Methodology for the evaluation of the quality of data in a Belgian risk assessment for *Salmonella* in pigs

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INTRODUCTION

Quantitative microbial risk assessment (QMRA) has its limits due to data quality, limited time, model uncertainty and quality of assumptions. The NUSAP method (Numeral Unit Spread Assessment Pedigree, Funtowicz and Ravetz, 1990) was implemented in a Belgian QMRA for *Salmonella* in pork. NUSAP is a notational system that aims to provide a better communication and management of uncertainty in science used for policy. Quality of data in QMRA is related to a variety of criteria such as the completeness, the validity, the comparability, the timeliness of data, the sampling methods and the use of (imperfect) diagnostic tests. We used the pedigree component from the NUSAP acronym to evaluate the quality of input parameters for the Belgian QMRA. This was done by a set of 4 pedigree criteria in a pedigree matrix.

MATERIAL AND METHODS

The Belgian QMRA was divided into 4 pathways: (1) primary production, (2) transport, slaughterhouse & post-processing, (3) distribution & storage, (4) consumption. Information for 101 model parameters, related to prevalence, concentration, process data, were summarised in a database.

Each parameter was specified in a parameter ID-card by means of its reference, its sample frame (study population, sample size, non-response, diagnostic test) and its information for central tendency, range and distribution. The pedigree matrix (**table 1**) included 4 criteria, namely proxy, empirical, method and validation.

Table 1 : Pedigree matrix for parameter strength (adapted from van der Sluijs et al., 2005)

Score	Proxy	Empirical	Method	Validation
4	Exact measure of the desired quantity (e.g. geographically representative)	Large sample direct measurements, recent data, controlled experiments	Best available practice in well-established discipline (accredited method for sampling / diagnostic test)	Compared with independent measurements of the same variable over long domain, rigorous correction of errors
3		small sample, direct measurements, less recent data, uncontrolled experiments, low non-response rate		
2			Acceptable method but limited consensus on reliability	
1	Weak correlation (very large geographical differences)	1 Expert opinion, rule of thumb estimate	Preliminary methods with unknown reliability	Weak very indirect validation
0	Not clearly correlated	Crude speculation	No discernible rigour	No validation

The input parameters were scored by 10 experts from the Belgian *Salmonella* project using the pedigree matrix. Kite diagram were used to visualise the scoring of the parameters for the different pedigree criteria.

An overall "parameter strength" (mean of the scores of the 4 pedigree criteria) was calculated by weighing 1. the expertise of the experts, 2. the consistency in rating between experts, and 3. the number of experts rating a pedigree criterion of a parameter.

RESULTS

The overall parameter strength, the aggregated scores of the 4 pedigree criteria, of the 101 parameters scored by the experts are presented (**figure 1a**). Two parameters are shown as examples (**figure 1b**) to visualize their pedigree components with a kite diagram.

Figure 1a :

Representation of the overall parameter strength for the scored parameters (Scores <0.2 = low strength, between 0.2 and 0.4 = moderate strength, >0.4 = high strength).

