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NDS Dynamics

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Welcome to NDS Newsletter

By David Weber DVM

NOT ONE MORE NEWSLETTER TO READ YOU SAY!

NDS Dynamics would like to send you a newsletter quarterly to keep you up to date with changes in NDS and the industry. If this is something you are not interested in please send us an email to take you off our list.

Inside This Issue

Feed Analysis and Re-sampling

By Ermanno Melli
Research & Development RUM&N Sas

Not knowing the nutritive value of a feedstuff can lead to less than optimum resource management such as not supplementing enough or spending excess money supplementing animals that do not need it. Livestock producers and nutritionists have far back recognized that laboratory feed testing is the recommended way to determine forage and feed nutrient content. It involves determining nutrient levels in forages and feeds and is one of the most effective feed and forage management tools. This eliminates speculation when trying to match forage and feed supplies to animal nutrient requirements, designing supplemental feeding programs, and evaluating forage production.

Submitting feed and forage samples to a laboratory for analysis is a common practice that gives a robust idea of the nutritional value of the feed, which in return can drive management decisions such as whether or not to supplement and how much to supplement.

In range of a strong analysis strategy, one feed is sampled and analyzed several times until its depletion, in order to keep up-to-date its nutritional characteristics and to allow a precise assessment of the ration in the course of time.

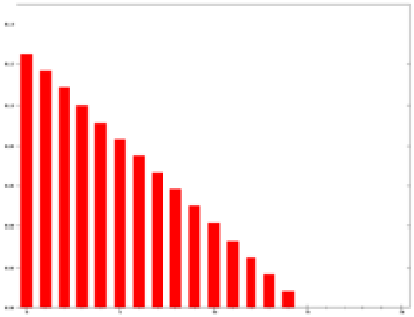
The most advanced nutrition platforms allow importing the analysis results coming from the laboratory; this makes the data acceptance process very efficient. On this matter, one very useful function would be the **re-sampling** feature. If a feed was already analyzed in the past, it allows you to import its laboratory data as an update on the previously analyzed sample and not as a new feed. This means that the new feed analysis data, if already existing in the data set, will update the current ones. Rations will be automatically re-evaluated, if the feed is already included.

Moving Average Re-sampling

This new approach adds the capability of re-sampling a feed with average values, calculated from a series of samples, each stored in a different import file. The term "Moving" indicates that only a sub-set of the available samples is used for the average (typically including the most recent ones); each time a new sample is added, the last one is excluded from the sub-set, in order to smooth out short-term fluctuations and highlight longer-term trends of the feed value. The number of the samples in the sub-set can be chosen for each feed.

Every time an analysis file is imported, its values are also saved as sample data in the database (the first sample is created when the related feed is created and cloned for the

Please see *Feed Analysis* on page 3



Above:
Linear weighted average assigns decreasing weights as the samples become older. In this way the most recent ones always have the highest weights.

A Few Points on the Reliability of Lipid Submodels

By Tom Jenkins
Clemson University

Lipid submodels in nutrition modeling programs attempt to estimate three important measures of total and individual fatty acid (FA) flows (g/day) in cows fed a specific TMR; 1) flow of FA consumed 2) rumen outflow of FA and 3) flow of absorbed FA in the intestines. Let's have a quick look at how good a job they do at each of these tasks.

