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

Kortney Paige Wagner

Iowa State University

Follow this and additional works at: https://lib.dr.iastate.edu/etd

Part of the Agriculture Commons, and the Bioresource and Agricultural Engineering Commons

Recommended Citation

Wagner, Kortney Paige, "A mass balance based model to evaluate the impact of amino acid profiles on the feeding and processed value of soybeans" (2017). Graduate Theses and Dissertations. 16233.
https://lib.dr.iastate.edu/etd/16233

This Thesis is brought to you for free and open access by the Iowa State University Capstones, Theses and Dissertations at Iowa State University Digital Repository. It has been accepted for inclusion in Graduate Theses and Dissertations by an authorized administrator of Iowa State University Digital Repository. For more information, please contact digirep@iastate.edu.
A mass balance based model to evaluate the impact of amino acid profiles on the feeding and processed value of soybeans

by

Kortney Wagner

A thesis submitted to the graduate faculty
in partial fulfillment of the requirements for the degree of

MASTER OF SCIENCE

Major: Agricultural and Biosystems Engineering

Program of Study Committee:
Charles R. Hurburgh Jr., Major Professor
Carl J. Bern
D. Raj Raman

The student author, whose presentation of the scholarship herein was approved by the program of study committee, is solely responsible for the content of this thesis. The Graduate College will ensure this thesis is globally accessible and will not permit alterations after a degree is conferred.

Iowa State University

Ames, Iowa

2017

Copyright © Kortney Wagner, 2017. All rights reserved.
# TABLE OF CONTENTS

<table>
<thead>
<tr>
<th>Section</th>
<th>Page</th>
</tr>
</thead>
<tbody>
<tr>
<td>ACKNOWLEDGEMENTS</td>
<td>iii</td>
</tr>
<tr>
<td>ABSTRACT</td>
<td>iv</td>
</tr>
<tr>
<td><strong>CHAPTER 1. GENERAL INTRODUCTION</strong></td>
<td>1</td>
</tr>
<tr>
<td>Literature Review</td>
<td>2</td>
</tr>
<tr>
<td>Soybean Meal</td>
<td>3</td>
</tr>
<tr>
<td>Soybean Solvent Extraction Process</td>
<td>5</td>
</tr>
<tr>
<td>Trading of Soybeans and Soybean Meal</td>
<td>8</td>
</tr>
<tr>
<td>Existing Soybean Solvent Extraction Models</td>
<td>9</td>
</tr>
<tr>
<td>Thesis Organization</td>
<td>12</td>
</tr>
<tr>
<td>References</td>
<td>12</td>
</tr>
<tr>
<td><strong>CHAPTER 2. DEVELOPMENT OF ADDITIONAL MASS BALANCE MODELING OF SOYBEAN SOLVENT EXTRACTION TO INCLUDE MINOR CONSTITUENTS</strong></td>
<td>15</td>
</tr>
<tr>
<td>Abstract</td>
<td>15</td>
</tr>
<tr>
<td>Introduction</td>
<td>16</td>
</tr>
<tr>
<td>Materials and Methods</td>
<td>22</td>
</tr>
<tr>
<td>Results and Discussion</td>
<td>35</td>
</tr>
<tr>
<td>Conclusion</td>
<td>41</td>
</tr>
<tr>
<td>Literature Cited</td>
<td>42</td>
</tr>
<tr>
<td><strong>CHAPTER 3. TECHNICAL NOTE – VALIDATION OF THE UPDATED SOYBEAN PROCESSING MODEL</strong></td>
<td>45</td>
</tr>
<tr>
<td>Abstract</td>
<td>45</td>
</tr>
<tr>
<td>Introduction</td>
<td>45</td>
</tr>
<tr>
<td>Technique</td>
<td>47</td>
</tr>
<tr>
<td>Results and Discussion</td>
<td>49</td>
</tr>
<tr>
<td>Conclusion</td>
<td>50</td>
</tr>
<tr>
<td>Literature Cited</td>
<td>52</td>
</tr>
<tr>
<td><strong>CHAPTER 4. GENERAL CONCLUSION</strong></td>
<td>53</td>
</tr>
<tr>
<td>Summary</td>
<td>53</td>
</tr>
<tr>
<td>Conclusions</td>
<td>53</td>
</tr>
<tr>
<td><strong>APPENDIX A: SPROC 3.0 USER MANUAL</strong></td>
<td>54</td>
</tr>
<tr>
<td><strong>APPENDIX B: SPROC 3.0 VBA CODE</strong></td>
<td>74</td>
</tr>
</tbody>
</table>
I would like to take this opportunity to thank all the people who helped complete my research project and thesis work. I would first like to thank my major professor, Dr. Charles Hurburgh, for giving me this opportunity and for his continued support and guidance throughout this process. Thank you to the United Soybean Board for the research support. I would also like to express my appreciation for my committee members, Drs. Carl J. Bern and D. Raj Raman. I would like to thank Dr. Thomas J. Brumm for allowing me to build upon his existing research. Thank you to Glen Rippke and Brian Kerr for answering all of my endless questions and to Dr. Erin Bowers for the constant writing guidance and support. Finally, I would like to thank my family, fiancé Wade, and cousin Sydney for their love and support throughout this whole process.
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.,
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).
Soybean Preparation

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>
<thead>
<tr>
<th>Model</th>
<th>Year</th>
<th>Prediction Calculations</th>
<th>Solvent Extraction Parameters</th>
<th>Meal Composition Data</th>
<th>Feed Formulation Software Included</th>
</tr>
</thead>
<tbody>
<tr>
<td>Updaw <em>et al.</em></td>
<td>1976</td>
<td>Linear Regression</td>
<td>No</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Abraham <em>et al.</em></td>
<td>1988</td>
<td>Mass Balance</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Brumm &amp; Hurburgh</td>
<td>1990</td>
<td>Mass Balance</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
</tbody>
</table>

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*.

