



Some considerations about near Infrared applications.

Pierre Dardenne

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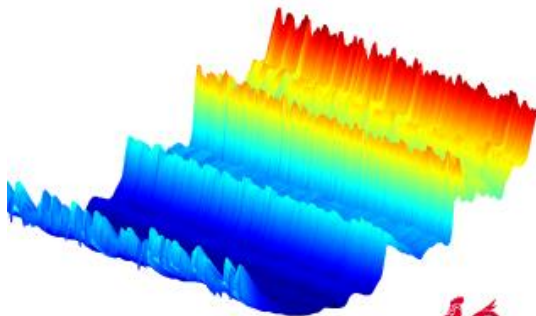
Vibrational Spectroscopy and Chemometrics

Training Session

13 March–17 March 2017



Anniversary
10th
Edition



Wallonie

Chemometrics applied to vibrational data

Exploratory analysis

Data visualisation

Principal component analysis

Outlier detection

Uncertainty estimation

Quantification and classification

Multivariate calibration

Partial Least squares PLS

Multiple linear regression MLR

Support vector machines SVM



Tom Fearn
Paolo Berzaghi
Mark Westerhaus

Abbas, Ouissam (MIR spectroscopy)

Baeten, Vincent (Raman / Sampling)

Dardenne, Pierre (NIR considerations)

Fernández Pierna, Juan Antonio (Chemometrics)

Vermeulen, Philippe (Hyperspectral Imaging)

Vincke, Damien (Hyperspectral Imaging)

Lecler, Bernard (Transfer/Standardization)

Minet, Olivier (NIR networks)

Sinnaeve, Georges (NIR online)

Vibrational Spectroscopy and Chemometrics

Training Session

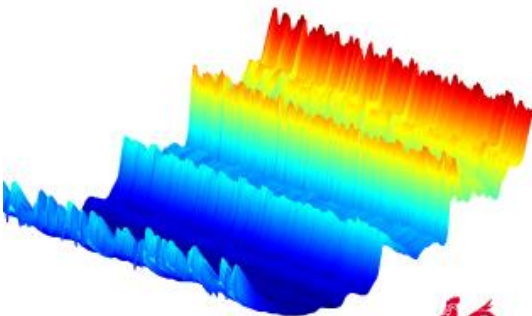
13 March–17 March 2017

Chemometrics applied to vibrational data

- Exploratory analysis
- Data visualisation
- Principal component analysis
- Outlier detection
- Uncertainty estimation
- Quantification and classification
- Multivariate calibration
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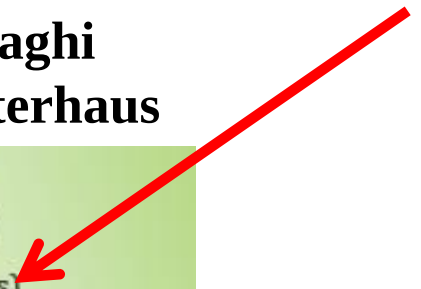
TIPS & TRICKS



Wallonie

Tom Fearn
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Abbas, Ouissam (MIR spectroscopy)
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1

The concept of the mixture model

Multivariate calibration and chemometrics for near infrared spectroscopy: which method?

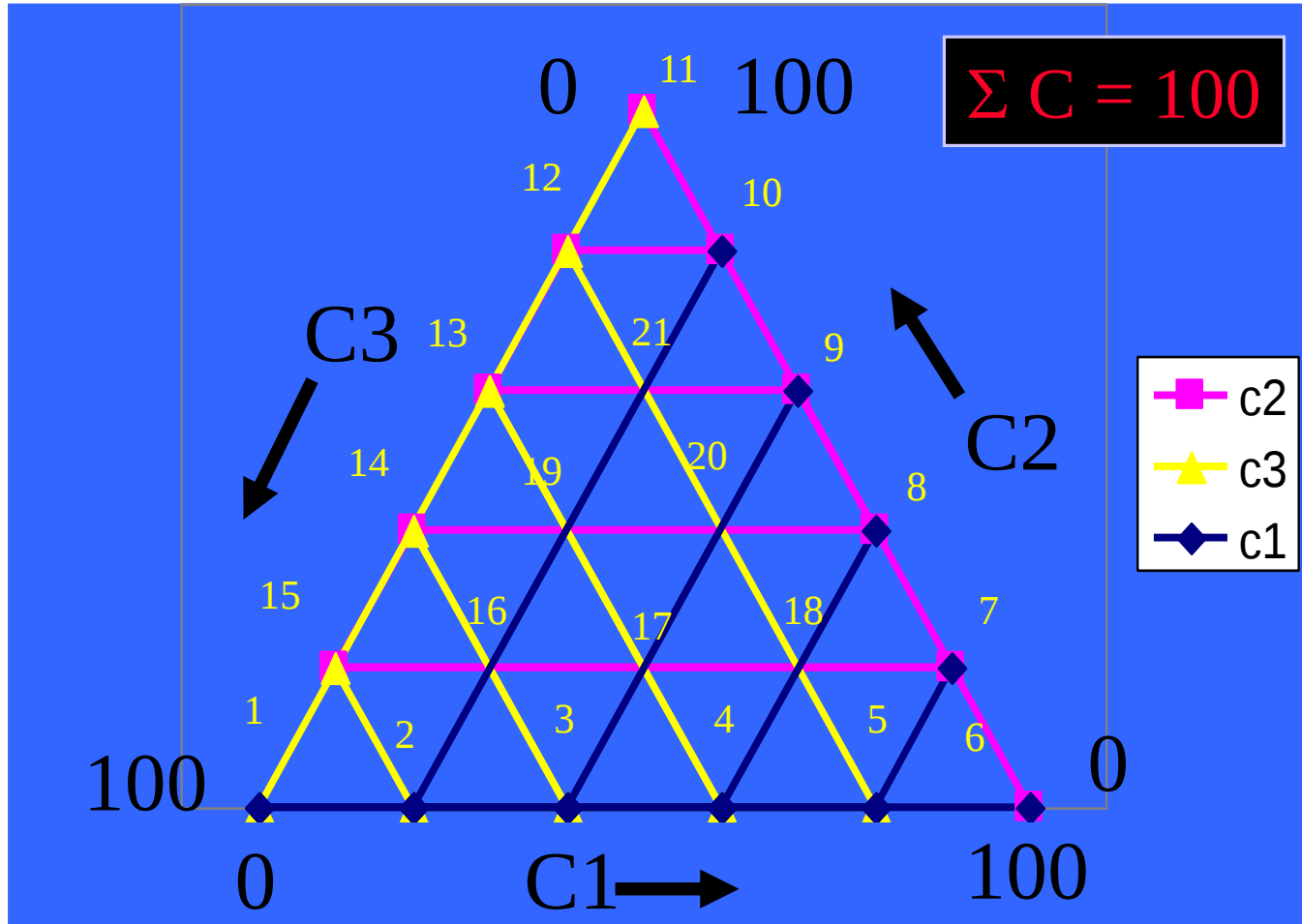
Pierre Dardenne, George Sinnaeve and Vincent Baeten

*Département Qualité des Productions Agricole, Centre de Recherches Agronomiques de Gembloux–CRAGx,
24 Chaussée de Namur, B-5030 Gembloux, Belgium*

