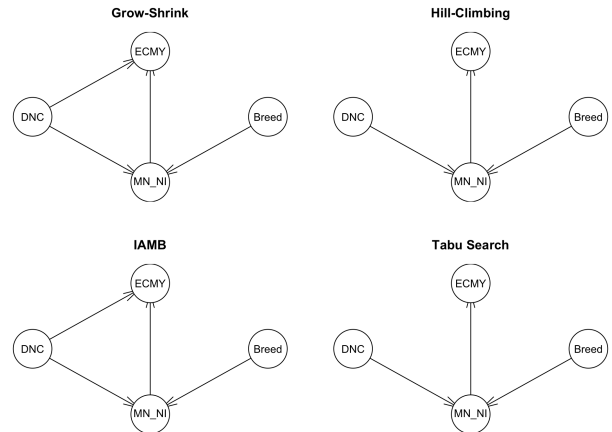

Fig. 4. BN structure learned based on different learning algorithms with pure data-driven approach corresponding normal curve.
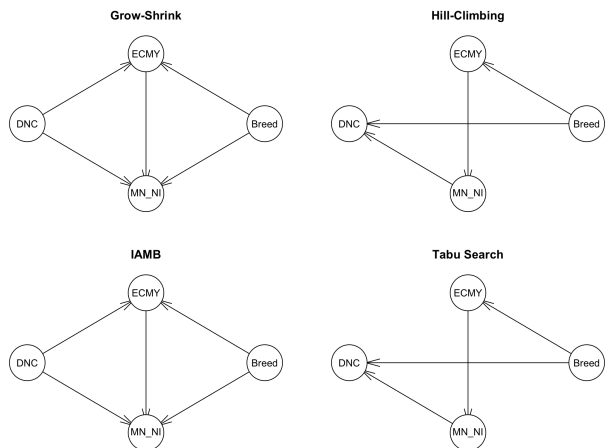

Fig. 5. BN structure learned using different learning algorithms with whitelists incorporated approach.

- The reasonable structures of BN were derived based on constrained-based algorithms with two whitelists incorporated (Fig. 5). However, the structure learned based on score-based algorithms contained two directed arcs (Breed → DNC, MN_NI → DNC) that did not match with the domain knowledge.

C. The selection of whitelist

The domain knowledge on data can be integrated in all learning algorithms by means of the whitelist which is the arc guaranteed to be present from the Bayesian network [20]. We compared the structure of BN derived based on Grow-Shrink algorithm by adding different whitelists as shown in Fig. 6. The whitelists included in this comparison are "Breed → ECMY", "ECMY → MN_NI", and "Breed → ECMY, ECMY → MN_NI".

- The structure of BN was influenced by selection of whitelist (WL). Compared to the structure derived with pure data-driven (without whitelist, lower right figure in Fig. 6), single whitelist incorporated in the learning process did not improve the structure. For example, adding whitelist "Breed → ECMY" or "ECMY → MN_NI" to learning process resulted in undirected arcs (between ECMY and MN_NI, between ECMY and DNC, respectively).
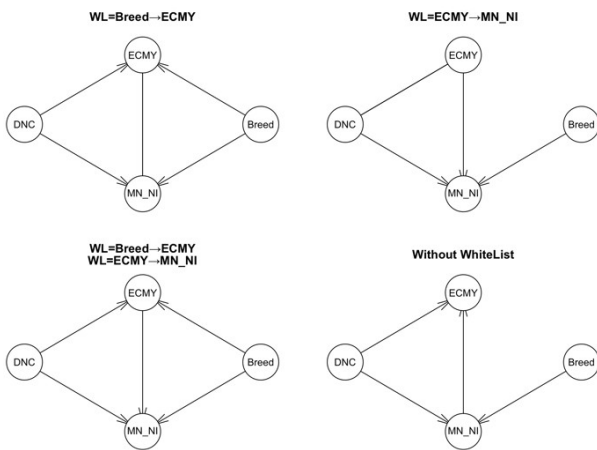

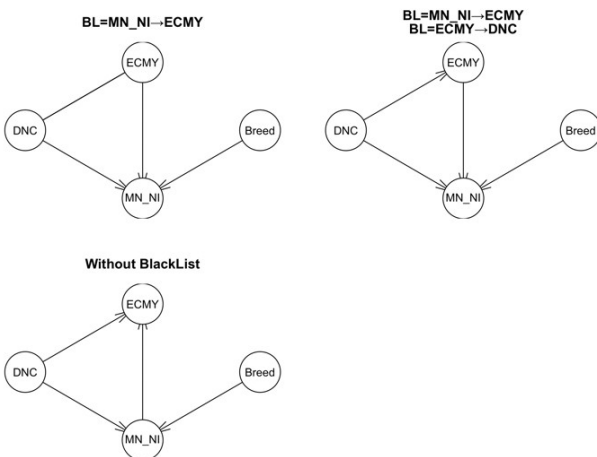Fig. 6. Influence of whitelist (WL) selection on BN structure.

Fig. 7. Influence of blacklists (BL) selection on BN structure.

- The results imply that ECMY may be the key variable in this model because it appeared in all the whitelist. It matches with domain knowledge as more milk produced less N excreted into manure.

D. The selection of blacklist

Blacklists are selected based on the domain knowledge. The arcs in the blacklists are guaranteed to be missing from the Bayesian network. Using the algorithm of Grow-Shrink, the structures of BN were derived by adding different blacklists as shown in Fig. 7. The blacklists involved are "MN_NI → ECMY", and ECMY → DNC". It's failed to construct the domain knowledge marched BN structure by using blacklist function particularly when pure data-driven process did not capture the relationship between nodes, e.g. adding blacklists did not help to build the arc between Breed and ECMY.

V. Conclusions

A number of models have been developed to assess the interactions among factors affecting manure N excretion from lactating dairy cows over the past decades and most of them are based on regression analysis. In the current study, we proposed a network-based model to examine and inference the effect of three main factors on manure output as a proportion of N intake in lactating dairy cows. The preliminary results indicate that Bayesian network model can be used to capture relationships among factors and to establish causal influence among predictors, which may provide an effective tool for optimizing the management of feed N resource and developing strategies to reduce N excretion in modern dairy production systems. In addition, the present modelling exercise demonstrates that a BN structure can be effectively constructed by incorporating the domain knowledge in the structure learning process using whitelists and blacklist functions in BN learn package.

Although the present results indicate that BN modelling is an effective approach to evaluate factors influencing N utilisation efficiency of lactating dairy cows, more work is needed to explore relationships among selected factors for prediction of N excretion of dairy production. For example, further research is required to investigate the impact of selection of parameters on the BN structure for prediction of manure N excretion and to compare the performance of BN models with that of statistical regression models which are commonly used to evaluate N utilization efficiency of dairy cows.

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