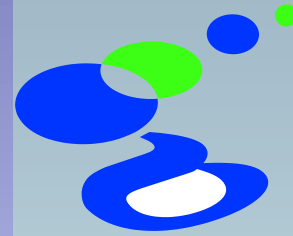


Joint ADSA-PSA-AMPA-ASAS Meeting
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Principal Components Approach for Estimating Heritability of Mid-Infrared Spectrum in Bovine Milk



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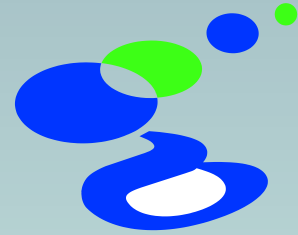
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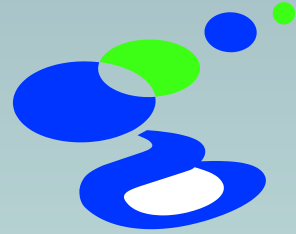
⁴FNRS, Brussels, Belgium

Introduction



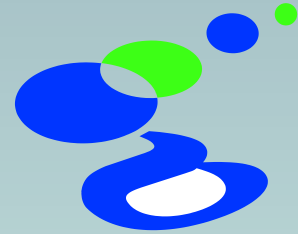
- MIR Spectrometry used in milk recording
- Absorptions of IR at frequencies correlated to the vibrations of specific chemical bonds within a molecule
 - MIR milk spectrum represents the milk composition
- Improve the nutritional quality of milk
- Difficulties:
 - 1,060 spectral data
 - Enough genetic variability ?

Objectives



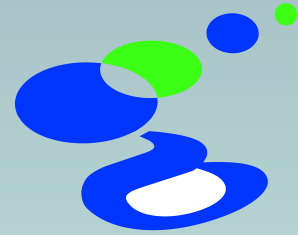
- Reduce the number of traits
- Estimate the genetic parameters of spectral data

Spectral Data



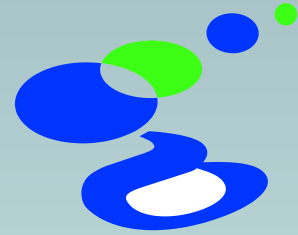
- 9,663 milk samples:
 - MilkoScan FT6000 during the Walloon milk recording
 - April 2005 and May 2006
 - 1,937 cows in 26 herds
 - 7 breeds :
 - Brown Swiss, Dual Purpose Belgian Blue, Holstein Friesian, Jersey, Montbeliarde, Normande and non Holstein Meuse-Rhine-Yssel type Red and White
- Limited data base: cows in first lactation:
 - 2,850 test-day spectral records
 - 750 cows

Trait Reduction



- PCA pre-treatment:
 - $\mathbf{V} = \mathbf{UDU}'$
 - \mathbf{V} = phenotypic (co)variances matrix for the 1,060 spectral initial traits
 - \mathbf{U} = matrix of eigenvectors
 - \mathbf{D} = diagonal matrix of eigenvalues
 - 48 principal components described 99.02% of phenotypic spectral variability

Trait Reduction

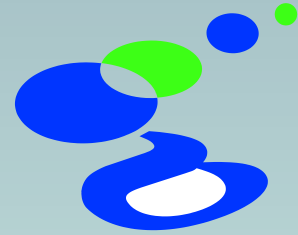


- 48 new traits were estimated:

$$\mathbf{y}_U = (\mathbf{I}_n \otimes \mathbf{U}_R') \mathbf{y}$$

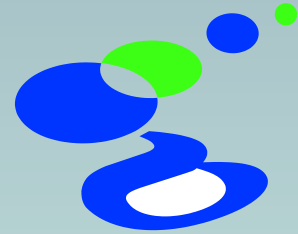
- \mathbf{U}_R = the reduced matrix containing the chosen eigenvectors
- \mathbf{I}_n = identity matrix of dimension n equal to the number of records
- \mathbf{y} = the vector including the 1,060 original traits
- \mathbf{y}_U = the vector including the 48 new traits

