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A mass balance based model to evaluate the impact of amino acid profiles on the feeding and processed value of soybeans

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A mass balance based model to evaluate the impact of amino acid profiles on the feeding and processed value of soybeans

by

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Charles R. Hurburgh Jr., Major Professor
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ABSTRACT

As the soybean industry continues to grow and become more globally competitive, the interest surrounding soybean quality has also increased. Historically, soybeans have been traded as a commodity, but over the past few decades, the idea of component based pricing as a way to assess quality has become more practical. Pricing soybeans based on components would account for the high variation in soybean composition and reward high quality and consistency, while commodity pricing does not. In order for component based pricing to become a viable option for the soybean industry, a rapid, reliable, and relatively low-cost method for evaluating soybeans of varying compositions must be available.

A soybean solvent extraction plant model was developed to evaluate raw soybeans by predicting product yields and compositions and determining an estimated monetary value for a bushel of soybeans based on both major and minor constituents. Previous models only included major constituents, such as protein and oil. All phases of the solvent extraction process (soybean preparation, oil extraction, and meal formulation) are accounted for in the model. The model runs in Microsoft Excel and utilizes inputs of raw soybean composition, including concentrations of moisture, protein, oil, fiber, amino acids, carbohydrates, and fatty acids, and processing conditions. These inputs allow the model to predict the yields and compositions for crude oil and soybean meal, as well as, the weight of net hulls and mill feed used, if applicable. This model allows producers, breeders, buyers, and nutritionists to evaluate a bushel of soybeans based on how its composition affects the end-use quality of the extraction products.

Additionally, the composition of the soybean meal predicted in the model is input into the U.S. Pork Center of Excellence, National Swine Nutrition Guide feed formulation software. The software formulates a swine diet based on common feed ingredients, including corn, synthetic

amino acids, monocalcium phosphate, limestone, salt, and the predicted soybean meal from the processing model. This software allows animal nutritionists to evaluate the feeding value of the predicted soybean meal based on factors such as metabolizable energy and neutral detergent fiber content of the feed, inclusion percentage, and the feed cost. Furthermore, this would provide a comparison tool for nutritionists and plant breeders to analyze the potential feeding values of raw soybeans before they are processed.

CHAPTER 1: GENERAL INTRODUCTION

Continuous agricultural developments have increased the efficiency of farming practices and grain processing and handling, outcomes that have been crucial for markets to stay competitive worldwide. The United States has played a key role in the development of these technologies; however, most of these advancements in the United States have focused on increasing quantity rather than quality. This allows the U.S. to remain competitive, but more countries are adopting similar technologies and closing the gap between both production and efficiency levels around the world. Addressing quality issues and determining an appropriate method for incentivizing producers to improve quality and consistency of their grain is a growing interest in the U.S. soybean industry.

Solvent extraction is the predominant type of processing utilized in the U.S. soybean industry. It is typically described in three phases: (1) Soybean Preparation, (2) Oil Extraction, and (3) Soybean Meal Formulation. The products produced in this process are crude soybean oil, soybean meal, and possibly mill run (extra hulls). Soybean meal is frequently utilized as a high protein feed concentrate for swine and poultry, and its nutritional composition (namely, its amino acid composition) determines its feeding value.

Historically, soybeans have been marketed based on a commodity pricing system, which rewards improvements in yield but not quality. It has been proposed that a component based pricing system (valuing soybeans and soybean meal on their components, such as protein and oil) would reward producers for higher quality products; thereby increasing their value for the end-user. A caveat to this proposed system is that valuing soybean meal strictly on protein content doesn’t account for differences in amino acids that make up the protein, which can be key to the products feeding value. For some feed markets, specific essential amino acid levels are the factors that feed nutritionists are most interested in.

To address these factors that affect the end-use quality of soybeans, a model was developed to place a value on a bushel of soybeans based on its intrinsic properties. The model developed follows key compositional traits of soybeans, including selected amino acids, through the solvent extraction process and calculates their distribution in the final products to determine the nutritional value of soybean meal. This determination, along with that of other extraction products, are used to calculate an estimated processed value useful for approximating the end-use value of a bushel of soybeans for producers, breeders, buyers, and nutritionists. Additionally, the soybean meal predicted in this model is input into the US Pork Center of Excellence, National Swine Nutrition Guide feed formulation software. This software allows nutritionists to compare soybean meal varying in composition based on its value in swine diets (includes amino acid profile, carbohydrate profile, crude protein, neutral detergent fiber, crude fiber, digestible energy, and metabolizable energy).

Literature Review

For the 2016 crop year, the U.S. achieved record high production and yield values for corn and soybeans, as well as increased production of total cotton from the previous year (White & Honig, 2017). The United States remains a leader in agricultural productivity, despite notable improvements to agricultural systems globally within the past few decades. Increases in yield and production stem from continual development of new technologies that improve harvesting, storing, processing, and shipping efficiencies, which allow the U.S. to compete in world markets (Brumm & Hurburgh, 1990). These improvements have created a system that focuses on quantity, instead of quality. As competition continues to develop in international grain markets, grain quality factors have become distinguishing traits used by foreign buyers (Office of Global Analysis, 2017).

In order to remain competitive internationally, the U.S. must address problems with inconsistent quality and understand the importance of intrinsic quality characteristics (or other factors) that are critical to end-users. Many countries, such as Argentina and Brazil, have integrated quality into their grain policy for decades by enforcing minimum receipt standards; the U.S. has yet to address this in an effective manner (U.S. Congress, Office of Technology Assessment, 1989). The main soybean product that varies in quality is soybean meal, which is used primarily for animal feed.

Soybean Meal

Soybean meal, a high protein animal feed ingredient that is internationally traded, is the predominant product produced by soybean solvent extraction (Park & Hurburgh, 2002). The industry's standard trading rules for soybean meal were developed by the National Oilseed Processors Association (NOPA), and they include fiber limitations, allowable tolerances, and penalty schedules. For example, the fiber limitation for high-protein (dehulled) meal is 3.5% with a tolerance of 0.3 percentage points allowed, and a 10% discount per percent point over the tolerance (NOPA, 2015). These rules provide standards for the buying and selling of soybean meal and influence conformity among soybean meal processors. In the U.S., out of 117 million metric tons of soybeans harvested, 57 million metric tons were processed into soybean meal for the 2016 crop year (USDA NASS, 2016). The main challenge with soybean meal is its highly variable composition depending on genetic varieties, agricultural practices, and environmental and processing conditions (Thakur & Hurburgh, 2007). The protein and oil content of soybeans can vary significantly between countries and among regions domestically (Medic, Atkinson, &

Hurburgh, 2014). For example, within the United States, the average soybean protein content for the 2016 crop year varied by 0.1 - 2.4 percentage points between the Midwest and East Coast (Miller-Garvin & Naeve, 2016). This variation leads to considerable differences in the nutritional value of resulting soybean meal, which introduces inconsistency into the commodity trading of soybean meal (Park & Hurburgh, 2002).

Soybean meal is the primary protein source utilized in swine and poultry diets worldwide; it accounts for an estimated 62% of the proteinaceous ingredients in feed for all food-producing animals (Karr-Lilienthal, Grieshop, Merchen, Mahan, & Fahey, 2004). The feeding value of soybean meal, determined through amino acid evaluation, is based on its nutritional quality; optimal animal growth and performance occurs when the protein contains the ideal proportions of the essential amino acids. The U.S. Soybean Export Council defines essential amino acids as those that cannot be produced sufficiently by the animal to meet their metabolic needs. Essential amino acid deficiencies cause compromised metabolic functions which typically lead to biological inefficiency and disease (Miller-Garvin & Naeve, 2016; Reese, et al., 1990).

Current research suggests that the 5 essential amino acids that are typically limiting in feed diets are lysine, cysteine, methionine, threonine, and tryptophan (Soybean Meal Information Center, 2012). When formulating swine diets, depending on the soybean meal composition, synthetic versions of these amino acids are added into the feed to obtain an appropriate balance, which adds to the feed cost (Stein, Berger, Drackley, Hernot, & Parons, 2008; Wendisch, 2014). Relative to all other plant based proteins, soybean protein contains a higher concentration of both lysine and tryptophan that complements the amino acid profile of cereal grains and causes soybean meal to be a valued ingredient for meeting the dietary requirements of pigs (Stein H. H., 2012; Reese, et al., 1990). For poultry, consistent amounts of lysine are crucial; inadequate lysine content can cause depigmentation of wing feathers in certain breeds of turkey and colored chicks. Similarly, abnormalities can occur in growing chicks if a deficiency of arginine, valine, leucine, or tyrosine occurs (National Research Council, 1994).

The amount of digestible and metabolizable energy available also significantly affects the feeding value of soybean meal (Opapeju, Golian, Nyachoti, & Campbell, 2006). The digestibility of feed is influenced by the amino acid and carbohydrate profiles of the meal; for example, the hulls, sugars, and non-starch polysaccharides are not well digested by monogastric animals (Swick, 2001; Ravindran, Abdollahi, & Bootwalla, 2014). One carbohydrate that swine are particularly sensitive to is stachyose, which decreases the digestibility of the meal (Van Kempen, Van Heugten, Moeser, Muley, & Sewalt, 2006). Determining the amino acid and carbohydrate profiles of the soybean meal would allow nutritionists to provide more accurately balanced diets, which could greatly improve animal performance. Additionally, determining the value of the soybean meal based on the amino acid profiles would more accurately represent its potential feed value, or its end-use value.

Soybean Solvent Extraction Process

U.S. soybean meal is produced primarily by soybean solvent extraction, a process which has been utilized since the 1850s (Figure 1). The typical solvent extraction operation can be divided into three phases: (1) Soybean Preparation, (2) Oil Extraction, and (3) Soybean Meal Formulation (Brumm & Hurburgh, 1990).

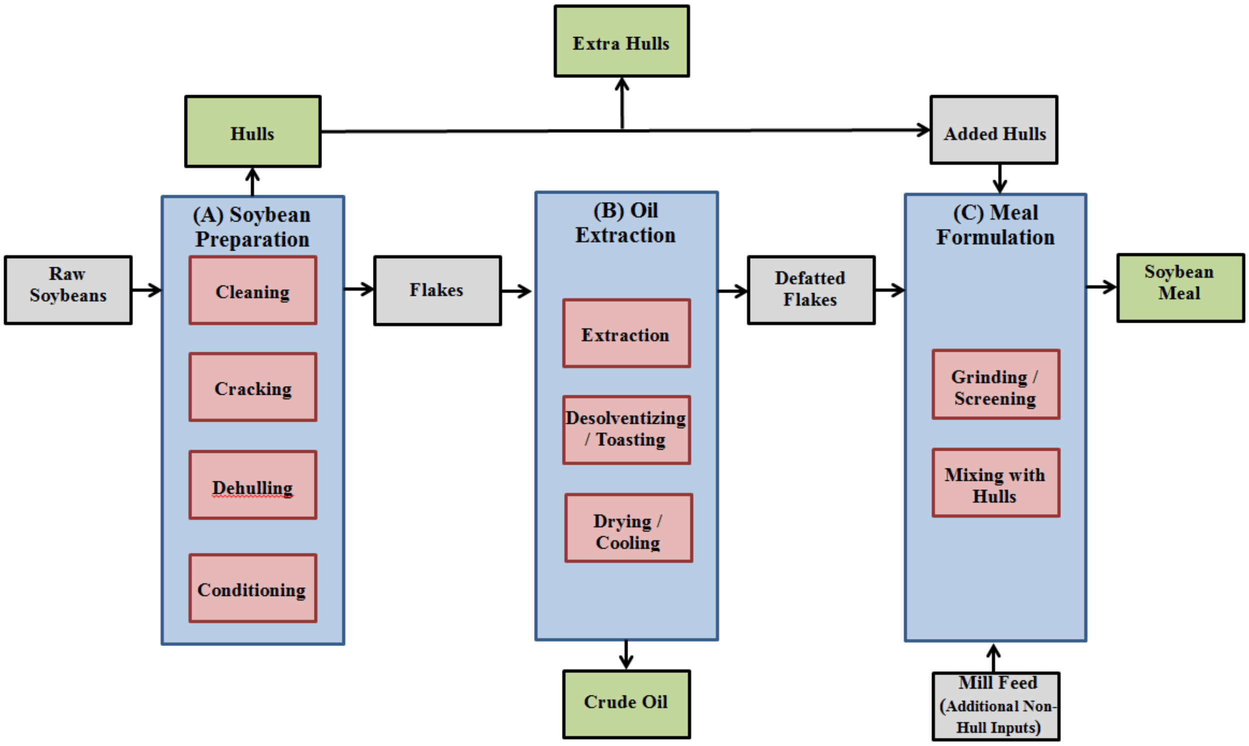


Figure 1: Soybean Solvent Extraction Flow Diagram

<u>Soybean Preparation</u>

Soybeans are oleaginous material (rich in oil) and must undergo preparation prior to the extraction process, which includes cleaning, cracking, dehulling, and conditioning (Kemper, 2005). The initial cleaning step is necessary because typical seed lots entering the processing plant will contain approximately 2% foreign material (sticks, pods, dust, stones, sands, etc.) (Serrato, 1981). Cracking reduces the size of the beans to facilitate further processing. The dehulling process applies aspiration to remove the outer seed coat, which is high in fiber and low in protein and oil when compared to the seed. This is a significant step in the process because it allows for the finished product to be higher in protein by weight than if the hulls were not removed, which in turn increases the finished product value per unit of weight (Kemper, 2005). Finally, the soybeans are conditioned into flakes, referred to as flaking, by distorting the structure of the bean into a thinner material (typically 0.015 inch), which reduces the distance the solvent needs to penetrate in the next step of extraction (Anderson, 2011).

Oil Extraction

In general, this process separates the oil fraction of the soybean flakes from the meal fraction (the remaining solid material). Once the soybeans are conditioned into flakes, they are conveyed through the solvent extractor, which utilizes hexane as the solvent. Hexane is widely utilized due to its high boiling point. This high boiling point allows it to remain in liquid phase in most processing temperatures; it also has a moderately high volatility and low sensible heat, which makes it easy to remove from the solid and oil fractions (Anderson, 2011; Williams, 2010). As the soybean flakes are conveyed through the extractor, the oil is removed through a series of four to eight miscella (solvent and oil solution) washes, with each wash decreasing in its oil concentration (Williams, 2010). The final wash contains only solvent, which is allowed to slowly drain from the meal fraction of the material before exiting the extractor (Kemper, 2005).

The remaining stages of the oil extraction phase involve desolventizing, drying, and cooling the defatted flakes. Depending on how much solvent the flakes retained after exiting the extractor, (typically between 29-35% wet basis) they are put through a desolventizing process that involves heating, or toasting, with steam to evaporate and recover the solvent (Williams, 2010; AOCS Press, 1995). Once the majority of the solvent is removed, the flakes are put through a dryer cooler which reduces the flake moisture down to a percentage that is within trading rule limits and prepares the meal for further formulation in phase 3 (Kemper, 2005). The final products of the oil extraction phase are crude soybean oil and defatted flakes.

Meal Formulation

During meal formulation, the product requirements of the end user (typically a nutritionist) and trading limits are taken into consideration. Initially, the soybean flakes are ground and screened to produce soybean meal. The hulls that were previously separated during soybean preparation are typically added to the meal to lower the total protein content to meet product specifications. If the separated hulls are not sufficient enough to lower the protein to the desired specification, mill feed, a mixture of hulls and other additives, can be bought and mixed into the meal to help lower the protein content as well. Finally, the remaining hulls can be saved for future meal formulation or traded (Brumm & Hurburgh, 1990).

Trading of Soybeans and Soybean Meal

Currently, the U.S. and Brazil are the top competitors in regards to soybean production and exports. Studies have shown that soybeans produced in Brazil contain higher protein and oil content when compared to U.S. beans (Karr-Lilienthal, Grieshop, Merchen, Mahan, & Fahey, 2004). However, when the amino acid profiles were determined, the U.S. soybeans proved to be more consistent and have higher feeding value because they had a more desirable amino acid profile (Park & Hurburgh, 2002). Utilizing a pricing system that accounts for these differences in composition would provide a better indication of soybean quality and feeding value than a traditional commodity pricing system.

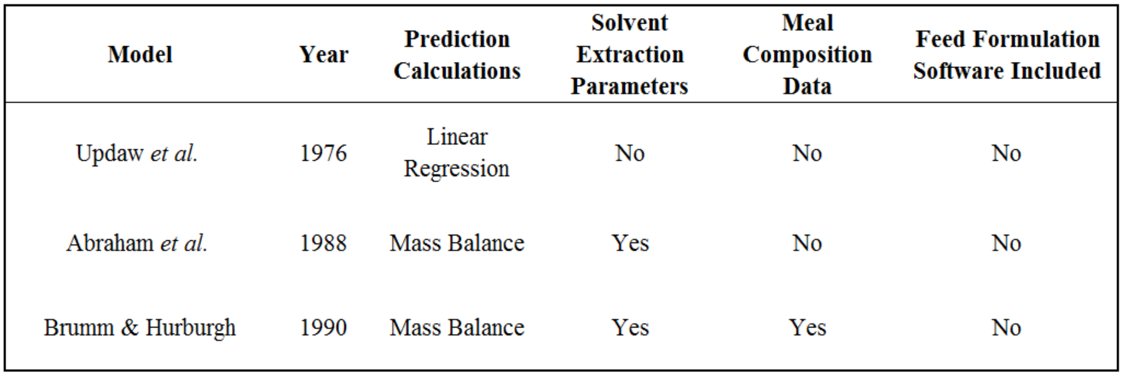
Soybean meal is currently evaluated based on weight, moisture, and protein levels at receiving, which can be easily measured at most elevators; however, the market has been reluctant to accept these values as pricing criteria (Swick, 2001; Park & Hurburgh, 2002). Near-Infrared Spectroscopy (NIRS) is becoming a common method used to determine compositional profiles of soybeans and soybean meal, and its widespread adoption increases the feasibility of implementing a component based pricing system. This concept is gaining interest, and market development for minor seed constituents is earning attention from soybean producers and nutritionists alike (Edmiston, 2000; Kovalenko, Rippke, & Hurburgh, 2006; Lee, et al., 2012).

Recently, the soybean industry (particularly solvent extraction processing) has shown increasing interest in utilizing a pricing system that provides incentives for the producer to improve grain quality rather than focus solely on increasing yields (Park & Hurburgh, 2002; United Soybean Board, 2016). This type of system would value grain based on its composition, such as, protein, oil, fiber, amino acid and carbohydrate levels, and reward producers for increasing the desired intrinsic factors that add to the end-use value of the grain (Edmiston, 2000).

Existing Soybean Solvent Extraction Models

Several prediction models for the soybean solvent extraction process and subsequent products have been developed. Table 1 lists the soybean models currently available in literature, and it includes some model characteristics for each.

Table 1: Existing Soybean Solvent Extraction Models
(Updaw, Bullock, & Nichols, 1976); (Abraham, Hron, & Koltun, 1987); (Brumm & Hurburgh, 1990)



Model	Year	Prediction Calculations	Solvent Extraction Parameters	Meal Composition Data	Feed Formulation Software Included
Updaw *et al.*	1976	Linear Regression	No	No	No
Abraham *et al.*	1988	Mass Balance	Yes	No	No
Brumm & Hurburgh	1990	Mass Balance	Yes	Yes	No

The first model was developed by Updaw *et al.* in 1976; it utilized limited material balances, or mass balances, to calculate soybean meal and oil yields for raw soybean samples containing a wide range of protein and oil contents. The correlation between product yields and protein and oil content was determined using linear regression, which resulted in the final prediction equations. Although the Updaw *et al.* model set the framework for developing component predictions, it did not account for any specific solvent extraction parameters or processing conditions. For example, this model ignored dehulling, meal formulation, and changes in process efficiencies (Updaw, Bullock, & Nichols, 1976).

The next approach, made in 1988 by Abraham *et al.*, was completely based on material balances and disregarded the linear regression equations that were previously used by Updaw *et al*. This model was developed specifically for the solvent extraction process with the purpose of supporting equipment selection and determining plant operation conditions. Although it included extraction conditions, it was based on mass flow rates, equilibrium data and extraction stages, rather than compositional data as the Updaw *et al.* model was (Abraham, Hron, & Koltun, 1987).

The most recent revision of a soybean solvent extraction prediction model was in 1990 by Brumm & Hurburgh. This model was developed to be a complete simulation of production operations in a soybean solvent extraction plant. It accounted for all phases of the extraction process, including dehulling and meal formulation, and included a calculation to regulate protein and fiber percentages based on product specifications and trading rule limitations. The model was developed on a computer-based interface that enabled input of different processing conditions for all phases, variations in marketing techniques, and soybean composition data. One advantage to this model was its ability to determine the estimated processed value (EPV) of the products produced during the solvent extraction process by calculating discounts based on trading rules or protein premiums. The current soybean meal price would then be discounted and multiplied by the soybean meal yield to generate the EPV ($/bu) (Brumm & Hurburgh, 1990).

Previous attempts to correlate raw soybean composition to end-use value have been successful for protein and oil content, and there is a need for further compositional analysis. The model developed in the current study extends the Brumm & Hurburgh model; it allows the user to evaluate the value of soybean meal and supplementary extraction products by inputting soybean compositional data, including amino acid, carbohydrate, and fatty acid profiles—the key factors influencing the end-use quality and feeding value of soybean meal (Miller-Garvin & Naeve, 2016). The model takes the composition of whole soybeans, and traces the nutrients through the solvent extraction process. The potential value of all the products is determined using the EPV developed by Brumm & Hurburgh (Brumm & Hurburgh, 1990). This EPV expands the feeding value estimates by utilizing the current prices for commercially produced synthetic amino acids, rather than solely the current market price for soybean meal at a standard protein content. By allowing adjustments for raw soybean composition and processing parameters, this model accounts for variability within the solvent extraction process and within soybean composition differences. Understanding this variation is an advantage from an animal nutrition perspective; the potential value of the soybean meal in swine diets can be determined using the connected feed formulation software. The soybean meal composition is input into the feed formulation software, which allows nutritionists to compare diet prices and formulations among varying meal compositions.

The overall goal of the current study was to develop a computer model that simulates soybean solvent extraction operations while considering amino acid, carbohydrate, and fatty acid profiles. The specific objectives of this research were to: (i) create a mass balance based model to predict the amounts of amino acids and carbohydrates in the meal and fatty acids in the oil extracted through the solvent extraction process; (ii) determine a processed value based on the amino acid profile of the meal; (iii) attach a swine feed formulation software to the model to determine feed cost and ration formulation based on the model's predicted meal composition.

Thesis Organization

This thesis is organized into three sections. The first section is a general introduction and literature review that discusses the importance of soybean meal composition, soybean solvent extraction, trading of soybeans and soybean meal, and existing soybean solvent extraction models. The second section of this thesis is research regarding the updated development of a model that predicts the compositions of products from the solvent extraction process, including amino acid, carbohydrate, and fatty acid profiles. This model also predicts the estimated processed value of all products based on their intrinsic properties, and it is titled "A mass balance based model to evaluate the impact of amino acid profiles on the feeding and processed value of soybeans". The third section of this thesis is a technical note, titled "Validation of the Updated Soybean Processing Model", discussing the results from using the previous Brumm & Hurburgh model compared to the current model that was developed in section 2. The results from this research are written in the format required for publication by the American Oil Chemists' Society (AOCS) in *Journal of the American Oil Chemists' Society*.

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CHAPTER 2: DEVELOPMENT OF ADDITIONAL MASS BALANCE MODELING OF SOYBEAN SOLVENT EXTRACTION TO INCLUDE MINOR CONSTITUENTS

A paper to be submitted to *Journal of the American Oil Chemists' Society*

Kortney Wagner and Charles R. Hurburgh Jr.

Abstract

As the soybean industry continues to grow and become more globally competitive, the interest surrounding soybean quality has also increased. Pricing soybeans based on components, rather than as a commodity as they are currently traded, would account for the high variation in soybean composition and reward high quality and consistency. A soybean solvent extraction plant model was developed to evaluate raw soybeans by predicting product yields and compositions to determine an estimated monetary value for a bushel of soybeans based on both major and minor constituents. The model runs in Microsoft Excel and utilizes inputs of raw soybean composition, including concentrations of moisture, protein, oil, fiber, amino acids, carbohydrates, and fatty acids, and processing conditions. These inputs allow the model to predict the yields and compositions for crude oil and soybean meal, as well as, the weight of net hulls and mill feed used, if applicable. This model allows producers, breeders, buyers, and nutritionists to evaluate a bushel of soybeans based on how its composition affects the end-use quality of the extraction products. Additionally, the composition of the soybean meal predicted in the model is input into the U.S. Pork Center of Excellence, National Swine Nutrition Guide feed formulation software. The software formulates a diet based on common feed ingredients, including corn, synthetic amino acids, monocalcium phosphate, limestone, salt, and the predicted soybean meal from the processing model. This software allows animal nutritionists to evaluate the feeding value of the predicted soybean meal based on factors such as metabolizable energy and neutral detergent fiber content of the feed, inclusion percentage, and the feed cost. There is a significant difference between evaluating soybeans based on the amino acid content of the meal versus the predicted product yields from the protein and oil content alone. The amino acid evaluation was greater for all samples. Feed costs of an example ration were estimated; the lowest average feed cost occurred for compositions with meal from low protein soybeans (<36.00%) that had high essential amino acids (>5.25%).

Introduction

The United States recorded record high production and yield values for corn and soybeans in 2016 and remains a world leader in agricultural productivity (White & Honig, 2017). Increases in yield and production, which keep the U.S. globally competitive, stem from continual development of new technologies that improve harvesting, storing, processing, and shipping efficiencies (Brumm & Hurburgh, 1990). However, these improvements have created a system that focuses on increasing quantity, instead of improving quality. As competition continues to develop in international grain markets, grain quality factors have become distinguishing traits among foreign buyers (Office of Global Analysis, 2017). As a result, many countries have been integrating quality into their grain policy by enforcing minimal receipt standards, but the U.S. has yet to address this in an effective manner (U.S. Congress, Office of Technology Assessment, 1989). In order to remain competitive internationally, the U.S. must address problems with inconsistent quality and understand the importance of intrinsic quality characteristics (or other factors) that are critical to the end-user. The major soybean product that is affected by these quality characteristics is soybean meal, which is used primarily for animal feed.

Soybean meal, a high protein animal feed concentrate that is internationally traded, is the predominant product produced by soybean solvent extraction (Park & Hurburgh, 2002). Soybean meal is the primary protein source utilized in swine and poultry diets worldwide; it accounts for an estimated 62% of the proteinaceous (protein-related) ingredients in all food-producing animals (Karr-Lilienthal, Grieshop, Merchen, Mahan, & Fahey, 2004). The industry's standard trading rules for soybean meal were developed by the National Oilseed Processors Association (NOPA), and they include fiber limitations and allowable tolerances (NOPA, 2015). These rules provide standards for the buying and selling of soybean meal and influence conformity among soybean meal processors. The main challenge with soybean meal is variable composition, which can vary significantly between countries and among regions domestically (Thakur & Hurburgh, 2007; Medic, Atkinson, & Hurburgh, 2014). Recent studies have shown that soybeans produced in Brazil contain higher protein and oil content when compared to U.S. beans (Karr-Lilienthal, Grieshop, Merchen, Mahan, & Fahey, 2004). This variation leads to considerable differences in the feeding value of soybean meal, which is based on its nutritional quality as estimated by amino acid evaluation.

Optimal animal growth and performance occurs when proteinaceous feed ingredients contain the ideal proportions of the essential amino acids. The U.S. Soybean Export Council defines essential amino acids as those that cannot be produced sufficiently by the animal to meet their metabolic needs; essential amino acid deficiencies cause compromised metabolic functions which typically lead to biological inefficiency and disease (Miller-Garvin & Naeve, 2016; Reese, et al., 1990). The 5 essential amino acids that are typically limiting in feed diets are lysine, cysteine, methionine, threonine, and tryptophan (Soybean Meal Information Center, 2012). In general, soybean protein contains a higher concentration of both lysine and tryptophan when compared to all other plant based proteins, which allows soybean meal to aid in meeting the diet requirements of pigs (Stein H. H., 2012; Reese, et al., 1990). The amount of available digestible and metabolizable energy also significantly affects the feeding value of soybean meal (Opapeju, Golian, Nyachoti, & Campbell, 2006). The digestibility of feed is influenced by the amino acid and carbohydrate profiles of the meal; for example, the hulls, sugars, and non-starch polysaccharides are not well digested by monogastric animals (Swick, 2001; Ravindran, Abdollahi, & Bootwalla, 2014). One carbohydrate that swine are particularly sensitive to is stachyose, which decreases the energy digestibility of the meal (Van Kempen, Van Heugten, Moeser, Muley, & Sewalt, 2006). Determining the amino acid and carbohydrate profiles of the soybean meal would allow nutritionists to provide more accurately balanced diets, which would improve animal performance. Additionally, determining the value of the soybean meal based on constituent profiles would more accurately represent its potential feed value, or its end-use value.

Soybean solvent extraction is the primary type of processing for soybean meal in the U.S. (Figure 2). The typical solvent extraction operation can be divided into three phases: (1) Soybean Preparation, (2) Oil Extraction, and (3) Soybean Meal Formulation (Brumm & Hurburgh, 1990).

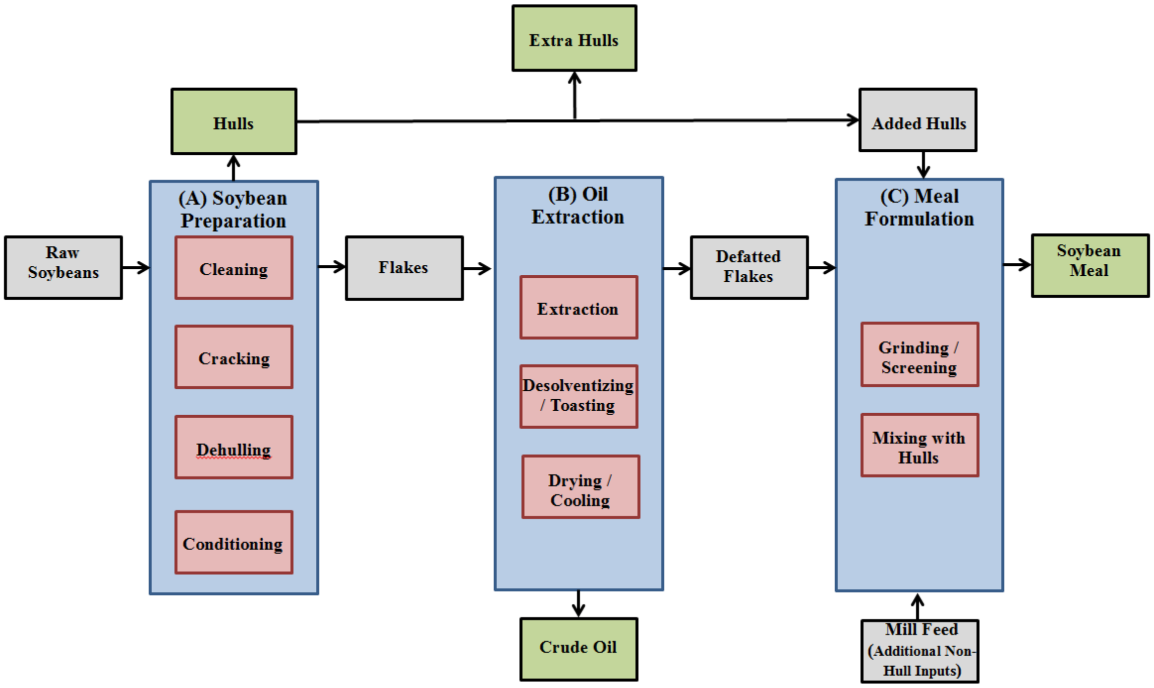


Figure 2: Soybean Solvent Extraction Flow Diagram

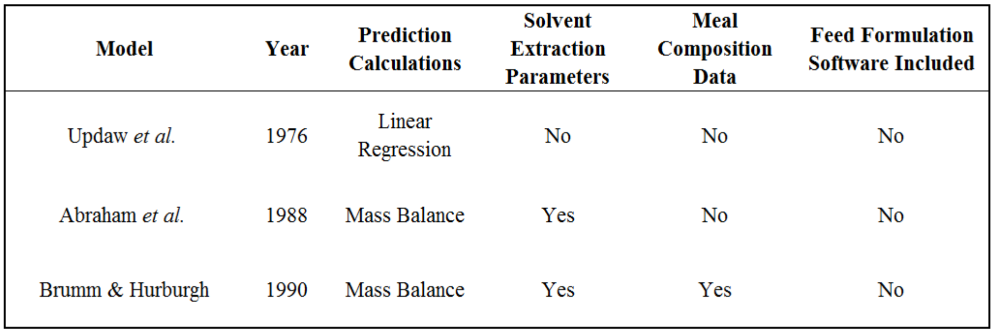
Soybean preparation consists of cleaning, cracking, dehulling, and conditioning (Kemper, 2005). Typical seed lots entering the processing plant will contain approximately 2% foreign material, which is removed in the initial step (Serrato, 1981). Cracking reduces the size of the beans to facilitate further processing. Dehulling allows for the finished product to be higher in protein and lower in fiber by weight, which increases the finished product value (Kemper, 2005). Finally, the soybeans are conditioned into flakes, referred to as flaking, which reduces the distance the solvent needs to penetrate in the next step of extraction (Anderson, 2011).

Oil extraction separates the oil fraction of the soybean flakes from the meal fraction. As the soybean flakes are conveyed through the extractor, the oil is removed through a series of four to eight miscella washes, with each wash decreasing in its oil concentration (Williams, 2010). The final wash contains only solvent, which is slowly drained from the meal fraction of the material before exiting the extractor; the flakes retain some solvent from the extractor (typically between 29-35% wet basis) (Kemper, 2005). The flakes are put through a desolventizing process that involves heating, or toasting, with steam to evaporate and recover the solvent (Williams, 2010; AOCS Press, 1995). Once the majority of solvent is removed, the flakes are put through a dryer cooler which reduces the flake moisture down to a percentage that is within NOPA trading rule limits (<12%) and prepares the meal for further formulation (Kemper, 2005). Crude soybean oil and defatted flakes are the products of oil extraction.

