

Combining fuzzy querying of imprecise data and predictive microbiology using category-based reasoning for prediction of the possible microbial spoilage in foods: application to [i]Listeria monocytogen[/i]es

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1	Combining fuzzy querying of imprecise data and predictive microbiology
2	using category-based reasoning
3	for prediction of the possible microbial spoilage in foods :
4	application to Listeria monocytogenes.
5	
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8 9 10 11 12 13 14 15 16 17 18	¹ UMR INA P-G/INRA, BIA Paris 16, rue Claude Bernard 75231 Paris Cédex 5 FRANCE Tel 331 44 08 16 75, Fax 331 44 08 16 66 E-mail: Patrice.Buche@inapg.inra.fr ² Agence Française de Sécurité Sanitaire des Aliments, Laboratoire d'Etudes et de Recherches sur,l'Hygiène et la Qualité des Aliments, 39/41, rue du 11 novembre 94700 Maisons-Alfort ³ Agence Française de Sécurité Sanitaire des Aliments/Ecole Nationale Vétérinaire de Toulouse , 23 chemin des Capelles 31076 Toulouse cedex 3 * corresponding author
19	Abstract

Various predictive models of microbial behavior have been created and extensive data 20 collection has been done by numerous private or public laboratories. However, significant 21 differences between predicted and observed values in foods have been observed and need to 22 be stressed, understood and explained as much as possible. In this paper, we present a 23 software tool (currently at the level of a prototype) able : (i) to store in a database all relevant 24 information expressed on one hand as qualitative or quantitative data and on the other hand as 25 precise or imprecise data, (ii) to retrieve the more relevant information from the database 26 using queries where criteria may be expressed as fuzzy values in order to enhance the 27 flexibility of the search, (iii) to compute, in addition to the nearest data, an estimation of 28 searched values using statistical models. The architecture of this software tool is structured as 29

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Key words : Predictive microbiology, *Listeria monocytogenes*, Fuzzy logic, Information
 retrieval system

34 Introduction

Numerous factors affect microbial growth in food systems and often synergistic or antagonist interactions are significant. Thus, microbial growth in foods can be enhanced or inhibited depending on multiple food ingredients and storage conditions (Eifert et al., 1996). This can explain why an understanding of microbial behavior usually requires large-scale experiments under a wide range of conditions and involving extensive data collection.

Since data collection can be very time-consuming and labor intensive, numerous
laboratories have developed predictive growth models, especially in Australia, the U.K., the
U.S.A. and France with particular reference to *L. monocytogenes*.

L. monocytogenes has been associated in the last 15 years with several food-borne illness outbreaks involving a large range of foods such as raw milk, cheeses (particularly soft-ripened varieties), raw vegetables, fermented raw-meat sausages, raw or cooked meats. Microbial safety of many food products depends on refrigeration after commercialization, as most microorganisms do not grow at refrigeration temperatures. However this is not the case for *L. monocytogenes* because of its ability to grow at temperatures as low as 3°C (even 0.1°C and – 0.4°C (Bajard et al., 1996).

In order to evaluate food safety relating to the *Listeria* growth hazard in "chilled prepared food products", temperature, pH and water activity are the main factors that must be taken into account in predictive models (Bajard et al., 1996). Various models are able to predict lag times and growth rates of *L. monocytogenes* (or other microorganisms) in many food matrices

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at constant temperatures (Ratkowsky et al., 1983; Zwietering et al., 1991; Duh and Schaffner, 54 1993; Rosso et al., 1993; Baranyi et al., 1993) and a small number of models also do so in a 55 dynamic temperature environment (Baranyi et al., 1995; Van Impe et al., 1995; Alavi et 56 al.,1999). Most of them have improved their predictions by including other environmental 57 58 factors such as the presence of organic acids, the nature of packaging atmosphere (Buchanan and Phillips, 1990; Murphy et al., 1996; Fernandez et al., 1997) or some other biological 59 factors such as the physiological state of inoculum cells and inoculum size (Mc Kellar et al., 60 1997). 61

However, some authors have observed significant differences between predicted values and 62 observed values in foods and suggest that these differences are due to factors not taken into 63 account in existing models (Brouillaud-Delattre et al., 1997; Dalgaard and Jorgensen, 1998). 64 For example, the growth response of L. monocytogenes can be modified by the strain 65 considered (Siswanto and Richard, 1992; Begot et al., 1997), the accumulation of inhibiting 66 substances (Guinot-Thomas et al., 1995), initial contamination level (Gay et al. 1996), 67 competitive interactions (Farrag and Marth, 1989) or microstructural texture (Guerzoni et al., 68 1994; Brouillaud-Delattre et al., 1997). 69

In some cases, failure of predictive models is due to insufficient knowledge of bacterial 70 behavior in complex environments such as food matrices. However, particularly over the last 71 few years, a lot of studies have provided better knowledge of new factors that may 72 significantly influence the growth of bacteria. The main problem concerns the quality of these 73 74 data : they might be imprecise and incomplete. On the one hand, experimental results are often synthesized as intervals of values obtained with or without statistical methods, in order 75 to represent variability, then the data are imprecise. On the other hand, experimental results 76 exist only for a limited amount of substrates, then the data are incomplete, in comparison to 77 the set of substrates on which users may query. The use of an computerized logical reasoning 78

Submitted to Special Issue of the International Journal of Food Microbiology Buche, P., Dervin, C., Brouillaud-Delattre, A., Gnanou-Besse, N. (2002). Combining fuzzy querying of imprecise data and predictive microbiology using category-based reasoning for prediction of the possible microbial spoilage in foods: application to Listeria monocytogenes. International Journal of Food Microbiology, 73 (2-3), 171-185. DOI: 10.1016/S0168-1605(01)00647-X may help to manage this incomplete and potentially imprecise information (Dubois and Prade,1995).

