

AMINOCow[®] Know How

Helpful hints for the effective use of AminoCow[®]

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Importation of Lab Samples Into AminoCow +: Guidelines for Users

AminoCow provides a semi-automated procedure for importing feed sample results from laboratories into AminoCow rations via e-mail. In order for you to take advantage of this procedure, the laboratory or laboratories that you use must be able to provide sample results to you in a prescribed format. Please check with the laboratories that you use to see if they provide this option.

Importing a Lab Sample and the Labs Folder

“Lab Sample” files are text files that are e-mailed to you by the lab. AminoCow provides a default folder for storing such text files in the AminoCowDocs folder created when you installed AminoCow. If you installed AminoCow on your C: drive, the folder is “C:\AminoCowDocs”, and the folder for storing lab samples is “C:\AminoCowDocs\Labs”. AminoCow always begins the process of managing lab samples by searching the Labs folder for new samples in the .txt format.

Any “.txt” files found in the Labs folder are presumed to be lab sample files and AminoCow will attempt to read these files. If a “.txt” file is not a lab sample file, AminoCow will generate a warning message and skip the file. If the file is a lab sample file, the samples will be read into the program and the “.txt” file will be deleted.

If you wish to keep copies of your lab samples files, make copies before running AminoCow and store the copies in a folder other than the Labs folder. AminoCow creates a sub-folder inside the Labs folder called “Archive”, and if you wish to, you can use the “Archive” folder for storing copies of sample files. However, AminoCow provides no management tools for this folder. The normal path for this folder is “C:\AminoCowDocs\Labs\Archive”.

If you receive lab samples via e-mail in a txt format, the simplest procedure is to save the .txt attachment to the Labs folder. However, many laboratories will include some type of standard report in a PDF or other document format, along with the sample file. If these files are also placed in the Labs folder, AminoCow will skip these files and will not remove them from the Lab folder. For those users with automatic download of zipped files, “Lab Sample” files should be downloaded into the normal download directory and unzipped. The unzipped .txt file can then be copied to the AminoCowDoc\Labs folder. Do not download zip files into the Labs folder.

If you wish to use a different procedure for stroing lab samples files, you will have to use the “SearchForSamples” utility. This utility is described in a later section of this documentation.

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To summarize, the basic recommended procedures for storing and accessing lab sample files are:

- AminoCow searches the Labs folder for files with .txt extension.
- Any files in the Labs folder with the .txt extension are assumed to be files containing lab samples.
- If the .txt file conforms to AminoCow requirements for lab sample files, the samples are read and placed in the Lab Queue for use in the AminoCow program and the lab sample file is deleted.
- If the .txt file is not a lab sample file, AminoCow displays a warning message and skips the file.
- Files in the “Labs” folder, which do not have the .txt extension are skipped.
- If you do not store lab sample “.txt” files in the Labs folder, you must use the “Sample Search” utility to locate your lab sample files.
- If, for some reason, you wish to keep copies of lab sample txt files, save your copies to a different folder before running AminoCow.

A Glossary of Terms

The following are terms used in this documentation.

Labs	the AminoCow labs folder described above.
Lab Sample Queue	the list of samples.
Lab or Sample Header	information about a sample provided by the lab.
Unused Samples	samples in the lab queue that have not been used.
Used Samples	samples that have been used to update an AminoCow feed, but have not been archived. Used samples are always associated with a specific client.
Archive	the list of used samples that have been deleted from the lab queue and moved to the archive.
Blended feed	the feed produced by updating an AminoCow feed with a lab sample, using some values from the current sample and some values from the AminoCow feed.
View	the samples currently displayed in the samples grid.
ACFeed	the name of the base AminoCow feed as found in the AminoCow feed's database. ACFeed is always stored with a used or archived sample to provide an audit trail.
Ration Feed/Feed	the name of the “blended feed” as found in the ration. The Ration Feed name is saved with the nutrients section of a used sample.

Overview of the Lab Sample Import Process

In AminoCow, begin the import process by selecting the ration that contains the feed that you wish to update. Then, from the Ration Worksheet, select the AminoCow feed that you wish to update. (AminoCow feeds are feeds with a feed type of “F”, “G”, “BP”, and “VM”. You cannot update user feeds, company feeds, mill feeds or mixes). Move to the ‘Feeds’ menu and select ‘Import Lab Analysis’. You will be asked if you wish to update the feed you selected. If you enter ‘Yes’, AminoCow will search the Labs folder for any new “Lab Sample” files and will automatically import new samples into the Lab Sample Queue. If new sample files are



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found, a message will indicate how many samples were added to the queue. If no new files were found but you have sample files that are not in the Labs folder, you can select 'Search for Samples' from the 'Lab Analysis' menu to display the file selection utility at the bottom of the "Lab Analysis" screen.