**References**


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](image-url)
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 eightmiscella 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)

<table>
<thead>
<tr>
<th>Model</th>
<th>Year</th>
<th>Prediction Calculations</th>
<th>Solvent Extraction Parameters</th>
<th>Meal Composition Data</th>
<th>Feed Formulation Software Included</th>
</tr>
</thead>
<tbody>
<tr>
<td>Updaw et al.</td>
<td>1976</td>
<td>Linear Regression</td>
<td>No</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Abraham et al.</td>
<td>1988</td>
<td>Mass Balance</td>
<td>Yes</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Brumm &amp; Hurburgh</td>
<td>1990</td>
<td>Mass Balance</td>
<td>Yes</td>
<td>Yes</td>
<td>No</td>
</tr>
</tbody>
</table>

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:

\[ PA = \frac{(WSoy \times P_1) - (WHull \times P_2)}{WSoy - WHull} \]  
\[ WOil = \frac{(WSoy - WHull) \times (PA_{Oil} - P_3)}{100 - P_3} \]  
\[ PC = \frac{WFlakes \times P_5 + WHull_{added} \times P_2 + WFeed \times P_6}{WMead} \]

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 (%)
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.
The potential value of the products is determined in two ways: (1) $EPV_{\text{protein/oil}}$: using the final product yields predicted by the protein and oil content alone and (2) $EPV_{\text{AA}}$: using the amino acid content. The $EPV_{\text{protein/oil}}$ 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 $EPV_{\text{protein/oil}}$ per bushel. The $EPV_{\text{AA}}$ 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 $EPV_{\text{AA}}$ 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 $EPV_{\text{protein/oil}}$ and $EPV_{\text{AA}}$. The $EPV_{\text{protein/oil}}$ 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 $EPV_{\text{AA}}$ equation for amino acid content (Equation 5) (Brumm T. J., 1990):

\[
EPV_{\text{protein/oil}} = \frac{PMeal \cdot WMeal}{2000} + POil \cdot WOil + \frac{PHull \cdot WHullNet}{2000} \quad (4)
\]

\[
EPV_{\text{AA}} = \sum_{i=1}^{n} (WAA_n \cdot PAA_n) + POil \cdot WOil + \frac{PHull \cdot WHullNet}{2000} \quad (5)
\]
Where: 

\[ EPV = \text{Estimated Processed Value ($/bu)} \]

\[ PMeal = \text{Meal Price, after discounted per trading rules ($/ton)} \]

\[ POil = \text{Oil Price ($/lb)} \]

\[ PHull = \text{Hull (mill run) Price ($/ton)} \]

\[ WMeal = \text{Weight of Soybean Meal (lb/bu)} \]

\[ WOil = \text{Weight of Crude Soybean Oil (lb/bu)} \]

\[ WHullNet = \text{Net Weight of the Hulls (lb/bu)} \]

\[ WAA = \text{Weight of Amino Acid (lb/bu)} \]

\[ PAA = \text{Amino Acid Price ($/lb)} \]

**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.

---

**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.
Figure 4: Inputs Worksheet

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).

\[ Y = \beta_0 * X + \beta_1 \]  

(6)

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

<table>
<thead>
<tr>
<th>Amino Acid</th>
<th>Slope ((\beta_0))</th>
<th>Intercept ((\beta_1))</th>
<th>(R^2)</th>
<th>Amino Acid</th>
<th>Slope ((\beta_0))</th>
<th>Intercept ((\beta_1))</th>
<th>(R^2)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alanine</td>
<td>0.029</td>
<td>0.460</td>
<td>0.854</td>
<td>Leucine</td>
<td>0.067</td>
<td>0.327</td>
<td>0.910</td>
</tr>
<tr>
<td>Arginine</td>
<td>0.094</td>
<td>-0.762</td>
<td>0.887</td>
<td>Lysine</td>
<td>0.047</td>
<td>0.597</td>
<td>0.866</td>
</tr>
<tr>
<td>Asparagine</td>
<td>0.112</td>
<td>-0.033</td>
<td>0.928</td>
<td>Methionine</td>
<td>0.009</td>
<td>0.180</td>
<td>0.643</td>
</tr>
<tr>
<td>Aparatic Acid</td>
<td>0.009</td>
<td>0.245</td>
<td>0.345</td>
<td>Phenylalanine</td>
<td>0.048</td>
<td>0.074</td>
<td>0.889</td>
</tr>
<tr>
<td>Cysteine</td>
<td>0.030</td>
<td>0.134</td>
<td>0.872</td>
<td>Proline</td>
<td>0.048</td>
<td>0.002</td>
<td>0.782</td>
</tr>
<tr>
<td>Glutamine</td>
<td>0.205</td>
<td>-1.081</td>
<td>0.883</td>
<td>Serine</td>
<td>0.042</td>
<td>0.111</td>
<td>0.658</td>
</tr>
<tr>
<td>Glutamic Acid</td>
<td>0.033</td>
<td>0.037</td>
<td>0.879</td>
<td>Threonine</td>
<td>0.026</td>
<td>0.433</td>
<td>0.802</td>
</tr>
<tr>
<td>Glycine</td>
<td>0.033</td>
<td>0.037</td>
<td>0.879</td>
<td>Tryptophan</td>
<td>0.008</td>
<td>0.144</td>
<td>0.238</td>
</tr>
<tr>
<td>Histidine</td>
<td>0.023</td>
<td>0.134</td>
<td>0.872</td>
<td>Tyrosine</td>
<td>0.030</td>
<td>0.233</td>
<td>0.820</td>
</tr>
<tr>
<td>Isoleucine</td>
<td>0.037</td>
<td>0.302</td>
<td>0.779</td>
<td>Valine</td>
<td>0.040</td>
<td>0.305</td>
<td>0.772</td>
</tr>
</tbody>
</table>