The object of this study is to develop a "logical tool" to include the incomplete and 81 imprecise information provided by the literature in the database of a "decision support system" 82 83 for prediction of microbial risk". Previous works have already proposed such a kind of system. Zwietering et al., (1992) takes only into account the fact that information is incomplete for 84 food products. He does not propose any solution to represent and manage imprecise 85 information. Estimation is only proposed for growth phenomena using a universal model. 86 Adair and Briggs (1993) presents only the concept and main stages of a dedicated expert 87 88 system.

Our logical approach suggests a new kind of predictive response. First, we propose a 89 unified framework based on fuzzy logic and theory of possibility which permits to : (i) express 90 the user's query preferences (and therefore to control the possible enlargement process of 91 92 database scanning) (ii) represent and manage the imprecise information. Second, the system presents the ability of delivering several hierarchical responses (experimental results obtained 93 from bibliography, unpublished experimental results, ...) brought by the database with an 94 indication of the respective degree of matching for each response. Third, the system is able to 95 propose a fuzzified estimated response using predictive models stored in its knowledge base. 96 Fourth, a case based reasoning system identifies the category of queried data. This support 97 system is part of a national project on predictive microbiology in food systems. 98

The originality of our approach is demonstrated using as an example to *L. monocytogenes* in this paper. But, our method and our tool are completely independent to any particular
 bacterium and can be used whatever studied bacterium.

102 Materials and methods

In this paper, we are concerned on one hand with the storage and handling of imprecise 103 information and on the other hand with the expression of querying using fuzzy values to 104 105 retrieve the more relevant information available in the database. In the first section, we introduce the relational model chosen to structure the information in the database. In the 106 107 second section, we present the unique framework selected to represent on one hand query preferences and on the other hand precise or imprecise values. In the third section, we present 108 statistical models we use to compute estimated values delivered to the user in addition to the 109 closest information found in the database. In the fourth section, we introduce resemblance 110 relations used to retrieve the closest information stored in the database in addition to query 111 preferences. Finally, in the fifth section, we present the main concepts of the information 112 retrieval system we have designed. 113

114 Information structured using the relational model.

The relational model is the most popular model used all over the world to represent 115 information in databases. It was proposed by Codd (1970) in the early 70's and it has been 116 available as a commercial product for 20 years. It manages large quantities of data using a 117 118 DBMS - Database Management System- such as Oracle for instance as well as personal databases using a DBMS such as Microsoft Access. The basic concept is very simple : 119 elementary information is gathered in *relations* which represent *objects* of the modeled world 120 121 or *links* between these objects. The concept of relation is implemented as a table. For instance, a bacterium is an object of the world we want to model. Elementary information such as the 122 name of the bacterium, the name of the strain, its identification (unique) number in the 123 database are gathered in a table called *Bacterium* and represent the object Bacterium in the 124 database. These 3 pieces of information are called attributes of the table. A domain of values 125 is associated to each attribute. For instance, the attribute BacteriumName must be a string as 126

Submitted to Special Issue of the International Journal of Food Microbiology Buche, P., Dervin, C., Brouillaud-Delattre, A., Gnanou-Besse, N. (2002). Combining fuzzy querying of imprecise data and predictive microbiology using category-based reasoning for prediction of the possible microbial spoilage in foods: application to Listeria monocytogenes the attribute *BacteriumId* must be a positive integer. All the bacteria represented in the database are described by the values associated to these 3 attributes and are called tuples of the table *Bacterium*. Now, if we want to represent the fact that a bacterium produces a bacteriocin, we will add two new tables. The table called *Bacteriocin* will represent the object Bacteriocin. Another table will represent the semantic link between the bacterium and the bacteriocin ; this table will be called *IsProducedBy*.

The relational model is built on solid theoretical foundations and useful normalization rules 133 have been provided to help the administrator of the database to define the table structures. 134 135 But, an important drawback of the relational model is that the modeled world is split into a great number of tables and the database structure composed of a long list of tables is very 136 137 complex to understand. This is the reason why the concept of view has been introduced. A view is a *virtual* table in which all the information needed by the user is brought together. For 138 instance, we can define the view BacteriocinProducedByBacterium which brings together the 139 140 information split into the 3 tables Bacterium, Bacteriocin and IsProducedBy. Only the administrator of the database needs to know the real and entire structure of the database. A 141 user only knows the view designed by the administrator to access the data he needs. 142

143 Query preferences and imprecision representation.

The fuzzy logic theory base approach presented in Zadeh (1965) has been largely used to represent values associated to selection attributes in order to enhance query flexibility (Cox, 1995; Bosc et al., 1999). More precisely, fuzzy sets are mathematical objects here used with a semantic of preferences. For example, if one queries a database with the selection attribute Duration associated to the fuzzy value *HighDuration* (presented in fig. 1), the database engine will first retrieve information corresponding to Duration value in the interval [50, 70] and

Submitted to Special Issue of the International Journal of Food Microbiology Buche, P., Dervin, C., Brouillaud-Delattre, A., Gnanou-Besse, N. (2002). Combining fuzzy querying of imprecise data and predictive microbiology using category-based reasoning for prediction of the possible microbial spoilage in foods: application to Listeria monocytogenes. second, with a decreasing degree of preference, information corresponding to duration in the
interval [20, 50[or]70, 100].

