

Standardisation of MIR milk spectra, a step to build an international spectral database



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PARTNERS

Investing in Opportunities



This project has received European Regional Development Funding through INTERREG IV B.



INTERREG IV B

5 Research units + 1 Laboratoire

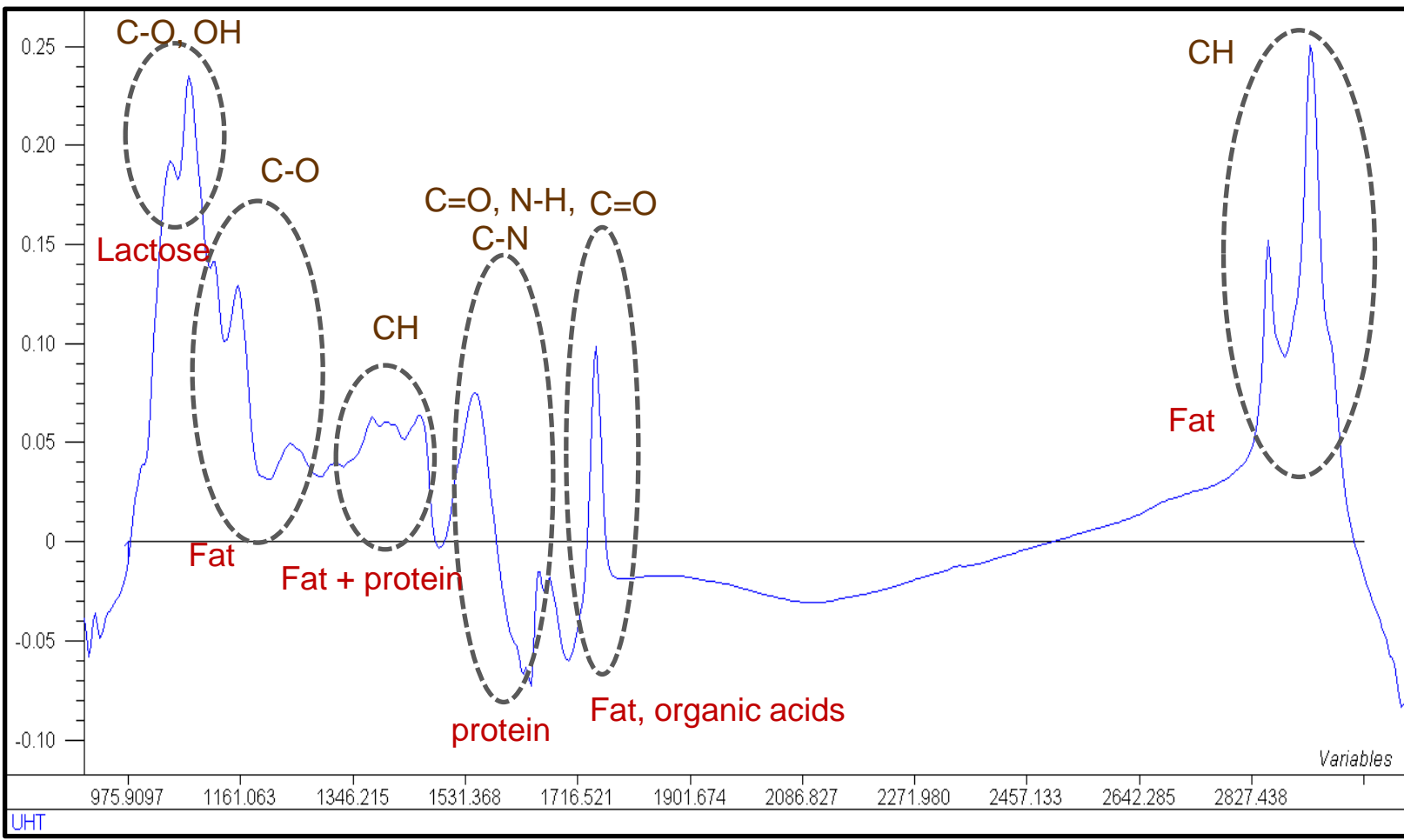
Name	Country
<i>Institut de l'Elevage</i>	FR
<i>Gembloux Agro-Bio Tech (Université de Liège)</i>	BE
<i>Centre wallon de Recherches agronomiques (Département Qualité Productions Animales)</i>	BE
<i>Comité du Lait</i>	BE
<i>Teagasc</i>	IR
<i>Scottish Agricultural College</i>	UK



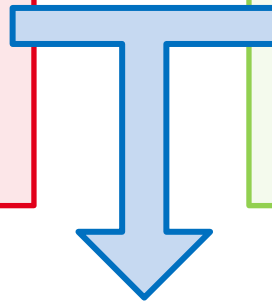
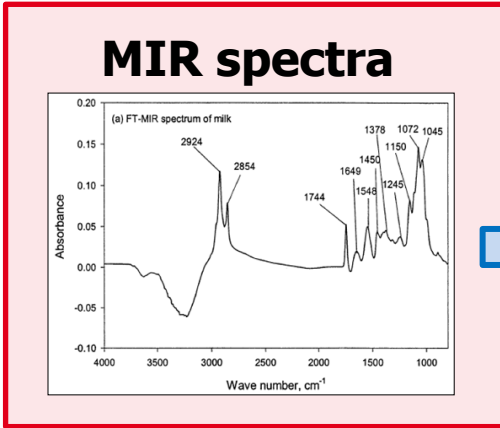
11 MILK CONTROL ORGANISATIONS

Name	Country
<i>Association Wallonne de l'Elevage</i>	BE
<i>Chambre régionale Agriculture Alsace</i>	FR
<i>ADECL62 (Pas-de-Calais)</i>	FR
<i>CLASEL (Sarthe & Mayenne)</i>	FR
<i>SCL du Doubs et du territoire de Belfort</i>	FR
<i>France Conseil Elevage</i>	FR
<i>LKV Baden-Württemberg</i>	DE
<i>LKV Nordrhein-Westfalen</i>	DE
<i>National Milk Recording</i>	UK
<i>Irish Cattle Breeding Federation</i>	IR
<i>CONVIS</i>	LU