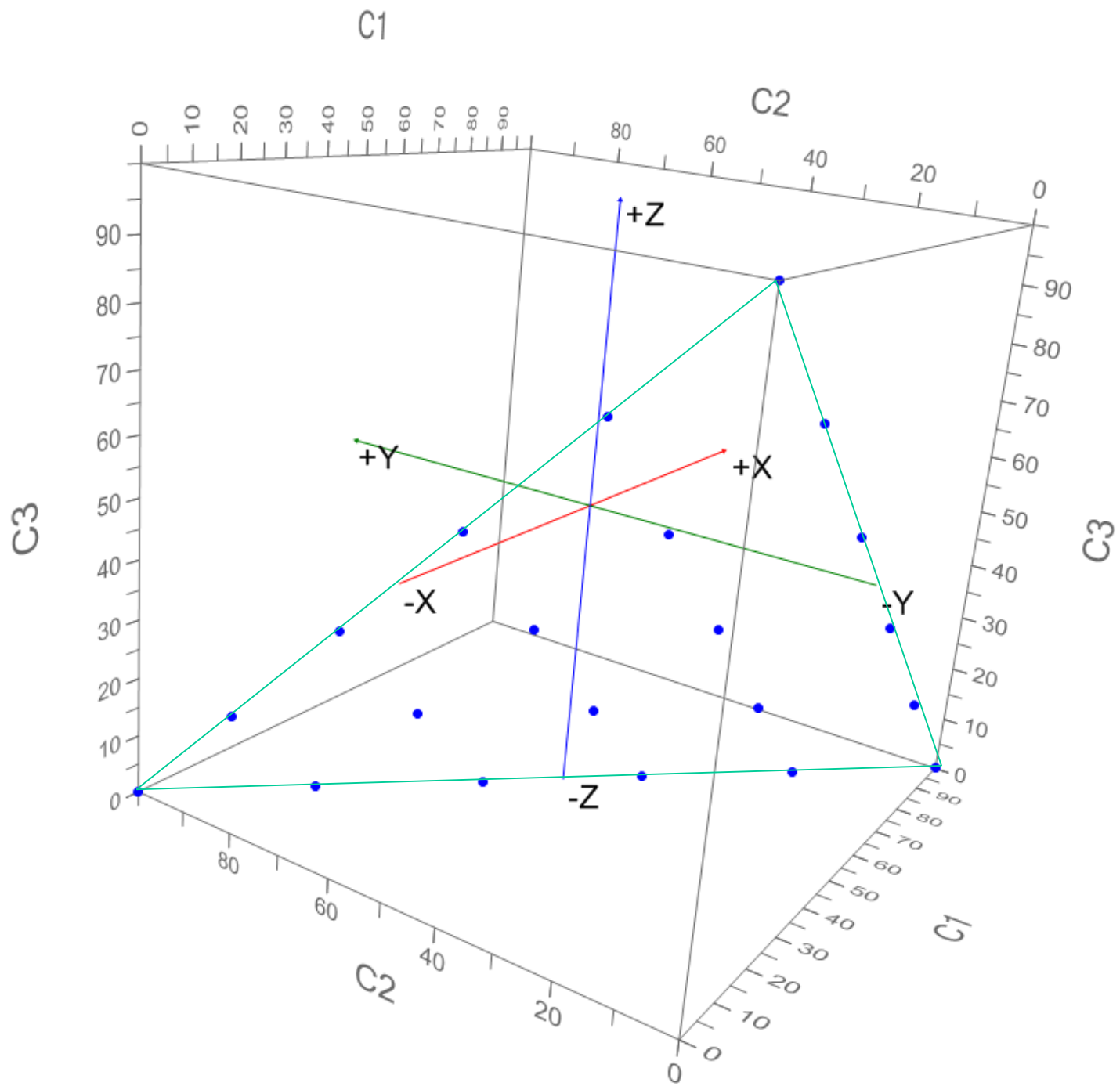
J. Near Infrared Spectrosc. **8**, 229–237 (2000)

3 Constituents : 2 dimensions

N=21



GHbar=1, NHmin=0.60



4 Constituents : 3 dimensions

SIMPLEX-LATTICE
Design

3rd order centroid
(face center)

$R=2, N=15$

$R=5, N=56$

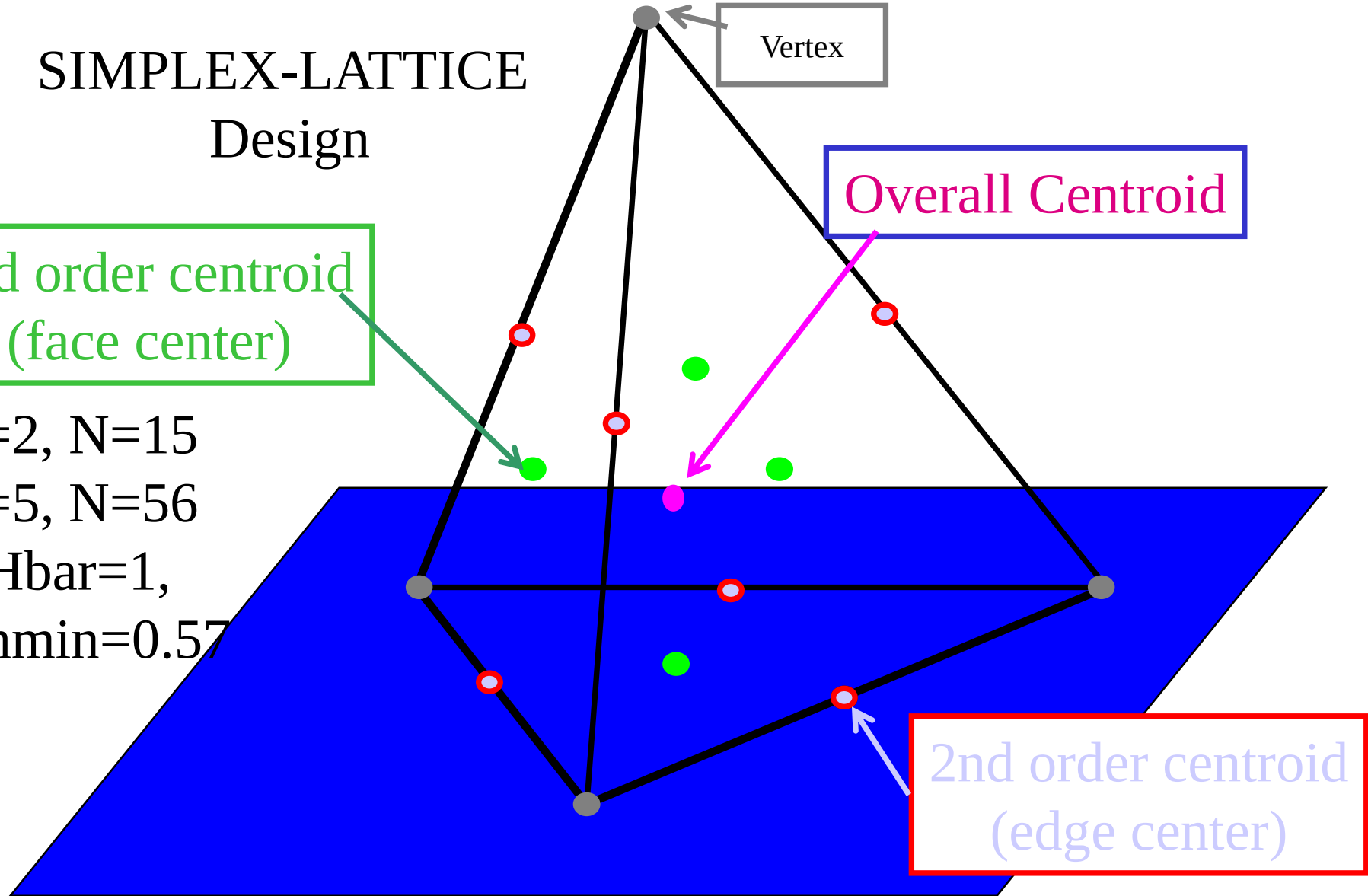
$\text{GHbar}=1,$

$N_{\text{hmin}}=0.57$

Vertex

Overall Centroid

2nd order centroid
(edge center)



p Constituents :

Excel:
=COMBIN()

$p-1$ dimensions

Ranges /5 $\rightarrow$ r=5

$$Nspl = C_{r+p-1}^{p-1} = \frac{(r+p-1)!}{r!(p-1)!}$$

$$C_{5+3-1}^{3-1} = \frac{(5+3-1)!}{5!(3-1)!} = \frac{7!}{5!*2!} = \frac{5040}{120*2} = 21$$

p Constituents :

$p-1$ dimensions

Ranges /5 $\rightarrow$ r=5

$$Nspl = C_{r+p-1}^{p-1}$$

$$C_{r+p-1}^{p-1} = \frac{(r+p-1)!}{r!(p-1)!}$$

GHbar=1, NHmin=0.57

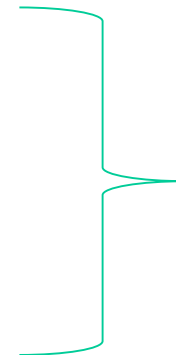
Const.	Dim.	Nspl
3	2	21
4	3	56
5	4	126
6	5	252
7	6	462
8	7	792
9	8	1287
10	9	2002
11	10	3003
13	12	6108
15	14	11628
:	:	:
25	24	118755

An example: calibrations for Milk Powder (Whole and Skimmed)

SMP – WMP

Protein :	20 – 40 %
Fat :	0 – 30 %
Carbohydrate :	35 – 55 %
Minerals :	5 - 10 %
Moisture :	0 – 5 %
Additives : ?	<1%

+ color
+ particle size
+ temperature
+ instrument
+.....