Regardless of whether or not there are new lab samples, the "Lab Analysis" screen will display. The "Lab Sample Analysis" form consists of 3 sections. The top of the form displays basic information regarding the sample. Typically this includes the feed laboratory supplying the sample, a laboratory reference number, and a return date as well as the client for which the analysis was performed and the laboratory description of the feed. Below this will be the client name known to AminoCow and the name of the AminoCow feed that will be updated. In the center section will be the name of the feed to be updated along with a list of basic nutrients. A grid at the bottom of the screen contains the lab samples currently available for use. When a lab sample is chosen, the name of the feed and the basic nutrients from the sample will display under the AminoCow feed.

Except for the "AminoCow Client" and "AminoCow Feed" boxes, the sample header boxes at the top of the screen are empty. The sample header boxes will be filled with information supplied by the laboratory when you select a lab sample. The "AminoCow Client" box contains the name of the client associated with the ration, while the "AminoCow Feed" box displays the name of the AminoCow feed as it appears in the AminoCow feeds database. Since it is possible to rename and modify AminoCow feeds at the ration level, this name may not be the same as the feed name used in the ration, and the nutrient profile of the current version of the feed may be different from the database version. Except for the application of 'AABByFormula', which always uses regression equations for the database version of the AminoCow feed, all calculations are based on the current version of the feed.

By default, the "Lab Sample" grid only displays unused samples. If there are no unused samples in the queue, the "Lab Sample" grid will be empty. If there are feeds in the archive for this client, you can click 'View Archived Samples' or you can select 'View Queue' to view all samples, including used samples for this client in the lab queue.

Choose the sample that you wish to work with from the "Lab Sample" grid. Selected basic nutrients for the sample will display below the AminoCow feed in the upper grid. If you are satisfied that the sample feed matches the profile of the AminoCow feed and is the correct feed, click 'Next'. If you are not satisfied, you can select a different feed from the sample queue or click 'Cancel' if there is no sample feed matching the AminoCow feed. In some situations, it may be necessary to return to the 'Ration Worksheet' and either select a different feed from the ration or perhaps even add an additional feed to the ration before returning to the 'Lab Analysis' screen.

In most situations, the unit of measure for energy and vitamins reported by the laboratory will be the same as the unit of measure for the ration. However, for nutritionists working with clients in different countries or using laboratories that report results using different units of measure, there may be an occasional miss-match. If AminoCow detects a miss-match, a warning message is displayed and any energy and vitamin values included in the sample are converted to the units used in the ration before the sample is copied. Discrepancies in the unit of measure – lbs, kg, or mj – only affects energy and vitamins.

If you click 'Next', you will be asked if you wish to archive the sample feed. If you answer 'Yes' the feed will be moved from the sample queue to the sample archive. If you answer 'No', the sample will be marked as



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used and will remain in the lab sample queue. Unless you are planning on maintaining a sample history or you plan to use the analysis in another context, it is not necessary to archive samples.

The “Feed Analysis” screen will display next. The name of the sample feed will replace the name of the AminoCow feed. Nutrient values from the sample feed will appear in bold blue, while values from the matching AminoCow feed will appear in black. All calculated nutrients are re-calculated on the basis of the lab analysis and these nutrients are also displayed in bold blue. Nutrients potentially affected by the lab analysis are the amino acids, which for feeds where AABByFormula is available are recalculated if CP changes, NFC, TDN and if Starch or Sugar changes the Glucose Precursor. RDP values included in a lab sample should be carefully evaluated before accepting them. Many labs present a calculated value for RDP and this may be different from the analytical value from the AminoCow feeds database. AminoCow rules for editing feeds apply. Except for calculated fields, any nutrient value can be edited and the name of the feed can be changed.

If you wish to put the “blended feed” on the “Ration Worksheet”, select ‘Save’. You will then be asked if you wish to overwrite the existing AminoCow feed in the ration. If you answer ‘Yes’, the feed name currently in the ration and the nutrient values will be replaced by the blended feed and the ration will be recalculated on the basis of the blended feed. If you answer ‘No’, the blended feed will be added as a new feed at the bottom of the ration.