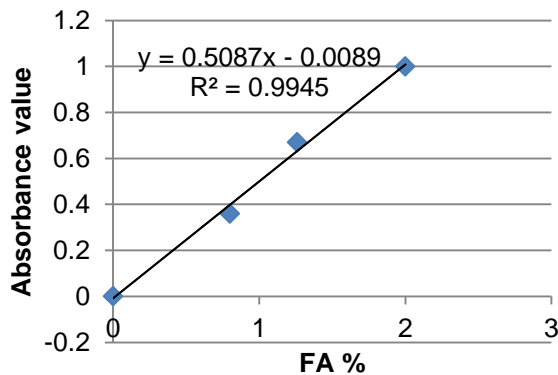




- **Position of the peaks** → **Qualitative analysis**
- **Intensity of the peaks** → **Quantitative analysis**



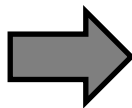
Saturated FA (g/100ml) = ax + b



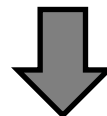
$$\begin{aligned} \text{Saturated FA (g/100ml)} = & 0.0985 + 4.6191 * X_1 + 1.1659 * X_2 + 1.4827 * X_3 \\ & + 4.1684 * X_4 + 7.3294 * X_5 + 9.8991 * X_6 + 11.183 * X_7 + 8.0711 * X_8 \\ & + 2.1599 * X_9 - 0.4619 * X_{10} - 1.7876 * X_{11} - 2.5708 * X_{12} - 2.8941 * X_{13} - \\ & 2.9217 * X_{14} - 2.7392 * X_{15} - 2.2543 * X_{16} - 1.2677 * X_{17} + 0.0676 * X_{18} \\ & + 1.0762 * X_{19} + 1.3228 * X_{20} + 1.0241 * X_{21} + 0.536 * X_{22} + 0.0177 * X_{23} - \\ & 0.5265 * X_{24} - 1.1445 * X_{25} - 1.8178 * X_{26} + 2.212 * X_{27} - 2.0766 * X_{28} + \\ & 8.3083 * X_{29} - 3.703 * X_{30} + 1.1999 * X_{31} + 0.5698 * X_{32} - 0.1674 * X_{33} \\ & + 0.246 * X_{34} + 0.666 * X_{35} + 1.2938 * X_{36} + 2.0946 * X_{37} - 0.0689 * X_{38} - \\ & 1.4774 * X_{39} - 1.7984 * X_{40} - 2.0553 * X_{41} - 2.9338 * X_{42} - 4.644 * X_{43} - 6.764 * X_{44} \\ & - 8.1475 * X_{45} - 5.6904 * X_{46} + 2.6657 * X_{47} + 10.9883 * X_{48} + 14.4346 * X_{49} \\ & + 13.8878 * X_{50} + 10.2135 * X_{51} + 4.8464 * X_{52} - 1.2081 * X_{53} - 7.4854 * X_{54} - \\ & 11.6799 * X_{55} - 12.6849 * X_{56} - 10.7724 * X_{57} - 4.8936 * X_{58} + 0.4425 * X_{59} \\ & + 3.583 * X_{60} + \dots \\ & .9636 * X_{310} + 6.4566 * X_{311} \end{aligned}$$

Classical use of MIR spectra :

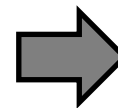
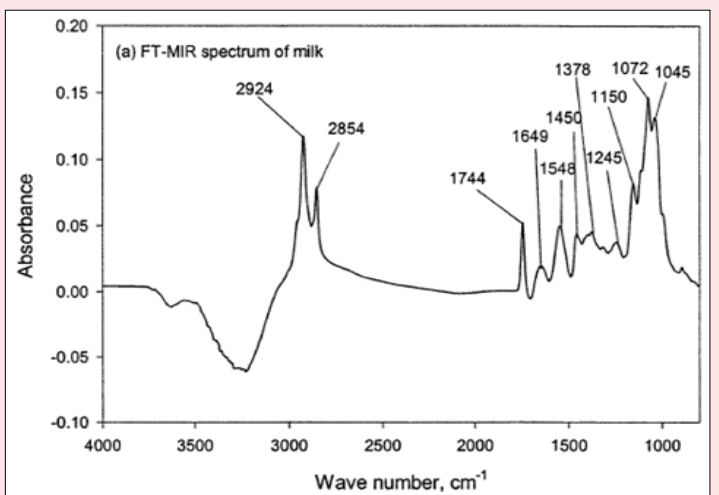
Milk control



