Appl Note 182. OnLine Analysis of Wheat using the CropScan 3000S On Silo Analyser

Introduction.

This study shows the use and accuracy of the CropScan 3000S On Silo Analyser to measure protein and moisture in wheat at the in-take elevator of a large flour mill. The data in this study compares the protein and moisture as analysed by the CropScan 3000S On Silo Analyser and the mills' bench top NIR analyser.

Instrumentation.

The CropScan 3000S Near Infrared Transmission spectrometer uses a remote sampling head to collect a sub sample of grain from the in-take elevator and collect the NIR spectra of the grain before returning it to the a conveyer belt. A fiber optic cable transmits the NIR light back to the CropScan 3000S NIT spectrometer located in a Nema IV enclosure that is mounted on the wall near the in-take elevator. The CropScan 3000S uses a diode array spectrometer to scan the wavelength region 720-1100nm. The instrument scans a sample every 11 seconds and displays the individual and averaged protein and moisture values on a PC located in the mill's laboratory for each load received by the mill.

Calibration:

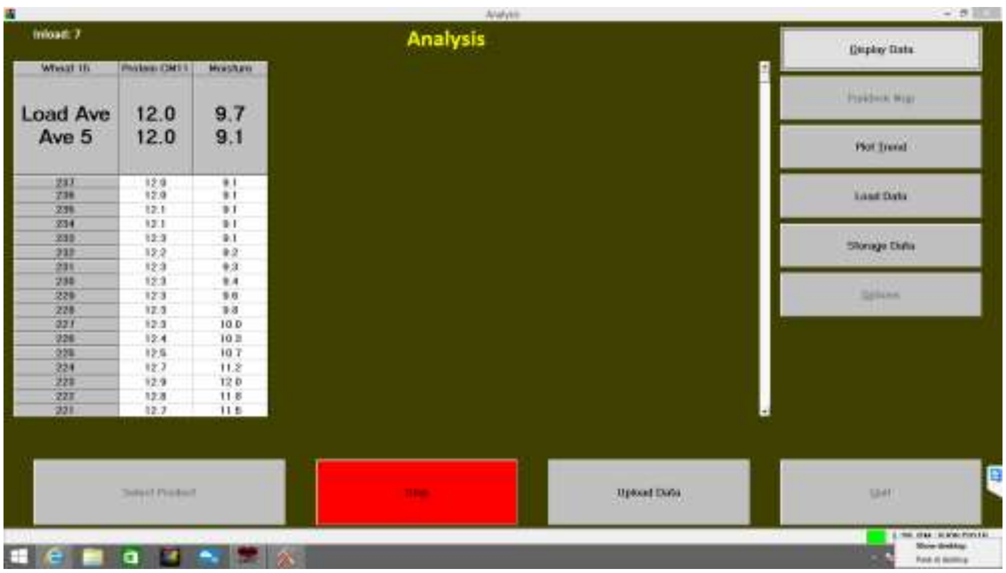
200 truckloads of wheat were speared and a 500ml sub sample was collected and analysed using the Foss Infratec 1214 NIR Analyser. Each truck load of wheat was emptied into the in-take elevator. The CropScan 3000S On Silo Analyser scanned sub sample from the in-take elevator every 11 seconds or 0.4 Tonne of grain loaded into the mill. The spectral data from the CropScan 3000S was averaged for each load. The lab data were collected from the Infratec 1241 and combined with the CropScan spectral file. A Partial Least Squares Regression was performed on the combined calibration file using NTAS (NIR Technology Analysis Software) to develop calibration model for protein and moisture. The calibration models were then used to predict the protein and moisture in the incoming wheat for a period of 1 week.

