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Multiple testing of food contact materials: A predictive algorithm for assessing the global migration from silicone moulds

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ABSTRACT

For reasons of food safety, packaging and food contact materials must be submitted to migration tests. Testing of silicone moulds is often very laborious, since three replicate tests are required to decide about their compliancy. This paper presents a general modelling framework to predict the sample's compliance or non-compliance using results of the first two migration tests. It compares the outcomes of models with multiple continuous predictors with a class of models involving latent and dummy variables. The model's prediction ability was tested using cross and external validations, i.e. model revalidation each time a new measurement set became available. At the overall migration limit of 10 mg dm^{-2}, the relative uncertainty on a prediction was estimated to be ~10%. Taking the default values for α and β equal to 0.05, the maximum value that can be predicted for sample compliance was therefore 7 mg dm^{-2}. Beyond this limit the risk for false compliant results increases significantly, and a third migration test should be performed. The result of this latter test defines the sample's compliance or non-compliance. Propositions for compliancy control inspired by the current dioxin control strategy are discussed.

1. Introduction

Polymerized siloxanes or polysiloxanes are mixed inorganic–organic polymers, consisting of an inorganic backbone of alternating silicon and oxygen atoms with organic side groups attached to the silicon atoms. Two organic functional groups, often methyl or phenyl groups, are attached to each silicon atom. Polysiloxanes are commonly termed silicones. These are generally considered as stable and inert. Silicone fluids are predominantly used as hydraulic fluids and as adhesives, lubricants, water repellents, and protective coatings. Silicone rubbers and elastomers, on the other hand, are used as electrical insulators in encapsulations, coatings, and varnishes; as gaskets and caulking material; in specialized tubing; as automobile engine components; as flexible windows in face masks and air locks; for laminating glass cloth; as surgical membranes and implants and also as non-stick moulds for baking and freezing processes in the food industry, in restaurants and pastry shops.

Bakery moulds can be used in both conventional and microwave ovens as well as in freezers. Moreover, they can be put directly from the freezer into the oven. The flexibility and non-stick features of silicones facilitate the extraction of food products after cooling down. Otherwise, frozen foods can be unmoulded without thawing. Bending or twisting silicone bakeware makes unmoulding considerably less challenging. Bakery moulds are readily advertised as soft, non-toxic and high conductivity silicones, reusable up to 1000 bakings and more. During the last decade flexible silicone baking moulds have achieved a quite significant market share; they are nowadays marketed as user friendly and cheaper alternatives to traditional metal bakeware.

It should not be forgotten, however, that food contact and packaging materials contain chemical substances, which can migrate into the food during processing and storage. The scientific literature emits some concern and recommends proper usage of the moulds to restrict migration into different foodstuffs [1–5]. Even when silicones are characterized by elevated thermal stability and pronounced resistance to aging, temperature rises lead to depolymerization of the elastomer and subsequent volatilization and migration [1–2]. Cyclic organosiloxane oligomers are commonly identified as migrating substances or migrants. Linear, partly hydroxyl-terminated, organosiloxanes are not frequently found in the samples [3]. Additionally, the type of food and especially its fat content are highly determining parameters for migration of the latter compounds [4]. Migrants are increasingly becoming subject to control and regulation [5,6]. For materials and articles intended to come into repeated contact with foodstuffs, the migration tests have to be carried out three times on one single object in accordance with the conditions laid

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down in both the recent EU regulation 10/2011 as well as the European Norm EN 1186. On each occasion another sample of the food or food simulant is to be used. The decision concerning compliance is then based on the migration value found in the third test. Conclusive proof that migration does not increase in the second and third tests when the migration limit is not exceeded in the first test makes further testing redundant.

