

Development of an Internet-based data explorer for a samples databases: the example of the STRATFEED project

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A key aspect of the European STRATFEED project on developing and validating analytical methods to detect animal meal in feed was the creation of a samples bank. To manage the 2,500 samples that were stored in the samples bank, another important objective was to build a database and develop an Internet-based data explorer – the STRATFEED explorer – to enable all laboratories and manufacturers working in the feed sector to make use of the database. The concept developed for the STRATFEED project could be used for samples management in other projects and it is easily adapted to meet a variety of requirements. The STRATFEED explorer can now be run from the public website <http://stratfeed.cra.wallonie.be>. Each webpage of this application is described in a documentation file aimed at helping the user to explore the database.

Keywords. Samples databases, Internet, computer systems (applications), data explorer.

1. INTRODUCTION

The creation of a samples bank was a key aspect of the European STRATFEED project (Dardenne *et al.*, 2004) implemented to develop and validate analytical methods for detecting animal meal in feed (Gizzi *et al.*, 2003): classical microscopy (EC, 1998b; Frick *et al.*, 2002), molecular biology (polymerase chain reaction [PCR]) (Berben *et al.*, 2000), and near-infrared technology (NIR) (Baeten *et al.*, 2004; Dardenne, Baeten, 2001; Perez-Marin *et al.*, 2003). Unlike the work done on gene banks, the research on feed banks has been quite limited (Garrido-Varo *et al.*, 2004). Nevertheless, during the past 20 years, with the increasing amount of data and the advances in computer and software technology, databases on the chemical composition and nutritional value of feed have been widely developed throughout Europe (Lapierre, 2004). In the 1990s, the European Union (EU) initiated and coordinated activities to harmonize the comprehensive information on animal feed and nutrition (ENFIC, 2001). The samples bank and the database built within the framework of the STRATFEED project focused in gathering samples and analytical data on feed contaminated (or not) with animal tissue. To manage the 2,500 samples of pure animal ingredients, and pure or spiked feeds stored in the samples bank, a second

key aspect of the project was to build a database to gather and store all the data so as to ensure the easy retrieval of specific data *via* the applications. The formulae of the samples in the bank are described following the EC guidelines in the Commission Directive 98/67/EC, which amended Council Directive 96/25/EC (EC, 1998a). The STRATFEED manager, a management tool, is used by the database administrator to incorporate data and update the database. It provides forms to input data, and reports to check data (Vermeulen *et al.*, 2003).

In order to enhance the use of the database, now a major source of descriptive and analytical information on feed samples contaminated (or not) with animal tissue, an Internet-based data explorer, described in this paper, was developed to enable all laboratories and manufacturers working in the feed sector to make use of the database.

2. CONCEPT

The STRATFEED explorer provides users with tools to explore the database via queries. The development of these tools was based on client-server architecture using the Internet to provide the link between the two sides, the client and the server (**Figure 1**). The client side supports the user interface, which is a web

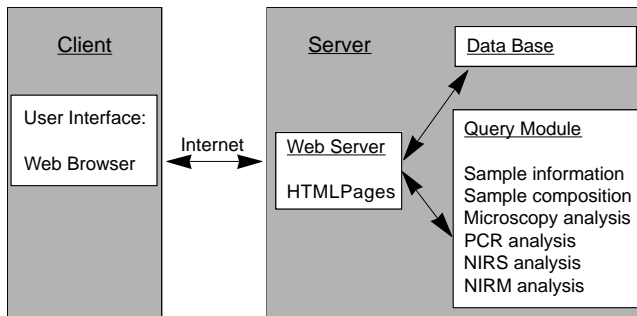


Figure 1. The Internet-based architecture of the STRATFEED explorer.

browser (Internet Explorer or Netscape). The server side supports the web server, the database and the query tools. The query module receives the request selected or formulated by the client (HTML pages), accesses the relevant material in the database and sends the answer to the client via the web server software and an Internet protocol. The MS Access platform was selected to operate the database and to manage numbers, texts, figures and files. In order to have maximum flexibility for development, updating and dissemination, tables were created to suit each of the methods studied in the project. The query tool was built within a development environment (Cold fusion web application server) that enables the user to create dynamic web pages. With this application, the user can quickly get an overview of the STRATFEED database through pre-determined queries, and those users with more expertise can build their own queries using the query modules that correspond to the methods studied in the project. The exploration process (**Figure 2**) is divided in four main steps. After selecting a pre-determined query from the overview module (Step 1A) or building a query using one of the query modules, and then selecting the value(s) of one or more of the proposed criteria (Step 1B), the system searches the database for the samples matching the query (Step 2).