**Out of the
constraint
 $\Sigma=100$**

**→9 dim. → 2000 samples required to fill the space with 6
points evenly spread for each dimension**

The questions are:

How long does it last to complete a calibration?

How many samples are needed to obtain a robust model?

NIR EQUATION STABILITY OVER TIME

Product: WHOLE PLANT MAIZE SILAGE

Constituents:

PROTEIN
(1600)

CRUDE FIBER
(1700)

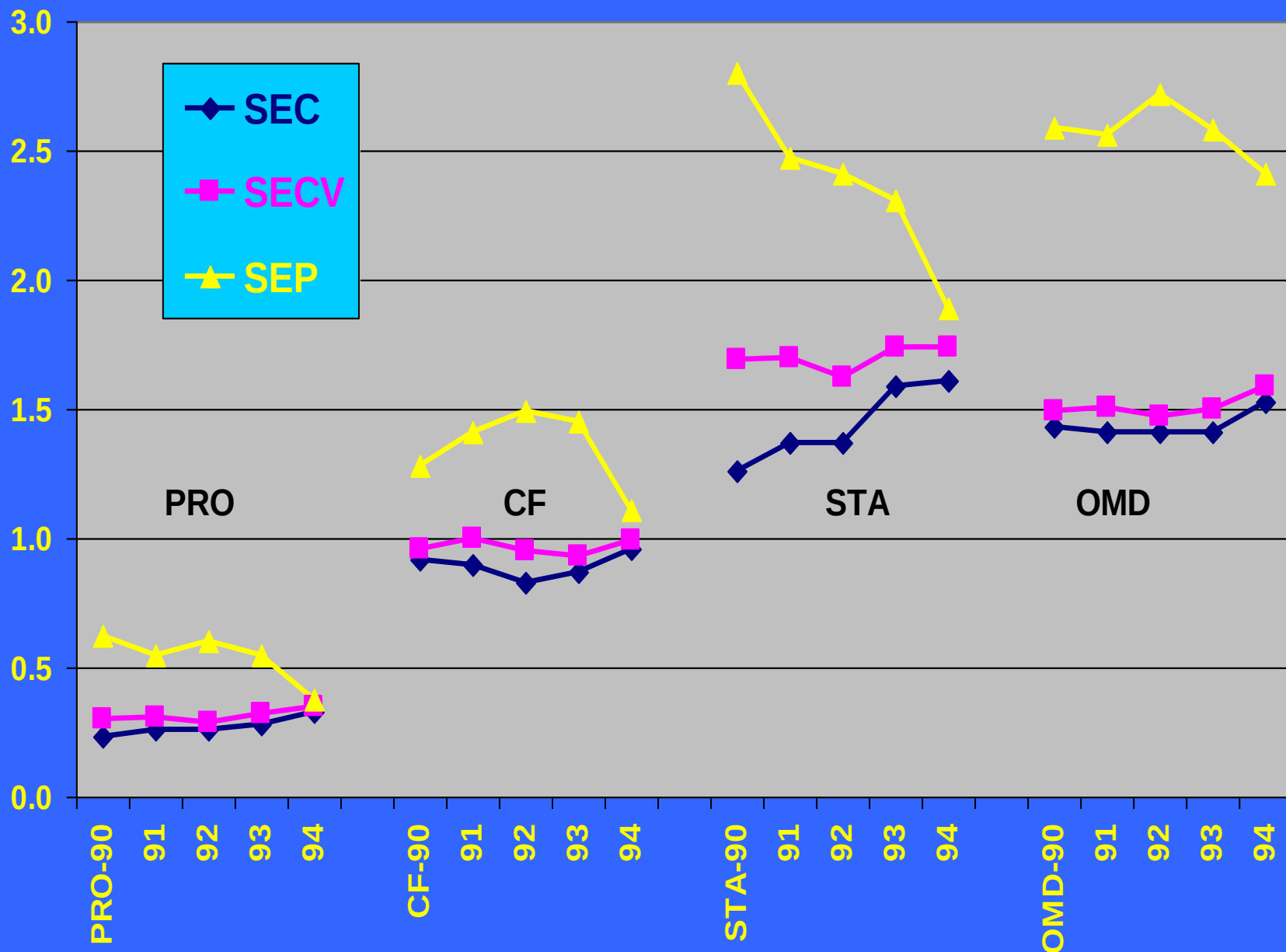
STARCH
(1950)

OMD
(2400)

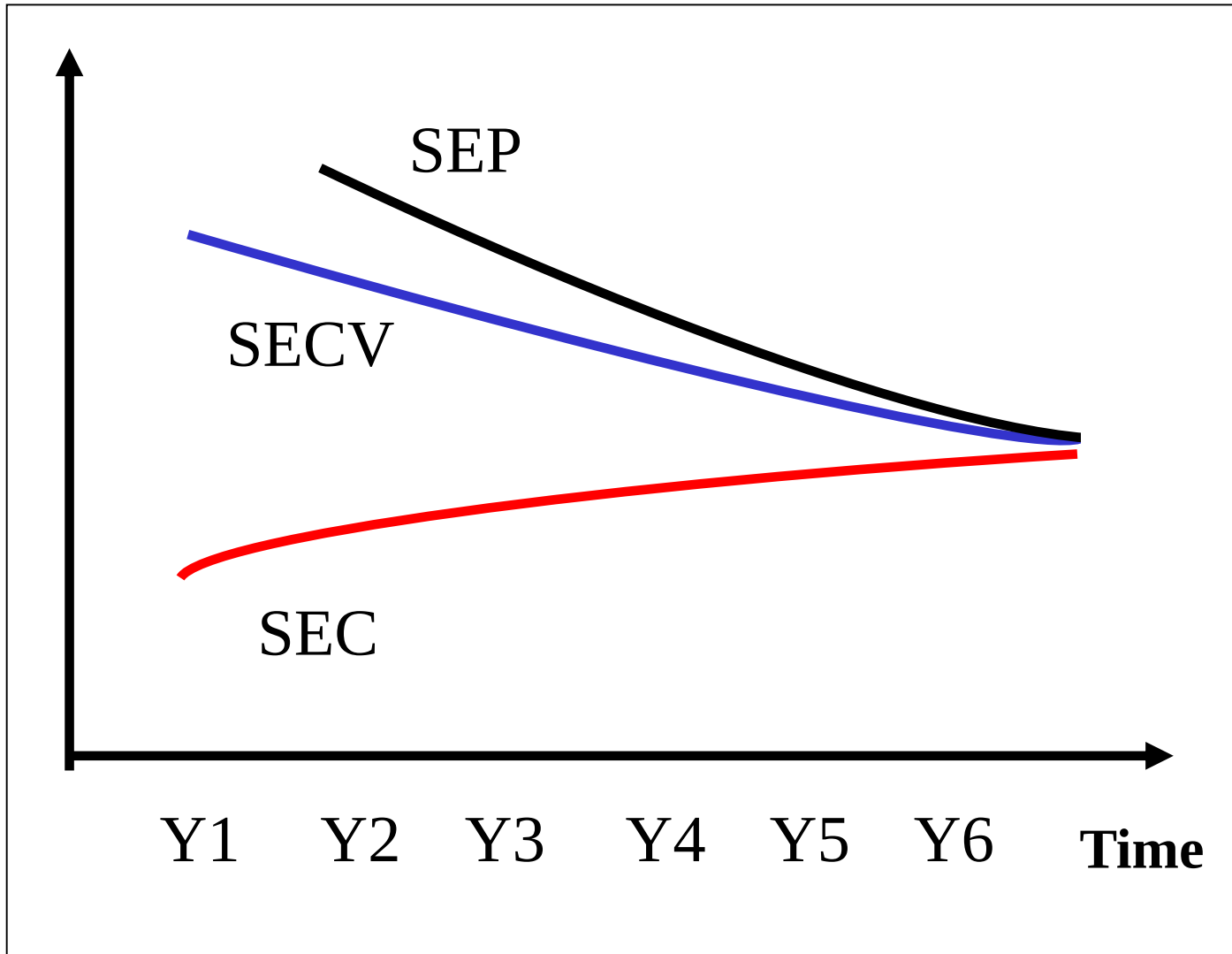
	90	91	92	93	94	95
Model 1	Calib	Validation				
Model 2	Calibration		Validation			
Model 3	Calibration			Validation		
Model 4	Calibration				Validation	
Model 5	Calibration					Valid

Validation is INDEPENDENT

NIR EQUATION STABILITY OVER TIME



GENERAL TRENDS OF MODEL STATS



In NIR models

ADD NEW INFORMATION
(new samples) & RECALIBRATE:

1) While SECV $\neq$ SEC

Rule of thumb: $(\text{SECV} < 1.1 * \text{SEC})$

2) While SEP $\neq$ SECV

Rule of thumb: $(\text{SEP} < 1.3 * \text{SECV})$

Agriculture Handbook, N°643 (1989)

Marten, G. C., J. S. Shenk, and F. E. Barton II,

CONCLUSION Multivariate models

- 1 multivariate space defines a lot of space**
- NIR needs numerous DIFFERENT samples to cover the actual variability (the rule of 10 #/term !!)**
- It takes time (years) to fill evenly the whole space to make the models stable and robust**
- Extrapolation is dangerous (empirical models)**
- Always good performance if the unknown samples are already represented in the calibration set (neighbors) : → Local approaches**

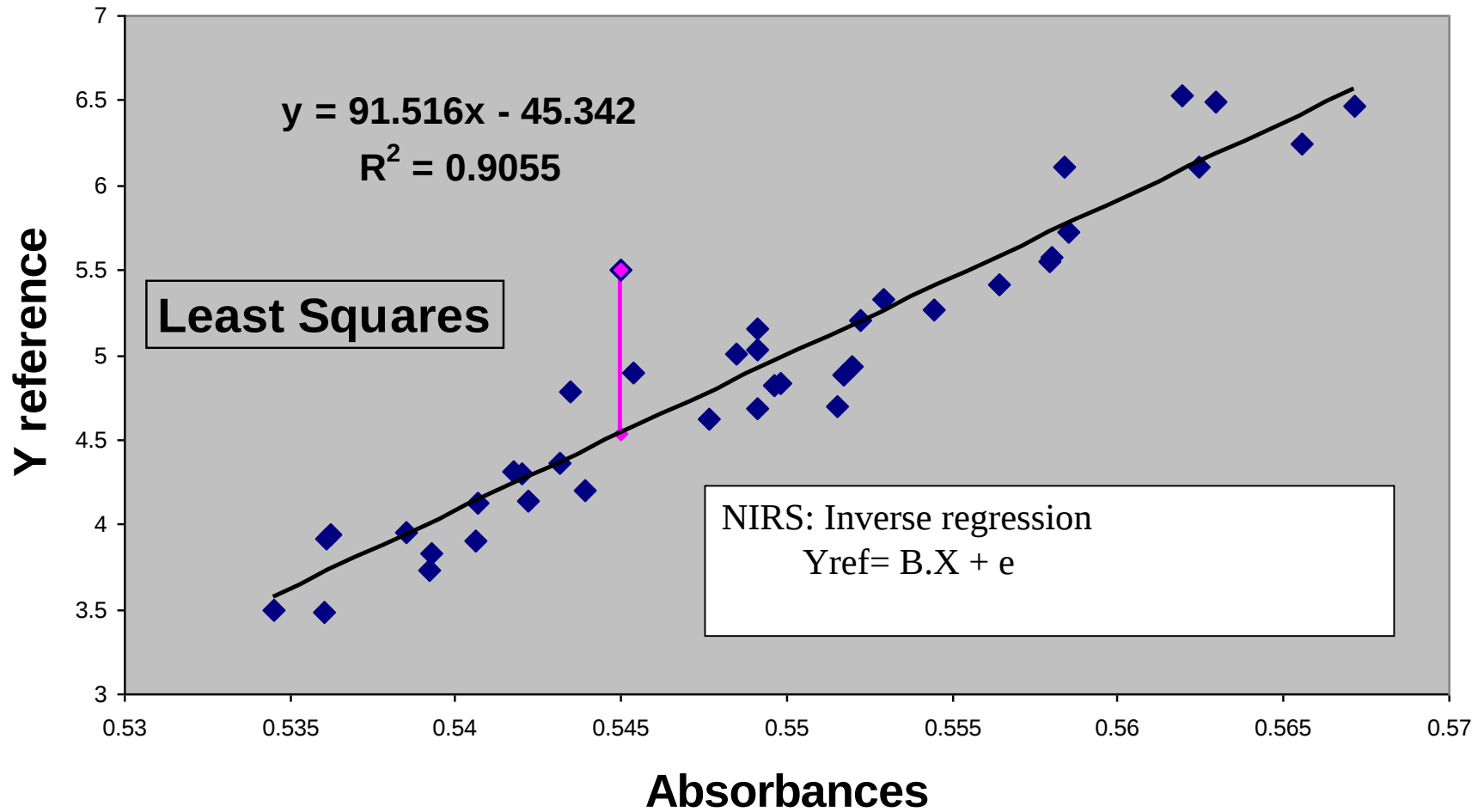
2

UNCERTAINTY

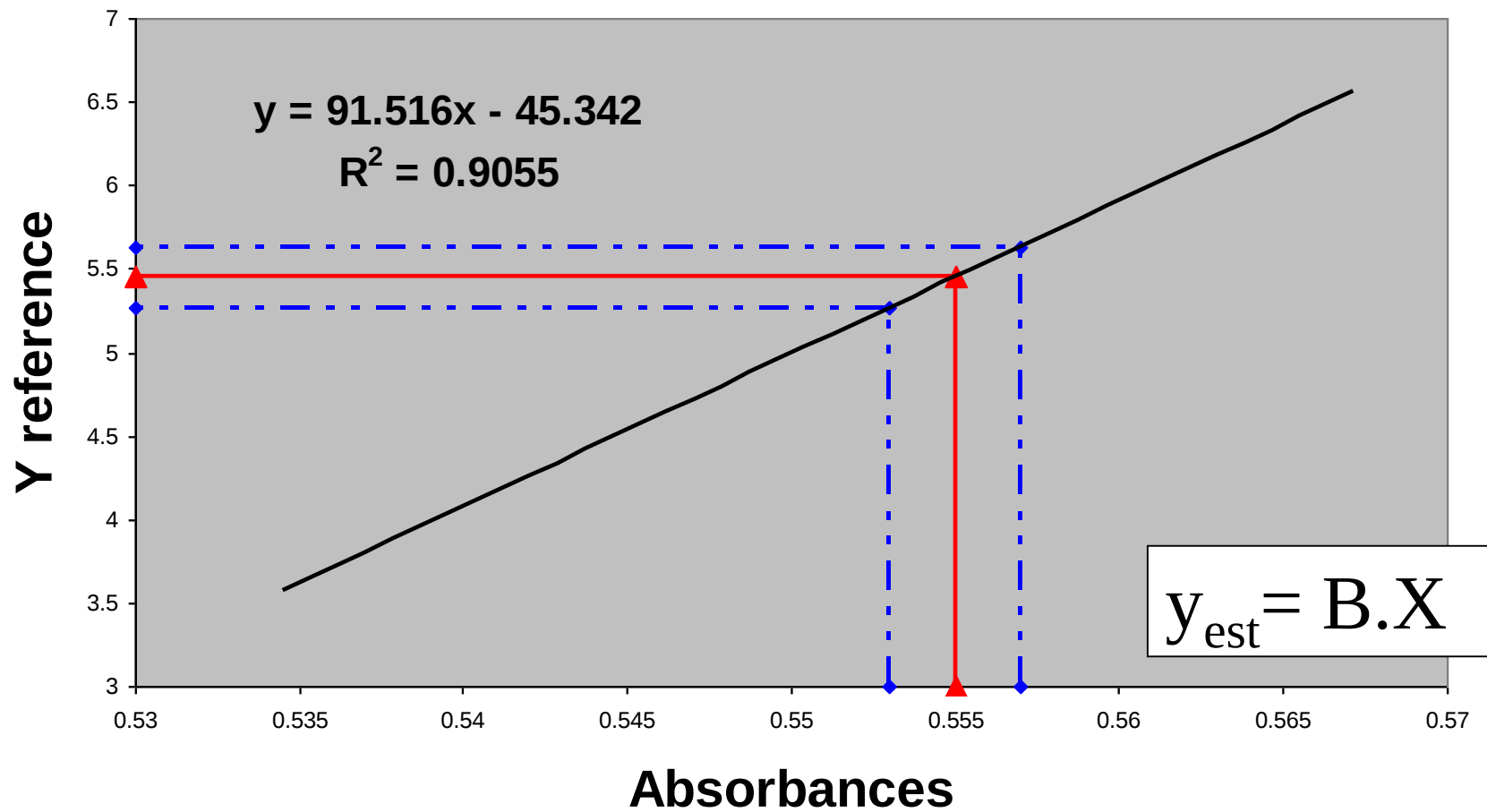
$$s(\hat{y}_i - y_i)?$$

uncertainty

CALIBRATION



PREDICTION

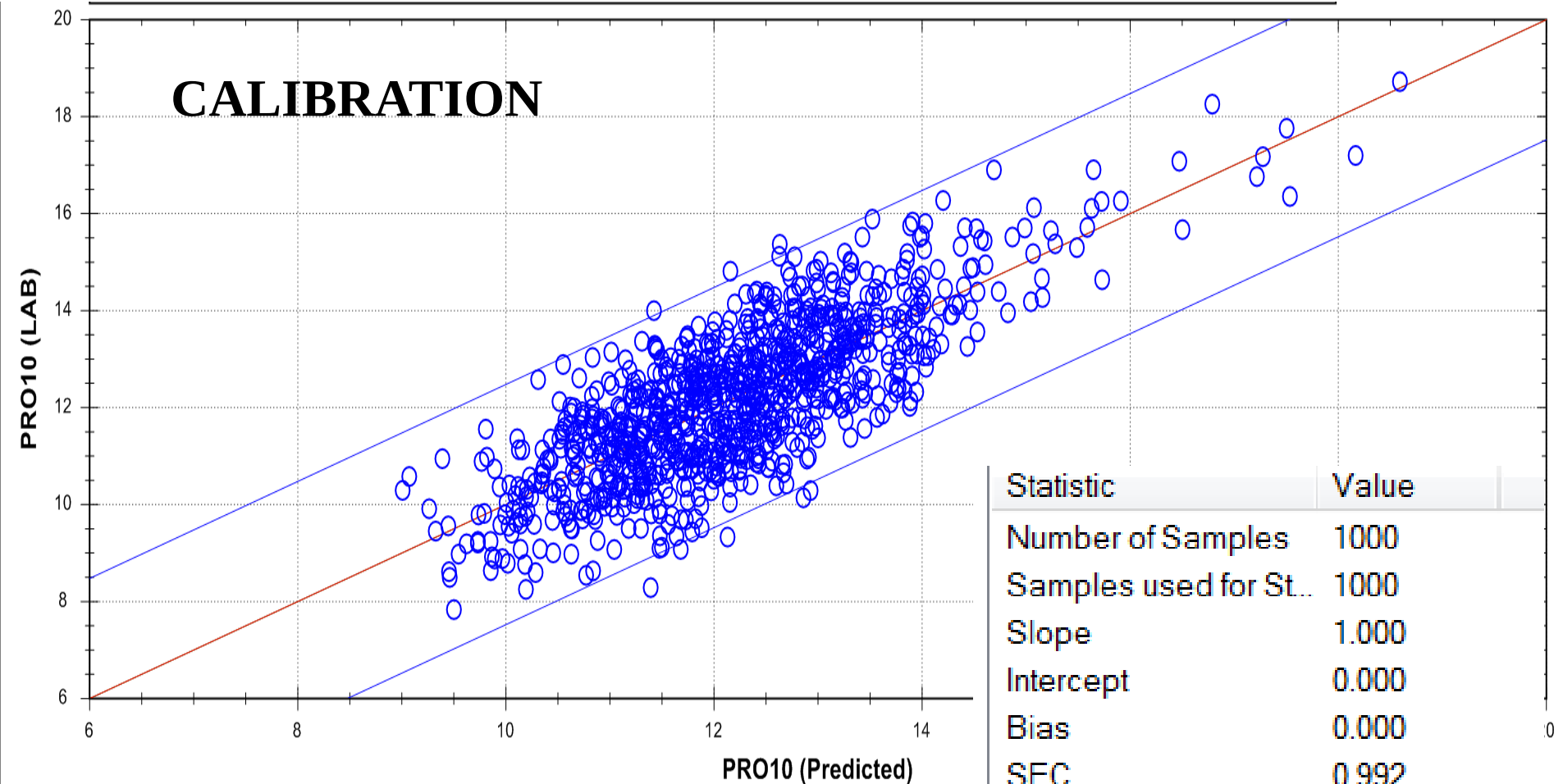


2000 spectra of ground wheat

Spilt $\frac{1}{2}$ -> CAL and VAL

CAL y values are modified by a vector of Gaussian noise of mean =0 and sd of 0.1, 0.2, ...1.0, ..1.5

