



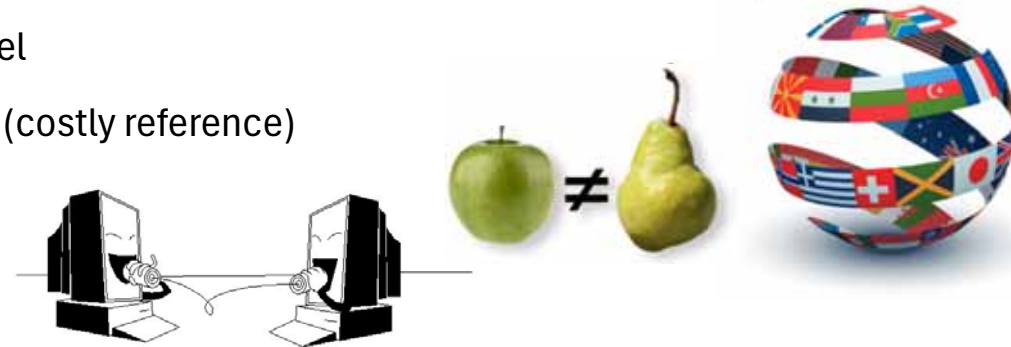
Action 3.5. : Comparison of methods for spectral standardization

Clément Grelet, Mazen Bahadi, Pierre Broutin, Malia Caputo, Octave Christophe, Laura Dale, Maria Frizzarin, Julie Leblois, André Mensching, Juliana Petrini, Silvia Orlandini, Kevin Vancleef, Per Waaben Hansen, Valérie Wolf, Hélène Soyeurt & Frédéric Dehareng

Objective and importance of MIR spectral standardization

Harmonization of spectra across instruments, labs, countries, continents

- Sharing of model
- Sharing of data (costly reference)



Harmonization of spectra across time

- Useability of models in time
- Stability of predictions



Harmonization of historical database

- Use of new models on historical spectra
- Power of big data
- Genetic evaluation



Different existing methods

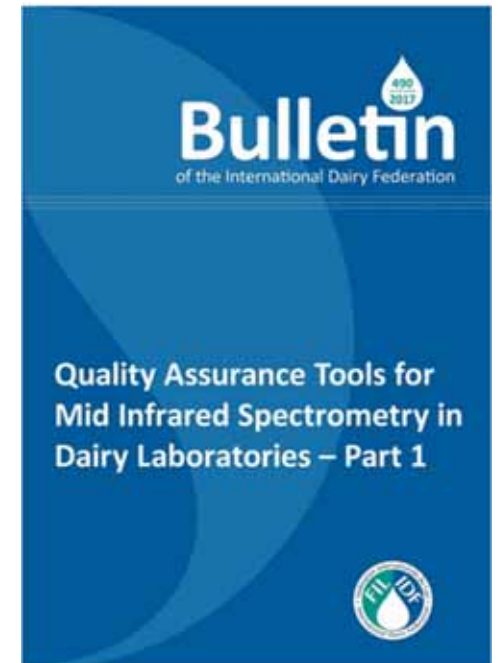
Manufacturers “baseline methods”

- Virtual Master Spectrum Approach (Foss)
- Universal Spectra Standardization (Bentley)

Additional spectral standardization methods

- Grelet et al., 2015
- Bonfatti et al., 2017
- Mensching et al., 2025

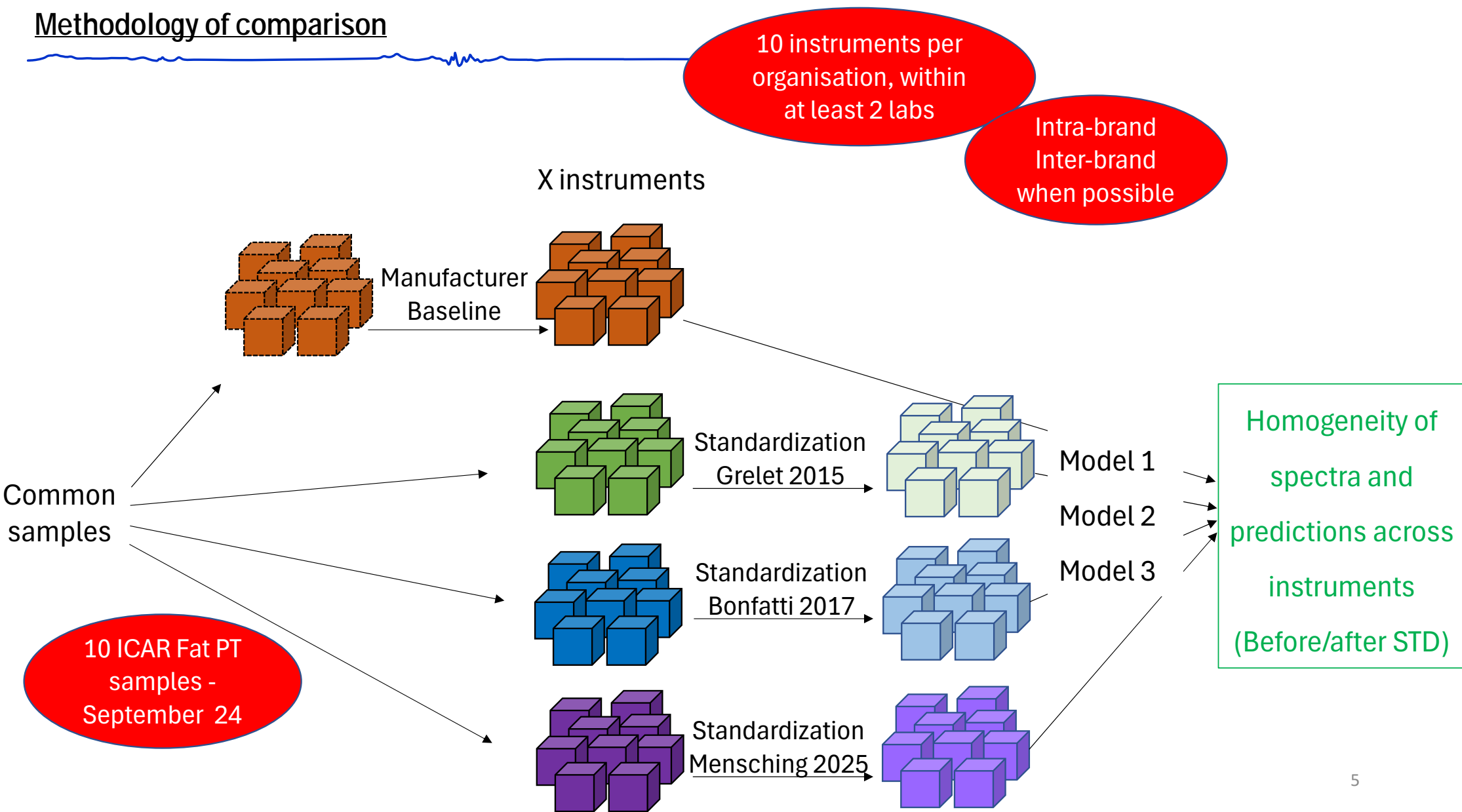
→ Main goal of ExtraMIR 3.5 task is to evaluate/compare the standardization procedure



Methods tested in the comparison

- Manufacturer Baseline
 - “FTIR Equalizer” method
 - Standardizing the intensity based on the intensity of the same chemical standard
 - The method ensure transferability within one instrument platform
- ◆ Grelet et al., 2015
 - Based on monthly exchange of common raw milk samples (specifically designed for this)
 - Across manufacturer brands
 - > 100 models already developed
- Bonfatti et al., 2017
 - Based on historical spectral records
 - No need for common samples exchange
 - Requires the accumulation of considerable amount of milk spectra
- ▲ Mensching et al., 2025
 - Based on a statistical standardization framework incorporating additional data sources
 - No common (additional) samples are required
 - Applicable to both historical and daily incoming data
 - Currently implemented for FOSS instruments