Meal formulation involves meeting product specifications determined by the end user and trading limits. The spent flakes are ground and screened to produce soybean meal. To lower the protein content of the meal to meet specifications, the hulls that were previously separated can be added back to the meal. If the separated hulls are not sufficient enough to lower the protein to the desired specification, mill feed, a mixture of hulls and other additives, can be bought and mixed into the meal to help lower the protein content as well. Finally, the soybean meal, crude oil, and remaining hulls, are traded commodities (Brumm & Hurburgh, 1990).

Soybean meal is currently evaluated based on weight, moisture, and protein levels for production, but the market does not use these values as pricing criteria for trading of soybeans (Swick, 2001; Park & Hurburgh, 2002). A component based pricing system would provide incentives for producers to improve grain quality rather than focus on increasing yields by valuing grain based on its composition, such as, protein, oil, fiber, amino acid and carbohydrate levels (Park & Hurburgh, 2002; Edmiston, 2000). The use of Near-Infrared Spectroscopy (NIR) is becoming a common method used to determine compositional profiles of soybeans, which increases the feasibility of adopting a component based pricing system. Utilizing a component based pricing system would provide a better indication of soybean quality and feeding value than a traditional commodity pricing system.

Table 2: Existing Soybean Solvent Extraction Models
(Updaw, Bullock, & Nichols, 1976); (Abraham, Hron, & Koltun, 1987); (Brumm & Hurburgh, 1990)



Model	Year	Prediction Calculations	Solvent Extraction Parameters	Meal Composition Data	Feed Formulation Software Included
Updaw *et al.*	1976	Linear Regression	No	No	No
Abraham *et al.*	1988	Mass Balance	Yes	No	No
Brumm & Hurburgh	1990	Mass Balance	Yes	Yes	No

There are several prediction models for the soybean solvent extraction process and subsequent product value. The available solvent extraction models in literature are listed in Table 2. The Updaw *et al.* model utilized limited material balances to calculate soybean meal and oil yields for raw soybean samples, but it didn’t account for any specific solvent extraction parameters or processing conditions. This model ignored dehulling, meal formulation, and changes in process efficiencies (Updaw, Bullock, & Nichols, 1976). The Abraham *et al.* model was completely based on material balances, and it was specifically developed for determining operating conditions and selecting equipment. Although it included extraction conditions, it was based on mass flow rates, equilibrium data and extraction stages, rather than compositional data (Abraham, Hron, & Koltun, 1987). The Brumm & Hurburgh model was developed to simulate solvent extraction operations, and account for all phases of the process. It included calculations for regulating protein and fiber percentages based on specifications and trading rule limitations. The main function of this model was to determine the estimated processed value (EPV) of the products produced during the solvent extraction process by calculating discounts based on trading rules or protein premiums (Brumm & Hurburgh, 1990).

The model developed in the current study allows the user to evaluate the value of soybean extraction products from soybean compositional data, including amino acid, carbohydrate, and fatty acid profiles. The $EPV_{protein/oil}$ developed by Brumm & Hurburgh is used to determine the potential value of the products from protein and oil alone (Brumm & Hurburgh, 1990). The EPV_{AA} is used to determine the value of the products based on their amino acid content. The feeding value of soybean meal is accounted for in the current model by formulating swine diets based on the predicted soybean meal composition. This allows nutritionists to compare diet prices and formulations among varying meal compositions. By allowing adjustments for raw soybean composition and processing parameters, this model accounts for variability within the solvent extraction process and within soybean composition differences.

Materials and Methods

This model was developed using Microsoft Excel 2013 (Microsoft Corporation, Redmond, WA), and runs using Visual Basic for Applications (VBA) coding. The model is divided into 4 separate worksheets: Introduction, Inputs, Outputs, and Report Sheet. The soybean meal outputs are transferred into the U.S. Pork Center of Excellence, National Swine Nutrition Guide feed formulation software (Iowa State University, Ames, IA).

Model Functionality

The soybean solvent extraction process was divided into 3 systems: System A (soybean preparation), System B (oil extraction), and System C (meal formulation). Material balances were written for each system to provide the final yields for soybean meal and crude soybean oil and their respective compositions. All components were found using the same general material balances for systems A and C; however, system B had a specific material balance written for the oil extracted. Additionally, system C included several steps that checked if the protein and fiber specifications were being met. The following equations are the material balances that were used in each system of the process:

$$PA = \frac{(WSoy*P_1)-(WHull*P_2)}{WSoy-WHull} \tag{1}$$

$$WOil = \frac{(WSoy-WHull)*(PA_{Oil}-P_3)}{100-P_3} \tag{2}$$

$$PC = \frac{WFlakes*P_5+WHull_{Added}*P_2+WFeed*P_6}{WMeal} \tag{3}$$

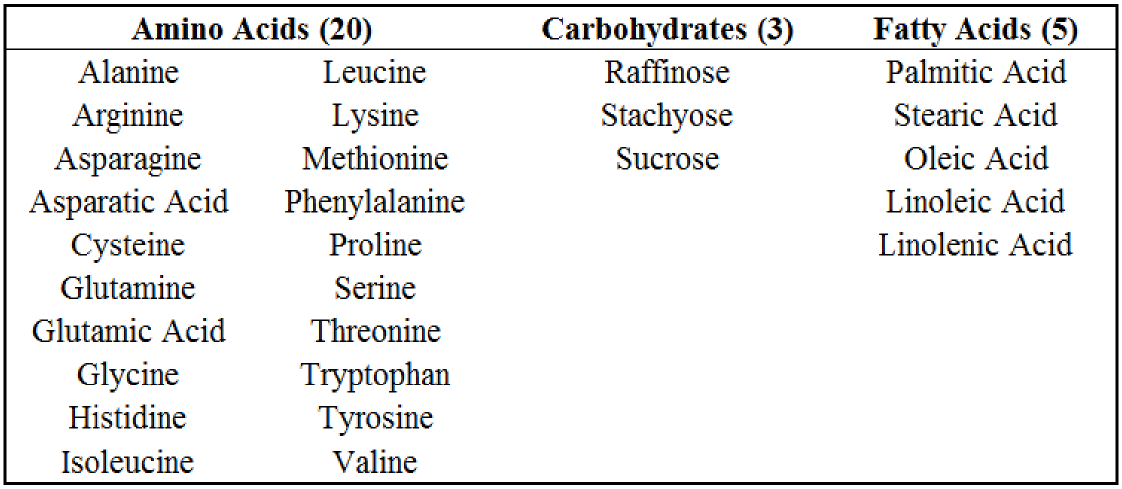
Where: PA = *Percent of Component Leaving System A (%)*
PC = *Percent of Component in Soybean Meal (%)*
PA_{Oil} = *Percent of Oil Leaving System A (%)*
$WSoy$ = *Weight of Soybeans (lb/bu)*
$WHull$ = *Weight of Hulls (lb/bu)*
$WOil$ = *Weight of Extracted Oil (lb/bu)*
$WFlakes$ = *Weight of Flakes Exiting Extraction (lb/bu)*
P_1 = *Percent of Component in Soybeans (%)*
P_2 = *Percent of Component in Hulls (%)*
P_3 = *Percent Oil of Flakes Leaving Extraction (%)*

P_5 = *Percent of Component in Flakes (%)*
P_6 = *Percent of Component in Mill Feed (%)*

The weight, protein, oil, fiber, amino acids, carbohydrates, and fatty acids were accounted for in the model on a dry-matter basis. The specific amino acids, carbohydrates, and fatty acids included in the model are listed below (Table 3). The input variables were converted from "as-is" moisture (or any other moisture basis) to dry-matter basis for all calculations within the model. The output end-product compositions and final yields can be adjusted to any moisture basis specified by the user. The model assumes an input weight of 60 lb, or one bushel, along with a given moisture content. The product yields and estimated processing values ($EPV_{protein/oil}$ & EPV_{AA}) are output on a per-bushel basis (Brumm T. J., 1990). The amount of hulls added back into the meal in system C is determined by the following NOPA trading rules for solvent extracted soybean meal:

1. Fiber limitation of 7% for 44% protein meal and 3.3-3.5% for high-protein (dehulled) meal. The discount for exceeding maximum fiber specification is 1% of the invoice price per 0.1% fiber in excess of specification. A tolerance of 0.3 percentage points fiber is allowed.
2. The protein discount of 2 times the unit price of protein per 1% protein below minimum specifications. A tolerance of 0.5 percentage points of protein is allowed.

Table 3: Amino Acids, Carbohydrates, and Fatty Acids Included in the Model



Amino Acids (20)		Carbohydrates (3)	Fatty Acids (5)
Alanine	Leucine	Raffinose	Palmitic Acid
Arginine	Lysine	Stachyose	Stearic Acid
Asparagine	Methionine	Sucrose	Oleic Acid
Asparatic Acid	Phenylalanine		Linoleic Acid
Cysteine	Proline		Linolenic Acid
Glutamine	Serine		
Glutamic Acid	Threonine		
Glycine	Tryptophan		
Histidine	Tyrosine		
Isoleucine	Valine		

The potential value of the products is determined in two ways: (1) $\text{EPV}_{\text{protein/oil}}$: using the final product yields predicted by the protein and oil content alone and (2) EPV_{AA}: using the amino acid content. The $\text{EPV}_{\text{protein/oil}}$ is based on the final product yields calculated from the material balances; it combines values for soybean meal, crude oil, and mill feed to determine the total $\text{EPV}_{\text{protein/oil}}$ per bushel. The EPV_{AA} is based on the amount of amino acids present in the soybean meal; it utilizes the current prices for commercially produced, synthetic amino acids to determine the EPV_{AA} of the meal. The estimated values for oil and mill feed are calculated using the product yield and current price for each product, and these values are the same for both $\text{EPV}_{\text{protein/oil}}$ and EPV_{AA}. The $\text{EPV}_{\text{protein/oil}}$ equation for final product yields (Equation 4) was adopted from the soybean processing model developed by Thomas J. Brumm; it was modified to produce the EPV_{AA} equation for amino acid content (Equation 5) (Brumm T. J., 1990):

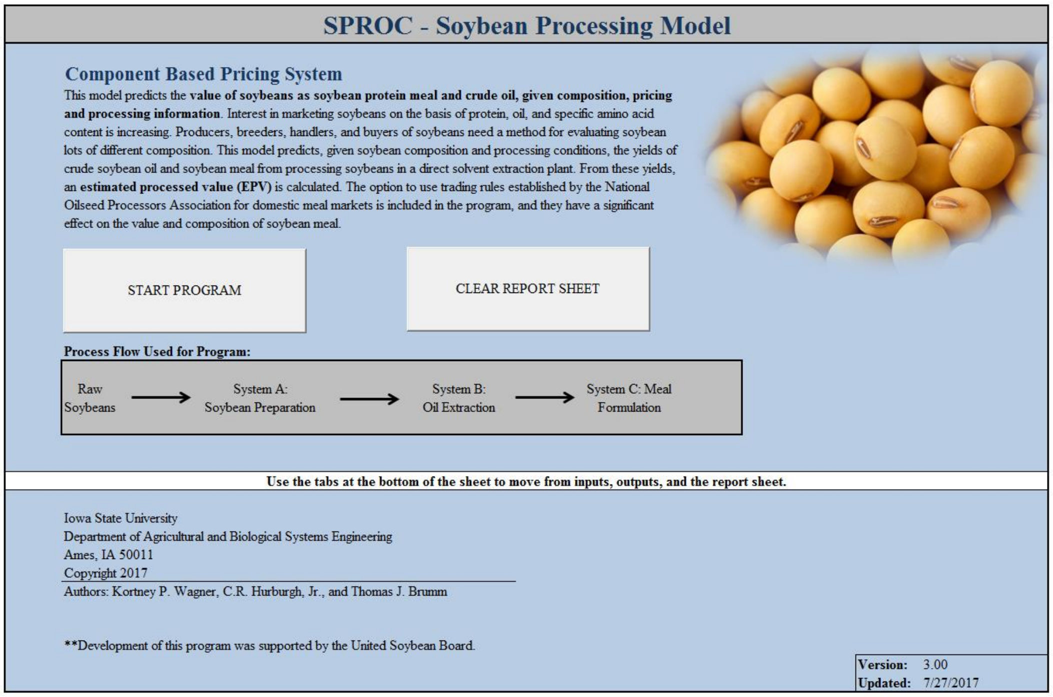
$$EPV_{protein/oil} = \frac{PMeal * WMeal}{2000} + POil * WOil + \frac{PHull * WHullNet}{2000} \qquad (4)$$

$$EPV_{AA} = \sum_{i=1}^{n}(WAA_n * PAA_n) + POil * WOil + \frac{PHull * WHullNet}{2000} \qquad (5)$$

Where: EPV = *Estimated Processed Value (\$/bu)*
PMeal = *Meal Price, after discounted per trading rules (\$/ton)*
POil = *Oil Price (\$/lb)*
PHull = *Hull (mill run) Price (\$/ton)*
WMeal = *Weight of Soybean Meal (lb/bu)*
WOil = *Weight of Crude Soybean Oil (lb/bu)*
$\mathit{WHullNet}$ = *Net Weight of the Hulls (lb/bu)*
WAA = *Weight of Amino Acid (lb/bu)*
PAA = *Amino Acid Price (\$/lb)*

Introduction Worksheet

The “Introduction” worksheet, shown when the user opens the model, provides a brief description of how the component-based pricing system is utilized in the SPROC model (which stands for Soybean PROCessing), and depicts the process flow of solvent extraction used for the model (Figure 3). This worksheet contains two buttons that allow the user to start the program (which opens the “Inputs” worksheet) or clear the report sheet.



SPROC - Soybean Processing Model

Component Based Pricing System

This model predicts the **value of soybeans as soybean protein meal and crude oil, given composition, pricing and processing information**. Interest in marketing soybeans on the basis of protein, oil, and specific amino acid content is increasing. Producers, breeders, handlers, and buyers of soybeans need a method for evaluating soybean lots of different composition. This model predicts, given soybean composition and processing conditions, the yields of crude soybean oil and soybean meal from processing soybeans in a direct solvent extraction plant. From these yields, an **estimated processed value (EPV)** is calculated. The option to use trading rules established by the National Oilseed Processors Association for domestic meal markets is included in the program, and they have a significant effect on the value and composition of soybean meal.

Process Flow Used for Program:

Use the tabs at the bottom of the sheet to move from inputs, outputs, and the report sheet.

Iowa State University
Department of Agricultural and Biological Systems Engineering
Ames, IA 50011
Copyright 2017
Authors: Kortney P. Wagner, C.R. Hurburgh, Jr., and Thomas J. Brumm

**Development of this program was supported by the United Soybean Board.

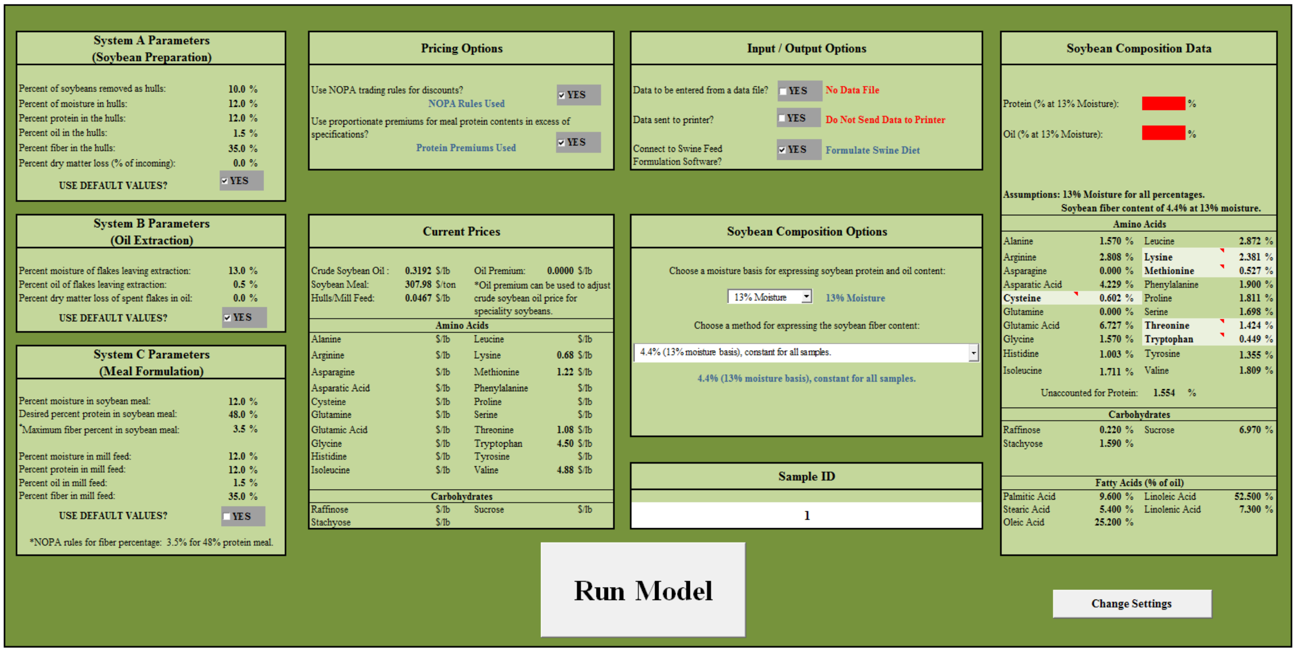
Version: 3.00
Updated: 7/27/2017

Figure 3: Introduction Worksheet

Inputs Worksheet

Model inputs are entered on the “Inputs” worksheet under one of five categories: System A Parameters, System B Parameters, System C Parameters, Current Prices, and Soybean Composition Data (Figure 4). The wide range of input parameters for Systems A-C allows the user to customize the model to reflect their current operation. The moisture basis and fiber content are chosen from a list of options. The user is also given the option to include the National Oilseed Processors Association (NOPA) trading rules for discounts or proportionate premiums for meal protein contents in excess of the provided specifications. There is an option to include an oil premium ($/lb) if specialty soybeans are being run through the model; however, a premium should only be specified for specialty soybeans. The model does not distinguish between normal and specialty soybeans based on the soybean composition. The processing condition defaults for Systems A-C are values determined by a major soybean processor in the U.S., and the soybean composition defaults for fatty acid and carbohydrate concentrations are from a recent study on the current knowledge of soybean composition (Medic, Atkinson, & Hurburgh, 2014). These defaults are assuming that normal soybeans are being run through the model, as opposed to specialty soybeans.

The amino acid, carbohydrate, and fatty acid profiles of the removed hulls were assumed to be equivalent to the same profiles for the soybeans. However, the user has the ability to change the hull profiles by adjusting the hull coefficients which are built into the model (Figure 5). Since the hull composition is assumed to be equivalent to the soybean composition, the coefficients are defaulted at 1. Values other than 1 cause the meal profile to change as well, to maintain the mass balance of each constituent.



System A Parameters (Soybean Preparation)

Percent of soybeans removed as hulls: 10.0 %
Percent of moisture in hulls: 12.0 %
Percent protein in the hulls: 12.0 %
Percent oil in the hulls: 1.5 %
Percent fiber in the hulls: 35.0 %
Percent dry matter loss (% of incoming): 0.0 %
USE DEFAULT VALUES? ☑ YES

System B Parameters (Oil Extraction)

Percent moisture of flakes leaving extraction: 13.0 %
Percent oil of flakes leaving extraction: 0.5 %
Percent dry matter loss of spent flakes in oil: 0.0 %
USE DEFAULT VALUES? ☑ YES

System C Parameters (Meal Formulation)

Percent moisture in soybean meal: 12.0 %
Desired percent protein in soybean meal: 48.0 %
*Maximum fiber percent in soybean meal: 3.5 %

Percent moisture in mill feed: 12.0 %
Percent protein in mill feed: 12.0 %
Percent oil in mill feed: 1.5 %
Percent fiber in mill feed: 35.0 %
USE DEFAULT VALUES? ☐ YES

*NOPA rules for fiber percentage: 3.5% for 48% protein meal.

Pricing Options

Use NOPA trading rules for discounts? ☑ YES
NOPA Rules Used
Use proportionate premiums for meal protein contents in excess of specifications? ☑ YES
Protein Premiums Used

Current Prices

Crude Soybean Oil : 0.3192 $/lb
Soybean Meal: 307.98 $/ton
Hulls/Mill Feed: 0.0467 $/lb
Oil Premium: 0.0000 $/lb
*Oil premium can be used to adjust crude soybean oil price for speciality soybeans.

Amino Acids			
Alanine	$/lb	Leucine	$/lb
Arginine	$/lb	Lysine	0.68 $/lb
Asparagine	$/lb	Methionine	1.22 $/lb
Asparatic Acid	$/lb	Phenylalanine	$/lb
Cysteine	$/lb	Proline	$/lb
Glutamine	$/lb	Serine	$/lb
Glutamic Acid	$/lb	Threonine	1.08 $/lb
Glycine	$/lb	Tryptophan	4.50 $/lb
Histidine	$/lb	Tyrosine	$/lb
Isoleucine	$/lb	Valine	4.88 $/lb

Carbohydrates			
Raffinose	$/lb	Sucrose	$/lb
Stachyose	$/lb		

Input / Output Options

Data to be entered from a data file? ☐ YES No Data File
Data sent to printer? ☐ YES Do Not Send Data to Printer
Connect to Swine Feed Formulation Software? ☑ YES Formulate Swine Diet

Soybean Composition Options

Choose a moisture basis for expressing soybean protein and oil content:
13% Moisture ▾ 13% Moisture
Choose a method for expressing the soybean fiber content:
4.4% (13% moisture basis), constant for all samples. ▾
4.4% (13% moisture basis), constant for all samples.

Sample ID

1

Soybean Composition Data

Protein (% at 13% Moisture): 🟥 %
Oil (% at 13% Moisture): 🟥 %

Assumptions: 13% Moisture for all percentages.
Soybean fiber content of 4.4% at 13% moisture.

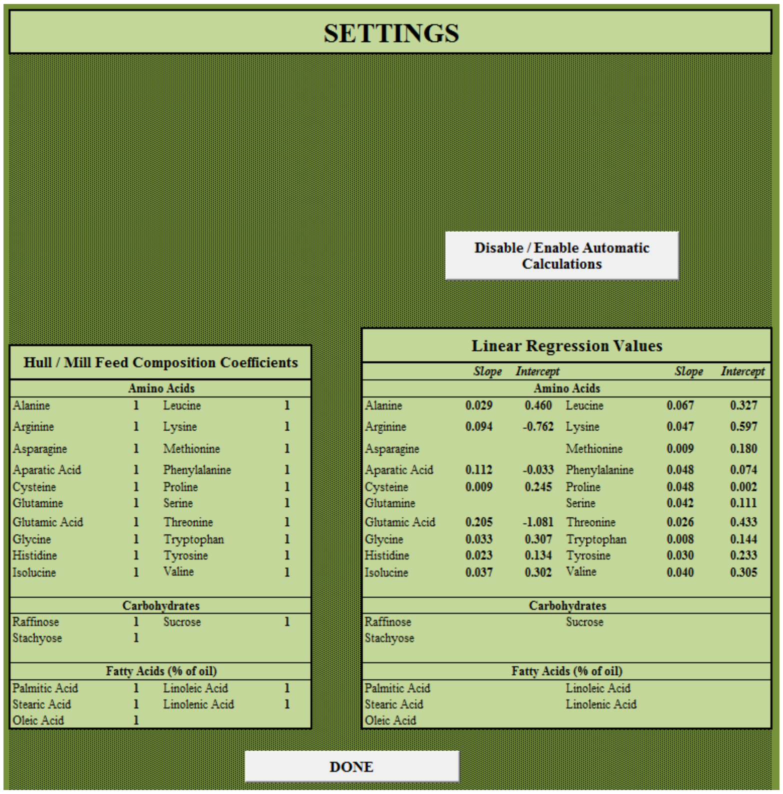
Amino Acids			
Alanine	1.570 %	Leucine	2.872 %
Arginine	2.808 %	**Lysine**	2.381 %
Asparagine	0.000 %	**Methionine**	0.527 %
Asparatic Acid	4.229 %	Phenylalanine	1.900 %
Cysteine	0.602 %	Proline	1.811 %
Glutamine	0.000 %	Serine	1.698 %
Glutamic Acid	6.727 %	**Threonine**	1.424 %
Glycine	1.570 %	**Tryptophan**	0.449 %
Histidine	1.003 %	Tyrosine	1.355 %
Isoleucine	1.711 %	Valine	1.809 %

Unaccounted for Protein: 1.554 %

Carbohydrates			
Raffinose	0.220 %	Sucrose	6.970 %
Stachyose	1.590 %		

Fatty Acids (% of oil)			
Palmitic Acid	9.600 %	Linoleic Acid	52.500 %
Stearic Acid	5.400 %	Linolenic Acid	7.300 %
Oleic Acid	25.200 %		

Figure 4: Inputs Worksheet



SETTINGS

Hull / Mill Feed Composition Coefficients

Amino Acids			
Alanine	1	Leucine	1
Arginine	1	Lysine	1
Asparagine	1	Methionine	1
Aparatic Acid	1	Phenylalanine	1
Cysteine	1	Proline	1
Glutamine	1	Serine	1
Glutamic Acid	1	Threonine	1
Glycine	1	Tryptophan	1
Histidine	1	Tyrosine	1
Isolucine	1	Valine	1

Carbohydrates			
Raffinose	1	Sucrose	1
Stachyose	1		

Fatty Acids (% of oil)			
Palmitic Acid	1	Linoleic Acid	1
Stearic Acid	1	Linolenic Acid	1
Oleic Acid	1		

Linear Regression Values

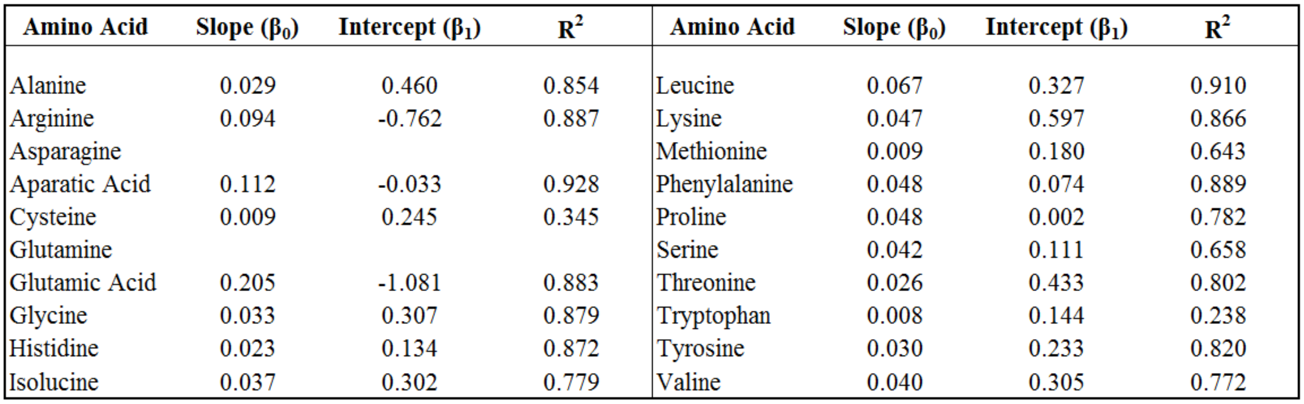
	Slope	*Intercept*		*Slope*	*Intercept*
Amino Acids					
Alanine	0.029	0.460	Leucine	0.067	0.327
Arginine	0.094	-0.762	Lysine	0.047	0.597
Asparagine			Methionine	0.009	0.180
Aparatic Acid	0.112	-0.033	Phenylalanine	0.048	0.074
Cysteine	0.009	0.245	Proline	0.048	0.002
Glutamine			Serine	0.042	0.111
Glutamic Acid	0.205	-1.081	Threonine	0.026	0.433
Glycine	0.033	0.307	Tryptophan	0.008	0.144
Histidine	0.023	0.134	Tyrosine	0.030	0.233
Isolucine	0.037	0.302	Valine	0.040	0.305
Carbohydrates					
Raffinose			Sucrose		
Stachyose					
Fatty Acids (% of oil)					
Palmitic Acid			Linoleic Acid		
Stearic Acid			Linolenic Acid		
Oleic Acid					

Figure 5: User Settings

If the amino acid profile of a sample is unknown, the amino acid concentrations can be predicted using linear regression equations developed by the Iowa Grain Quality Initiative (Medic, Atkinson, & Hurburgh, 2014). The general linear regression equation is used for all amino acids (Equation 6), and the corresponding default coefficients are listed in Table 4. These coefficients can be modified by the user or can be disabled, which allows for customization of the amino acid predictions to a specific soybean profile, if known (Figure 5).

$$Y = \beta_0 * X + \beta_1 \qquad (6)$$

Table 4: Linear Regression Coefficients (Medic, Atkinson, & Hurburgh, 2014)



Amino Acid	Slope (β_0)	Intercept (β_1)	R^2	Amino Acid	Slope (β_0)	Intercept (β_1)	R^2
Alanine	0.029	0.460	0.854	Leucine	0.067	0.327	0.910
Arginine	0.094	-0.762	0.887	Lysine	0.047	0.597	0.866
Asparagine				Methionine	0.009	0.180	0.643
Aparatic Acid	0.112	-0.033	0.928	Phenylalanine	0.048	0.074	0.889
Cysteine	0.009	0.245	0.345	Proline	0.048	0.002	0.782
Glutamine				Serine	0.042	0.111	0.658
Glutamic Acid	0.205	-1.081	0.883	Threonine	0.026	0.433	0.802
Glycine	0.033	0.307	0.879	Tryptophan	0.008	0.144	0.238
Histidine	0.023	0.134	0.872	Tyrosine	0.030	0.233	0.820
Isolucine	0.037	0.302	0.779	Valine	0.040	0.305	0.772

Outputs Worksheet

The “Outputs” worksheet displays all the model outputs formatted as a flow process diagram to allow the user to visualize the entire process (Figure 6). All compositional values are displayed as percent by weight. Results displayed include: results for the hulls separated and added back into the meal formulation (lb/bu); crude soybean oil final yield (lb/bu); fatty acid composition of the oil (%); soybean meal final yield (lb/bu) and the amino acid and carbohydrate profiles (%); total $EPV_{protein/oil}$ and EPV_{AA} of all products and the separated EPVs ($/bu). This results section also displays any price adjustments made from NOPA trading rules or from protein premium discounts. All outputs are given on a per bushel basis, and the soybean meal compositional values are given on the moisture basis specified by the user.

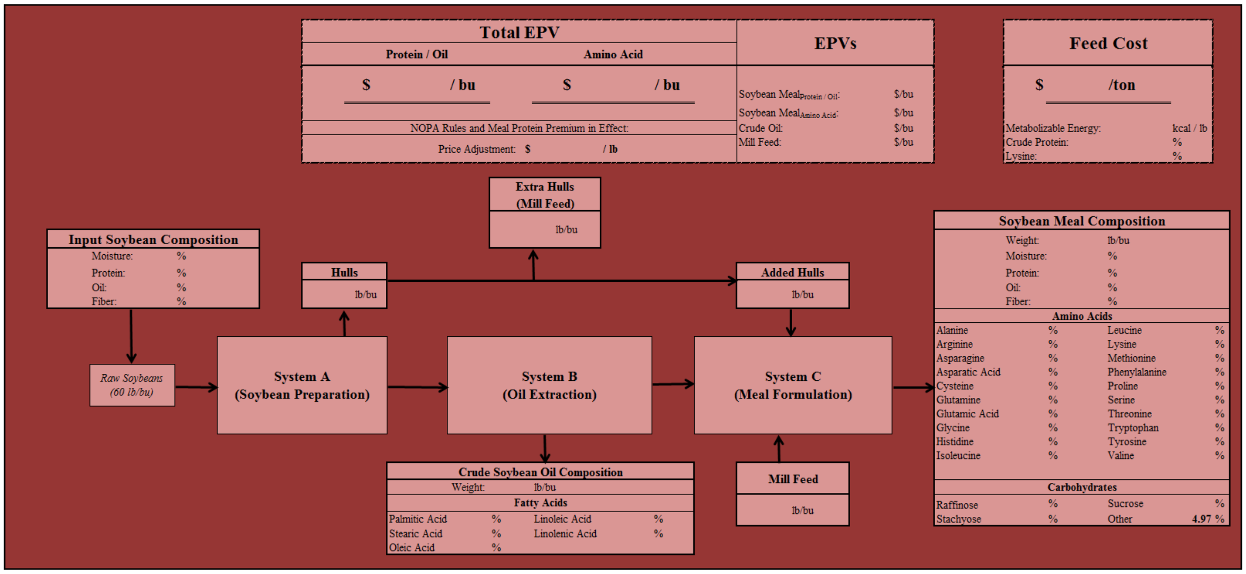
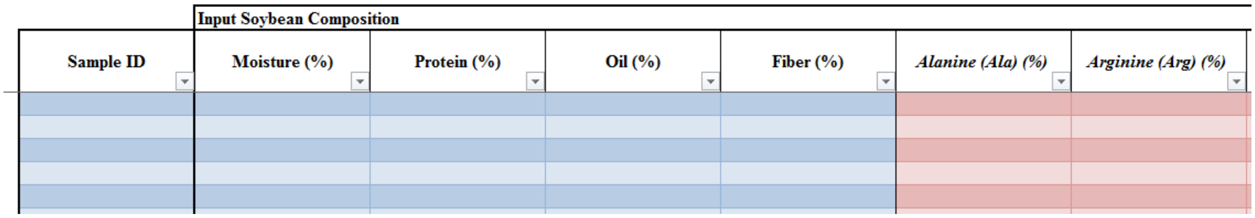


Figure 6: Outputs Worksheet

Report Sheet

The "Report Sheet" worksheet allows the user to automatically save all sample values in a data table and sort the results (Figure 7). Additionally, if the "Send Data to Printer" option is selected on the "Inputs" worksheet, this worksheet can be automatically sent to a printer of the user's choice.