Formally, for each element in a fuzzy set, there is a grade of membership score that represents the degree to which the element belongs to the set. These scores are assumed to vary between 0 and 1 inclusive. A 0 indicates that the element has no membership in the set and a 1 indicates that the element has complete, or crisp, membership in the set.

It is a common think to find imprecise data in the bibliography, expressed as intervals of 156 value, without any reference to the manner it has been obtained. The reason why we have 157 chosen the possibility theory is that we want to represent imprecision that is characterized by 158 an inherent vagueness (as high duration) and not uncertainty which occurs when one can 159 accurately predict the behavior of many similar experiments (Laviolette et al., 1995). The 160 161 framework of fuzzy logic restated in the possibility theory base approach presented in Zadeh (1978) has been used to represent precise or imprecise values of data and to realize fuzzy 162 163 pattern matching. A lot of works have focussed on the management of this kind of data in 164 databases (Dubois and Prade, 1995; Bosc and Pivert, 1997; Bosc and Pivert, 1998; Galindo et al., 1998). 165

Representation of precise or imprecise values on continuous or discrete domain are illustrated 166 here with 3 examples. In Figure 1, the fuzzy set *HighDuration* represents an imprecise value : 167 the duration is completely possible in the interval 50-70 seconds, but it is still possible with a 168 169 decreasing degree of possibility until the interval 20-100 seconds. Figure 2 illustrates the 170 imprecise value *SterilizedMilk* which can be whole sterilized milk with a degree of possibility of 1 and which may be also skimmed sterilized milk with a degree of possibility of 0.5. The 171 figure 3 shows that the same framework may also represent a precise value (here the precise 172 value 80 seconds for the attribute Duration), it may be used to represent both kinds of 173 174 information (precise or imprecise).

More formally, the value associated to an attribute *A* for a tuple *t* is defined as a possibility distribution $\pi_{A(t)}$ on the underlying domain *D*. The possibility distribution $\pi_{A(t)}$ can be viewed as a fuzzy restriction of the possible value of A(t) by a fuzzy subset *F*. Given χ the membership function associated to *F*:

$$\begin{cases} \forall d \in D, \, \chi_F(d) \in [0,1] \\ \pi_{A(t)}(d) = \chi_F(d) \,. \end{cases}$$
⁽¹⁾

For instance, the information *« thermisation t has a high duration »* will be represented by: $\pi_{Duration(t)}(d) = \chi_{HighDuration}(d)$. Here, $\chi_{HighDuration}$ is a membership function which represents the vague predicate *HighDuration* defined as a fuzzy subset. We consider two kinds of membership functions depending on the domain : *(i)* on an ordered and continuous underlying domain, a trapezoidal fuzzy subset is associated to each value (see fig. 1), *(ii)* on a discrete and non ordered domain, a standard fuzzy subset is associated to each value (see fig. 2).

185 Statistical models

186 Two types of models are used in order to give an estimation of the data sought. The first one 187 concerns growth model and the second one inactivation model.

The growth model comes from a bacterial growth simulation model with two levels (Rosso et 188 al., 1993). Primary level model F (adaptive model) describes how microbial density x changes 189 with time t in a specified environment $x(t)=F(p_i, t)$ where p_i are at most 6 characteristic 190 parameters (maximum growth rate μ_{max} or generation time $t_g = ln2/\mu_{max}$, lag phase duration λ , 191 inoculum x_0 , maximal density x_{max} , and eventually initial growth rate μ_0 , adaptation rate ρ_a). 192 Secondary level models indicate how parameters μ_{max} and λ of primary model change with 193 respect to cardinal values (maximum, minimum and optimal) of temperature T and of pH and 194 a fourth parameter μ_{opt} (value of μ at optimal temperature and optimal pH). With this model we 195

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are able to give a fuzzy estimation of the parameter μ_{max} (or the generation time t_g) using fuzzy arithmetic (Pedrycz and Gomide, 1998, pp129-150).

Inactivation models (Augustin, 1996) used are linear models : primary modeling is a linear 198 relation between log_{10} (cell population N) and time $t : log_{10}(N) = at+b$, allowing us to define 199 D=1/a, time of decimal reduction. Then a linear regression of $log_{10}(D)$ on the temperature T: 200 $log_{10}(D) = cT + d$, is calculated from numerous data found in the literature. This model allows us 201 to calculate the estimation of the duration D for a given temperature value and moreover to 202 203 calculate a fuzzy estimation of it. This calculus takes into account two kinds of variability : the limits of the fuzzy subset representing the user's preferences and the confidence interval 204 on the coefficients of the regression model (Buche and Dervin, 1999). 205

Two conditions must be fulfilled to obtain a fuzzy estimation using those both models : *(i)* values for each model parameter must be expressed in the selection attributes (for example, temperature and pH for the selected growth model and temperature for the selected inactivation model) ; *(ii)* values associated to each attribute expressed as fuzzy subset must be included in the limits of the model. If the second condition is not fulfilled, we deliver a precise estimation using precise values for model parameters (defined as the center of the 'core of the trapezoidal fuzzy subsets).

However, our method is not dependent on those previous models because : first, our system incorporates in its knowledge base predictive models which can be replaced or enhanced if necessary; second, different models may be used for different categories of data (see section The Information Retrieval System for more details).