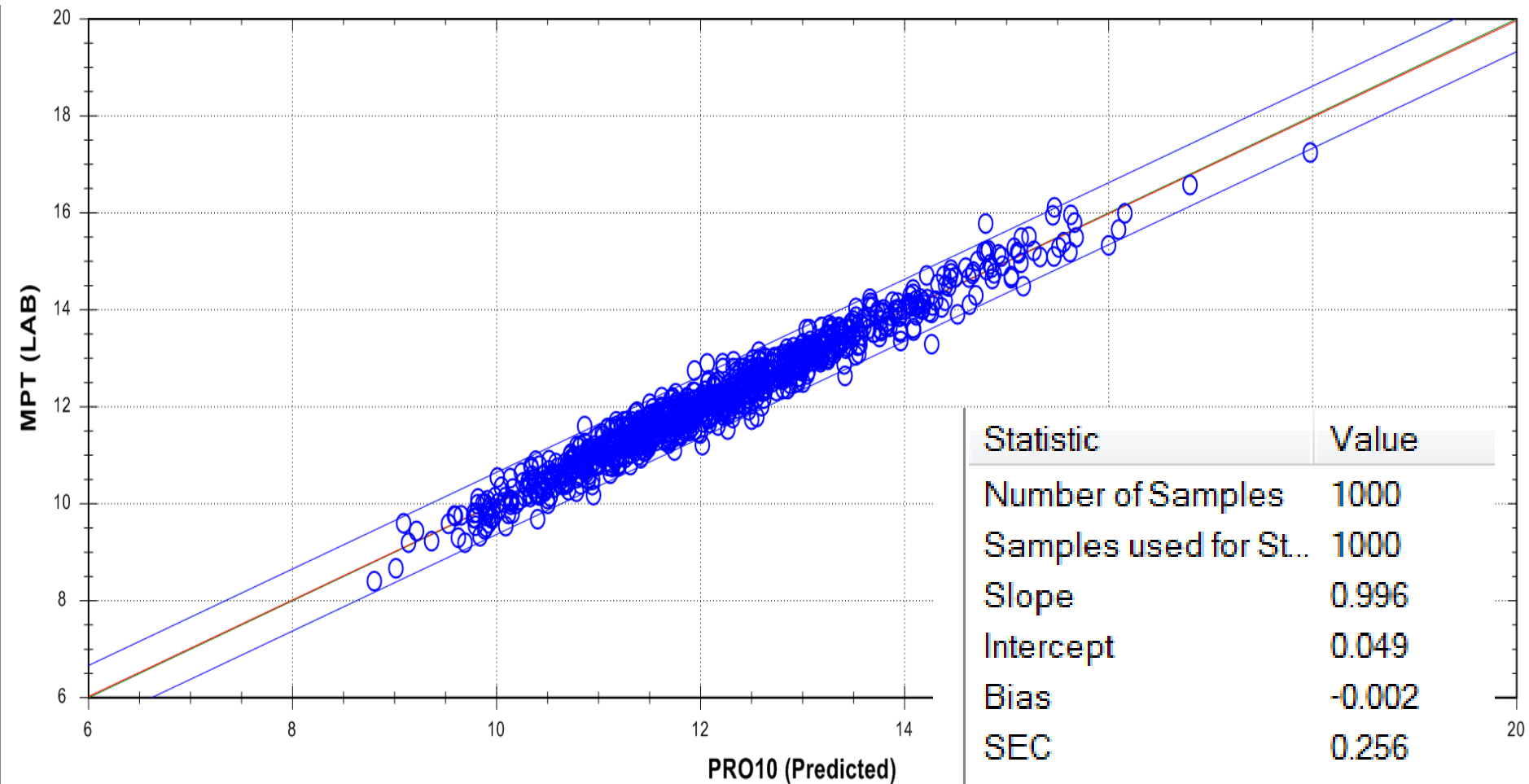
CALIBRATION



Y modified with noise $N(0,1)$

mean = 0

sd = 1

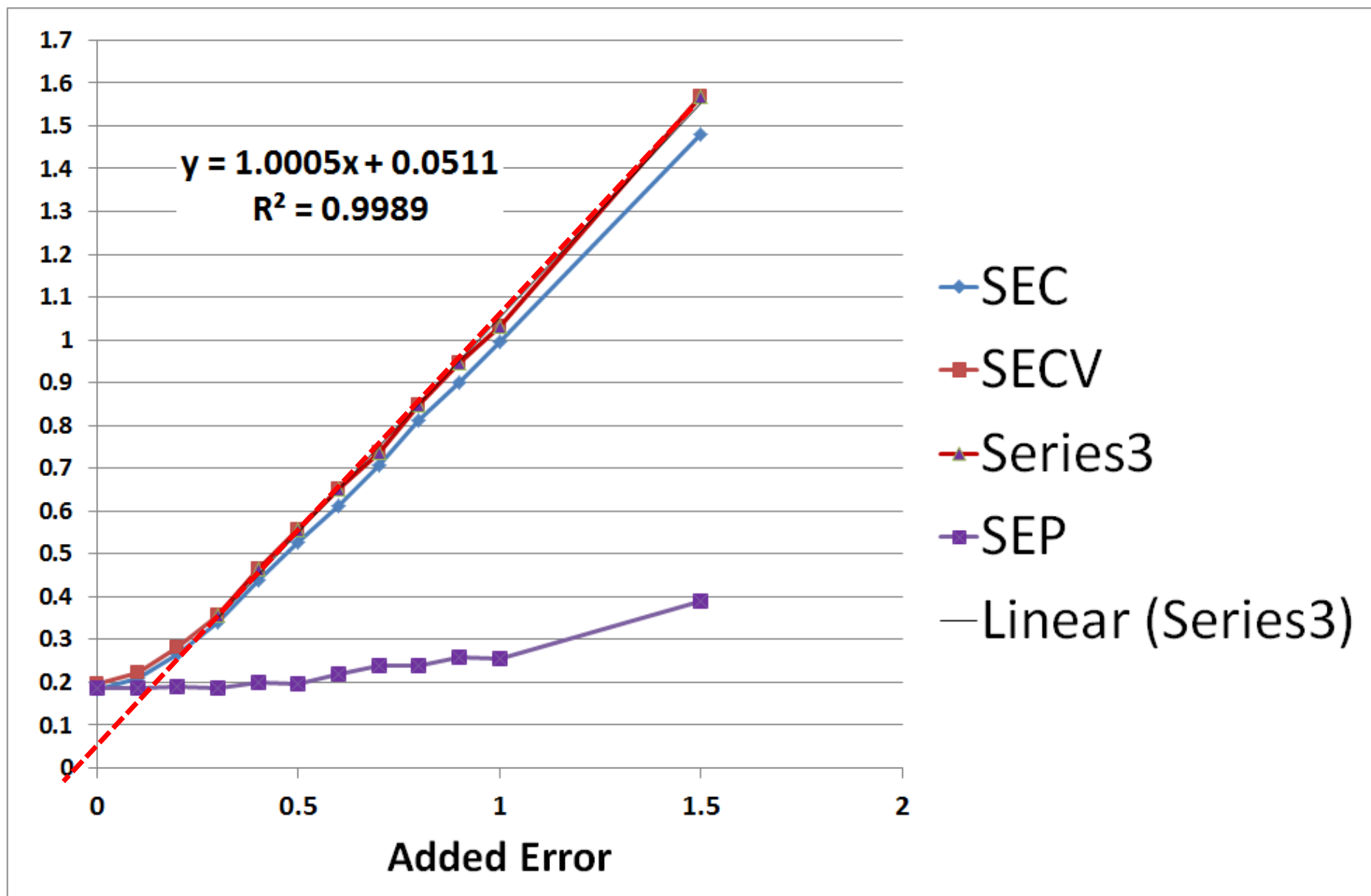


TEST SET N= 1000

Statistic	Value
Number of Samples	1000
Samples used for St...	1000
Slope	0.996
Intercept	0.049
Bias	-0.002
SEC	0.256
SEP	0.256
SEP(C)	0.256
RSQ	0.960
Predicted Average	12.150
Actual Average	12.148
Predicted SD	1.268
Actual SD	1.268

Added

Error	SECV	SEP
0.0	0.20	0.19
0.1	0.22	0.19
0.2	0.28	0.19
0.3	0.36	0.19
0.4	0.47	0.20
0.5	0.56	0.20
0.6	0.65	0.22
0.7	0.74	0.24
0.8	0.85	0.24
0.9	0.95	0.26
1.0	1.03	0.26
1.5	1.57	0.39



Uncertainty of the NIR analyses

$$s(\hat{y}_i - y_i) = \left[(1 + h_i) \cdot SEC^2 - S_{ref}^2 \right]^{1/2}$$

Faber and Bro, *Chemom., Intell. Lab. Syst.* 61, 133 (2002)

Fernandez Pierna & al., *Chemom., Intell. Lab. Syst.* 65,281 (2003)

$$SEP_{actual}^2 = SEP_{observed}^2 - SEL_{ref}^2$$

$$SEP_{actual}^2 = SEP_{observed}^2 - SEL_{ref}^2$$

An example:

Protein in wheat: SEL = 0,15

SEP_{observed} = 0,21

