

Explorative analysis of microbial communities in chicken production



ORCHESTRATING FOOD SYSTEM MICROBIOMES TO
MINIMIZE FOOD WASTE
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Context

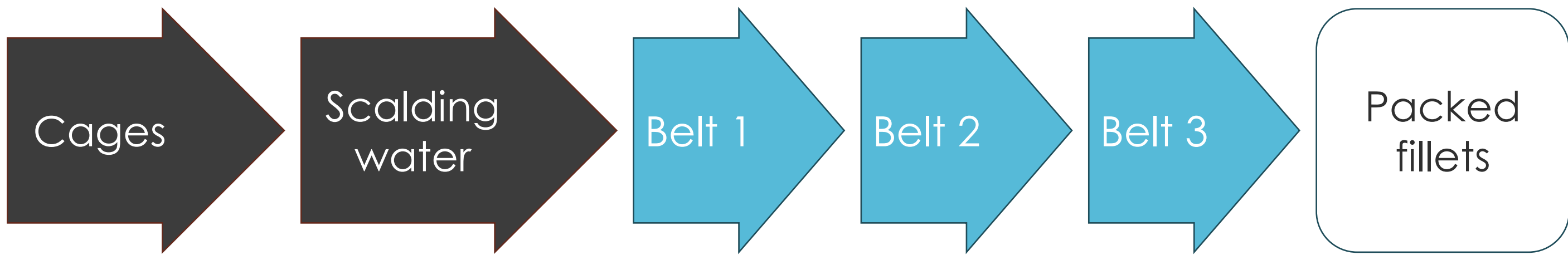
This study is part of the MICROORC project, which aims to reduce food waste by monitoring and utilizing microbiomes in the food processing chain. A key aspect of the project involves mapping microbiome variations along the chicken production line, to identify patterns and potential key control points.

Research question

What is the best chemometric tool for exploring variations in complex industrial microbiome data, and interpreting these variations with respect to time, space, and microbial signatures?

Data

Samples were collected from two chicken slaughterhouses, A and B, located in Norway and Portugal, over a one-year period. In each factory, sampling occurred on seven separate days, both early and late in the day, and at multiple locations along the production line:

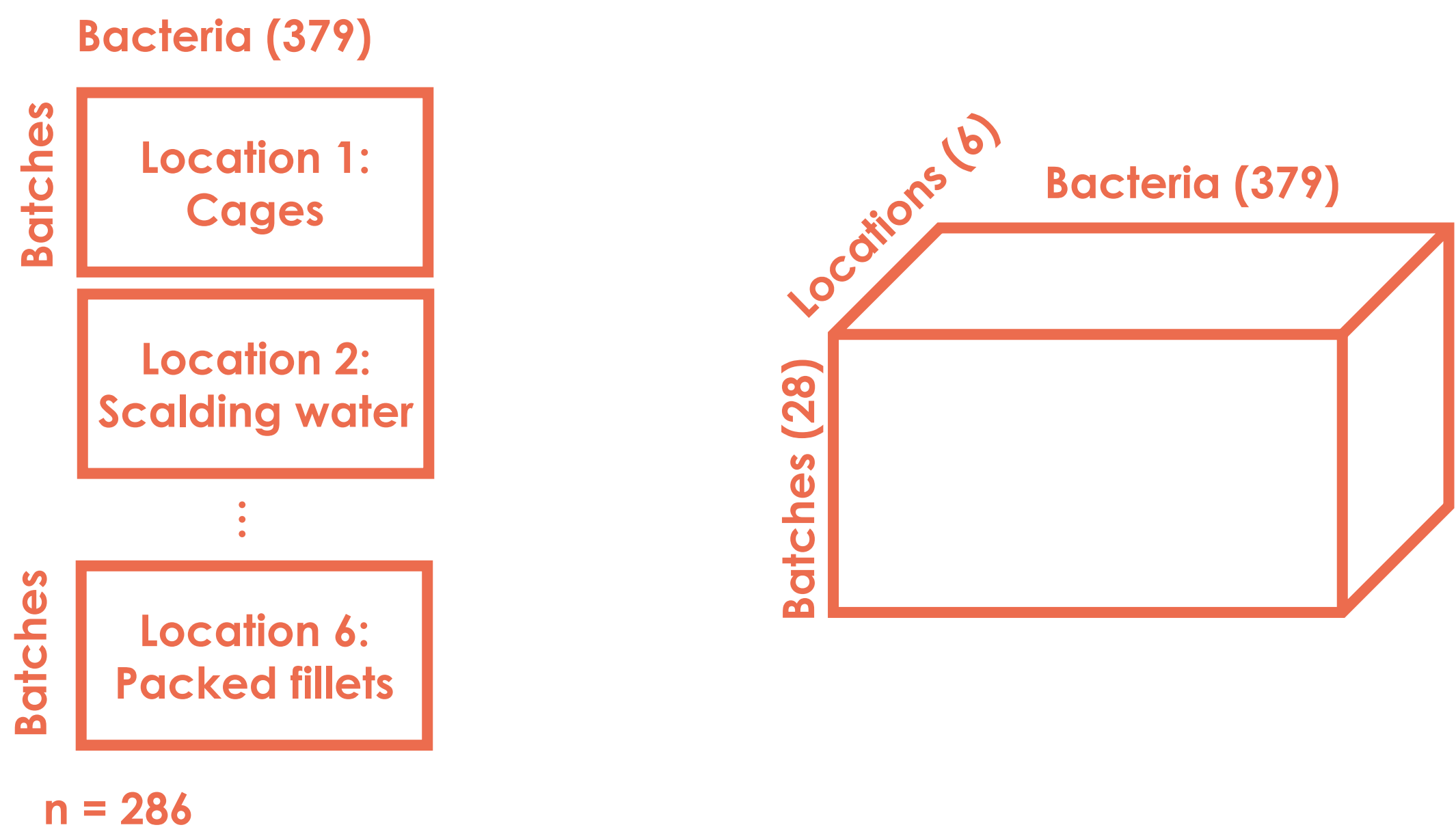


The colors represent different hygienic zones (black = dirty, blue = clean).

Microbial community composition was measured using 16s DNA sequencing, amounting to a total of 379 microbial features after filtering out low-abundant features. As with all industry data, there are challenges with missing data, inconsistent sampling procedures and other uncontrollable factors.

Methods

The data can be structured either in a two-way or three-way array. The rows in the batch mode represent 28 independent production batches (2 factories x 7 production days x 2 times a day). There are varying numbers of replicates per batch and sampling location, which are averaged in the three-way representation but kept intact in the two-way data.

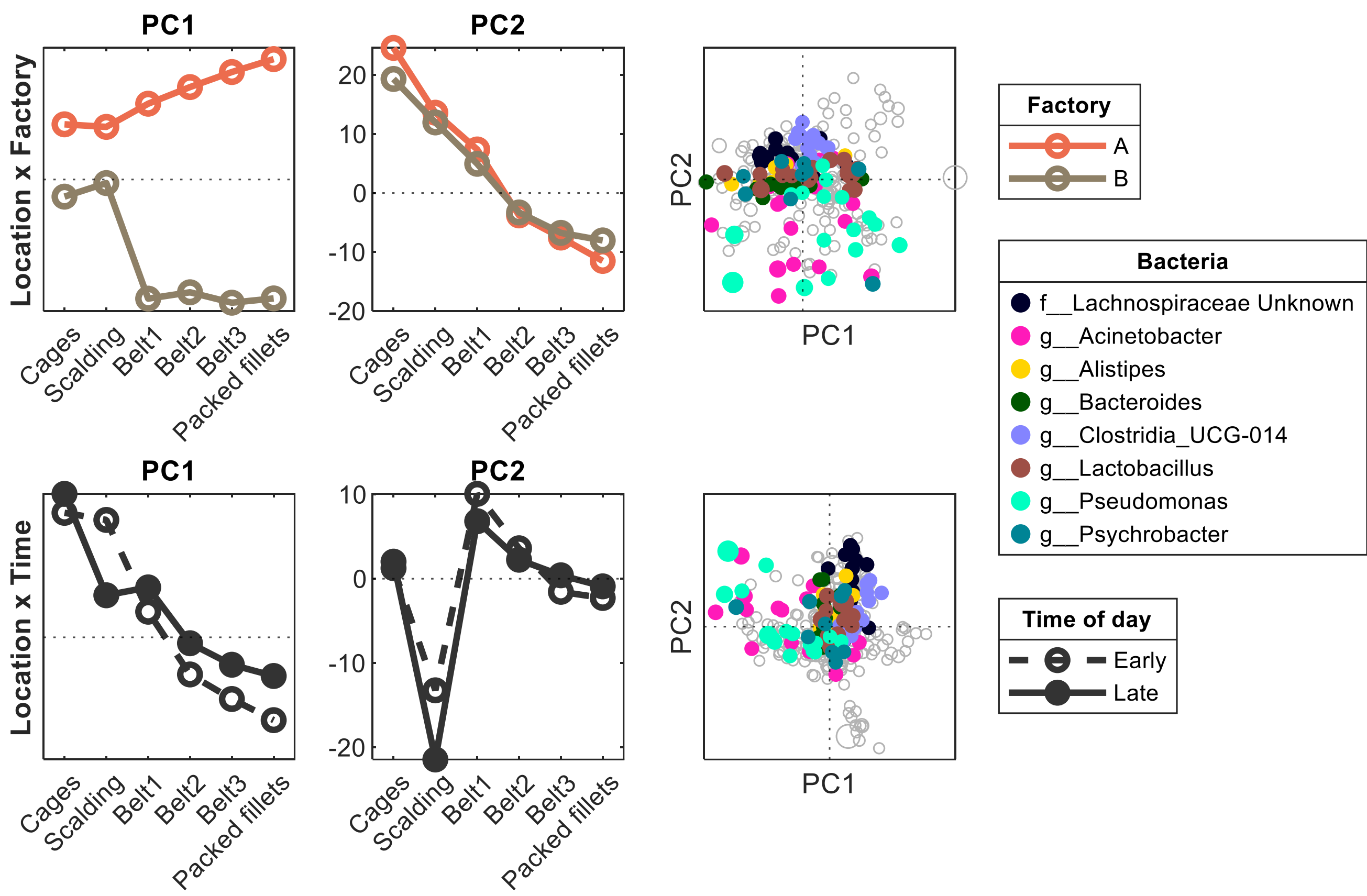


The two-way array was analysed using ASCA with factors *Factory*, *Location* and *Time of day*, while the three-way array was decomposed by PARAFAC. The three-way array contains 4% missing elements, as some locations are missing for some batches.