1. Flow of FA Consumed – This is the most easily controlled of the three. Content and profile of FA in feed ingredients in the library are based on actual wet chemistry values that are accurate and dependable for that specific ingredient. If you are feeding ingredients that have similar nutrient composition (such as protein, fiber, etc) as the same ingredients listed in the library you will come very close to actual FA intakes by the cow. If any of your feed ingredients don't match the library counterpart closely, you are risking errors in estimating FA intakes. This is easily solved though. Several commercial laboratories offer FA analysis at a reasonable cost and you can enter actual values from the analysis of your ingredients.
2. Rumen Outflow of FAs – Definitely the most difficult of the three to estimate. The program probably includes a lipolysis rate for FA assigned to each ingredient, which estimates how quickly FA are released from a "bound" state in the feed material to a "free state" in rumen contents. Once FA are in the free state they can then undergo the process of biohydrogenation, which converts unsaturated to saturated FA in the rumen along with the accumulation of a number of trans FA and CLA intermediates. High lipolysis rates mean FA are quickly released and undergo extensive biohydrogenation leading to a rumen outflow with high saturated and low unsaturated FA profile. Low lipolysis rates mean FA are slowly released from their bound state thus limiting biohydrogenation resulting in a higher rumen outflow of unsaturated FA. If lipolysis rates are incorrect, calculations of biohydrogenation and their intermediates also will be in error. Where do lipolysis rates come from? The great majority were computer generated based on intakes and rumen outflow of FA taken from published studies with duodenally-cannulated cows. Sometimes there were very few published studies on a specific feed ingredient leading to considerable uncertainty about their lipolysis rate. As of now, there is not a way to have a feed ingredient analyzed for its lipolysis rates.
3. Flow of Absorbed FA from the Intestines – this one falls somewhere between the other two in dependability. Digestibility values for FA in feed ingredients are compiled from published studies. For the most part, the digestibility values vary little from one ingredient to another. The main exception would be new fat supplements where FA digestibility could be a function of its specific chemical and physical properties. FA digestibility's can be measured in vivo, although metabolism trials are lengthy and expensive.

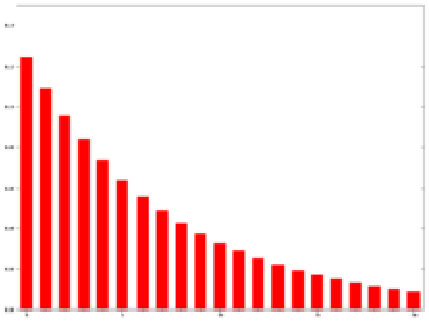
We still have room for improvement in building nutrition programs that more accurately reflect FA status of cows fed specific diets. Of course, the same could be said of most other nutrients as well including amino acids and carbohydrates. Despite limitations with the current lipid submodels, they have already provided valuable assistance into decisions about manipulating lipid intakes by cows to enhance performance. Accurate and dependable lipid submodels are needed more today than ever – let's keep striving for improvement.

Free Tips for your NDS!

Did you know:

- There are PDF tutorials in a zip file on our website!
- We even have some audio tutorials on the website that use your Windows Media Player to run through the tutorials.
- An easier way to get NDS Updates on your program; make sure the 'Automatic update' box is checked in the 'Options' under 'Settings.'
- A new commercial feed library is being built and is being made available for download now, with more ingredients added monthly!
- You can also pick where you want to save your recipes, in an external or internal file structure. To learn more visit "File Structure" tutorial from our website!

Feed Analysis from page 1



Above:

Exponential average applies weighting factors which decrease exponentially as the samples become older. With the effect of enhancing even more the recent samples in the average calculations.

first time). The link between the sample and the feed is set through the feed selection step of the re-sampling.

At least two samples of the feed to be re-sampled are needed in order to get the moving average applied; in this case some additional functions are available:

- Number of samples: if more samples are available you can choose how many of them have to be included in the sub-set used to calculate the average values; if this equals or exceeds the number of available samples, the average is calculated using all the available samples. It is also possible to choose just one sample; in this case the re-sampling is not based on an average, since the values are just those of the most recent sample.
- Moving Average methods: three different average methods are available:
  - Simple (non-weighted) Average;
  - Linear Weighted Average;
  - Exponential Average.

Simple Moving Average (SMA) is a non-weighted average; in other words, it assigns the same weights to all the sample values. Since SMA could be disproportionately affected by "old" data, two more different weighted average have been developed to give higher weights to the most recent samples and lower weights to the older ones.

NDS Training Session during ADSA

By Rachel Eickman

Where: Indianapolis at the Hampton Inn Downtown
When: July 10th - 12th
Why: We will be hosting two different sessions for you to pick from:

Wednesday July 10th 'Starting with the Basics' from 5-9 pm

This is designed to give an overview of the program from start to building diets. We will explore all parts and aspects of the NDS Program.

Thursday July 11th and Friday July 12th 'What's new and digging deeper with NDS'

This two day seminar will be for people starting with or already using NDS. Using the NDS software the time will be used going through basic to more complex functions and features also looking at new features.

Hampton Inn Downtown
105 S Meridian Street
Indianapolis, IN 46225

$50 Registration fee for Wednesday
$500 Registration fee for Thursday & Friday
RSVP now to save your seat!
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