Methodology of comparison



Data treatment

Collect and anonymization of data

Interpolation of all spectra into a common range

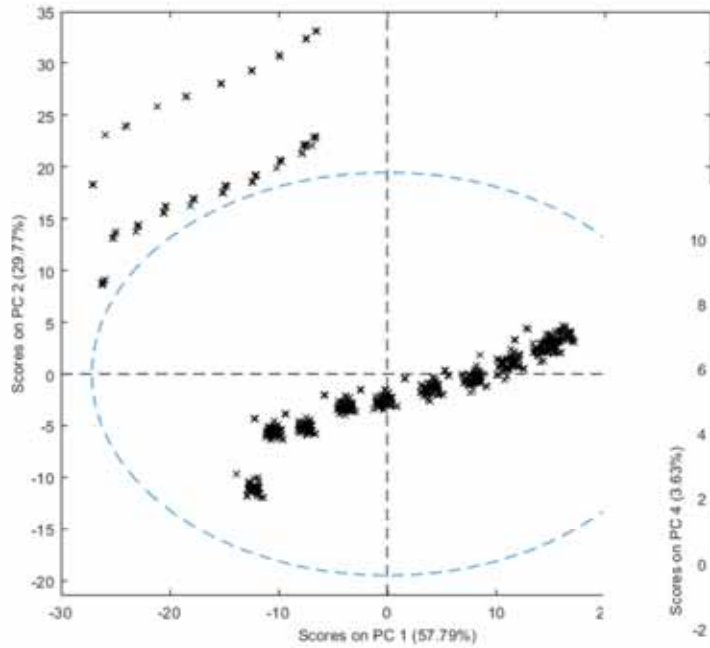
Switch of all spectra in absorbance

Application of 10 models from CRA-W/Ulg with different phenotypes and accuracies

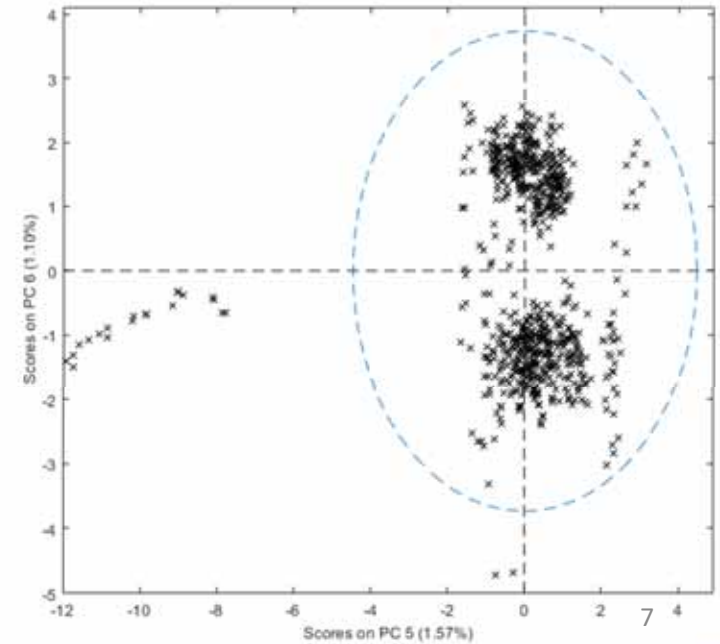
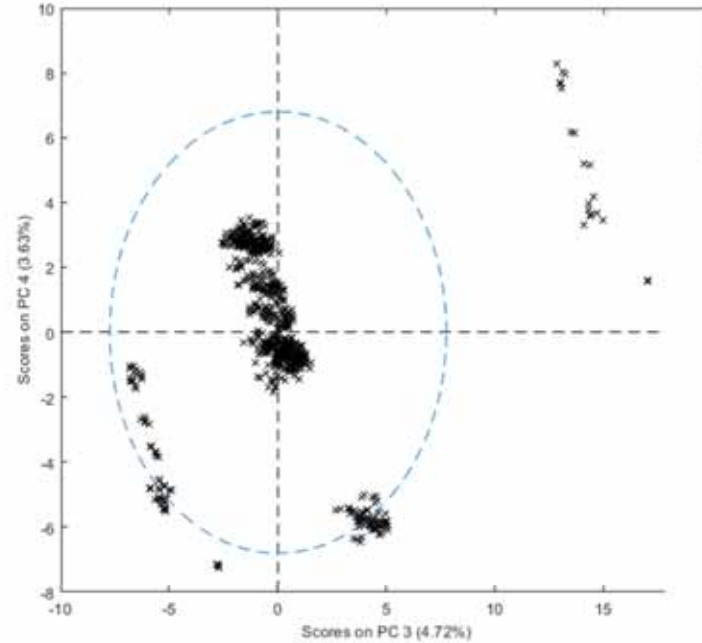
| | Models | R ² cv | RMSEcv |
|-------------|------------------------|-------------------|--------|
| Fatty acids | Fat (g/100ml) | 1.00 | 0.040 |
| | SAT (g/100ml) | 0.99 | 0.072 |
| | C18_1cis9 (g/100ml) | 0.95 | 0.062 |
| | C8 (g/100ml) | 0.91 | 0.0040 |
| | PUFA (g/100ml) | 0.77 | 0.0210 |
| Cow status | N efficiency (%) | 0.74 | 5% |
| | Blood BHB (mmol/L) | 0.70 | 0.270 |
| | CH4 (g/day) | 0.68 | 57.0 |
| | Milk BHB (μmol/L) | 0.61 | 64.6 |
| | Blood Glucose (mmol/L) | 0.44 | 0.360 |

Editing of data (deletion of inconsistent results, mixing of samples...)

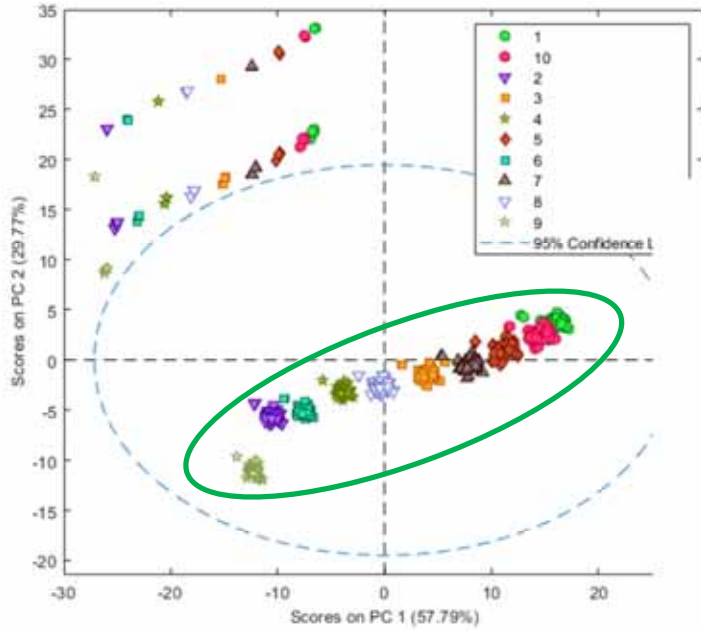
Evaluation on **spectral homogeneity across instruments** before standardization (within each methodology)



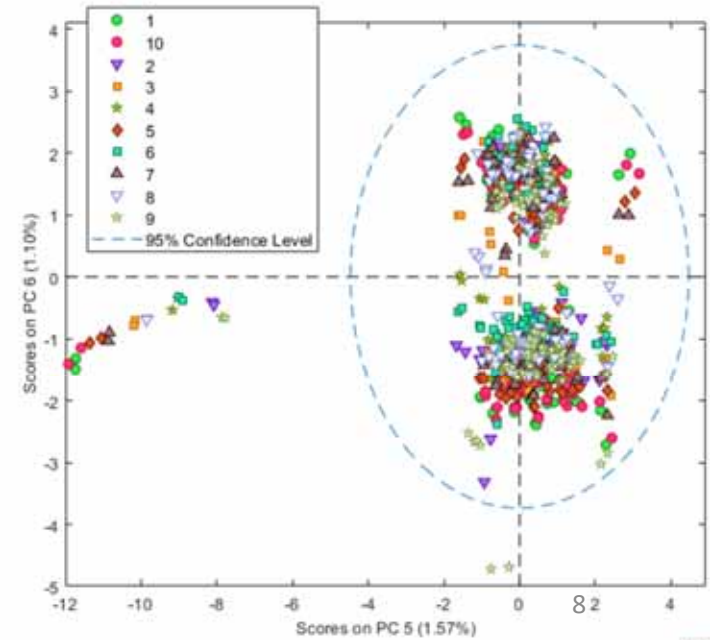
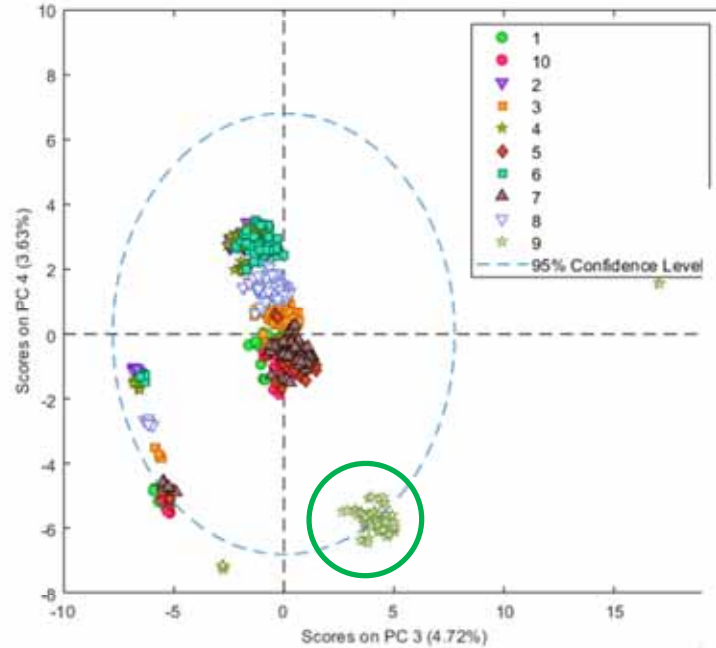
- BEFORE standardization
- PCA on 212 repeatable wavenumbers and 1st derivative
- All brands



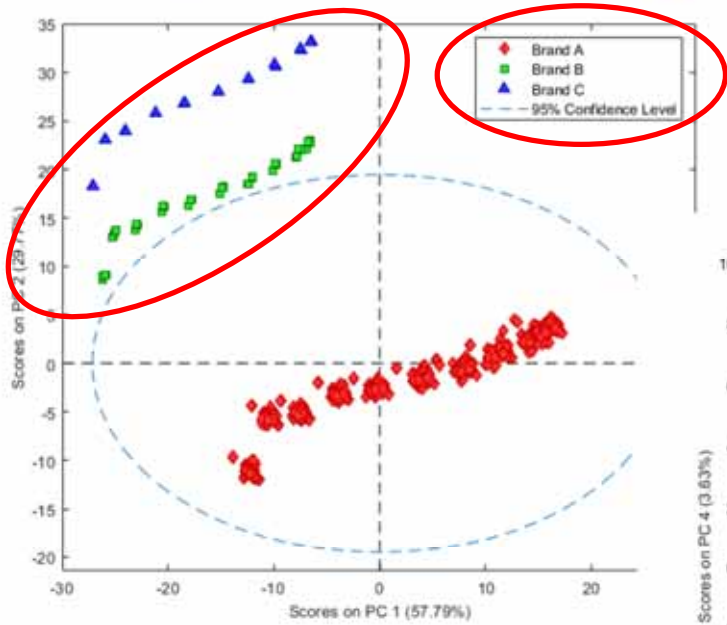
Evaluation on **spectral homogeneity across instruments** before standardization (within each methodology)



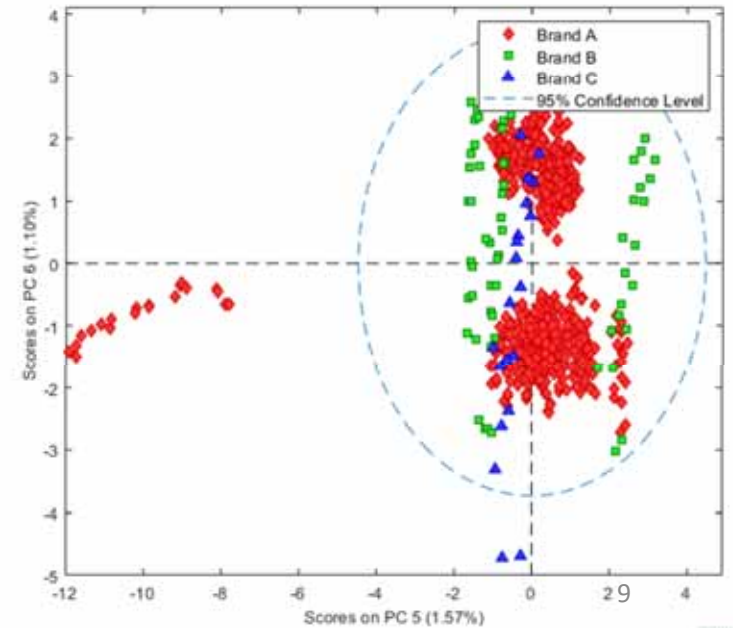
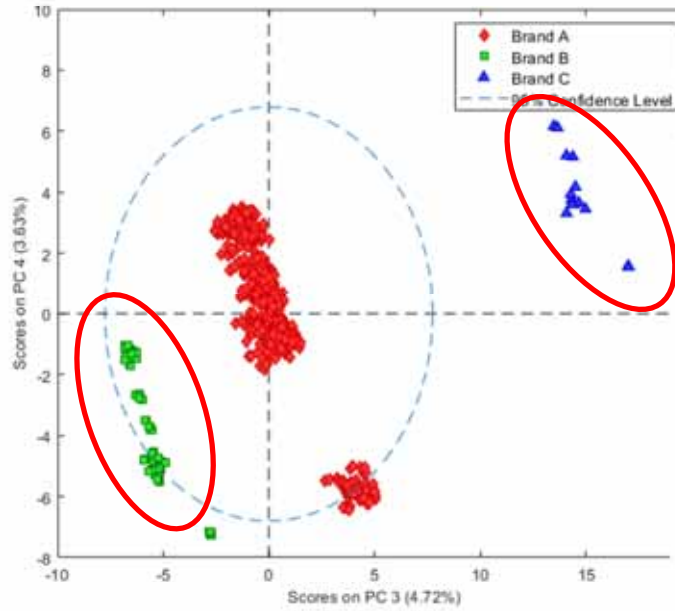
- BEFORE standardization
- PCA on 212 repeatable wavenumbers and 1st derivative
- All brands
- **Sample effect**