Estimation of (Co)Variances



- Model:
 - Fixed effects:
 - Herd * test date
 - Class of 15 days in milk
 - Random effects:
 - Permanent environment effect
 - Animal genetic effect
 - Residual effect
- Multiple diagonalization and REML
- Back transformation

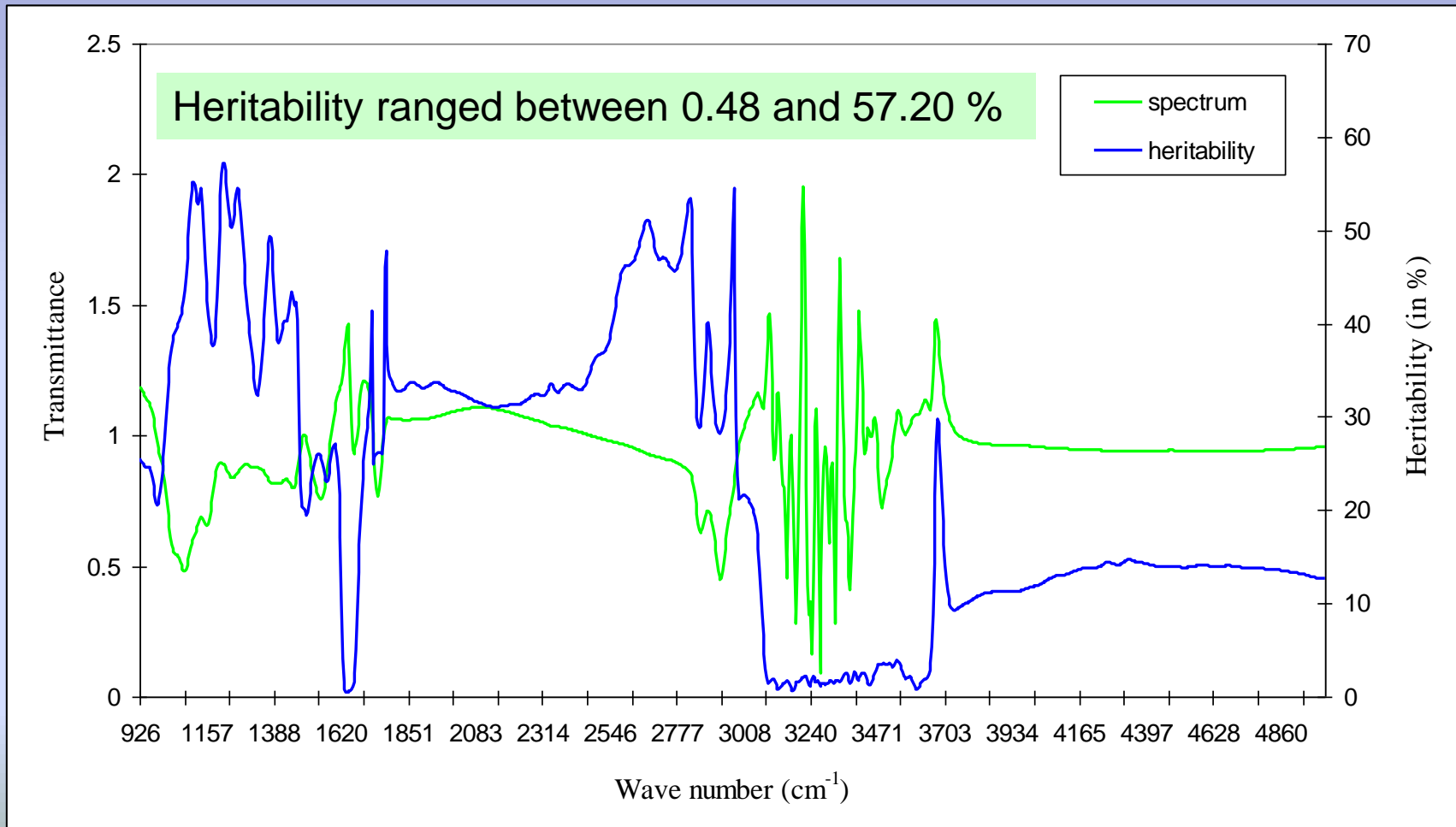
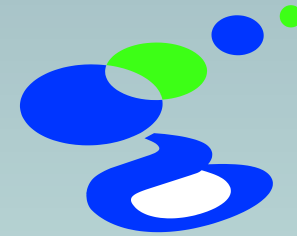
Estimation of (Co)Variances



