Optimisation of the measurement of meat and meat products; valorisation of the databases

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Introduction

Near infrared (NIR) Spectrometry gives us a quick and non-destructive answer to the determination of the intrinsic meat quality what means to determine the concentration of major compounds such as water, protein and lipids.[1,2] NIR also shows a strong potential to estimate some physicochemical properties of meat such as collagen contents, jutosity and tenderness, partially linked to organoleptic quality.[3–5]

Different factors influence the NIR spectra:[7] i.e. particle size, temperature, stocking effect. In this work, we analyse the effect of sample temperature, speed and grinding time.

During the last eight years, NIR spectra and corresponding reference values (moisture, fat, protein and collagen) were gathered into three major databases: beef-pork, chicken and meat derived products. The aim of this work was to reorganise these different databases and to test their performances. The use of specific databases can improve the accuracy.[8] Different separations of the global databases had thus been considered.

Methods

Temperature influence

Sample of mixed meat (beef meat) were bring at a fixed temperature (10, 15, 20 and 25°C) in a bain-marie. After 40 minutes, temperature is considered reached and the sample is analysed with a Foss NIRSystems 5000 (spinning module).

Grinding optimisation

A grindomix GM200 knife grinder was used. To determine the optimal time and speed of grinding, several combinations were tested. Four speeds (3000, 5000, 7000 and 9000 rpm) and four times (5, 10, 20 and 30 seconds) of grinding were performed. For each analyse, 100 g bacon (which is rather heterogeneous) were mixed. Five cups were filled and analysed with a Foss NIRSystems 6500 (spinning module).

Database valorisation

Meat database contains at least 700 samples, chicken database 400 samples and meat-derived products 250. The first step was to reorganise these different databases and to identify clearly all the samples. After that, these populations were evaluated qualitatively and quantitatively. Finally, specifications following different criteria were tested to improve the accuracy.

Results and discussion

Temperature influence

Figure 1 shows the spectra of samples at different temperatures in a space formed by the first two axis of principal components analysis. The temperature clearly influences the spectra.
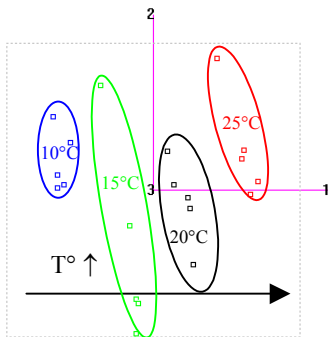

Figure 1. Principal component analysis of mixed meat samples at different temperatures.

Figure 2 shows the wavelength correlated with the temperature. The wavelengths pointed (1150, 1400 and 1900 nm) correspond with those from water.
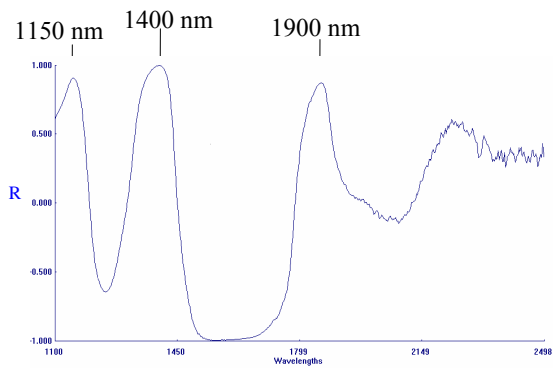

Figure 2. Correlogram of temperature with wavelength.

The increase of temperature allows liberating a part of fixed water.[9] The intensity of the peak at 1400 nm, which corresponds to free water, increases thus with temperature as shown in Figure 3.
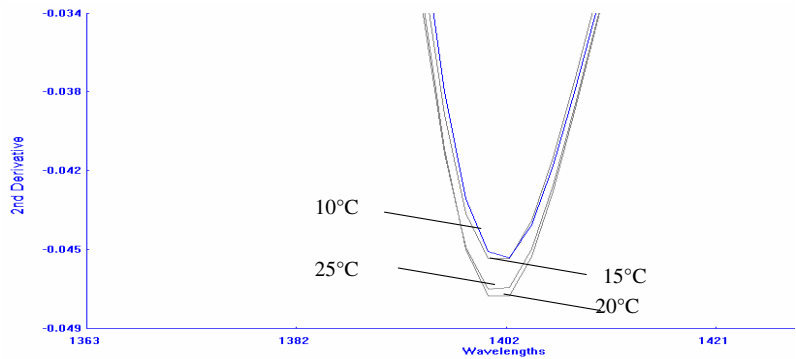
Figure 3. Evolution of the peak at 1400 nm (second derivative) with temperature.