Software

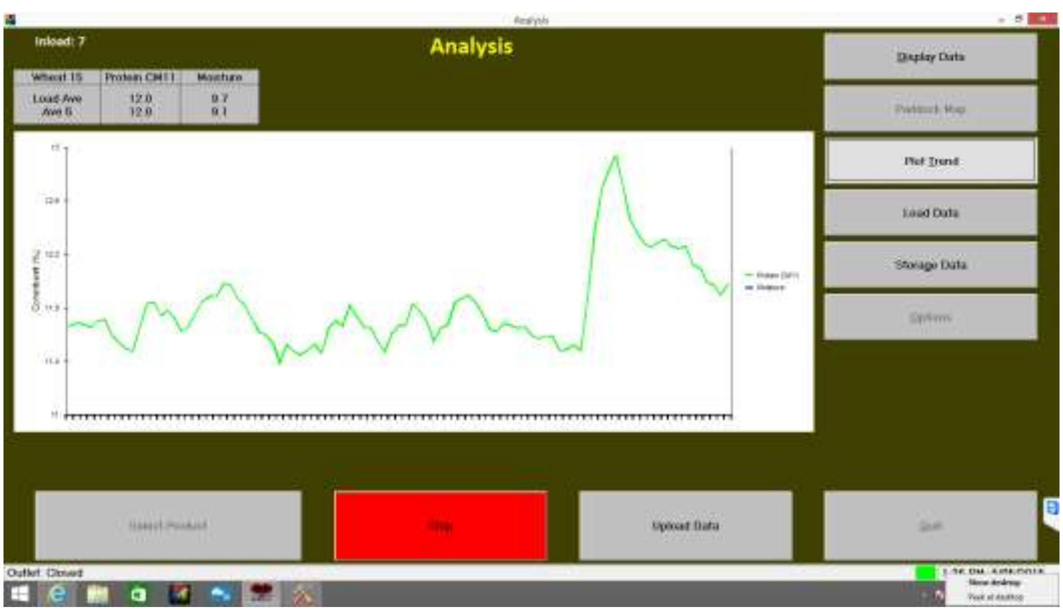
The CropScan 3000S Analysis software displays results and tables in an easy to read format to monitor protein and moisture in the wheat coming into the mill. The data provided by the CropScan 3000S allows the mill operators see the real variability of the protein and moisture of the wheat being received and potentially enabling the grain to be segregated in real time as it is received.

The Analysis Software displays 4 screens for the operator to toggle between to retrieve the information quickly.

Display Data screen shows the Load Average, Moving Average and the last 100 results scanned by the CropScan 3000S.