MIR



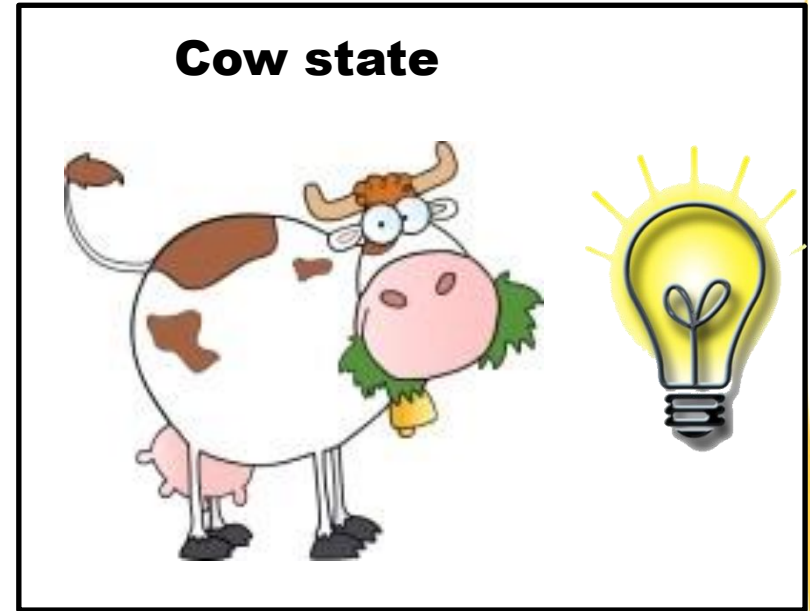
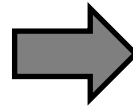
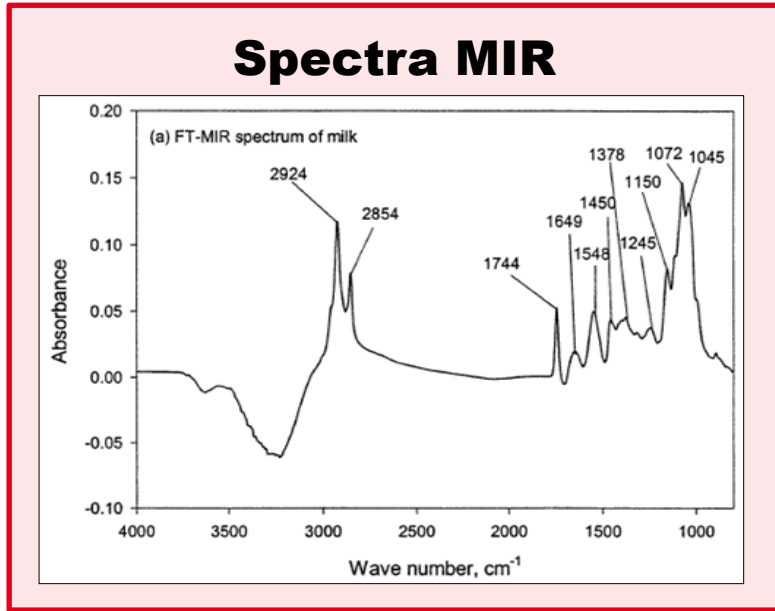
MIR spectra of each cow



Milk composition

- Fat*
- Proteins*
- Urea*
- FA*
- ...

**Fast
Cheap**



Prediction tools fast, cheap, via milk control organisations

Informations on :

- fertility**
- feeding**
- health**
- environmental impact**

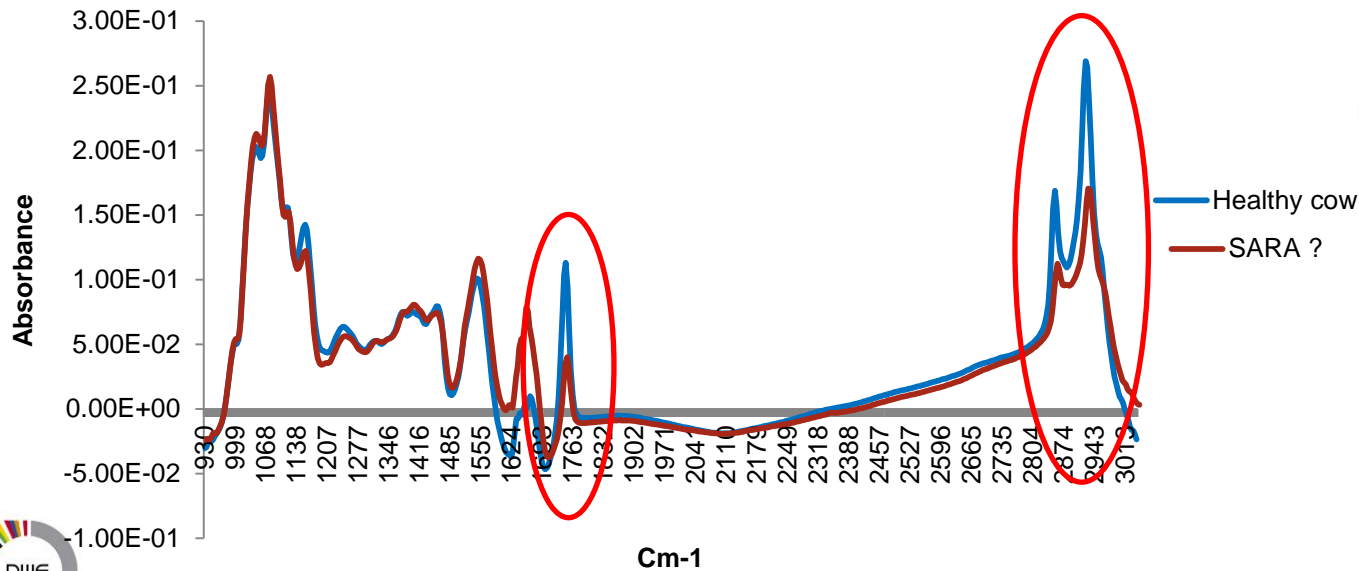
Concrete example: SARA



Impact of SARA on fat rate, fatty acid profile... (Sauvant et al., 1999; Colman et al., 2010)



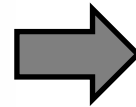
Hypothetic spectra of healthy cow and cow suffering of SARA



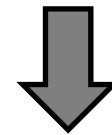
STEP N°1

Combine data from each MRO :

Spectra MIR + Fertility, health, feeding and environmental data

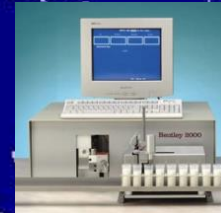
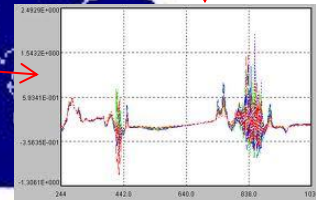