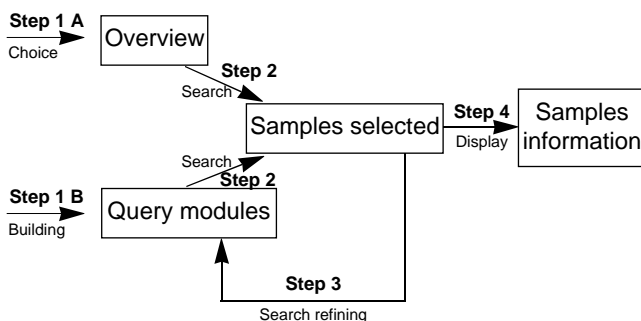


Figure 2. The exploration process used by the STRATFEED explorer.

If the result of the search is not refined enough, users can refine their query by doing step 1B again (Step 3). If the result is refined enough, the sample information, the analyses results and the conclusions are displayed (Step 4). To help users to explore the database, each web page is described by a documentation file. The file carries a picture of the web page concerned, a description of the content and a description of the actions that can be run from this web page. The full user guide can be viewed on the first page of the application by clicking on the help icon.

3. QUERY MODULES

The list of pre-determined queries shown in **figure 3** gives the user an overview of the STRATFEED database. By clicking on a pre-determined query, the user can access a table listing the samples (compound feed or feed materials) stored in the samples bank corresponding to the query. The criteria for the query include: type of ingredient (mean-and-bone meal [MBM], poultry, fish, etc.), chemical constituent (H_2O , N, Ca, P, etc.), partner providing the sample, and analytical method used (classical microscopy, PCR, near-infrared spectroscopy [NIRS] and near-infrared microscopy [NIRM]). There are also criteria relating to storage: physical presentation (pellet, meal, etc.), level of conservation (good, bad, medium), type of bag (vacuum, plastic, etc.) and quantity available. Other criteria relate to classification: destination of the feed (poultry, pig, ruminant, etc.) and the set name used in the project to develop and validate the new methods. By clicking on one of these numbers, another table is created giving the list of samples corresponding to the query.

Another approach is for the users themselves to build their queries. For each method, the criteria are defined by the respective Work Packages (WPs) of the project. These criteria include pictures and graphs and have been defined to identify the sample and the laboratory and to describe the analyses. There are query modules for each topic, based on these criteria. **Figure 4** shows the query module for classical microscopy criteria, which are classified under two topics. The laboratory identification topic describes the fields used to identify the institute and the people in charge of the analysis. The observations topic describes the classical microscopy criteria: percentage of sediment obtained during sample preparation, type of constituent observed (bones, scales, etc.), type of criteria observed for each constituent, value observed for each criterion, frequency of observation for each criterion and availability of pictures to illustrate the observations for each constituent. After completing the query form, by clicking on the search button a table is created giving the list of samples corresponding to the query.