ASCA Results

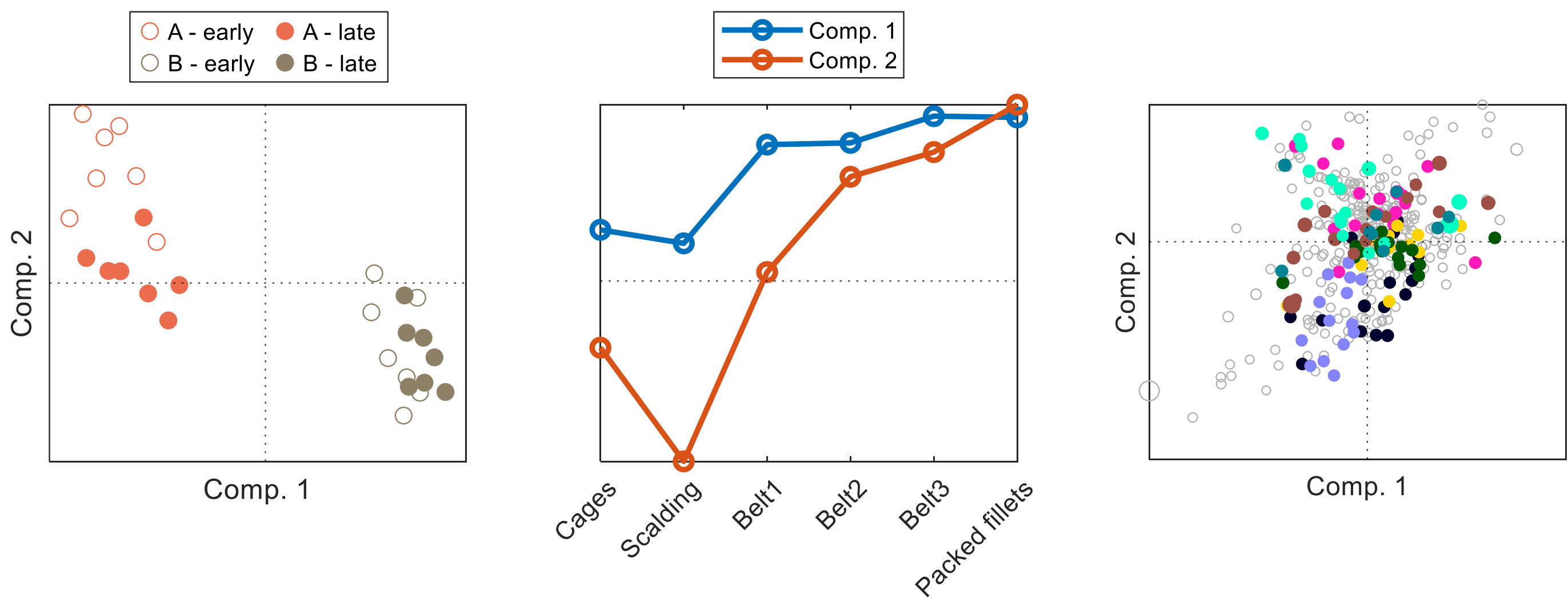
Differences between factories and locations had the highest contribution to the microbial variation. Interestingly, there was also systematic variation due to time of day. SCA was performed to interpret these differences, revealing that the shift along the processing line is related to different genera. The difference between factories (top row) is largest in the clean zone, while the difference between early and late batches (bottom row) is largest in the scalding water.

Effect	Df	Explained variance
Factory	1	14***
Location	5	12.5***
Time of day	1	1.2***
Factory x Location	5	5.2***
Factory x Time	1	0.7***
Location x Time	5	2.1***
Factory x Location x Time	5	1.2
Error	262	63.2



PARAFAC Results

A PARAFAC model with two components explains 23% of the variation in the data. In line with the ASCA result, the loadings reveal that the first component represents the difference between factories, which increases along the processing line. The second component represents variation that also differs between factories, and separates early and late batches in factory A.



Conclusion

The main systematic variation is the difference between factories, which increases along the production line. This is represented in both models.

The more subtle differences between early and late batches are more challenging to understand, and the methods provide different perspectives on this. Both methods indicate that the difference between early and late batches is largest in the scalding water but also evident in the latest locations. While the PARAFAC model indicates that this effect is only found in factory A, the ASCA results suggest that it is present in both factories.

The large residual variation within both models stems from the natural uncertainty within industry level microbial data, as well as from variation between sampling days throughout the year, which is particularly interesting for the project and will be investigated further.