	Input Soybean Composition					
Sample ID	Moisture (%)	Protein (%)	Oil (%)	Fiber (%)	*Alanine (Ala) (%)*	*Arginine (Arg) (%)*

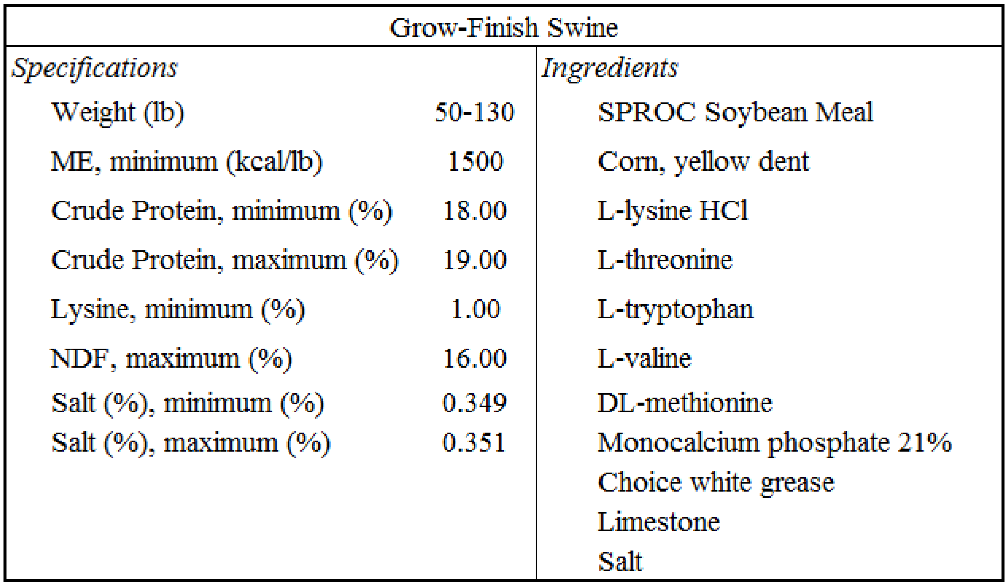
Figure 7: Report Sheet Worksheet Example

Swine Feed Formulation Software

This model is connected to the U.S. Pork Center of Excellence, National Swine Nutrition Guide feed formulation software (Iowa State University, Ames, IA). Once the processing model is run, the calculated soybean meal outputs are automatically entered into the feed ingredients library on an "as-fed" basis. The values entered into the library include the following: amino acid profile, fat, linoleic concentration, crude protein, neutral detergent fiber, crude fiber, digestible energy, and metabolizable energy.

The amino acid, fat, linoleic, crude protein, and crude fiber concentrations are entered directly into the feed library from the processing model's output sheet. The metabolizable and digestible energy values are calculated using Equations 7 and 8 (Li, et al., 2015). The swine guide uses calculated averages for neutral detergent fiber and acid detergent fiber, which are found in the feed ingredients library under the soybean meal ingredient with the closest crude protein concentration to the meal's predicted protein concentration (Dahlke, 2012). The diet specifications and ingredients used in the test run are based on the Nutrient Requirements of Swine for grow-finish swine (Table 5) (National Research Council, 1988).

Table 5: Diet Specifications and Ingredients (National Research Council)



Grow-Finish Swine		
Specifications		*Ingredients*
Weight (lb)	50-130	SPROC Soybean Meal
ME, minimum (kcal/lb)	1500	Corn, yellow dent
Crude Protein, minimum (%)	18.00	L-lysine HCl
Crude Protein, maximum (%)	19.00	L-threonine
Lysine, minimum (%)	1.00	L-tryptophan
NDF, maximum (%)	16.00	L-valine
Salt (%), minimum (%)	0.349	DL-methionine
Salt (%), maximum (%)	0.351	Monocalcium phosphate 21%
		Choice white grease
		Limestone
		Salt

$$ME = 2.74 + 0.97 * DE - 0.06 * CP \tag{7}$$

$$DE = 38.44 - 0.43 * CF - 0.98 * GE + 0.11 * ADF \tag{8}$$

Where: *ME* = *Metabolizable Energy (MJ/kg)*

DE = *Digestible Energy (MJ/kg)*

CP = *Crude Protein (%)*

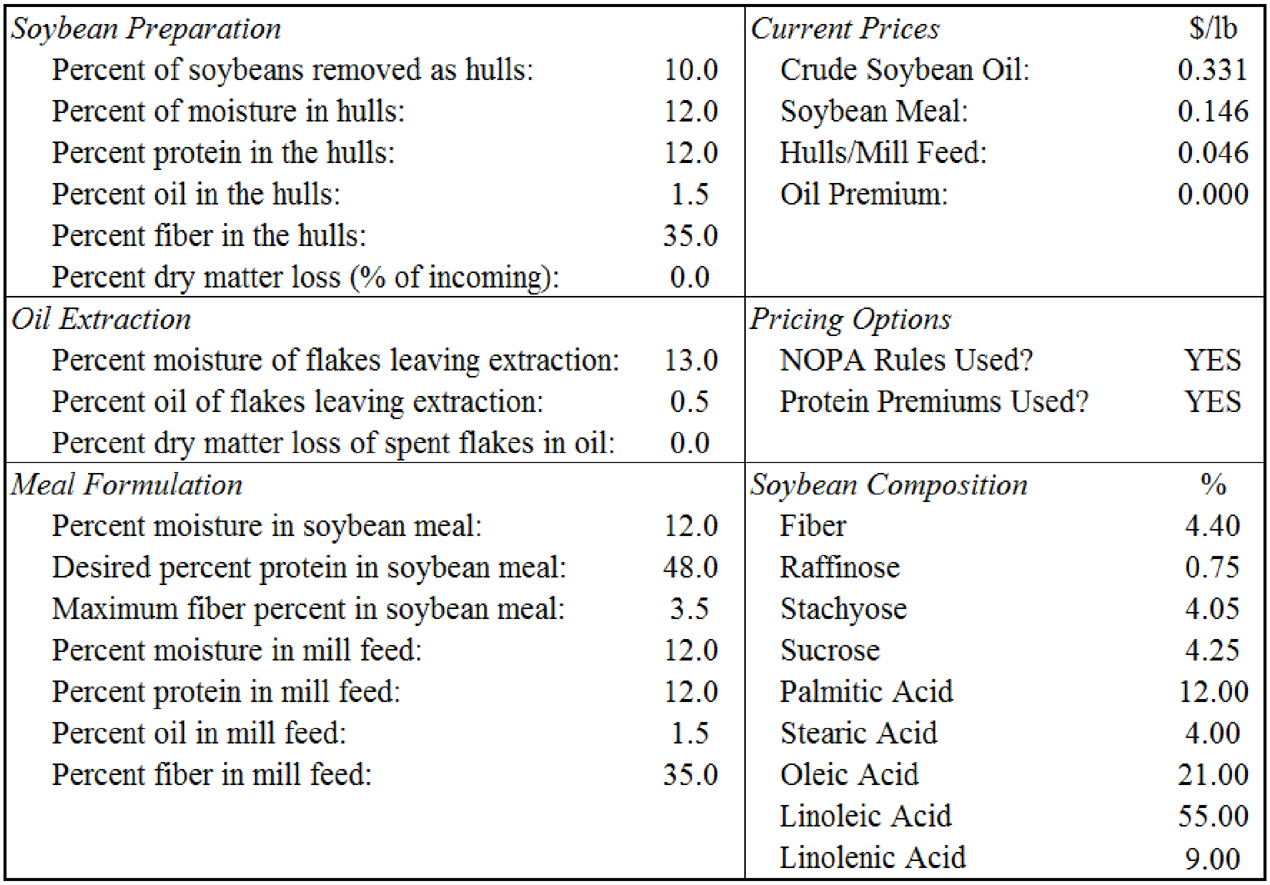
CF = *Crude Fiber (%)*
GE = *Gross Energy (MJ/kg)*
ADF = *Acid Detergent Fiber (%)*

Test on Actual Data

The test sample set was selected from unpublished data from the Iowa Grain Quality Initiative (Iowa State University, Ames, IA). The samples were taken from a 20-year whole soybean reference database that contains proximate analysis values from Eurofins Nutrition Analysis Center (Eurofins Scientific Inc., Des Moines, IA) and amino acid analysis from the Experiment Station Chemistry Labs (University of Missouri, Columbia, MO). The soybean samples were from varying regions within the United States, Canada, Japan, Brazil, Argentina, and Chile, and the harvest dates ranged from 1993 to 2012. Systematic sampling was used to determine an evenly distributed sample set of data. The dataset was maintained for calibration of NIRS analyzers. The components from the sample set entered into the model include moisture, crude protein, oil, and amino acid concentrations. Due to inconsistent and missing data, fiber, fatty acid, and carbohydrate concentrations were assumed to be standard industry values. All assumptions for the test run are listed in table 6.

The processing conditions are the same as those used as defaults in the original SPROC model, and the current prices are the averages for June 2017 reported by the USDA (Agricultual Marketing Service, 2017; Brumm & Hurburgh, 1990). The data were summarized to show the range within the variables of interest (Table 7). The samples were divided into the following 4 categories based on their crude protein and essential amino acid concentrations: High Protein-High Essential Amino Acids (HP, HEAA), High Protein-Low Essential Amino acids (HP, LEAA), Low Protein-High Essential Amino Acids (LP, HEAA), and Low Protein-Low Essential Amino Acids (LP, LEAA). Essential amino acids considered were cysteine, lysine, methionine, threonine, and tryptophan. The thresholds established for high protein and high essential amino acids were concentrations above 36.00% and 5.25%, respectively. These thresholds represent the approximate population median for protein and essential amino acids. It should be noted that the number of samples chosen from each category was balanced to obtain an even distribution for the test run. The following is the percent of samples in each category from the entire dataset: 40.9% HP,HEAA; 10.3% HP, LEAA; 3.2% LP,HEAA; 45.6% LP, LEAA. The amount of samples in each category is not a representation of the distribution typically found in the current market. Statistical analysis was performed using JMP Pro 13.0.0 (SAS Institute Inc., Cary, NC).

Table 6: Processing condition and soybean composition assumptions made in test run (Brumm and Hurburgh; Agricultual Marketing Service; Medic, Atkinson and Hurburgh)



Soybean Preparation		*Current Prices*	$/lb
Percent of soybeans removed as hulls:	10.0	Crude Soybean Oil:	0.331
Percent of moisture in hulls:	12.0	Soybean Meal:	0.146
Percent protein in the hulls:	12.0	Hulls/Mill Feed:	0.046
Percent oil in the hulls:	1.5	Oil Premium:	0.000
Percent fiber in the hulls:	35.0		
Percent dry matter loss (% of incoming):	0.0		
Oil Extraction		*Pricing Options*	
Percent moisture of flakes leaving extraction:	13.0	NOPA Rules Used?	YES
Percent oil of flakes leaving extraction:	0.5	Protein Premiums Used?	YES
Percent dry matter loss of spent flakes in oil:	0.0		
Meal Formulation		*Soybean Composition*	%
Percent moisture in soybean meal:	12.0	Fiber	4.40
Desired percent protein in soybean meal:	48.0	Raffinose	0.75
Maximum fiber percent in soybean meal:	3.5	Stachyose	4.05
Percent moisture in mill feed:	12.0	Sucrose	4.25
Percent protein in mill feed:	12.0	Palmitic Acid	12.00
Percent oil in mill feed:	1.5	Stearic Acid	4.00
Percent fiber in mill feed:	35.0	Oleic Acid	21.00
		Linoleic Acid	55.00
		Linolenic Acid	9.00

Table 7: Sample Data Set Summary

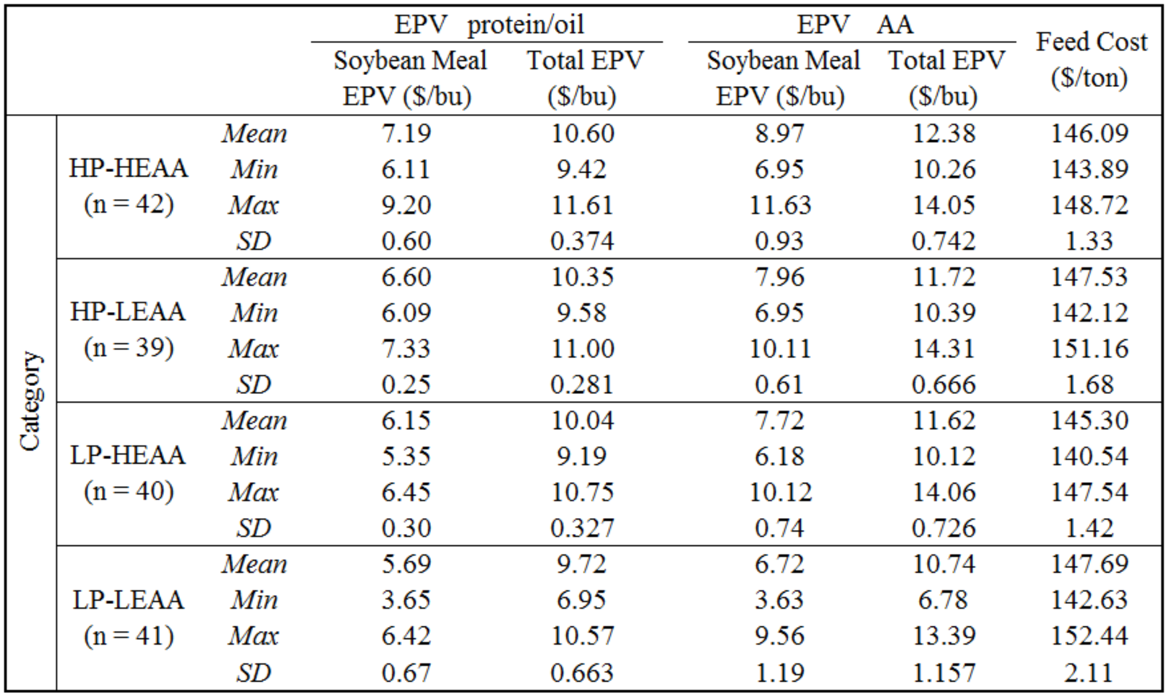
	Category															
13% Moisture	HP-HEAA (n = 42)				HP-LEAA (n = 39)				LP-HEAA (n = 40)				LP-LEAA (n = 41)			
Basis	Mean	Min	Max	SD	Mean	Min	Max	SD	Mean	Min	Max	SD	Mean	Min	Max	SD
Protein	40.07	36.13	50.73	3.02	37.06	36.00	40.63	1.09	35.11	33.17	35.98	0.88	33.77	27.91	35.85	1.67
Oil	16.87	12.16	19.91	1.88	18.39	15.99	20.62	1.23	18.93	16.77	21.32	1.07	19.46	14.91	22.46	1.49
Fiber	4.40	4.40	4.40	0.00	4.40	4.40	4.40	0.00	4.40	4.40	4.40	0.00	4.40	4.40	4.40	0.00
Amino Acids																
Alanine	4.52	3.92	5.93	0.39	4.06	3.83	4.37	0.12	4.06	3.87	4.22	0.09	3.76	3.23	4.20	0.22
Arginine	1.48	1.36	1.68	0.08	1.38	1.29	1.45	0.04	1.41	1.33	1.49	0.04	1.30	1.08	1.42	0.06
Aspartic Acid	1.78	1.49	2.21	0.16	1.60	1.26	1.79	0.11	1.66	1.49	1.82	0.07	1.51	1.14	1.80	0.12
Cysteine	7.14	6.20	8.33	0.55	6.37	5.24	6.96	0.31	6.36	5.92	6.76	0.23	5.84	4.79	6.53	0.41
Glutamic Acid	1.90	1.65	2.24	0.14	1.73	1.63	1.91	0.06	1.72	1.43	2.05	0.09	1.59	1.27	1.83	0.11
Glycine	1.64	1.47	1.92	0.11	1.52	1.42	1.59	0.04	1.52	1.41	1.63	0.05	1.43	1.30	1.56	0.07
Histidine	1.64	1.50	1.89	0.10	1.53	1.47	1.63	0.04	1.53	1.46	1.66	0.04	1.45	1.30	1.58	0.06
Isoleucine	0.62	0.51	0.81	0.06	0.57	0.48	0.66	0.04	0.60	0.51	0.74	0.05	0.55	0.39	0.63	0.05
Leucine	1.88	1.50	2.16	0.13	1.78	1.56	1.93	0.08	1.73	1.54	1.88	0.08	1.65	1.49	1.82	0.09
Lysine	0.55	0.48	0.65	0.04	0.50	0.45	0.55	0.02	0.53	0.47	0.58	0.03	0.48	0.41	0.54	0.03
Methionine	1.79	1.44	2.05	0.12	1.67	1.43	1.78	0.07	1.66	1.41	1.78	0.07	1.56	1.30	1.71	0.09
Phenylalanine	3.01	2.75	3.34	0.16	2.78	2.63	2.93	0.07	2.76	2.63	2.91	0.06	2.59	2.25	2.87	0.14
Proline	1.42	1.31	1.60	0.08	1.32	1.21	1.40	0.05	1.31	1.21	1.43	0.05	1.23	1.08	1.36	0.07
Serine	2.00	1.80	2.31	0.12	1.84	1.72	1.99	0.06	1.81	1.69	1.95	0.06	1.69	1.40	1.87	0.10
Threonine	2.49	2.29	2.81	0.14	2.30	2.14	2.42	0.06	2.33	2.22	2.51	0.07	2.19	1.92	2.36	0.10
Tryptophan	1.05	0.93	1.23	0.07	0.97	0.91	1.08	0.04	0.96	0.89	1.02	0.03	0.90	0.76	1.00	0.04
Tyrosine	3.04	2.59	4.92	0.45	2.68	2.41	2.94	0.12	2.61	2.46	2.81	0.08	2.42	2.03	2.71	0.14
Valine	0.48	0.37	0.57	0.05	0.40	0.28	0.51	0.05	0.45	0.37	0.56	0.05	0.41	0.30	0.58	0.06
Total EAA	5.61	5.26	6.23	0.27	5.15	4.98	5.25	0.07	5.32	5.25	5.58	0.07	4.93	4.39	5.20	0.19

Notes: HP = High Protein (>36.00%); LP = Low Protein (<36.00%); HEAA = High Essential Amino Acids (>5.25%); LEAA = Low Essential Amino Acids (<5.25%); SD = Standard Deviation; Fiber was assumed at 4.40%; Essential amino acids are highlighted; 13% Moisture Basis.

Results and Discussion

The sample set was divided into categories to show the differences in evaluations based on their varying crude protein (P) and essential amino acid (EAA) concentrations and to display a comprehensive range of results. In this test, oil premiums were not included. The two evaluations that were analyzed were the estimated processed values ($EPV_{protein/oil}$ & EPV_{AA}), based on protein/oil content and amino acid concentrations ($/bu) (Table 8). The swine feed cost ($/ton) was determined by the feed formulation software. The total EPV_{AA}, which includes the product values for soybean meal, oil, and extra mill run, proved to be greater than the $EPV_{protein/oil}$ in every category when the amino acid concentrations were used for determination instead of the protein and oil. The highest EPV_{AA} of $12.38/bu occurred for the HP-HEAA category. However, the variation within the results was greater for the EPV_{AA} with standard deviations ranging from $0.74/bu to $1.16/bu.

Table 8: Estimated Processed Value and Swine Feed Cost

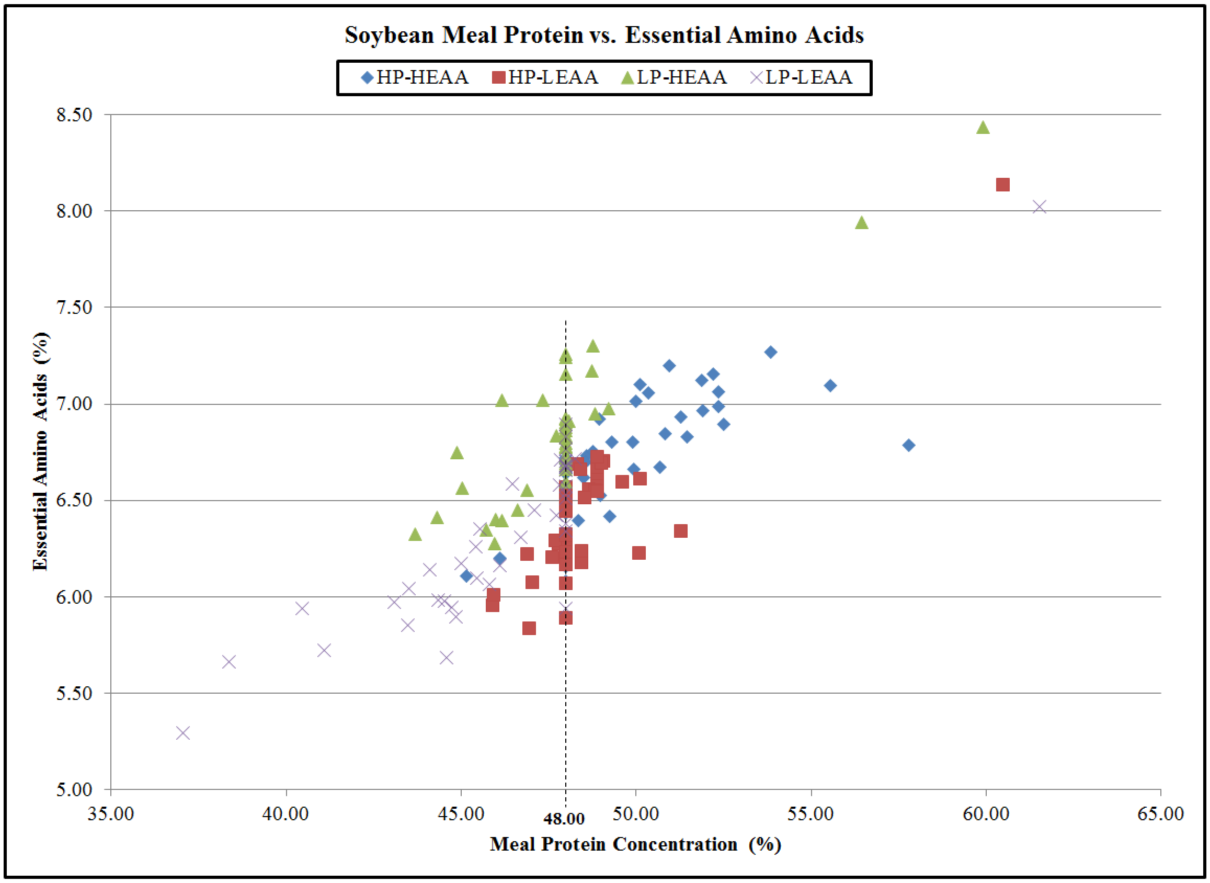


			EPV protein/oil		EPV AA		Feed Cost ($/ton)
			Soybean Meal EPV ($/bu)	Total EPV ($/bu)	Soybean Meal EPV ($/bu)	Total EPV ($/bu)	
Category	HP-HEAA (n = 42)	*Mean*	7.19	10.60	8.97	12.38	146.09
		Min	6.11	9.42	6.95	10.26	143.89
		Max	9.20	11.61	11.63	14.05	148.72
		SD	0.60	0.374	0.93	0.742	1.33
	HP-LEAA (n = 39)	*Mean*	6.60	10.35	7.96	11.72	147.53
		Min	6.09	9.58	6.95	10.39	142.12
		Max	7.33	11.00	10.11	14.31	151.16
		SD	0.25	0.281	0.61	0.666	1.68
	LP-HEAA (n = 40)	*Mean*	6.15	10.04	7.72	11.62	145.30
		Min	5.35	9.19	6.18	10.12	140.54
		Max	6.45	10.75	10.12	14.06	147.54
		SD	0.30	0.327	0.74	0.726	1.42
	LP-LEAA (n = 41)	*Mean*	5.69	9.72	6.72	10.74	147.69
		Min	3.65	6.95	3.63	6.78	142.63
		Max	6.42	10.57	9.56	13.39	152.44
		SD	0.67	0.663	1.19	1.157	2.11

Notes: HP = High Protein (>36.00%); LP = Low Protein (<36.00%); HEAA = High Essential Amino Acids (>5.25%); LEAA = Low Essential Amino Acids (<5.25%); EPV = Estimated Processed Value. The AA evaluation is calculated as the sum of amino acid valuations for the soybean meal.

The significant difference between the $\mathrm{EPV}_{\mathrm{protein/oil}}$ and $\mathrm{EPV}_{\mathrm{AA}}$ is caused by the current market prices of soybean meal and commercially produced, synthetic amino acids. Synthetic amino acids currently have a high market price; therefore, the $\mathrm{EPV}_{\mathrm{AA}}$ of soybean meal logically increases because the value is based on its amino acid profile. It should be noted that the $\mathrm{EPV}_{\mathrm{protein/oil}}$ evaluation is significantly influenced by the current price of soybean meal as well. Therefore, the difference between the two evaluations is driven by the current state of the market and will vary according to market conditions.

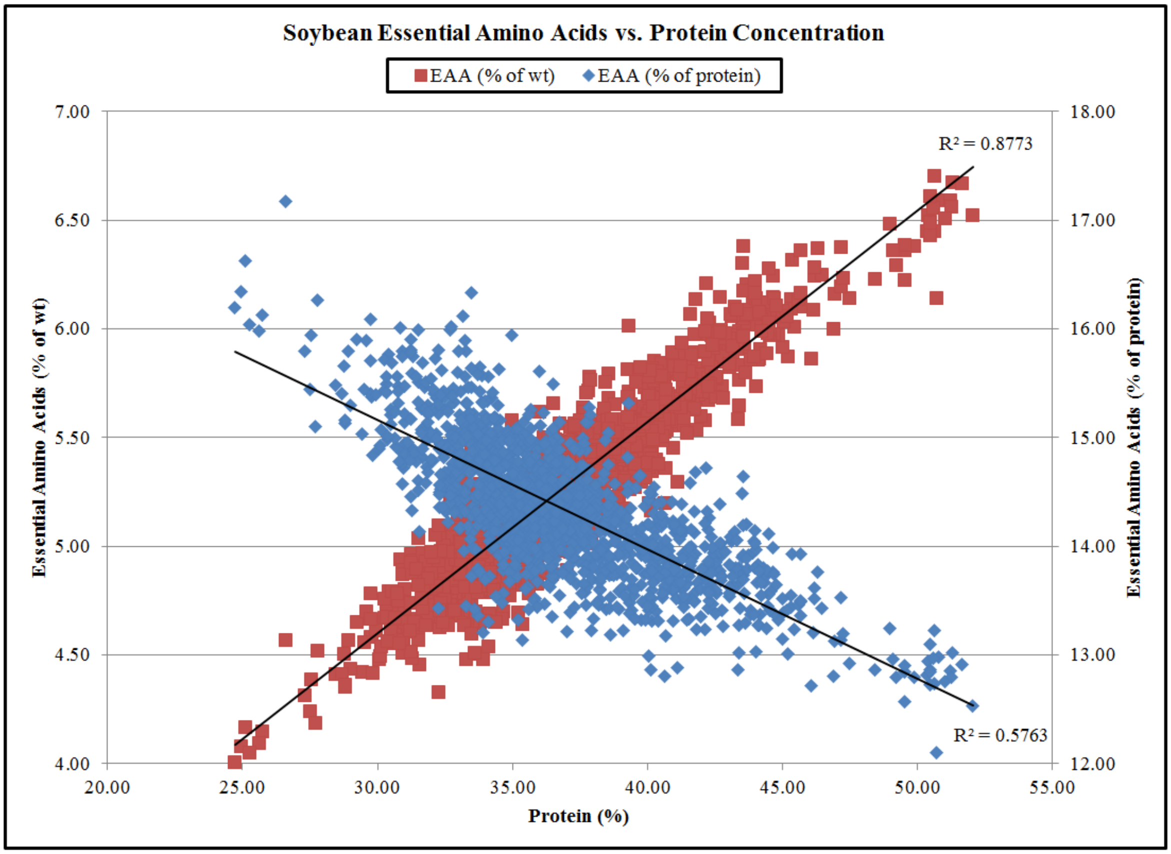
The feeding value of the meal was analyzed by plotting EAA concentration against protein concentration (Figure 8). Because the meal protein specification for the test run was 48.00%, a large amount of samples were formulated to exactly 48.00% meal protein. The outlying samples with meal protein of approximately 55.00% or higher were limited by the fiber specification of 3.50%, which restricted the model's ability to regulate the protein content. Additionally, it is important to realize the difference between a higher $\mathrm{EPV}_{\mathrm{AA}}$ and the corresponding feeding value of the soybean meal. The highest $\mathrm{EPV}_{\mathrm{AA}}$ occurred for the HP-HEAA category, but figure 8 shows the highest EAA concentration in the meal occurred for the LP-HEAA category at the majority of protein concentrations. This shows that the total amount of essential amino acids in the meal can be high (resulting in a high $\mathrm{EPV}_{\mathrm{AA}}$), but the relative concentration of EAA to protein is the key factor that affects the feeding value.



Notes: HP = High Protein (>36.00%); LP = Low Protein (<36.00%); HEAA = High Essential Amino Acids (>5.25%); LEAA = Low Essential Amino Acids (<5.25%); Dotted Line = 48.00% Meal Protein.

Figure 8: Soybean Meal Protein vs. Essential Amino Acid Concentration

The difference between total amount of EAA and the relative concentration of EAA to protein of the entire dataset (n = 1461) is shown in figure 9. The percent of EAA by weight shows a positive linear relationship against protein concentration; however, the EAA as a percent of protein (relative concentration of EAA to protein) decreases as protein increases. This suggests that soybeans with lower protein content will have a higher relative concentration of EAA to protein. If the relative concentration of essential amino acids to protein is high, then less meal needs to be added into the feed to reach the amino acid requirements. As a result, more ingredients that are less expensive than soybean meal can be added into the diet, which lowers the total feed cost. However, if the relative concentration of essential amino acids to protein was low, the amount of soybean meal added to the diet would need to be higher, which increases the feed cost. Therefore, this suggests the LP-HEAA category would have the highest feeding value, resulting in a low feed cost.



Notes: EAA = Essential Amino Acids; EAA considered: cysteine, lysine, methionine, threonine, and tryptophan.

Figure 9: Essential Amino Acid Concentration vs. Protein Concentration of Soybeans

The feed cost and diet formulation results are shown in table 9. All diets had the option to include the soybean meal predicted from the model and a consistent list of other common ingredients utilized in swine diets. Choice white grease was available for each formulation as a source of fat for the diet; however, due to the estimated current price of this ingredient at $500/ton, it was not included in any diet. The feed cost ($/ton) varied depending on the CP and EAA concentrations of the soybeans. The lowest average feed cost of $145.30/ton occurred for the low protein-high essential amino acid (LP-HEAA) category, which is consistent with the results found in figure 8. This is logical because this category utilized the least amount of added synthetic amino acids (0.26% as fed), and it allowed for the most use of other, less expensive ingredients. The highest average feed cost of $147.69/ton occurred for the low protein-low essential amino acid (LP-LEAA) category. The feed costs are higher for both LEAA categories because they incurred the added feed cost resulting from adding more soybean meal and more synthetic amino acids to achieve the required amino acid content in the diet.

Conclusions

An existing mass balance model was updated to a spreadsheet-based model that tracked amino acids, fatty acids, and carbohydrates through the soybean solvent extraction process. The soybean meal, crude oil, and extra mill run yields and compositions were used to determine the estimated processed values. Furthermore, these nutrients were connected to feed formulation software that allows the user to formulate swine diets based on the predicted soybean meal components. This model improves upon existing models by accounting for the large variation found in minor (but valuable) constituents of soybeans and using these constituents to predict the end-use value of a bushel of soybeans. The ability of the model user to compare product compositions and resulting predicted values gives producers, breeders, buyers, and nutritionists an idea of how varying compositional profiles change the worth of the end products. Additionally, this model displays the importance of a component based pricing system for the soybean industry. This system would value grain based on its composition, such as, protein, oil, fiber, amino acid and carbohydrate levels, and reward producers for increasing the desired intrinsic factors, which have been shown to increase the end-use value of the grain.

A large sample set of soybean data provides an example of how a large range in compositions can affect the potential product value when based on product yield, amino acid concentrations, or feeding value in a swine diet. Table 8 displays how these different evaluations

Table 9: Feed Formulation Results

	Category															
	HP-HEAA (n = 42)				HP-LEAA (n = 39)				LP-HEAA (n = 40)				LP-LEAA (n = 41)			
	Mean	Min	Max	SD	Mean	Min	Max	SD	Mean	Min	Max	SD	Mean	Min	Max	SD
Meal Ingredients (% as fed)																
Soybean Meal	25.50^{a}	21.16	28.17	1.40	26.15^{a}	20.32	28.22	1.28	26.41^{a}	20.69	29.25	1.67	27.77^{b}	19.92	36.46	2.61
Corn, Yellow Dent	71.81^{a}	69.20	75.88	1.36	71.14^{a}	69.08	76.90	1.25	70.98^{a}	68.27	76.63	1.62	69.58^{b}	61.10	77.28	2.54
L-Lysine, HCl	0.22^{ab}	0.16	0.33	0.04	0.24^{a}	0.17	0.32	0.04	0.19^{c}	0.07	0.27	0.05	0.21^{bc}	0.11	0.33	0.05
L-Threonine	0.07^{a}	0.03	0.12	0.02	0.07^{a}	0.03	0.13	0.02	0.05^{b}	0.01	0.08	0.02	0.06^{a}	0.02	0.13	0.02
Monocalcium Phosphate	1.04^{a}	1.02	1.07	0.01	1.04^{a}	1.02	1.07	0.01	1.03^{a}	1.02	1.07	0.01	1.03^{b}	0.98	1.07	0.02
Limestone	0.96^{a}	0.95	0.99	0.01	0.96^{a}	0.95	0.99	0.01	0.96^{a}	0.94	0.99	0.01	0.95^{b}	0.90	1.00	0.01
Salt	0.35	0.35	0.35	0.00	0.35	0.35	0.35	0.00	0.35	0.35	0.35	0.00	0.35	0.35	0.35	0.00
Choice White Grease	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
L-Tryptophan	0.01^{a}	0.00	0.02	0.01	0.01^{b}	0.00	0.04	0.01	0.00^{a}	0.00	0.01	0.00	0.01^{a}	0.00	0.03	0.01
DL-Methionine	0.04^{a}	0.01	0.09	0.02	0.05^{a}	0.01	0.09	0.02	0.02^{b}	0.00	0.05	0.01	0.04^{a}	0.00	0.13	0.02
Meal Characteristics																
ME (kcal/lb)	1543^{c}	1523	1583	13.71	1552^{bc}	1519	1584	16.77	1560^{b}	1519	1593	19.08	1575^{a}	1517	1637	25.02
Crude Protein (%)	18.92^{a}	18.00	19.00	0.21	18.9^{ab}	18.23	19.00	0.20	18.74^{b}	18.00	19.00	0.37	18.79^{ab}	18.00	19.00	0.35
Lysine (%)	1.12^{a}	1.11	1.13	0.00	1.12^{a}	1.11	1.12	0.00	1.12^{b}	1.12	1.13	0.00	1.12^{a}	1.11	1.13	0.00
NDF (%)	9.18^{a}	9.15	9.52	0.07	9.19^{a}	9.14	9.51	0.11	9.33^{a}	9.16	10.45	0.33	9.64^{b}	9.15	10.72	0.59
Cost ($/ton)	146.09^{a}	143.89	148.72	1.33	147.53^{b}	142.12	151.16	1.68	145.3^{a}	140.54	147.54	1.42	147.69^{b}	142.63	152.44	2.11
Total Synthetic EAA	0.34^{ab}	0.20	0.56	0.08	0.37^{a}	0.22	0.57	0.09	0.26^{c}	0.08	0.41	0.08	0.32^{b}	0.13	0.62	0.10

Notes: ^{a,b,c} Least square means within each row with different superscript letters are considered significantly different; HP = High Protein (>36.00%); LP = Low Protein (<36.00%); HEAA = High Essential Amino Acids (>5.25%); LEAA = Low Essential Amino Acids (<5.25%); ME = Metabolizable Energy; NDF= Neutral Detergent Fiber; SD = Standard Deviation.

change based on the protein and essential amino acid concentrations found in the soybeans. The average lowest feed cost of $145.30/ton was found for the low protein-high essential amino acid category, which suggests that the relative concentration of essential amino acids to protein is an accurate indication of end-use feeding value of the soybean meal.