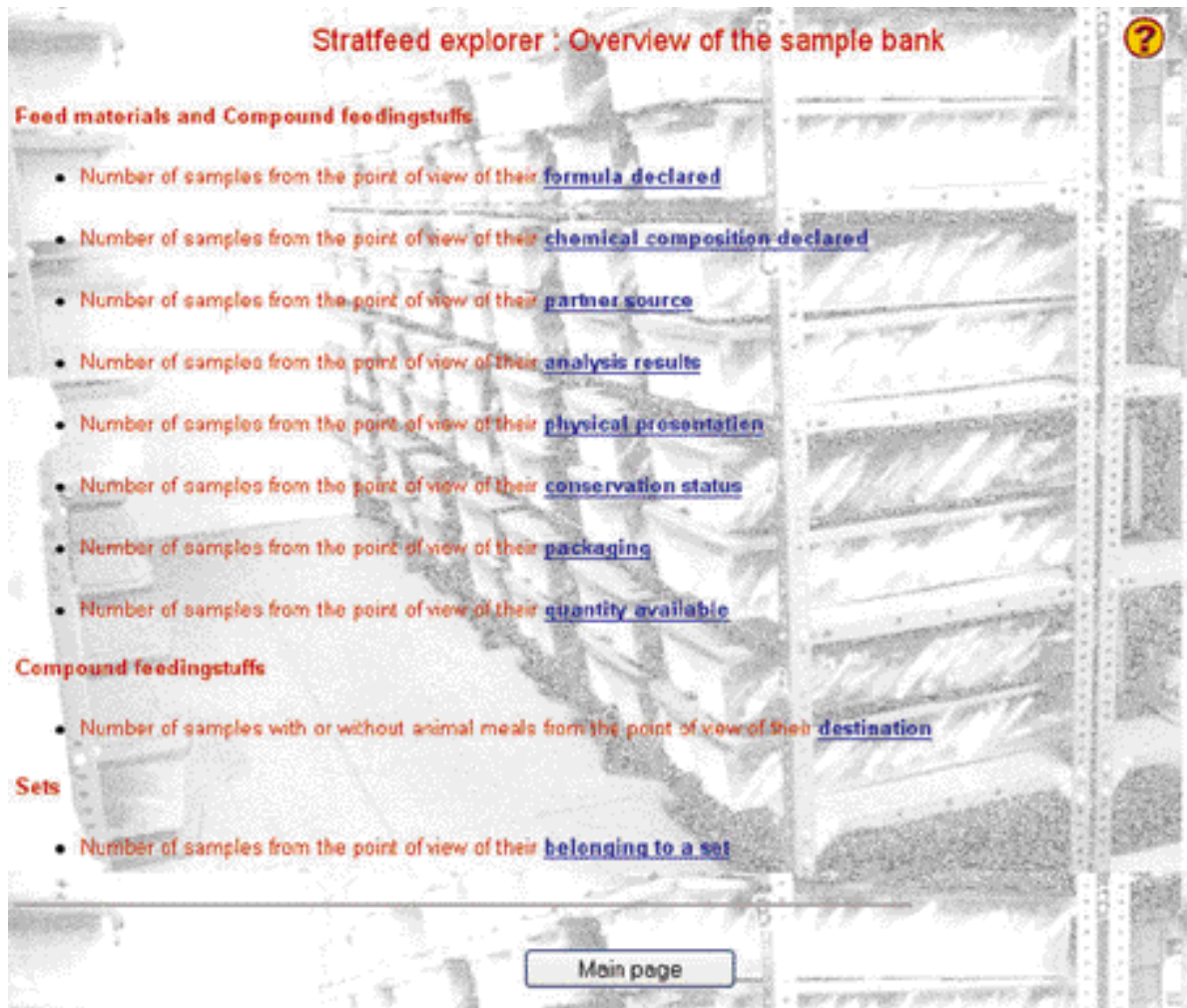


Figure 3. The pre-determined query module provided by the STRATFEED explorer.