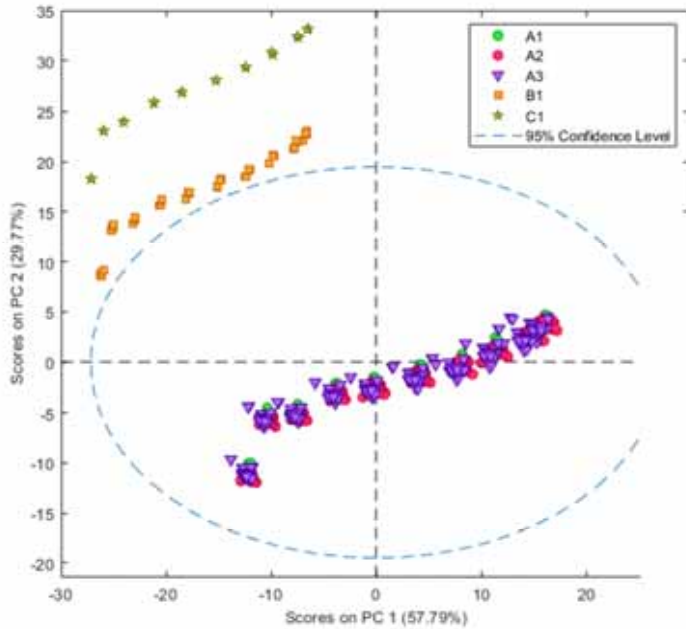
Evaluation on **spectral homogeneity across instruments** before standardization (within each methodology)



- BEFORE standardization
- PCA on 212 repeatable wavenumbers and 1st derivative
- All brands
- **Brand effect**

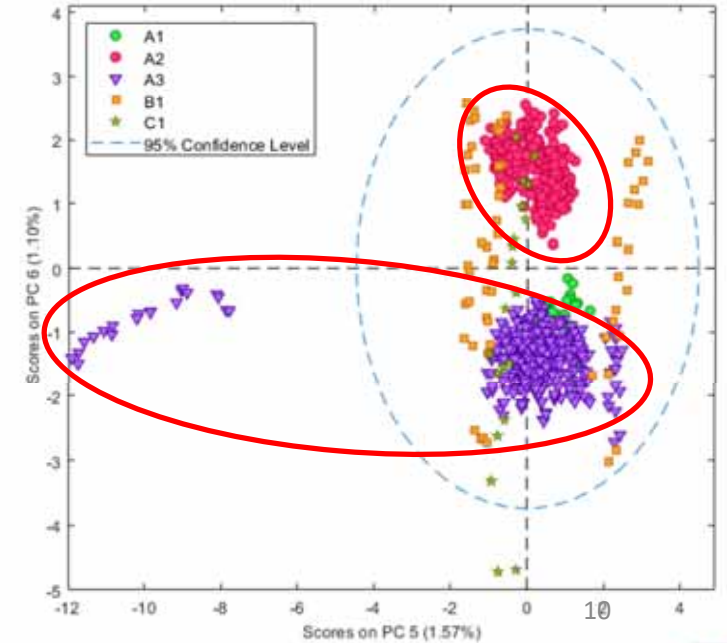
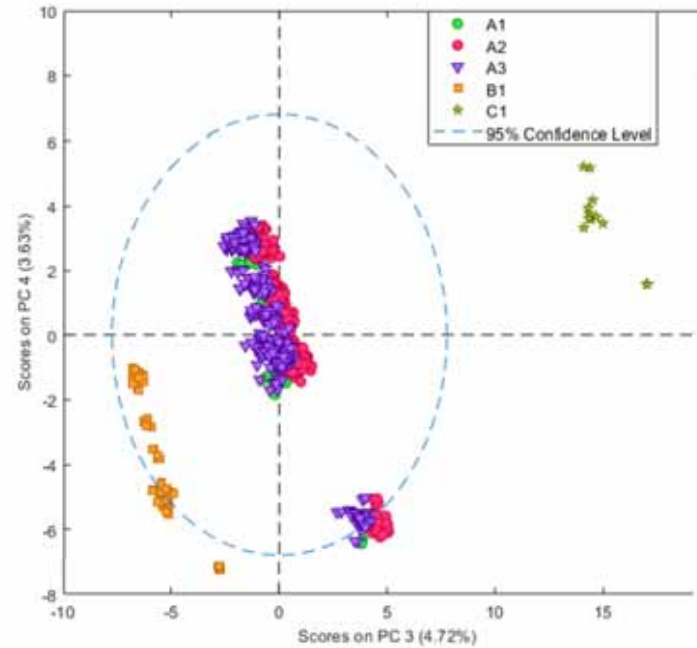


Evaluation on **spectral homogeneity across instruments** before standardization (within each methodology)



- BEFORE standardization
- PCA on 212 repeatable wavenumbers and 1st derivative
- All brands
- **Instrument model effect**

| Brand | Model |
|---------|-------|
| Brand A | A1 |
| Brand A | A2 |
| Brand A | A3 |
| Brand B | B1 |
| Brand C | C1 |

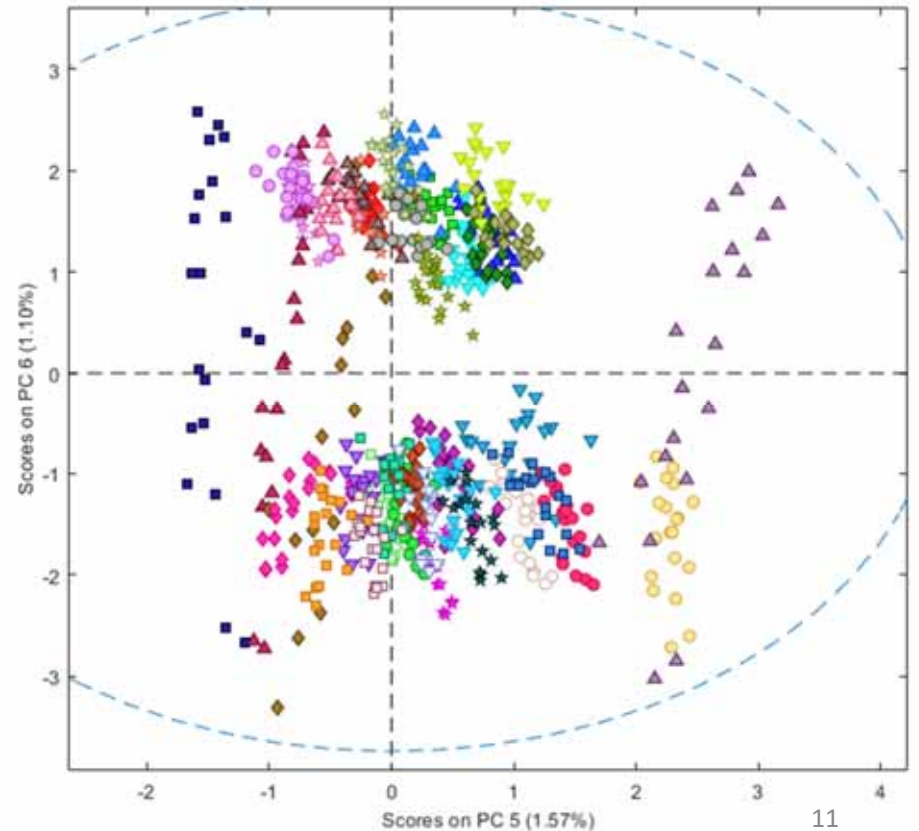


Evaluation on **spectral homogeneity across instruments** before standardization (within each methodology)

- BEFORE standardization
- PCA on 212 repeatable wavenumbers and 1st derivative
- All brands
- Machine effect

Conclusion 1:
Spectra vary according to

- **samples**
- instrument brands
- instrument models
- individual machines

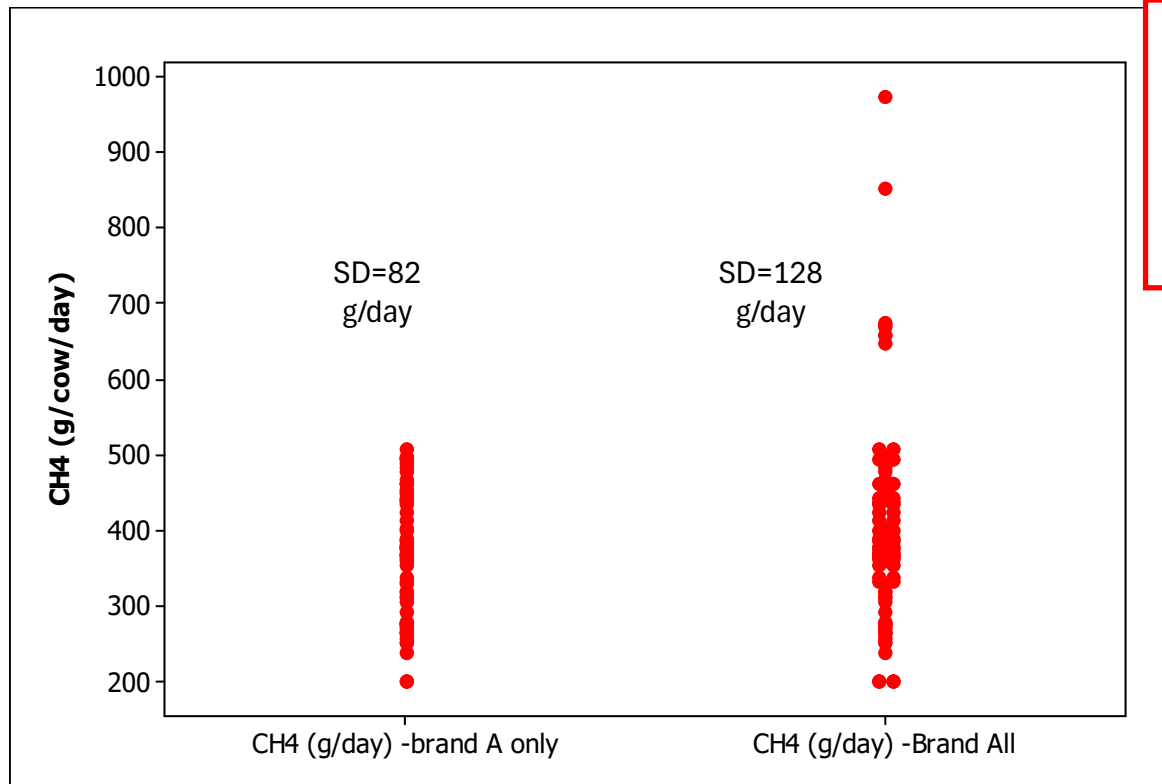


Evaluation on **spectral homogeneity across instruments** before standardization (within each methodology)