Triplicate testing of silicone objects is a laborious and expensive matter, which can be avoided by mathematically determining the final migration value with a predictive algorithm, based on the first and second migration values. This mathematical approach is here illustrated with data obtained for overall migration from silicones; it is, however, applicable to all compliance tests, requiring triplicate analyses. On one hand, the suggested procedure could reduce the test period by one third, e.g. a time saving of ~10 days for traditional global migration experiments (10 days at 40 °C) and of ~1 day at the test conditions of the present study. Moreover, there is an additional benefit since many molecule specific analyses are carried out in duplicate. The EU regulation strongly recommends strict quality control and the European norm NBN EN 1186 requires three repetitions of chromatographic analyses.

In this paper, we apply multivariate modelling [7] to predict the migration values from silicone moulds. We compare the outcomes of different regression methods such as multiple linear regression (MLR), principal components regression (PCR) and partial least squares (PLS). These models do not compete with deterministic migration models based on diffusion and repartition coefficients (e.g. in [8]); they involve linear combinations of explanatory variables instead of hypothetical functional forms derived from an underlying theory. Therefore, multivariate modelling is also applicable, when no fundamental theory exists, and can provide an independent check on the validity of existing deterministic models.

2. Materials and methods

2.1. Migration testing

Silicone moulds from various manufacturers were submitted to overall migration tests; moulds from supermarkets and from retail trade were sampled by the Belgian Federal Agency for the Safety of the Food Chain (FASFC). Prior to testing, surface dust of the sample moulds was removed. The samples were neither rinsed with water nor cleaned with household detergents. Following the European Standard EN 1186-1, all samples were brought into contact with volatile food simulants, which were evaporated to dryness after migration. The remaining residues were gravimetrically determined. For each reusable object the overall migration test was 3 times repeated (European Norm EN 1186). As laid down in the EU Regulation 10/2011, the migration experiments were done with the substitute fatty food simulant ethanol (95%, v-v). Ethanol (AnalaR NORMAPUR, BDH Prolabo®), obtained from VWR International (Haasrode, Belgium), and Millipore Milli Q water were used. The moulds were tested during 4.5 h at 60 °C following the Directive 82/711/EC, since the most recent EU Regulation 10/2011 was not applicable at the moment the experiments were carried out. For the tests a Binder drying oven was used; residues were weighed with a Mettler Toledo precision balance.

The contact interface of the silicone moulds and the food simulant depended on their shapes and sizes. For samples with a large flat surface the migration cell type B, as described in Annex C of the European Standard 1186, was used. All cell spare parts are manufactured in stainless steel; sealing between food contact material and food simulant is done with O-rings. The food simulant contact area amounts to 1 dm^2. Objects in a tub or tray form were filled with a known volume of the simulant. Objects with very complex shapes were immersed in the simulant; determined contact areas of the samples were taken into account. Overall migration tests were carried out in duplicate; the results were expressed in mg dm^{-2}. Weighed residues were divided by a factor 5. This reduction factor was always applied to evaluate the observed migration levels, since migration into the simulant is generally accepted to exceed the migration into real foodstuffs (85/572/EEC). The new EU Regulation 10/2011 imposes the food simulant oil and mentions a reduction factor of 3. These new test conditions will be effective in 2013.

2.2. MLR/PCR/PLS regressions

Multivariate regressions methods such as MLR, PCR and PLS have the common characteristic of generating models that involve linear combinations of explanatory variables, their differences lie in the way how correlations between variables are handled. In MLR the dependent variable is regressed on the predictor variables directly. Yet, when several predictors are linearly correlated with each other, this may result in: (i) regression coefficients that are very sensitive to even small fluctuations of the response variable, (ii) standard errors that are high for the regression coefficients, and hence (iii) degradation of the predictions' precision [9]. PCR and PLS are both methods that solve the colinearity problem. In those methods, new predictors, known as components, are constructed as linear combinations of the original predictor variables. PCR creates these new components to explain the observed variability in the predictors, without taking into account the response variable [10]. PLS achieves a compromise between two objectives [11,12], i.e. maximize the explained variance of the predictors (principle of PCA) and (ii) optimize the correlations between the predictors and the dependent variable(s) (principle of regression). Regardless of the procedure (either MLR, PCR or PLS), the best model is chosen to provide an optimal balance between fit and predictive ability.

