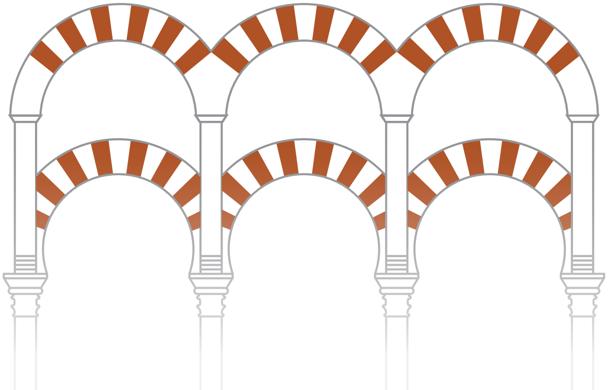

10TH INTERNATIONAL CONFERENCE ON PREDICTIVE MODELLING IN FOOD

CORDOBA, SPAIN, 26-29 SEPTEMBER, 2017

GOVERNMENT BUILDING OF THE UNIVERSITY OF CÓRDOBA

CÓRDOBA, SEPTEMBER, 2017
ICPMF10
INTERNATIONAL CONFERENCE ON PREDICTIVE MODELLING IN FOOD

ICFMH
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UNIVERSIDAD Ð CÓRDOBA

www.icpmf10.com

Dear Colleagues and friends,

On behalf of the organizing committee, We kindly invite you to attend the 10th International Conference of Predictive Modelling in Food (ICPMF10) to be held in Córdoba from 26th to 29th September, 2017. As you may know the International Committee on Predictive Modelling in Food (www.icpmf.org), which was founded in 2011, has the mission to promote the development of predictive models and to generate new knowledge in the field that are relevant to food stakeholders, risk assessors and governmental authorities. This objective is primarily achieved through advancing the success and sustainability of the biennial ICPMF-conferences.

Historically, Córdoba city has been an interplay of cultures, ideas and traditions, so we would like to extend this to the field of **Predictive Modelling in Food.**

The scientific program we are preparing will include plenary sessions, oral communications and panels, where the most relevant topics related to our area will be addressed:

- Systems biology and whole-cell modelling
- Individual-based models
- Modelling approaches using metagenomics (food) data
- Complex systems modelling approaches for food safety and quality
- Modelling microbial dynamics in relation to food microstructure
- Data Bases, software and decision-support tools in predictive modelling on foods
- Predictive models for food safety and quality: decontamination, food formulation, bacterial transfer, microbial spoilage, etc.
- Predictive models for food process simulation: dehydrating, mixing, forming, heat transfer, etc.
- Modelling the impact of microbiological interactions in foods
- Interdisciplinary approaches and new advances in predictive modelling in foods
- Quantitative Microbial Risk Assessment and Management
- Predictive mycology.

Besides that, the organizing committee has decided to organize three workshops, included in the conference registration (e.g. free access to workshops). They will be take place during the day before the scientific program, that is, 26th of September, 2017.

The local organizing committee is preparing a comprehensive and challenging program, and we expect to gather a significant number of participants from over the world. We also encourage the participation of students; whose fresh ideas and enthusiasm are always welcome. To this end, two students supporting programs will be developed consisting of a Travel Support Scholarship sponsored by Elsevier and a Developing Scientist Poster Competition organized by International Committee of Food Hygiene and Microbiology (ICFHM).

The International Journal of Food Microbiology will be the publication supporting ICPMF10 which will host the Special issue of the conference containing the most relevant works presented at ICPMF10, which will be published, after the conferences, according to a peer review process.

In addition to the scientific program, we are preparing an attractive social and recreational program with which we could enjoy weather, history and gastronomy of Córdoba, a city declared a World Heritage Site by UNESCO.

The website www.icpmf10.com will be our platform to manage your participation in ICPMF10 and provide you the latest news on the conference. Registration to the Conference will be easily done through the website as well as submission of abstracts, booking rooms in the recommended hotels, and including the main travelling tips for Córdoba, eating places, transport, etc.

We look forward to meeting you for the Conference, in Cordoba, a lovely town, located in the south of Spain.

Kind Regards,
The Organizing Committee

Committees

ORGANIZING COMMITTEE

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WEDNESDAY, SEPTEMBER 27th 2017