**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.
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.

**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)

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

\[
ME = 2.74 + 0.97 \times DE - 0.06 \times CP \quad (7)
\]

\[
DE = 38.44 - 0.43 \times CF - 0.98 \times GE + 0.11 \times ADF \quad (8)
\]

Where:

- \( ME \) = Metabolizable Energy (MJ/kg)
- \( DE \) = Digestible Energy (MJ/kg)
- \( CP \) = Crude Protein (%)
**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 (Agricultural 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; Agricultural Marketing Service; Medic, Atkinson and Hurburgh)

<table>
<thead>
<tr>
<th>Soybean Preparation</th>
<th>Current Prices</th>
<th>$/lb</th>
</tr>
</thead>
<tbody>
<tr>
<td>Percent of soybeans removed as hulls:</td>
<td>10.0</td>
<td></td>
</tr>
<tr>
<td>Percent of moisture in hulls:</td>
<td>12.0</td>
<td></td>
</tr>
<tr>
<td>Percent protein in the hulls:</td>
<td>12.0</td>
<td></td>
</tr>
<tr>
<td>Percent oil in the hulls:</td>
<td>1.5</td>
<td></td>
</tr>
<tr>
<td>Percent fiber in the hulls:</td>
<td>35.0</td>
<td></td>
</tr>
<tr>
<td>Percent dry matter loss (% of incoming):</td>
<td>0.0</td>
<td></td>
</tr>
<tr>
<td>Oil Extraction</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Percent moisture of flakes leaving extraction:</td>
<td>13.0</td>
<td></td>
</tr>
<tr>
<td>Percent oil of flakes leaving extraction:</td>
<td>0.5</td>
<td></td>
</tr>
<tr>
<td>Percent dry matter loss of spent flakes in oil:</td>
<td>0.0</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Pricing Options</th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>NOPA Rules Used?</td>
<td>YES</td>
<td></td>
</tr>
<tr>
<td>Protein Premiums Used?</td>
<td>YES</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Meal Formulation</th>
<th>Soybean Composition</th>
</tr>
</thead>
<tbody>
<tr>
<td>Percent moisture in soybean meal:</td>
<td>12.0</td>
</tr>
<tr>
<td>Desired percent protein in soybean meal:</td>
<td>48.0</td>
</tr>
<tr>
<td>Maximum fiber percent in soybean meal:</td>
<td>3.5</td>
</tr>
<tr>
<td>Percent moisture in mill feed:</td>
<td>12.0</td>
</tr>
<tr>
<td>Percent protein in mill feed:</td>
<td>12.0</td>
</tr>
<tr>
<td>Percent oil in mill feed:</td>
<td>1.5</td>
</tr>
<tr>
<td>Percent fiber in mill feed:</td>
<td>35.0</td>
</tr>
<tr>
<td>Fiber</td>
<td>4.40</td>
</tr>
<tr>
<td>Raffinose</td>
<td>0.75</td>
</tr>
<tr>
<td>Stachyose</td>
<td>4.05</td>
</tr>
<tr>
<td>Sucrose</td>
<td>4.25</td>
</tr>
<tr>
<td>Palmitic Acid</td>
<td>12.00</td>
</tr>
<tr>
<td>Stearic Acid</td>
<td>4.00</td>
</tr>
<tr>
<td>Oleic Acid</td>
<td>21.00</td>
</tr>
<tr>
<td>Linoleic Acid</td>
<td>55.00</td>
</tr>
<tr>
<td>Linolenic Acid</td>
<td>9.00</td>
</tr>
</tbody>
</table>
Table 7: Sample Data Set Summary

<table>
<thead>
<tr>
<th>Basis</th>
<th>HP-HEAA (n = 42)</th>
<th>HP-LEAA (n = 39)</th>
<th>LP-HEAA (n = 40)</th>
<th>LP-LEAA (n = 41)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Min</td>
<td>Max</td>
<td>SD</td>
</tr>
<tr>
<td>Protein</td>
<td>40.07</td>
<td>36.13</td>
<td>50.73</td>
<td>3.02</td>
</tr>
<tr>
<td>Fiber</td>
<td>4.40</td>
<td>4.40</td>
<td>4.40</td>
<td>0.00</td>
</tr>
<tr>
<td>Alanine</td>
<td>4.52</td>
<td>3.92</td>
<td>5.93</td>
<td>0.39</td>
</tr>
<tr>
<td>Arginine</td>
<td>1.48</td>
<td>1.36</td>
<td>1.68</td>
<td>0.08</td>
</tr>
<tr>
<td>Aspartic Acid</td>
<td>1.78</td>
<td>1.49</td>
<td>2.21</td>
<td>0.16</td>
</tr>
<tr>
<td>Cysteine</td>
<td>7.14</td>
<td>6.20</td>
<td>8.33</td>
<td>0.55</td>
</tr>
<tr>
<td>Glutamic Acid</td>
<td>1.90</td>
<td>1.65</td>
<td>2.24</td>
<td>0.14</td>
</tr>
<tr>
<td>Glycine</td>
<td>1.64</td>
<td>1.47</td>
<td>1.92</td>
<td>0.11</td>
</tr>
<tr>
<td>Histidine</td>
<td>1.64</td>
<td>1.50</td>
<td>1.89</td>
<td>0.10</td>
</tr>
<tr>
<td>Isoleucine</td>
<td>0.62</td>
<td>0.51</td>
<td>0.81</td>
<td>0.06</td>
</tr>
<tr>
<td>Leucine</td>
<td>1.88</td>
<td>1.50</td>
<td>2.16</td>
<td>0.13</td>
</tr>
<tr>
<td>Lysine</td>
<td>0.55</td>
<td>0.48</td>
<td>0.65</td>
<td>0.04</td>
</tr>
<tr>
<td>Methionine</td>
<td>1.79</td>
<td>1.44</td>
<td>2.05</td>
<td>0.12</td>
</tr>
<tr>
<td>Phenylalanine</td>
<td>3.01</td>
<td>2.75</td>
<td>3.34</td>
<td>0.16</td>
</tr>
<tr>
<td>Proline</td>
<td>1.42</td>
<td>1.31</td>
<td>1.60</td>
<td>0.08</td>
</tr>
<tr>
<td>Serine</td>
<td>2.00</td>
<td>1.80</td>
<td>2.31</td>
<td>0.12</td>
</tr>
<tr>
<td>Threonine</td>
<td>2.49</td>
<td>2.29</td>
<td>2.81</td>
<td>0.14</td>
</tr>
<tr>
<td>Tryptophan</td>
<td>1.05</td>
<td>0.93</td>
<td>1.23</td>
<td>0.07</td>
</tr>
<tr>
<td>Tyrosine</td>
<td>3.04</td>
<td>2.59</td>
<td>4.92</td>
<td>0.45</td>
</tr>
<tr>
<td>Valine</td>
<td>0.48</td>
<td>0.37</td>
<td>0.57</td>
<td>0.05</td>
</tr>
<tr>
<td>Total EAA</td>
<td>5.61</td>
<td>5.26</td>
<td>6.23</td>
<td>0.27</td>
</tr>
</tbody>
</table>