2.3. Model selection criteria

In the assessment of model performance and relevance three quality indices were used.

- The coefficient of multiple determinations (R^2), which indicates the proportion of variability in a data set accounted for by the statistical model. During the selection stage of model building, we used the determination coefficient adjusted for the number of explanatory terms in the model:

  $$AdjR^2 = 1-(1-R^2)\cdot\left(\frac{n-1}{df}\right),$$

  where df is the degrees of freedom. Unlike R^2, $AdjR^2$ increases only if the new term improves the model more than would be expected by chance.
- The root mean squared error (RMSE) or residual standard deviation, which yields a measure of the spread of the measurements around the fitted model:

  $$RMSE = \sqrt{\frac{\sum (y_i - f(x_i))^2}{df}}$$

- The root mean squared prediction error (RMSPE), which yields a measure of how the outcome of an experiment can reliably be predicted. RMSPE involves the predicted residual error sum

Table 1
Descriptive statistics for silicone moulds. According to the European Norm EN 1186, the overall migration test was 3 times repeated (X_1, X_2, X_3). Values in mg dm^{-2} are medians with interquartile range in brackets.

Treatment groups	X_1	X_2	X_3
Filled samples	18.0 (17.1)	10.5 (10.4)	6.4 (7.2)
Immersed samples	18.4 (7.5)	9.6 (4.0)	5.3 (2.6)
Single-side tested samples	15.8 (3.5)	10.8 (2.4)	7.4 (1.8)

of squares or PRESS statistic that requires a cross-validation [13]:

$$Press = \sum (y_i - f(x_i)_{(-i)})^2$$

where $f(x_i)_{(-i)}$ is the prediction of the ith observation when it is not included in the training set used for the estimation of the model parameters. RMSPE is then computed according to:

$$RMSPE = \sqrt{\frac{Press}{df}}$$

Moreover, a large difference between RMSPE and RMSE indicates that the model is sensitive to the presence or absence of certain observations in the model.

2.4. Outlier diagnostics

There are a variety of statistics for detecting outliers available [14]. We choose to consider only two of these tools, the studentized deleted residuals and Cook's distance, as they have a natural interpretation in the context of the cross validation used in this study:

- The studentized deleted residual (SDR) is a useful index to find those values of the response variable which are unusual with respect to the fitted model:

$$SDR_i = \frac{y_i - f(x_i)_{(-i)}}{RMSE \cdot \sqrt{1-h_{ii}}}$$

where h_{ii} is the ith diagonal element of the hat matrix: $X^T \cdot (X^T \cdot X)^{-1} \cdot X$. Since the degree of freedom is quite large here ($df > 200$), we could use the rule of thumb that SDR > 2 should be uncommon and SDR > 3 should be rare.
- Cook's distance (D_i) combines both the hat-diagonal and studentized deleted residual to give a statistic for detecting observations that actually influence the estimation of model parameters:

$$D_i = \frac{SDR_i^2}{p} \cdot \frac{h_{ii}}{1-h_{ii}}$$

where p is the number of parameters in the model. Potentially influential points are characterized by D_i − values > 1.

2.5. Predictions of new response

The uncertainty in a new response predicted from a linear combination of predictor-values is composed of (i) the uncertainty of the regression line that can be assessed with the variance–covariance matrix $= MSE \cdot (X^T \cdot X)^{-1}$, and (ii) the variability of the measurements that can be estimated by RMSE (see above). Consequently the standard deviation of a new response y_0 predicted at x_0 is given by [9]:

$$s_{y_0} = RMSE \cdot \sqrt{\frac{1}{m} + x_0^T \cdot (X^T \cdot X)^{-1} \cdot x_0} \quad (1)$$

where x_0 is the matrix of the predictor-values, x_0^T its transpose and m is the number of replicates.