217 **Resemblance relations**

¹ Defined as the set of values where the membership function is equal to 1

If no information stored in the database corresponds to the values specified for the selection attributes, it is still possible to retrieve the closest information if resemblance relations have been defined. Resemblance relations res_i are defined on the domain D_i of an attribute *i* which belongs to the query. Given a distance d_i on the domain D_i , the resemblance relations between *x* and *y* are defined as follows:

$$\begin{cases} res_i: D_i \times D_i \to [0,1] \\ \forall (x,y) \in D_i \times D_i, res_i(x,y) = \frac{1}{1 + d_i(x,y)}. \end{cases}$$
(2)

223 We have defined two kinds of distance d_i :

for biological qualitative information (e.g., substrates or serotypes), called concepts in 224 (i) defined 225 the following, we have а semantic distance d_i computed in 226 generalization/specialization trees, called GS trees. A GS tree is defined as follows : concept C_1 is the father of C_2 (i.e. C_1 is above C_2 in the tree) if C_1 is more general than C_2 (C_2 is more 227 specific than C_1). An example of GS tree is given in Fig. 4, representing the distance 228 associated to the attribute Substrate. We drew upon the work of (Foo et al., 1989) to build a 229 semantic distance function on GS trees. Given two concepts C_1 and C_2 , we consider C_3 , the 230 more specific concept which generalizes C_1 and C_2 ; then the semantic distance $d_i(C_1, C_2)$ is 231 equal to $d_i(C_1, C_3) + d_i(C_2, C_3)$. By example, in the fig.4, the distance between concepts 232 Skimmed milk and Whole milk is 2 (d_i (Skimmed milk, Sterilized Milk) + d_i (Whole Milk, 233 Sterilized Milk) = 1 + 1 = 2) and the distance between Skimmed milk and Raw milk is 4 (d_i) 234 (Skimmed milk, Milk) + d_i (Raw Milk, Milk) = 3 + 1 = 4). 235

(ii) for information defined on an ordered domain, we have defined a distance d_i between 237 two values x and y of an attribute i, as follows : given an increasing ordered series of values Δ_n ($\Delta_n < \Delta_{n+1}$) on the domain D_i associated to increasing numerical values α_n , d_i (x,y) = α_n *where* α_n *is the value associated to* Δ_n *such as* $\Delta_n \leq |x-y| < \Delta_{n+1}$ By example, the following values α_n may be associated to the values Δ_n on the domain D_i of

the attribute Temperature

n	1	2	3	4	
Δ_{n}	0	1	3	5	
α_n	0	1	2	3	

- 242 Then for values 2,3,7 of attribute Temperature
- 243 d_{température}(2, 3) = 1 because $\Delta_2 \leq |2-3| < \Delta_3$
- 244 $d_{\text{température}}(3, 7) = 2 \text{ because } \Delta_3 \leq |3-7| < \Delta_4$

245 The information retrieval system

Using a graphical user interface called GUI in the following (see fig 7), the user queries the database specifying selection criteria using the form attribute/value. The value associated to each selection attribute is a fuzzy subset. It represents the user's preferences. Result attributes are the closest values retrieved from the database for the selection attributes and specific attributes depending on the view through which the query is executed.

The system scans the database through the different views available in its knowledge base and 251 252 retrieves the results associating an adequation degree to each of them. More precisely, the GUI translates and submits to the engine the user's preferences as a set of queries Q_V . For each 253 available view V, the syntax of Q_V is a set $\{V, a_1, \ldots, a_n, \langle a_{n+1}, v_{n+1}, r_{n+1}, ft_{n+1} \rangle, \ldots, \langle a_m, v_m, v_n \rangle$ 254 r_m , ft_m>, nb, t} where V is the name of the view through which the query is executed; a_1, \ldots, a_n 255 are the expected attributes (limited to 1 in the examples), $\langle a_{n+1}, v_{n+1}, r_{n+1}, ft_{n+1} \rangle$,..., $\langle a_m, v_m, v_n \rangle$ 256 r_m, ft_m> are quadruplets defining the selection criteria, nb and t define respectively the 257 maximum number of tuples and the minimum degree of matching of each tuple in the result (t 258 in [0, 1]). The quadruplets defining the selection criteria have the following meaning: 259

260 For all i in [n+1, m]:

- a_i is a selection attribute and v_i is a fuzzy set defining the value associated with a_i. We
 distinguish two kinds of labels depending on the underlying domain of the attribute :
 discrete or continuous. Two examples of fuzzy sets are given in fig 1 and fig 2.
- r_i is a boolean value specifying to the engine whether the ressemblance relations available in the engine knownledge base may be used or not.
- ft_i is a boolean value specifying to the engine whether the users' preferences expressed in the fuzzy sets may be enlarged or not.
- 268 For instance, we consider the following query Q_{ex} :
- 269 *V=HeatResistance*
- 270 $a_1 = DecimalReductionTime$,
- 271 $\langle a_2 = Substrate, v_2 = MyEggProductPreferences$, $r_2 = true, ft_2 = false \rangle$,
- 272 $\langle a_3 = DecimalReductionTime, v_3 = HighDuration, r_3 = false, ft_3 = true \rangle$
- 273 nb = 40, t = 0.3

The value represented by the fuzzy subset $MyEggProductPreferences = \{(egg yolk, 1), \}$ 274 (whole egg, 0.5) indicates that the user is first interested by information about egg yolk and 275 second by whole egg. The definition of the fuzzy set is made by the user using the GUI. This 276 is the first way to enlarge the query, completely controlled by the user. The second way of 277 278 enlargement is also controlled by the user : he may activate or desactivate the automatic enlargement based on the set of resemblance relations defined in the previous section and 279 stored in the knowledge base of the engine. The boolean value r_i , specified in the above 280 quadruplet definition, permits to control this mecanism. In the above example Q_{ex} , $(r_2 = true)$ 281 the engine is authorized to realize enlargement using the resemblance relation defined on the 282 domain of values of the attribute Substrate. The third way of enlargement is also controlled 283 by the user : he may activate or desactivate the automatic enlargement of his preferences based 284 on fuzzy tolerance coefficients defined in the knowledge base of the engine for each category 285

of data. The boolean value ft_i , specified in the above quadruplet definition, permits to control this mecanism. In the above example Q_{ex} , ($ft_3 = true$) the engine is authorized to realize enlargement on the user's preferences represented by the fuzzy set *HighDuration* for the attribute *DecimalReductionTime*.