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\textsubscript{protein/oil} & EPV\textsubscript{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\textsubscript{AA}, which includes the product values for soybean meal, oil, and extra mill run, proved to be greater than the EPV\textsubscript{protein/oil} in every category when the amino acid concentrations were used for determination instead of the protein and oil. The highest EPV\textsubscript{AA} of $12.38/bu occurred for the HP-HEAA category. However, the variation within the results was greater for the EPV\textsubscript{AA} with standard deviations ranging from $0.74/bu to $1.16/bu.

Table 8: Estimated Processed Value and Swine Feed Cost

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

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 EPV\textsubscript{protein/oil} and EPV\textsubscript{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 EPV\textsubscript{AA} of soybean meal logically increases because the value is based on its amino acid profile. It should be noted that the EPV\textsubscript{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 EPV\textsubscript{AA} and the corresponding feeding value of the soybean meal. The highest EPV\textsubscript{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 EPV\textsubscript{AA}), but the relative concentration of EAA to protein is the key factor that affects the feeding value.
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.

![Soybean Essential Amino Acids vs. Protein Concentration](image.png)

**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

<table>
<thead>
<tr>
<th>Meal Ingredients (% as fed)</th>
<th>Category</th>
<th>HP-HEAA (n = 42)</th>
<th>HP-LEAA (n = 39)</th>
<th>LP-HEAA (n = 40)</th>
<th>LP-LEAA (n = 41)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>Min</td>
<td>Max</td>
<td>SD</td>
<td>Mean</td>
</tr>
<tr>
<td>Corn, Yellow Dent</td>
<td>71.81a</td>
<td>69.20</td>
<td>75.88</td>
<td>1.36</td>
<td>71.14a</td>
</tr>
<tr>
<td>L-Lysine, HCl</td>
<td>0.22ab</td>
<td>0.16</td>
<td>0.33</td>
<td>0.04</td>
<td>0.24a</td>
</tr>
<tr>
<td>L-Threonine</td>
<td>0.07a</td>
<td>0.03</td>
<td>0.12</td>
<td>0.02</td>
<td>0.07a</td>
</tr>
<tr>
<td>Monocalcium Phosphate</td>
<td>1.04a</td>
<td>1.02</td>
<td>1.07</td>
<td>0.01</td>
<td>1.04a</td>
</tr>
<tr>
<td>Limestone</td>
<td>0.96c</td>
<td>0.95</td>
<td>0.99</td>
<td>0.01</td>
<td>0.96a</td>
</tr>
<tr>
<td>Salt</td>
<td>0.35</td>
<td>0.35</td>
<td>0.35</td>
<td>0.00</td>
<td>0.35</td>
</tr>
<tr>
<td>Choice White Grease</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
<td>0.00</td>
</tr>
<tr>
<td>L-Tryptophan</td>
<td>0.01b</td>
<td>0.00</td>
<td>0.02</td>
<td>0.01</td>
<td>0.01b</td>
</tr>
<tr>
<td>DL-Methionine</td>
<td>0.04a</td>
<td>0.01</td>
<td>0.09</td>
<td>0.02</td>
<td>0.05a</td>
</tr>
<tr>
<td>ME (kcal/lb)</td>
<td>1543ab</td>
<td>1523</td>
<td>1583</td>
<td>13.71</td>
<td>1552bc</td>
</tr>
<tr>
<td>Crude Protein (%)</td>
<td>18.92a</td>
<td>18.00</td>
<td>19.00</td>
<td>0.21</td>
<td>18.9b</td>
</tr>
<tr>
<td>Lysine (%)</td>
<td>1.12a</td>
<td>1.11</td>
<td>1.13</td>
<td>0.00</td>
<td>1.12a</td>
</tr>
<tr>
<td>NDF (%)</td>
<td>9.18a</td>
<td>9.15</td>
<td>9.52</td>
<td>0.07</td>
<td>9.19a</td>
</tr>
<tr>
<td>Cost ($/ton)</td>
<td>146.09a</td>
<td>143.89</td>
<td>148.72</td>
<td>1.33</td>
<td>147.53b</td>
</tr>
<tr>
<td>Total Synthetic EAA</td>
<td>0.34ab</td>
<td>0.20</td>
<td>0.56</td>
<td>0.08</td>
<td>0.37a</td>
</tr>
</tbody>
</table>

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.

Literature Cited


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.