**Transnational
database**

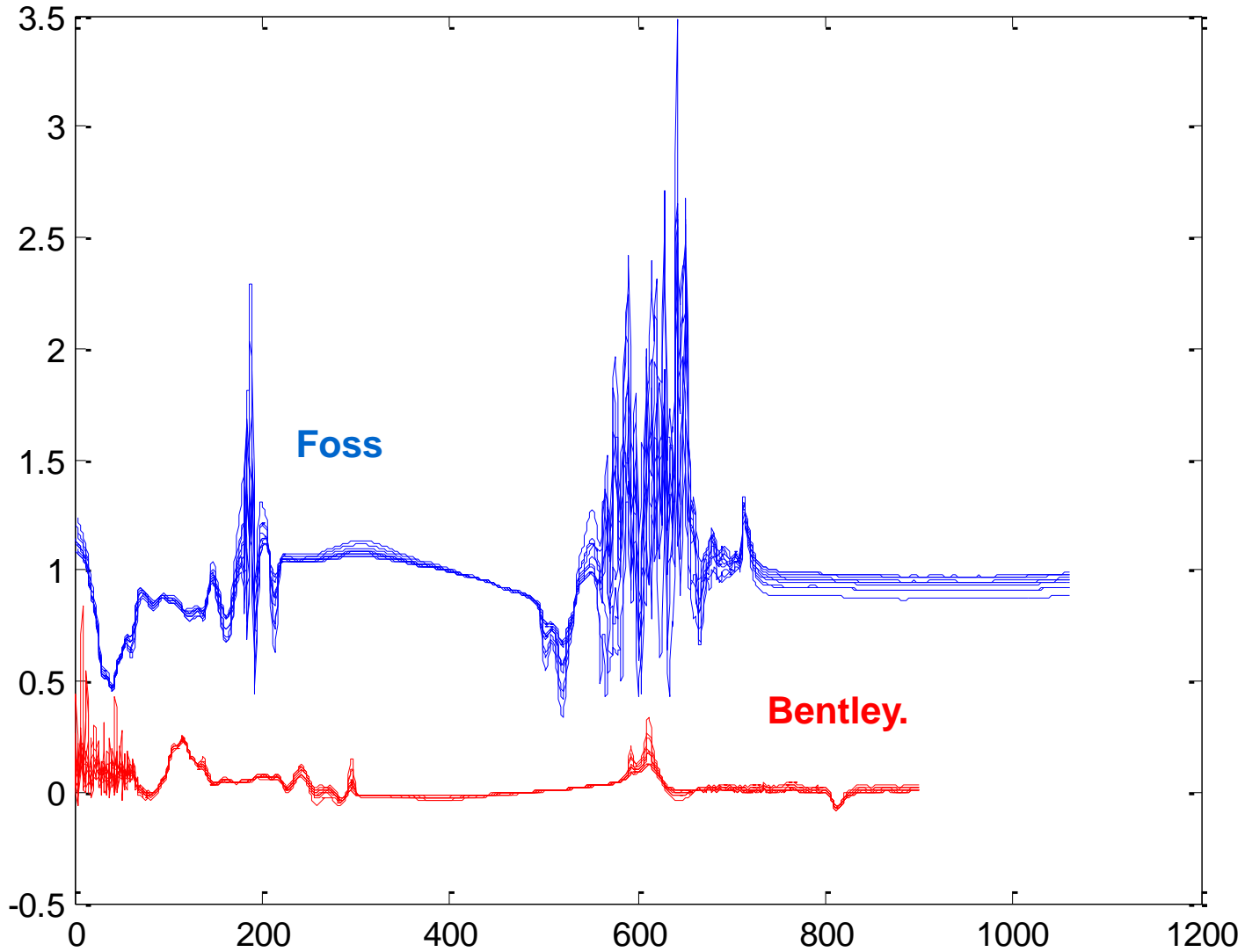


**Prediction tools of
cows states**

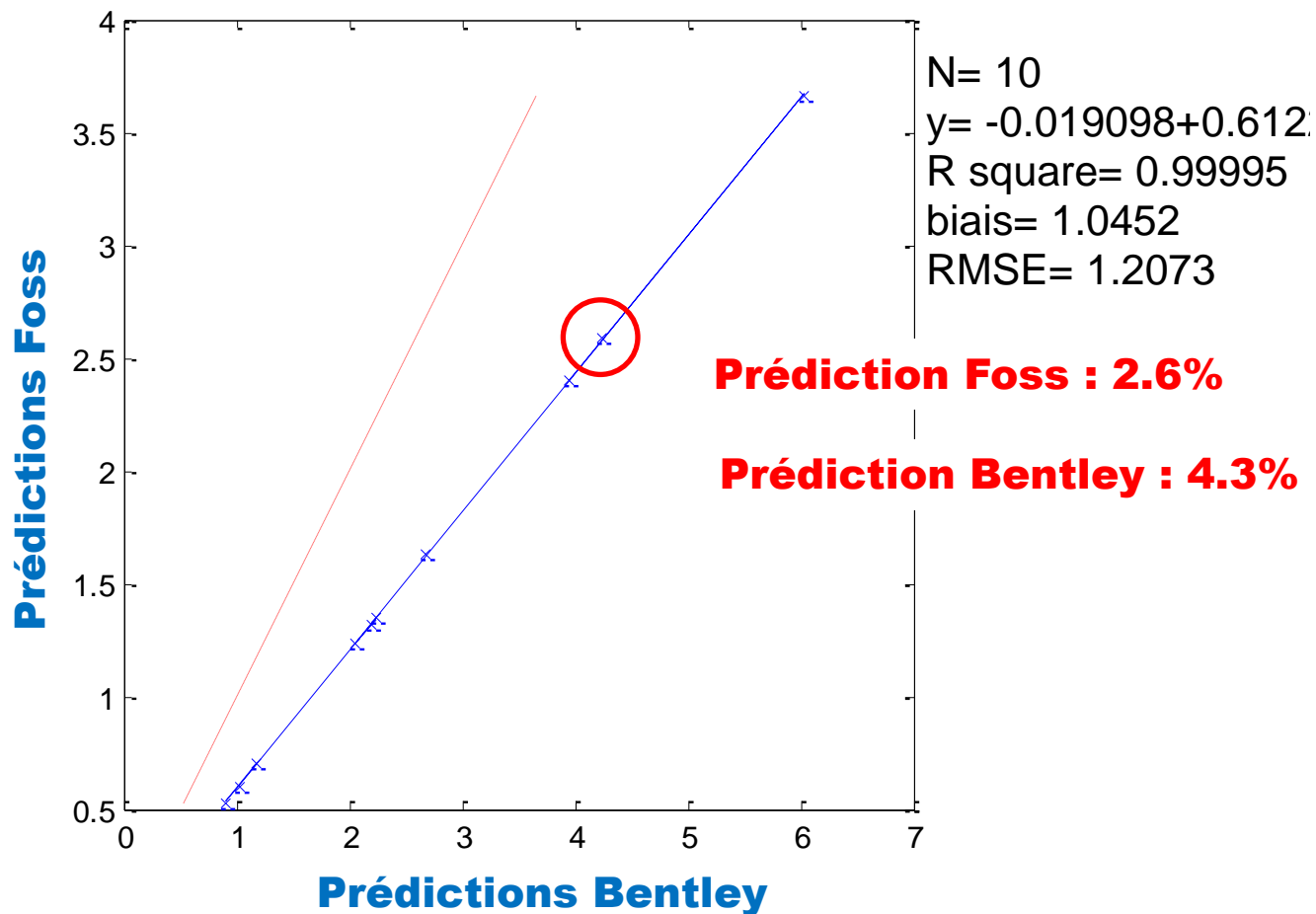
No standard
format !!