Analysis of one common sample by all machines (sample 5 ~ 4.13 g/100g)

Application of 1 common CH4 model

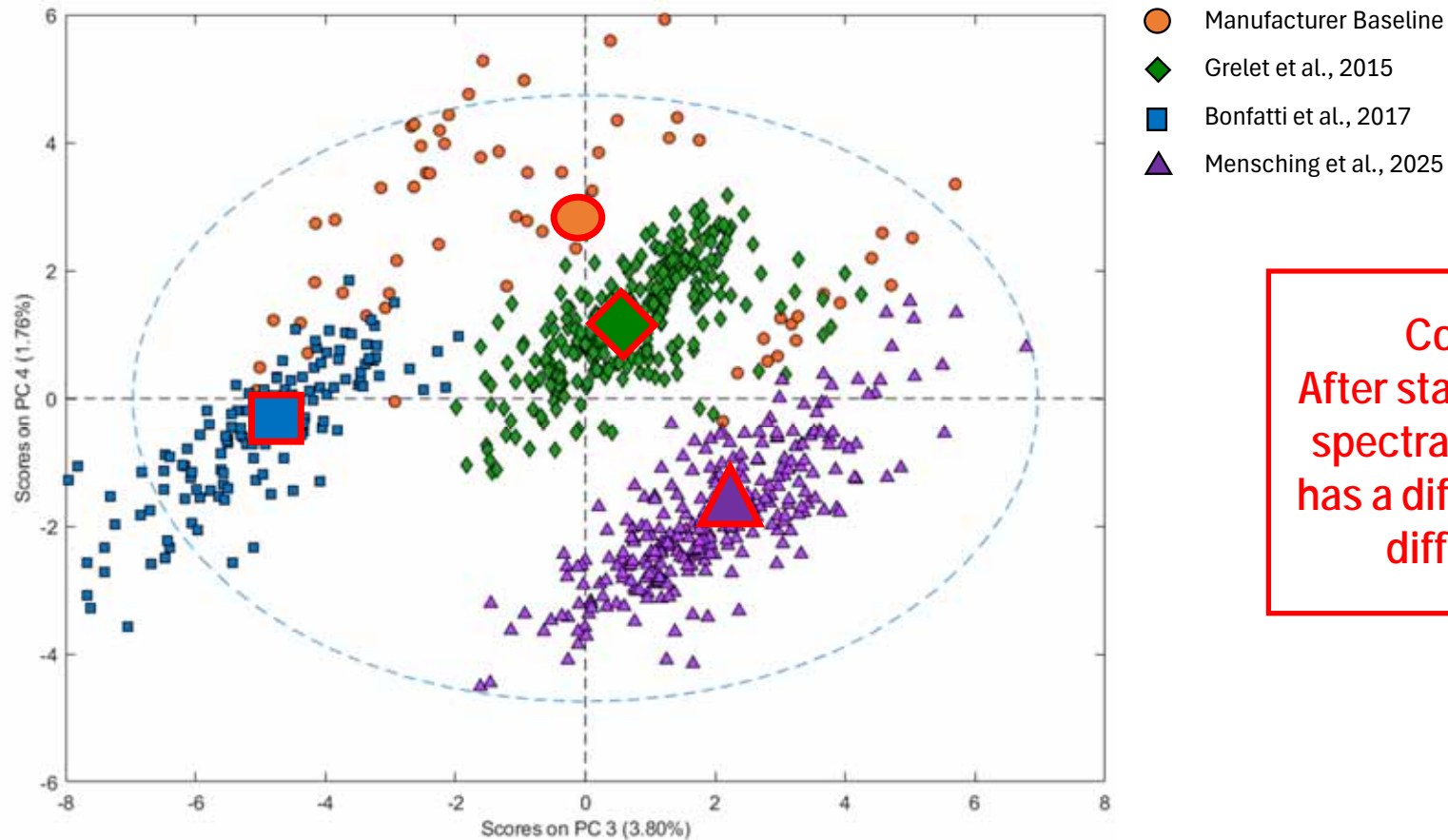
→ Impact on predictions



Conclusion 2:
Spectral heterogeneity across instruments leads to prediction heterogeneity across instruments

Evaluation on **spectral homogeneity across instruments** after standardization (within each methodology)

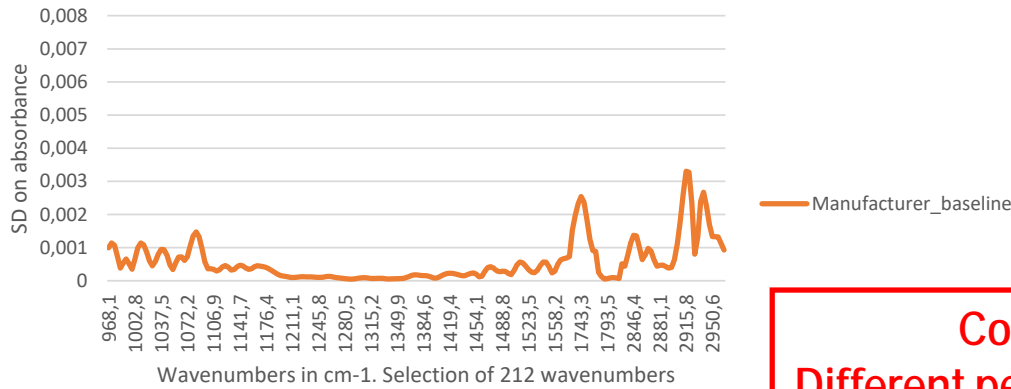
- AFTER standardization within each methodology
- PCA on 212 repeatable wavenumbers and 1st derivative
- Brand A only
- Method effect



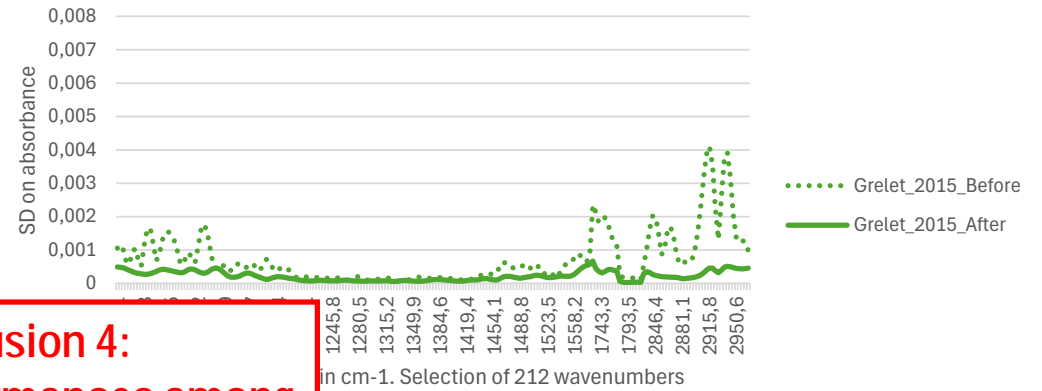
Conclusion 3:
After standardization, the spectra of each network has a different centroid, a different format

Evaluation on **spectral homogeneity across instruments** before and after standardization (within each methodology)

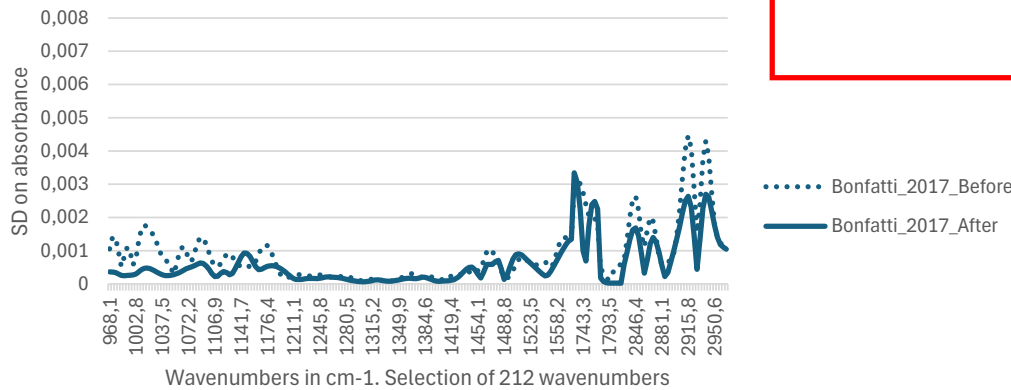
Wavenumber homogeneity of **Manufacturer Baseline -brand A**



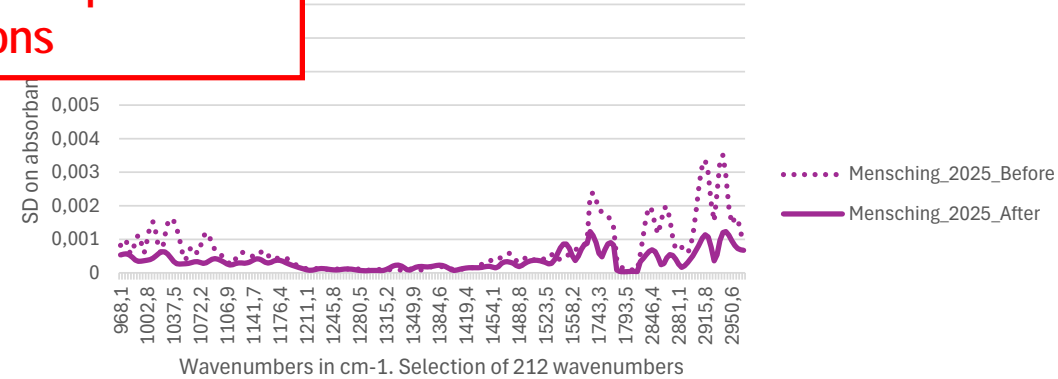
Wavenumber homogeneity BEFORE and AFTER standardization - Grelet 2015 -brand A