SEP_{actual} = SQRT(0,21² – 0,15²) = 0,15



Journal of Near Infrared Spectroscopy
25(2) 85–90

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DOI: 10.1177/0967033517702395

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2 FIGURES OF MERIT: RMSEP SEL

Original Article

Tutorial: Items to be included in a report on a near infrared spectroscopy project

Phil Williams¹, Pierre Dardenne² and Peter Flinn³

What is the MOST important in a model ?

Not the stats : sec, sep, R2,... = gauges

B coefficients = engine

$$\hat{Y} = X.b$$

$$n.1 = (n.m) * (m.1)$$

CONCLUSION UNCERTAINTY

In many NIR applications, NIR values are more accurate than the reference method ones.

But it is not easy to prove it!

Do not try to obtain the smallest SEC (outliers)

Just try to compute stable Bcoefficients from spectra containing the expected future variation.

3

LOD



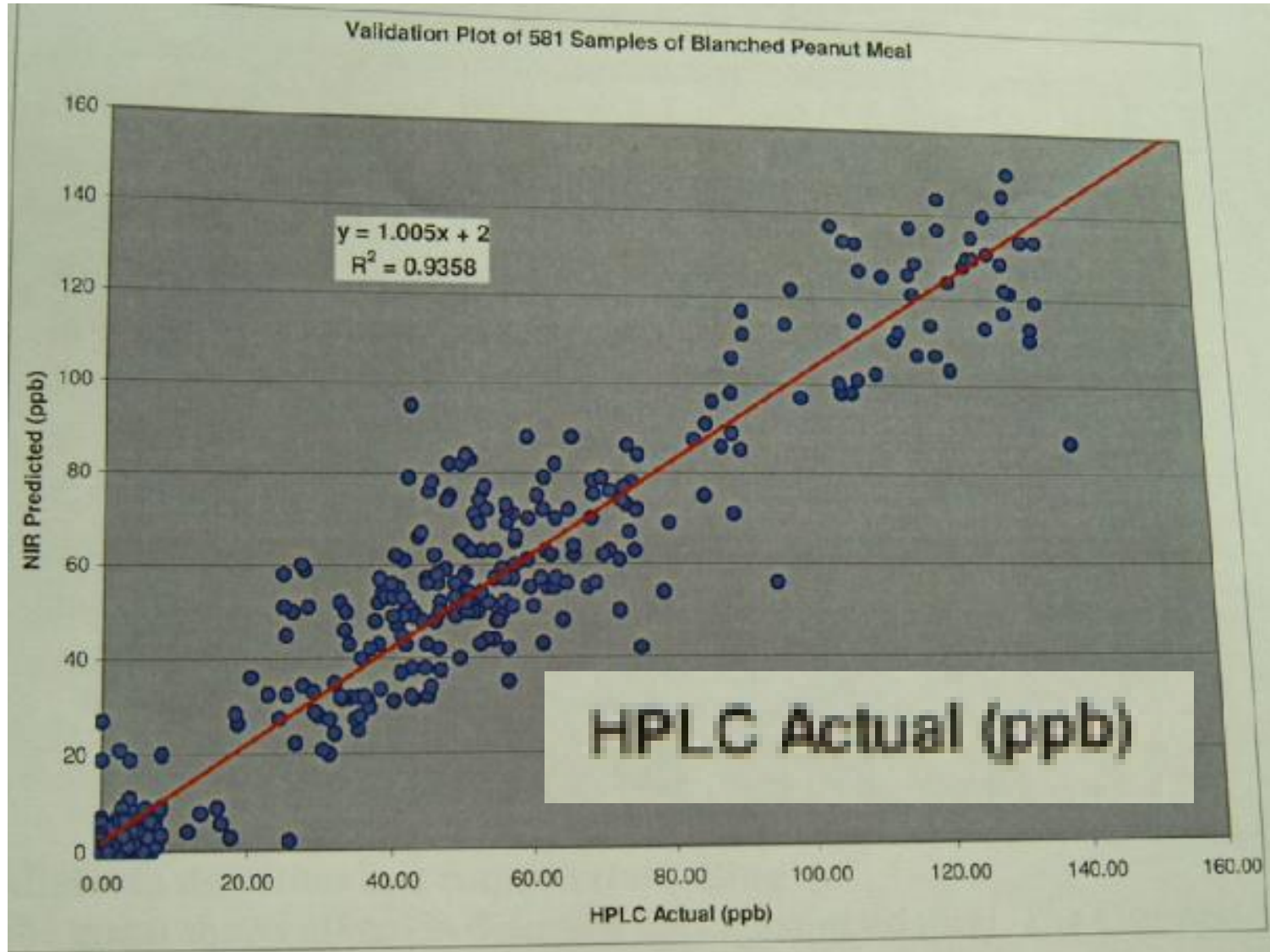
Rapid detection of melamine in milk powder by near infrared spectroscopy