290 In the running version of the system prototype, the selection attributes available for each view are substrate, conditions of the process step (temperature and pH) and bacterium. For the 291 moment, views available concern growth, heat resistance (inactivation) and bacteriocin 292 interaction. In this information retrieval system, we have introduced the new concept of 293 category-based fuzzy view (Buche and Loiseau, 1999; Buche and Dervin, 1999). This notion 294 is an extension of the classical view concept in databases, e.g. a virtual table in which all the 295 information needed by the user is brought together. This view is fuzzy because the selection 296 attributes are expressed as fuzzy predicates as in (Galindo et al., 1998; Zadrozny and 297 Kacprzyk, 1998). This view is category-based because the system identifies the category of 298 299 queried information (defined in the information retrieval system knowledge base). Three 300 advantages are provided by this category-based reasoning system implemented in the category-based fuzzy view. First, if the user authorized it, the view engine enlarges user's 301 preferences expressed in his query if they are too restrictive due to the real content of the 302 database: it provides an additional degree of flexibility not available in the previous systems. 303 Second, the view engine is able to propose, in addition to the nearest information retrieved 304 from the database, an estimation of the data sought. For this purpose, statistical models well-305 306 adapted to each category of data (choice of the model and associated parameters) are incorporated into the knowledge base of the engine. Third, the view engine optimizes the 307 fuzzy matching processing because the user's preferences are only compared to the 308 information associated to the category selected : in the previous systems, all the information 309 stored in the queried tables are compared to the user's preferences. 310

Adequation between, on one hand, sought values and their category definition and, on the other hand, sought values and values from the database are computed using pattern matching techniques presented in (Dubois and Prade, 1995) and fuzzy object comparison measures proposed in (Bosc and Pivert, 1997). A detailed description of the engine processing can be find in (Buche and Loiseau, 1999).

We have implemented the concept of category-based fuzzy view in a prototype called CFQ 316 (for Category-based Fuzzy Querying). This software is written in Java language. Thus, CFQ is 317 available on the Web. The information is stored in an Oracle DBMS using the imprecision 318 representation model of FSQL (Galindo et al., 1998). A CFQ query is executed using a three 319 tier process architecture (see fig 8): (i) the CFQ Java client applet running under a usual Web 320 browser, (ii) a database connectivity middleware (running on the Web server due to security 321 checking on applet execution), (iii) an Oracle/FSQL database server. First, the user loads the 322 CFQ engine applet from the Web server on his Web browser. Second, he expresses his 323 preferences using the GUI of CFQ and asks for information scanning. Third, the GUI tranfers 324 the user's query to the CFQ engine. The engine identifies the queried category of data and 325 builds the fuzzy filter. To retrieve the closest tuples stored in the database, the engine submits 326 SQL queries to the Oracle database server through the Web server. 327

328 **Results**

In this section, we present four results provided by our system CFQ corresponding to four different examples of queries. Each query illustrates functionalities provided by the system : in example 1, automatic category-based enlargement of data sought by the user to take into account variability of data values stored in the database ; in the second and third examples, comparison between estimated values and closest experimental values retrieved from the database may provide on one hand a validation of the estimation or on the other hand important differences which need to be explained by a sound bibliographical analysis; in thefourth example, proposal of values unknown by the user but essential to obtain an estimation.

The first example is about the behavior of L. monocytogenes in egg products under 337 inactivation conditions. It is a sort of process validation query. The user specifies as querying 338 339 attributes, substrate, temperature conditions and decimal reduction time of his process and wants to compare it to the decimal reduction time values stored in the database. Values sought 340 for decimal reduction time are represented by the fuzzy set *HighDuration* (see fig 1). Values 341 sought for temperature are in the interval [60, 64]. Values sought for substrates are 342 represented by the following fuzzy set called *MyEggProductPreferences*={(egg yolk, 1), 343 (whole egg, 0.5). It means that the user is first interested by information about egg yolk and 344 second by information about whole egg. The 3 views available in the system are executed and 345 only the view HeatResistance provides results (with a adequation degree superior to a 346 threshold, set arbitrarily to 0.3). The syntax of the query Q generated by the GUI 347 corresponding to the view *HeatResistance* is the following : 348

349 $Q = \{V = HeatResistance, a_1 = DecimalReductionTime, \}$

350 $\langle a_2 = Substrate, v_2 = MyEggProductPreferences$, $r_2 = true, ft_2 = false \rangle$,

351 $\langle a_3 = DecimalReductionTime, v_3 = HighDuration, r_3 = true, ft_3 = true \rangle$