Wavenumber homogeneity BEFORE and AFTER standardization - Bonfatti 2017 -brand A

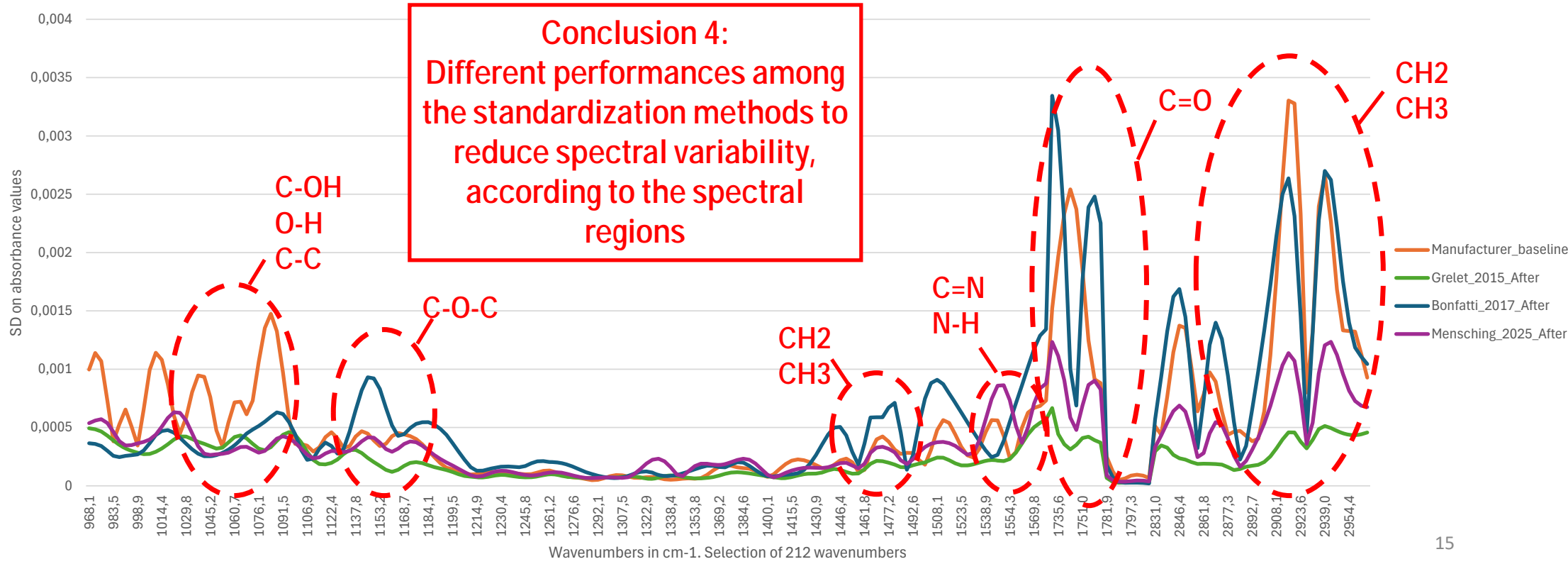
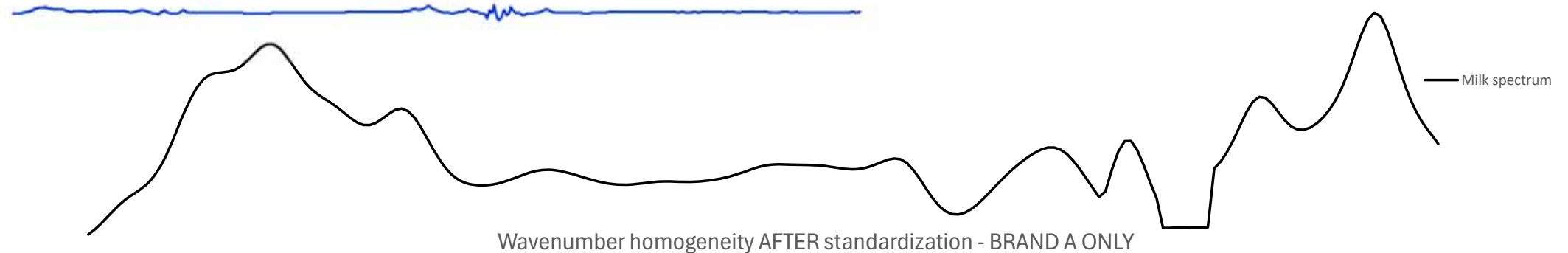


Wavenumber homogeneity BEFORE and AFTER standardization - Mensching 2025 -brand A



Conclusion 4:
Different performances among the standardization methods to reduce spectral variability, according to the spectral regions

Evaluation on **spectral homogeneity across instruments** after standardization (within each methodology)

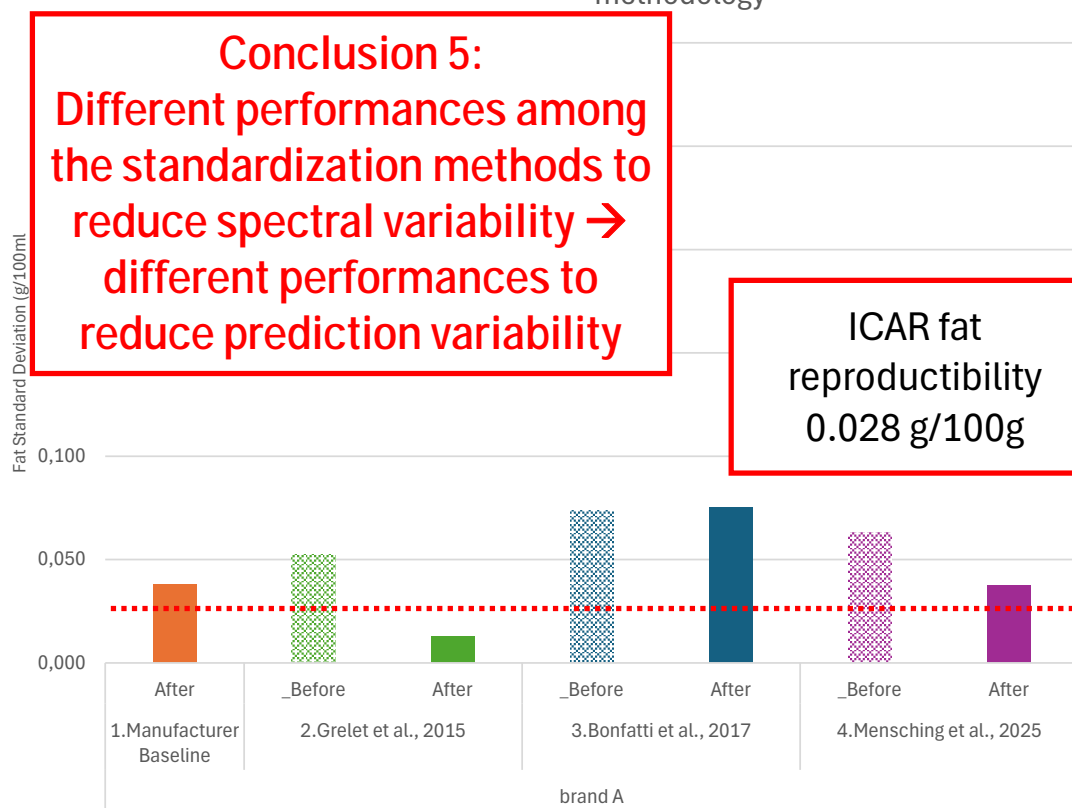


Evaluation on Predictions homogeneity across instruments before and after standardization (within each methodology)

Standard deviation calculated per samples and equation and averaged per methodology (for the 10 samples)

| | Method | STD | n machines | Fat (g/100ml) |
|---------|------------------------|--------|------------|---------------|
| brand A | Manufacturer Baseline | | 5 | 0.038 |
| | Grelet et al., 2015 | Before | 11 | 0.053 |
| | Grelet et al., 2015 | After | 11 | 0.013 |
| | Bonfatti et al., 2017 | Before | 7 | 0.074 |
| | Bonfatti et al., 2017 | After | 7 | 0.075 |
| | Mensching et al., 2025 | Before | 14 | 0.063 |
| | Mensching et al., 2025 | After | 14 | 0.038 |

Standard deviation of fat predictions, for the 10 samples individually and per methodology



Lab results (all labs): Slope and bias corrected fat
SD=0.042 g/100g

Evaluation on Predictions homogeneity across instruments before and after standardization (within each methodology)

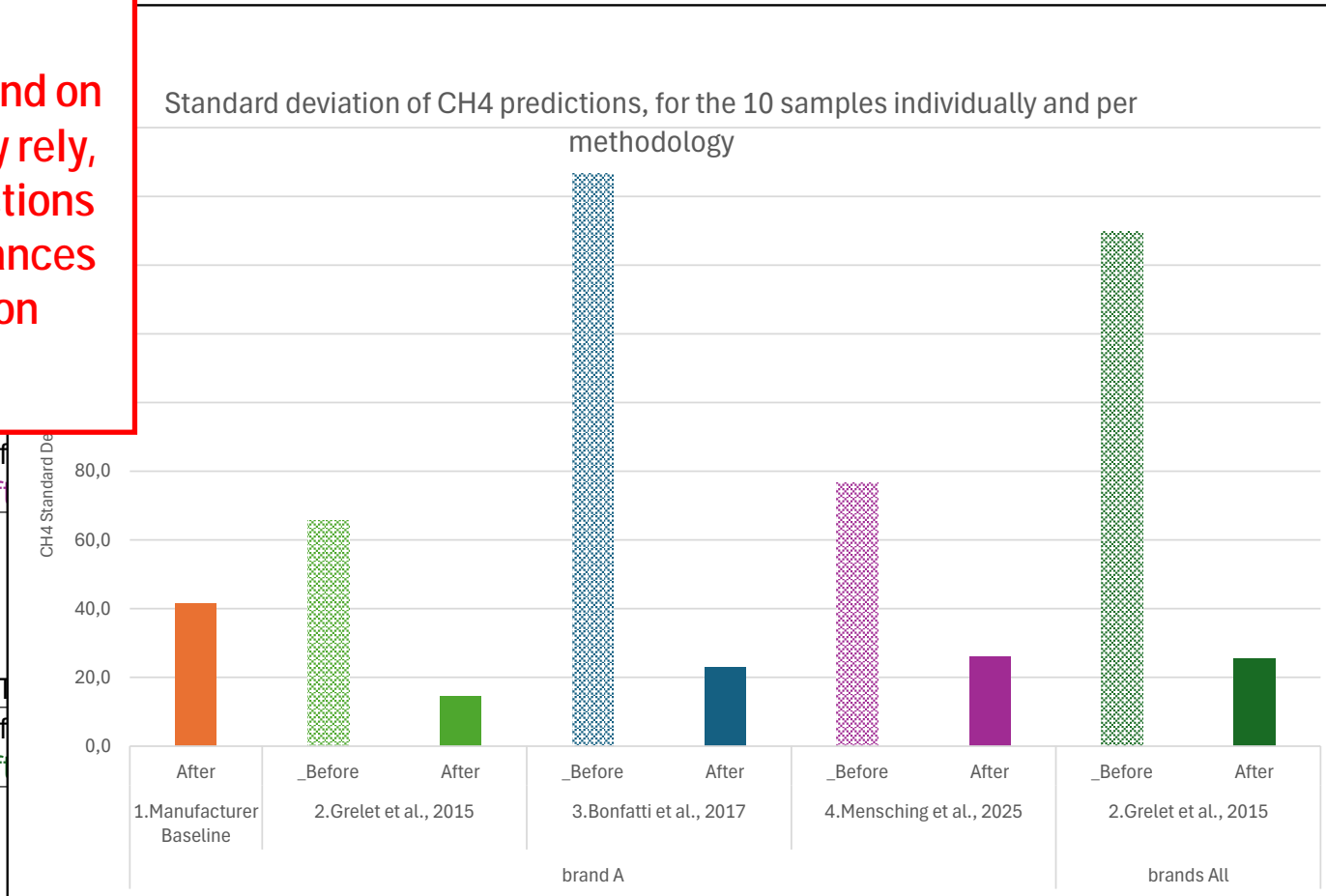
Standard deviation calculated per samples and equation and averaged per methodology (for the 10 samples)