Important Considerations and Limitations of the Importing Lab Samples

While importing a lab sample into AminoCow is straightforward, there are several important considerations and limitations that must be kept in mind for the import procedure to produce satisfactory results. Overall “local knowledge” concerning the source of the sample feed is the most critical factor in matching an AminoCow feed to a lab sample and is the best safeguard against miss-matched feeds. The considerations for choosing a matching AminoCow feed for the lab import process are no different than the considerations used for manually modifying a feed based on a feed analysis, but they are worth repeating.

First and foremost the AminoCow protein model requires accurate information on the amino acid content of feeds as well as accurate information on the feed’s likely contribution to microbial synthesis. Very few lab analyses contain information on the amino acid content of feeds so this information must come from the matching AminoCow feed. As for microbial protein, some of the major nutrients, including CP, NDF and Ash, used to calculate microbial protein are included in most feed analyses, but other important nutrients such as NDCIP, ADICP, fat, lignin and the processing factor may not be included in the feed analysis.

The point is that an imported sample feed is a “blended feed” with some nutrients coming from the sample, but with any nutrients not provided by the sample coming from the AminoCow feed. The following are critical points:

1. The sample feed must be a good match with the AminoCow feed that it will modify. If the match is not good, the amino acid nutrient contribution of the blended feed cannot be accurately calculated.
2. AABByFormula must be used to calculate the amino acid content of the blended feed. AABByFormula uses regression equations to calculate the amino acid content of a feed based on changes to CP. If the sample feed is poorly matched to an AminoCow feed, the wrong set of regression equations will be used, and the amino acid values will not be correct.



3. When calculating microbial synthesis using a blended feed, the AminoCow feed provides default values for any nutrients not included in the lab analysis. If there is a poor match, the microbial protein contribution of the blended feed cannot be correctly calculated.
4. For forages, grains and by-products, the processing factor is a critical component in the calculation of microbial protein. Among the common feeds, varieties of corn grain and corn silage vary significantly in their processing factors. Of particular concern is corn silage where there is a significant difference between processed and non-processed corn silage. Since a lab analysis typically cannot distinguish between processed and non-processed corn silage, the user must know if the corn silage in the sample is processed or not.
5. Legumes, including alfalfa and clover, tend to vary in terms of the nutrients in the carbohydrate group including lignin. For feeds in this group, matching the lab sample to an AminoCow feed on the basis of the carbohydrate group is more important than matching on CP. “Local knowledge” concerning the age and type of the legume is a critical component in achieving a good match.

Problem Feeds

Mixed hays and forages present a special case in that the AminoCow feeds database has only two mixed samples to represent these ingredients, and the AminoCow samples may or may not be representative of any given real world sample. Laboratories may provide some information on the content of a mixed sample, and of course “local knowledge” is another important factor. If the mixed sample is used in small quantities in a ration, then choosing one of the two AminoCow mixed forages may be “close enough”. However, if the mixed forage is a major ingredient in a ration, then it might be worth considering using the primary feed in the sample as the basis for choosing an AminoCow feed. For example, if the sample is a mix of legumes and timothy and is mostly legume, choose the legume as the AminoCow feed. For mixed forages the primary problem is choosing an AminoCow feed that is a reasonable match in terms of lignin, sugar and the amino acid profile.

TMR's and other mixes

Samples consisting of TMR's and mixes such as energy mixes and protein blends cannot be imported into AminoCow. AminoCow cannot calculate the amino acid content of these feeds as they do not correspond to any standard AminoCow feed. However, if a laboratory includes a report as part of the feed analysis, the results of the analysis as included in the report can be used to validate calculated results for an AminoCow mix or TMR.

This restriction does not apply to mineral mixes as AminoCow allows mixes that do not contain protein to be modeled as single feeds. However, if a mineral mix is imported and matched to an AminoCow mineral, make sure that all non-reported nutrient values are set to zero.

The Lab Analysis Screen

The “Lab Analysis Screen” briefly described in the overview section displays the lab queue and provides some basic management tools for the lab queue. If you are not interested in maintaining an archive of lab samples, then this screen should provide all of the tools necessary to import lab samples and maintain the lab queue. If you are interested in maintaining an archive of lab samples, a more extensive set of tools is available by selecting ‘Feeds’ from the AminoCow “Main Menu” and then selecting ‘Manage Lab Samples’. This option is discussed in the following section.