than 1 ppm.²¹ In order to overcome the limitation of the methods which had already been evaluated, this study tried to establish a fast detection method for pure melamine in milk powder by near infrared (NIR) spectrometry together with LS-SVM and has shown some promise. The detection limit of this method was lower than 1 ppm. It conforms to the national standard for melamine in infant milk products. The

Melamine Detection in Infant Formula Powder Using Near- and Mid-Infrared Spectroscopy

models are not matrix independent. New calibration models are required for application to different brands or formulations of infant formula powders or other food products. It is expected that the analytical approach for quantifying or detecting melamine using NIR or FTIR spectroscopy would be applicable to other products. The NIR and FTIR methods meet the need for a rapid, simple, and available technique for detecting 1 ppm melamine in infant formula powder.

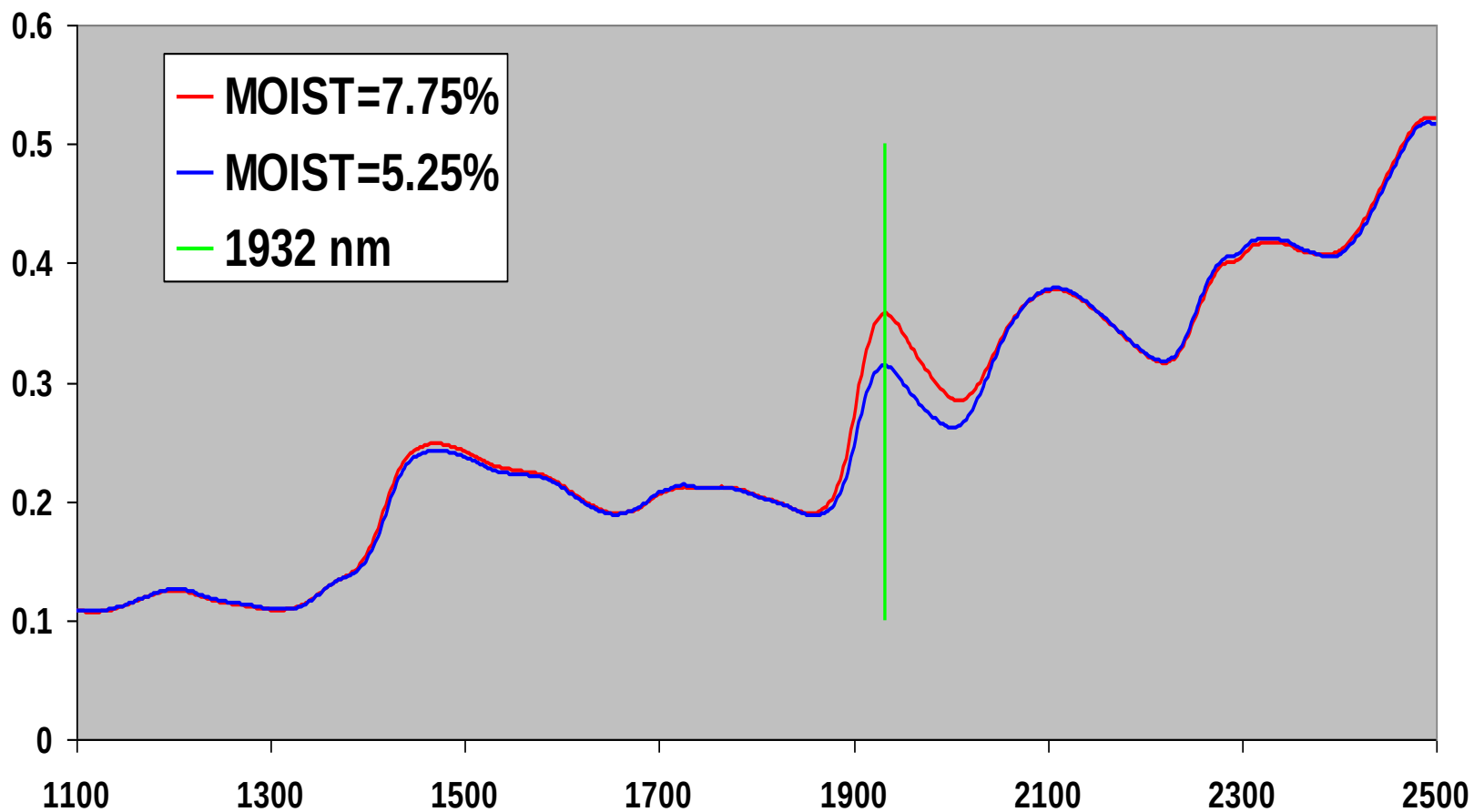
Rapid and Non-destructive Mycotoxin Assay with NIRS, *Russel Wilkie* (ICNIR2005, Auckland)



LOD of NIRS

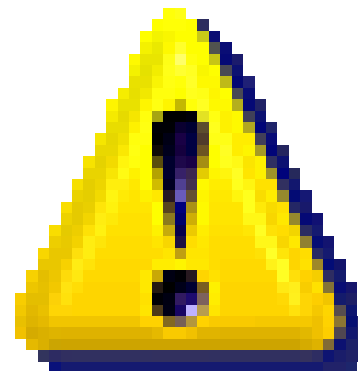
CORN SILAGE DATA SET 4816 spectra sorted/H2O %

CORN SILAGE - AVERAGE OF 2 x 2408 SPECTRA



LOD of NIRS

	1932
MOIST=7.75%	0.357243
MOIST=5.25%	0.313645
2.5	0.043598
1	0.017439



If <0.1%

A units	Water %	ppm	ppb
0.020 000	1	10 000	10 000 000
0.002 000	0.1	1 000	1 000 000
0.000 200	0.01	100	100 000
0.000 020	0.001	10	10 000



Villeneuve d'ascq, 5-6 Décembre 2012

Polytech'Lille, Université Lille1, FRANCE

Connexion

NAVIGATION

Accueil

Lieu de la conférence

Conférenciers invités

Liste de communications
acceptées

Programme
CHIMIOMETRIE 2012

Comités ▼

Résumé et inscription ▼

Publication dans
CHEMOLAB

Challenge 2012

Prix et récompenses

Hébergement

Exposants / Partenaires /
Sponsors

Devenir partenaire /
Sponsoriser cette
conférence

CHALLENGE 2012



Le Challenge est ouvert !

Le challenge organisé par le Groupe Français de Chimiométrie se présente sous la forme d'une énigme. Il s'agit de trouver les réponses d'un fichier "test" à partir d'un fichier dit d'étalonnage. Les données de ce dernier fichier peuvent être polluées (données manquantes, données aberrantes, etc.).

Le fichier d'étalonnage et le fichier "test" sont mis à votre disposition ci-dessous. L'analyse des solutions se fait au cours du congrès. Les congressistes ayant proposé les meilleurs solutions seront invités à présenter brièvement leur méthodologie lors d'une session spéciale CHALLENGE. Les meilleures solutions seront primées.

NOUVEAUTÉ : Afin de favoriser la participation des jeunes chimiométriciens (moins de 30 ans), le comité scientifique a décidé cette année de créer une catégorie spécifique dite "Junior". Ces contributions au Challenge seront ainsi étudiées séparément de celles des seniors.