| | | Method | STD | n machines | Fat (g/100ml) | SAT (g/100ml) | C18_1cis9 (g/100ml) | C8 (g/100ml) | PUFA (g/100ml) | Blood BHB (mmol/L) | Blood Glucose (mmol/L) | Milk BHB (μmol/L) | CH4 (g/day) | N efficiency (%) |
|------------|--|------------------------------|--------|------------|---------------|---------------|---------------------|--------------|----------------|--------------------|------------------------|-------------------|-------------|------------------|
| | | Manufacturer Baseline | | 5 | 0.038 | 0.045 | 0.033 | 0.0035 | 0.0261 | 0.031 | 0.084 | 31.6 | 41.6 | 5% |
| brand A | | Grelet et al., 2015 | Before | 11 | 0.053 | 0.079 | 0.085 | 0.0030 | 0.0348 | 0.091 | 0.101 | 17.8 | 65.7 | 6% |
| | | Grelet et al., 2015 | After | 11 | 0.013 | 0.027 | 0.024 | 0.0014 | 0.0060 | 0.029 | 0.039 | 8.4 | 14.4 | 1% |
| | | Bonfatti et al., 2017 | Before | 7 | 0.074 | 0.087 | 0.076 | 0.0028 | 0.0431 | 0.057 | 0.119 | 34.5 | 166.7 | 6% |
| | | Bonfatti et al., 2017 | After | 7 | 0.075 | 0.070 | 0.056 | 0.0022 | 0.0099 | 0.064 | 0.048 | 11.1 | 21.7 | 2% |
| | | Mensching et al., 2025 | Before | 14 | 0.063 | 0.069 | 0.085 | 0.0029 | 0.0374 | 0.062 | 0.110 | 22.6 | 76.8 | 5% |
| | | Mensching et al., 2025 | After | 14 | 0.038 | 0.047 | 0.040 | 0.0019 | 0.0093 | 0.072 | 0.083 | 17.3 | 26.1 | 3% |
| | | | | | | | | | | | | | | |
| | | Method | STD | n machines | Fat (g/100ml) | SAT (g/100ml) | C18_1cis9 (g/100ml) | C8 (g/100ml) | PUFA (g/100ml) | Blood BHB (mmol/L) | Blood Glucose (mmol/L) | Milk BHB (μmol/L) | CH4 (g/day) | N efficiency (%) |
| all brands | | Grelet et al., 2015 | Before | 15 | 0.271 | 0.764 | 0.350 | 0.0330 | 0.0618 | 0.964 | 0.539 | 41.0 | 149.7 | 35% |
| | | Grelet et al., 2015 | After | 15 | 0.017 | 0.058 | 0.045 | 0.0024 | 0.0138 | 0.037 | 0.102 | 16.2 | 25.5 | 4% |

Evaluation on Predictions homogeneity across instruments before and after standardization (within each methodology)

Standard deviation calculated per samples and equation and averaged per methodology (for the 10 samples)

Conclusion 6:
 Depending on models, and on which spectral area they rely, harmonization of predictions show different performances across standardization methodologies



| CH4 (g/day) | N efficiency (%) |
|-------------|------------------|
| 41.6 | 5% |
| 65.7 | 6% |
| 14.4 | 1% |
| 166.7 | 6% |
| 21.7 | 2% |
| 76.8 | 5% |
| 26.1 | 3% |
| CH4 (g/day) | N efficiency (%) |
| 149.7 | 35% |
| 25.5 | 4% |

Mensching et al., 2025 Bef
 Mensching et al., 2025 Af

Method ST
 Grelet et al., 2015 Bef
 Grelet et al., 2015 Af

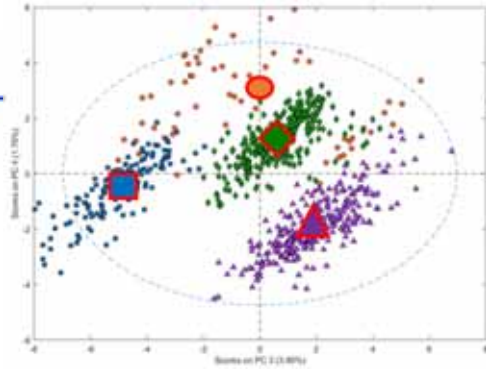
all brands

Conclusions



- MIR instruments show a very large spectral variability without standardization (brands, models, machines...)
- Spectral heterogeneity impacts **prediction reproducibility across spectrometers**
- 4 methodologies of standardization compared
 - 1 Baseline method & 3 *A posteriori* methods
 - Different concepts (historical dataset, sharing of common samples...)
 - Different limitations (sufficient routine amount of samples, cost, transport of samples...)
 - 3 methods intra-brand & 1 inter-brand
- Standardization methodologies enable to reduce spectral variability
- **Very different performances among the standardization methods** to reduce spectral variability, **according to the spectral regions**
- Depending of models (quality), and on which spectral area they rely, **harmonization of predictions show different performances across standardization methodologies**

Conclusions

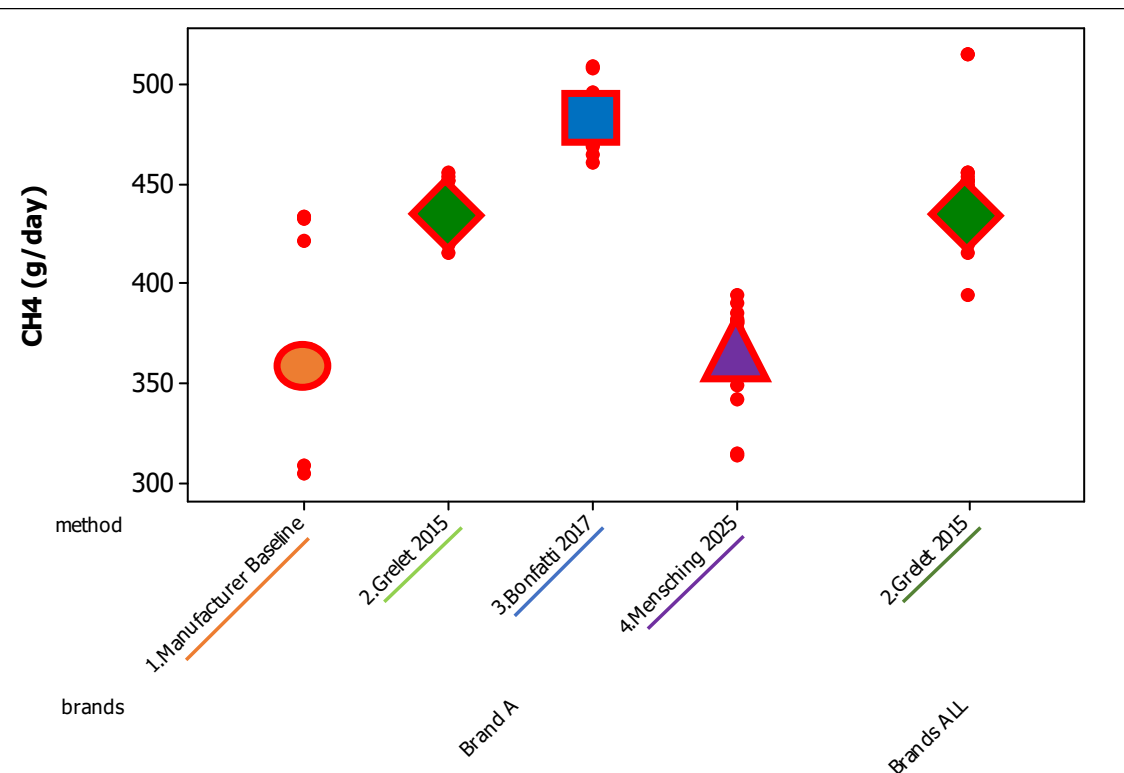


→ application of 1 common CH₄ model on standardized spectra of one milk sample across the different methodologies

Differences in spectral standardization (centroids) across methodologies

→ **may constrain model transferability between networks** (i.e. sharing models may require standardising spectra to the same standardization process to build the model and for predictions).

Need for further research to better understand and potentially overcome these limitations





Thank you for
your attention!

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Evaluation of data



- Evaluation of **spectral homogeneity across all instruments** before standardization
Spectral homogeneity through PCA and predictions homogeneity
- Within each methodology, evaluation on **spectral homogeneity across instruments** before and after standardization.
To calculate the Standard Deviation of absorbance intensities per wavenumber, across 10 instruments, before and after standardization. To be applied only on stable wavenumbers only.
- Within each methodology, evaluation on **prediction homogeneity across instruments** before and after standardization.
To calculate the Standard deviation of predictions across 10 instruments before and after standardization for each methodology and each model.

Dataset description

4 methodologies (44 machines in total)

- Manufacturer Baseline – network 1
 - 5 instruments brand A (7 in total but 2 with missing spectra)
 - After standardization only (5)