3. Results

3.1. Data structure and analysis

The data, used to develop and validate the regression models, represents a set of 229 silicone moulds from various manufacturers sampled between 2007 and 2011 as part of a monitoring programme for food security. The effect of mould size/shape was first investigated since this effect could impact the estimation of the model parameters and, hence, the determination of the predicted values for all observations. The samples were splitted in three groups: filled, immersed and single-sided tested samples. Table 1 indicates that the differences in the median values among the treatment groups are not statistically significant (Kruskal–Wallis test, $p = 0.168$). The measurements decreased monotonically from the first (X_1) to the third (X_3) migration tests (Kruskal–Wallis test, $p < 0.001$), although very rarely a measurement exceeded a previous one with $X_1 \leq X_2$ in 1% cases and $X_2 \leq X_3$ in 2% cases.

A Principal Component Analysis (PCA) results in a two-factor model explaining 99.5% of the variance. The first factor is the more important and accounts for more than 91% of the modelled variation. The score plot, which provides a map of the observations, is depicted in Fig. 1. Data points close to each other have similar properties, whereas those far from each other are dissimilar with respect to their migration profiles. For example, single-sided tested samples appear close to the centre (origin) of the plane, indicating that they have average properties. In contrast herewith, several data points belonging to the group of filled samples are located together in the upper right corner; these observations (#10, 29, 37, 43, 151 and 165) are characterized by the highest values for migration test 3. Finally, it can be observed that 5 data points (#10, 29, 37, 43, 55 and 151) fall outside the ellipse corresponding to the 99% confidence region, as specified by the Hotelling's T^2 statistic [15]. From a statistical point of view, instead of the expected 1% that exceeds the 99th percentiles, 2% does so. This is well acceptable since the 229 results do not

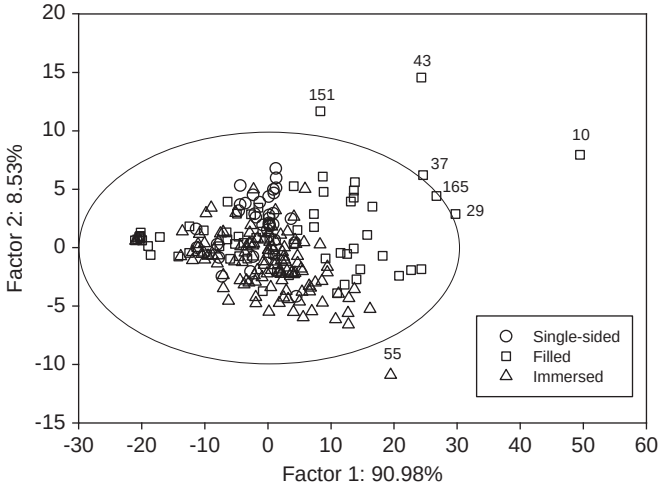

Fig. 1. PCA score plot of the silicone mould dataset. The numbering of the observations refers to the sampling sequence. The ellipse corresponds to the 99% confidence region as given by Hotelling's T^2.