352 , nb = 40, t = 0.3

In this view, the system has determined that the category of queried data is *Egg Product*. For this category, the system has found in its knowledge base an enlargement coefficient (called fuzzy tolerance coefficient) for the selection attribute DecimalReductionTime. Fig. 5 shows user's preferences enlargement for this selection attribute. The values sought for decimal reduction time are compared to the values stored in the database which are represented as imprecise values defined by the interval given by the two attributes *Duration Min* and *Duration Max*. Table 2 shows results obtained without or with enlargement of preferences

computed for the decimal reduction time attribute. The first five tuples appear in the two 360 query results. An additional tuple is provided in the second result set thanks to the 361 enlargement mechanism even if the threshold set on the adequation degree is the same for the 362 two queries (set arbitrarily to 0.3 as said previously). This additional datum concerns a 363 364 substrate which does not belong to the user's preferences expressed by MyEggProductPreferences. Therefore, it has been retrieved thanks to the fuzzy resemblance 365 relation defined on the domain of values associated to the attribute Substrate and thanks to the 366 category-based enlargement mechanism adapted to the category EggProduct. In the context of 367 this example, it may be a relevant piece of information which indicates that the addition of salt 368 or sugar to eggs provides a high increase in the decimal reduction time. 369

The second example is about the behavior of L. monocytogenes in dairy products under 370 growth conditions. The user wants to retrieve the generation time and queries on substrate, 371 temperature and pH attributes. Values sought are the following : for substrate, the fuzzy set 372 MyDairyProductPreferences is {(Sterilized milk, 1)} which means that user queries sterilized 373 milk only; for temperature, the fuzzy set MyTemperaturePreferences is the interval [2.2, 2.8] 374 ; for the pH, the fuzzy set *MypHPreferences* is the precise value 6.6. The 3 views available in 375 the system are executed and only the view *Growth* provides results. The syntax of the query 376 Q generated by the GUI corresponding to the view *Growth* is the following : 377

- 378 $Q = \{V = Growth, a_1 = GenerationTime,$
- 379 $\langle a_2 = Substrate, v_2 = MyDairyProductPreferences, r_2 = true, ft_2 = false \rangle$,
- 380 $\langle a_3 = Temperature, v_3 = MyTemperaturePreferences, r_3 = true, ft_3 = false \rangle$,
- 381 $\langle a_4 = pH, v4 = MypHPreferences, r_4 = true, ft_4 = false \rangle$
- 382 , nb = 40, t = 0.3

In this case, the system CFQ is able to compute a fuzzified estimation thanks to the statistical growth model stored in the system knowledge base for the queried category *Dairy Product*. The generation time estimation (in hours) computed with the sought values is the interval [66.18, 105.27]. Simultaneously, CFQ system retrieves the closest experimental data stored in the database (see table 3). The closest experimental value retrieved from the database (identified by number 33) is out of the estimated interval of values (duration = 28.5 hours). This value has been published in Walker et al. (1990), this bibliographical reference may also be provided by the querying system. In this case, this experimental value tends to invalidate the estimation.

The third example is about the behavior of L. monocytogenes in dairy products under 392 inactivation conditions. The user queries using substrate and temperature as selection 393 attributes. Values sought the following : for substrate, 394 are the fuzzy set *MyDairyProductPreferences* is {(Raw milk, 1)}; for temperature, the value is defined by the 395 fuzzy set ImpreciseTemperature (see fig. 6). The 3 views available in the system are executed 396 and only the view *HeatResistance* (due essentially to the temperature values) provides results. 397 398 The syntax of the query Q generated by the GUI corresponding to the view *HeatResistance* is 399 the following :

400
$$Q = \{V = HeatResistance, a_1 = DecimalReductionTime,$$

401 $\langle a_2 = Substrate, v_2 = MyDairyProductPreferences, r_2 = true, ft_2 = false \rangle$,

402 $\langle a_3 = Temperature, v_3 = ImpreciseTemperature, r_3 = true, ft_3 = false \rangle$

As in the previous example, the CFQ system is also able to compute a fuzzified estimation thanks to the statistical inactivation model stored in its knowledge base for the category of queried data, here Dairy Products. The fuzzy kernel (values with a membership degree equal to 1) of the estimated decimal reduction time (expressed in seconds) is the interval [4.83, 287.18]. The fuzzy support (values with a membership degree > 0) of the estimated decimal reduction time is the interval [1.99, 697.99]. Most experimental values retrieved from the

^{403 ,} nb = 40, t = 0.3

database (see table 4) are included in the fuzzy estimation support. Only one experimental
value (ID = 8 in table 4) is far from the kernel (but still belongs to the support). Therefore, the
great majority of experimental values confirm the estimation.

The fourth example is about the behavior of *L. monocytogenes* in meat products under growth conditions. In this case, we suppose that the user only knows the values for the substrate and the temperature. He has no idea about the value of the pH. It is then possible to use the CFQ system to perform an initial screening to retrieve possible values for the unknown parameter (here the pH) and a second scan to obtain simultaneously an estimated value of the growth (which can be computed only if temperature and pH are simultaneously provided in the query) and a comparison with the closest experimental values.