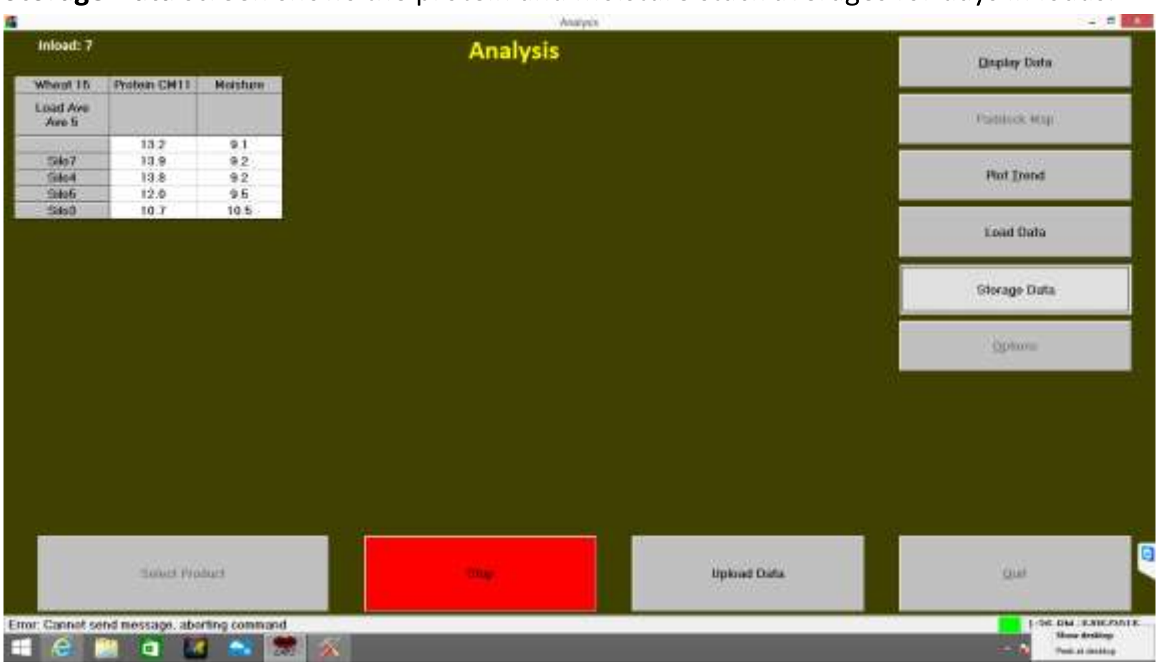


Plot Trend screen shows the results in a trend line plot to show the protein distributing across the entire load.



Load Data screen shows the summary days load averages for protein and moisture with the Weighbridge No, Supplier Name and which Silo the grain was stored into. This allows the operator to quickly view any previous loads results and receival information throughout the day.

Storage Data screen shows the protein and moisture stack averages for days in loads.



Results

Calibration Data

Figure 2.1, below, shows the NIT spectra for the Wheat samples.

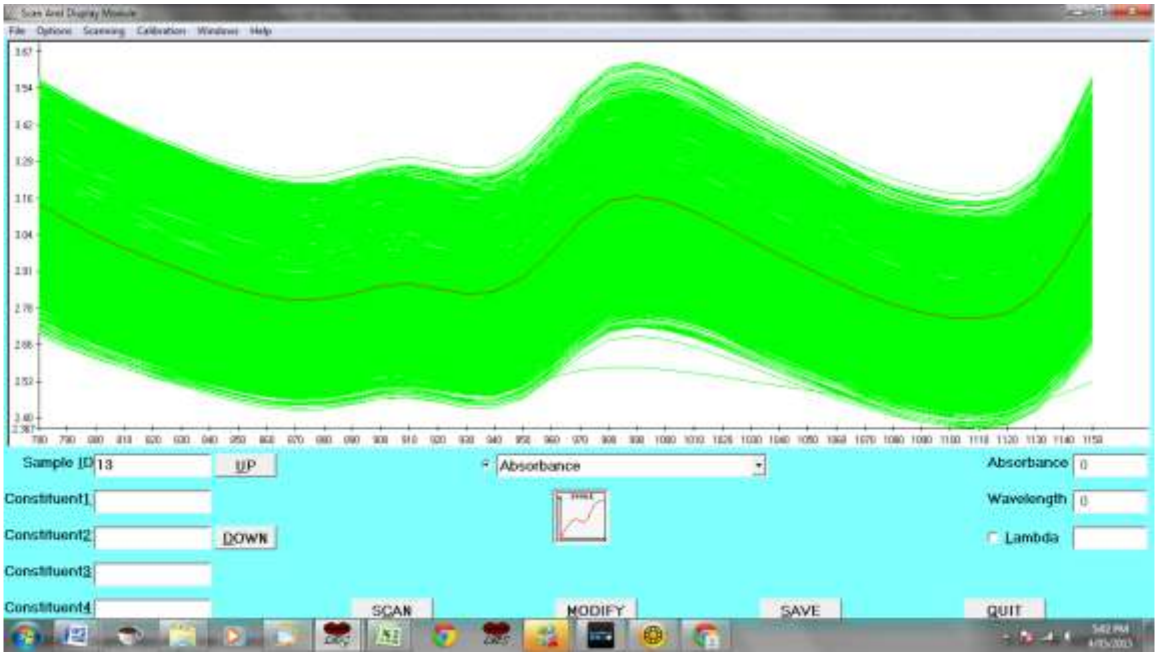


Figure 2.1: Plot of NIR Spectra for Wheat.

Figure 2.2 shows the calibration statistics for the protein. The Standard Error of Calibration (SEC) is 0.25% with a correlation (R2) of 0.97.