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CHAPTER 3: TECHNICAL NOTE - VALIDATION OF THE UPDATED SOYBEAN PROCESSING MODEL

Abstract

As the soybean solvent extraction industry continues to grow, more emphasis has been placed on the factors that affect the quality of the final products. These factors include the major and minor constituents within raw soybeans, such as, protein, oil, amino acids, carbohydrates, and fatty acids. In order to evaluate lots of soybeans with varying compositions, a model (SPROC) was developed by Brumm & Hurburgh in 1990 that placed an estimated processed value (EPV) on a bushel of raw soybeans based on its protein and oil content. An updated version of this model (SPROC 3.0) was developed to evaluate soybeans based on minor constituents, rather than protein and oil. SPROC 3.0 runs in Microsoft Excel and requires inputs of whole soybean composition and processing conditions. Initially, the updated model was based on protein and oil to allow a comparison between the two models before including minor constituents.

To validate that SPROC 3.0 is an accurate representation of the original model for protein and oil alone, case study samples from the original model's publication were utilized to compare results sets between the two models. This is important to maintain continuity for users of the original model. The deviations between results were analyzed. The EPV of all products only varied for two samples and by only $0.01 / bu (greater than the original model for both samples). A logical explanation of this deviation would be the error produced from the lack of precision in the original model's programming. Therefore, continuity was established between both models.

Introduction

The soybean industry has grown significantly competitive over the past few decades due to the development of new production technologies. These advancements have increased productivity, but have left overall grain quality relatively unchanged. As more countries have achieved similar levels of efficiency and productivity, the soybean industry has begun to focus on grain quality. In particular, intrinsic factors, such as, amino acids, carbohydrates, and fatty acids, that affect the end-user have acquired significant interest (Office of Global Analysis, 2017).

Utilizing these intrinsic factors to place a value on soybeans is challenging because of the significant variation among these components due to agricultural practices, genetic varieties, and environmental conditions (Thakur & Hurburgh, 2007). In 1990, a model was developed by Brumm & Hurburgh, titled SPROC for soybean processing, to address this issue of evaluating soybeans with varying compositions. This model estimated a monetary value for a bushel of soybeans based on its protein and oil content. Because solvent extraction is the primary type of processing performed on soybeans, the model simulated the production operations in a soybean solvent extraction plant, including soybean preparation, dehulling, oil extraction, and meal formulation. A calculation for regulating protein and fiber content of the soybean meal was also included to account for trading rule limitations and product specifications. The estimated processed value (EPV) was found by predicting the product yields and determining discounts based on marketing techniques chosen by the user (Brumm & Hurburgh, 1990).

Although the original SPROC model effectively correlated raw soybean composition to end-use value, the soybean industry is now focusing on further compositional analysis. To address these issues, an updated SPROC model (SPROC 3.0) was developed to determine the EPV of a bushel of soybeans based on its amino acid, carbohydrate, and fatty acid content, rather than only protein and oil content. The current study evaluates the validity of SPROC 3.0 by comparing results with the original model using case study samples found in the original SPROC publication (Brumm & Hurburgh, 1990).

Technique

The original SPROC model was developed using Microsoft QuickBasic (Microsoft Corporation, Redmond, WA), a computer-based interface that has since been eliminated. This interface will not run on Windows 7 and above. The updated SPROC model, titled SPROC 3.0, was developed using Microsoft Excel 2013 (Microsoft Corporation, Redmond, WA). It runs using Visual Basic for Applications (VBA) coding. The model utilized the original mass balance equations developed by Brumm & Hurburgh for moisture, protein, oil, and fiber, and the EPV equation for all extraction products. The flow diagram of the mass balance model is shown in figure 10.

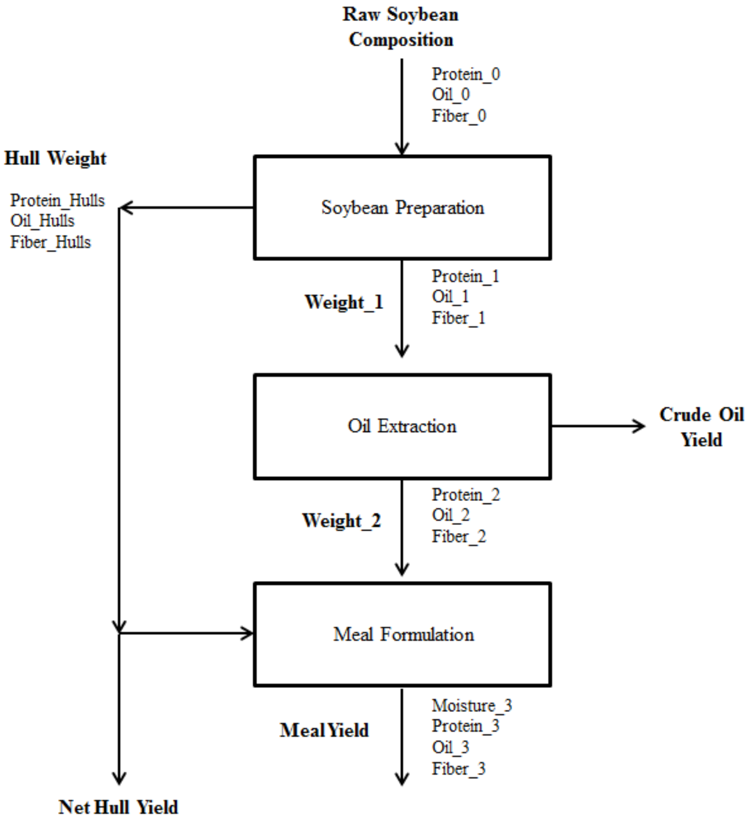
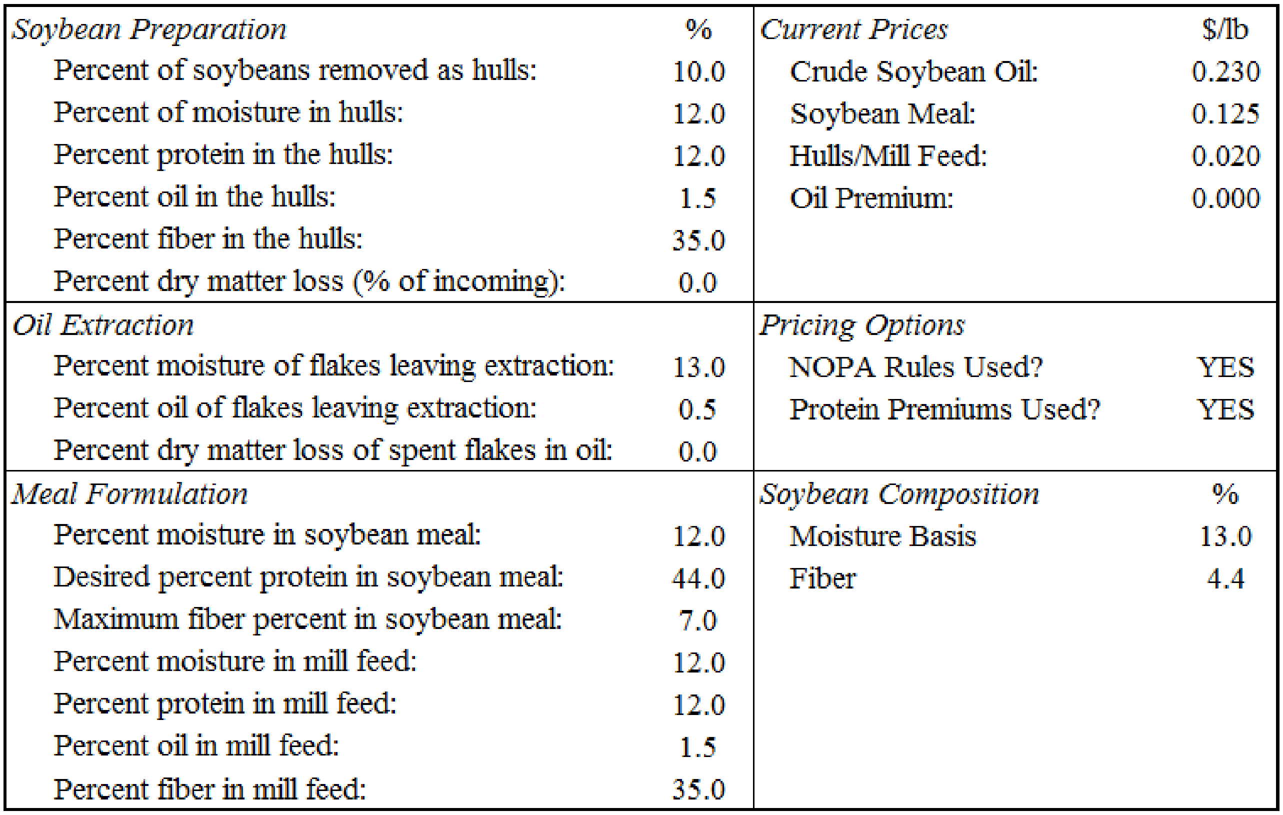


Figure 10: Flow Diagram of the Mass Balance Model

The samples used for analysis were taken from original publication; ten samples were chosen from 52 entries in the 1987 Iowa State Fair Open Market Soybean Class to show the variability in the EPV determined by the model. The protein and oil contents were determined at the time with a Dickey-john Instalab 800 near-infrared instrument. The soybean fiber content was assumed at 4.4% on a 13% moisture basis in the original sample set. All processing conditions and assumptions were kept constant in the updated model to assure continuity between the two models (Table 10).

Table 10: Processing Conditions for Comparison Model Run (Brumm & Hurburgh, 1990)



Soybean Preparation	%	*Current Prices*	$/lb
Percent of soybeans removed as hulls:	10.0	Crude Soybean Oil:	0.230
Percent of moisture in hulls:	12.0	Soybean Meal:	0.125
Percent protein in the hulls:	12.0	Hulls/Mill Feed:	0.020
Percent oil in the hulls:	1.5	Oil Premium:	0.000
Percent fiber in the hulls:	35.0		
Percent dry matter loss (% of incoming):	0.0		
Oil Extraction		*Pricing Options*	
Percent moisture of flakes leaving extraction:	13.0	NOPA Rules Used?	YES
Percent oil of flakes leaving extraction:	0.5	Protein Premiums Used?	YES
Percent dry matter loss of spent flakes in oil:	0.0		
Meal Formulation		*Soybean Composition*	%
Percent moisture in soybean meal:	12.0	Moisture Basis	13.0
Desired percent protein in soybean meal:	44.0	Fiber	4.4
Maximum fiber percent in soybean meal:	7.0		
Percent moisture in mill feed:	12.0		
Percent protein in mill feed:	12.0		
Percent oil in mill feed:	1.5		
Percent fiber in mill feed:	35.0		

Results and Discussion

The case study samples were run through the updated SPROC model to obtain the soybean meal yield (lb/bu) and protein (%), mill feed used (lb/bu), crude oil yield (lb/ bu), extra hull yield (lb/bu), price adjustment ($/lb), and EPV of all products ($/bu). The averages of all 10 samples were calculated, and the total deviation from the original model results was found by summing the absolute differences for each sample. The original model only outputs to the 0.1 precision for percentages and 0.01 for the EPV of all products. To keep the results consistent, the results of the updated model were rounded to match these precisions (Table 11).

Because the same background mass balance equations were used for each model, the averages and deviations found are logical. There was no deviation found in all categories except the EPV of all products. For samples 9 and 10, SPROC 3.0 estimated a value of $0.01 / bu greater than the original SPROC model. The original SPROC model only accounted for 5 significant digits for each variable (Noggle, 1993). This could lead to rounding errors when compared to the updated model programming which accounts for at least 15 significant digits for each variable. Therefore, the updated model would have greater accuracy in the two cases where the EPV showed slight deviation.

Conclusion

The original SPROC model was developed to evaluate lots of whole soybeans with varying compositions based on protein and oil content. The updated model was developed in a current program with the intention of including minor constituents, such as, amino acids, carbohydrates, and fatty acids, which affect the end-use value of the extraction products. Case study samples that were used in the original model publication were employed to validate the updated model. There were no deviations found among the results, except for the EPV of all products. This deviation could be explained by the significant difference in precision of both models. Therefore, SPROC 3.0 is an accurate representation of the original model, and it is a valid platform to use for the addition of the minor constituents. Existing users not considering minor constituents, such as breeding programs for high protein, will not experience loss of continuity.

Table 11: Comparison Table of Results between the Original and Updated SPROC Models

Sample ID	Protein (%)[c]	Oil (%)[c]	Original SPROC, Brumm-Hurburgh[b]							SPROC 3.0[b]						
			Yield (lb/bu)	Protein (%)	Mill Feed Used (lb/bu)	Crude Oil Yield (lb/bu)	Extra Hulls (lb/bu)	Price Adjustment ($/lb)	EPV of All Products ($/bu)	Yield (lb/bu)	Protein (%)	Mill Feed Used (lb/bu)	Crude Oil Yield (lb/bu)	Extra Hulls (lb/bu)	Price Adjustment ($/lb)	EPV of All Products ($/bu)
1	31.6	20.1	42.0	44.0	0.0	11.8	3.9	0.000	8.04	42.0	44.0	0.0	11.8	3.9	0.000	8.04
2	33.1	18.9	44.5	44.0	0.0	11.0	2.2	0.000	8.15	44.5	44.0	0.0	11.0	2.2	0.000	8.15
3	33.9	19.0	46.1	44.0	0.0	11.1	0.6	0.000	8.32	46.1	44.0	0.0	11.1	0.6	0.000	8.32
4	34.6	18.1	47.1	44.0	0.0	10.6	0.2	0.000	8.32	47.1	44.0	0.0	10.6	0.2	0.000	8.32
5	34.8	19.1	47.8	44.0	1.1	11.2	0.0	0.000	8.52	47.8	44.0	1.1	11.2	0.0	0.000	8.52
6	35.5	18.2	48.8	44.0	1.6	10.6	0.0	0.000	8.52	48.8	44.0	1.6	10.6	0.0	0.000	8.52
7	35.5	17.7	48.7	44.0	1.1	10.3	0.0	0.000	8.44	48.7	44.0	1.1	10.3	0.0	0.000	8.44
8	36.6	17.5	50.2	44.3	2.5	10.2	0.0	0.001	8.62	50.2	44.3	2.5	10.2	0.0	0.001	8.62
9	38.0	16.6	51.0	45.3	2.7	9.7	0.0	0.004	8.73	51.0	45.3	2.7	9.7	0.0	0.004	8.74
10	38.4	17.4	50.3	46.4	2.5	10.1	0.0	0.007	8.90	50.3	46.4	2.5	10.1	0.0	0.007	8.91
Average	35.2	18.3	47.7	44.4	1.2	10.7	0.7	0.001	8.46	47.7	44.4	1.2	10.7	0.7	0.001	8.46
Deviation[a]										0.0	0.0	0.0	0.0	0.0	0.000	0.02

Notes: SPROC = Soybean Processing Model. Highlighted regions show area of deviation. [a]The deviation is calculated using the absolute difference between the results for both models and for each sample. [b]7.0% fiber limitation by NOPA trading rules, hulls added to dehulled meal to obtain 44% protein unless fiber is limiting, basis 12.0% moisture. [c]Basis 13.0% moisture.

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Thakur, M., & Hurburgh, C. R. (2007). Quality of US Soybean Meal Compared to the Quality of Soybean Meal from Other Origins. *Journal of the American Oil Chemists' Society*, *84*(9), 835-843.

CHAPTER 4: GENERAL CONCLUSION

Summary

Soybeans have been historically marketed based on a commodity pricing system, based on weight only. However, this type of system doesn’t account for the differences in composition which leads to significant variation in quality as well. In order to diminish issues of quality variability, it would be beneficial to have a systemized incentive for producers to select seeds with superior genetics and adjust some cultural practices. To address this issue, a soybean solvent extraction model was designed to predict extraction product yields and compositions to determine estimated processed values for a bushel of soybeans based on amino acid, carbohydrate, and fatty acid content. This model was built upon an existing model that utilized mass balance equations to make yield and composition predictions based on protein and oil content. The new model takes into account soybean composition and processing conditions. This provides a tool for producers, breeders, buyers, and nutritionists to evaluate a bushel of soybeans based on how its composition affects the end-use quality of the extraction products.

The second part of this research involved using the original model to validate the results of the updated model. The case study samples presented in the original model publication provided a representative range of protein and oil contents to display the variability in the model. The results showed that there was insignificant deviation due to the difference in precision between the models, and that the updated model was a valid platform for the addition of minor constituents.

Conclusions

This research could be augmented by including feed formulation software for poultry and determining an overall feeding value based on swine and poultry feed. Additional economic factors and energy considerations could expand the model’s capability as well. A sensitivity analysis using simulated market prices would be beneficial to further test how the model predicts value in varying market conditions. Finally, an annual nationwide prediction of soybean quality profiles could provide valuable marketing information for U.S. soybeans, as production moves more to lower protein in northern and western areas.

APPENDIX A: SPROC 3.0 USER MANUAL

SPROC 3.0 USER MANUAL

SPROC 3.0 connected with the National Swine Nutrition Guide is a model that can be used by solvent extraction plants, buyers, breeders, and animal nutritionists to determine an estimated value of extraction products. The inputs to the model are soybean composition, operating conditions, and current prices, which is utilized by the model to determine product compositions and yields. These results are outputted into the feed library of the formulation software. This allows the user to compare different soybean meals by evaluating their feeding value in common swine diets.

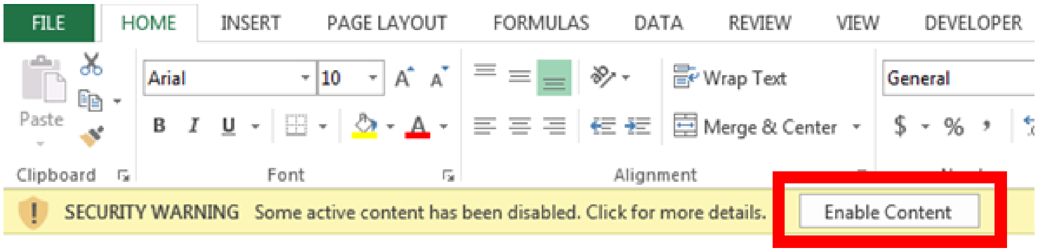
SOFTWARE REQUIREMENT

To run this model, you will need Microsoft Excel. The model runs using Visual Basic macros, which requires the “Macro” setting to be enabled.

ENABLING MACROS

A. Enable content when the model opens:

1. Select “Enable Content” in the security warning banner at the top of the spreadsheet.
    - This will enable the macros for the model to run properly.

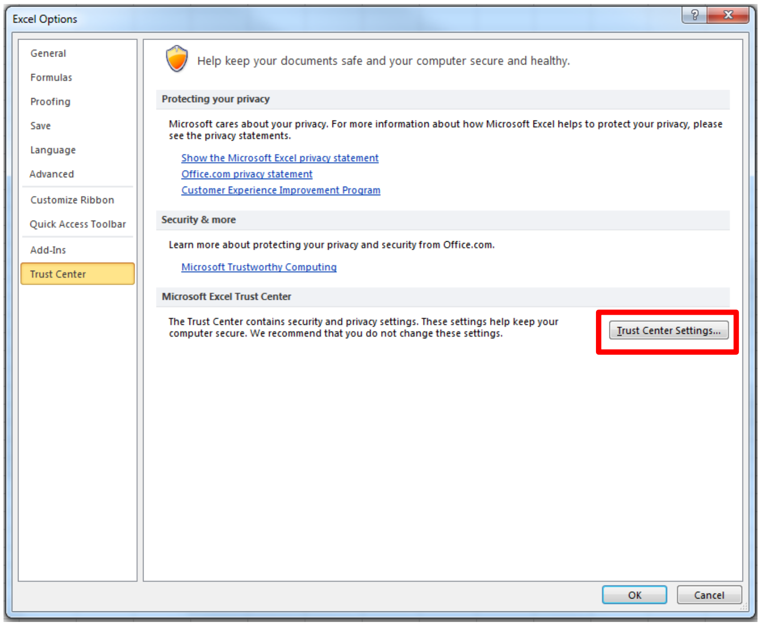


SECURITY WARNING Some active content has been disabled. Click for more details.

OR

B. MS Excel 2007 or later versions:

1. Select ‘File’
2. Select ‘Options’
3. Select ‘Trust Center’
4. Select ‘Trust Center Settings’
5. Select ‘Macro Settings’
6. Select ‘Enable All Macros’
    - A warning message may appear because enabling macros is not recommended by Microsoft. **You must enable macros to run the model.**



Help keep your documents safe and your computer secure and healthy.

Protecting your privacy

Microsoft cares about your privacy. For more information about how Microsoft Excel helps to protect your privacy, please see the privacy statements.

Show the Microsoft Excel privacy statement
Office.com privacy statement
Customer Experience Improvement Program

Security & more

Learn more about protecting your privacy and security from Office.com.

Microsoft Trustworthy Computing

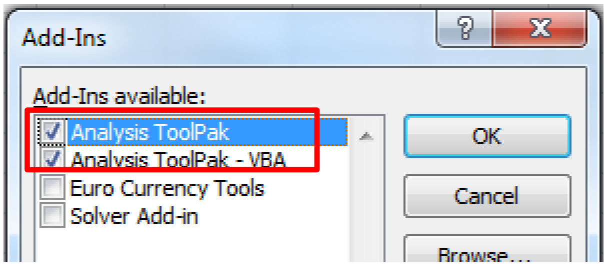
Microsoft Excel Trust Center

The Trust Center contains security and privacy settings. These settings help keep your computer secure. We recommend that you do not change these settings.

OR

C. Earlier versions of Excel:

1. Select ‘Tools’ from the menu bar
2. Select ‘Macro’
3. Select ‘Security’
4. Select ‘Low’
    - You also must select 2 Excel Add-Ins for the model to run properly.
5. Select ‘Tools’ from the menu bar
6. Select ‘Add-Ins’
7. Select the boxes for both ‘Analysis Tool Pack’ **AND** ‘Analysis Tool Pack-VBA’



Add-Ins available:

☑ Analysis ToolPak
☑ Analysis ToolPak - VBA
☐ Euro Currency Tools
☐ Solver Add-in

PROGRAM OPERATION

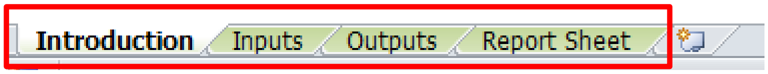
A. Overview:

1. The program may ask for a password when opened for the first time, the password is found below.

PASSWORD: Arnold Ziffel

Password: Arnold Ziffel

2. All red boxes indicate a user input.
    - There <u>must</u> be a valid value in all red boxes before the program will run.
    - The red boxes will turn green when a valid value is input into the box.
3. Navigate from page to page using the tabs on the bottom of the screen.

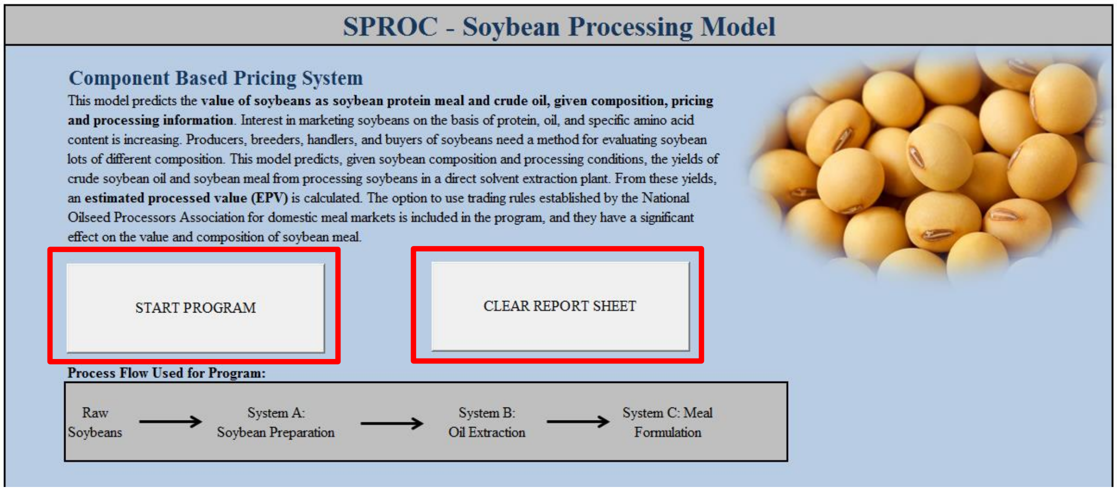


B. Introduction Tab:

1. This tab will automatically be displayed when the program is opened.
    - There's a brief description of what a component based pricing system is, and how the model works.
2. Choose 'Start Program' to be directed to the 'Inputs' sheet

OR

3. Choose 'Clear Report Sheet' to clear any existing samples on the 'Report Sheet' tab



SPROC - Soybean Processing Model

Component Based Pricing System

This model predicts the **value of soybeans as soybean protein meal and crude oil, given composition, pricing and processing information**. Interest in marketing soybeans on the basis of protein, oil, and specific amino acid content is increasing. Producers, breeders, handlers, and buyers of soybeans need a method for evaluating soybean lots of different composition. This model predicts, given soybean composition and processing conditions, the yields of crude soybean oil and soybean meal from processing soybeans in a direct solvent extraction plant. From these yields, an **estimated processed value (EPV)** is calculated. The option to use trading rules established by the National Oilseed Processors Association for domestic meal markets is included in the program, and they have a significant effect on the value and composition of soybean meal.

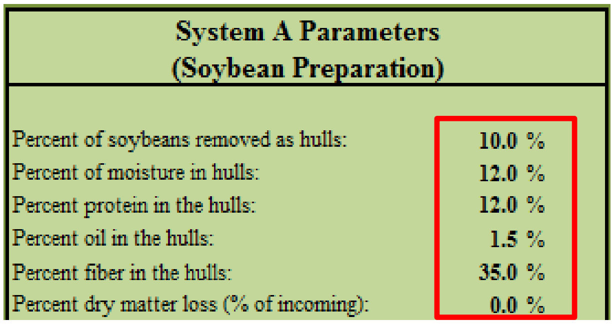
Process Flow Used for Program:

Raw Soybeans → System A: Soybean Preparation → System B: Oil Extraction → System C: Meal Formulation

C. Inputs Tab:

1. System A Parameters (Soybean Preparation):
    - This section includes all the operating conditions for the soybean preparation process.

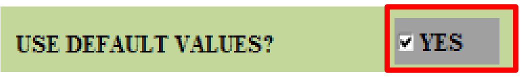
    a. Enter the values in percentages to the desired decimal place.
    - The program will only display the first decimal place, but if more decimal places were entered, the entire value will be used in the program.



System A Parameters (Soybean Preparation)	
Percent of soybeans removed as hulls:	10.0 %
Percent of moisture in hulls:	12.0 %
Percent protein in the hulls:	12.0 %
Percent oil in the hulls:	1.5 %
Percent fiber in the hulls:	35.0 %
Percent dry matter loss (% of incoming):	0.0 %

OR

b. Choose the 'USE DEFAULT VALUES' box to automatically enter common values for each input.



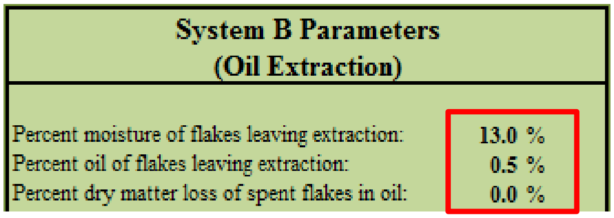
USE DEFAULT VALUES? ☑ YES

2. System B Parameters (Oil Extraction):

- This section includes all the operating conditions for the oil extraction process.

a. Enter the values in percentages to the desired decimal place.

- The program will only display the first decimal place, but if more decimal places were entered, the entire value will be used in the program.

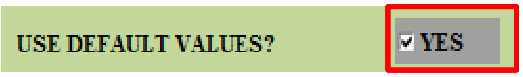


System B Parameters (Oil Extraction)

Percent moisture of flakes leaving extraction:	13.0 %
Percent oil of flakes leaving extraction:	0.5 %
Percent dry matter loss of spent flakes in oil:	0.0 %

OR

b. Choose the ‘USE DEFAULT VALUES’ box to automatically enter common values for each input.



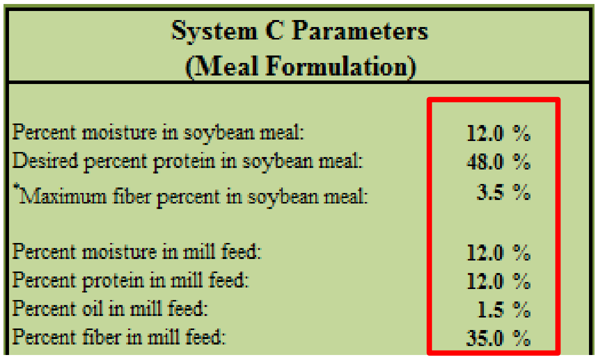
USE DEFAULT VALUES? ☑ **YES**

3. System C Parameters (Meal Formulation):

- This section includes all the operating conditions for the meal formulation process.

a. Enter the values in percentages to the desired decimal place.

- The program will only display the first decimal place, but if more decimal places were entered, the entire value will be used in the program.
- If using the National Oilseed Processors Association (NOPA) trading rules, the fiber percentage limit for <u>48% protein meal</u> is <u>3.5% fiber</u>.

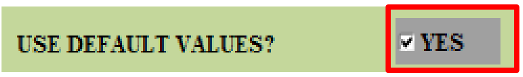


System C Parameters (Meal Formulation)

Percent moisture in soybean meal:	12.0 %
Desired percent protein in soybean meal:	48.0 %
*Maximum fiber percent in soybean meal:	3.5 %
Percent moisture in mill feed:	12.0 %
Percent protein in mill feed:	12.0 %
Percent oil in mill feed:	1.5 %
Percent fiber in mill feed:	35.0 %

OR

b. Choose the ‘USE DEFAULT VALUES’ box to automatically enter common values for each input.


USE DEFAULT VALUES? ☑ YES

4. Pricing Options:
   - This section includes the options to use the National Oilseed Processors Association (NOPA) trading rules for price discounts or the proportionate premiums for meal protein contents that are in excess of specifications.

   a. Click ‘YES’ beside the NOPA trading rules option to choose to these discounts.
   - This option affects the EPV results by discounting the $/bu if the protein or fiber content of the soybean meal is outside of the allowable tolerance set by NOPA. The rules are listed below.

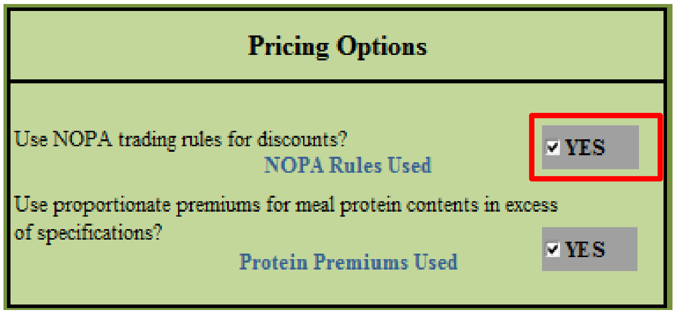
NOPA Rules

1. Fiber limitation of 7.0% for 44% protein meal and 3.3 – 3.5% for high protein (47.5-49.0%) (dehulled) meal.

2. The discount for exceeding the maximum fiber specifications is 1% of the invoice price per 0.1% fiber in excess of specification. A 0.3 percentage point tolerance for fiber is allowed.

3. The protein discount of 2 times the unit price of protein per 1% protein below minimum specifications. A 0.5 percentage point tolerance for protein is allowed.

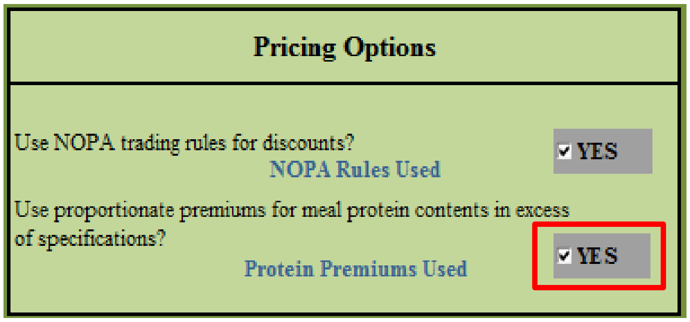
***Complete soybean meal specifications can be found in the NOPA trading rules.**


Pricing Options

Use NOPA trading rules for discounts? ☑ YES
NOPA Rules Used

Use proportionate premiums for meal protein contents in excess of specifications? ☑ YES
Protein Premiums Used

   b. Click ‘YES’ besides the protein premiums option to choose to use the protein premiums.
   - This option affects the EPV results by adding the unit price of protein per 1% protein above specifications. No tolerance is used for protein premiums.