The Structure of a Lab Sample

Lab samples as generated by participating laboratories have two parts (1) a lab header providing basic information about the lab sample and (2) sample nutrients providing the actual analysis. Laboratories may provide somewhat different sets of information in the lab header section and will also provide a somewhat different set of nutrients in a lab analysis. AminoCow leaves the definition of the content of the lab header to the individual laboratories. While AminoCow requires that the nutrient fields follow AminoCow rules, AminoCow does not require that any particular set of nutrients be included in a lab analysis. In addition, laboratories may include nutrients not found in AminoCow. If such nutrients are included, AminoCow ignores them, but they may appear in a report provided by the laboratory.

The lab queue displays header information for samples as transmitted by a laboratory plus some additional fields that may or may not have values. The sample header information as provided by the laboratory is found in Columns 1 through 6. If the laboratory follows AminoCow recommendations on the structure of the sample header, then Column 1 contains the name of the laboratory; Column 2 contains a laboratory id or account number; Column 3 contains the date the analysis was performed; Column 4 contains the name of the client as known to the laboratory; Column 5 contains the name of the feed as known to the laboratory; and Column 6 contains a feed type code as assigned by the laboratory. However, because feed analysis laboratories are not required to follow this format, the lab queue display may or may not reflect this structure.

The first five columns in the lab queue are assigned by AminoCow and, except for the “Delete” and “LogDate” columns, will be blank until the lab sample is used. The “Delete” column is used for removing samples from the lab queue. A value of “Yes” indicates that the feed will be deleted when exiting the “Lab Analysis Screen” or when the ‘Delete’ button is clicked. The default is “No”. The “LogDate” is the date on which the sample was imported into the lab queue. The queue is sorted by log date. The remaining three fields are only filled if the sample has been matched to an AminoCow feed. When the “Lab Analysis Screen” is exited by selecting ‘Next’, the sample feed is stamped with a “used date” and is assigned the AminoCow client code associated with the ration and the name of the AminoCow feed the sample is modifying. If you click ‘Yes’ when asked whether or not to archive a sample, the sample feed is deleted from the lab queue and moved to the archive. If you answer ‘No’, the sample remains in the queue, and will be listed only when working with the client associated with the feed and then only when the ‘View Queue’ button is clicked.

To select a sample, simply click on it. The lab header information will display in the upper frame while certain common nutrient values from the lab analysis will display underneath the AminoCow feed. If a nutrient in the grid was not included in the analysis, it will have a value of -1 or will be blank. If the sample seems to be a correct match for the AminoCow feed, click ‘Next’ to move to the next step. Otherwise, you can select a different sample from the queue, or you can exit without selecting a sample by clicking ‘Cancel’ or choosing ‘Exit’ from the menu.

If you cannot find the sample you are looking for in the list of unused samples, you can click ‘View Queue’ to expand the list to include all used samples for the current client. If you suspect that the sample may be in the archive, you can click the ‘View Archived Samples’ button. This will display all archived samples for the AminoCow client and order them by the date on which they were used.



Deleting Feeds

You can delete samples that are in the lab queue by setting the “Delete” field to “Yes”. To do this, enter a ‘Y’ in the Delete column of the sample to be deleted. Once you have selected the samples to be deleted, you can click the ‘Delete’ button to complete the process. While you can mark the currently selected sample for deletion, you cannot delete it by using the ‘Delete’ button. Otherwise samples marked for deletion will be deleted when you exit the “Lab Analysis Screen”. Samples in the archive cannot be deleted from this screen.

It is a good practice to delete all TMR’s and mixes from the lab queue. If you are not interested in maintaining an archive, delete samples when you are done with them. If you have marked the current sample for deletion, it will be deleted when you exit the “Lab Analysis Screen” by clicking ‘Next’.

The AminoCow “Manage Lab Samples” Screen

For those users who are interested in maintaining some type of lab sample history, the “Lab Sample Manager” screen provides some basic tools for viewing data, managing the archive and lab queue and exporting selected lab samples to a text file. The exported text file can easily be imported into a spreadsheet such as Excel or most statistical programs for further analysis. The “Lab Manager” itself, however, does not include any statistical analysis or reporting functions.