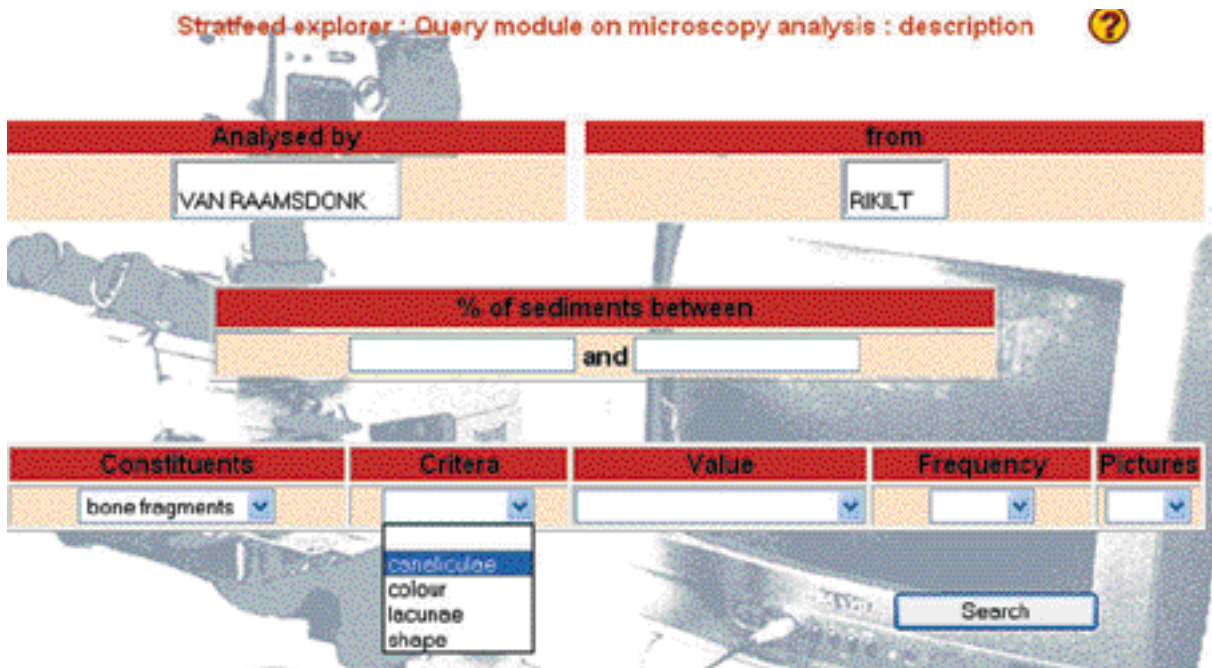


Figure 4. The query module on microscopy analysis provided by the STRATFEED explorer.

Based on the results from a pre-determined query or from a query a user has built, the search can be refined by building a new query. This will be performed on the list of samples selected in the first query, and so on. A queries history frame indicates the results of the previous queries.

4. RESULTS DISPLAY

The results of each analysis are displayed according to laboratory, method and sample. The conclusions for each of these levels are also presented. The conclusions relate to each taxon or species detected, to a result and to the reliability of this result.

The results legend is as follows:

- + Clearly positive for the presence of the taxon or species studied
- +/- Slightly positive for the presence of the taxon or species studied
- Negative for the presence of the taxon or species studied
- ? No clear result

The reliability legend is as follows:

- Yellow Single result (only one result is provided in this field)
- Green Highly reliable result (all results provided are identical)
- Orange Most results provided are in agreement with each other
- Red Results provided are contradictory

Figure 5 provides details of analyses by one laboratory. It indicates that the results of an NIRM analysis of sample 112 obtained by the CRA-W laboratory are as follows: using the raw method, without sedimentation, 680 particles were analysed by NIRM; the mathematical models predicted the presence of 541 vegetal particles and 26 animal particles; among these 26 animal particles, 0 fish particles and 22 terrestrial particles; among these 22 terrestrial particles, 16 poultry particles and two mammal particles. Using the sedimentation method, 130 particles were analysed by NIRM. The mathematical models predicted the presence of 52 animal particles.

The laboratory's conclusions are displayed at the bottom of the figure. The table indicates that for sample 112, analysed by NIRM in the CRA-W laboratory, the presence of animal meal and, more precisely, of terrestrial meal (mammal and poultry meal) is clearly predicted, as is the absence of fish meal. For the animal prediction, both methods (with and without sedimentation) gave the same result (green in the figure). For the others species or taxon studied, only one method was used for the study (yellow).

Figure 6 shows the conclusions about taxon or species detected, derived from the analyses using one method conducted by all the laboratories involved. It indicates that for sample 112 analysed by PCR by four laboratories, the presence of animal meal and, more precisely, of its fish, poultry, mammal, pig, ruminant and bovine origin is clearly detected. These results are highly reliable (green). All the laboratories involved gave the same results. For fish and mammal meal (yellow), only one lab was involved in the study.