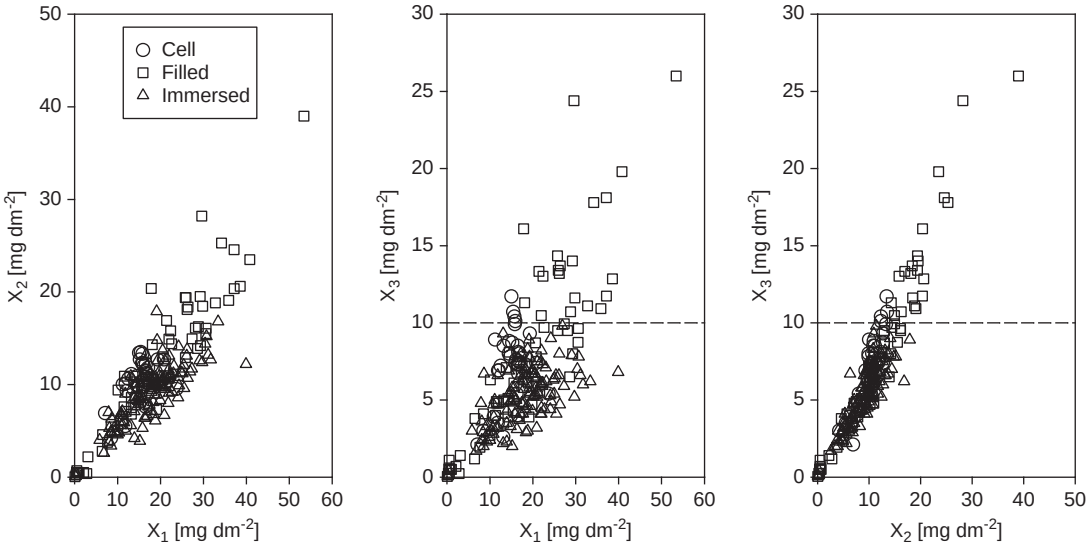

Fig. 2. Multiple two-variable scatterplots of the silicone mould dataset. The dashed line indicates the limits to be found in the third migration test for sample compliance.

represent 229 realizations of the same experiment, but correspond to a four year sampling period. Therefore, the variability is not only due to random noise, but also due to changes in laboratory conditions. As seen in Fig. 2, X_2 is the best predictor of X_3, while X_1 appears as a covariate that could impact the relationship between X_2 and X_3. About 11% of the samples are not compliant, i.e., the third migration value is greater than the overall limit of 10 mg dm^{-2}, and many of those belong to the group filled samples. A regression trees indicate moreover that if X_1 lies in [15.0, 53.4[then $X_3 \geq 10$ in 20% cases; if X_2 lies in [12.3, 39.0[then $X_3 \geq 10$ in 50% cases, whereas if both $X_1 \geq 20.0$ and $X_2 \geq 15.0$ then $X_3 \geq 10$ in 75% cases.

3.2. Model building

To test whether X_3 could accurately be predicted using the first and second migration values, cross and external validations were carried out in the following way: (i) the dataset was split into two moieties, (ii) the model was developed on data gathered between 10/2007 and 06/2010 using the leave-one-out method (cross validation), and (iii) the model was tested on data gathered between 08/2010 and 12/2011 (external validation). In the case of MLR regressions, we considered additive type models only to avoid mathematical difficulties that can result in unreliable predictions (see Section 2):

$$Y = \beta_0 + \sum \beta_i \cdot X_i + \varepsilon \quad (2)$$

In practice Eq. (2) may not be fully suitable and increasing model complexity is achieved by adding squared ($i=j$) and interaction terms ($i \neq j$) between predictor variables:

$$Y = \beta_0 + \sum \beta_i \cdot X_i + \sum \beta_{i,j} \cdot X_i \cdot X_j + \varepsilon \quad (3)$$

With Eq. (3), conditions are fulfilled for PCR and/or PLS modelling, i.e. regression analysis with many noisy and collinear sets of predictors and response variables. Additionally, for both type of equations, models including quantitative (X_1, X_2) and dummy predictors that reflect attachment to categories (filled, immersed and single-sided tested samples) were tested. Table 2 summarizes the results for all different models applied to the training and validation sets. Criteria for model selection (see Section 2) was chosen to provide an optimal balance between fit (R^2 and $AdjR^2$) and predictive ability (RMSPE and RMSE).

Table 2
Statistics for different models applied to the silicone mould data. TG is a dummy variable reflecting the attachment to groups (filled, immersed and single-sided tested samples).