10 spectra from identical milks :



Predictions fat with raw spectra :



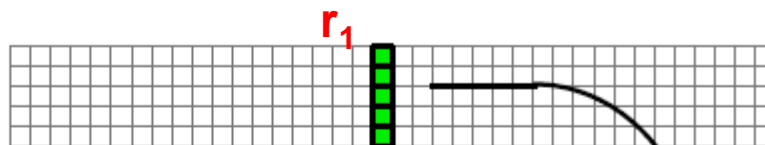
Need of spectral standardisation

PIECE-WISE DIRECT STANDARDIZATION (PDS)

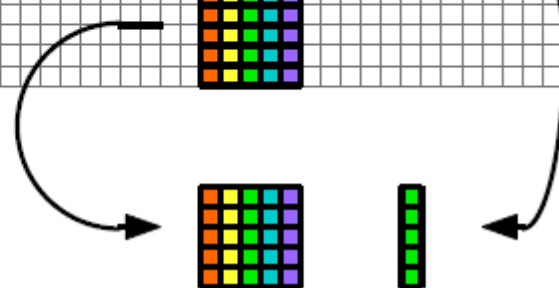
Absorbance in the area of r_1 (master)

→ correlated to R_2 (slaves)

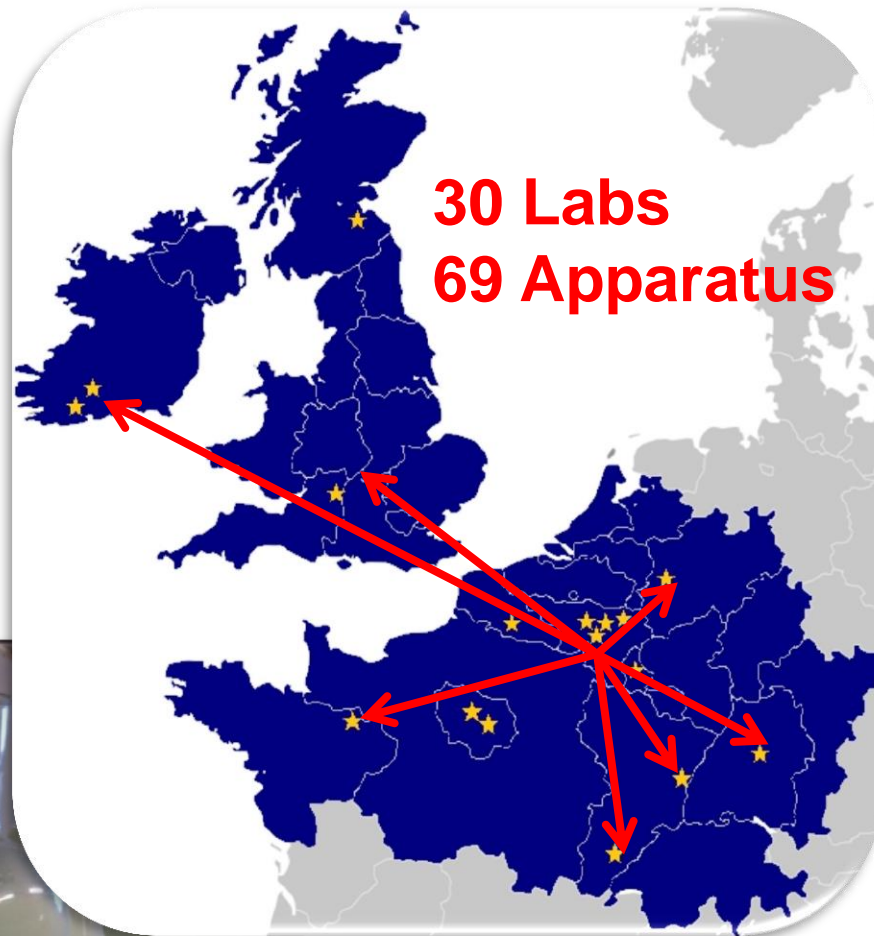
« Master »