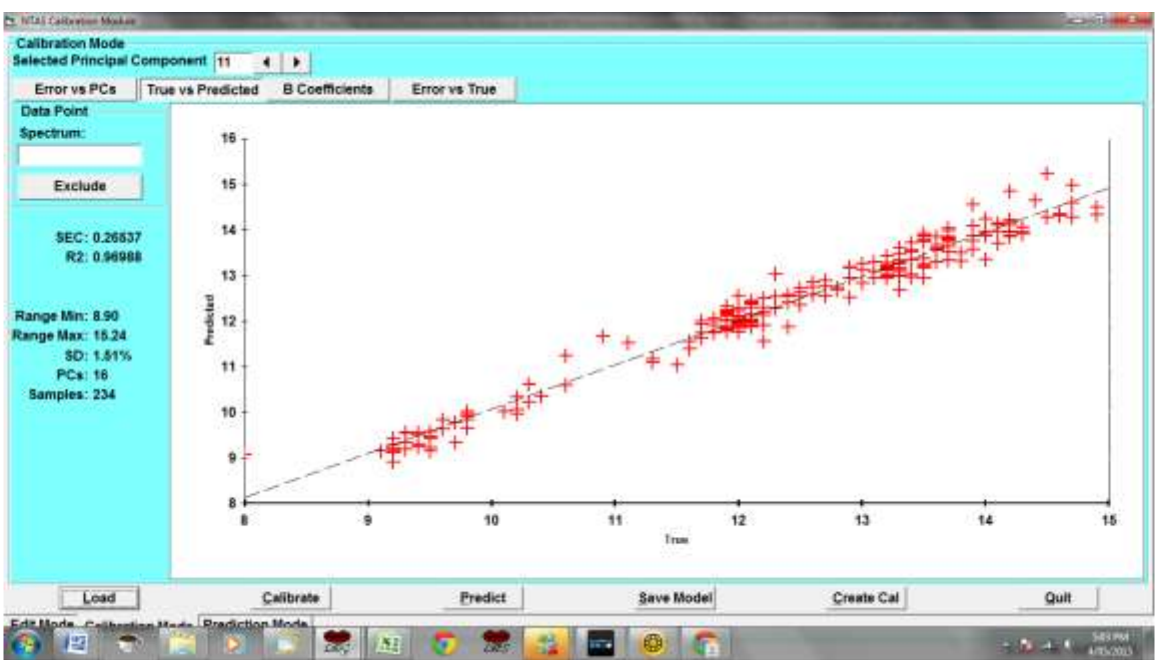


Figure 2.2: Protein Calibration Plot

Figure 2.3 shows the calibration statistics for the moisture. The Standard Error of Calibration (SEC) is 0.2% with a correlation (R2) of 0.96.