![Flow Diagram of the Mass Balance Model](image)

**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)

<table>
<thead>
<tr>
<th>Soybean Preparation</th>
<th>%</th>
<th>Current Prices</th>
<th>$/lb</th>
</tr>
</thead>
<tbody>
<tr>
<td>Percent of soybeans removed as hulls:</td>
<td>10.0</td>
<td>Crude Soybean Oil:</td>
<td>0.230</td>
</tr>
<tr>
<td>Percent of moisture in hulls:</td>
<td>12.0</td>
<td>Soybean Meal:</td>
<td>0.125</td>
</tr>
<tr>
<td>Percent protein in the hulls:</td>
<td>12.0</td>
<td>Hulls/Mill Feed:</td>
<td>0.020</td>
</tr>
<tr>
<td>Percent oil in the hulls:</td>
<td>1.5</td>
<td>Oil Premium:</td>
<td>0.000</td>
</tr>
<tr>
<td>Percent fiber in the hulls:</td>
<td>35.0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Percent dry matter loss (% of incoming):</td>
<td>0.0</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Oil Extraction</th>
<th></th>
<th>Pricing Options</th>
</tr>
</thead>
<tbody>
<tr>
<td>Percent moisture of flakes leaving extraction:</td>
<td>13.0</td>
<td>NOPA Rules Used?</td>
</tr>
<tr>
<td>Percent oil of flakes leaving extraction:</td>
<td>0.5</td>
<td>Protein Premiums Used?</td>
</tr>
<tr>
<td>Percent dry matter loss of spent flakes in oil:</td>
<td>0.0</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Meal Formulation</th>
<th></th>
<th>Soybean Composition</th>
<th>%</th>
</tr>
</thead>
<tbody>
<tr>
<td>Percent moisture in soybean meal:</td>
<td>12.0</td>
<td>Moisture Basis</td>
<td>13.0</td>
</tr>
<tr>
<td>Desired percent protein in soybean meal:</td>
<td>44.0</td>
<td>Fiber</td>
<td>4.4</td>
</tr>
<tr>
<td>Maximum fiber percent in soybean meal:</td>
<td>7.0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Percent moisture in mill feed:</td>
<td>12.0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Percent protein in mill feed:</td>
<td>12.0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Percent oil in mill feed:</td>
<td>1.5</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Percent fiber in mill feed:</td>
<td>35.0</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**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

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

Notes: SPROC = Soybean Processing Model. Highlighted regions show area of deviation. *The deviation is calculated using the absolute difference between the results for both models and for each sample. ^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. ¨Basis 13.0% moisture.
Literature Cited


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.
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.

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.
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’

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

2. All red boxes indicate a user input.
   • There must 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

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.

   OR

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

   OR

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

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 48% protein meal is 3.5% fiber.

   ![System C Parameters (Meal Formulation)](image)

   OR

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

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.
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.

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.
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 0 or leave the box blank.

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.

![Image of data entry screen]

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

![Image of printer data entry]

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

![Image of swine feed software]

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
```

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
```