The “Lab Manager” works on the principle of selecting views of samples. Each view is a set of data from either the archive or the lab queue. All operations after the selection of a view affect only the samples in the view. The top grid on the “Lab Manager Screen” displays the header information for lab samples in the current view. The “ACClient” field is the AminoCow client code associated with the sample. The “ACFeed” field displays the database name of the AminoCow feed associated with the sample. Note that since feeds can be renamed at anytime, the “ACFeed” name may be different than the name of the blended feed saved in a ration. For example, the original AminoCow feed may have been “Corn sil 40% grain”, while the blended feed is “Big Silo Corn 06/01/06”. In this case the “ACFeed” field will contain “Corn sil 40% grain”, while the “Feed” field in the nutrient display will show “Big Silo Corn 06/01/06.” If you are viewing unused feeds in the lab queue, the “ACFeed”, “ACClient” and the “UsedDate” field will be blank. The “LogDate” field always contains the date the sample was imported into AminoCow, while fields “Col 1” – “Col 6” contain sample information supplied by the laboratory.

The three options available from the “Lab Manager Menu” are ‘Manage Archive Samples’, ‘Manage Lab Queue’, and ‘Utilities’. The ‘Manage Archive Samples’ options are ‘Selected Client’ and ‘All’. The sample archive is organized on the basis of client codes with each sample associated with a particular client. To display the samples associated with a particular client, choose the ‘Selected Client’ option and then from the drop-down list, choose the appropriate client. All samples in the archive associated with the selected client are displayed in the upper grid organized by “ACFeed” and “UsedDate”. Note that as you scroll through the top grid, the nutrients for the sample are displayed in the bottom grid. If you select the ‘All’ option, all samples in the archive are displayed organized by “Client”, “ACFeed” and “UsedDate”. If you select ‘Manage Lab Queue’, the available options are: ‘Selected Client’, ‘Unused’, ‘Used’ and ‘All’. If you select a client, any samples in the queue that have been associated with the client are displayed organized by “ACFeed” and “UsedDate”. If you select ‘Unused’, all samples that have not been used are displayed and are organized by “LogDate”. If ‘Used’ is selected, all samples in the queue that have been used are displayed and are organized by “Client”, “ACFeed”, and “UsedDate”. If ‘All’ is chosen, all samples in the queue are displayed and are organized by “Client”, “ACFeed”, “UsedDate” and “LogD”.



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The Utility Menu has one option, 'Select Display Columns'. This option presents a drop-down list of available nutrient columns. Check the columns that you wish to see displayed on the screen or exported to a text file.

Operations on the Archive

The operations available for the Archive are 'Delete By Date', 'Sort' and 'Export'. The 'Delete By Date' option allows you to select one of several pre-defined date ranges for deleting samples from the archive or allows you to select your own deletion date. All samples with dates older than the selected delete date are removed from the archive when you confirm the deletion option.

The 'Sort' option allows you to select a column from the upper grid for changing the sort order of the display. For example, if you use several labs, and all labs use 'Col 1' for the lab name, selecting 'Col 1' as the sort column, sorts the display by laboratory.

'Export' exports the current samples, including the nutrient columns to a tab-delimited text file named 'AC_LabSamples.txt'. This file is always in the AminoCow documents folder, usually C:\AminoCowDocs. At the time of export you have the option of including the lab columns in the header as part of the file. (The lab columns are Col 1 – Col 6). If these columns are not included, the export file will contain the "ACClient", "ACFeed", "LogDate", and "UsedDate" fields, plus the nutrient columns that are displayed in the lower grid. The export file will contain one entry for each sample in the current display.

The format of the AC_LabSamples file is designed to make it easy to import the data into a spreadsheet such as Excel or any other application that allows the import of tab-delimited files. To import the AC_Log Sample file into Excel 2000 or later, open Excel and under the 'Data' tab select 'Get External Data'. From the options select 'Import Text File' and select "C:\AminoCowDocs\AC_LogSamples.txt" as the file to import. At the first Text Import Wizard screen accept the default options and click 'Next'. At the second screen, make sure that "Tab" is checked as the delimiter and then click 'Next'. At the third screen, accept the default options and then finish the import. Excel will import and then display the text file.

Operations on the Lab Queue

The operations on the Lab Queue are 'Delete By Date', 'Sort', 'Export', 'Delete Unused Samples' and 'Archive Used Samples'. The first three operations are identical to the operations on the Archive. 'Delete Unused Samples' allows you to delete unused samples older than a selected date. This option is only available when viewing unused samples in the lab queue. The 'Archive Used' procedure used samples older than a selected date. The default is to archive all used samples older than 15 days. Note that only samples in the current view are archived. Thus if you are viewing samples for a selected client and click 'Archive Used Samples', only samples for that client will be archived.

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