Grinding optimisation

Meat is, for an analytical point, a complex matrix. The muscle fibres diffuse the light what is against us for measure in reflexion. The grinding allows to homogenise the sample by destruction of muscle fibre.

The optimisation of the speed of the Grindomix GM200 knife grinder and of the grinding time was achieved on the basis of a response map of the SEP values obtained while predicting the fat content of a bacon sample which is rather heterogeneous. The best *SEP* was obtained at a speed of 5000 rpm with a 20 seconds grinding time (Figure 4).
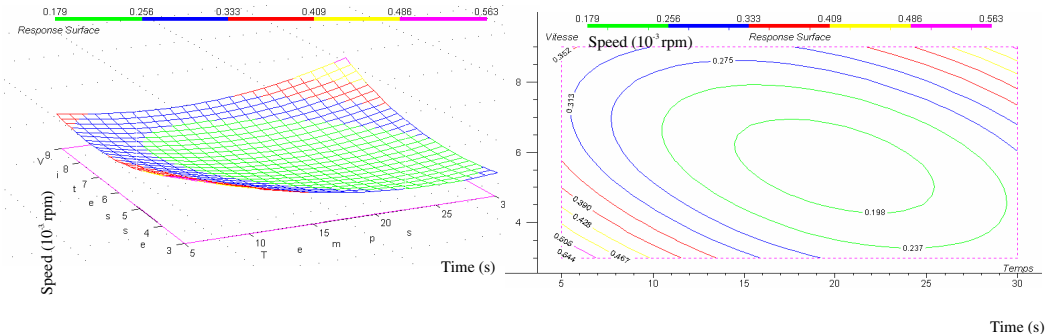

Figure 4. Response map and his outlines of the SEP value obtained while predicting the fat content of a bacon sample.

Database valorisation

Beef Pork database

If the beef samples are considered separately, the SEP values are slightly improved. The beef meat samples positively contribute to the accuracy achieved on the pork (Figure 5).
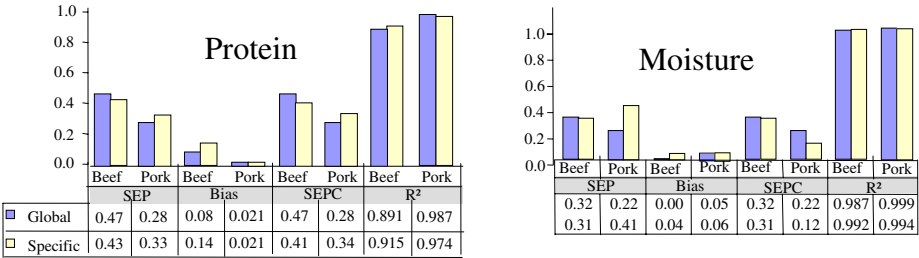
Figure 5. Prediction of protein and moisture content of beef and pork samples.

	Protein								Moisture							
	Beef	Pork	Beef	Pork	Beef	Pork	Beef	Pork	Beef	Pork	Beef	Pork	Beef	Pork	Beef	Pork
	SEP		Bias		SEPC		R²		SEP		Bias		SEPC		R²	
Global	0.47	0.28	0.08	0.021	0.47	0.28	0.891	0.987	0.32	0.22	0.00	0.05	0.32	0.22	0.987	0.999
Specific	0.43	0.33	0.14	0.021	0.41	0.34	0.915	0.974	0.31	0.41	0.04	0.06	0.31	0.12	0.992	0.994