Training set	**Predictors in Eq.**	***AdjR*^{2}**	***RMSPE***
MLR	X_1, X_2	0.910	1.18
PCR	X_1, X_1^2, X_2, X_2^2 and product terms	0.907	1.43
PLS	X_1, X_1^2, X_2, X_2^2 and product terms	0.916	1.25
MLR	X_1, X_2, TG	0.914	1.19
PCR	X_1, X_1^2, X_2, X_2^2, TG and product terms	0.914	1.46
PLS	X_1, X_1^2, X_2, X_2^2, TG and product terms	0.916	1.30
Validation sets	**Predictors in Eq.**	***R*^{2}**	***RMSE***
MLR	X_1, X_2	0.953	0.86
PCR	X_1, X_1^2, X_2, X_2^2 and product terms	0.955	0.89
PLS	X_1, X_1^2, X_2, X_2^2 and product terms	0.955	0.88
MLR	X_1, X_2, TG	0.951	0.86
PCR	X_1, X_1^2, X_2, X_2^2, TG and product terms	0.289	3.53
PLS	X_1, X_1^2, X_2, X_2^2, TG and product terms	0.949	1.02

Overall, the goodness of fit does not increase significantly with model complexity, and MLR, characterized by the lowest values of RMSPE and RMSE, appear to be the best for prediction purposes. Almost identical RMSPE and RMSE values are obtained with the model including the dummy variables but the simpler model involving X_1 and X_2 is to be preferred:

$$X_3 = -0.17 \cdot X_1 (SE = 0.015) + 0.92 \cdot X_2 (SE = 0.026) \quad (4)$$

where X_i variables are expressed in mg/dm^2.

3.3. Predictions made on the basis of the fitted line

The relationship between the measured and predicted values for the whole dataset is illustrated in Fig. 3. Seven data points (#29, 43, 49, 50, 76, 96, and 125) have unusual responses relative to the regression model because they lie off the line defined by the other observations. For those samples, the absolute values of the studentized deleted residual are high (>3) but Cook's distances remain below the cut-off value of 1 usually quoted for spotting influential or leverage points (Table 3). We can therefore conclude that these observations have a minimal impact on the estimation of model parameters, but could alter the predictive power by inflating the residual standard deviation or RMSE. As seen in Table 3 RMSE, which yields a measure of the spread of the data points around the fitted line, increases from ~0.8 to

$\sim$1.0 mg dm^{-2}; whether the outlying observations are considered or not. It is important to note that this variance inflation does not impact the mean and the variability of the predicted values amongst treatment groups. In other words, although the model was built using a set of relatively heterogeneous data, the quality of the prediction is equivalent whatever the type of mould tested, and whether the testing was done by ethanol volume vs. mould surface area (Table 3). The uncertainty of a response predicted from a new set of measurements is calculated with Eq. (1). At the overall migration limit of 10 mg dm^{-2}, this uncertainty amounts to 1.04 mg dm^{-2}, i.e. about 10%. Keeping the risk for both false positive or false negative results at an acceptable level ($\alpha=\beta=0.05$) [16] the maximum value that can be predicted by the model for compliance with the regulations is then $\sim$7 mg dm^{-2} (i.e. $10-3.29s_{y_0}$). Beyond this limit the risk for false negative results may increase significantly. From Fig. 3, it can be seen that with a prediction value of ≤ 7, the third migration value never exceeded 10 mg dm^{-2}.

4. Discussion

4.1. Suggestions for compliancy control

Consumers are nowadays very concerned about food safety, since contaminating chemicals are known to enter the environment and, inherently, the food chain by many different pathways. In addition to deploying molecule specific strategies for the ecological as well as public health risk assessments of the pollutants, it is necessary to apply and explore other strategies, such as the use of bio-assays and biosensors for the identification of pollutants responsible for particular adverse effects [17]. This strengthens the need for a well-organized food control and elevated numbers of sample analyses. Recent and modern control strategies often apply a two-step approach, whereby screening of multifold samples by rapid and cheaper techniques is combined with sophisticated and very expensive confirmatory techniques for suspect samples.

An interesting showcase is the commonly accepted approach for control on dioxin contaminations in food and feed. In a first step, high numbers of samples are rapidly screened; for this purpose the CALUX technique is very often used [18]. Afterwards suspect samples and a restricted number of QC/QA samples are analyzed by sophisticated chromatographic techniques. Similar to this system, we suggest either the green–orange–red or the green–red approach (Fig. 4).