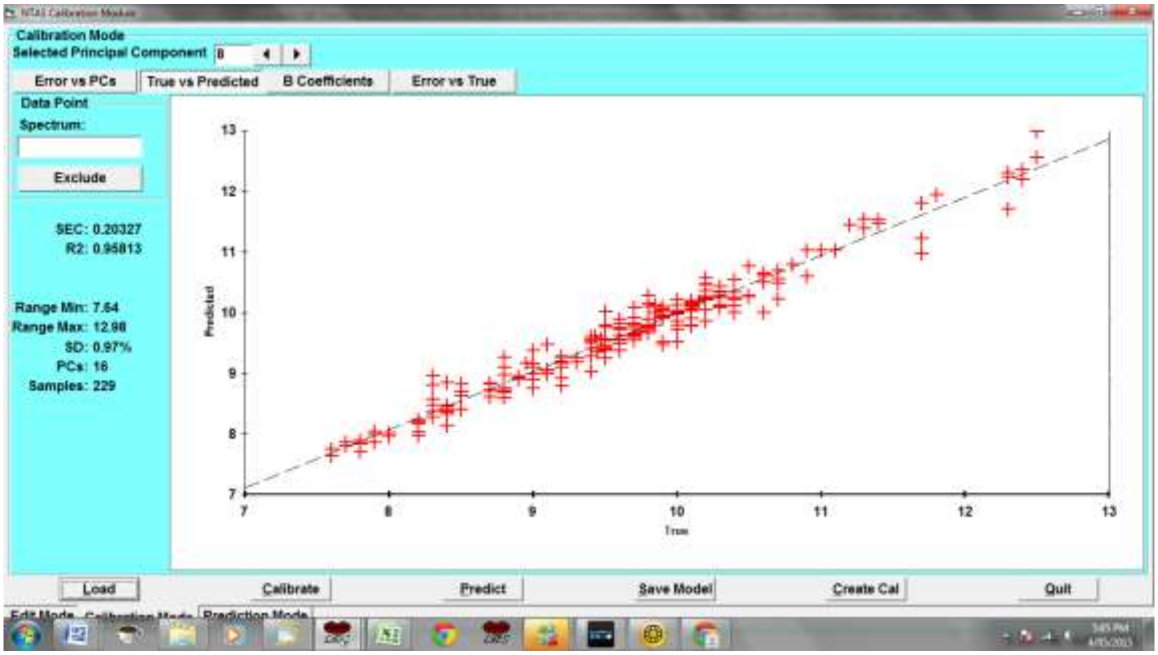


Figure 2.3: Moisture Calibration Plot

Prediction.

42 truckloads of wheat were measured over one week period to check for accuracy and stability. The table below shows the average protein and moisture results from the CropScan 3000S versus the average results from the laboratory NIR analyser.

Table 1: Predicted CropScan Protein Vs Lab Protein.

	CropScan	CropScan	Lab	CropScan	Lab	
	AS-IS	S & B	AS-IS	CM 11%	CM 11%	CM 11%
Sample ID	**Protein**	**Protein**	**Protein**	**Protein**	**Protein**	**Difference**
20M1	12.4	12.3	11.9	12.1	11.7	0.4
20M3	9.7	9.4	9.4	9.4	9.4	0.0
20M4	9.5	9.1	9.3	9.1	9.3	-0.2
20M5	13.8	13.9	13.3	13.7	13.1	0.6
20M6	12.1	12.1	11.8	12.0	11.8	0.2
20M7	12.0	11.9	12.0	11.5	11.6	-0.1
20M8	12.0	11.9	11.9	11.8	11.8	0.0
20M9	13.0	13.0	13.2	12.6	12.8	-0.2
20M10	13.4	13.5	13.5	13.5	13.6	-0.1
20M11	11.8	11.6	11.9	11.6	11.8	-0.2
21T1	14.5	14.6	14.4	14.3	14.1	0.2
21T2	12.7	12.7	13.1	12.2	12.6	-0.4
21T3	13.5	13.6	13.6	13.1	13.2	-0.1

21T4	11.9	11.8	11.9	11.7	11.8	-0.1
21T5	13.1	13.1	12.6	12.9	12.4	0.5
21T7	11.7	11.6	11.8	11.5	11.7	-0.2
21T9	9.4	9.1	9.3	9.1	9.3	-0.2
21T11	13.9	13.9	13.9	13.4	13.4	0.0
22W1	12.8	12.8	12.9	12.4	12.5	-0.1
22W2	14.3	14.4	14.3	14.1	14.0	0.1
22W3	13.2	13.2	13.1	12.9	12.8	0.1
22W4	10.0	9.7	9.4	9.7	9.4	0.3
22W5	14.0	14.1	14.6	13.8	14.3	-0.5
22W6	14.0	14.1	14.1	13.7	13.8	0.0
22W7	12.7	12.7	12.4	12.5	12.3	0.3
22W8	13.5	13.5	13.8	13.2	13.4	-0.2
22W9	13.8	13.8	14.3	13.5	14.0	-0.5
22W11	9.6	9.3	9.3	9.3	9.3	0.0
23TH1	13.9	13.9	14.3	13.7	14.0	-0.3
23TH2	9.6	9.2	9.6	9.2	9.4	-0.2
23TH3	14.1	14.2	14.3	13.9	14.1	-0.1
23TH4	13.5	13.6	13.7	13.3	13.3	-0.1
23TH5	13.7	13.8	13.7	13.5	13.5	0.0
23TH7	14.0	14.1	14.9	13.9	14.6	-0.7
23TH8	11.9	11.8	11.9	11.7	11.8	-0.1
23TH9	13.6	13.6	13.9	13.4	13.6	-0.2
23TH10	13.6	13.7	14.3	13.4	14.0	-0.6
24F1	13.1	13.2	12.9	12.8	12.5	0.3
24F2	12.0	11.8	11.8	11.7	11.7	0.0
24F3	9.7	9.4	9.4	9.4	9.3	0.0
24F4	11.8	11.7	11.9	11.6	11.8	-0.3
24F5	12.0	11.9	11.9	11.8	11.8	0.0
					Bias	**-0.06**
					SEP	**0.27**