Figure 7 shows the conclusions for one sample regarding the taxon or species detected, derived from analyses using all the methods studied in the project. It indicates, for example, that the presence of mammal meal in sample 112 was clearly detected by classical microscopy (highly reliable result), by PCR (single result) and by NIRM (single result). In this case, the different methods gave the same results (green). The presence of fish meal in sample 112, however, was clearly detected by classical microscopy (highly reliable result) and by PCR (single result) but not detected by NIRM (single result). In this case, the different methods gave contradictory results (red). By clicking on the method link, the detailed results relating to the method selected are displayed for the sample in question.

5. DISCUSSION AND PERSPECTIVES

The most important step in a wide-ranging project such as STRATFEED is data collection and validation. In the STRATFEED project it involved close collaboration between the research WPs and the information technology team. The STRATFEED explorer can now be run from the public website <http://stratfeed.cra.wallonie.be> on a database reduced to the common sets of samples used in developing the methods. On the private part of the website, STRATFEED partners can explore the complete database, including 2,500 feed samples. This application provides a real added value to the database, which is the first reference samples bank to have gathered so many feed samples, contaminated (or not) with animal tissue. The bank is maintained by the research team headed by Ana Garrido at the University of Cordoba (Dardenne *et al.*, 2004).

The modular structure of the system, based on the project topics, facilitates updating and the development of other tools for other methods. The concept developed by the STRATFEED project can be used for sample management in other projects and can easily be adapted to meet new requirements. The other applications developed under the project are described in more detail in an earlier publication (Vermeulen *et al.*, 2003) and are available on <http://stratfeed.cra.wallonie.be>. These include: a tool for the dissemi-

Detail of the analysis n° 1

Analysed by BAETEN from CRA-W

Methods	Number of particles analysed	Group	Number of particles predicted	Analyses
Raw	680	Animal	26	CRA-112c
	Fish	0	
	Terrestrial	22	
	Poultry	16	
	Mammal	2	
		Vegetal	541	
Sed	130	Animal	52	

Conclusions of analysis for the laboratory CRA-W

Taxon or species detected	Result - Reliability
Animal	+
....Fish	-
....Terrestrial	+
.....Poultry	+
.....Mammal	+
Vegetal	+

Figure 5. NIRM results summary at the laboratory level provided by the STRATFEED explorer.

Stratfeed explorer - PCR analysis for sample 112

Conclusion of 4 analyses

Taxon or species detected	Result - Reliability
Animal	
....Fish	+
....Terrestrial	
.....Poultry	+
.....Mammal	+
.....Frog	+
.....Reptilian	+
.....Insect	+
Vegetal	



Figure 6. PCR results summary at the technique level provided by the STRATFEED explorer.

Stratfeed explorer - Results summary for sample 112



Taxon or species detected	Analyse by				Conclusion
	Microscopy	PCR	NIR	NIRM	
	Result Reliability	Result Reliability	Result Reliability	Result Reliability	Result Reliability
Animal	+			+	+
....Fish	+	+		+	+
....Terrestrial			+	+	+
.....Poultry	-	+		+	+
.....Mammal	+	+		+	+
.....Frog		+			+
.....Reptilian		+			+
.....Insect		+			+
Vegetal				+	+

Sample information page

Figure 7. Results summary at the sample level provided by the STRATFEED explorer.

nation of results (*STRATFEED website*, comprising a public and a private section); a tool for data management (*STRATFEED manager*); and two tools for decision-making (ARIES Decision Support System — on CD-ROM; *STRATFEED Decision Support System* — on the Internet).

The international symposium on 'Food and feed safety in the context of prion diseases', organized in Namur, Belgium on 16–18 June 2004, provided an opportunity to disseminate the project results and to inform a wider public about the computer information system (Vermeulen *et al.*, 2004).

The STRATFEED explorer, and the website hosting the application, will be maintained and updated by CRA-W for at least three years after the end of the project (June 2004), or longer, depending on the status of the bovine spongiform encephalopathy (BSE) problem and on the number of hits on the website.

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