The former one distinguishes a green zone with all compliant values, a red zone with all non-compliant values and an intermediate orange zone. Values within the green zone do not exceed the value of 7 mg dm^{-2}, this zone corresponds per definition to those samples that are fit for the market. Values within the red zone exceed the value of 10 mg dm^{-2}; the corresponding samples should not become available to the consumers. The orange zone from 7 to 10 mg dm^{-2} gathers migration values that are not significantly different from the legal norm value of 10 mg dm^{-2}. A third migration test would then be required and the results of the third tests define the sample's compliance or non-compliance.

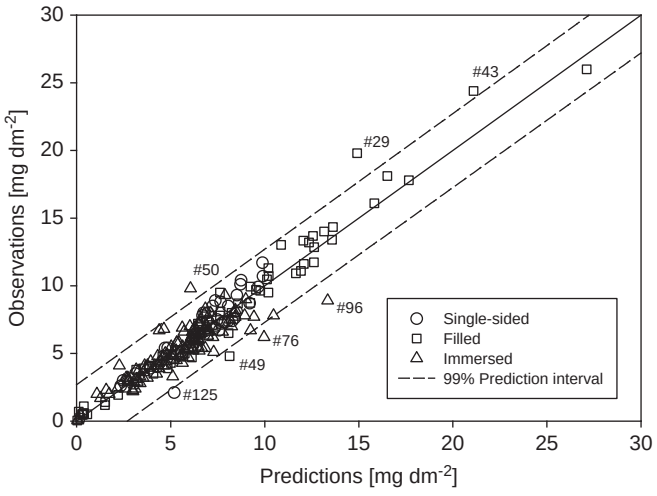

Fig. 3. Relationship between measured and predicted migration values found for the silicone mould dataset.

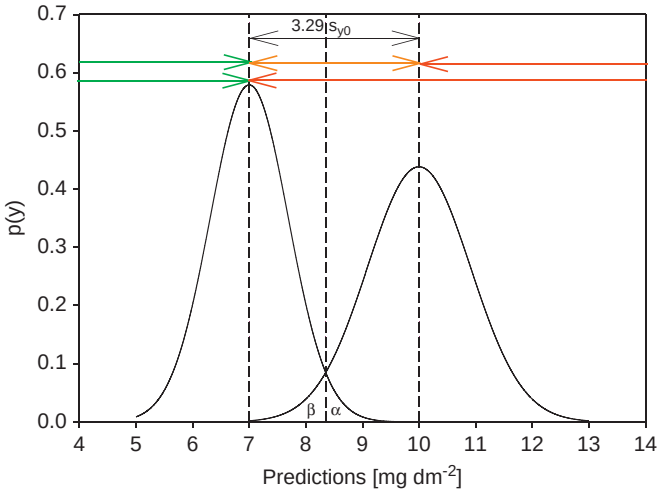

Fig. 4. Probability distribution function $p(y)$ for the migration values predicted with Eq. (3). Taking the default values $\alpha=\beta=0.05$, the multiplication factor for the expected uncertainty s_{y_0} (Eq. (1)) is 3.29($=2\times1.645$).

Table 3
Studentized deleted residuals and Cook′ distance from Eq. (3) for observations #29, 43, 49, 50, 76, 96, and 125.

Treatment groups	OBS	Stud. del. res.	Cook's dist.	$RMSE_{\text{without outliers}}$	$RMSE_{\text{with outliers}}$
Filled samples	29	5.02	0.304	0.7	1.1
	43	3.41	0.421		
	49	−3.29	0.060		
Immersed samples	50	3.73	0.076	0.8	1.0
	76	−3.77	0.097		
	96	−4.54	0.22		
Single sided tested samples	125	−3.02	0.045	0.9	1.0
Overall RMSE				0.8	1.0

The green–red system, on the other hand, distinguishes compliant and suspect samples only. This approach is inspired by the current dioxin control strategy and requires an additional third migration test for all samples with a predicted migration value exceeding 7 mg dm^{-2}. The result of the third test would then be decisive about compliance or non-compliance of the sample.