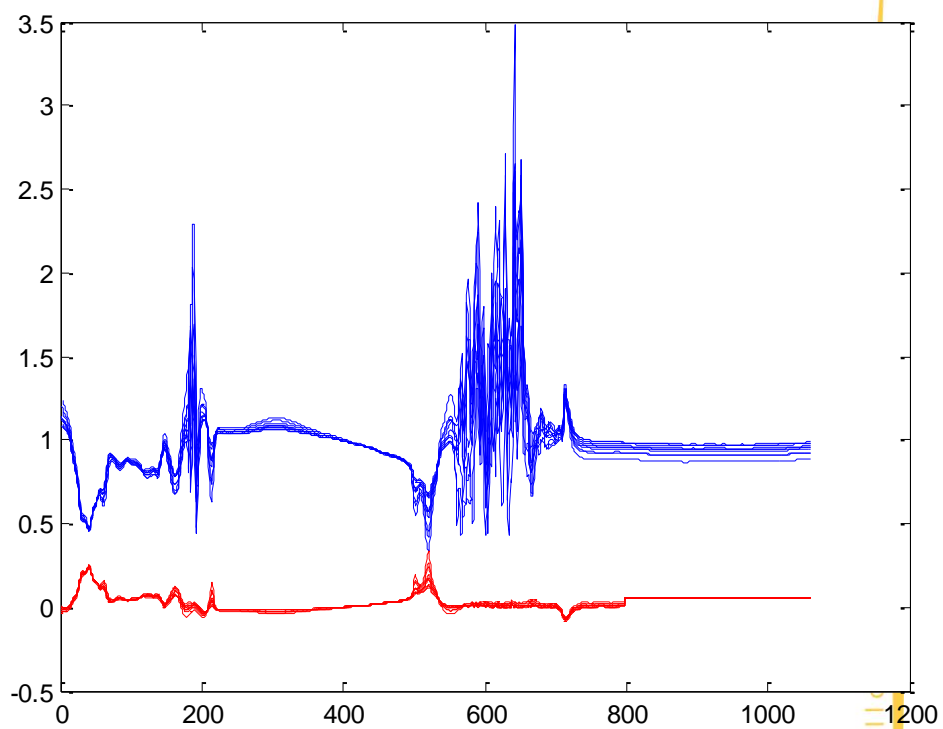
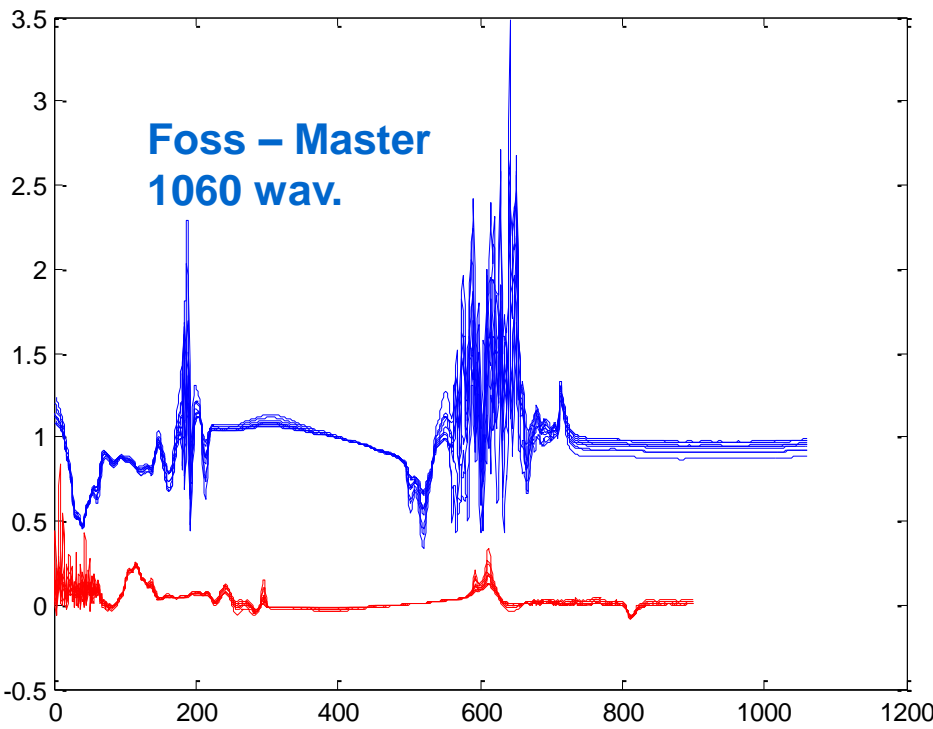


« Slave »

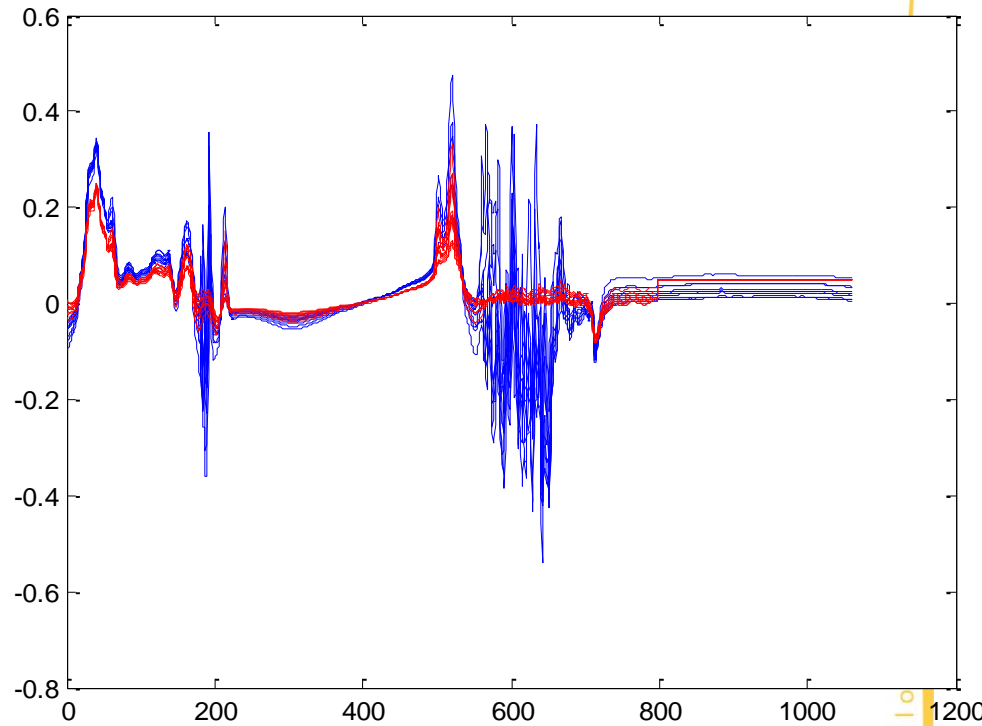
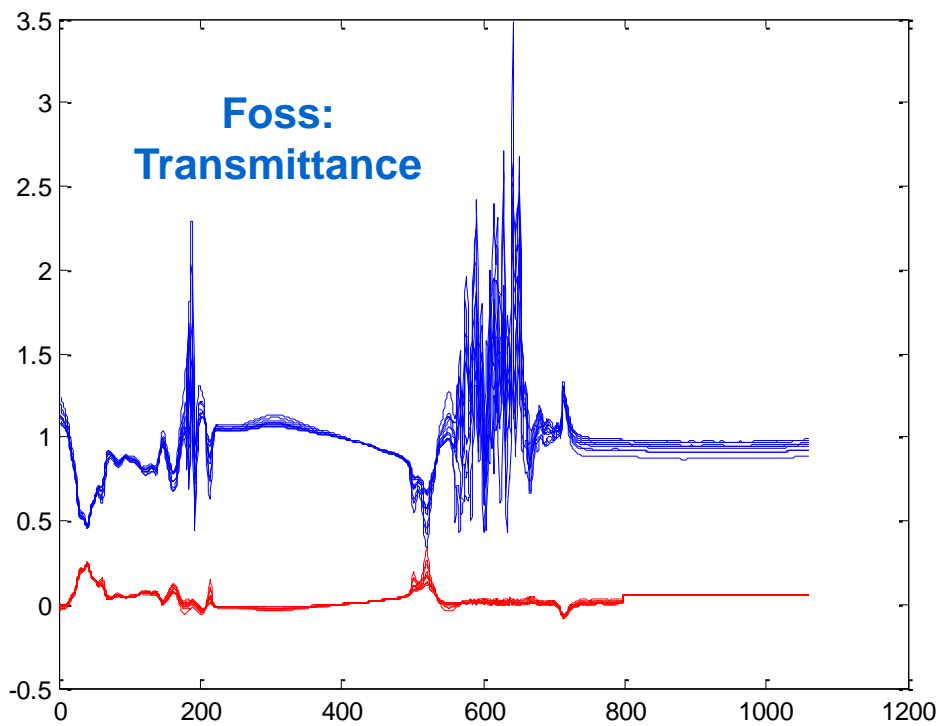