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.
```

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 will not run if this box is empty.

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.
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.

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 MUST 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 text files (.txt) or excel files (.xlsx)
   c. Type the name of your file in the ‘Data File Name’ box.
   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’.
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.
h. If amino acid concentrations are unknown, 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.

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.
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.

<table>
<thead>
<tr>
<th>Amino Acids</th>
<th>Slope</th>
<th>Intercept</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alanine</td>
<td>0.029</td>
<td>0.460</td>
</tr>
<tr>
<td>Arginine</td>
<td>0.094</td>
<td>-0.762</td>
</tr>
<tr>
<td>Asparagine</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Aspartic Acid</td>
<td>0.112</td>
<td>-0.035</td>
</tr>
<tr>
<td>Cysteine</td>
<td>0.009</td>
<td>0.245</td>
</tr>
<tr>
<td>Glutamine</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Glutamic Acid</td>
<td>0.205</td>
<td>-1.081</td>
</tr>
<tr>
<td>Glycine</td>
<td>0.033</td>
<td>0.307</td>
</tr>
<tr>
<td>Histidine</td>
<td>0.023</td>
<td>0.154</td>
</tr>
<tr>
<td>Isoleucine</td>
<td>0.037</td>
<td>0.302</td>
</tr>
</tbody>
</table>

| Carbohydrates | | |
|---------------|--|
| Raffinose     | |
| Stachyose     | |

<table>
<thead>
<tr>
<th>Fatty Acids (% of oil)</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>Palmitic Acid</td>
<td>Linolenic Acid</td>
</tr>
<tr>
<td>Stearic Acid</td>
<td>Linolenic Acid</td>
</tr>
<tr>
<td>Oleic Acid</td>
<td></td>
</tr>
</tbody>
</table>

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

- If the calculations are DISABLED, all amino acid values MUST 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.
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.

   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.
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.

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

<table>
<thead>
<tr>
<th>Total EPV</th>
<th>EPVs</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yield Evaluation</td>
<td>Amino Acid Evaluation</td>
</tr>
<tr>
<td>$ 8.65 / bu</td>
<td>$ 11.46 / bu</td>
</tr>
</tbody>
</table>

NOPA Rules and Meal Protein Premium in Effect:

Price Adjustment: $ 0.003 / lb

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
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.
   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.

   b. Click the ‘Save’ button.

4. Repeat steps 1-3 for all desired formulations.
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
  End If
ElseIf Worksheets("Inputs").Range("AF7") = "Enter From User" 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
  End If
End If

ErrorHandler:
  Exit Sub
End If
ElseIf Worksheets("Inputs").Range("AF8") = "AA = YES" And Workshee\ts("Inputs").Range("AF9") = "Carb = YES" And Workshee\ts("Inputs").Range("AF10") = "FA = YES" Then

    VariableNum = 34

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

    VariableNum = 9

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

    VariableNum = 10

ElseIf Worksheets("Inputs").Range("AF8") = "AA = NO" And Workshee\ts("Inputs").Range("AF9") = "Carb = YES" And Workshee\ts("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 = NO" And Worksheets("Inputs").Range("AF10")
    = "FA = NO" Then
        VariableNum = 29
    ElseIf Worksheets("Inputs").Range("AF8") = "AA = NO" And
    Worksheets("Inputs").Range("AF9") = "Carb = YES" And
    Worksheets("Inputs").Range("AF10") = "FA = NO" 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


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" AndWorksheets("Inputs").Range("AF9") = "Carb = NO" AndWorksheets("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("AC27") = file_data(16, i + 1)
    Worksheets("Inputs").Range("AC28") = file_data(17, i + 1)
    Worksheets("Inputs").Range("AC29") = file_data(18, i + 1)
    Worksheets("Inputs").Range("AC30") = file_data(19, i + 1)
    Worksheets("Inputs").Range("AC31") = file_data(20, i + 1)
    Worksheets("Inputs").Range("AC32") = file_data(21, i + 1)
    Worksheets("Inputs").Range("AC33") = file_data(22, i + 1)
    Worksheets("Inputs").Range("AC34") = file_data(23, i + 1)
    Worksheets("Inputs").Range("AC35") = file_data(24, i + 1)
    Worksheets("Inputs").Range("AC36") = file_data(25, i + 1)
    Worksheets("Inputs").Range("AC37") = file_data(26, i + 1)
    Worksheets("Inputs").Range("AC38") = file_data(27, i + 1)
    Worksheets("Inputs").Range("AC39") = file_data(28, i + 1)
    Worksheets("Inputs").Range("AC40") = file_data(29, i + 1)
    Worksheets("Inputs").Range("AC41") = file_data(30, i + 1)
    Worksheets("Inputs").Range("AC42") = file_data(31, i + 1)
    Worksheets("Inputs").Range("AC43") = file_data(32, i + 1)
    Worksheets("Inputs").Range("AC44") = file_data(33, i + 1)
    Worksheets("Inputs").Range("AC45") = 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_Alpha = 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_Tyr = Worksheets("Inputs").Range("N31").Value
Price_Val = Worksheets("Inputs").Range("N32").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