Proxy : Pigs from USA, *Salmonella* Choleraesuis un-frequent in Belgium

Validation : No validation, Validation status unknown

Empirical : Aggregated data, small sample

Method : Unclear, insufficient information available to score

Proxy : Whole Belgium, good measure for the desired quantity

Validation : Data validated with private data

Empirical : Very direct and recent data

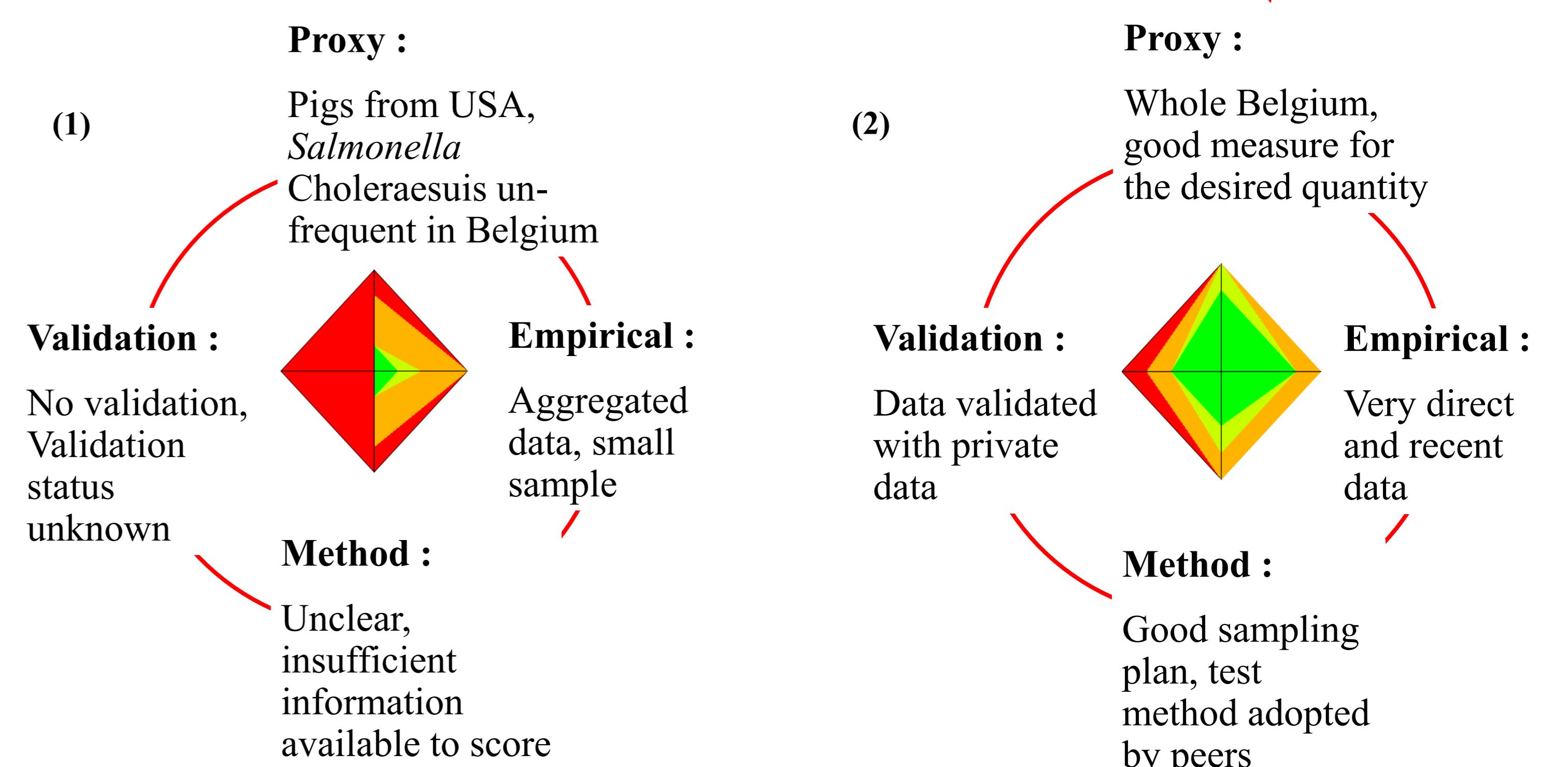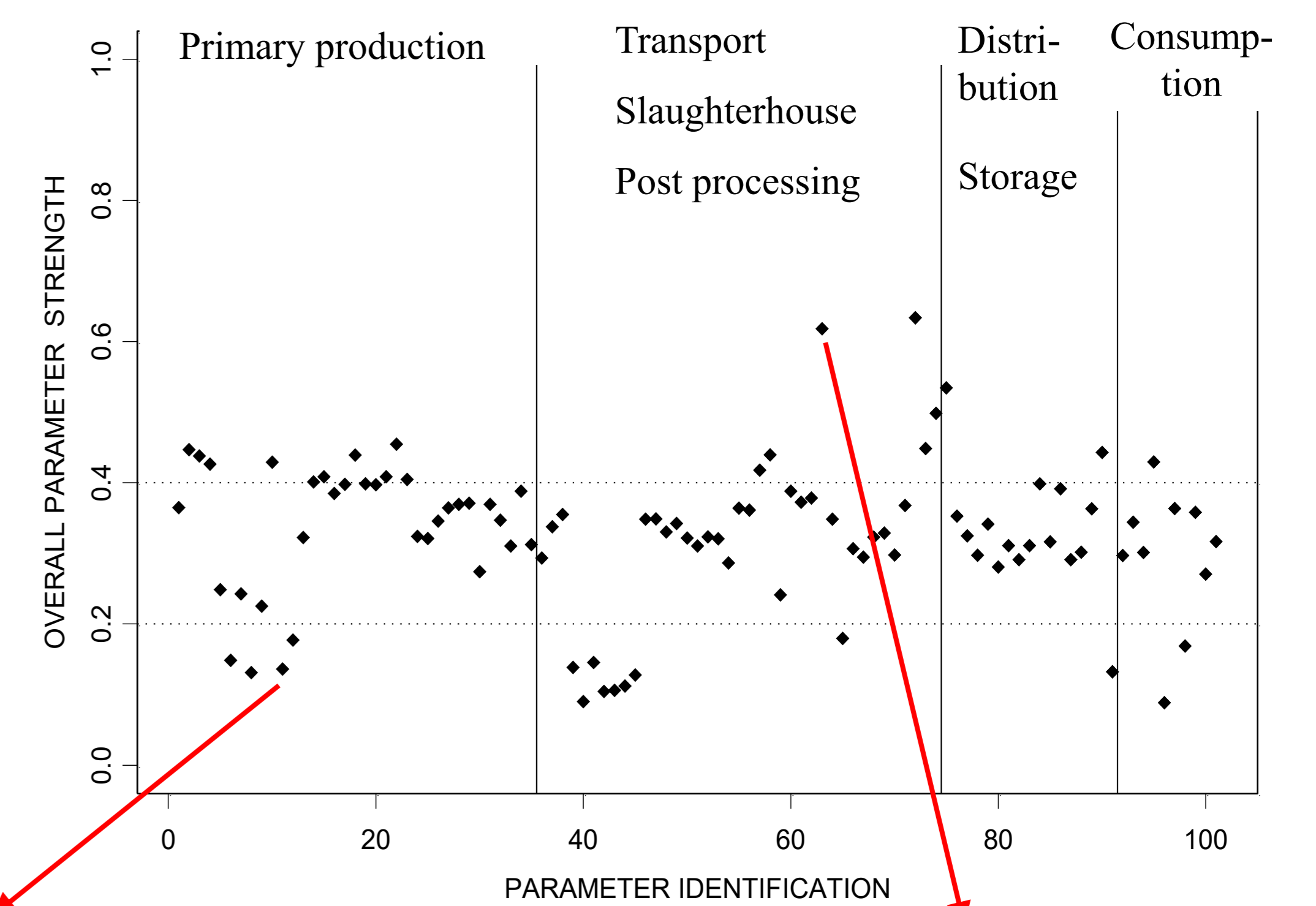**Method :** Good sampling plan, test method adopted by peers