Pricing Options

Use NOPA trading rules for discounts? ☑ YES

NOPA Rules Used

Use proportionate premiums for meal protein contents in excess of specifications? ☑ YES

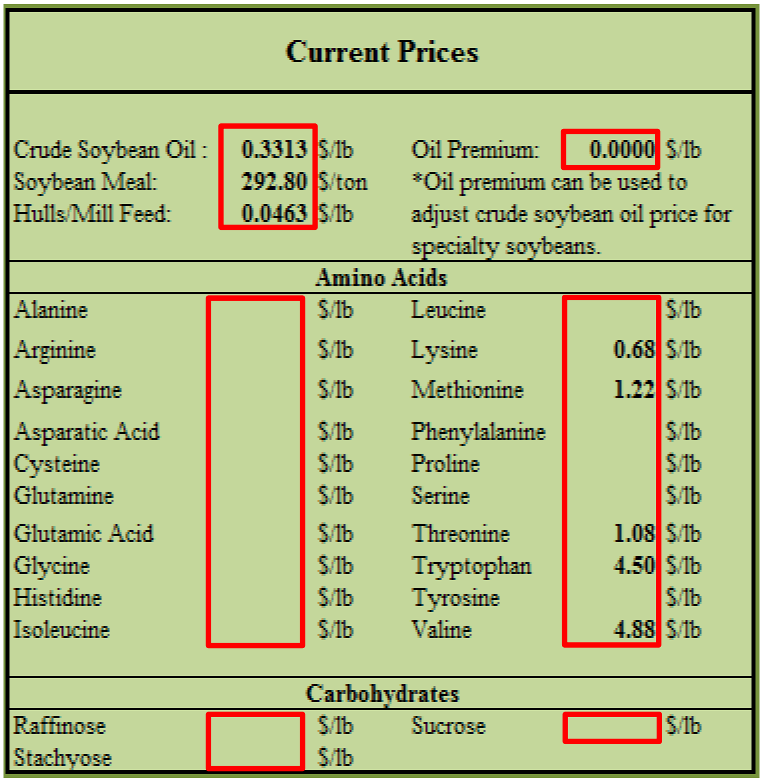
Protein Premiums Used

5. Current Prices:

- This section includes all current market prices used in the program.
- Because market prices fluctuate daily, there is not a 'Default Values' option available for this section.

a. Enter the values in the specified units (either $/lb or $/ton) to the desired decimal place.

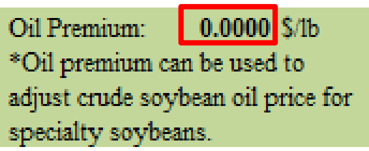
- The program will only display up to four decimal places, but if more decimal places were entered, the entire value will be used in the program.



Current Prices

Crude Soybean Oil :	0.3313	$/lb	Oil Premium:	0.0000	$/lb
Soybean Meal:	292.80	$/ton	*Oil premium can be used to adjust crude soybean oil price for specialty soybeans.		
Hulls/Mill Feed:	0.0463	$/lb			
Amino Acids					
Alanine		$/lb	Leucine		$/lb
Arginine		$/lb	Lysine	0.68	$/lb
Asparagine		$/lb	Methionine	1.22	$/lb
Asparatic Acid		$/lb	Phenylalanine		$/lb
Cysteine		$/lb	Proline		$/lb
Glutamine		$/lb	Serine		$/lb
Glutamic Acid		$/lb	Threonine	1.08	$/lb
Glycine		$/lb	Tryptophan	4.50	$/lb
Histidine		$/lb	Tyrosine		$/lb
Isoleucine		$/lb	Valine	4.88	$/lb
Carbohydrates					
Raffinose		$/lb	Sucrose		$/lb
Stachyose		$/lb			

b. Oil premium: This value is to allow the user to adjust for specialty soybeans (ex: high linoleic soybeans) which would typically bring a higher market price than regular soybeans.



Oil Premium: 0.0000 $/lb

*Oil premium can be used to adjust crude soybean oil price for specialty soybeans.

c. Amino acids & carbohydrates: The majority of these components are not commercially available currently, but enter the $/lb price for the components that are commercially available.

- For components not available, either enter <u>0</u> or <u>leave the box blank</u>.

6. Input / Output Options:

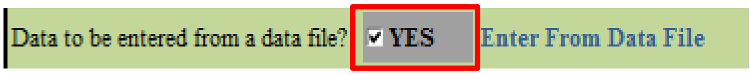
- This section contains three options for entering data, printing data, and connecting to the feed formulation software.

a. To enter data from a data file click the 'YES' box next to this option.

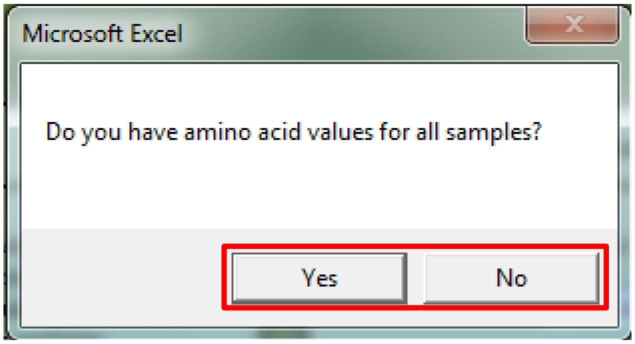
b. The 'Soybean Composition Data' section will change to have you enter your data file information.

- See section 9 (Soybean Composition Data) for instructions on how to enter data file information.

c. The program will open a box that asks 'Do you have amino acid values for all samples?'. Choose 'Yes' or 'No' depending on what data you have included in your data file.



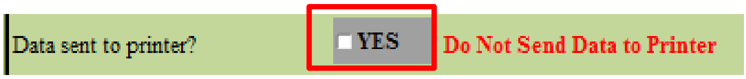
Data to be entered from a data file? ☑ YES Enter From Data File



Microsoft Excel

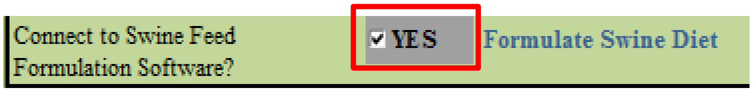
Do you have amino acid values for all samples?

d. To send data straight to a printer, click the 'YES' box next to this option.



Data sent to printer? ☐ YES Do Not Send Data to Printer

e. To connect results to the swine feed formulation software, click the 'YES' box next to this option.

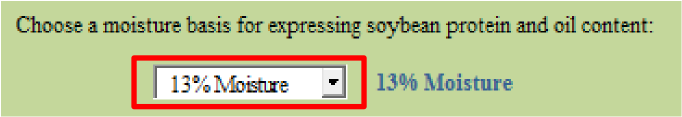


Connect to Swine Feed Formulation Software? ☑ YES Formulate Swine Diet

7. Soybean Composition Options:

- This section contains the options for entering the soybean moisture basis and fiber content.

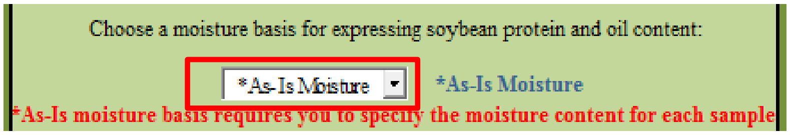
a. To assume a 13% moisture basis for all samples, choose the '13% Moisture' option in the drop-down menu for moisture basis.


Choose a moisture basis for expressing soybean protein and oil content:

13% Moisture 13% Moisture

OR

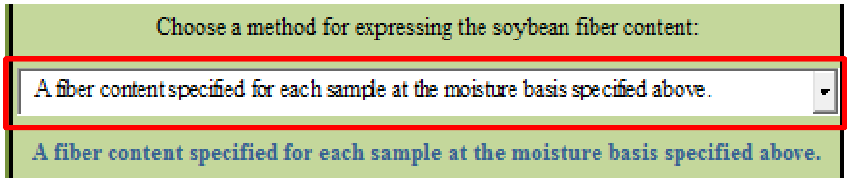
b. To enter a different moisture basis for all samples, choose the '*As-Is Moisture' option in the drop-down menu for moisture basis.


Choose a moisture basis for expressing soybean protein and oil content:

*As-Is Moisture *As-Is Moisture

*As-Is moisture basis requires you to specify the moisture content for each sample

c. To enter a different fiber content for all samples, choose the 'A fiber content specified for each sample at the moisture basis specified above.' option in the drop-down menu for fiber content.

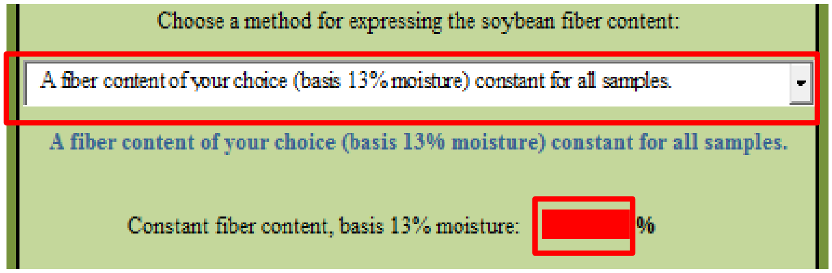

Choose a method for expressing the soybean fiber content:

A fiber content specified for each sample at the moisture basis specified above.

A fiber content specified for each sample at the moisture basis specified above.

d. To enter a constant fiber content of your choice for all samples, choose the 'A fiber content of your choice (basis 13% moisture) constant for all samples.' option in the drop-down menu for fiber content.

- A box prompting the user to enter a constant fiber content at a 13% moisture basis will appear at the bottom of this section.
- The model <u>will not run</u> if this box is empty.

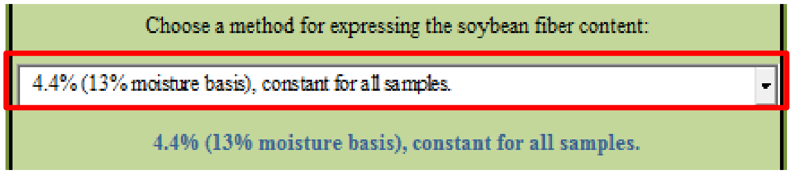

Choose a method for expressing the soybean fiber content:

A fiber content of your choice (basis 13% moisture) constant for all samples.

A fiber content of your choice (basis 13% moisture) constant for all samples.

Constant fiber content, basis 13% moisture: %

e. To assume a 4.4% fiber content for all samples, choose the '4.4% (13% moisture basis), constant for all samples.' option in the drop-down menu for fiber content.



Choose a method for expressing the soybean fiber content:

4.4% (13% moisture basis), constant for all samples.

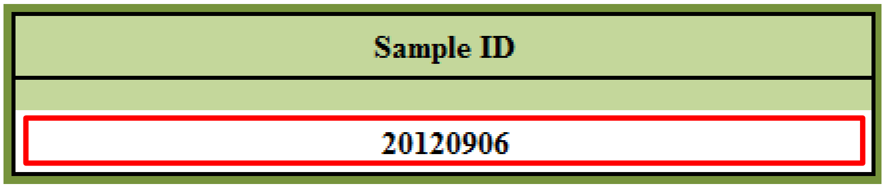
4.4% (13% moisture basis), constant for all samples.

8. Sample ID:

- This section contains the sample ID for each sample.
- The program will automatically increase the sample ID by 1 for each new sample.

a. Enter the sample ID for the sample in the white portion of the sample ID box.

- The program will run even if a sample ID is not specified.



Sample ID

20120906

9. Soybean Composition Data:

- This section contains all the soybean composition data used in the program.

a. If you are entering data from a data file, the 'YES' box for this option in the 'Input / Output Options' section <u>MUST</u> be selected.

- See section 6 (Input / Output Options) for instructions on how to change this option.

b. Choose the type of data file you are using from the drop-down menu for 'Type of Data File'.

- The program only supports <u>text files (.txt)</u> or <u>excel files (.xlsx)</u>

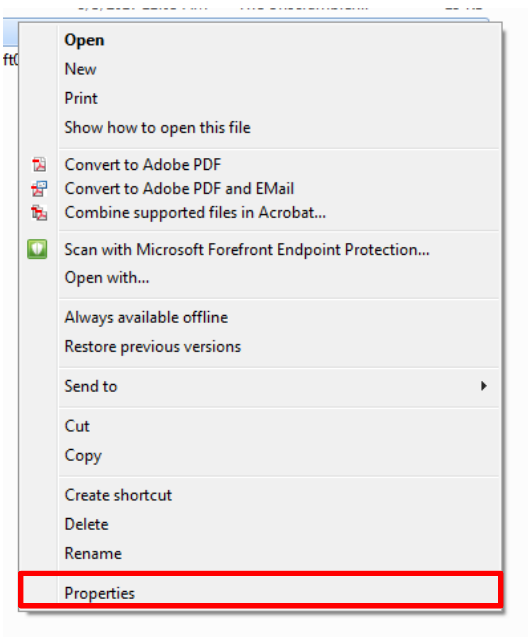
Type of File: Excel File (.xlsx)

c. Type the name of your file in the 'Data File Name' box.

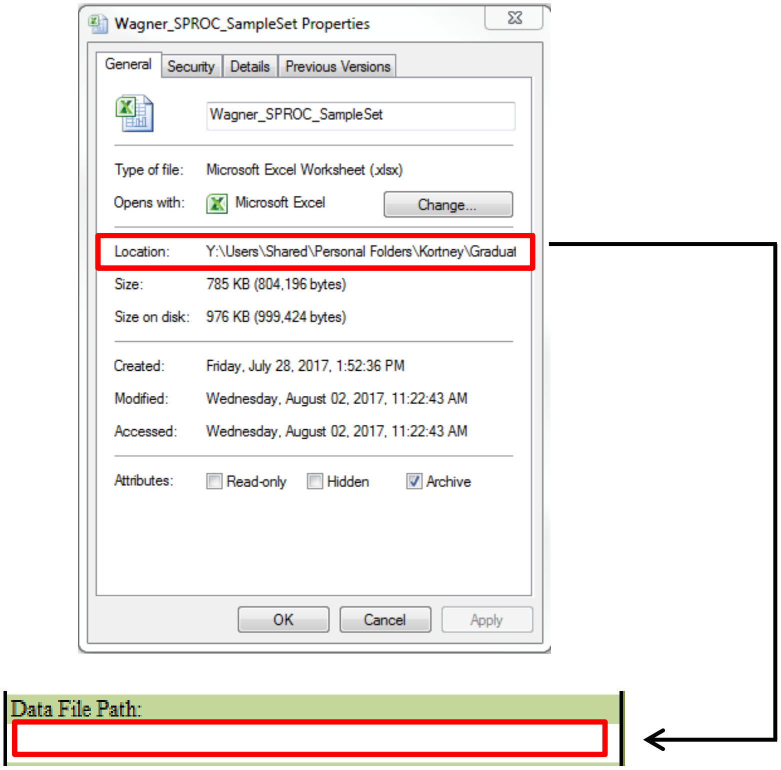
Data File Name:

d. Type the file path in the 'Data File Path' box.

- The file path of any file can typically be found by right-clicking on the file and choosing 'Properties'.



- The file path will be shown next to ‘Location’. Copy and paste that location into the ‘Data File Path’ box.



Wagner_SPROC_SampleSet

Type of file: Microsoft Excel Worksheet (.xlsx)

Opens with: Microsoft Excel

Location: Y:\Users\Shared\Personal Folders\Kortney\Graduat

Size: 785 KB (804,196 bytes)

Size on disk: 976 KB (999,424 bytes)

Created: Friday, July 28, 2017, 1:52:36 PM

Modified: Wednesday, August 02, 2017, 11:22:43 AM

Accessed: Wednesday, August 02, 2017, 11:22:43 AM

Attributes: ☐ Read-only ☐ Hidden ☑ Archive

Data File Path:

e. If you don’t have all the amino acid values for the samples, the program will automatically predict the amino acid concentrations based on the protein content of each sample.

- The program will only predict these values if this setting is ENABLED.
- See section 10 (Settings) for instructions on how to enable / disable this option.

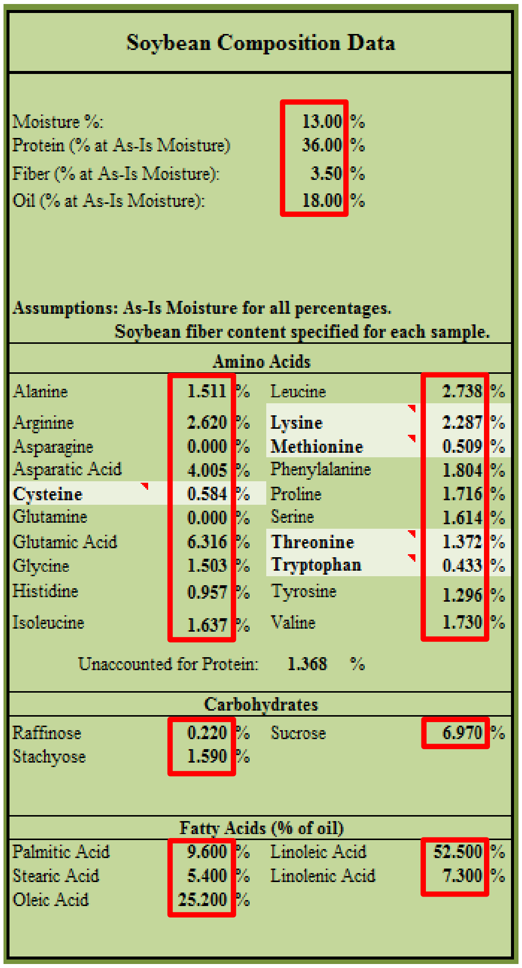
OR

f. If you are manually entering the soybean composition data, the ‘YES’ box for this option in the ‘Input / Output Options’ section MUST NOT be selected.

- See section 6 (Input / Output Options) for instructions on how to change this option.

g. Enter the values in percentages to the desired decimal place for the values requested.

- The program will only display up to three decimal places, but if more decimal places were entered, the entire value will be used in the program.
- The inputs will change based on the options chose in the ‘Soybean Composition Options’ section. See section 7 (Soybean Composition Options) for instructions on how to change these options.
- The highlighted amino acids are typically considered ‘limiting’ for swine diets.



Soybean Composition Data

Moisture %:	13.00	%
Protein (% at As-Is Moisture)	36.00	%
Fiber (% at As-Is Moisture):	3.50	%
Oil (% at As-Is Moisture):	18.00	%

Assumptions: As-Is Moisture for all percentages.
Soybean fiber content specified for each sample.

Amino Acids

Alanine	1.511	%	Leucine	2.738	%
Arginine	2.620	%	**Lysine**	2.287	%
Asparagine	0.000	%	**Methionine**	0.509	%
Asparatic Acid	4.005	%	Phenylalanine	1.804	%
Cysteine	0.584	%	Proline	1.716	%
Glutamine	0.000	%	Serine	1.614	%
Glutamic Acid	6.316	%	**Threonine**	1.372	%
Glycine	1.503	%	**Tryptophan**	0.433	%
Histidine	0.957	%	Tyrosine	1.296	%
Isoleucine	1.637	%	Valine	1.730	%

Unaccounted for Protein: 1.368 %

Carbohydrates

Raffinose	0.220	%	Sucrose	6.970	%
Stachyose	1.590	%			

Fatty Acids (% of oil)

Palmitic Acid	9.600	%	Linoleic Acid	52.500	%
Stearic Acid	5.400	%	Linolenic Acid	7.300	%
Oleic Acid	25.200	%			

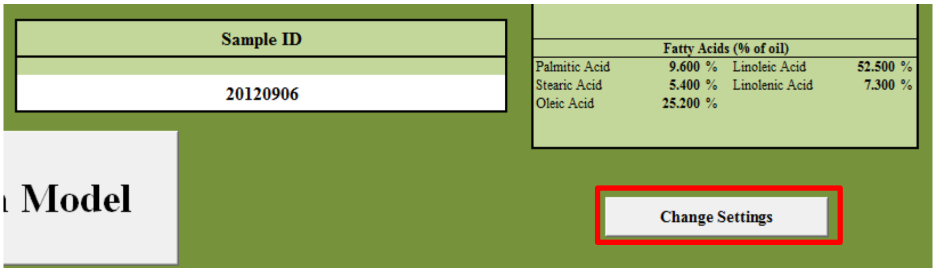
h. If amino acid concentrations are <u>unknown</u>, the program will automatically predict these values based on the protein percentage entered if this option is enabled.

- See section 10 (Settings) for instructions on how to enable / disable this option.

10. Settings:

- This section contains the different program settings that the user can adjust.

a. To adjust the program's settings, click the 'Change Settings' button in the bottom-right corner of the screen.



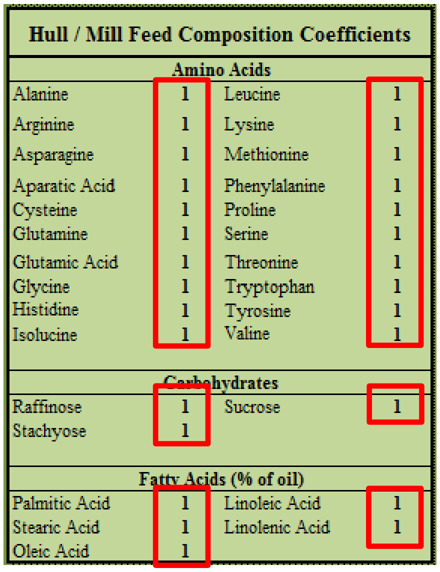
Sample ID
20120906

Fatty Acids (% of oil)

Palmitic Acid	9.600 %	Linoleic Acid	52.500 %
Stearic Acid	5.400 %	Linolenic Acid	7.300 %
Oleic Acid	25.200 %		

b. Hull / Mill Feed Composition Coefficients: This box allows the user to change the assumed composition of the hulls / mill feed. The program default assumes that the hulls have the same composition as the soybeans, so all the coefficients are defaulted at 1.

- Example: If the hulls are known to have half the amount of methionine as the soybeans, the user would change the methionine coefficient to 0.5.

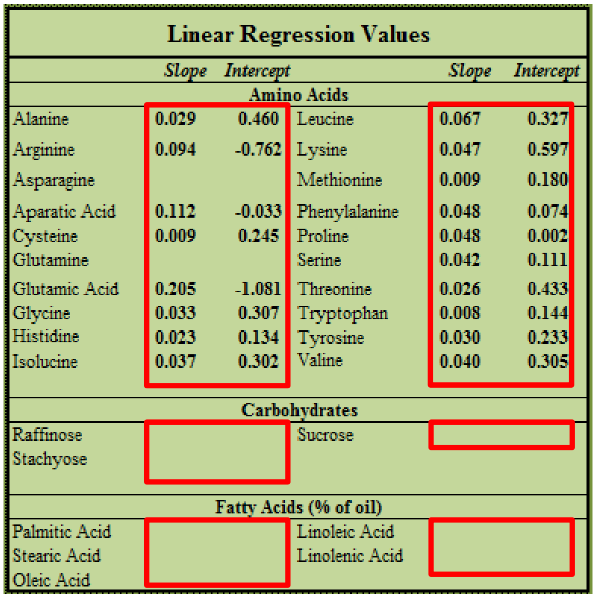


Hull / Mill Feed Composition Coefficients

Amino Acids			
Alanine	1	Leucine	1
Arginine	1	Lysine	1
Asparagine	1	Methionine	1
Aparatic Acid	1	Phenylalanine	1
Cysteine	1	Proline	1
Glutamine	1	Serine	1
Glutamic Acid	1	Threonine	1
Glycine	1	Tryptophan	1
Histidine	1	Tyrosine	1
Isolucine	1	Valine	1
Carbohydrates			
Raffinose	1	Sucrose	1
Stachyose	1		
Fatty Acids (% of oil)			
Palmitic Acid	1	Linoleic Acid	1
Stearic Acid	1	Linolenic Acid	1
Oleic Acid	1		

c. Linear Regression Values: This box allows the user to change the regression equations used to predict the amino acid values. The slope and intercept for each component can be changed which will change how the program predicts the concentrations.

- Slopes and intercepts for carbohydrates and fatty acids were left blank because there isn't a common correlation between these components. If the user knows these slope and intercept values, they should enter them in the corresponding boxes.

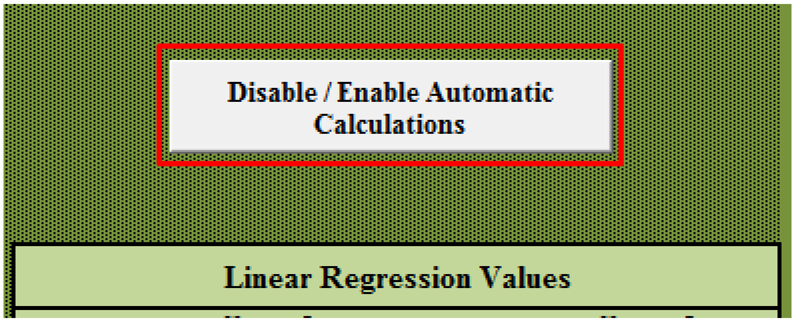


Linear Regression Values

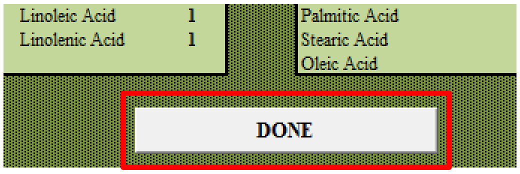
	Slope	*Intercept*		*Slope*	*Intercept*
Amino Acids					
Alanine	0.029	0.460	Leucine	0.067	0.327
Arginine	0.094	-0.762	Lysine	0.047	0.597
Asparagine			Methionine	0.009	0.180
Aparatic Acid	0.112	-0.033	Phenylalanine	0.048	0.074
Cysteine	0.009	0.245	Proline	0.048	0.002
Glutamine			Serine	0.042	0.111
Glutamic Acid	0.205	-1.081	Threonine	0.026	0.433
Glycine	0.033	0.307	Tryptophan	0.008	0.144
Histidine	0.023	0.134	Tyrosine	0.030	0.233
Isolucine	0.037	0.302	Valine	0.040	0.305
Carbohydrates					
Raffinose			Sucrose		
Stachyose					
Fatty Acids (% of oil)					
Palmitic Acid			Linoleic Acid		
Stearic Acid			Linolenic Acid		
Oleic Acid					

d. To enable / disable the prediction equations, click the 'Disable / Enable Automatic Calculations' button above the 'Linear Regression Values' box.

- If the calculations are <u>DISABLED</u>, all amino acid values <u>MUST</u> be manually entered in the 'Soybean Composition Data' box. See section 9 (Soybean Composition Data) for instructions on how to manually enter the data.



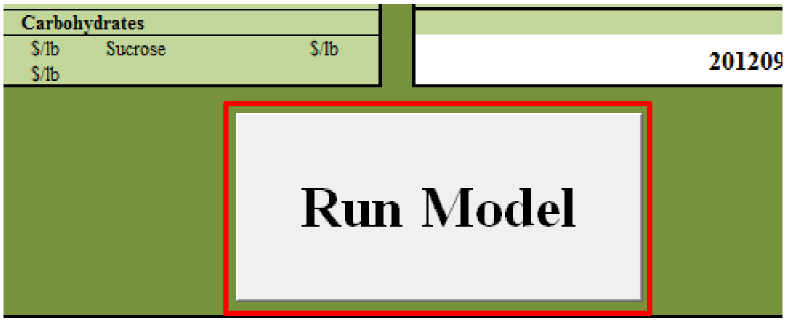
e. To exit the settings, click the 'DONE' button at the bottom of the screen.


Linoleic Acid 1
Linolenic Acid 1
Palmitic Acid
Stearic Acid
Oleic Acid

RUNNING THE MODEL

A. Run Model:

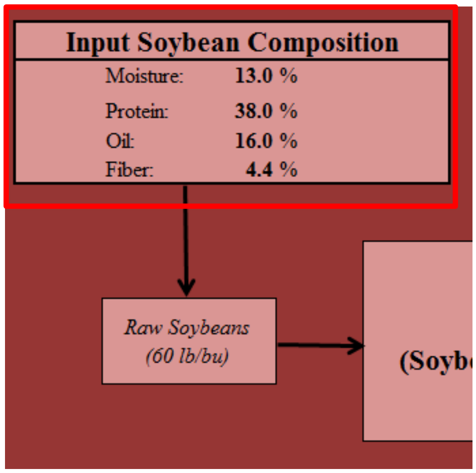
1. Once all the inputs have been put into the model, the program can be run by clicking on the 'RUN MODEL' button on the bottom of the 'Inputs' tab. This will run the program.


Carbohydrates
$/lb Sucrose $/lb
$/lb
201209

2. Once the 'Run Model' button has been clicked, the program will run and you will be automatically directed to the 'Outputs' tab to view the results.
   - If the option to send data to the printer is chosen in the 'Input / Output Options' box, then the program will automatically direct to the 'Report Sheet' tab and a printer box will appear on the screen.

B. Outputs Tab:

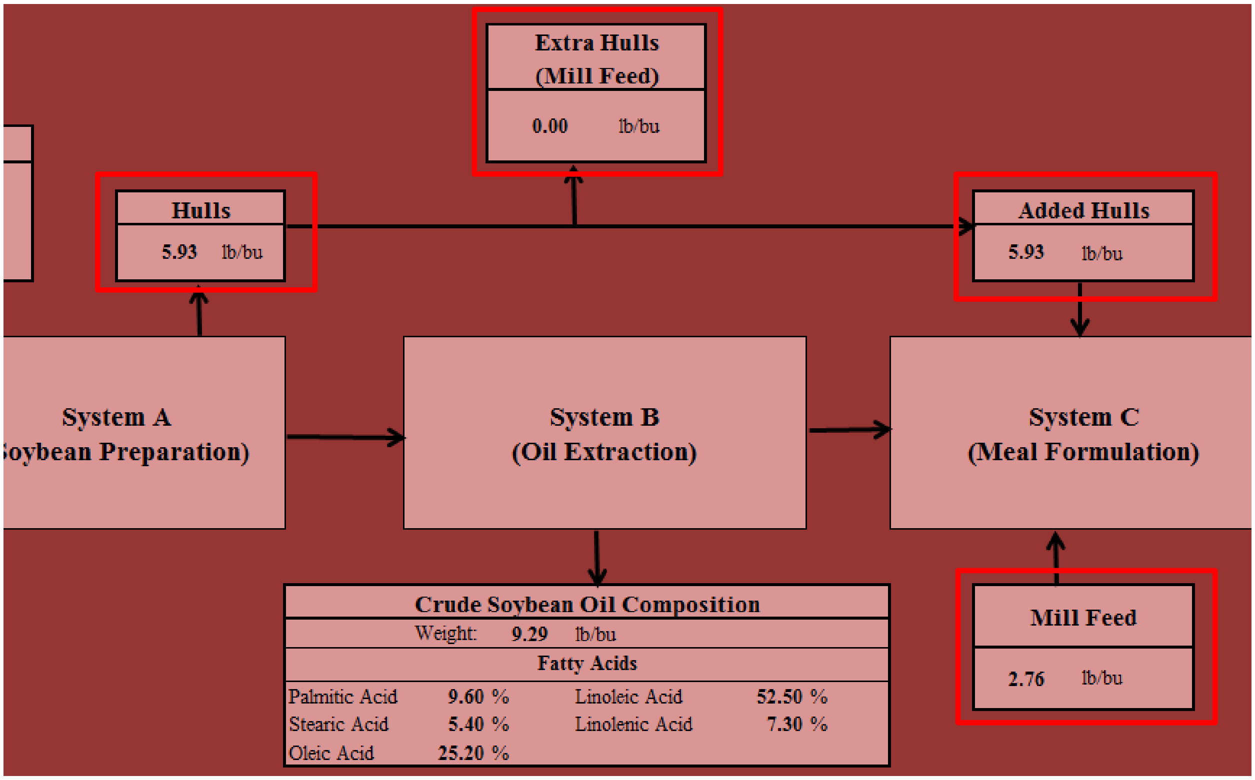
1. The 'Outputs' tab shows the majority of the model results in a flow diagram format.
   a. Input Soybean Composition: Found at the left of the screen. This box displays the moisture, protein, oil, and fiber contents that were entered on the 'Inputs' tab.
      - The entered amino acid, carbohydrate, and fatty acid profiles are only shown on the 'Report Sheet' tab.



Input Soybean Composition

Moisture:	13.0 %
Protein:	38.0 %
Oil:	16.0 %
Fiber:	4.4 %

b. Hulls / Mill Feed: Found in the center of the screen. The total removed hulls is found exiting system A. The extra hulls or mill feed is found underneath the Total EPV box. The added hulls that were reformulated into the soybean meal are found above the system C box. If any mill feed was needed, that amount is found below the system C box.



Extra Hulls (Mill Feed)
0.00 lb/bu

Hulls
5.93 lb/bu

Added Hulls
5.93 lb/bu

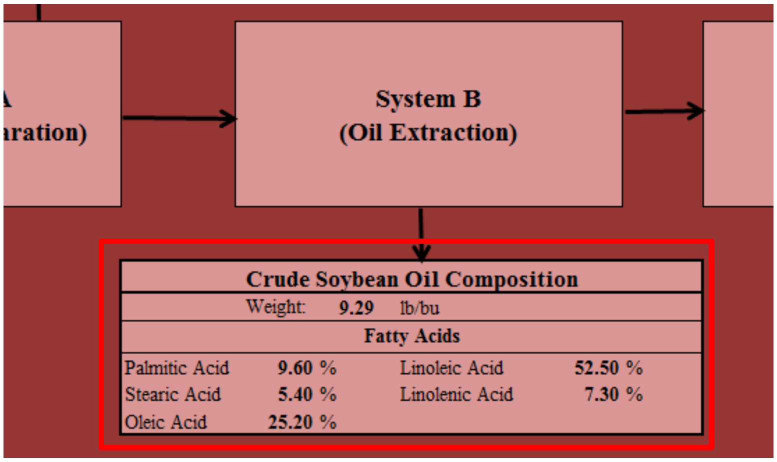
Mill Feed
2.76 lb/bu

Crude Soybean Oil Composition
Weight: 9.29 lb/bu

Fatty Acids

Palmitic Acid	9.60 %	Linoleic Acid	52.50 %
Stearic Acid	5.40 %	Linolenic Acid	7.30 %
Oleic Acid	25.20 %		

c. Crude Soybean Oil Composition: Found at the bottom of the screen. This displays the total oil yield and composition of the oil.