Splitting up the database according to the quality of meat (first or second grade) (Figure 6) or according to the fat content (lean and fat group) doesn't improve much the SEP values (Figure 7).
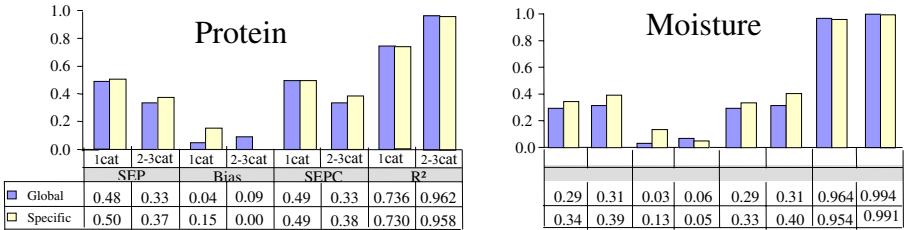

	Protein								Moisture							
	1cat	2-3cat	1cat	2-3cat	1cat	2-3cat	1cat	2-3cat	1cat	2-3cat	1cat	2-3cat	1cat	2-3cat	1cat	2-3cat
	SEP		Bias		SEPC		R²		SEP		Bias		SEPC		R²	
Global	0.48	0.33	0.04	0.09	0.49	0.33	0.736	0.962	0.29	0.31	0.03	0.06	0.29	0.31	0.964	0.994
Specific	0.50	0.37	0.15	0.00	0.49	0.38	0.730	0.958	0.34	0.39	0.13	0.05	0.33	0.40	0.954	0.991

Figure 6. Prediction of protein and moisture content of first and second grade of meat quality samples.

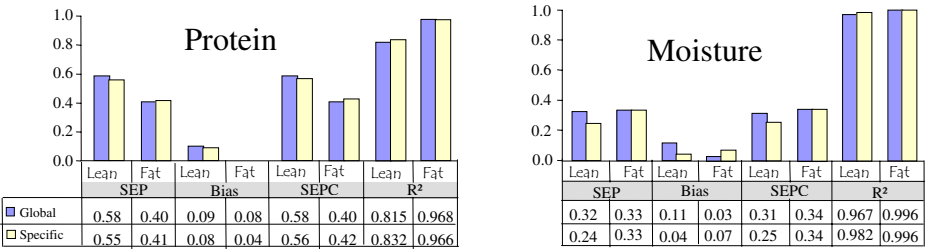|	Protein								Moisture							
	Lean	Fat	Lean	Fat	Lean	Fat	Lean	Fat	Lean	Fat	Lean	Fat	Lean	Fat	Lean	Fat
	SEP		Bias		SEPC		R²		SEP		Bias		SEPC		R²	
Global	0.58	0.40	0.09	0.08	0.58	0.40	0.815	0.968	0.32	0.33	0.11	0.03	0.31	0.34	0.967	0.996
Specific	0.55	0.41	0.08	0.04	0.56	0.42	0.832	0.966	0.24	0.33	0.04	0.07	0.25	0.34	0.982	0.996

Figure 7. Prediction of protein and moisture content of lean and fat meat samples.

Chicken samples database

The principal component analysis of this database shows clearly that two sample types formed this population (Figure 8). In the case of chicken, the use of specific databases improves the *SEP* values (Figure 9).

Breasts (□) and leg (◇) on global database (+)

Figure 8. Representation of the breast and leg database on the global following first axis of PCA.

Protein

	Breast	Leg	Breast	Leg	Breast	Leg	Breast	Leg
	SEP		Bias		SEPC		R²	
Global	0.52	0.38	0.00	0.02	0.53	0.39	0.752	0.891
Specific	0.44	0.34	0.02	0.04	0.45	0.35	0.836	0.911