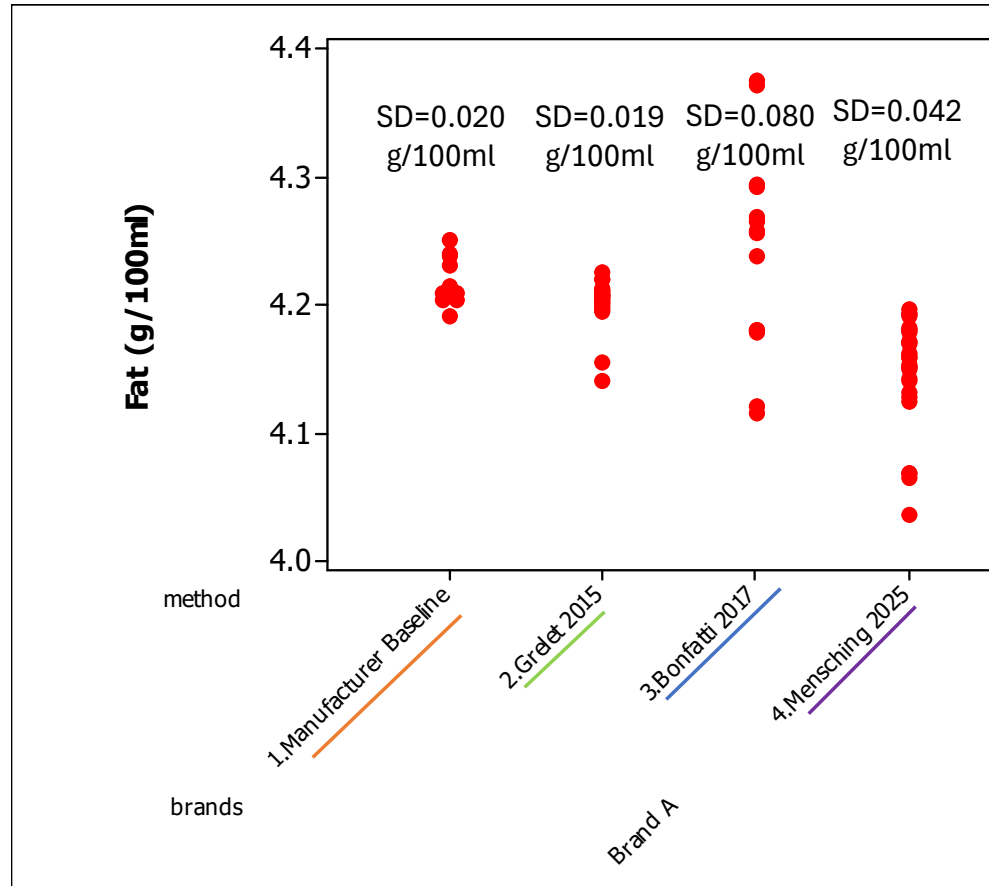
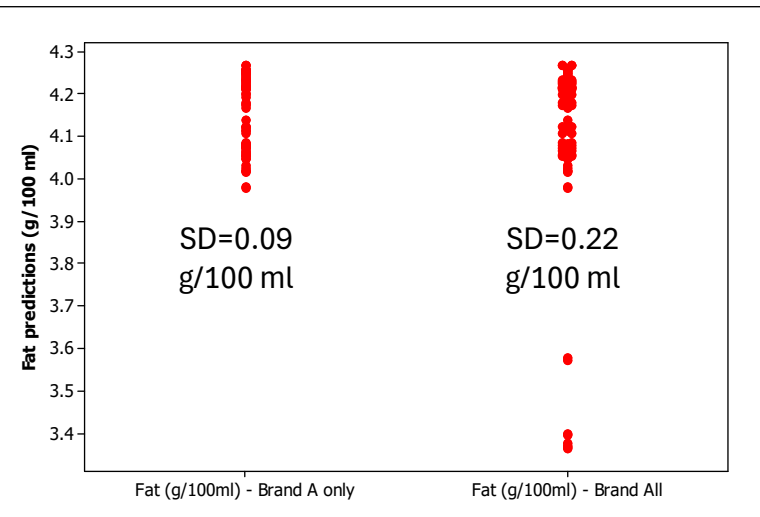
- ◆ Grelet et al., 2015– network 2
 - 15 instruments
 - 11 instruments brand A
 - 3 instruments brand B
 - 1 instrument brand C
 - All instruments Before and After standardization

- Bonfatti et al., 2017 – network 3
 - 10 instruments brand A
 - Before (8 instrument) and After (7 instruments) standardization
 - One machine excluded because of technical limitation (not enough samples analyzed on the instrument)

- ▲ Mensching et al., 2025– network 4
 - 14 instruments brand A
 - All instruments Before and After standardization

Evaluation on Predictions homogeneity across instruments before and after standardization (within each methodology)

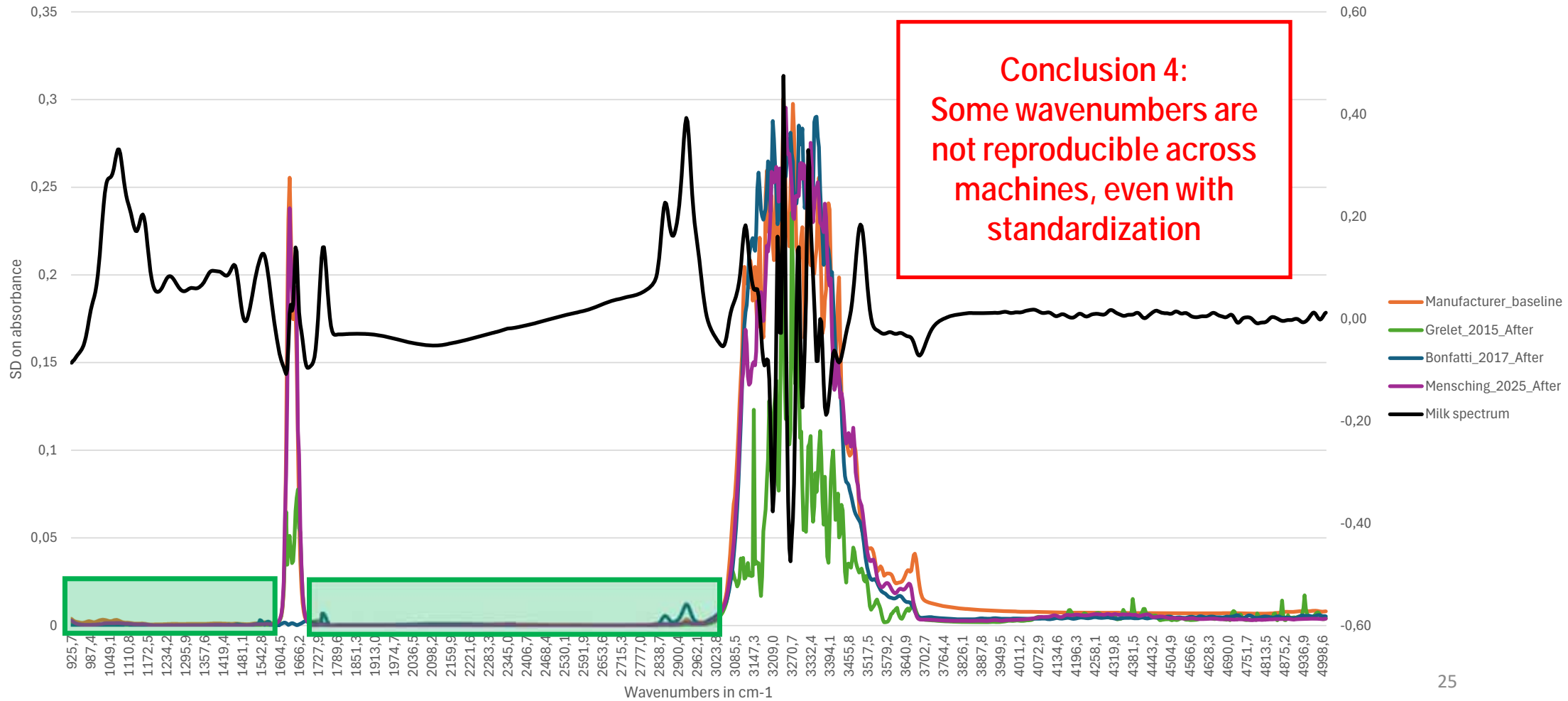
→ Impact on predictions homogeneity across instruments, application of 1 common fat model (one sample only, sample 5 ~ 4.13 g/100g)



Evaluation on spectral homogeneity across instruments AFTER standardization (within each methodology)

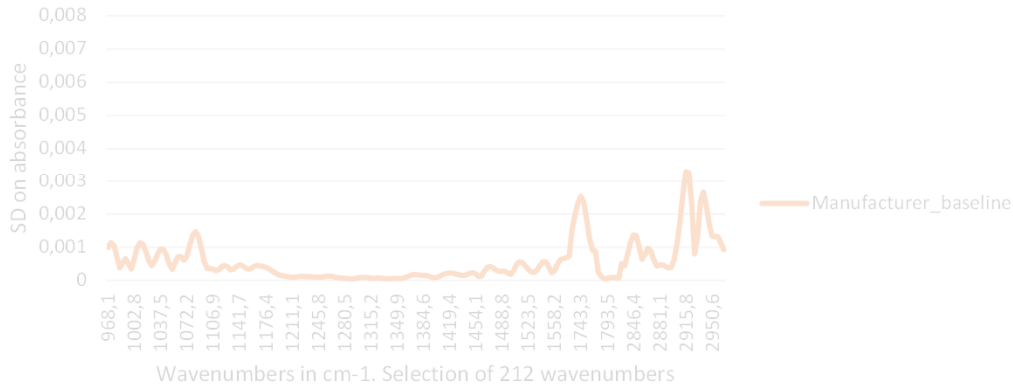


Wavenumber homogeneity AFTER standardization on the full spectrum - brand A only

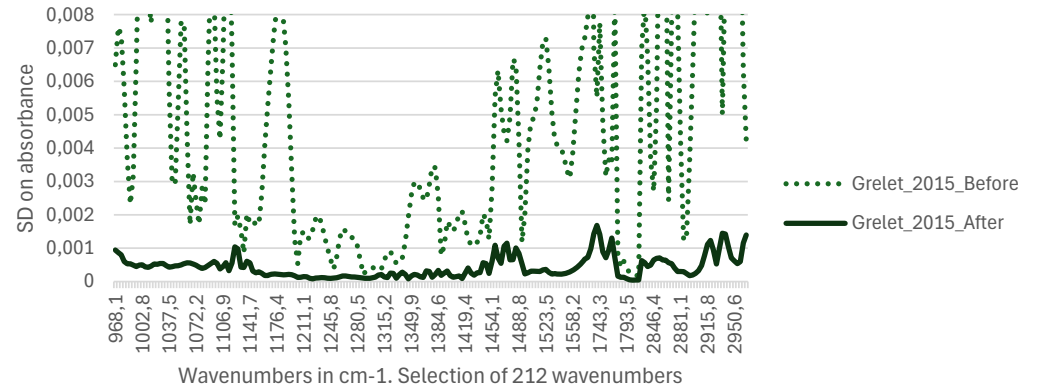


Evaluation on spectral homogeneity across instruments before and after standardization (within each methodology)

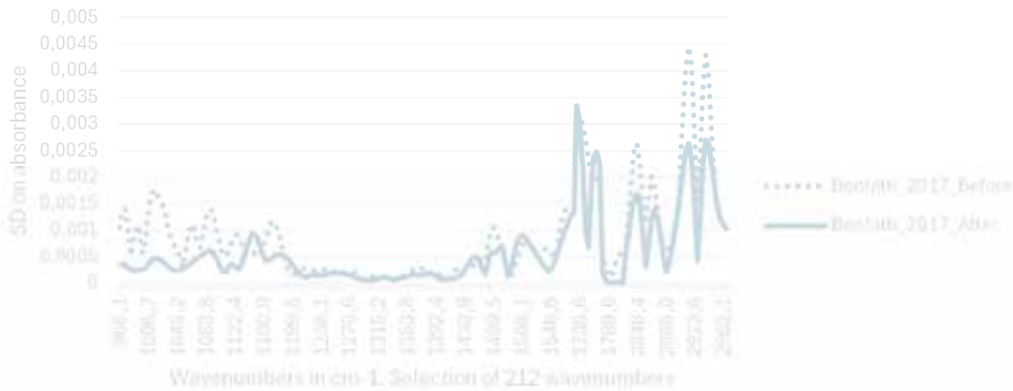
Wavenumber homogeneity of
Manufacturer Baseline -brand A