Crude Soybean Oil Composition

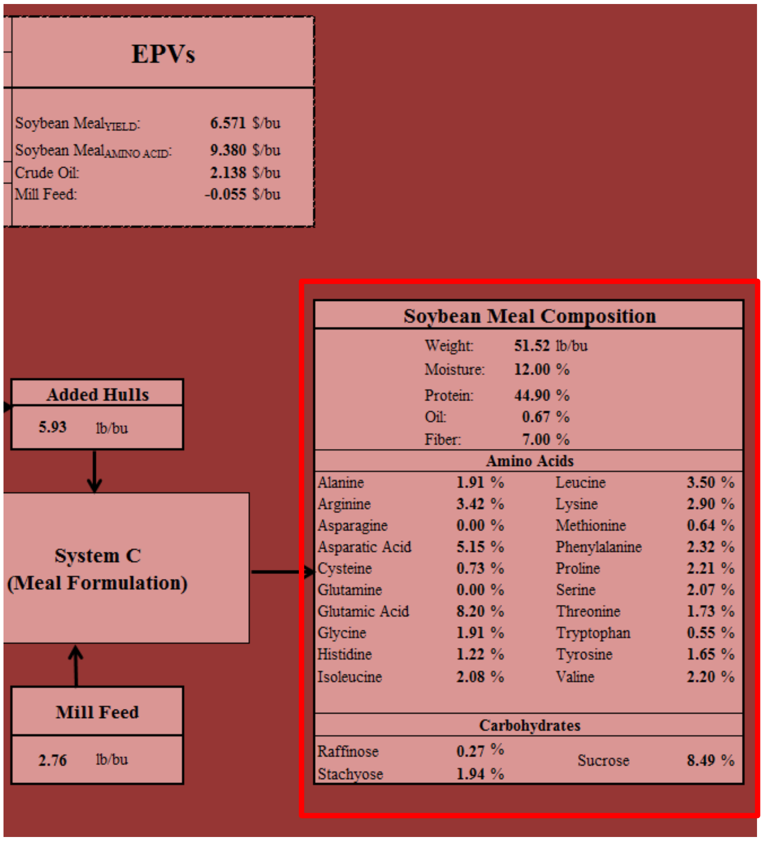
Weight: **9.29** lb/bu

Fatty Acids

Palmitic Acid	**9.60** %	Linoleic Acid	**52.50** %
Stearic Acid	**5.40** %	Linolenic Acid	**7.30** %
Oleic Acid	**25.20** %		

d. Soybean Meal Composition: Found at the right of the screen. This displays the yield and composition of the soybean meal.

- Most of these values are copied into the U.S. Pork Center of Excellence, National Swine Nutrition Guide feed formulation software, if that option is chosen.
- See section 7 (Input / Output Options) under **Inputs Tab** for instructions on how to choose this option.



EPVs

Soybean Meal$_{YIELD}$:	**6.571** $/bu
Soybean Meal$_{AMINO\ ACID}$:	**9.380** $/bu
Crude Oil:	**2.138** $/bu
Mill Feed:	**-0.055** $/bu

Soybean Meal Composition

Weight: **51.52** lb/bu
Moisture: **12.00** %
Protein: **44.90** %
Oil: **0.67** %
Fiber: **7.00** %

Amino Acids

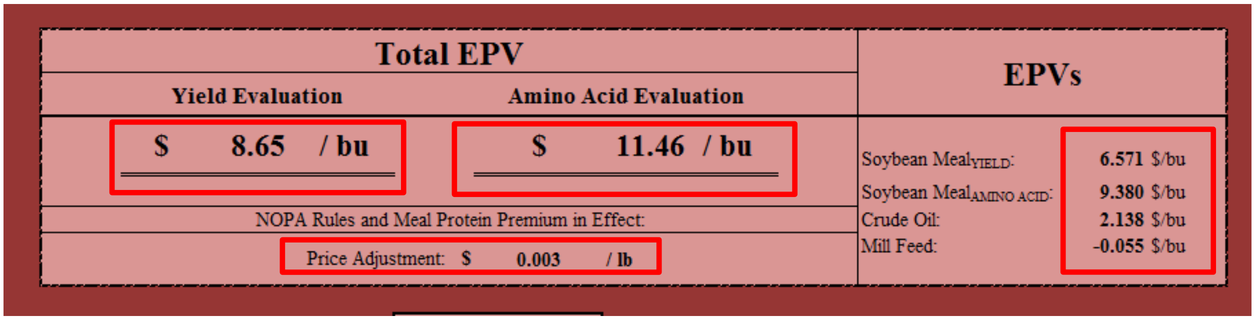
Alanine	**1.91** %	Leucine	**3.50** %
Arginine	**3.42** %	Lysine	**2.90** %
Asparagine	**0.00** %	Methionine	**0.64** %
Asparatic Acid	**5.15** %	Phenylalanine	**2.32** %
Cysteine	**0.73** %	Proline	**2.21** %
Glutamine	**0.00** %	Serine	**2.07** %
Glutamic Acid	**8.20** %	Threonine	**1.73** %
Glycine	**1.91** %	Tryptophan	**0.55** %
Histidine	**1.22** %	Tyrosine	**1.65** %
Isoleucine	**2.08** %	Valine	**2.20** %

Carbohydrates

Raffinose	**0.27** %	Sucrose	**8.49** %
Stachyose	**1.94** %		

e. Total EPV / EPVs: Found at the top of the screen. This displays the EPV ($/bu) for both the yield and amino acid evaluations. This also displays the individual EPVs for all the extraction products. If NOPA trading rules or protein premiums are used, the effective price adjustment will be displayed at the bottom of this box.

- Yield Evaluation: Accounts for the total soybean meal yield and current market price for determination.
- Amino Acid Evaluation: Accounts for the content of amino acids and the current market price for the corresponding commercially produced synthetic amino acid.



Total EPV

Yield Evaluation	Amino Acid Evaluation
$ 8.65 / bu	$ 11.46 / bu

NOPA Rules and Meal Protein Premium in Effect:

Price Adjustment: $ 0.003 / lb

EPVs

Soybean Meal$_{YIELD}$:	6.571 $/bu
Soybean Meal$_{AMINO\ ACID}$:	9.380 $/bu
Crude Oil:	2.138 $/bu
Mill Feed:	-0.055 $/bu

C. Report Sheet Tab:

1. This sheet is separated into 5 separate sections: Input Soybean Composition, Soybean Meal Composition, Crude Oil, Evaluations, and Swine Feed Formulation.
   - The categories in this sheet are color coded based on the type of result:

Color Coding

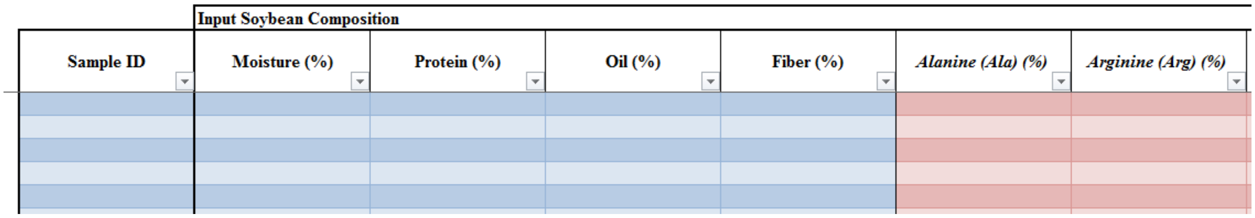
1. Blue = Proximate Analysis (Moisture, Protein, Oil, Fiber) (%), Yields (lb/bu), EPVs ($/bu)

2. Red = Amino Acid Concentrations (%)

3. Green = Fatty Acid Concentrations (%)

4. Orange = Carbohydrate Concentrations (%)

5. Purple = Feed Formulation Results



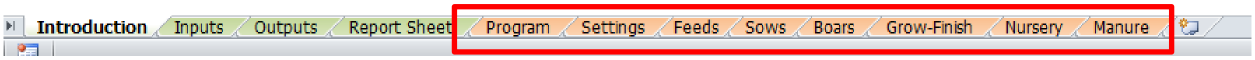
Input Soybean Composition

Sample ID	Moisture (%)	Protein (%)	Oil (%)	Fiber (%)	*Alanine (Ala) (%)*	*Arginine (Arg) (%)*

RUNNING THE FEED FORMULATION SOFTWARE

A. Use the Pre-Formulated Diet:

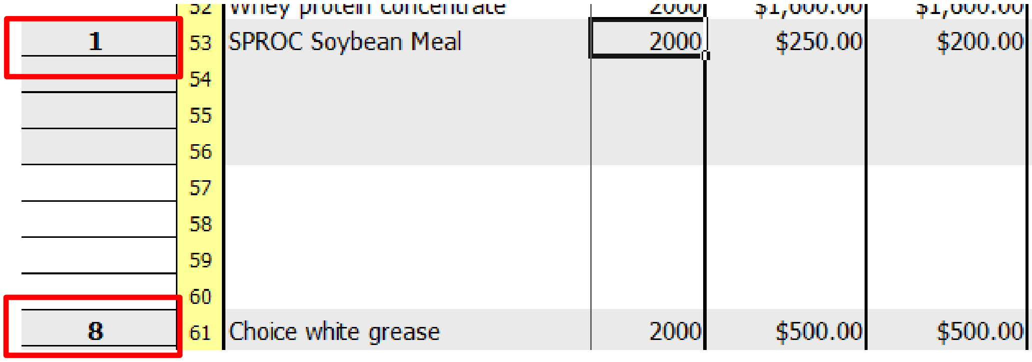
1. If the option to 'Connect to Swine Feed Formulation Software' is chosen, when the model is run it will automatically formulate a diet and the results will appear in the 'Report Sheet' tab.
   - The feed formulation tabs will appear at the bottom of the screen, colored orange.
   - The pre-formulated diet includes the following ingredients: Corn – yellow dent, SPROC Soybean Meal, Choice White Grease, L-Lysine HCl, DL-Methionine, L-Threonine, L-Tryptophan, L-Valine, Monocalcium Phosphate 21%, Limestone, Salt.
   - The diet is formulated for 'Grow-Finish' swine, and all assumptions can be found on the 'Grow-Finish' tab.



OR

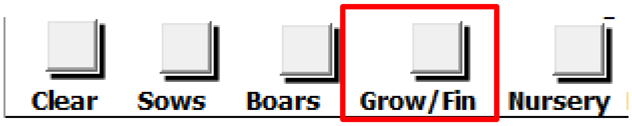
B. Use a Customized Diet:

1. Choose Custom Ingredients:
   a. Select the 'Feeds' tab.
   b. Scroll down to the desired feed and double-click in the far left column to add the feed to your formulation.
      - The composition of the ingredients is found by scrolling to the right.
      - The number indicates the order that the ingredients get added to the diet.

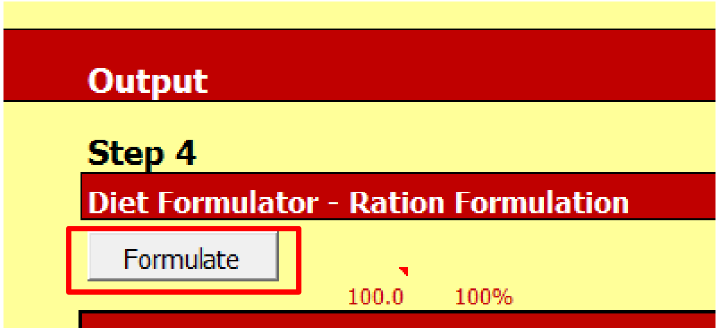


	52	Whey protein concentrate	2000	$1,000.00	$1,000.00
1	53	SPROC Soybean Meal	2000	$250.00	$200.00
	54				
	55				
	56				
	57				
	58				
	59				
	60				
8	61	Choice white grease	2000	$500.00	$500.00

2. Formulate the Diet:
   a. Select the 'Grow / Finish' button at the top of the screen.



b. Execute the formulation by clicking the ‘Grow-Finish’ tab at the bottom of the screen and clicking the ‘Formulate’ button under STEP 4 on this tab.

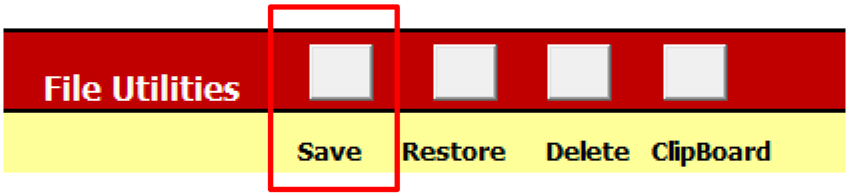


3. Saving and Restoring the Feed Library:

a. To save results, scroll to the top of the ‘Grow-Finish’ tab and give the file a name in the drop down box.

Producer: SPROC USER
Phone #: 0
0
Date: 8/16/2017
File Name:

b. Click the ‘Save’ button.