Figure 1b : Kite diagram with the pedigree scores elicited by the group of experts
(1) Duration of shedding of *Salmonella* Typhimurium & Choleraesuis in pig,
(2) *Salmonella* prevalence in pig carcasses at the end of the slaughter line.

Expert disagreement

Maximum score

Minimum score if one outlier is removed

Minimum score
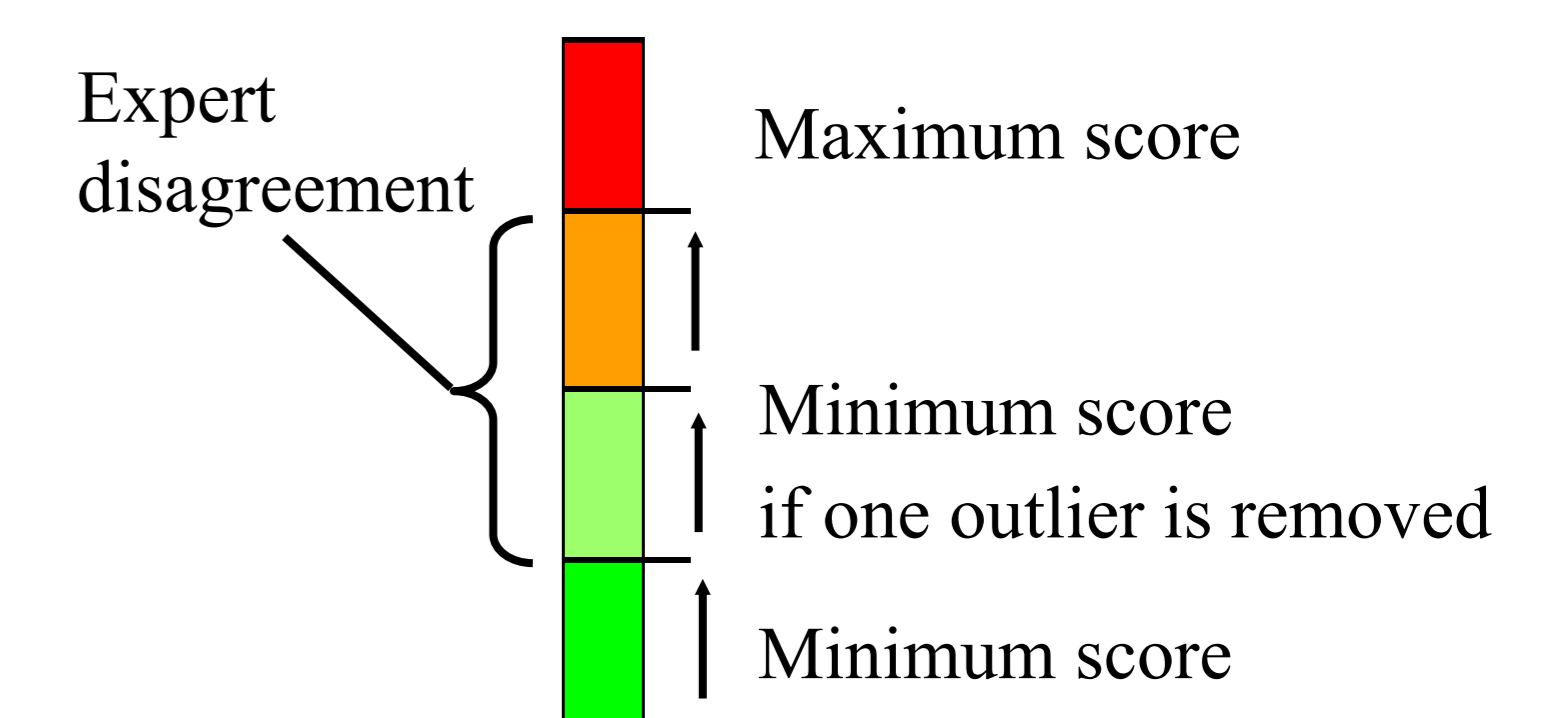
DISCUSSION AND CONCLUSION

Experts attributed mostly low scores to parameters for the validation criterion. Two explanations can be given for this: 1. parameters had not been validated, 2. experts were not sure if there had been a validation. The overall strengths of the parameters allows a quick overview of the scored parameters. The applied pedigree method allows a structured reflection on the quality of parameters used in QMRA. When several sources are available for the same parameters, the pedigree process can help in selecting the parameter with the highest strength. In a future study, the parameter strength will be combined with the results of a sensitivity analysis to produce a diagnostic diagram. Plotting both the sensitivity and the strength on this type of diagram allows the identification of critical model parameters, i.e. with a low strength and having a high contribution to the sensitivity of the output. The pedigree method improves the decision makers' confidence in the conclusion of a QMRA.

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