For reasons of food safety control the green–orange–red approach only would be acceptable. It eliminates non-compliant samples from the market and consumers do not face negative effects of excessive migration from silicone baking forms. Migration limits, and more particularly specific migration limits, are derived from toxicological evidence and set tolerable daily intake values. Higher intakes, and hence exposures, might generate adverse health effects.

Otherwise, the green–red approach provides a third migration value for those samples that are considered suspect. This might prove interesting for reasons of research and development.

In either cases substantial time and energy profit can be expected. Additionally, it might be a good idea to use this approach for other problems, such as the migration of contaminants from kitchen utensils. The Rapid Alert System for Food and Feed (https://webgate.ec.europa.eu/rasff-window/portal/index) publishes approximately 10% notifications on packaging and food contact materials. Very often these notifications refer to organic food contamination, such as the migration of melamine from kitchen utensils into acetic acid. Sometimes they refer to metal contaminations, such as migration of lead, cadmium and chromium.

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References

[1] R. Meuwly, K. Brunner, C. Fragnière, F. Sager, V. Dudler, Mitt. Geb. Lebensmittelunters. Hyg. 96 (2005) 281–297.
[2] R. Meuwly, F. Sager, K. Brunner, V. Dudler, Dtsch. Lebensm.-Rundsch. 103 (2007) 561–568.
[3] R. Helling, A. Mieth, S. Altmann, T.J. Simat, Food Addit. Contam. 26 (2009) 395–407.
[4] R. Helling, K. Kutschbach, T.J. Simat, Food Addit. Contam. 27 (2010) 396–405.
[5] M.F. Poças, T. Hogg, Trends Food Sci. Technol. 18 (2007) 219–230.
[6] K. Grob, M. Biedermann, E. Scherbaum, M. Roth, K. Rieger, Crit. Rev. Food Sci. Nutr. 46 (2006) 1–7.
[7] L. Eriksson, E. Johansson, N. Kettaneh-Wold, J. Trygg, C. Wilström, S. Wold, Multi- and Megavariate Data Analysis Part I, Basic Principles and Applications, Second revised and enlarged edition, Umetrics Academy, Umea, Sweden, 2006.
[8] M.F. Pocas, J.C. Oliveira, J.R. Pereira, R. Brandsch, T. Hogg, Food Control 22 (2011) 303–312.
[9] D.L. Massart, B.G.M. Vandeginste, L.M.C. Buydens, S. De Jong, P.J. Lewi, J. Smeyers-Verbeke, Handbook of Chemometrics and Qualimetrics, vol. 20A, Elsevier, 1997.
[10] I.T. Jolliffe, J. R. Stat. Soc., Ser. C (Appl. Stat.) 31 (1982) 300–303.
[11] S. Wold, M. Sjöström, L. Eriksson, Chemom. Intell. Lab. Syst. 58 (2001) 109–130.
[12] S. Wold, J. Trygg, A. Berglund, H. Antii, Chemom. Intell. Lab. Syst. 58 (2001) 131–150.
[13] D.M. Allen, Technometrics 16 (1974) 125–127.
[14] P.J. Rousseeuw, A.M. Leroy, Robust Regression and Outlier Detection, John Wiley & Sons, 1987.
[15] H. Hotteling, Ann. Math. Stat. 2 (1931) 360–378.
[16] L.A. Currie, Pure Appl. Chem. 67 (1995) 1699–1723.
[17] C. Blasco, Y. Pico, Trends Anal. Chem. 28 (2009) 745–757.
[18] M.S. Denison, B. Zhao, D.S. Baston, G.C. Clark, H. Murata, D. Han, Talanta 63 (2004) 1123–1133.