For instance, in the first query, values sought are the following : for substrate, the fuzzy set MyMeatProductPreferences is {(Cuts of beef, 1)}; for temperature, the fuzzy set MyTemperaturePreferences is the precise value 4°C. The 3 views available in the system are executed and only the view *Growth* provides results (due to the temperature values). The syntax of the query Q generated by the GUI corresponding to the view *Growth* is the following :

426
$$Q = \{V = Growth, a_1 = pH, a_2 = GenerationTime\}$$

427 $\langle a_3 = Substrate, v_3 = MyMeatProductPreferences, r_3 = true, ft_3 = false \rangle$,

428 $\langle a_4 = Temperature, v_4 = MyTemperaturePreferences, r_4 = true, ft_4 = false \rangle$,

429 ,
$$nb = 40, t = 0.3$$

The results of the interrogation are given in table 5. In the entire set of experiments, the pH is included in the interval [5.5, 6.7]. In the second query, the user considers the same values for substrate and temperature and adds the first screening for the pH value, i.e. the fuzzy set

Submitted to Special Issue of the International Journal of Food Microbiology Buche, P., Dervin, C., Brouillaud-Delattre, A., Gnanou-Besse, N. (2002). Combining fuzzy 433 *MypHPreferences* corresponding to the interval [5.5, 6.7].). The syntax of the query Q434 generated by the GUI corresponding to the view *Growth* is the following :

435 $Q = \{V = Growth, a_1 = GenerationTime,$

436 $\langle a_2 = Substrate, v_2 = MyMeatProductPreferences, r_2 = true, ft_2 = false \rangle$,

437 $\langle a_3 = Temperature, v_3 = MyTemperaturePreferences, r_3 = true, ft_3 = false \rangle$,

438
$$< a_4 = pH, v4 = MypHPreferences, r_4 = true, ft_4 = false >$$

439 ,
$$nb = 40$$
, $t = 0.3$

The estimated generation time (expressed in hours) obtained during the second screening is the interval [6.38, 76.3]. The closest set of experimental values is identical to the one obtained in the first screening.

443 **Discussion**

One of the great difficulties in predicting microbial behavior in complex food matrix concerns 444 the fact that we have to take into account the variability of biological systems (bacteria and 445 food matrices) in a large range of environmental conditions (experimental or industrial 446 447 conditions). Moreover, in most cases, we are not able to determine all of the factors that could interfere with the bacterial response. First, quantification cannot be done precisely (chemical 448 449 or physical gradients are not easy to establish), second, we do not always know the influence of one factor (ingredient, other bacteria, physical conditions, etc.) on bacterial behavior. For 450 example, the ability of L. monocytogenes to grow in many food products is mainly evaluated 451 with regards to a small number of factors such as temperature, pH, etc. Nevertheless, other 452 factors (physiological, biological or other physical factors) could significantly modify the 453 growth response of L. monocytogenes. Because our knowledge in microbiology and 454 particularly in microbial ecology is growing, predictive microbiology models will be able to 455 take into account this new information in order to improve prediction. This new knowledge is 456 incomplete and/or can be imprecise. Our information retrieval system allows us to take into 457

account these data that can (*i*) modulate or specify the prediction obtained with mathematical
models or (*ii*) can propose a response when mathematical models have failed to calculate
growth or inactivation parameters.

We have also to mention two main drawbacks the user will have to manage with this new 461 462 querying approach. First, the adequation degree of a retrieved information may be the combining result of three different enlargement mechanisms (user's preferences expression, 463 category-based enlargement of user's preferences, enlargement by resemblance relation 464 definition on the domain of values). Then, it is not easy to explain to the user how it has been 465 computed by the system. Second, the user has to be careful if he realizes comparisons between 466 closest experimental data retrieved from the database and fuzzy estimation using statistical 467 models. He has to check that retrieved experimental data are close enough compared to his 468 selection criteria, knowing that the adequation degree only provides a relative ranking of 469 retrieved information. For instance, in the result of the second query presented in the previous 470 section, only the first closest information (ID 33) checks completely the selection criteria and 471 472 can be really used to be compared to the fuzzified estimation.

473 Conclusion

474 In this paper, we have introduced the concept of category-based fuzzy view to design an information retrieval system adapted to microbial risk analysis of food products. In the query, 475 the user has to specify his fuzzy preferences. Then the CFQ engine scans the database through 476 the views available in its knowledge base. For each view, the engine builds a fuzzy filter with 477 478 the user preferences adapted to the category of queried data - thanks to knowledge associated to each category. It brings three benefits : (i) The CFQ engine optimizes the processing time 479 of the filtering because it only scans the data associated to the selected category; (ii) the CFQ 480 engine can deliver an estimate of the queried data if an estimation method has been defined 481 for the selected category of data; (iii) the CFQ engine can enlarge users' preferences to adapt 482

them to the real content of the database. The CFQ engine has been developed in Java language. Therefore, the information retrieval system is available through the WEB. It has been coupled to Oracle extended for fuzzy SQL (Buche and Loiseau, 1999; Buche and Dervin, 1999). CFQ is complementary with classical simulation software because :

487 - It can be used when classical software does not work; for example when parameters are
488 outside the limits of the model.

It allows fuzzy expression of the parameters (selection attribute values) and takes into
 account this imprecision in the database scan and in the calculation of the estimated
 values.

It allows comparison between estimated and experimental data, underlining possible
 contradictions and then acting as a basic tool to understand unknown phenomena.

494 - It may provide information on an original domain, such as interaction between bacteria.

495 - It produces synthesized information, and provides bibliographical references to the
 496 corresponding publications.

497 - It is a flexible tool able to evolve by incorporating new experimental results and/or new
498 simulation models.

In order to improve this information retrieval system, it is now necessary to add data that come from more complete bibliography references. In the future, the database will have to integrate other pathogens in order to carry out a better microbial prediction of food products, predictive microbiology being an interesting tool for risk analysis..