Table 2 Prediction of Moisture CropScan 3000S vs Lab NIR

	CropScan	**Lab**	
Sample ID	**Moisture**	**Moisture**	**Difference**
20M1	9.8	9.6	0.2
20M3	10.6	10.7	-0.1
20M4	11.2	11.2	0.0
20M5	9.5	9.6	-0.1
20M6	10.3	10.7	-0.4
20M7	7.7	7.6	0.1
20M8	10.3	10.3	0.0

20M9	8.2	8.2	0.0
20M10	11.3	11.6	-0.3
20M11	10.5	10.3	0.2
21T1	9.2	9.3	-0.1
21T2	7.8	7.8	0.0
21T3	8.1	8.2	-0.1
21T4	10.4	10.3	0.1
21T5	10.0	9.8	0.2
21T7	10.3	10.3	0.0
21T9	11.3	11.0	0.3
21T11	7.6	7.7	-0.1
22W1	8.0	8.0	0.0
22W2	9.1	8.9	0.2
22W3	9.3	9.0	0.3
22W4	10.8	11.0	-0.2
22W5	9.3	9.1	0.2
22W6	8.9	8.9	0.0
22W7	10.2	10.1	0.1
22W8	8.6	8.3	0.3
22W9	8.9	9.0	-0.1
22W11	10.8	10.8	0.0
23TH1	9.4	9.3	0.0
23TH2	10.9	8.9	2.0
23TH3	9.5	9.5	0.0
23TH4	8.9	8.6	0.3
23TH5	9.3	9.5	-0.2
23TH7	9.4	9.2	0.2
23TH8	10.1	10.3	-0.2
23TH9	9.6	9.3	0.3
23TH10	9.3	9.3	0.0
24F1	8.2	7.9	0.3
24F2	10.0	10.1	-0.1
24F3	10.5	10.5	0.0
24F4	10.3	10.5	-0.2
24F5	10.2	10.2	0.0
		Bias	**0.10**
		SEP	**0.35**

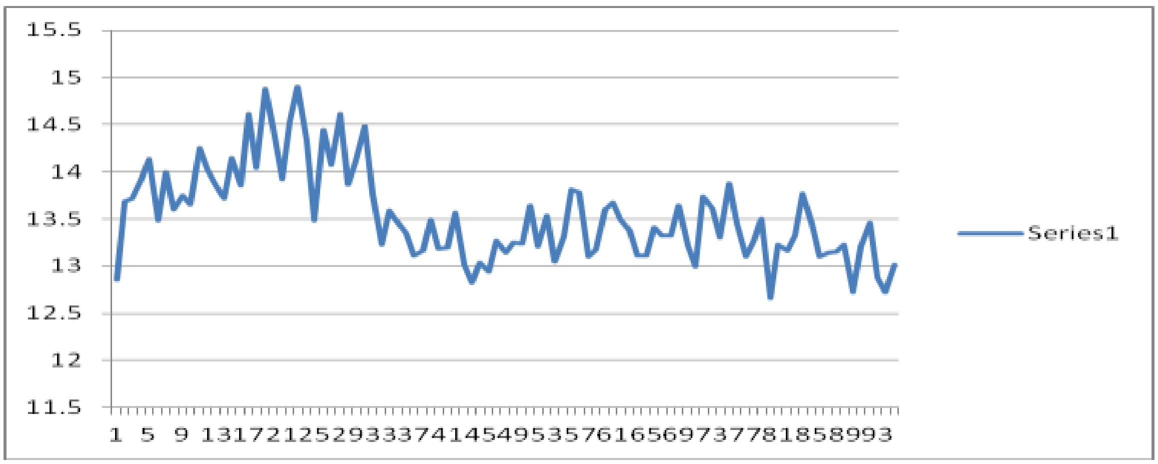
Discussion:

Protein Outliers

The prediction data for protein over the week of testing is 0.27% which is typical of comparative studies between the CropScan 1000B benchtop NIR analysers and the Infratec 1241 NIR analyser.

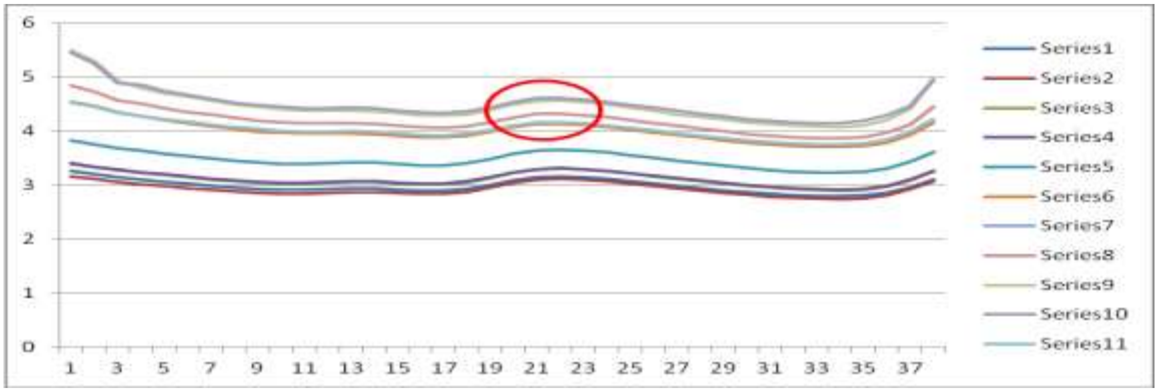
In the tables above, it can be seen where several samples that have difference greater than 0.3%. It is considered that this occurs when loads have a larger variation in protein across the load and therefore the spear samples may not truly represent the variation in the load.

The plot below shows 95 protein readings made across load 20M5 which has a difference of 0.6% against the lab. The plot shows that the first third of the load has a 1% higher protein level than other two thirds of the load.



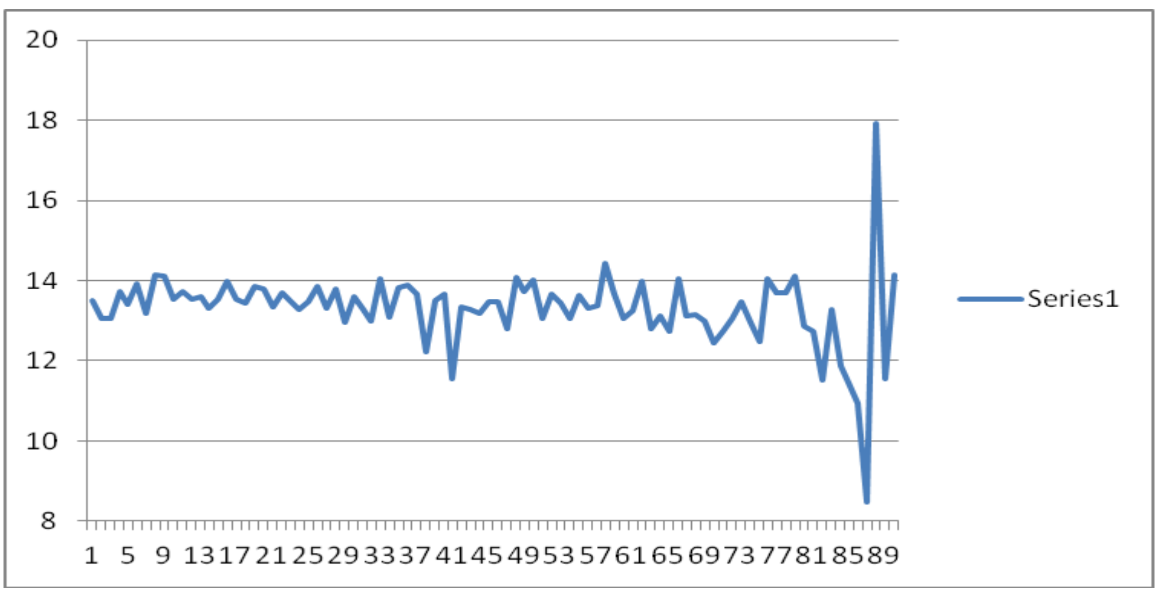
The 500ml load sample as measured by the lab NIR only provides an average across the load. If 2 spears are taken from the front of the load and 3 from the back of the load, then there is a disproportion of the protein across the load. Whereas the CropScan measures approximately 95 individual sub samples from start to finish and thereby provides a far more accurate average of the protein in the truck.