4. Repeat steps 1-3 for all desired formulations.

APPENDIX B: SPROC 3.0 VBA CODE

```
Sub SPROC_Code()

'Checks input sheet for missing data before running the rest of the code
For Each Rng In
Worksheets("Inputs").Range("G7:G12,G19:G21,G28:G30,G32:G35,K19:K21,N19,AC17:AC26,
AG17:AG26,AC30:AC31,AG30:AG31,AC35:AC37,AG35:AG36")
   If IsEmpty(Rng.Value) Then
      UserForm1.Hide  'Hides the progress bar
      Application.StatusBar = False
      MsgBox ("Please enter data in all the red boxes.")
      Exit Sub
   End If
Next

If Worksheets("Inputs").Range("V7") = "No Data File" And
((IsEmpty(Worksheets("Inputs").Range("AE8").Value) = True) Or
(IsEmpty(Worksheets("Inputs").Range("AE10").Value) = True)) Then
   UserForm1.Hide  'Hides the progress bar
   Application.StatusBar = False
   MsgBox ("Please enter data in all the red boxes.")
   Exit Sub
ElseIf Worksheets("Inputs").Range("V7") = "No Data File" And
Worksheets("Inputs").Range("V21") = "*As-Is Moisture" And
IsEmpty(Worksheets("Inputs").Range("AE7").Value) = True Then
   UserForm1.Hide  'Hides the progress bar
   Application.StatusBar = False
   MsgBox ("Please enter data in all the red boxes.")
   Exit Sub
ElseIf Worksheets("Inputs").Range("V7") = "No Data File" And
Worksheets("Inputs").Range("Q26") = "A fiber content specified for each sample at the moisture
basis specified above." _
      And IsEmpty(Worksheets("Inputs").Range("AE9").Value) = True Then
         UserForm1.Hide  'Hides the progress bar
         Application.StatusBar = False
         MsgBox ("Please enter data in all the red boxes.")
         Exit Sub
ElseIf Worksheets("Inputs").Range("V7") = "No Data File" And
Worksheets("Inputs").Range("Q26") = "A fiber content of your choice (basis 13% moisture)
constant for all samples." _
      And IsEmpty(Worksheets("Inputs").Range("W29").Value) = True Then
         UserForm1.Hide  'Hides the progress bar
         Application.StatusBar = False
         MsgBox ("Please enter data in all the red boxes.")
         Exit Sub
```

```
ElseIf Worksheets("Inputs").Range("V7") = "Enter From Data File" And
((IsEmpty(Worksheets("Inputs").Range("AF7").Value) = True) Or _
        (IsEmpty(Worksheets("Inputs").Range("AA11").Value) = True) Or
(IsEmpty(Worksheets("Inputs").Range("AA13").Value) = True)) Then
    UserForm1.Hide  'Hides the progress bar
    Application.StatusBar = False
    MsgBox ("Please enter your file name, path, and type into the composition data box.")
    Exit Sub
End If


'----------------------------------------------------------------------------------------------------

'Sets status bar to in progress while program is running
Application.StatusBar = "Please wait... calculations in progress."

'----------------------------------------------------------------------------------------------------

'Reads data from data file if that input option is chosen
On Error GoTo ErrorHandler
Dim file_data() As Variant
If Worksheets("Inputs").Range("V7") = "Enter From Data File" Then
    If Worksheets("Inputs").Range("AF7") = "Text File (.txt)" Then
        If Worksheets("Inputs").Range("AF8") = "AA = NO" And
Worksheets("Inputs").Range("AF9") = "Carb = NO" And Worksheets("Inputs").Range("AF10")
= "FA = NO" Then

            VariableNum = 5

        ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And
Worksheets("Inputs").Range("AF9") = "Carb = NO" And Worksheets("Inputs").Range("AF10")
= "FA = NO" Then

            VariableNum = 25

        ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And
Worksheets("Inputs").Range("AF9") = "Carb = YES" And
Worksheets("Inputs").Range("AF10") = "FA = NO" Then

            VariableNum = 29

        ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And
Worksheets("Inputs").Range("AF9") = "Carb = NO" And Worksheets("Inputs").Range("AF10")
= "FA = YES" Then

            VariableNum = 30
```

```
    ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And
Worksheets("Inputs").Range("AF9") = "Carb = YES" And
Worksheets("Inputs").Range("AF10") = "FA = YES" Then

      VariableNum = 34

    ElseIf Worksheets("Inputs").Range("AF8") = "AA = NO" And
Worksheets("Inputs").Range("AF9") = "Carb = YES" And
Worksheets("Inputs").Range("AF10") = "FA = NO" Then

      VariableNum = 9

    ElseIf Worksheets("Inputs").Range("AF8") = "AA = NO" And
Worksheets("Inputs").Range("AF9") = "Carb = NO" And Worksheets("Inputs").Range("AF10")
= "FA = YES" Then

      VariableNum = 10

    ElseIf Worksheets("Inputs").Range("AF8") = "AA = NO" And
Worksheets("Inputs").Range("AF9") = "Carb = YES" And
Worksheets("Inputs").Range("AF10") = "FA = YES" Then

      VariableNum = 14

    End If

    ReDim file_data(VariableNum, 700) As Variant

    file_name = Worksheets("Inputs").Range("AA11")     'Reads the file path
    file_path = Worksheets("Inputs").Range("AA13")     'Reads the file name

    file = file_path + "\" + file_name + ".txt"        'Concatenates string of file name and path

    Open file For Input As #1                          'Opens the correct file for use

    N = -1                                  'Sets n = -1 so that the column titles will be stored as
sample_number 0
    i = 1

    Do Until EOF(1)
      N = N + 1

      Line Input #1, LineFromFile                  'Reads the first line of the text file
      LineItems = Split(LineFromFile, vbTab)       'Splits the line into each variable
```

```
            For i = 1 To VariableNum
                file_data(i, N) = LineItems(i - 1)          'Saves each variable into the array
            Next i

        Loop

        Close #1

    End If

    If Worksheets("Inputs").Range("AF7") = "Excel File (.xlsx)" Then
        If Worksheets("Inputs").Range("AF8") = "AA = NO" And Worksheets("Inputs").Range("AF9") = "Carb = NO" And Worksheets("Inputs").Range("AF10") = "FA = NO" Then

            VariableNum = 5

        ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And Worksheets("Inputs").Range("AF9") = "Carb = NO" And Worksheets("Inputs").Range("AF10") = "FA = NO" Then

            VariableNum = 25

        ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And Worksheets("Inputs").Range("AF9") = "Carb = YES" And Worksheets("Inputs").Range("AF10") = "FA = YES" Then

            VariableNum = 34

        ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And Worksheets("Inputs").Range("AF9") = "Carb = YES" And Worksheets("Inputs").Range("AF10") = "FA = NO" Then

            VariableNum = 29

        ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And Worksheets("Inputs").Range("AF9") = "Carb = NO" And Worksheets("Inputs").Range("AF10") = "FA = YES" Then

            VariableNum = 30

        ElseIf Worksheets("Inputs").Range("AF8") = "AA = NO" And Worksheets("Inputs").Range("AF9") = "Carb = YES" And Worksheets("Inputs").Range("AF10") = "FA = NO" Then

            VariableNum = 9
```

```
    ElseIf Worksheets("Inputs").Range("AF8") = "AA = NO" And
Worksheets("Inputs").Range("AF9") = "Carb = NO" And Worksheets("Inputs").Range("AF10")
= "FA = YES" Then

      VariableNum = 10

    ElseIf Worksheets("Inputs").Range("AF8") = "AA = NO" And
Worksheets("Inputs").Range("AF9") = "Carb = YES" And
Worksheets("Inputs").Range("AF10") = "FA = YES" Then

      VariableNum = 14

    End If


    Dim OpenWB As Workbook
    ReDim file_data(VariableNum, 700) As Variant

    file_name = Worksheets("Inputs").Range("AA11")      'Reads the file path
    file_path = Worksheets("Inputs").Range("AA13")      'Reads the file name

    file = file_path + "\" + file_name + ".xlsx"        'Concatenates string of file name and path

    Application.ScreenUpdating = False                  'Stops screen from updating
    Set OpenWB = Workbooks.Open(file)                      'Opens source data file

    N = Excel.Application.Cells.SpecialCells(xlLastCell).Row

    For r = 1 To N
      For c = 1 To VariableNum
        file_data(c, r - 1) = Workbooks(file_name).Worksheets("Sheet1").Cells(r, c)
      Next c
    Next r

    N = N - 1

    OpenWB.Close (True)                             'Closes source data file
    Application.ScreenUpdating = True                   'Restarts screen updating

  End If
Else
  N = 1                                         'Sets n = 1 if data is manually entered (this is used in
loop below to determine how many times to run the code)

End If
```

```
sample_number = N                                   'Saves number of samples into variable
"sample_number"

progress 10 'Sets progress bar to 10%

'----------------------------------------------------------------------------------------------------------
i = 0

On Error GoTo ErrorHandler_2

Do

'Sets the file data into the correct input cells
If Worksheets("Inputs").Range("V7") = "Enter From Data File" Then

    If Worksheets("Inputs").Range("AF8") = "AA = NO" And
Worksheets("Inputs").Range("AF9") = "Carb = NO" And Worksheets("Inputs").Range("AF10")
= "FA = NO" Then
        Worksheets("Inputs").Range("Q36") = file_data(1, i + 1)
        Worksheets("Inputs").Range("AE7") = file_data(2, i + 1)
        Worksheets("Inputs").Range("AE8") = file_data(3, i + 1)
        Worksheets("Inputs").Range("AE9") = file_data(4, i + 1)
        Worksheets("Inputs").Range("AE10") = file_data(5, i + 1)

    ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And
Worksheets("Inputs").Range("AF9") = "Carb = NO" And Worksheets("Inputs").Range("AF10")
= "FA = NO" Then

        Worksheets("Inputs").Range("AQ18") = "DISABLED"

        Worksheets("Inputs").Range("Q36") = file_data(1, i + 1)
        Worksheets("Inputs").Range("AE7") = file_data(2, i + 1)
        Worksheets("Inputs").Range("AE8") = file_data(3, i + 1)
        Worksheets("Inputs").Range("AE9") = file_data(4, i + 1)
        Worksheets("Inputs").Range("AE10") = file_data(5, i + 1)

        Worksheets("Inputs").Range("AC17") = file_data(6, i + 1)
        Worksheets("Inputs").Range("AC18") = file_data(7, i + 1)
        Worksheets("Inputs").Range("AC19") = file_data(8, i + 1)
        Worksheets("Inputs").Range("AC20") = file_data(9, i + 1)
        Worksheets("Inputs").Range("AC21") = file_data(10, i + 1)
        Worksheets("Inputs").Range("AC22") = file_data(11, i + 1)
        Worksheets("Inputs").Range("AC23") = file_data(12, i + 1)
        Worksheets("Inputs").Range("AC24") = file_data(13, i + 1)
        Worksheets("Inputs").Range("AC25") = file_data(14, i + 1)
```

```
        Worksheets("Inputs").Range("AC26") = file_data(15, i + 1)
        Worksheets("Inputs").Range("AG17") = file_data(16, i + 1)
        Worksheets("Inputs").Range("AG18") = file_data(17, i + 1)
        Worksheets("Inputs").Range("AG19") = file_data(18, i + 1)
        Worksheets("Inputs").Range("AG20") = file_data(19, i + 1)
        Worksheets("Inputs").Range("AG21") = file_data(20, i + 1)
        Worksheets("Inputs").Range("AG22") = file_data(21, i + 1)
        Worksheets("Inputs").Range("AG23") = file_data(22, i + 1)
        Worksheets("Inputs").Range("AG24") = file_data(23, i + 1)
        Worksheets("Inputs").Range("AG25") = file_data(24, i + 1)
        Worksheets("Inputs").Range("AG26") = file_data(25, i + 1)

        Worksheets("Inputs").Range("AQ18") = ""

    ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And
Worksheets("Inputs").Range("AF9") = "Carb = YES" And
Worksheets("Inputs").Range("AF10") = "FA = NO" Then

        Worksheets("Inputs").Range("AQ18") = "DISABLED"

        Worksheets("Inputs").Range("Q36") = file_data(1, i + 1)
        Worksheets("Inputs").Range("AE7") = file_data(2, i + 1)
        Worksheets("Inputs").Range("AE8") = file_data(3, i + 1)
        Worksheets("Inputs").Range("AE9") = file_data(4, i + 1)
        Worksheets("Inputs").Range("AE10") = file_data(5, i + 1)

        Worksheets("Inputs").Range("AC17") = file_data(6, i + 1)
        Worksheets("Inputs").Range("AC18") = file_data(7, i + 1)
        Worksheets("Inputs").Range("AC19") = file_data(8, i + 1)
        Worksheets("Inputs").Range("AC20") = file_data(9, i + 1)
        Worksheets("Inputs").Range("AC21") = file_data(10, i + 1)
        Worksheets("Inputs").Range("AC22") = file_data(11, i + 1)
        Worksheets("Inputs").Range("AC23") = file_data(12, i + 1)
        Worksheets("Inputs").Range("AC24") = file_data(13, i + 1)
        Worksheets("Inputs").Range("AC25") = file_data(14, i + 1)
        Worksheets("Inputs").Range("AC26") = file_data(15, i + 1)
        Worksheets("Inputs").Range("AG17") = file_data(16, i + 1)
        Worksheets("Inputs").Range("AG18") = file_data(17, i + 1)
        Worksheets("Inputs").Range("AG19") = file_data(18, i + 1)
        Worksheets("Inputs").Range("AG20") = file_data(19, i + 1)
        Worksheets("Inputs").Range("AG21") = file_data(20, i + 1)
        Worksheets("Inputs").Range("AG22") = file_data(21, i + 1)
        Worksheets("Inputs").Range("AG23") = file_data(22, i + 1)
        Worksheets("Inputs").Range("AG24") = file_data(23, i + 1)
        Worksheets("Inputs").Range("AG25") = file_data(24, i + 1)
        Worksheets("Inputs").Range("AG26") = file_data(25, i + 1)
```

```
        Worksheets("Inputs").Range("AC30") = file_data(26, i + 1)
        Worksheets("Inputs").Range("AC31") = file_data(27, i + 1)
        Worksheets("Inputs").Range("AG30") = file_data(28, i + 1)
        Worksheets("Inputs").Range("AG31") = file_data(29, i + 1)

        Worksheets("Inputs").Range("AQ18") = ""

    ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And
Worksheets("Inputs").Range("AF9") = "Carb = NO" And Worksheets("Inputs").Range("AF10")
= "FA = YES" Then

        Worksheets("Inputs").Range("AQ18") = "DISABLED"

        Worksheets("Inputs").Range("Q36") = file_data(1, i + 1)
        Worksheets("Inputs").Range("AE7") = file_data(2, i + 1)
        Worksheets("Inputs").Range("AE8") = file_data(3, i + 1)
        Worksheets("Inputs").Range("AE9") = file_data(4, i + 1)
        Worksheets("Inputs").Range("AE10") = file_data(5, i + 1)

        Worksheets("Inputs").Range("AC17") = file_data(6, i + 1)
        Worksheets("Inputs").Range("AC18") = file_data(7, i + 1)
        Worksheets("Inputs").Range("AC19") = file_data(8, i + 1)
        Worksheets("Inputs").Range("AC20") = file_data(9, i + 1)
        Worksheets("Inputs").Range("AC21") = file_data(10, i + 1)
        Worksheets("Inputs").Range("AC22") = file_data(11, i + 1)
        Worksheets("Inputs").Range("AC23") = file_data(12, i + 1)
        Worksheets("Inputs").Range("AC24") = file_data(13, i + 1)
        Worksheets("Inputs").Range("AC25") = file_data(14, i + 1)
        Worksheets("Inputs").Range("AC26") = file_data(15, i + 1)
        Worksheets("Inputs").Range("AG17") = file_data(16, i + 1)
        Worksheets("Inputs").Range("AG18") = file_data(17, i + 1)
        Worksheets("Inputs").Range("AG19") = file_data(18, i + 1)
        Worksheets("Inputs").Range("AG20") = file_data(19, i + 1)
        Worksheets("Inputs").Range("AG21") = file_data(20, i + 1)
        Worksheets("Inputs").Range("AG22") = file_data(21, i + 1)
        Worksheets("Inputs").Range("AG23") = file_data(22, i + 1)
        Worksheets("Inputs").Range("AG24") = file_data(23, i + 1)
        Worksheets("Inputs").Range("AG25") = file_data(24, i + 1)
        Worksheets("Inputs").Range("AG26") = file_data(25, i + 1)

        Worksheets("Inputs").Range("AC35") = file_data(26, i + 1)
        Worksheets("Inputs").Range("AC36") = file_data(27, i + 1)
        Worksheets("Inputs").Range("AC37") = file_data(28, i + 1)
        Worksheets("Inputs").Range("AG35") = file_data(29, i + 1)
        Worksheets("Inputs").Range("AG36") = file_data(30, i + 1)
```

```
    Worksheets("Inputs").Range("AQ18") = ""

  ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And
Worksheets("Inputs").Range("AF9") = "Carb = YES" And
Worksheets("Inputs").Range("AF10") = "FA = YES" Then

    Worksheets("Inputs").Range("AQ18") = "DISABLED"

    Worksheets("Inputs").Range("Q36") = file_data(1, i + 1)
    Worksheets("Inputs").Range("AE7") = file_data(2, i + 1)
    Worksheets("Inputs").Range("AE8") = file_data(3, i + 1)
    Worksheets("Inputs").Range("AE9") = file_data(4, i + 1)
    Worksheets("Inputs").Range("AE10") = file_data(5, i + 1)

    Worksheets("Inputs").Range("AC17") = file_data(6, i + 1)
    Worksheets("Inputs").Range("AC18") = file_data(7, i + 1)
    Worksheets("Inputs").Range("AC19") = file_data(8, i + 1)
    Worksheets("Inputs").Range("AC20") = file_data(9, i + 1)
    Worksheets("Inputs").Range("AC21") = file_data(10, i + 1)
    Worksheets("Inputs").Range("AC22") = file_data(11, i + 1)
    Worksheets("Inputs").Range("AC23") = file_data(12, i + 1)
    Worksheets("Inputs").Range("AC24") = file_data(13, i + 1)
    Worksheets("Inputs").Range("AC25") = file_data(14, i + 1)
    Worksheets("Inputs").Range("AC26") = file_data(15, i + 1)
    Worksheets("Inputs").Range("AG17") = file_data(16, i + 1)
    Worksheets("Inputs").Range("AG18") = file_data(17, i + 1)
    Worksheets("Inputs").Range("AG19") = file_data(18, i + 1)
    Worksheets("Inputs").Range("AG20") = file_data(19, i + 1)
    Worksheets("Inputs").Range("AG21") = file_data(20, i + 1)
    Worksheets("Inputs").Range("AG22") = file_data(21, i + 1)
    Worksheets("Inputs").Range("AG23") = file_data(22, i + 1)
    Worksheets("Inputs").Range("AG24") = file_data(23, i + 1)
    Worksheets("Inputs").Range("AG25") = file_data(24, i + 1)
    Worksheets("Inputs").Range("AG26") = file_data(25, i + 1)

    Worksheets("Inputs").Range("AC30") = file_data(26, i + 1)
    Worksheets("Inputs").Range("AC31") = file_data(27, i + 1)
    Worksheets("Inputs").Range("AG30") = file_data(28, i + 1)
    Worksheets("Inputs").Range("AG31") = file_data(29, i + 1)

    Worksheets("Inputs").Range("AC35") = file_data(30, i + 1)
    Worksheets("Inputs").Range("AC36") = file_data(31, i + 1)
    Worksheets("Inputs").Range("AC37") = file_data(32, i + 1)
    Worksheets("Inputs").Range("AG35") = file_data(33, i + 1)
    Worksheets("Inputs").Range("AG36") = file_data(34, i + 1)
```

```
        Worksheets("Inputs").Range("AQ18") = ""

    ElseIf Worksheets("Inputs").Range("AF8") = "AA = NO" And
Worksheets("Inputs").Range("AF9") = "Carb = NO" And Worksheets("Inputs").Range("AF10")
= "FA = YES" Then

        Worksheets("Inputs").Range("Q36") = file_data(1, i + 1)
        Worksheets("Inputs").Range("AE7") = file_data(2, i + 1)
        Worksheets("Inputs").Range("AE8") = file_data(3, i + 1)
        Worksheets("Inputs").Range("AE9") = file_data(4, i + 1)
        Worksheets("Inputs").Range("AE10") = file_data(5, i + 1)

        Worksheets("Inputs").Range("AC35") = file_data(6, i + 1)
        Worksheets("Inputs").Range("AC36") = file_data(7, i + 1)
        Worksheets("Inputs").Range("AC37") = file_data(8, i + 1)
        Worksheets("Inputs").Range("AG35") = file_data(9, i + 1)
        Worksheets("Inputs").Range("AG36") = file_data(10, i + 1)

        Worksheets("Inputs").Range("AQ18") = ""

    ElseIf Worksheets("Inputs").Range("AF8") = "AA = NO" And
Worksheets("Inputs").Range("AF9") = "Carb = YES" And
Worksheets("Inputs").Range("AF10") = "FA = NO" Then

        Worksheets("Inputs").Range("Q36") = file_data(1, i + 1)
        Worksheets("Inputs").Range("AE7") = file_data(2, i + 1)
        Worksheets("Inputs").Range("AE8") = file_data(3, i + 1)
        Worksheets("Inputs").Range("AE9") = file_data(4, i + 1)
        Worksheets("Inputs").Range("AE10") = file_data(5, i + 1)

        Worksheets("Inputs").Range("AC30") = file_data(6, i + 1)
        Worksheets("Inputs").Range("AC31") = file_data(7, i + 1)
        Worksheets("Inputs").Range("AG30") = file_data(8, i + 1)
        Worksheets("Inputs").Range("AG31") = file_data(9, i + 1)

        Worksheets("Inputs").Range("AQ18") = ""

    ElseIf Worksheets("Inputs").Range("AF8") = "AA = NO" And
Worksheets("Inputs").Range("AF9") = "Carb = YES" And
Worksheets("Inputs").Range("AF10") = "FA = YES" Then

        Worksheets("Inputs").Range("Q36") = file_data(1, i + 1)
        Worksheets("Inputs").Range("AE7") = file_data(2, i + 1)
        Worksheets("Inputs").Range("AE8") = file_data(3, i + 1)
        Worksheets("Inputs").Range("AE9") = file_data(4, i + 1)
```

```
        Worksheets("Inputs").Range("AE10") = file_data(5, i + 1)

        Worksheets("Inputs").Range("AC30") = file_data(6, i + 1)
        Worksheets("Inputs").Range("AC31") = file_data(7, i + 1)
        Worksheets("Inputs").Range("AG30") = file_data(8, i + 1)
        Worksheets("Inputs").Range("AG31") = file_data(9, i + 1)

        Worksheets("Inputs").Range("AC35") = file_data(10, i + 1)
        Worksheets("Inputs").Range("AC36") = file_data(11, i + 1)
        Worksheets("Inputs").Range("AC37") = file_data(12, i + 1)
        Worksheets("Inputs").Range("AG35") = file_data(13, i + 1)
        Worksheets("Inputs").Range("AG36") = file_data(14, i + 1)

        Worksheets("Inputs").Range("AQ18") = ""

    End If

    Worksheets("Report Sheet").Activate
    ActiveSheet.Range("A1").Select
End If

ClearOutputs 'Clears "Outputs" sheet

'Set sample number:
    SampleID = Worksheets("Inputs").Range("Q36")

'System A, B, & C Parameter INPUTS:
    Wa = 60
    DMLa = Worksheets("Inputs").Range("G12").Value
    Pah = Worksheets("Inputs").Range("G7").Value
    ph1 = Worksheets("Inputs").Range("G8").Value
    ph2 = Worksheets("Inputs").Range("G9").Value
    ph3 = Worksheets("Inputs").Range("G10").Value
    Ph5 = Worksheets("Inputs").Range("G11").Value
    Pc1 = Worksheets("Inputs").Range("G19").Value
    Pc3 = Worksheets("Inputs").Range("G20").Value
    DMLc = Worksheets("Inputs").Range("G21").Value
    Pd1 = Worksheets("Inputs").Range("G28").Value
    Pd2spec = Worksheets("Inputs").Range("G29").Value
    Pd5spec = Worksheets("Inputs").Range("G30").Value 'Can be From NOPA trading rules
(3.5%)
    Pf1 = Worksheets("Inputs").Range("G32").Value
    Pf2 = Worksheets("Inputs").Range("G33").Value
    Pf3 = Worksheets("Inputs").Range("G34").Value
    Pf5 = Worksheets("Inputs").Range("G35").Value
```

```
'Current Prices Inputs
    PriceOil = Worksheets("Inputs").Range("K19").Value
    PriceOil_Premium = Worksheets("Inputs").Range("N19").Value
    PriceMeal = Worksheets("Inputs").Range("K20").Value
    PriceHMF = Worksheets("Inputs").Range("K21").Value

    Price_Ala = Worksheets("Inputs").Range("K24").Value
    Price_Arg = Worksheets("Inputs").Range("K25").Value
    Price_Asn = Worksheets("Inputs").Range("K26").Value
    Price_Asp = Worksheets("Inputs").Range("K27").Value
    Price_Cys = Worksheets("Inputs").Range("K28").Value
    Price_Gln = Worksheets("Inputs").Range("K29").Value
    Price_Glu = Worksheets("Inputs").Range("K30").Value
    Price_Gly = Worksheets("Inputs").Range("K31").Value
    Price_His = Worksheets("Inputs").Range("K32").Value
    Price_Ile = Worksheets("Inputs").Range("K33").Value
    Price_Leu = Worksheets("Inputs").Range("N24").Value
    Price_Lys = Worksheets("Inputs").Range("N25").Value
    Price_Met = Worksheets("Inputs").Range("N26").Value
    Price_Phe = Worksheets("Inputs").Range("N27").Value
    Price_Pro = Worksheets("Inputs").Range("N28").Value
    Price_Ser = Worksheets("Inputs").Range("N29").Value
    Price_Thr = Worksheets("Inputs").Range("N30").Value
    Price_Trp = Worksheets("Inputs").Range("N31").Value
    Price_Tyr = Worksheets("Inputs").Range("N32").Value
    Price_Val = Worksheets("Inputs").Range("N33").Value

    Price_Raffinose = Worksheets("Inputs").Range("K36").Value
    Price_Stachyose = Worksheets("Inputs").Range("K37").Value
    Price_Sucrose = Worksheets("Inputs").Range("N36").Value

'Amino Acid Inputs:
    Ala_In = Worksheets("Inputs").Range("AC17").Value
    Arg_In = Worksheets("Inputs").Range("AC18").Value
    Asn_In = Worksheets("Inputs").Range("AC19").Value
    Asp_In = Worksheets("Inputs").Range("AC20").Value
    Cys_In = Worksheets("Inputs").Range("AC21").Value
    Gln_In = Worksheets("Inputs").Range("AC22").Value
    Glu_In = Worksheets("Inputs").Range("AC23").Value
    Gly_In = Worksheets("Inputs").Range("AC24").Value
    His_In = Worksheets("Inputs").Range("AC25").Value
    Ile_In = Worksheets("Inputs").Range("AC26").Value
    Leu_In = Worksheets("Inputs").Range("AG17").Value
    Lys_In = Worksheets("Inputs").Range("AG18").Value
    Met_In = Worksheets("Inputs").Range("AG19").Value
    Phe_In = Worksheets("Inputs").Range("AG20").Value
```

```
    Pro_In = Worksheets("Inputs").Range("AG21").Value
    Ser_In = Worksheets("Inputs").Range("AG22").Value
    Thr_In = Worksheets("Inputs").Range("AG23").Value
    Trp_In = Worksheets("Inputs").Range("AG24").Value
    Tyr_In = Worksheets("Inputs").Range("AG25").Value
    Valine_In = Worksheets("Inputs").Range("AG26").Value

'Carbohydrate Inputs:
    Raffinose_In = Worksheets("Inputs").Range("AC30").Value
    Stachyose_In = Worksheets("Inputs").Range("AC31").Value
    Sucrose_In = Worksheets("Inputs").Range("AG30").Value
    OtherCarb_In = Worksheets("Inputs").Range("AG31").Value

'Fatty Acid Inputs:
    Palmitic_In = Worksheets("Inputs").Range("AC35").Value
    Stearic_In = Worksheets("Inputs").Range("AC36").Value
    Oleic_In = Worksheets("Inputs").Range("AC37").Value
    Linoleic_In = Worksheets("Inputs").Range("AG35").Value
    Linolenic_In = Worksheets("Inputs").Range("AG36").Value

'Hull Composition Coefficient Inputs:
    Ala_Co = Worksheets("Inputs").Range("AL24").Value
    Arg_Co = Worksheets("Inputs").Range("AL25").Value
    Asn_Co = Worksheets("Inputs").Range("AL26").Value
    Asp_Co = Worksheets("Inputs").Range("AL27").Value
    Cys_Co = Worksheets("Inputs").Range("AL28").Value
    Gln_Co = Worksheets("Inputs").Range("AL29").Value
    Glu_Co = Worksheets("Inputs").Range("AL30").Value
    Gly_Co = Worksheets("Inputs").Range("AL31").Value
    His_Co = Worksheets("Inputs").Range("AL32").Value
    Ile_Co = Worksheets("Inputs").Range("AL33").Value
    Leu_Co = Worksheets("Inputs").Range("AO24").Value
    Lys_Co = Worksheets("Inputs").Range("AO25").Value
    Met_Co = Worksheets("Inputs").Range("AO26").Value
    Phe_Co = Worksheets("Inputs").Range("AO27").Value
    Pro_Co = Worksheets("Inputs").Range("AO28").Value
    Ser_Co = Worksheets("Inputs").Range("AO29").Value
    Thr_Co = Worksheets("Inputs").Range("AO30").Value
    Trp_Co = Worksheets("Inputs").Range("AO31").Value
    Tyr_Co = Worksheets("Inputs").Range("AO32").Value
    Valine_Co = Worksheets("Inputs").Range("AO33").Value

    Raffinose_Co = Worksheets("Inputs").Range("AL36").Value
    Stachyose_Co = Worksheets("Inputs").Range("AL37").Value
    Sucrose_Co = Worksheets("Inputs").Range("AO36").Value
    OtherCarb_Co = Worksheets("Inputs").Range("AO37").Value
```

```
   Palmitic_Co = Worksheets("Inputs").Range("AL40").Value
   Stearic_Co = Worksheets("Inputs").Range("AL41").Value
   Oleic_Co = Worksheets("Inputs").Range("AL42").Value
   Linoleic_Co = Worksheets("Inputs").Range("AO40").Value
   Linolenic_Co = Worksheets("Inputs").Range("AO41").Value

'Soybean Composition INPUTS:
   Pa2 = Worksheets("Inputs").Range("AE8").Value
   Pa3 = Worksheets("Inputs").Range("AE10").Value

   'Determines correct value for moisture % based on moisture basis chosen.
   If Worksheets("Inputs").Range("V21").Value = "13% Moisture" Then
      Pa1 = 13
      Worksheets("Inputs").Range("AE7") = ""
   Else
      Pa1 = Worksheets("Inputs").Range("AE7").Value
   End If

   'Determines correct value for fiber % based on fiber content chosen.
   If Worksheets("Inputs").Range("Q26").Value = "A fiber content specified for each sample at
the moisture basis specified above." Then
      Pa5 = Worksheets("Inputs").Range("AE9").Value
   ElseIf Worksheets("Inputs").Range("Q26").Value = "A fiber content of your choice (basis
13% moisture) constant for all samples." Then
      Pa5 = Worksheets("Inputs").Range("W29").Value
      Worksheets("Inputs").Range("AE9") = ""
   Else
      Pa5 = 4.4 'Default fiber value for 13% moisture basis.
      Worksheets("Inputs").Range("AE9") = ""
   End If

progress 20 'Sets progress bar to 20%

'----------------------------------------------------------------------------------------------------

'Converting the AA, Carb, and FA values to hull components using the HULL COEFFICIENTS:

'Amino Acid Inputs:
   Ala_Hulls = Ala_In * Ala_Co
   Arg_Hulls = Arg_In * Arg_Co
   Asn_Hulls = Asn_In * Asn_Co
   Asp_Hulls = Asp_In * Asp_Co
   Asx_Hulls = Asx_In * Asx_Co
   Cys_Hulls = Cys_In * Cys_Co
   Gln_Hulls = Gln_In * Gln_Co
```

```
   Glu_Hulls = Glu_In * Glu_Co
   Glx_Hulls = Glx_In * Glx_Co
   Gly_Hulls = Gly_In * Gly_Co
   His_Hulls = His_In * His_Co
   Ile_Hulls = Ile_In * Ile_Co
   Leu_Hulls = Leu_In * Leu_Co
   Lys_Hulls = Lys_In * Lys_Co
   Met_Hulls = Met_In * Met_Co
   Phe_Hulls = Phe_In * Phe_Co
   Pro_Hulls = Pro_In * Pro_Co
   Ser_Hulls = Ser_In * Ser_Co
   Thr_Hulls = Thr_In * Thr_Co
   Trp_Hulls = Trp_In * Trp_Co
   Tyr_Hulls = Tyr_In * Tyr_Co
   Valine_Hulls = Valine_In * Valine_Co

'Carbohydrate Inputs:
   Raffinose_Hulls = Raffinose_In * Raffinose_Co
   Stachyose_Hulls = Stachyose_In * Stachyose_Co
   Sucrose_Hulls = Sucrose_In * Sucrose_Co
   OtherCarb_Hulls = OtherCarb_In * OtherCarb_Co

'Fatty Acid Inputs:
   Palmitic_Hulls = Palmitic_In * Palmitic_Co
   Stearic_Hulls = Stearic_In * Stearic_Co
   Oleic_Hulls = Oleic_In * Oleic_Co
   Linoleic_Hulls = Linoleic_In * Linoleic_Co
   Linolenic_Hulls = Linolenic_In * Linolenic_Co

'-------------------------------------------------------------------------------------------------------------------

'Converting to DRY-WEIGHT BASIS:

   Wa = Wa * (1 - (Pa1 / 100))
   Pa2 = Pa2 / (1 - (Pa1 / 100))
   Pa3 = Pa3 / (1 - (Pa1 / 100))
   Pa5 = Pa5 / (1 - (Pa1 / 100))

   ph2 = ph2 / (1 - (ph1 / 100))
   ph3 = ph3 / (1 - (ph1 / 100))
   Ph5 = Ph5 / (1 - (ph1 / 100))

   Pc3 = Pc3 / (1 - (Pc1 / 100))

   Pf2 = Pf2 / (1 - (Pf1 / 100))
   Pf3 = Pf3 / (1 - (Pf1 / 100))
```

```
Pf5 = Pf5 / (1 - (Pf1 / 100))

Pd2max = Pd2spec / (1 - (Pd1 / 100))
Pd5max = Pd5spec / (1 - (Pd1 / 100))

Ala = Ala_In / (1 - (Pa1 / 100))
arg = Arg_In / (1 - (Pa1 / 100))
Asn = Asn_In / (1 - (Pa1 / 100))
Asp = Asp_In / (1 - (Pa1 / 100))
cys = Cys_In / (1 - (Pa1 / 100))
Gln = Gln_In / (1 - (Pa1 / 100))
Glu = Glu_In / (1 - (Pa1 / 100))
Gly = Gly_In / (1 - (Pa1 / 100))
his = His_In / (1 - (Pa1 / 100))
ile = Ile_In / (1 - (Pa1 / 100))
leu = Leu_In / (1 - (Pa1 / 100))
lys = Lys_In / (1 - (Pa1 / 100))
met = Met_In / (1 - (Pa1 / 100))
phe = Phe_In / (1 - (Pa1 / 100))
pro = Pro_In / (1 - (Pa1 / 100))
Ser = Ser_In / (1 - (Pa1 / 100))
thr = Thr_In / (1 - (Pa1 / 100))
trp = Trp_In / (1 - (Pa1 / 100))
tyr = Tyr_In / (1 - (Pa1 / 100))
valine = Valine_In / (1 - (Pa1 / 100))

Raffinose = Raffinose_In / (1 - (Pa1 / 100))
Stachyose = Stachyose_In / (1 - (Pa1 / 100))
Sucrose = Sucrose_In / (1 - (Pa1 / 100))
OtherCarb = OtherCarb_In / (1 - (Pa1 / 100))

Ala_Hulls = Ala_Hulls / (1 - (ph1 / 100))
Arg_Hulls = Arg_Hulls / (1 - (ph1 / 100))
Asn_Hulls = Asn_Hulls / (1 - (ph1 / 100))
Asp_Hulls = Asp_Hulls / (1 - (ph1 / 100))
Asx_Hulls = Asx_Hulls / (1 - (ph1 / 100))
Cys_Hulls = Cys_Hulls / (1 - (ph1 / 100))
Gln_Hulls = Gln_Hulls / (1 - (ph1 / 100))
Glu_Hulls = Glu_Hulls / (1 - (ph1 / 100))
Glx_Hulls = Glx_Hulls / (1 - (ph1 / 100))
Gly_Hulls = Gly_Hulls / (1 - (ph1 / 100))
His_Hulls = His_Hulls / (1 - (ph1 / 100))
Ile_Hulls = Ile_Hulls / (1 - (ph1 / 100))
Leu_Hulls = Leu_Hulls / (1 - (ph1 / 100))
Lys_Hulls = Lys_Hulls / (1 - (ph1 / 100))
Met_Hulls = Met_Hulls / (1 - (ph1 / 100))
```

```
    Phe_Hulls = Phe_Hulls / (1 - (ph1 / 100))
    Pro_Hulls = Pro_Hulls / (1 - (ph1 / 100))
    Ser_Hulls = Ser_Hulls / (1 - (ph1 / 100))
    Thr_Hulls = Thr_Hulls / (1 - (ph1 / 100))
    Trp_Hulls = Trp_Hulls / (1 - (ph1 / 100))
    Tyr_Hulls = Tyr_Hulls / (1 - (ph1 / 100))
    Valine_Hulls = Valine_Hulls / (1 - (ph1 / 100))

    Raffinose_Hulls = Raffinose_Hulls / (1 - (ph1 / 100))
    Stachyose_Hulls = Stachyose_Hulls / (1 - (ph1 / 100))
    Sucrose_Hulls = Sucrose_Hulls / (1 - (ph1 / 100))
    OtherCarb_Hulls = OtherCarb_Hulls / (1 - (ph1 / 100))

'----------------------------------------------------------------------------------------------------

'SYSTEM A (SOYBEAN PREPARATION):

'Mass Calculations:
    WaNet = Wa * (1 - (DMLa / 100))
    Wh = WaNet * (Pah / 100)
    Wb = WaNet - Wh

'Protein Calculations:
    Pb2 = (WaNet * Pa2 - Wh * ph2) / Wb

'Oil Calculations:
    Pb3 = (WaNet * Pa3 - Wh * ph3) / Wb

'Fiber Calculations:
    Pb5 = (WaNet * Pa5 - Wh * Ph5) / Wb

'----------------------------------------------------------------------------------------------------

'SYSTEM B (SOLVENT EXTRACTION):

'Oil Calculations:
    Wo = (Wb * (Pb3 - Pc3)) / (100 - Pc3)

'Mass Calculations:
    Wc = (Wb - Wo) * (1 - (DMLc / 100))

'Protein Calculations:
    Pc2 = (Wb * Pb2) / Wc

'Fiber Calculations:
    Pc5 = (Wb * Pb5) / Wc
```

```
'Product Weight for System C:
   W1c = Wc

progress 30 'Sets progress bar to 30%
'----------------------------------------------------------------------------------------------------------

'SYSTEM C (MEAL FORMULATION FOR SOYBEAN MEAL):
   'Note: The protein content of the meal (Pd2) is intially set equal to the deisred protein content (Pd2spec).
   '      This may change depending on the amount of hulls that can be blended back. Steps I and II are initially performed as if hulls are not blended in.

Pd2 = Pd2max
Mode = "SystemC_1"
W1f = 0
W1h = 0

Do While Mode <> "DONE"
Select Case Mode
   Case "SystemC_1"
      If Pd2 <= Pc2 Then 'Can the protein specification be met?
         Mode = "SystemC_2"
      Else
         Pd2 = Pc2
         Pd5 = Pc5
         W1h = 0 'Weight of hulls added to soybean meal
         W1f = 0 'Weight of mill feed added to soybean meal
         W1d = W1c
         Mode = "DONE"
      End If

   Case "SystemC_2"
      If Pd5max >= Pc5 Then 'Can the fiber specification be met?
         Mode = "SystemC_3"
      Else
         Pd2 = Pc2
         Pd5 = Pc5
         W1h = 0 'Weight of hulls added to soybean meal
         W1f = 0 'Weight of mill feed added to soybean meal
         W1d = W1c
         Mode = "DONE"
      End If

   Case "SystemC_3"
      'Protein Calculations:
```

```
            W1d = (W1c * (Pc2 - ph2)) / (Pd2 - ph2)

        'Mass Calculations:
            W1h = W1d - W1c

        If W1h <= Wh Then 'How much hulls were added? Less than the amount removed in
dehulling?
            Mode = "SystemC_5"
        Else
            W1h = Wh
            Mode = "SystemC_4"
        End If

    Case "SystemC_4"
       'Add mill feed to meet the protein specification
        'Protein Calculations:
            W1d = (W1c * (Pc2 - Pf2) + W1h * (ph2 - Pf2)) / (Pd2 - Pf2)

        'Mass Calculations:
            W1f = W1d - W1c - W1h
            Mode = "SystemC_5"

    Case "SystemC_5"
        'Hulls (and possible mill feed) are added to meet the protein specification.
        'Fiber Calculations:
            Pd5 = (W1c * Pc5 + W1h * Ph5 + W1f * Pf5) / W1d

        If Pd5 <= Pd5max Then
            Mode = "DONE"
        Else
            Mode = "SystemC_6"  'Recalculate based on the fiber limit in step 4.
        End If

    Case "SystemC_6"
        'Recalculate meal formation based on fiber limit.
        Pd5 = Pd5max
        'Fiber Calculations:
            W1d = (W1c * (Pc5 - Pf5) + W1h * (Ph5 - Pf5)) / (Pd5 - Pf5)

        'Mass Calculations:
            W1f = W1d - W1c - W1h

        'Can we add any filler?
        If W1f >= 0 Then
            Mode = "SystemC_7"
        Else
```

```
         W1f = 0
         'Recalculate on fiber limit using hulls only.
         'Mass Calculations:
            W1d = W1c * (Pc5 - Ph5) / (Pd5 - Ph5)
            W1h = W1d - W1c
            Mode = "SystemC_7"
      End If

   Case "SystemC_7"
      'Calculate protein content after adding hulls/mill feed to meet the fiber specification.
      'Protein Calculations:
         Pd2 = (W1c * Pc2 + W1h * ph2 + W1f * Pf2) / W1d
         Mode = "DONE"

   Case Else
      MsgBox "Problem with code. Proper mode was not selected."
      Mode = "DONE"

End Select
Loop

'Soybean Meal Oil Calculation:
   Pd3 = (W1c * Pc3 + W1h * ph3 + W1f * Pf3) / W1d

progress 40 'Sets progress bar to 40%

'---------------------------------------------------------------------------------------------------------

'AMINO ACID & CARBOHYDRATE COMPOSITION VALUES:

Ala = ((WaNet * Ala) - ((Wh - W1h) * Ala_Hulls) + (W1f * Ala_Hulls)) / W1d
arg = ((WaNet * arg) - ((Wh - W1h) * Arg_Hulls) + (W1f * Arg_Hulls)) / W1d
Asn = ((WaNet * Asn) - ((Wh - W1h) * Asn_Hulls) + (W1f * Asn_Hulls)) / W1d
Asp = ((WaNet * Asp) - ((Wh - W1h) * Asp_Hulls) + (W1f * Asp_Hulls)) / W1d
cys = ((WaNet * cys) - ((Wh - W1h) * Cys_Hulls) + (W1f * Cys_Hulls)) / W1d
Gln = ((WaNet * Gln) - ((Wh - W1h) * Gln_Hulls) + (W1f * Gln_Hulls)) / W1d
Glu = ((WaNet * Glu) - ((Wh - W1h) * Glu_Hulls) + (W1f * Glu_Hulls)) / W1d
Gly = ((WaNet * Gly) - ((Wh - W1h) * Gly_Hulls) + (W1f * Gly_Hulls)) / W1d
his = ((WaNet * his) - ((Wh - W1h) * His_Hulls) + (W1f * His_Hulls)) / W1d