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Figure 1. A trapezoidal fuzzy subset representing an imprecise value

(MD stands for Membership function)

Discrete domain Sterilized milk



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Version postprint

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MD

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Figure 5. Enlargement mechanism of the user's preferences using fuzzy tolerance coefficient for the category EggProduct (first example of query)



Figure 6. Temperature value for the third query

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650 Figure 7. The Graphical User Interface permits to express the selection criteria of a query and to 651 display the results. It is organized as a thumbnail formular. In the above example, the selected thumbnail 652 shows the value (expressed as a fuzzy set) associated by the user to the attribute temperature.

653

654



Figure 8. Category-based Fuzzy Querying engine is a software based on a three tier architecture : the
 Java applet is available on the Web server, the Java applet is loaded on the client to run in the Web
 browser, the CFQ engine running in the client applet queries the database through the Web server to
 retrieve the closest information



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Table 1. View BacteriocinProducedByBacterium

BACTERIOCIN	BACTERIUM	STRAIN
NAME	NAME	NAME
Pediocin ACH	Lactobacillus	WHE92
	Plantarum	
Pediocin ACH	Pediococcus	Н
	Acidilacti	

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670	Table 2. Closest data retrieved through the view Heat Resistance corresponding to the first query without
671	enlargement of preferences (Adequation Degree (AD) > 0.3) are the first five tuples. With enlargement of
672	preferences, same first five tuples are obtained plus the additionnal sixth tuple.
673	

ID	AD	SUBSTRATE	TEMP (°C)	DURATION MIN (Sec)	DURATION MAX (Sec)
80	0.905	egg yolk	60	55.2	101.4
82	0.905	egg yolk	60	55.2	101.4
85	0.786	egg yolk	64.4	26.4	26.4
78	0.5	whole egg	60	78	84
81	0.5	whole egg	60	90	126
86	0.319	egg +	64.4	366.6	366.6
		salt or sugar			

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Submitted to Special Issue of the International Journal of Food Microbiology Buche, P., Dervin, C., Brouillaud-Delattre, A., Gnanou-Besse, N. (2002). Combining fuzzy querying of imprecise data and predictive microbiology using category-based reasoning for prediction of the possible microbial spoilage in foods: application to Listeria monocytogenes. International Journal of Food Microbiology, 73 (2-3), 171-185. DOI : 10.1016/S0168-1605(01)00647-X

		× ×		0 /	
ID	AD	SUBSTRAT	TEMP	PH	GENERATION TIME (hours)
33	0.76	Sterilized_milk_(UHT)	2.5	6.6	28.5
4	0.35	Skimmed_milk	4	6.4	32.5
7	0.35	Skimmed_milk	4	6.4	30.6
10	0.35	Skimmed_milk	4	6.4	37.5
13	0.35	Skimmed_milk	4	6.4	38
16	0.35	Skimmed_milk	4	6.6	48.9
17	0.35	Skimmed_milk	4	6.6	53.5
20	0.35	Sterilized_whole_milk	4	6.4	30.6
23	0.35	Sterilized_whole_milk	4	6.4	30.5
26	0.35	Sterilized_whole_milk	4	6.4	36
29	0.35	Sterilized_whole_milk	4	6.4	36.5

Table 3. Closest data retrieved through the view Growth corresponding to the second query (AD means Adequation Degree)

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Table 4. Closest experimental values for the third query (AD means Adequation Degree)

ID	AD	SUBSTRATE	TEMP	DURATION	DURATION
				MIN	MAX
	0.70			(Sec)	(sec)
9	0.76	Raw_milk	63.3	19.8	19.8
8	0.5	Milk	61.7	570	570
11	0.2	Raw_milk	71.7	1.6	1.6
12	0.2	Raw_milk	71.7	1.9	1.9
13	0.2	Skimmed_milk	62.7	54	54
14	0.2	Sterilized_whole_milk	62.7	60	60
15	0.2	Half_skimmed_milk	62.7	54	54
16	0.2	Half_skimmed_milk	62	6	24
17	0.2	Half_skimmed_milk	62	6	24
18	0.2	Sterilized_whole_milk	63.3	19.8	34.8
19	0.2	Skimmed_milk	63.3	25.8	28.2
21	0.2	Sterilized_whole_milk	71.7	3.1	3.1
22	0.2	Sterilized_whole_milk	71.7	5	5
23	0.2	Half_skimmed_milk	72	0.05	1.5
24	0.2	Half_skimmed_milk	72	0.02	1.4
25	0.2	Sterilized_whole_milk	71.7	2.7	2.7
26	0.2	Sterilized_whole_milk	71.7	1.3	1.3
27	0.2	Sterilized_whole_milk	71.7	0.7	0.7
28	0.2	Sterilized_whole_milk	71.7	2	2
29	0.2	Sterilized_whole_milk	71.7	1.4	1.4
30	0.2	Sterilized_whole_milk	71.7	0.6	0.6
31	0.2	Sterilized_whole_milk	71.7	1.2	1.2
32	0.2	Pasteurized_whole_milk	57.8	138	138

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690			Table 5. Closest experiment	al values for the	e fourth	query		
691 692 693		(AD means Adequation Degree)						
	ID	AD	SUBSTRATE	TEMP	PH	GENERATION TIME (hours)		
	86	0.58	Cuts_of_fat_beef	4.7	5.6	11.9		
	81	0.5	Cuts_of_lean_beef	5	6.3	17.1		
	79	0.4	Cuts_of_lean_beef	5.5	5.5	22.1		
	77	0.38	Cuts_of_lean_beef	5.6	5.6	22.9		
	87	0.24	Cuts_of_fat_beef	7.5	5.6	7.1		
	85	0.21	Cuts_of_lean_beef	10	6.7	4.08		

10.1

5.6

4.62

Cuts_of_fat_beef

694

88

0.20

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