Téléchargez le fichier de données : [ICI](#)

Description du CHALLENGE CHIMIOMETRIE 2012 :

270 spectra in a CAL set with known concentration of a contaminant.

276 spectra in a TEST set to be predicted.

CAL SET (only soya meal (SM))

240 with 4 concentrations (0.10, 0.25, 0.50, 1.00%)

+30 randomly selected from the clean set

270 spectra

TEST SET

T1 = 40 SM randomly selected with high contamination (2, 3, 4, 5%)

T2 = 50 randomly selected from the **clean** set

T3 = 43 soyameal spl from another origin + another instrument

T4 = 78 wheat gluten (39 in duplicates)

T5 = 65 maize gluten

Total : 276

Foss XDS

Foss 6500
Clean & Conta.
Melamine
Cyanuric Acid

Step-up Regression Statistics

Input File	calset1 s.cal	REP File	None
Validation File	None	Equation File	mlr2.eqa
Math Treatment	0, 0, 1, 1	Number of variables	550
Scatter Corrected	None	Downweight outliers	Yes
Constituent	mela	Number of samples	300
Cross validation	By groups, no pre-sort, form groups by blocks, group duplicates together		
Mean	0.370	Range	0.00 - 1.00
		Standard deviation	0.358

Number of terms 3 SEC 0.082 AdjRSQ 0.948

	Coefficient	Data Point	Wavelength	F
B(0) =	-0.131			
B(1) =	-1768.915	83	1464.0	5102.85
B(2) =	2269.486	84	1466.0	5246.59
B(3) =	-501.577	87	1472.0	1979.13

MLR : Multi Linear Regression – manual step up

WinISI Global

File Options Tables Graphs Help



Click on an option to continue

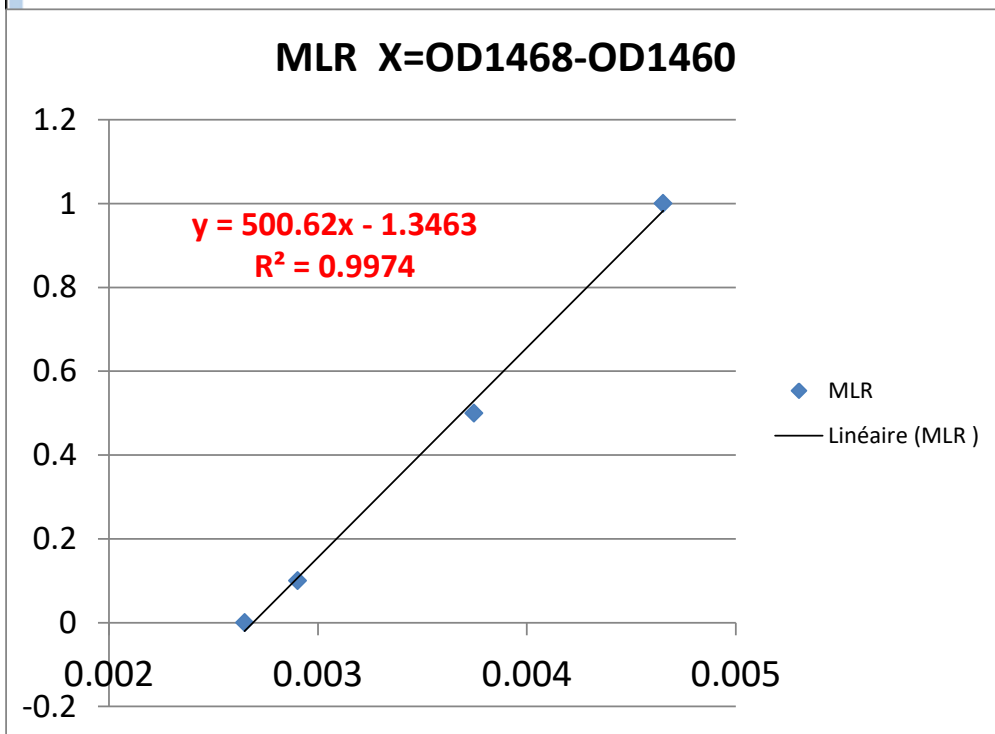
Percent C

Step-up Regression Statistics

Input File	CALSET1S.CAL	REP File	None
Validation File	None	Equation File	None
Math Treatment	0, 0, 1, 1	Number of variables	550
Scatter Corrected	None	Downweight outliers	Yes
Constituent	mela	Number of samples	300
Cross validation	By groups, no pre-sort, form groups by blocks, group duplicates together		
Mean	0.370	Range	0.00 - 1.00
		Standard deviation	0.358
Number of terms	3	SEC	0.081
		AdjRSQ	0.949
	Coefficient	Data Point	Wavelength
B(0) =	-0.143		
B(1) =	-792.693	86	1470.0
B(2) =	1714.127	84	1466.0
B(3) =	-922.584	82	1462.0
			F
			1634.24
			3500.19
			5463.41

Average by group of 60 samples : 0.0, 0.10, 0.25, 0.50, 1%

Step-up Regression Statistics				
Input File	totmeans6.cal		REP File	None
Validation File	None		Equation File	None
Math Treatment	0, 0, 1, 1		Number of variables	550
Scatter Corrected	None		Downweight outliers	Yes
Constituent	mela		Number of samples	5
Cross validation	By groups, no pre-sort, form groups by blocks, group duplicates together			
Mean	0.370	Range	0.00 - 1.00	Standard deviation 0.399
Number of terms	2	SEC	0.032	AdjRSQ 0.994
	Coefficient	Data Point	Wavelength	F
B[0] =	-0.209			
B[1] =	518.336	85	1468.0	613.22
B[2] =	-521.870	81	1460.0	614.07



$$1/500 = 0.002$$

A OD difference of
0.002 = 1% melamine

A Units	μLog	Melamine %	ppm	ppb
0.002	2000	1	10 000	10 000 000
0.000 2	200	0.1	1 000	1 000 000
0.000 02	20	0.01	100	100 000
0.000 002	2	0.001	10	10 000

MELAMINE ABSORBS 10 x LESS THEN WATER !!



Detection of melamine and cyanuric acid in feed ingredients by near infrared spectroscopy and chemometrics

O. Abbas,* B. Lecler, P. Dardenne and V. Baeten

Food and Feed Quality Unit, Valorisation of Agricultural Products Department, Walloon Agricultural Research Centre (CRA-W),
Chaussée de Namur 24, B-5030 Gembloux, Belgium. E-mail: o.abbas@cra.wallonie.be



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journal homepage: www.elsevier.com/locate/chemolab

Use of a multivariate moving window PCA for the untargeted detection of contaminants in agro-food products, as exemplified by the detection of melamine levels in milk using vibrational spectroscopy☆

J.A. Fernández Pierna, D. Vincke, V. Baeten, C. Grelet, F. Dehareng, P. Dardenne *

Walloon Agricultural Research Centre (CRA-W), Valorisation of Agricultural Products Department, Chaussée de Namur n°24, 5030 Gembloux, Belgium

MID-IR MILK & Melamine → 250 ppm

**NIR SOYAMEAL & Melamine → 1000 ppm
(60 samples at 0.1 = 4 misses)**



Virtual Issue: [Papers Presented at NIR-2015, October 2015, Foz do Iguassu, Brazil](#)

LOCAL regression algorithm improves near infrared spectroscopy predictions when the target constituent evolves in breeding populations

F. Davrieux,^{a,*} D. Dufour,^{b,e} P. Dardenne,^c J. Belalcazar,^d M. Pizarro,^d J. Luna,^d L. Londoño,^e A. Jaramillo,^e T. Sanchez,^d N. Morante,^d F. Calle,^d L.A. Becerra Lopez-Lavalle^d and H. Ceballos^d

carotenoids content of cassava roots

TCC values ranged from 0.11 $\mu\text{g g}^{-1}$ to 29.0 $\mu\text{g g}^{-1}$ (ppm)

>6000 samples and cross year validation

CONCLUSION LOD

**When $Y < 0.1$ %, be sure what you analyze is
(significantly) present in the spectra;
Look at the ratio absorptivity/noise**

**Analytes < 0.1 % can be well predicted and provide
useful results
But these analytes are likely correlated with something
else into the matrix.**

**Hyperspectral Imaging can improve the LOD significantly
→ ppm ?**

Conclusions

- 1. Mixture model and multivariate space – Number of samples>>**
- 2. Uncertainty**
- 3. Limit of detection**

As Karl Norris and John Shenk recommendations

- Look at the spectra**
- Make the models simple**
- Challenge (validate) the models with new sets**