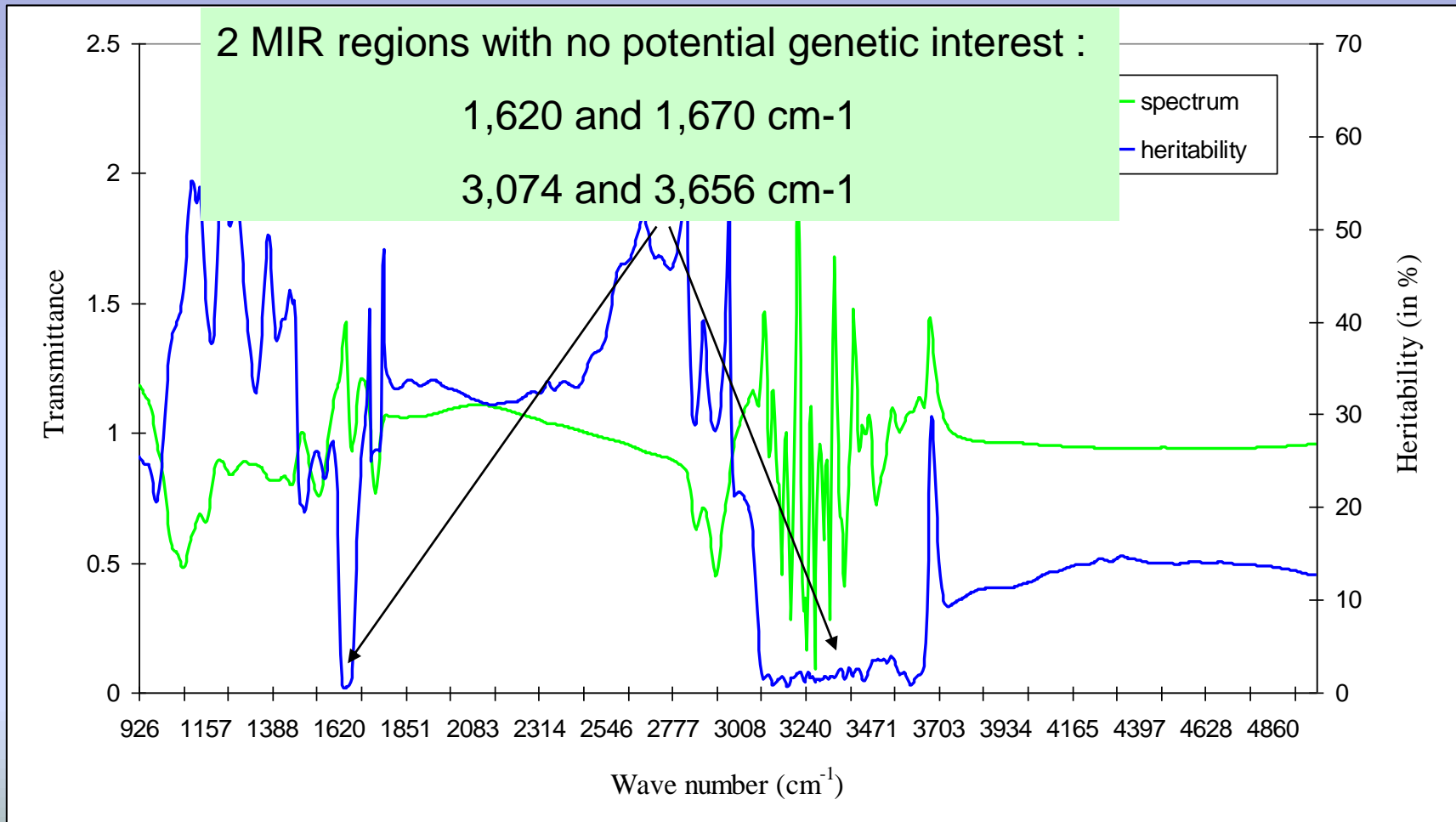
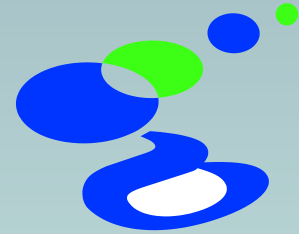
PC	Relative eigenvalues	Heritability		Permanent Environment		Residual	
		Estimate	SE	Estimate	SE	Estimate	SE
1	45.95	21.13	1.82	10.51	1.71	68.36	1.50
2	18.92	18.89	1.99	7.45	1.15	73.66	1.58
3	14.17	49.66	3.00	3.11	3.35	47.24	1.06
4	3.59	2.96	0.39	2.51	0.42	94.53	1.95
5	3.34	15.54	3.54	16.65	2.35	67.81	1.47
6	1.73	2.19	0.25	1.58	0.31	96.23	1.94
7	0.93	35.54	2.99	1.58	1.76	62.88	1.32
8	0.82	31.37	3.47	1.11	2.48	67.52	1.40