$$r_{1j} = R_{2j} b_j + b_{0j}$$





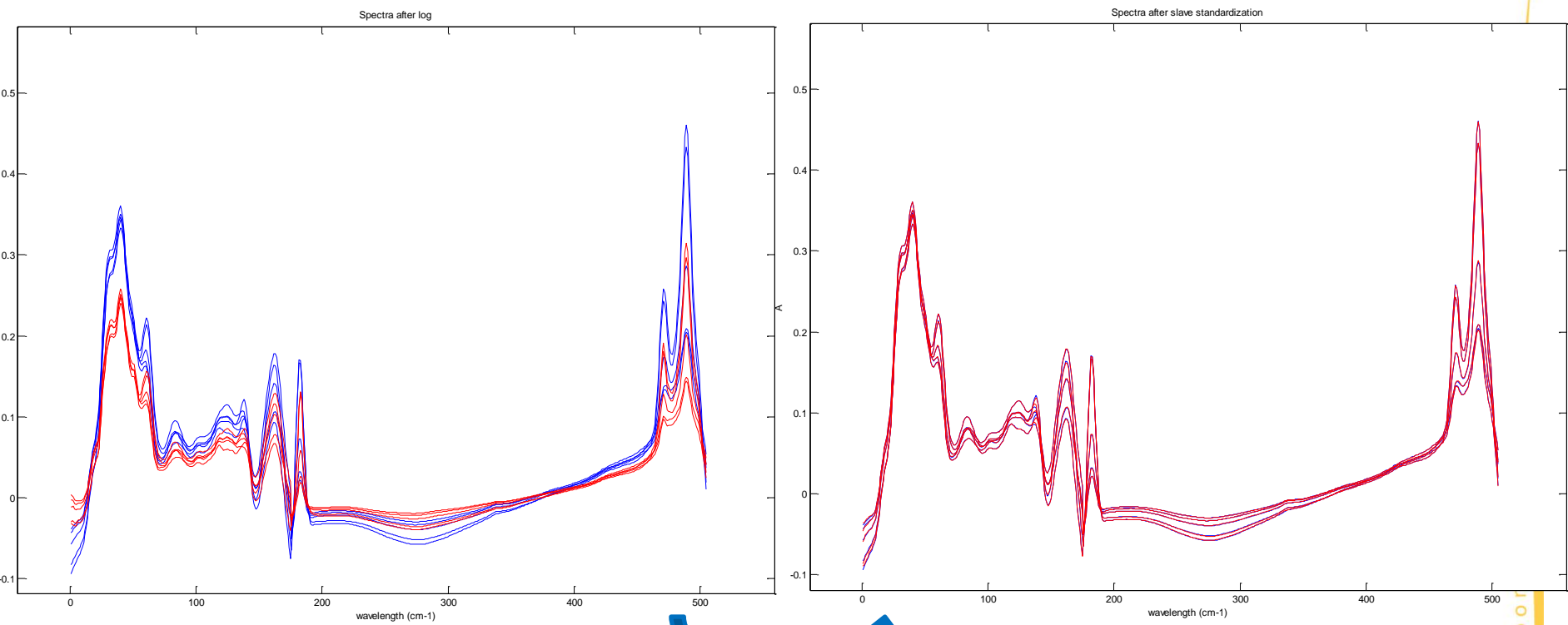
Interpolation



Bentley: Absorbance



**Logarithmic
transformation**



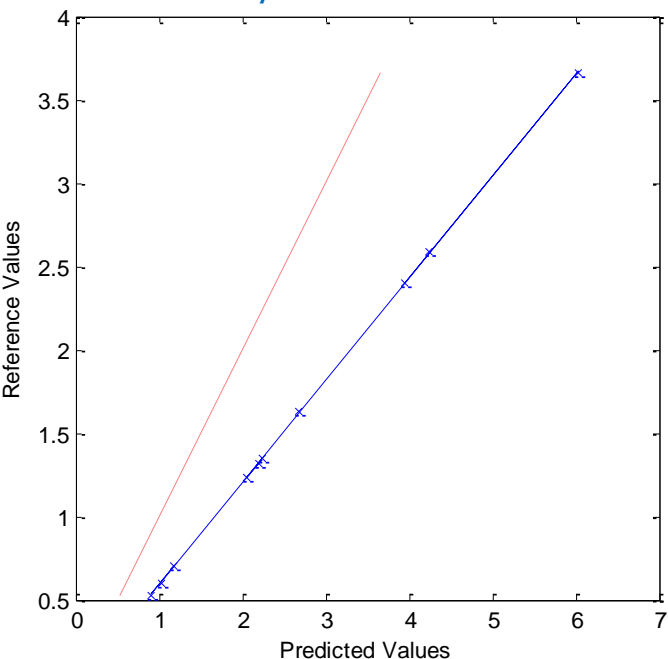
PDS

Possibility to merge spectra into a common database

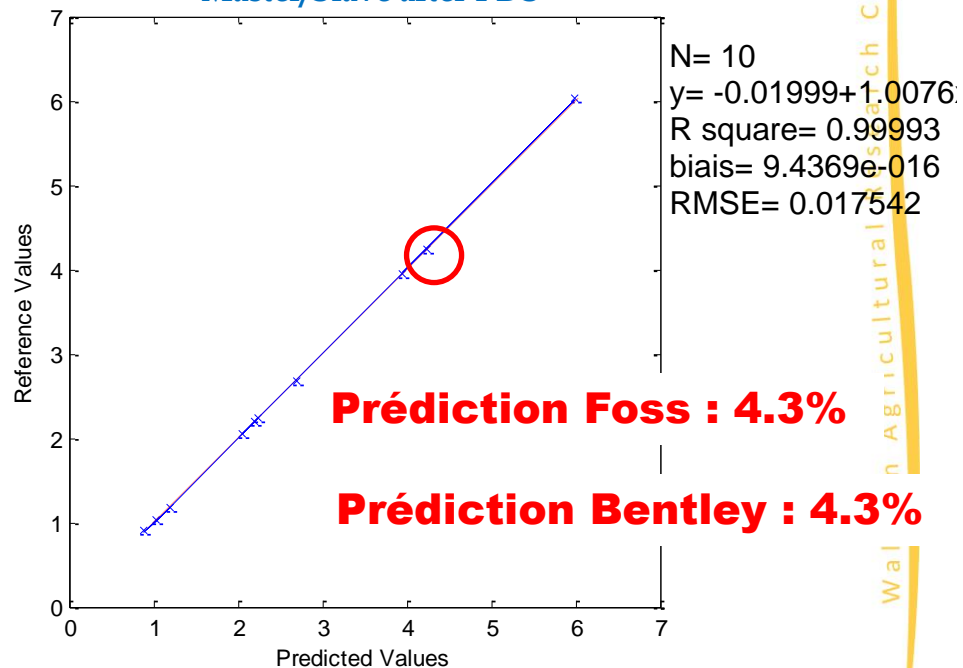
Test: application of fat prediction



Regression of fat prediction
Master/Slave before PDS



Regression of fat prediction
Master/Slave after PDS



Possibility to create and use models on all apparatus