'Raffinose 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("AL33").Value
Lys_Co = Worksheets("Inputs").Range("AO24").Value
Met_Co = Worksheets("Inputs").Range("AO25").Value
Phe_Co = Worksheets("Inputs").Range("AO26").Value
Pro_Co = Worksheets("Inputs").Range("AO27").Value
Ser_Co = Worksheets("Inputs").Range("AO28").Value
Thr_Co = Worksheets("Inputs").Range("AO29").Value
Trp_Co = Worksheets("Inputs").Range("AO30").Value
Tyr_Co = Worksheets("Inputs").Range("AO31").Value
Valine_Co = Worksheets("Inputs").Range("AO32").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").Value = ""
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").Value = ""
Else
  Pa5 = 4.4 'Default fiber value for 13% moisture basis.
  Worksheets("Inputs").Range("AE9").Value = ""
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))
\[
Pf5 = \frac{Pf5}{1 - (Pf1 / 100)}
\]
\[
Pd2max = \frac{Pd2spec}{1 - (Pd1 / 100)}
\]
\[
Pd5max = \frac{Pd5spec}{1 - (Pd1 / 100)}
\]
\[
Ala = \frac{Ala_{In}}{1 - (Pa1 / 100)}
\]
\[
arg = \frac{Arg_{In}}{1 - (Pa1 / 100)}
\]
\[
Asn = \frac{Asn_{In}}{1 - (Pa1 / 100)}
\]
\[
Asp = \frac{Asp_{In}}{1 - (Pa1 / 100)}
\]
\[
cys = \frac{Cys_{In}}{1 - (Pa1 / 100)}
\]
\[
Gln = \frac{Gln_{In}}{1 - (Pa1 / 100)}
\]
\[
Glu = \frac{Glu_{In}}{1 - (Pa1 / 100)}
\]
\[
Gly = \frac{Gly_{In}}{1 - (Pa1 / 100)}
\]
\[
his = \frac{His_{In}}{1 - (Pa1 / 100)}
\]
\[
ile = \frac{Ile_{In}}{1 - (Pa1 / 100)}
\]
\[
leu = \frac{Leu_{In}}{1 - (Pa1 / 100)}
\]
\[
lys = \frac{Lys_{In}}{1 - (Pa1 / 100)}
\]
\[
met = \frac{Met_{In}}{1 - (Pa1 / 100)}
\]
\[
phe = \frac{Phe_{In}}{1 - (Pa1 / 100)}
\]
\[
pro = \frac{Pro_{In}}{1 - (Pa1 / 100)}
\]
\[
Ser = \frac{Ser_{In}}{1 - (Pa1 / 100)}
\]
\[
thr = \frac{Thr_{In}}{1 - (Pa1 / 100)}
\]
\[
trp = \frac{Trp_{In}}{1 - (Pa1 / 100)}
\]
\[
ty = \frac{Tyr_{In}}{1 - (Pa1 / 100)}
\]
\[
valine = \frac{Valine_{In}}{1 - (Pa1 / 100)}
\]
\[
Raffinose = \frac{Raffinose_{In}}{1 - (Pa1 / 100)}
\]
\[
Stachyose = \frac{Stachyose_{In}}{1 - (Pa1 / 100)}
\]
\[
Sucrose = \frac{Sucrose_{In}}{1 - (Pa1 / 100)}
\]
\[
OtherCarb = \frac{OtherCarb_{In}}{1 - (Pa1 / 100)}
\]
\[
Ala_Hulls = \frac{Ala_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Arg_Hulls = \frac{Arg_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Asn_Hulls = \frac{Asn_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Asp_Hulls = \frac{Asp_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Asx_Hulls = \frac{Asx_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Cys_Hulls = \frac{Cys_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Gln_Hulls = \frac{Gln_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Glu_Hulls = \frac{Glu_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Glx_Hulls = \frac{Glx_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Gly_Hulls = \frac{Gly_{Hulls}}{1 - (ph1 / 100)}
\]
\[
His_Hulls = \frac{His_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Ile_Hulls = \frac{Ile_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Leu_Hulls = \frac{Leu_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Lys_Hulls = \frac{Lys_{Hulls}}{1 - (ph1 / 100)}
\]
\[
Met_Hulls = \frac{Met_{Hulls}}{1 - (ph1 / 100)}
\]
\[
\begin{align*}
Phe_{\text{Hulls}} &= \frac{Phe_{\text{Hulls}}}{1 - (\text{ph1} / 100)} \\
Pro_{\text{Hulls}} &= \frac{Pro_{\text{Hulls}}}{1 - (\text{ph1} / 100)} \\
Ser_{\text{Hulls}} &= \frac{Ser_{\text{Hulls}}}{1 - (\text{ph1} / 100)} \\
Thr_{\text{Hulls}} &= \frac{Thr_{\text{Hulls}}}{1 - (\text{ph1} / 100)} \\
Trp_{\text{Hulls}} &= \frac{Trp_{\text{Hulls}}}{1 - (\text{ph1} / 100)} \\
Tyr_{\text{Hulls}} &= \frac{Tyr_{\text{Hulls}}}{1 - (\text{ph1} / 100)} \\
\text{Valine}_{\text{Hulls}} &= \frac{\text{Valine}_{\text{Hulls}}}{1 - (\text{ph1} / 100)} \\
\text{Raffinose}_{\text{Hulls}} &= \frac{\text{Raffinose}_{\text{Hulls}}}{1 - (\text{ph1} / 100)} \\
\text{Stachyose}_{\text{Hulls}} &= \frac{\text{Stachyose}_{\text{Hulls}}}{1 - (\text{ph1} / 100)} \\
\text{Sucrose}_{\text{Hulls}} &= \frac{\text{Sucrose}_{\text{Hulls}}}{1 - (\text{ph1} / 100)} \\
\text{OtherCarb}_{\text{Hulls}} &= \frac{\text{OtherCarb}_{\text{Hulls}}}{1 - (\text{ph1} / 100)}
\end{align*}
\]

'SYSTEM A (SOYBEAN PREPARATION):

'Mass Calculations:
\[
\begin{align*}
\text{WaNet} &= \text{Wa} \times (1 - (\text{DMLa} / 100)) \\
\text{Wh} &= \text{WaNet} \times (\text{Pah} / 100) \\
\text{Wb} &= \text{WaNet} - \text{Wh}
\end{align*}
\]

'Protein Calculations:
\[
\begin{align*}
\text{Pb2} &= \frac{(\text{WaNet} \times \text{Pa2} - \text{Wh} \times \text{ph2})}{\text{Wb}}
\end{align*}
\]

'Oil Calculations:
\[
\begin{align*}
\text{Pb3} &= \frac{(\text{WaNet} \times \text{Pa3} - \text{Wh} \times \text{ph3})}{\text{Wb}}
\end{align*}
\]

'Fiber Calculations:
\[
\begin{align*}
\text{Pb5} &= \frac{(\text{WaNet} \times \text{Pa5} - \text{Wh} \times \text{Ph5})}{\text{Wb}}
\end{align*}
\]

'SYSTEM B (SOLVENT EXTRACTION):

'Oil Calculations:
\[
\begin{align*}
\text{Wo} &= \frac{(\text{Wb} \times (\text{Pb3} - \text{Pc3}))}{(100 - \text{Pc3})}
\end{align*}
\]

'Mass Calculations:
\[
\begin{align*}
\text{Wc} &= \frac{(\text{Wb} - \text{Wo})}{(1 - (\text{DMLc} / 100))}
\end{align*}
\]

'Protein Calculations:
\[
\begin{align*}
\text{Pc2} &= \frac{(\text{Wb} \times \text{Pb2})}{\text{Wc}}
\end{align*}
\]

'Fiber Calculations:
\[
\begin{align*}
\text{Pc5} &= \frac{(\text{Wb} \times \text{Pb5})}{\text{Wc}}
\end{align*}
\]
'Product Weight for System C:
  \[ W_{1c} = W_c \]

progress 30 'Sets progress bar to 30%

'SYSTEM C (MEAL FORMULATION FOR SOYBEAN MEAL):