Heritability values ranged between 0.80 and 49.66%.

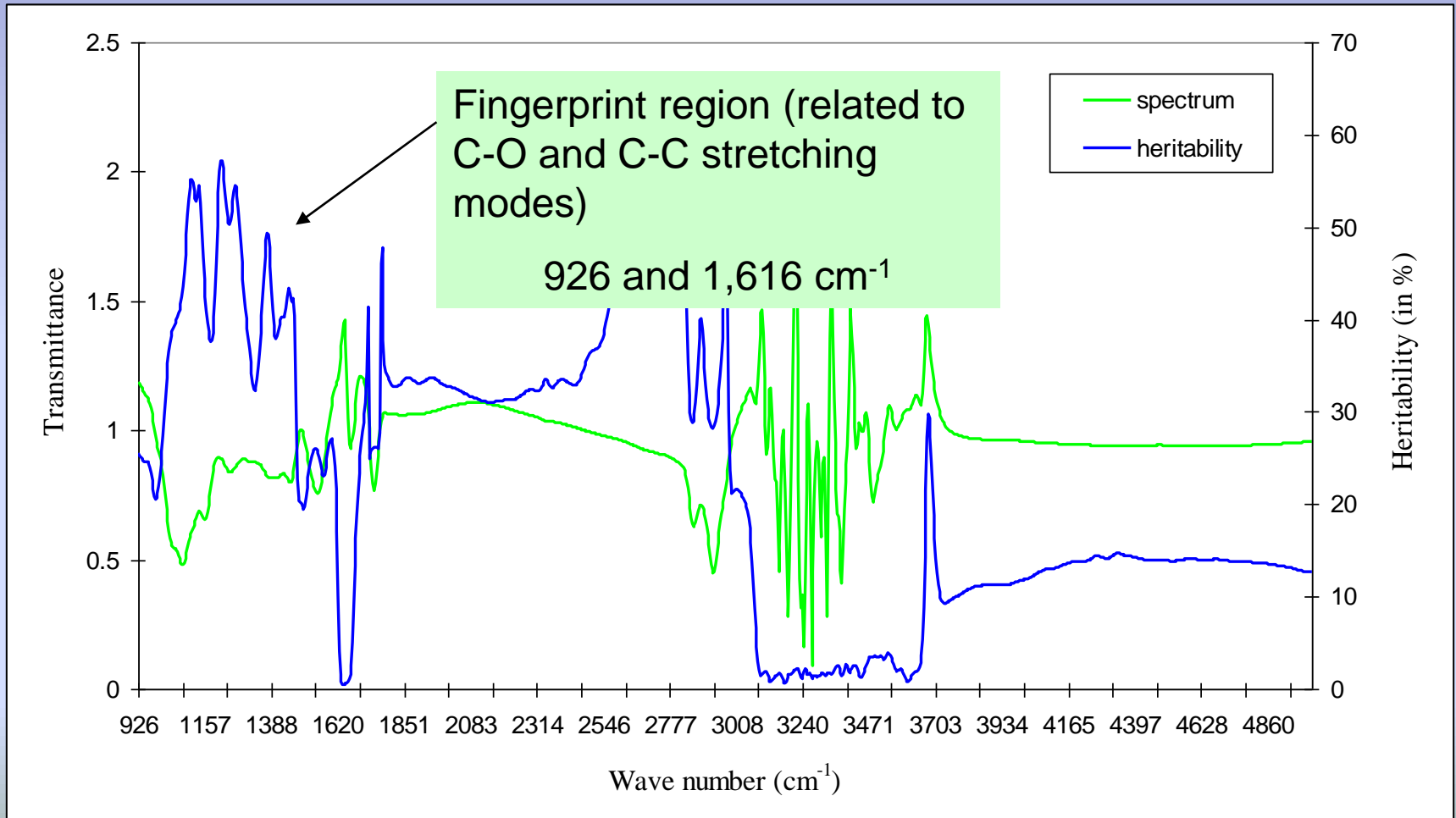
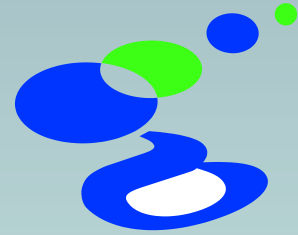
Heritability of MIR Spectrum