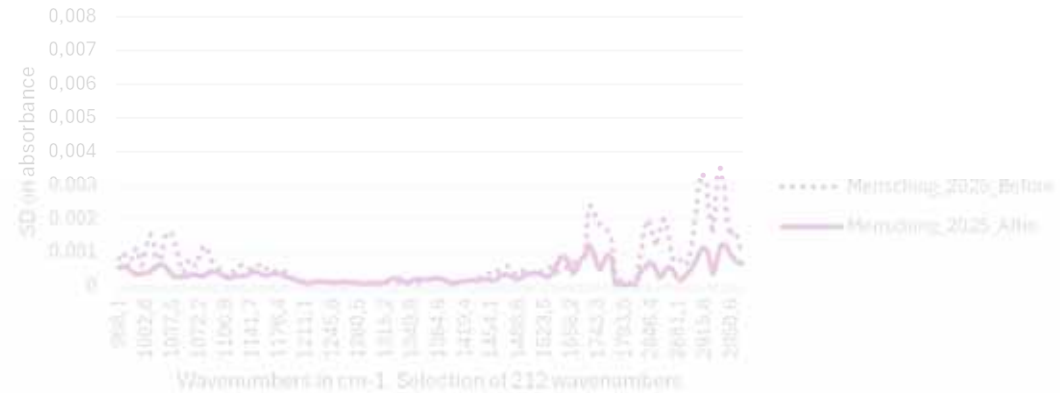
Wavenumber homogeneity BEFORE and AFTER standardization-
Grelet 2015 - all brands



Wavenumber homogeneity BEFORE and AFTER standardization -
Bonfatti 2017 -brand A

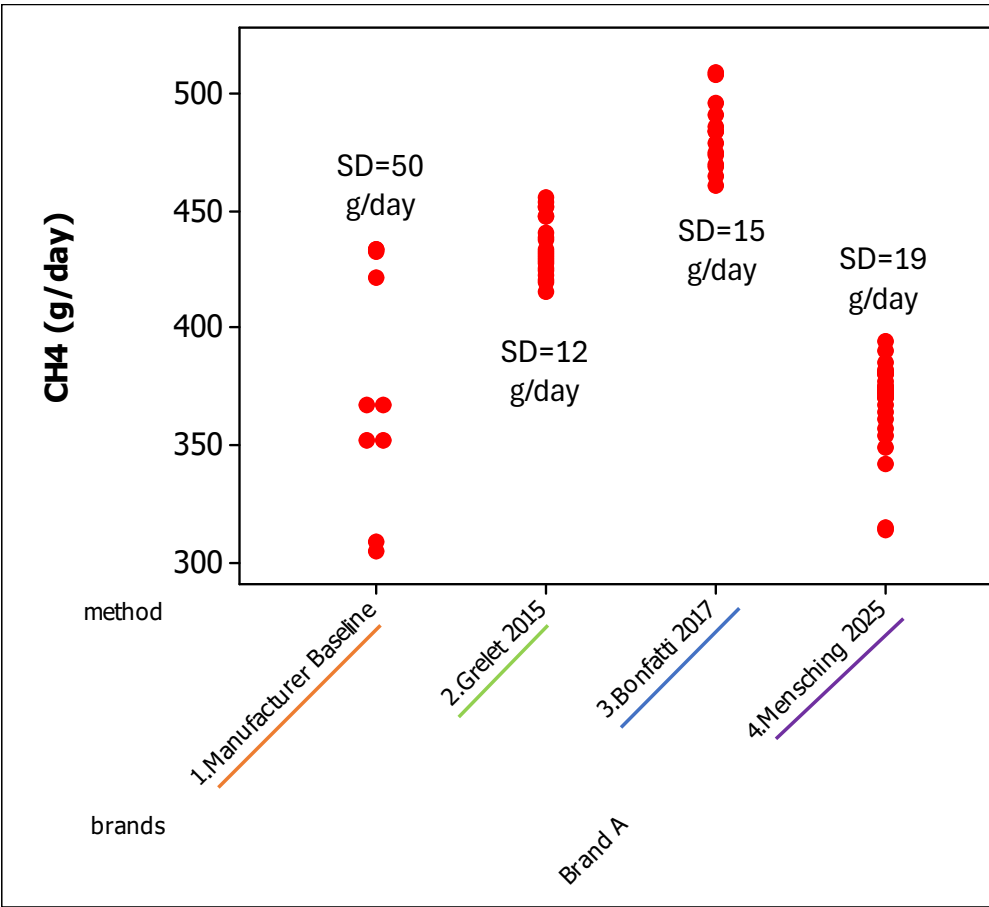
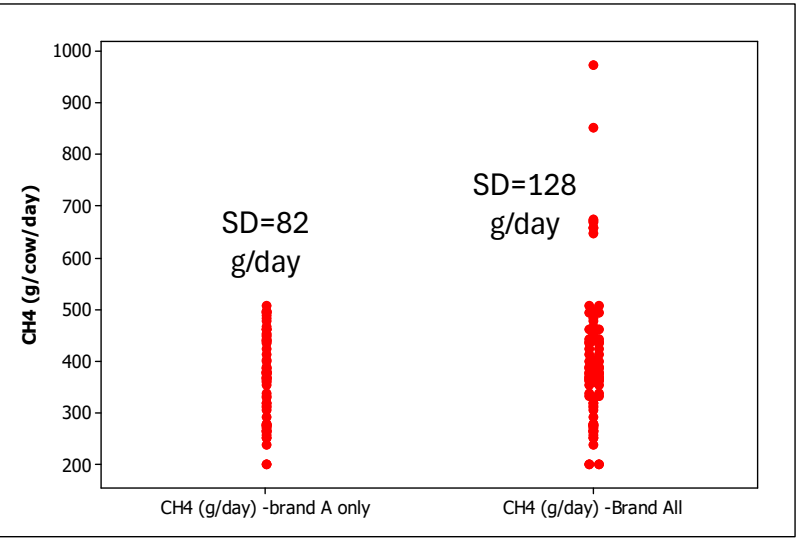


Wavenumber homogeneity BEFORE and AFTER standardization -
Mensching 2025 -brand A



Evaluation on Predictions homogeneity across instruments before and after standardization (within each methodology)

→ Impact on predictions homogeneity across instruments, application of 1 common CH4 model (one sample only, sample 5 ~ 4.13 g/100g)



Evaluation on Predictions homogeneity across instruments before and after standardization (within each methodology)

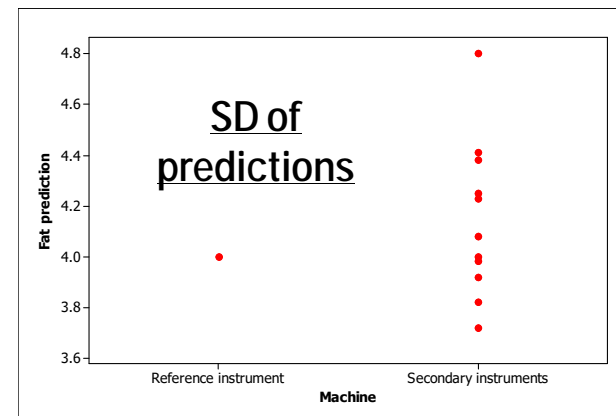
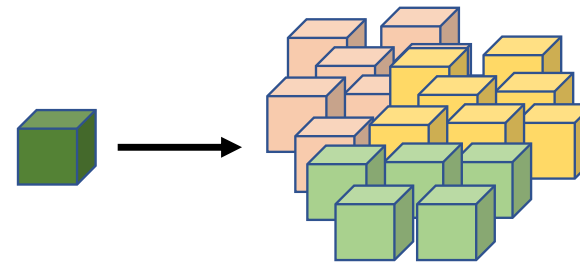
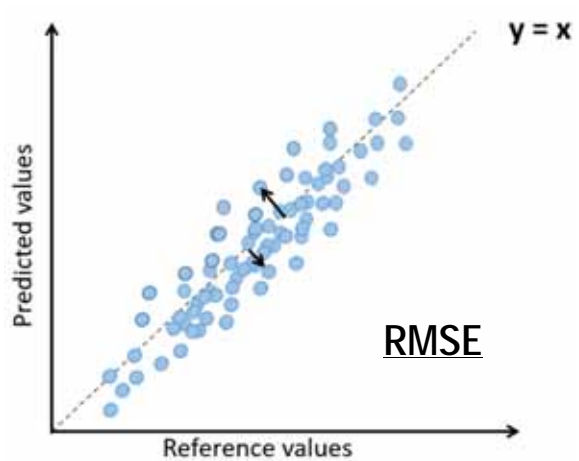
What does it mean in lab real life ?

Real total error of prediction when using a MIR model on a spectrometer

Error of the model itself

+ / &

Error due to the transfer of model on this instrument



Evaluation on Predictions homogeneity across instruments before and after standardization (within each methodology)

Error of the model itself

| | Fat (g/100ml) | SAT (g/100ml) | C18_1cis9 (g/100ml) | C8 (g/100ml) | PUFA (g/100ml) | Blood BHB (mmol/L) | Blood Glucose (mmol/L) | Milk BHB (μmol/L) | CH4 (g/day) | N efficiency (%) |
|-------------------|------------------|------------------|------------------------|-----------------|-------------------|-----------------------|------------------------------|----------------------|----------------|---------------------|
| R ² cv | 1.00 | 0.99 | 0.95 | 0.91 | 0.77 | 0.70 | 0.44 | 0.61 | 0.68 | 0.74 |
| RMSEcv | 0.040 | 0.072 | 0.062 | 0.0040 | 0.0210 | 0.270 | 0.360 | 64.6 | 57.0 | 5% |

Error due to the transfer of model on this instrument

Relative homogeneity, SD compared to model error

| Method | STD | n machines | Fat | SAT | C18_1cis9 | C8 | PUFA | Blood BHB | Blood Glucose | Milk BHB | CH4 | N efficiency |
|------------------------------|--------|---------------|-----------|-----------|-----------|-----------|-----------|-----------|------------------|----------|---------|--------------|
| | | | (g/100ml) | (g/100ml) | (g/100ml) | (g/100ml) | (g/100ml) | (mmol/L) | (mmol/L) | (μmol/L) | (g/day) | (%) |
| Manufacturer Baseline | | | 95% | 63% | 53% | 87% | 124% | 11% | 23% | 49% | 73% | 88% |
| Grelet et al., 2015 | Before | 11 | 132% | 109% | 138% | 76% | 166% | 34% | 28% | 28% | 115% | 104% |
| Grelet et al., 2015 | After | 11 | 31% | 37% | 39% | 35% | 29% | 11% | 11% | 13% | 25% | 22% |
| brand A | | | | | | | | | | | | |
| Bonfatti et al., 2017 | Before | 7 | 185% | 121% | 123% | 69% | 205% | 21% | 33% | 53% | 292% | 110% |
| Bonfatti et al., 2017 | After | 7 | 186% | 98% | 91% | 54% | 47% | 24% | 13% | 17% | 38% | 45% |
| Mensching et al., 2025 | Before | 14 | 157% | 96% | 137% | 73% | 178% | 23% | 31% | 35% | 135% | 85% |
| Mensching et al., 2025 | After | 14 | 94% | 65% | 64% | 47% | 44% | 27% | 23% | 27% | 46% | 52% |
| all brands | | | | | | | | | | | | |
| Grelet et al., 2015 | Before | | 17% | | | | | 150% | | 63% | 263% | 670% |
| Grelet et al., 2015 | After | | 1% | | | | | 28% | | 25% | 45% | 71% |

Conclusion 7:
 Interaction with models. Standardization is adding less (relative) error to predictions from models with large errors