Secondly, we have found that some of the loads contain a higher amount of dust and this can result in protein predicted higher than the lab NIR. As all NIR analyser measures the light transmitted through the grain, dust can reduce the amount of light reaching the detector. Dust was observed at the beginning and end of the loads which caused the energy going through the sample to be reduced by 10%. The below figure shows the difference in the absorbance spectra between a clean sample and a dusty sample.



The effect of dust on the average protein and moisture across the loads is minimal, ie, 0.3%, however the agreement between the CropScan 3000S and the Lab NIR would be improved if the system was located after the grain is cleaned or at least the dust removed.

Thirdly, we have found that at the end of a load we can see that the samples become extreamly dusty and causes the system to read higher or lower than the average. If these scans are removed from the average through software then the accuarcy would be improved. The figure below shows the protein plotted for load 22W9 where it be can seen that at the end of the load the protein prediction becomes higher due to dust in the sample stream.



Moisture Outliers:

The moisture results from the CropScan 3000S are excellent except for load 23TH2 that shows a difference of 2% for moisture higher than the labs moisture. This is a significantly higher error compared to the other 38 moisture analysis. If load 23TH2 is removed from the results table the Standard Error of Prediction for moisture drops from 0.4% to 0.2% against the lab. Since the protein prediction for this load was within 0.1% of the lab moisture it is hard to explain the reason for the difference in the moisture. It may be due to a recoding error however 1 outlier out of 38 analyses gives a high level of confidence the moisture prediction is accurate.

Conclusion.

The Wheat 15 calibration model which was developed specifically for the mill was used to measure the protein and moisture in the wheat received during the week of the April 20^{th}. Having collected calibration samples at different protein and moisture ranges and with varying temperatures, has built in a high degree of accuracy and robustness into the calibration. The data in this report shows a SEP for protein 0.27% and moisture 0.2% against the lab NIR analyser.

It is considered that by adding extra samples over time to handle the different wheat varieties will result in an even more robust on line analysis system.

As a result of the data collected from the CropScan 3000S On Silo Analyser over the last two months, Next Instruments has decided to make some improvements to the system to make it more accurate and robust for use with a flour mill operation.

1. The temperature inside the spectrometer enclosure is varies by 10^0C. By insulating the NIR spectrometer enclosure it will be possible maintain a more stable operating temperature of +/-5^0C.
2. Implement a rejection algorithm to reject results that are statistically different from the load average. This will reject outliers caused by the dusty samples, which will help improve accuracy.
3. Re-locate the sample head to where it samples the grain after the cleaning. This will further reduce the chance of dusty samples and improve accuracy.
4. The sample head needs to be inspected to see if any design changes are required. However the sample head has cycled over 100,000 times during the trial and is obviously working well.

Applying these three changes will improve the accuracy and robustness of the system.