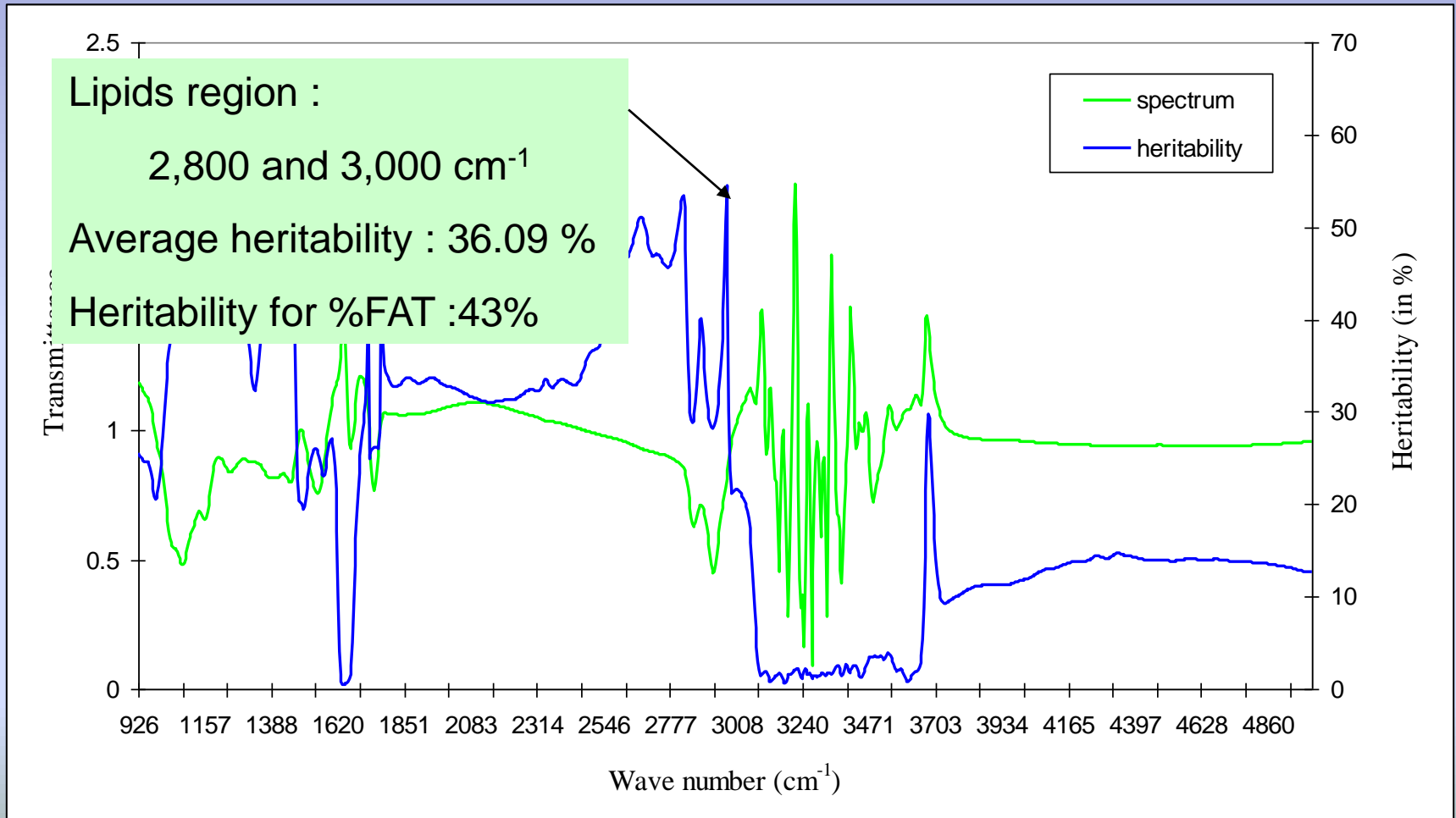
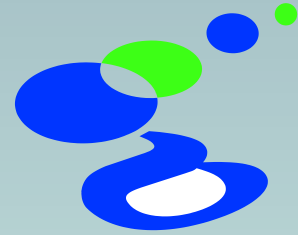
Heritability of MIR Spectrum