ile = ((WaNet * ile) - ((Wh - W1h) * Ile_Hulls) + (W1f * Ile_Hulls)) / W1d
leu = ((WaNet * leu) - ((Wh - W1h) * Leu_Hulls) + (W1f * Leu_Hulls)) / W1d
lys = ((WaNet * lys) - ((Wh - W1h) * Lys_Hulls) + (W1f * Lys_Hulls)) / W1d
met = ((WaNet * met) - ((Wh - W1h) * Met_Hulls) + (W1f * Met_Hulls)) / W1d
phe = ((WaNet * phe) - ((Wh - W1h) * Phe_Hulls) + (W1f * Phe_Hulls)) / W1d
pro = ((WaNet * pro) - ((Wh - W1h) * Pro_Hulls) + (W1f * Pro_Hulls)) / W1d
Ser = ((WaNet * Ser) - ((Wh - W1h) * Ser_Hulls) + (W1f * Ser_Hulls)) / W1d
```

```
thr = ((WaNet * thr) - ((Wh - W1h) * Thr_Hulls) + (W1f * Thr_Hulls)) / W1d
trp = ((WaNet * trp) - ((Wh - W1h) * Trp_Hulls) + (W1f * Trp_Hulls)) / W1d
tyr = ((WaNet * tyr) - ((Wh - W1h) * Tyr_Hulls) + (W1f * Tyr_Hulls)) / W1d
valine = ((WaNet * valine) - ((Wh - W1h) * Valine_Hulls) + (W1f * Valine_Hulls)) / W1d

Raffinose = ((WaNet * Raffinose) - ((Wh - W1h) * Raffinose_Hulls) + (W1f * Raffinose_Hulls)) / W1d
Stachyose = ((WaNet * Stachyose) - ((Wh - W1h) * Stachyose_Hulls) + (W1f * Stachyose_Hulls)) / W1d
Sucrose = ((WaNet * Sucrose) - ((Wh - W1h) * Sucrose_Hulls) + (W1f * Sucrose_Hulls)) / W1d
OtherCarb = ((WaNet * OtherCarb) - ((Wh - W1h) * OtherCarb_Hulls) + (W1f * OtherCarb_Hulls)) / W1d

'-----------------------------------------------------------------------------------------------------

'ESTIMATED PROCESSED VALUE (EPV):

'Convert $/ton to $/lb:
    PriceMeal = PriceMeal / 2000
    PriceOil = PriceOil + PriceOil_Premium

Mode = "EPV_1"

Do While Mode <> "DONE"
Select Case Mode

    Case "EPV_1"
        'Converting to AS-IS WEIGHT BASIS:

        W1d = W1d / (1 - (Pd1 / 100))

        Wa = Wa / (1 - (Pa1 / 100))
        Pa2 = Pa2 * (1 - (Pa1 / 100))
        Pa3 = Pa3 * (1 - (Pa1 / 100))
        Pa5 = Pa5 * (1 - (Pa1 / 100))

        Pd2 = Pd2 * (1 - (Pd1 / 100))
        Pd3 = Pd3 * (1 - (Pd1 / 100))
        Pd5 = Pd5 * (1 - (Pd1 / 100))

        Wh = Wh / (1 - (ph1 / 100))
        W1h = W1h / (1 - (ph1 / 100))

        W1f = W1f / (1 - (Pf1 / 100))

        Ala = Ala * (1 - (Pd1 / 100))
```

```
    arg = arg * (1 - (Pd1 / 100))
    Asn = Asn * (1 - (Pd1 / 100))
    Asp = Asp * (1 - (Pd1 / 100))
    cys = cys * (1 - (Pd1 / 100))
    Gln = Gln * (1 - (Pd1 / 100))
    Glu = Glu * (1 - (Pd1 / 100))
    Gly = Gly * (1 - (Pd1 / 100))
    his = his * (1 - (Pd1 / 100))
    ile = ile * (1 - (Pd1 / 100))
    leu = leu * (1 - (Pd1 / 100))
    lys = lys * (1 - (Pd1 / 100))
    met = met * (1 - (Pd1 / 100))
    phe = phe * (1 - (Pd1 / 100))
    pro = pro * (1 - (Pd1 / 100))
    Ser = Ser * (1 - (Pd1 / 100))
    thr = thr * (1 - (Pd1 / 100))
    trp = trp * (1 - (Pd1 / 100))
    tyr = tyr * (1 - (Pd1 / 100))
    valine = valine * (1 - (Pd1 / 100))

    Raffinose = Raffinose * (1 - (Pd1 / 100))
    Stachyose = Stachyose * (1 - (Pd1 / 100))
    Sucrose = Sucrose * (1 - (Pd1 / 100))
    OtherCarb = OtherCarb * (1 - (Pd1 / 100))

    Mode = "EPV_2"

Case "EPV_2"
    'Calculates the soybean meal value based on the amino acid & carbohydrate prices.
    Price_Ala_Meal = Price_Ala * (Ala / 100)
    Price_Arg_Meal = Price_Arg * (arg / 100)
    Price_Asn_Meal = Price_Asn * (Asn / 100)
    Price_Asp_Meal = Price_Asp * (Asp / 100)
    Price_Cys_Meal = Price_Cys * (cys / 100)
    Price_Gln_Meal = Price_Gln * (Gln / 100)
    Price_Glu_Meal = Price_Glu * (Glu / 100)
    Price_Gly_Meal = Price_Gly * (Gly / 100)
    Price_His_Meal = Price_His * (his / 100)
    Price_Ile_Meal = Price_Ile * (ile / 100)
    Price_Leu_Meal = Price_Leu * (leu / 100)
    Price_Lys_Meal = Price_Lys * (lys / 100)
    Price_Met_Meal = Price_Met * (met / 100)
    Price_Phe_Meal = Price_Phe * (phe / 100)
    Price_Pro_Meal = Price_Pro * (pro / 100)
    Price_Ser_Meal = Price_Ser * (Ser / 100)
    Price_Thr_Meal = Price_Thr * (thr / 100)
```

```
        Price_Trp_Meal = Price_Trp * (trp / 100)
        Price_Tyr_Meal = Price_Tyr * (tyr / 100)
        Price_Val_Meal = Price_Val * (valine / 100)

        Price_Raffinose_Meal = Price_Raffinose * (Raffinose / 100)
        Price_Stachyose_Meal = Price_Stachyose * (Stachyose / 100)
        Price_Sucrose_Meal = Price_Sucrose * (Sucrose / 100)

        PriceMeal_AA = Price_Ala_Meal + Price_Arg_Meal + Price_Asn_Meal + Price_Asp_Meal
+ Price_Cys_Meal + Price_Gln_Meal + Price_Glu_Meal + Price_Gly_Meal _
                        + Price_His_Meal + Price_Ile_Meal + Price_Leu_Meal + Price_Lys_Meal +
Price_Met_Meal + Price_Phe_Meal + Price_Pro_Meal + Price_Ser_Meal _
                        + Price_Thr_Meal + Price_Trp_Meal + Price_Tyr_Meal + Price_Val_Meal +
Price_Raffinose_Meal + Price_Stachyose_Meal + Price_Sucrose_Meal

        Mode = "EPV_3"

    Case "EPV_3"
        'Calculate the protein discount for the soybean meal.
        'PROTEIN DISCOUNT: 2 times the unit protein price, 0.5% allowance, 12% moisture
basis.
        If Worksheets("Inputs").Range("K8") = "NOPA Rules Used" Then

            DiscP = 0 'Sets product discount to 0 initially.
            DiscP_AA = 0 'Sets product discount to 0 initially.

            If Pd2 * 88 / (100 - Pd1) >= Pd2spec * 88 / (100 - Pd1) - 0.5 Then
                Mode = "EPV_4" 'No protein discount.
            Else
                DiscP = DiscP + 2 * PriceMeal * (Pd2spec - Pd2) / Pd2spec 'Calculates protein
discount for product.
                DiscP_AA = DiscP_AA + 2 * PriceMeal_AA * (Pd2spec - Pd2) / Pd2spec 'Calculates
protein discount for product.
                Mode = "EPV_4"
            End If

        Else
            Mode = "EPV_5"
        End If

    Case "EPV_4"
        'Calculate the fiber discount for the soybean meal, if NOPA trading rules are being used.
        'NOTE: Pd5spec is the as-is moisture equivalent of Pd5max.
        'FIBER DISCOUNT: 1% of the invoice price per 0.1% in excess of specification, 0.3%
allowance, 12% moisture basis.
```

```
      If Pd5 * 88 / (100 - Pd1) <= Pd5spec * 88 / (100 - Pd1) + 0.3 Then
         Mode = "EPV_5" 'No fiber discount.
      Else
         DiscP = DiscP + 0.1 * PriceMeal * (Pd5 - Pd5spec) 'Calculates fiber discount.
         DiscP_AA = DiscP_AA + 0.1 * PriceMeal_AA * (Pd5 - Pd5spec) 'Calculates fiber
discount.
         Mode = "EPV_5"
      End If

   Case "EPV_5"
      'Calculate the protein premium for the soybean meal, if such a premium is being used.
      'PROTEIN PREMIUM: The per unit price of protein times the amount of protein in excess
of specifications.
      If Worksheets("Inputs").Range("K11") = "Protein Premiums Used" Then

         If Pd2 * 88 / (100 - Pd1) <= Pd2spec * 88 / (100 - Pd1) Then
            Mode = "EPV_6" 'No protein premium.
         Else
            DiscP = DiscP - (Pd2 - Pd2spec) * (PriceMeal / Pd2spec) 'Calculates protein premium.
            DiscP_AA = DiscP_AA - (Pd2 - Pd2spec) * (PriceMeal_AA / Pd2spec) 'Calculates
protein premium.
            Mode = "EPV_6"
         End If

      Else
         Mode = "EPV_6"
      End If

   Case "EPV_6"
      'Calculate the EPV.
      EPVMeal = (PriceMeal - DiscP) * W1d
      EPVMeal_AA = (PriceMeal_AA - DiscP_AA) * W1d
      EPVOil = PriceOil * Wo
      EPVMillFeed = PriceHMF * (Wh - W1h - W1f)
      EPV_AA = EPVMeal_AA + EPVOil + EPVMillFeed
      EPV = EPVMeal + EPVOil + EPVMillFeed

      Mode = "DONE"

   Case Else
      MsgBox "Problem with code. Proper mode was not selected."
      Mode = "DONE"

End Select
Loop
```

```
progress 50 'Sets progress bar to 50%

'----------------------------------------------------------------------------------------------------

'Additional calculations for output varibles:

'Net Hull Weight Calculation:
   Whn = Wh - W1h

'Unaccounted for Protein (SBM):
   Unacct_ProteinSBM = Pd2 - (Ala + arg + Asn + Asp + cys + Gln + Glu + Gly + his + ile + leu
_
                  + lys + met + phe + pro + Ser + thr + trp + tyr + valine)

'----------------------------------------------------------------------------------------------------

'FEED FORMULATION CALCULATIONS:

If Worksheets("Inputs").Range("V11") = "Formulate Swine Diet" Then
   If Sheets("Feeds").Range("D61") = "" Then 'Only fills in if library has been cleared
      Sheets("Feeds").Range("C61").Value = "SPROC Soybean Meal"
      Sheets("Feeds").Range("D61").Value = 2000 'lb / ton
      Sheets("Feeds").Range("Q61").Value = 39 'From existing 47.5% meal in library
      Sheets("Feeds").Range("V61").Value = 90
      Sheets("Feeds").Range("X61").Value = 87
      Sheets("Feeds").Range("Z61").Value = 91
      Sheets("Feeds").Range("AB61").Value = 87
      Sheets("Feeds").Range("AD61").Value = 90
      Sheets("Feeds").Range("AF61").Value = 89
      Sheets("Feeds").Range("AH61").Value = 88
      Sheets("Feeds").Range("AJ61").Value = 94
      Sheets("Feeds").Range("AL61").Value = 91
      Sheets("Feeds").Range("AN61").Value = 89
      Sheets("Feeds").Range("AP61").Value = 89
      Sheets("Feeds").Range("AR61").Value = 90
      Sheets("Feeds").Range("AU61").Value = 0.34
      Sheets("Feeds").Range("AV61").Value = 0.69
      Sheets("Feeds").Range("AW61").Value = 0.16
      Sheets("Feeds").Range("AX61").Value = 0.22
      Sheets("Feeds").Range("AY61").Value = 0.02
      Sheets("Feeds").Range("AZ61").Value = 0.05
      Sheets("Feeds").Range("BA61").Value = 0.3
      Sheets("Feeds").Range("BB61").Value = 2.14
      Sheets("Feeds").Range("BC61").Value = 0.44
      Sheets("Feeds").Range("BE61").Value = 20
      Sheets("Feeds").Range("BF61").Value = 0.2
```

```
        Sheets("Feeds").Range("BG61").Value = 176
        Sheets("Feeds").Range("BH61").Value = 36
        Sheets("Feeds").Range("BI61").Value = 0.3
        Sheets("Feeds").Range("BJ61").Value = 55
        Sheets("Feeds").Range("BL61").Value = 24
        Sheets("Feeds").Range("BN61").Value = 1.6
        Sheets("Feeds").Range("BP61").Value = 1.4
        Sheets("Feeds").Range("BQ61").Value = 10
        Sheets("Feeds").Range("BR61").Value = 6.8
        Sheets("Feeds").Range("BS61").Value = 1239
        Sheets("Feeds").Range("BT61").Value = 0.1
        Sheets("Feeds").Range("BV61").Value = 0.6
        Sheets("Feeds").Range("BW61").Value = 2.9
        Sheets("Feeds").Range("BX61").Value = 1.5
        Sheets("Feeds").Range("CD61").Value = 15
    End If

    If Pd2 >= 47 Then 'Determines correct values based on protein %
        NE_Meal = 907
        ADF_Meal = 5.4
        NDF_Meal = 8.9
    ElseIf Pd2 >= 45 Then
        NE_Meal = 894
        ADF_Meal = 6.4
        NDF_Meal = 10.2
    Else
        NE_Meal = 881
        ADF_Meal = 9.4
        NDF_Meal = 13.3
    End If

    Pd2 = Pd2 / (1 - (Pd1 / 100)) 'Converting protein to dry matter basis
    Pd5 = Pd5 / (1 - (Pd1 / 100)) ' Converting fiber to dry matter basis
    ADF_Meal = ADF_Meal / (1 - (Pd1 / 100)) ' Converting ADF to dry matter basis
    GE = 19.59 'Average from Taylor & Francis

    DE_Meal = 38.44 - 0.43 * Pd5 - 0.98 * GE + 0.11 * ADF_Meal 'Equation from Taylor &
Francis (dry matter basis)
    ME_Meal = 2.74 + 0.97 * DE_Meal - 0.06 * Pd2 'Equation from Taylor & Francis (dry matter
basis)
    Linoleic_Meal = ((Linoleic_In / 100) * Pd3) 'Linoleic % of meal
    Meal_Price_In = Worksheets("Inputs").Range("K20").Value
    Meal_Price_Out = 200

    ME_Meal = ME_Meal * 108.411 'Converts to kcal/lb
    DE_Meal = DE_Meal * 108.411 'Converts to kcal/lb
```

```
    ME_Meal = ME_Meal * (1 - (Pd1 / 100)) 'Converts to as-fed basis
    DE_Meal = DE_Meal * (1 - (Pd1 / 100)) 'Converts to as-fed basis

    Pd2 = Pd2 * (1 - (Pd1 / 100)) 'Converting protein to as-fed basis
    Pd5 = Pd5 * (1 - (Pd1 / 100)) ' Converting fiber to as-fed basis
    ADF_Meal = ADF_Meal * (1 - (Pd1 / 100)) ' Converting ADF to as-fed basis


    Sheets("Feeds").Range("E61").Value = Meal_Price_In
    Sheets("Feeds").Range("F61").Value = Meal_Price_Out
    Sheets("Feeds").Range("G61").Value = 100 - Pd1
    Sheets("Feeds").Range("H61").Value = DE_Meal
    Sheets("Feeds").Range("I61").Value = ME_Meal
    Sheets("Feeds").Range("J61").Value = NE_Meal
    Sheets("Feeds").Range("K61").Value = Pd2
    Sheets("Feeds").Range("L61").Value = ADF_Meal
    Sheets("Feeds").Range("M61").Value = NDF_Meal
    Sheets("Feeds").Range("N61").Value = Pd5
    Sheets("Feeds").Range("O61").Value = Pd3
    Sheets("Feeds").Range("P61").Value = Linoleic_Meal
    Sheets("Feeds").Range("U61").Value = lys
    Sheets("Feeds").Range("W61").Value = thr
    Sheets("Feeds").Range("Y61").Value = met
    Sheets("Feeds").Range("AA61").Value = cys
    Sheets("Feeds").Range("AC61").Value = trp
    Sheets("Feeds").Range("AE61").Value = ile
    Sheets("Feeds").Range("AG61").Value = valine
    Sheets("Feeds").Range("AI61").Value = arg
    Sheets("Feeds").Range("AK61").Value = his
    Sheets("Feeds").Range("AM61").Value = leu
    Sheets("Feeds").Range("AO61").Value = phe
    Sheets("Feeds").Range("AQ61").Value = tyr

    If i = 0 Then 'Only fills in on the first sample, these values don't change after the first sample
is run
        Sheets("Feeds").Range("E80").Value = Price_Lys * 2000 'Current price of lysine
        Sheets("Feeds").Range("F80").Value = Price_Lys * 2000 'Current price of lysine
        Sheets("Feeds").Range("E87").Value = Price_Thr * 2000 'Current price of threonine
        Sheets("Feeds").Range("F87").Value = Price_Thr * 2000 'Current price of threonine
        Sheets("Feeds").Range("E88").Value = Price_Trp * 2000 'Current price of tryptophan
        Sheets("Feeds").Range("F88").Value = Price_Trp * 2000 'Current price of tryptophan
        Sheets("Feeds").Range("E84").Value = Price_Met * 2000 'Current price of methionine
        Sheets("Feeds").Range("F84").Value = Price_Met * 2000 'Current price of methionine
        Sheets("Feeds").Range("E90").Value = Price_Val * 2000 'Current price of methionine
        Sheets("Feeds").Range("F90").Value = Price_Val * 2000 'Current price of methionine
```

```
        Sheets("Feeds").Range("A61").Value = 1 'Adds the SPROC soybean meal to the feed diet
        Sheets("Feeds").Range("A18").Value = 2 'Adds corn to the feed diet
        Sheets("Feeds").Range("A80").Value = 3 'Adds lysine to the feed diet
        Sheets("Feeds").Range("A87").Value = 4 'Adds threonine to the feed diet
        Sheets("Feeds").Range("A94").Value = 5 'Adds phosphate to the feed diet
        Sheets("Feeds").Range("A98").Value = 6 'Adds limestone to the feed diet
        Sheets("Feeds").Range("A101").Value = 7 'Adds salt to the feed diet
        Sheets("Feeds").Range("A69").Value = 8 'Adds fat to the feed diet
        Sheets("Feeds").Range("A88").Value = 9 'Adds tryptophan to the feed diet
        Sheets("Feeds").Range("A84").Value = 10 'Adds methionine to the feed diet
        Sheets("Feeds").Range("A90").Value = 11 'Adds valine to the feed diet

        'Enters info on Grow-Finish tab (suggestions from Brian Kerr)
        Sheets("Grow-Finish").Range("E13").Value = "Mixed"
        Sheets("Grow-Finish").Range("E15").Value = 50
        Sheets("Grow-Finish").Range("E17").Value = 130
        Sheets("Grow-Finish").Range("K24").Value = 0
        Sheets("Grow-Finish").Range("E24").Value = 3.68
    End If

    Sheets("Feeds").CommandButton7 = True 'Saves the feed library with the new ingredients
    Sheets("Feeds").CommandButton7 = vbClick

progress 60 'Sets progress bar to 60%

    Sheets("Grow-Finish").CommandButton14 = True 'Fills in nutrient specifications
    Sheets("Grow-Finish").CommandButton14 = vbClick

    Sheets("Grow-Finish").Range("E81") = 0.35 'Sets salt min and max to be .35 (From Brian Kerr)
    Sheets("Grow-Finish").Range("F81") = 0.35
    Sheets("Grow-Finish").Range("E37") = 18 'Sets crude protein to 18-19% (From Brian Kerr)
    Sheets("Grow-Finish").Range("F37") = 19

    Sheets("Grow-Finish").CommandButton6 = True 'Formulates diet
    Sheets("Grow-Finish").CommandButton6 = vbClick

    If i = 0 Then
        'Unhides the Feed Formualtion Tabs (only on 1st sample)
        Application.ScreenUpdating = False 'Freezes screen temporarily
        Worksheets("Program").Visible = True
        Worksheets("Settings").Visible = True
        Worksheets("Feeds").Visible = True
        Worksheets("Sows").Visible = True
        Worksheets("Boars").Visible = True
```

```
        Worksheets("Grow-Finish").Visible = True
        Worksheets("Nursery").Visible = True
        Worksheets("Manure").Visible = True
        Application.ScreenUpdating = True 'Unfreezes screen
    End If

Else
    If i = 0 Then
        'Hides the Feed Formulation Tabs When Not in Use
        Application.ScreenUpdating = False
        Worksheets("Program").Visible = False
        Worksheets("Settings").Visible = False
        Worksheets("Feeds").Visible = False
        Worksheets("Sows").Visible = False
        Worksheets("Boars").Visible = False
        Worksheets("Grow-Finish").Visible = False
        Worksheets("Nursery").Visible = False
        Worksheets("Manure").Visible = False
        Application.ScreenUpdating = True
    End If

End If

progress 70 'Sets progress bar to 70%

'-----------------------------------------------------------------------------------------------------
'OUTPUTS
If Worksheets("Inputs").Range("V7") = "No Data File" Then
    'Activates "Outputs" Sheet
    Worksheets("Outputs").Activate
    ActiveSheet.Range("A1").Select
End If

'OUTPUTS - For "Outputs" Sheet:
    Worksheets("Outputs").Range("E15") = Pa1
    Worksheets("Outputs").Range("E16") = Pa2
    Worksheets("Outputs").Range("E17") = Pa3
    Worksheets("Outputs").Range("E18") = Pa5
    Worksheets("Outputs").Range("K5") = EPV
    Worksheets("Outputs").Range("O5") = EPV_AA
    Worksheets("Outputs").Range("T6") = EPVMeal
    Worksheets("Outputs").Range("T7") = EPVMeal_AA
    Worksheets("Outputs").Range("T8") = EPVOil
    Worksheets("Outputs").Range("T9") = EPVMillFeed
    Worksheets("Outputs").Range("K9") = -1 * DiscP
    Worksheets("Outputs").Range("P9") = -1 * DiscP_AA
```

```
Worksheets("Outputs").Range("I17") = Wh
Worksheets("Outputs").Range("M13") = Whn
Worksheets("Outputs").Range("R17") = W1h
Worksheets("Outputs").Range("X14") = W1d
Worksheets("Outputs").Range("X15") = Pd1
Worksheets("Outputs").Range("X16") = Pd2
Worksheets("Outputs").Range("X17") = Pd3
Worksheets("Outputs").Range("X18") = Pd5
Worksheets("Outputs").Range("R32") = W1f
Worksheets("Outputs").Range("M31") = Wo
Worksheets("Outputs").Range("L33") = Palmitic_In
Worksheets("Outputs").Range("L34") = Stearic_In
Worksheets("Outputs").Range("L35") = Oleic_In
Worksheets("Outputs").Range("O33") = Linoleic_In
Worksheets("Outputs").Range("O34") = Linolenic_In
Worksheets("Outputs").Range("W20") = Ala
Worksheets("Outputs").Range("W21") = arg
Worksheets("Outputs").Range("W22") = Asn
Worksheets("Outputs").Range("W23") = Asp
Worksheets("Outputs").Range("W24") = cys
Worksheets("Outputs").Range("W25") = Gln
Worksheets("Outputs").Range("W26") = Glu
Worksheets("Outputs").Range("W27") = Gly
Worksheets("Outputs").Range("W28") = his
Worksheets("Outputs").Range("W29") = ile
Worksheets("Outputs").Range("Z20") = leu
Worksheets("Outputs").Range("Z21") = lys
Worksheets("Outputs").Range("Z22") = met
Worksheets("Outputs").Range("Z23") = phe
Worksheets("Outputs").Range("Z24") = pro
Worksheets("Outputs").Range("Z25") = Ser
Worksheets("Outputs").Range("Z26") = thr
Worksheets("Outputs").Range("Z27") = trp
Worksheets("Outputs").Range("Z28") = tyr
Worksheets("Outputs").Range("Z29") = valine
'Worksheets("Outputs").Range("Y30") = Unacct_ProteinSBM
Worksheets("Outputs").Range("W32") = Raffinose
Worksheets("Outputs").Range("W33") = Stachyose
Worksheets("Outputs").Range("Z32") = Sucrose
Worksheets("Outputs").Range("Z33") = OtherCarb

If Worksheets("Inputs").Range("V11") = "Formulate Swine Diet" Then
   Worksheets("Outputs").Range("X5") = Worksheets("Grow-Finish").Range("J110").Value
   Worksheets("Outputs").Range("Y8") = Worksheets("Grow-Finish").Range("K115").Value
   Worksheets("Outputs").Range("Y9") = Worksheets("Grow-Finish").Range("K117").Value
   Worksheets("Outputs").Range("Y10") = Worksheets("Grow-Finish").Range("K141").Value
```

```
    Else
        Worksheets("Outputs").Range("X5") = "-"
        Worksheets("Outputs").Range("Y8") = "-"
        Worksheets("Outputs").Range("Y9") = "-"
        Worksheets("Outputs").Range("Y10") = "-"
    End If

progress 80 'Sets progress bar to 80%

 Row = 4

 Do
    If IsEmpty(Worksheets("Report Sheet").Cells(Row, 2).Value) = True Then

        'Soybean Composition Inputs
        Worksheets("Report Sheet").Cells(Row, 2) = SampleID
        Worksheets("Report Sheet").Cells(Row, 3) = Pa1
        Worksheets("Report Sheet").Cells(Row, 4) = Pa2
        Worksheets("Report Sheet").Cells(Row, 5) = Pa3
        Worksheets("Report Sheet").Cells(Row, 6) = Pa5
        Worksheets("Report Sheet").Cells(Row, 7) = Ala_In
        Worksheets("Report Sheet").Cells(Row, 8) = Arg_In
        Worksheets("Report Sheet").Cells(Row, 9) = Asn_In
        Worksheets("Report Sheet").Cells(Row, 10) = Asp_In
        Worksheets("Report Sheet").Cells(Row, 11) = Cys_In
        Worksheets("Report Sheet").Cells(Row, 12) = Gln_In
        Worksheets("Report Sheet").Cells(Row, 13) = Glu_In
        Worksheets("Report Sheet").Cells(Row, 14) = Gly_In
        Worksheets("Report Sheet").Cells(Row, 15) = His_In
        Worksheets("Report Sheet").Cells(Row, 16) = Ile_In
        Worksheets("Report Sheet").Cells(Row, 17) = Leu_In
        Worksheets("Report Sheet").Cells(Row, 18) = Lys_In
        Worksheets("Report Sheet").Cells(Row, 19) = Met_In
        Worksheets("Report Sheet").Cells(Row, 20) = Phe_In
        Worksheets("Report Sheet").Cells(Row, 21) = Pro_In
        Worksheets("Report Sheet").Cells(Row, 22) = Ser_In
        Worksheets("Report Sheet").Cells(Row, 23) = Thr_In
        Worksheets("Report Sheet").Cells(Row, 24) = Trp_In
        Worksheets("Report Sheet").Cells(Row, 25) = Tyr_In
        Worksheets("Report Sheet").Cells(Row, 26) = Valine_In
        Worksheets("Report Sheet").Cells(Row, 27) = Palmitic_In
        Worksheets("Report Sheet").Cells(Row, 28) = Stearic_In
        Worksheets("Report Sheet").Cells(Row, 29) = Oleic_In
        Worksheets("Report Sheet").Cells(Row, 30) = Linoleic_In
        Worksheets("Report Sheet").Cells(Row, 31) = Linolenic_In
        Worksheets("Report Sheet").Cells(Row, 32) = Raffinose_In
```

```
Worksheets("Report Sheet").Cells(Row, 33) = Stachyose_In
Worksheets("Report Sheet").Cells(Row, 34) = Sucrose_In
Worksheets("Report Sheet").Cells(Row, 35) = OtherCarb_In
'Soybean Meal Composition
Worksheets("Report Sheet").Cells(Row, 36) = W1d
Worksheets("Report Sheet").Cells(Row, 37) = Pd1
Worksheets("Report Sheet").Cells(Row, 38) = Pd2
Worksheets("Report Sheet").Cells(Row, 39) = Pd3
Worksheets("Report Sheet").Cells(Row, 40) = Pd5
Worksheets("Report Sheet").Cells(Row, 41) = W1h
Worksheets("Report Sheet").Cells(Row, 42) = W1f
Worksheets("Report Sheet").Cells(Row, 43) = Ala
Worksheets("Report Sheet").Cells(Row, 44) = arg
Worksheets("Report Sheet").Cells(Row, 45) = Asn
Worksheets("Report Sheet").Cells(Row, 46) = Asp
Worksheets("Report Sheet").Cells(Row, 47) = cys
Worksheets("Report Sheet").Cells(Row, 48) = Gln
Worksheets("Report Sheet").Cells(Row, 49) = Glu
Worksheets("Report Sheet").Cells(Row, 50) = Gly
Worksheets("Report Sheet").Cells(Row, 51) = his
Worksheets("Report Sheet").Cells(Row, 52) = ile
Worksheets("Report Sheet").Cells(Row, 53) = leu
Worksheets("Report Sheet").Cells(Row, 54) = lys
Worksheets("Report Sheet").Cells(Row, 55) = met
Worksheets("Report Sheet").Cells(Row, 56) = phe
Worksheets("Report Sheet").Cells(Row, 57) = pro
Worksheets("Report Sheet").Cells(Row, 58) = Ser
Worksheets("Report Sheet").Cells(Row, 59) = thr
Worksheets("Report Sheet").Cells(Row, 60) = trp
Worksheets("Report Sheet").Cells(Row, 61) = tyr
Worksheets("Report Sheet").Cells(Row, 62) = valine
Worksheets("Report Sheet").Cells(Row, 63) = Raffinose
Worksheets("Report Sheet").Cells(Row, 64) = Stachyose
Worksheets("Report Sheet").Cells(Row, 65) = Sucrose
Worksheets("Report Sheet").Cells(Row, 66) = OtherCarb
'Crude Oil Composition
Worksheets("Report Sheet").Cells(Row, 67) = Wo
Worksheets("Report Sheet").Cells(Row, 68) = Palmitic_In
Worksheets("Report Sheet").Cells(Row, 69) = Stearic_In
Worksheets("Report Sheet").Cells(Row, 70) = Oleic_In
Worksheets("Report Sheet").Cells(Row, 71) = Linoleic_In
Worksheets("Report Sheet").Cells(Row, 72) = Linolenic_In
Worksheets("Report Sheet").Cells(Row, 73) = Whn

If DiscP = "" Then
   Worksheets("Report Sheet").Cells(Row, 74) = "-"
```

```
    Else
      Worksheets("Report Sheet").Cells(Row, 74) = DiscP
    End If

    'EPVs
    Worksheets("Report Sheet").Cells(Row, 75) = EPVOil
    Worksheets("Report Sheet").Cells(Row, 76) = EPVMillFeed
    Worksheets("Report Sheet").Cells(Row, 77) = EPVMeal
    Worksheets("Report Sheet").Cells(Row, 78) = EPV
    Worksheets("Report Sheet").Cells(Row, 79) = EPVMeal_AA
    Worksheets("Report Sheet").Cells(Row, 80) = EPV_AA

progress 90 'Sets progress bar to 90%

    'Feed Formulation Outputs
    If Worksheets("Inputs").Range("V11") = "Formulate Swine Diet" Then
      N = 81
      For N = 81 To 91

        If Worksheets("Grow-Finish").Cells(N + 32, 5).Value = "" Then
          Worksheets("Report Sheet").Cells(Row, N) = "-"
        Else
          Worksheets("Report Sheet").Cells(Row, N) = Worksheets("Grow-Finish").Cells(N
+ 32, 5).Value * 100
        End If

      Next N

      Worksheets("Report Sheet").Cells(Row, 92) = Worksheets("Grow-
Finish").Range("K115").Value
      Worksheets("Report Sheet").Cells(Row, 93) = Worksheets("Grow-
Finish").Range("K117").Value
      Worksheets("Report Sheet").Cells(Row, 94) = Worksheets("Grow-
Finish").Range("K141").Value
      Worksheets("Report Sheet").Cells(Row, 95) = Worksheets("Grow-
Finish").Range("K119").Value
      Worksheets("Report Sheet").Cells(Row, 96) = Worksheets("Grow-
Finish").Range("J110").Value
    Else
      Worksheets("Report Sheet").Cells(Row, 81) = "-"
      Worksheets("Report Sheet").Cells(Row, 82) = "-"
      Worksheets("Report Sheet").Cells(Row, 83) = "-"
      Worksheets("Report Sheet").Cells(Row, 84) = "-"
      Worksheets("Report Sheet").Cells(Row, 85) = "-"
      Worksheets("Report Sheet").Cells(Row, 86) = "-"
      Worksheets("Report Sheet").Cells(Row, 87) = "-"
```

```
            Worksheets("Report Sheet").Cells(Row, 88) = "-"
            Worksheets("Report Sheet").Cells(Row, 89) = "-"
            Worksheets("Report Sheet").Cells(Row, 90) = "-"
            Worksheets("Report Sheet").Cells(Row, 91) = "-"
            Worksheets("Report Sheet").Cells(Row, 92) = "-"
            Worksheets("Report Sheet").Cells(Row, 93) = "-"
            Worksheets("Report Sheet").Cells(Row, 94) = "-"
            Worksheets("Report Sheet").Cells(Row, 95) = "-"
            Worksheets("Report Sheet").Cells(Row, 96) = "-"
        End If

        PrintRow = Row

        Exit Do

    Else
        Row = Row + 1
    End If

Loop Until Row = 700

'----------------------------------------------------------------------------------------------------

i = i + 1   'Counts the number of loops until the number of loops matches the number of samples

Loop Until i >= sample_number    'Loop for the entire code to run for each sample (If
sample_number = 1 than code will only run once)

'----------------------------------------------------------------------------------------------------

'Increasing sample number by one
SampleIDFunc SampleID

'----------------------------------------------------------------------------------------------------

'Printing Option
Printer PrintRow

Dim ws As Worksheet

'Clears the page breaks created by the print preview
Application.ScreenUpdating = False
For Each ws In ThisWorkbook.Worksheets
    ws.DisplayPageBreaks = False
Next ws
Application.ScreenUpdating = True
```

```
'----------------------------------------------------------------------------------------------------

'Clears input cells, ready for next sample
ClearInputs

'----------------------------------------------------------------------------------------------------

'Resets status bar
   Application.StatusBar = False
'Set progress bar to 100%
   progress 100
   UserForm1.Hide  'Hides the progress bar

   Exit Sub
ErrorHandler:
   UserForm1.Hide  'Hides the progress bar
   Application.StatusBar = False
   MsgBox "ERROR: Please check your file name and file path."
   Exit Sub

ErrorHandler_2:
   UserForm1.Hide  'Hides the progress bar
   Application.StatusBar = False
   MsgBox "ERROR: Problem occurred when running the program. Please check all inputs and try again."

End Sub

'Code for the progress indicator bar
Sub progress(pctCompl As Single)

UserForm1.Text.Caption = pctCompl & "% Completed"
UserForm1.Bar.Width = pctCompl * 2

DoEvents

End Sub

'Initially shows the progress bar and activates userform1
Sub RUN_MODEL_Click()

UserForm1.Show

End Sub
```

```
Sub MissingData()

'Checks input sheet for missing data before running the rest of the code
For Each Rng In
Worksheets("Inputs").Range("G7:G12,G19:G21,G28:G30,G32:G35,K19:K21,N19,AC17:AC26,
AG17:AG26,AC30:AC31,AG30:AG31,AC35:AC37,AG35:AG36")
    If IsEmpty(Rng.Value) Then
        UserForm1.Hide  'Hides the progress bar
        Application.StatusBar = False
        MsgBox ("Please enter data in all the red boxes.")
        Exit Sub
    End If
Next

If Worksheets("Inputs").Range("V7") = "No Data File" And
((IsEmpty(Worksheets("Inputs").Range("AE8").Value) = True) Or
(IsEmpty(Worksheets("Inputs").Range("AE10").Value) = True)) Then
    UserForm1.Hide  'Hides the progress bar
    Application.StatusBar = False
    MsgBox ("Please enter data in all the red boxes.")
    Exit Sub
ElseIf Worksheets("Inputs").Range("V7") = "No Data File" And
Worksheets("Inputs").Range("V21") = "*As-Is Moisture" And
IsEmpty(Worksheets("Inputs").Range("AE7").Value) = True Then
    UserForm1.Hide  'Hides the progress bar
    Application.StatusBar = False
    MsgBox ("Please enter data in all the red boxes.")
    Exit Sub
ElseIf Worksheets("Inputs").Range("V7") = "No Data File" And
Worksheets("Inputs").Range("Q26") = "A fiber content specified for each sample at the moisture
basis specified above." _
        And IsEmpty(Worksheets("Inputs").Range("AE9").Value) = True Then
            UserForm1.Hide  'Hides the progress bar
            Application.StatusBar = False
            MsgBox ("Please enter data in all the red boxes.")
            Exit Sub
ElseIf Worksheets("Inputs").Range("V7") = "No Data File" And
Worksheets("Inputs").Range("Q26") = "A fiber content of your choice (basis 13% moisture)
constant for all samples." _
        And IsEmpty(Worksheets("Inputs").Range("W29").Value) = True Then
            UserForm1.Hide  'Hides the progress bar
            Application.StatusBar = False
            MsgBox ("Please enter data in all the red boxes.")
            Exit Sub
ElseIf Worksheets("Inputs").Range("V7") = "Enter From Data File" And
((IsEmpty(Worksheets("Inputs").Range("AF7").Value) = True) Or _
```

```
        (IsEmpty(Worksheets("Inputs").Range("AA11").Value) = True) Or
(IsEmpty(Worksheets("Inputs").Range("AA13").Value) = True)) Then
    UserForm1.Hide  'Hides the progress bar
    Application.StatusBar = False
    MsgBox ("Please enter your file name, path, and type into the composition data box.")
    Exit Sub
End If

End Sub

Sub ClearOutputs()

'Clears "Outputs" sheet:
    Worksheets("Outputs").Range("E15:E18").ClearContents
    Worksheets("Outputs").Range("K5") = ""
    Worksheets("Outputs").Range("O5") = ""
    Worksheets("Outputs").Range("K9") = ""
    Worksheets("Outputs").Range("P9") = ""
    Worksheets("Outputs").Range("I17") = ""
    Worksheets("Outputs").Range("M13") = ""
    Worksheets("Outputs").Range("R17") = ""
    Worksheets("Outputs").Range("R32") = ""
    Worksheets("Outputs").Range("M31").ClearContents
    Worksheets("Outputs").Range("L33:L35").ClearContents
    Worksheets("Outputs").Range("O33:O34").ClearContents
    Worksheets("Outputs").Range("T6:T9").ClearContents
    Worksheets("Outputs").Range("X14:X18").ClearContents
    Worksheets("Outputs").Range("W20:W29").ClearContents
    Worksheets("Outputs").Range("Z20:Z29").ClearContents
    Worksheets("Outputs").Range("W32:W33").ClearContents
    Worksheets("Outputs").Range("Z32") = ""

End Sub

Sub Printer(PrintRow)

'If "send to printer" was chosen on the input sheet, this code will display the printer options
dialog box.


    If Worksheets("Inputs").Range("V9") = "Send Data to Printer" Then
        UserForm1.Hide  'Hides the progress bar
        Worksheets("Report Sheet").Activate
        ActiveSheet.Range(Cells(2, 2), Cells(PrintRow, 94)).Select
        Printer_Setup
        'Application.Dialogs(xlDialogPrint).Show
```

```
        Worksheets("Report Sheet").Activate
        ActiveSheet.Range("A1").Select
    End If


End Sub

Sub ClearInputs()

'Clears input cells, ready for next sample
    Worksheets("Inputs").Range("AE7") = ""
    Worksheets("Inputs").Range("AE8") = ""
    Worksheets("Inputs").Range("AE9") = ""
    Worksheets("Inputs").Range("AE10") = ""

End Sub

Sub SampleIDFunc(SampleID)

'Increasing sample number by one
    SampleID = SampleID + 1
    Worksheets("Inputs").Range("Q36") = SampleID

End Sub

Sub Printer_Setup()

    Application.PrintCommunication = False
    With ActiveSheet.PageSetup
        .PrintTitleRows = ""
        .PrintTitleColumns = ""
    End With
    Application.PrintCommunication = True
    ActiveSheet.PageSetup.PrintArea = ""
    Application.PrintCommunication = False
    With ActiveSheet.PageSetup
        .LeftHeader = ""
        .CenterHeader = ""
        .RightHeader = ""
        .LeftFooter = ""
        .CenterFooter = ""
        .RightFooter = ""
        .LeftMargin = Application.InchesToPoints(0.25)
        .RightMargin = Application.InchesToPoints(0.25)
        .TopMargin = Application.InchesToPoints(0.25)
        .BottomMargin = Application.InchesToPoints(0.25)
```

```
    .HeaderMargin = Application.InchesToPoints(0)
    .FooterMargin = Application.InchesToPoints(0)
    .PrintHeadings = False
    .PrintGridlines = False
    .PrintComments = xlPrintNoComments
    .PrintQuality = 1200
    .CenterHorizontally = True
    .CenterVertically = False
    .Orientation = xlPortrait
    .Draft = False
    .PaperSize = xlPaperLetter
    .FirstPageNumber = xlAutomatic
    .Order = xlOverThenDown
    .BlackAndWhite = False
    .Zoom = False
    .FitToPagesWide = 14
    .FitToPagesTall = 1
    .PrintErrors = xlPrintErrorsDisplayed
    .OddAndEvenPagesHeaderFooter = False
    .DifferentFirstPageHeaderFooter = False
    .ScaleWithDocHeaderFooter = True
    .AlignMarginsHeaderFooter = True
    .EvenPage.LeftHeader.Text = ""
    .EvenPage.CenterHeader.Text = ""
    .EvenPage.RightHeader.Text = ""
    .EvenPage.LeftFooter.Text = ""
    .EvenPage.CenterFooter.Text = ""
    .EvenPage.RightFooter.Text = ""
    .FirstPage.LeftHeader.Text = ""
    .FirstPage.CenterHeader.Text = ""
    .FirstPage.RightHeader.Text = ""
    .FirstPage.LeftFooter.Text = ""
    .FirstPage.CenterFooter.Text = ""
    .FirstPage.RightFooter.Text = ""
End With
Application.PrintCommunication = True
Application.PrintCommunication = False
With ActiveSheet.PageSetup
    .PrintTitleRows = ""
    .PrintTitleColumns = ""
End With
Application.PrintCommunication = True
ActiveSheet.PageSetup.PrintArea = ""
Application.PrintCommunication = False
With ActiveSheet.PageSetup
    .LeftHeader = ""
```

```
    .CenterHeader = ""
    .RightHeader = ""
    .LeftFooter = ""
    .CenterFooter = ""
    .RightFooter = ""
    .LeftMargin = Application.InchesToPoints(0.25)
    .RightMargin = Application.InchesToPoints(0.25)
    .TopMargin = Application.InchesToPoints(0.25)
    .BottomMargin = Application.InchesToPoints(0.25)
    .HeaderMargin = Application.InchesToPoints(0)
    .FooterMargin = Application.InchesToPoints(0)
    .PrintHeadings = False
    .PrintGridlines = False
    .PrintComments = xlPrintNoComments
    .PrintQuality = 1200
    .CenterHorizontally = True
    .CenterVertically = False
    .Orientation = xlPortrait
    .Draft = False
    .PaperSize = xlPaperLetter
    .FirstPageNumber = xlAutomatic
    .Order = xlOverThenDown
    .BlackAndWhite = False
    .Zoom = False
    .FitToPagesWide = 14
    .FitToPagesTall = 1
    .PrintErrors = xlPrintErrorsDisplayed
    .OddAndEvenPagesHeaderFooter = False
    .DifferentFirstPageHeaderFooter = False
    .ScaleWithDocHeaderFooter = True
    .AlignMarginsHeaderFooter = True
    .EvenPage.LeftHeader.Text = ""
    .EvenPage.CenterHeader.Text = ""
    .EvenPage.RightHeader.Text = ""
    .EvenPage.LeftFooter.Text = ""
    .EvenPage.CenterFooter.Text = ""
    .EvenPage.RightFooter.Text = ""
    .FirstPage.LeftHeader.Text = ""
    .FirstPage.CenterHeader.Text = ""
    .FirstPage.RightHeader.Text = ""
    .FirstPage.LeftFooter.Text = ""
    .FirstPage.CenterFooter.Text = ""
    .FirstPage.RightFooter.Text = ""
End With

Application.Dialogs(xlDialogPrint).Show
```

```
    Application.PrintCommunication = True
End Sub
```