  'Note: The protein content of the meal (P_{d2}) is initially set equal to the desired protein content (P_{d2spec}).
  '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.

P_{d2} = P_{d2max}
Mode = "SystemC_1"
W_{1f} = 0
W_{1h} = 0

Do While Mode <> "DONE"
Select Case Mode
  Case "SystemC_1"
    If P_{d2} <= P_{c2} Then 'Can the protein specification be met?
      Mode = "SystemC_2"
    Else
      P_{d2} = P_{c2}
P_{d5} = P_{c5}
      W_{1h} = 0 'Weight of hulls added to soybean meal
      W_{1f} = 0 'Weight of mill feed added to soybean meal
      W_{1d} = W_{1c}
      Mode = "DONE"
  End If

  Case "SystemC_2"
    If P_{d5max} >= P_{c5} Then 'Can the fiber specification be met?
      Mode = "SystemC_3"
    Else
      P_{d2} = P_{c2}
P_{d5} = P_{c5}
      W_{1h} = 0 'Weight of hulls added to soybean meal
      W_{1f} = 0 'Weight of mill feed added to soybean meal
      W_{1d} = W_{1c}
      Mode = "DONE"
  End If

  Case "SystemC_3"
    'Protein Calculations:
\[ W_{1d} = \frac{(W_{1c} \cdot (P_{c2} - P_{h2}))}{(P_{d2} - P_{h2})} \]

'Mass Calculations:
\[ W_{1h} = W_{1d} - W_{1c} \]

If \( W_{1h} \leq W_h \) Then 'How much hulls were added? Less than the amount removed in dehulling?
     Mode = "SystemC_5"
Else
     \( W_{1h} = W_h \)
     Mode = "SystemC_4"
End If

Case "SystemC_4"
'Add mill feed to meet the protein specification
'Protein Calculations:
\[ W_{1d} = \frac{(W_{1c} \cdot (P_{c2} - P_{f2}) + W_{1h} \cdot (P_{h2} - P_{f2}))}{(P_{d2} - P_{f2})} \]

'Mass Calculations:
\[ W_{1f} = W_{1d} - W_{1c} - W_{1h} \]
     Mode = "SystemC_5"

Case "SystemC_5"
'Hulls (and possible mill feed) are added to meet the protein specification.
'Fiber Calculations:
\[ P_{d5} = \frac{(W_{1c} \cdot P_{c5} + W_{1h} \cdot P_{h5} + W_{1f} \cdot P_{f5})}{W_{1d}} \]

If \( P_{d5} \leq P_{d5\text{max}} \) 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.
\[ P_{d5} = P_{d5\text{max}} \]
'Fiber Calculations:
\[ W_{1d} = \frac{(W_{1c} \cdot (P_{c5} - P_{f5}) + W_{1h} \cdot (P_{h5} - P_{f5}))}{(P_{d5} - P_{f5})} \]

'Mass Calculations:
\[ W_{1f} = W_{1d} - W_{1c} - W_{1h} \]

'Can we add any filler?
If \( W_{1f} \geq 0 \) 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))
il = 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)


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.
            Mode = "EPV_6"
        End If
    Else
        Mode = "EPV_6"
    End If

Case "EPV_6"
    'Calculate the EPV.
    EPVM = (PriceMeal - DiscP) * W1d
    EPVM_AA = (PriceMeal_AA - DiscP_AA) * W1d
    EPVMo = PriceOil * Wo
    EPVMillFeed = PriceHMF * (Wh - W1h - W1f)
    EPV_AA = EPVM + EPVMo + EPVMillFeed
    EPV = EPVM + EPVMo + 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 variables:

'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
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") = Whn
Worksheets("Outputs").Range("M13") = W1h
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") = argn
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
    End If

    Row = Row + 1
End Do
Soybean Meal Composition

<table>
<thead>
<tr>
<th>Worksheet Cell</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Row, 33</td>
<td>Stachyose_In</td>
</tr>
<tr>
<td>Row, 34</td>
<td>Sucrose_In</td>
</tr>
<tr>
<td>Row, 35</td>
<td>OtherCarb_In</td>
</tr>
<tr>
<td>Row, 36</td>
<td>W1d</td>
</tr>
<tr>
<td>Row, 37</td>
<td>Pd1</td>
</tr>
<tr>
<td>Row, 38</td>
<td>Pd2</td>
</tr>
<tr>
<td>Row, 39</td>
<td>Pd3</td>
</tr>
<tr>
<td>Row, 40</td>
<td>Pd5</td>
</tr>
<tr>
<td>Row, 41</td>
<td>W1h</td>
</tr>
<tr>
<td>Row, 42</td>
<td>W1f</td>
</tr>
<tr>
<td>Row, 43</td>
<td>Ala</td>
</tr>
<tr>
<td>Row, 44</td>
<td>arg</td>
</tr>
<tr>
<td>Row, 45</td>
<td>Asn</td>
</tr>
<tr>
<td>Row, 46</td>
<td>Asp</td>
</tr>
<tr>
<td>Row, 47</td>
<td>cys</td>
</tr>
<tr>
<td>Row, 48</td>
<td>Gln</td>
</tr>
<tr>
<td>Row, 49</td>
<td>Glu</td>
</tr>
<tr>
<td>Row, 50</td>
<td>Gly</td>
</tr>
<tr>
<td>Row, 51</td>
<td>his</td>
</tr>
<tr>
<td>Row, 52</td>
<td>ile</td>
</tr>
<tr>
<td>Row, 53</td>
<td>leu</td>
</tr>
<tr>
<td>Row, 54</td>
<td>lys</td>
</tr>
<tr>
<td>Row, 55</td>
<td>met</td>
</tr>
<tr>
<td>Row, 56</td>
<td>phe</td>
</tr>
<tr>
<td>Row, 57</td>
<td>pro</td>
</tr>
<tr>
<td>Row, 58</td>
<td>Ser</td>
</tr>
<tr>
<td>Row, 59</td>
<td>thr</td>
</tr>
<tr>
<td>Row, 60</td>
<td>trp</td>
</tr>
<tr>
<td>Row, 61</td>
<td>tyr</td>
</tr>
<tr>
<td>Row, 62</td>
<td>valine</td>
</tr>
<tr>
<td>Row, 63</td>
<td>Raffinose</td>
</tr>
<tr>
<td>Row, 64</td>
<td>Stachyose</td>
</tr>
<tr>
<td>Row, 65</td>
<td>Sucrose</td>
</tr>
<tr>
<td>Row, 66</td>
<td>OtherCarb</td>
</tr>
</tbody>
</table>

Crude Oil Composition

<table>
<thead>
<tr>
<th>Worksheet Cell</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>Row, 67</td>
<td>Wo</td>
</tr>
<tr>
<td>Row, 68</td>
<td>Palmitic_In</td>
</tr>
<tr>
<td>Row, 69</td>
<td>Stearic_In</td>
</tr>
<tr>
<td>Row, 70</td>
<td>Oleic_In</td>
</tr>
<tr>
<td>Row, 71</td>
<td>Linoleic_In</td>
</tr>
<tr>
<td>Row, 72</td>
<td>Linolenic_In</td>
</tr>
<tr>
<td>Row, 73</td>
<td>Whn</td>
</tr>
</tbody>
</table>

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
        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
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
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 & ": " & pctCompl & "/100% 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
    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 _
If (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)

End Sub
.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