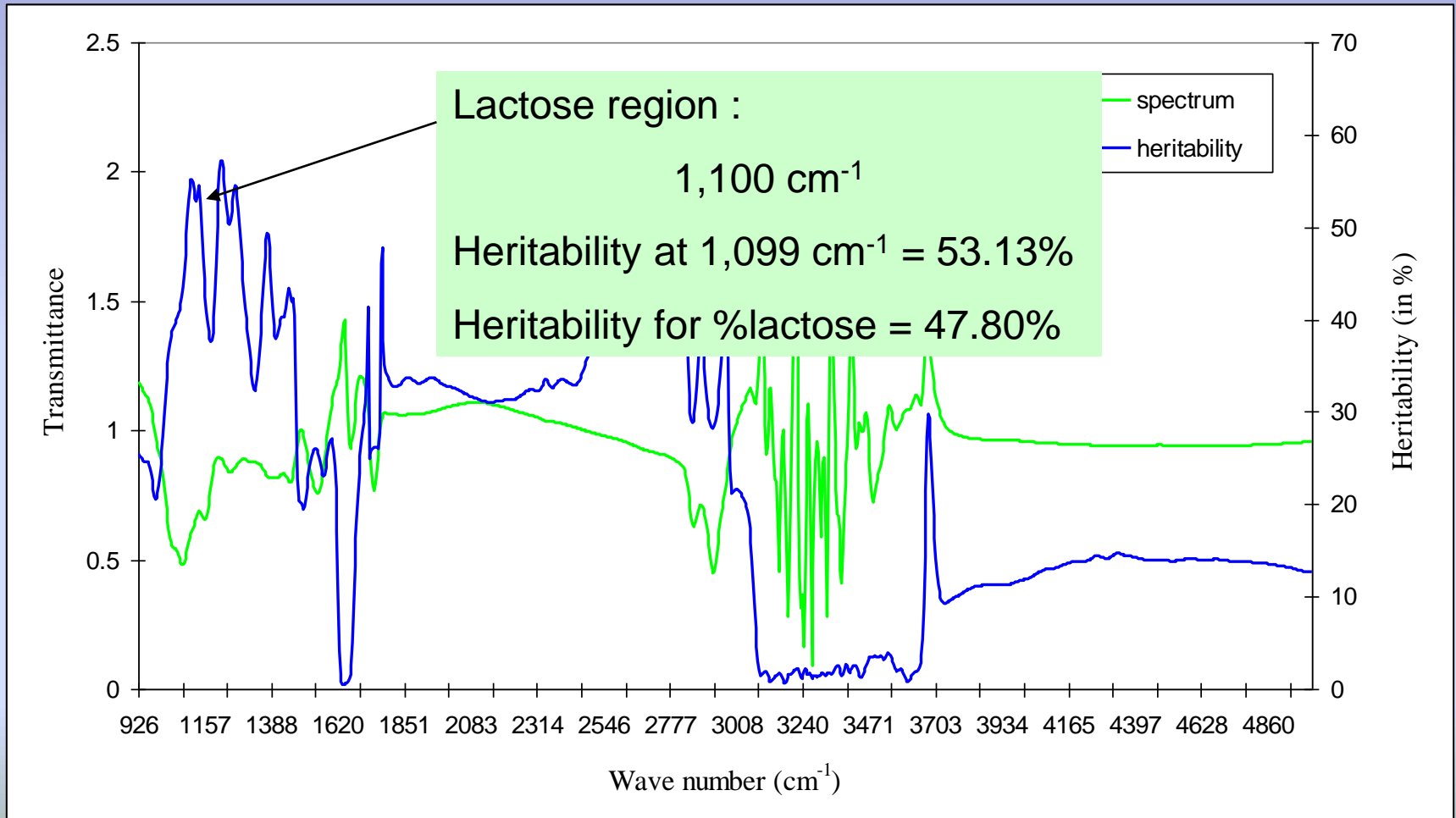
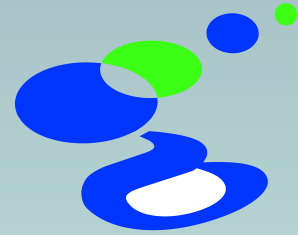
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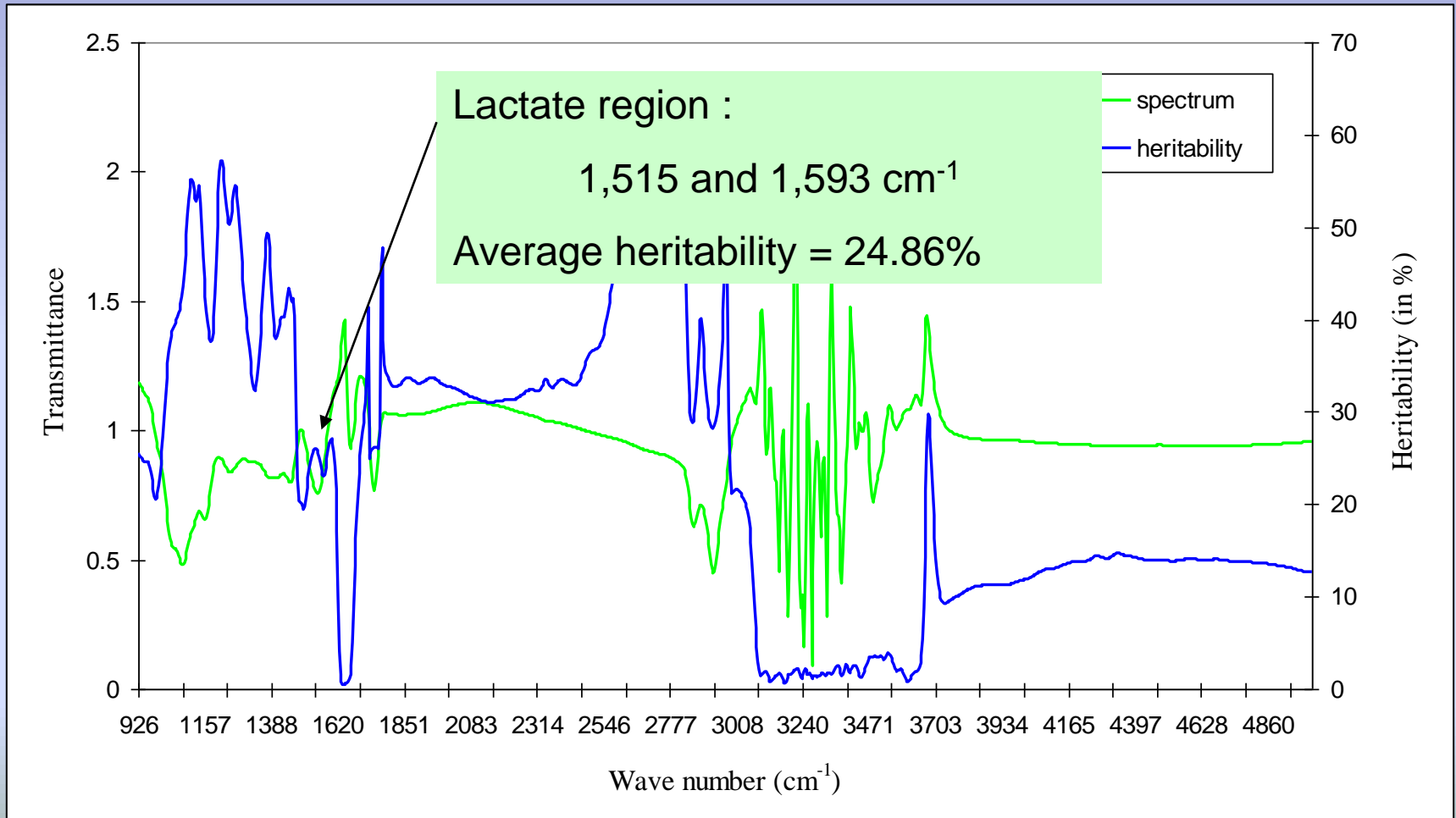
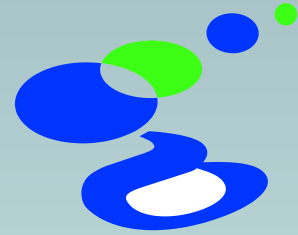
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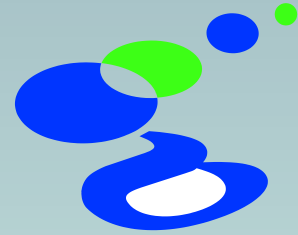
Heritability of MIR Spectrum



Heritability of MIR Spectrum

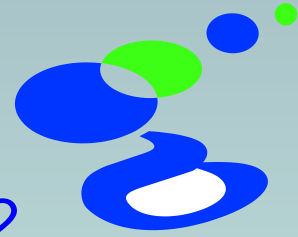


Conclusion



- PCA pre-treatment is interesting
- All wave numbers are not necessary for genetic improvement
- Genetic variability of MIR milk spectrum exists
 - Enough genetic variability to improve the nutritional quality of milk by animal selection.
- Perspectives:
 - Increase the spectral data
 - Improve the model
 - Study in details the link between milk components and spectral data

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Thank you for your attention

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