

## **Abstract**

A correct identification and quantification of the different sources of variance in an experimental dataset is of utmost importance, for instance, when comparing treatment groups, or in the case where there is a need for describing the (future) behaviour of a batch of biological products. The total data variance can be split up into two different parts, one describing the biological variance due to the natural heterogeneity of the batch and the other describing the uncertainty due to the imperfect measurement of the attribute considered. The classical approach to include biological variance in postharvest research is to use a two stage approach in which in a first stage a (non-linear) model is built for each product individually, whereafter inferences are based on the parameters obtained from the first stage. In this contribution, we propose a methodological approach to identify and quantify the different sources of biological variance, using the concept of (non-linear) mixed effects models. Such models are a useful tool to handle repeated measures data containing a high biological variance. The concept is demonstrated on a practical dataset of postharvest firmness changes in mangoes. It is shown that aside from the differences in biological age of the mangoes, the decay rate also varies among mangoes. Furthermore, it is shown that the biological variance is the dominating source of variance during the experiment.