Moisture

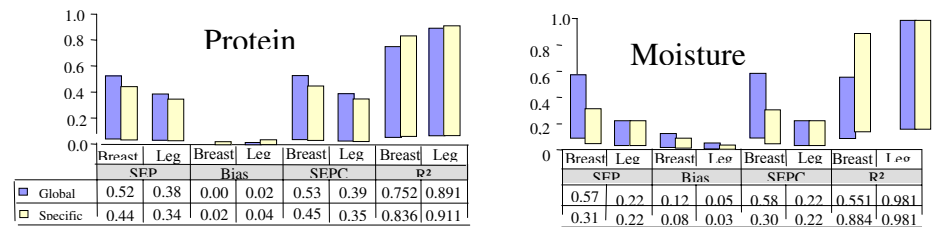|	Breast	Leg	Breast	Leg	Breast	Leg	Breast	Leg
	SEP		Bias		SEPC		R²	
	0.57	0.22	0.12	0.05	0.58	0.22	0.551	0.981
	0.31	0.22	0.08	0.03	0.30	0.22	0.884	0.981

Figure 9. Prediction of protein and moisture content of breast and leg chicken samples.

Meat-derived products databases

Meat-derived products database is clearly composed of 3 sample types as shown at Figure 10.

Pâté (□), Ham (◇) and Sausage (x) on Meat derived products database
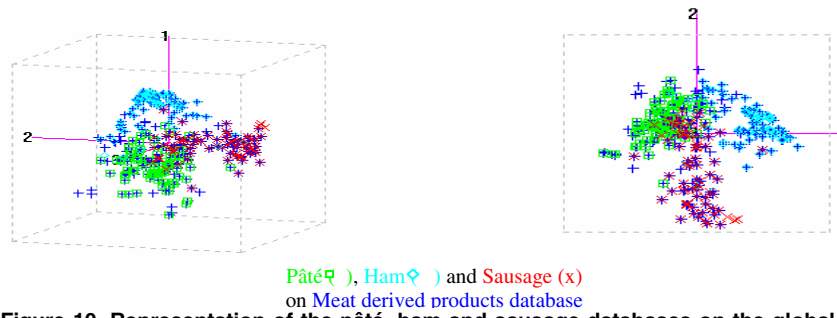
Figure 10. Representation of the pâté, ham and sausage databases on the global one following the first axis of PCA.

As far as the pâtés and hams are concerned, specific calibration can lead to better SEP values. It was not the case for sausages (Figure 11).

Protein

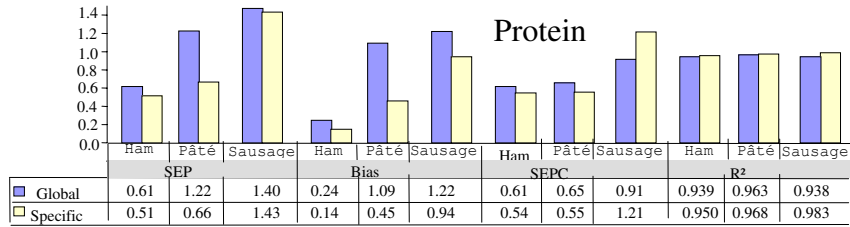|	Ham	Pâté	Sausage	Ham	Pâté	Sausage	Ham	Pâté	Sausage	Ham	Pâté	Sausage
	SEP			Bias			SEPC			R²		
Global	0.61	1.22	1.40	0.24	1.09	1.22	0.61	0.65	0.91	0.939	0.963	0.938
Specific	0.51	0.66	1.43	0.14	0.45	0.94	0.54	0.55	1.21	0.950	0.968	0.983

Figure 11. Prediction of protein content of pâtés, hams and sausages.

Conclusions and further prospects

Sampling parameters

To reduce the temperature influence (clearly observed here), databases samples measured at different temperatures were included in order to bring the thermal variation.[10,11]

The response map allows us to determine the best combination of grinding speed and time.

Database valorisation

In the actual configuration, the global beef-pork database is still the more useful. The use of specific databases requires a lot of work for a poor improvement of the accuracy. In the case of chicken samples, the isolation of two sample types is performing better. For the meat-derived products database, additional samples are required to improve accuracy of the prediction model.

Further prospects

Further work is required to study the possibility of using a local calibration. In this calibration mode, the software search, on the basis of the Mahalanobis distance or the correlation coefficient, the nearest samples in the whole database. It builds a specific calibration with these samples and predicts the composition of unknown samples. This calibration mode works well with great databases and multiproducts databases.[12] Gathering the different databases would be, at this time, interesting.

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