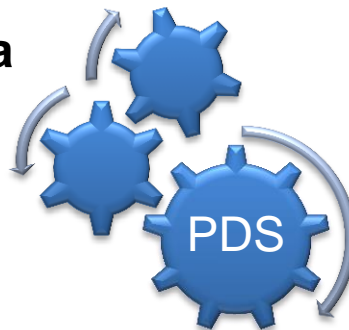
Example of first tools: Methane prediction equation (A.Vanlierde, 2013)



368 Foss spectra

+

84 Delta spectra

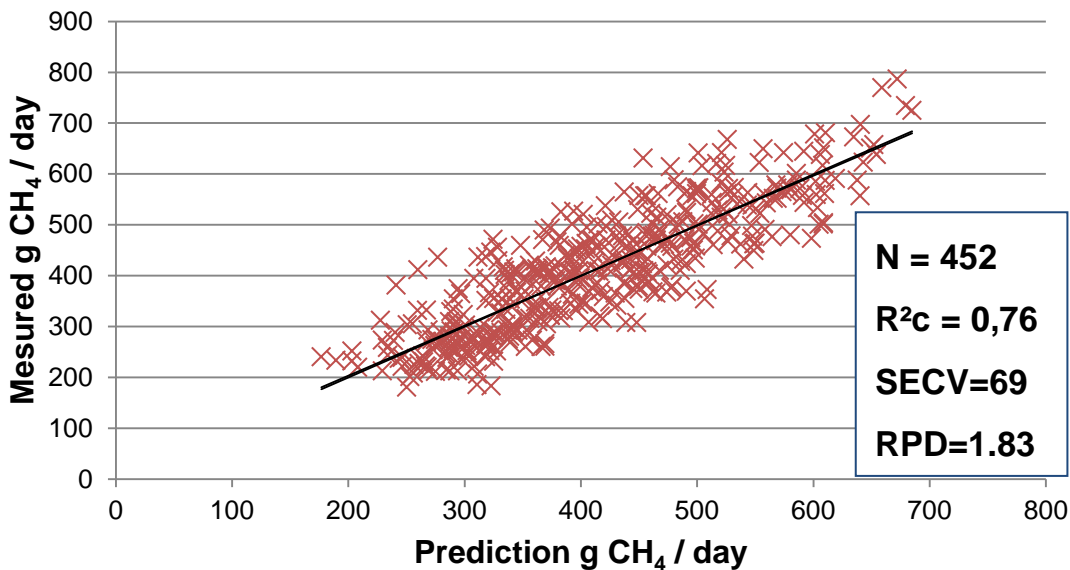


=

452 spectra in a common format

+

Reference values (SF6)



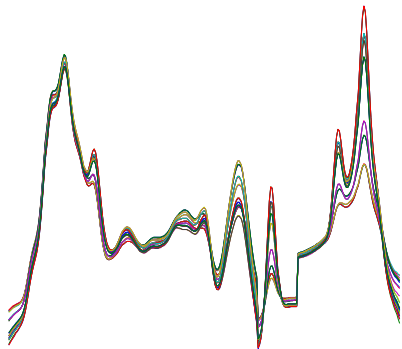
- ✓ PDS allows to group spectra from all apparatus in a common database



- ✓ Allows to create and use universal equation on all apparatus



2015



Thanks for your attention !



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