What is claimed is:

1. A method of developing a computer model for analyzing feed for swine or poultry comprising steps of:

(a) digesting in vitro a plurality of samples of animal feed each having an animal feed composition to generate a plurality of digested animal feed samples, wherein each of the plurality of digested animal feed samples comprises at least one residual component, wherein the at least one residual component is selected from the group consisting of protein, phosphorous, fat, gross energy, and carbohydrates, wherein the samples of animal feed consist of swine feed, poultry feed, and mixtures thereof, wherein each animal feed composition comprises one or more of corn, soybean, grain(s), distiller grain(s), legumes, molasses, or a mixture of any thereof, wherein digesting comprises two phases, wherein a phase is conducted at a pH of less than about 7 and includes use of at least one enzyme comprising pepsin, and wherein another phase is conducted at a neutral to acidic pH and includes at least one enzyme comprising pancreatin, and wherein digesting further comprises separating each of the plurality of digested animal feed samples into a solid component and a liquid component;

(b) scanning the solid component of each of the plurality of digested animal feed samples using a near infrared (NIR) spectrophotometer to generate spectral data for each of the plurality of digested animal feed samples;

(c) determining the concentration of the at least one residual component in each of the plurality of digested animal feed samples using a wet chemistry method; and

(d) generating a computer model comprising a computer implemented method comprising steps of:

i) receiving spectral data for each of the plurality of digested animal feed samples;

ii) relating the spectral data for each of the plurality of digested animal feed samples to the concentration of the at least one residual component in a corresponding sample of the plurality of digested animal feed samples; and

iii) establishing a predictive relationship based on the spectral data and the concentration of the at least one residual component of the plurality of digested animal feed samples to generate the computer model.

2. The method of claim 1, wherein the step of scanning the solid component of each of the plurality of digested feed samples further comprises the step of mathematically manipulating the spectral data of each of the plurality of digested animal feed samples.

3. The method of any one of claims 1-2, wherein the wet chemistry method comprises analyzing each sample of the digested feed for the concentration of the at least one residual component selected from the group consisting of protein, phosphorous, fat, gross energy, and carbohydrates.

4. The method of claim 1, wherein each of the plurality of samples of animal feed is swine feed, wherein the phase is conducted for 1 to 6 hours at a pH of less than about 7 and the other phase is conducted for 18 hours to 48 hours at neutral pH to an acidic pH of at least 6.0, to generate the digested animal feed.

5. The method of claim 1, wherein each of the plurality of samples of animal feed is poultry feed, and wherein the digesting further comprises an in vitro digestion phase conducted on each of the samples of animal feed that includes at least one enzyme comprising phytase.

6. The method of claim 4, wherein the phase that includes pepsin is conducted at a pH of less than about 7 for 30 minutes to 2 hours and the other phase that includes pancreatin is conducted at neutral pH to an acidic pH of at least 6.0 for 30 minutes to 2 hours, to generate the digested animal feed.

7. The method of claim 1, wherein the at least one residual component is selected from the group consisting of protein, phosphorous, fat, and gross energy.