08:30 - 09:00 h	Opening conference
09:00 - 09:30 h	Keynote Speech: "Predictive modelling transforming food microbiology: where to next?" **by Dr. Tom Ross**. University of Tasmania, Australia
09:30 - 10:30 h	**SESSION 1.-** Interdisciplinary approaches and new advances
09.30-9.45	MODELLING APPROACHES FOR GENOTYPE-PHENOTYPE ASSOCIATION STUDIES BASED ON NGS: APPLICATION ON LISTERIA MONOCYTOGENES Lena Fritsch, Meryl Vila Nova, Jean-François Mariet, Nicolas Radomski, Arnaud Felten, Michel-Yves Mistou, Jean-Christophe Augustin, Laurent Guillier
09.45-10.00	MICROBIAL MODELLING COUPLING THE DYNAMICS OF DIFFUSED GASES AND MICROBIAL GROWTH IN MODIFIED ATMOSPHERE PACKAGING Kirk D. Dolan, Hazel Meredith, Declan J. Bolton, Vasilis P. Valdramidis
10.00-10.15	ZERO-INFLATED REGRESSIONS FOR MODELLING MICROBIAL LOW PREVALENCE AND SAMPLING PERFORMANCE FOR FOODBORNE PATHOGENS Ursula Gonzales-Barron, Marta Hernández, David Rodríguez-Lázaro, Vasco Cadavez, Antonio Valero
10.15-10.30	MEAT SPOILAGE PREDICTION MODELS USING FINGERPRINTING(‘OMICS,SURFACE CHEMISTRY)IN TANDEM WITH AUTOMATED RANKING PLATFORM Fady Mohareb, Stathis Panagou, George - John Nychas
10:30 - 11:00 h	COFFEE BREAK AND POSTER SESSION
11:00 - 13:00 h	**SESSION 2.-** Predictive models and complex modelling approaches for food safety and quality
11.00-11.15	RAPID DETECTION OF MICROBIOLOGICAL QUALITY OF RAW MINCED BEEF BY MEANS OF ELECTRONIC NOSE AND MULTIVARIATE ANALYSIS Dimitris Pavlidis, Stathis Panagou, George - John Nychas
11.15-11.30	MODELLING OF TTI SMART LABELS RESPONSE FOR MONITORING SHELF-LIFE AND *VIBRIO PARAHAEMOLYTICUS* RISK IN OYSTERS Kalliopi Kallioupi, Marianna Giannoglou, Theofania Tsironi, Petros Taoukis
11.30-11.45	MODELING ADHESION AND BIOFILM FORMATION ON STAINLESS STEEL BY FIVE DIFFERENT SEROTYPES OF SALMONELLA ENTERICA Marciane Magnani, Juliana de Oliveira Moraes, Ellen Abreu da Cruz, Tereza C R Moreira Oliveira, Verônica Ortiz Alvarenga, Anderson de Souza Sant’Ana
11.45-12.00	EXTENSIVE CARDINAL PARAMETER MODEL TO PREDICT GROWTH OF PSEUDOMONADS IN SALT-REDUCED LIGHTLY PRESERVED SEAFOOD Veronica Martinez-Rios, Paw Dalgaard
12.00-12.15	THE PROPAGATION OF UNCERTAINTY FROM DATA TO PREDICTIONS Akkermans Simen, Nimmegeers Philippe, Telen Dries, Van Impe Jan
12.15-12.30	MODELLING AND IDENTIFICATION OF RELEVANT PATHWAYS FOR NUCLEOTIDE DEGRADATION IN FRESH HAKE DURING STORAGE Carlos Vilas, Míriam R. García, Antonio A. Alonso, Juan R. Herrera, Marta Bernárdez
12.30-12.45	IMPACT OF NATURAL DIVERSITY IN HEAT RESISTANCE OF BACTERIAL CELLS AND SPORES ON SAFETY AND QUALITY

O03.- ZERO-INFLATED REGRESSIONS FOR MODELLING MICROBIAL LOW PREVALENCE AND SAMPLING PERFORMANCE FOR FOODBORNE PATHOGENS

Ursula Gonzales-Barron[1], Marta Hernández[2], David Rodríguez-Lázaro[3], Vasco Cadavez [1], Antonio Valero[4]

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Keywords: zero inflated binomial, prevalence, poultry meat, markov chain MonteCarlo

INTRODUCTION AND OBJECTIVES

Microbial contamination of raw poultry meat could occur because of improper handling at primary production and slaughterhouse levels. Low microbial prevalence data often consists of a high amount of non-detections (zero positives), so a flexible framework is required to characterise the underlying microbial distribution and conduct reliable inferential statistics. Thus, the objective of this work was to evaluate the performance of zero-inflated binomial (ZIB) regression models to describe the effects of sampling site (carcass, thigh, breast, wings) on the measured incidences of *Salmonella*, *Listeria monocytogenes* and *Staphylococcus aureus* on chicken meat. For this aim, a number of fixed- and random-effects models were evaluated and compared, while sampling performance based on mean prevalence estimates was assessed.

MATERIAL AND METHODS

Poultry samples were taken during three consecutive years from a Spanish slaughterhouse (36 sampled batches from 144 sampling periods). Analyses were carried following ISO methods for each pathogen taking 25 g samples from each site. Carcasses samples were collected before jointing, while thigh, breast and wings were sampled afterwards. For each pathogen, four ZIB models were fitted to the presence/absence data with sampling site as covariate and random-effects due to sampling occasion either in the binomial probability (p) or in the extra-proportion of zero counts (w0). Models were fitted using the Markov chain Monte Carlo (MCMC) technique via WINBUGS 1.4.3.

RESULTS

The data sets of the three pathogens presented a high proportion of non-detections. While *Salmonella* spp. was the pathogen least frequently detected from poultry meat (90.9% non-detections), *L. monocytogenes* and *S. aureus* gave positive results slightly more often (14-15% detections); although in general the frequency of positive results were conditional upon the sampling site. For the three data sets, the sampling site exerted a greater effect on the extra proportion of non-detections than on the binomial prevalence itself, with breast bearing the lowest prevalence estimates of *Salmonella* spp. (mean: 0.0088; 95% CI: 0.0002-0.0195) and *S. aureus* (mean 0.0148; 95% CI: 0.0001-0.0400). The fitting capacity of the models was further improved when random effects due to sampling occasion were placed in the extra proportion of non-detections (deviances decreased from 146.7-156.7 to 140.2-140.6). At any sampling site (breast, carcass, thigh or wings), the mean prevalence was estimated as 0.0135 (95% CI: 0.0015 – 0.0270) for *Salmonella*, 0.0211 (95% CI: 0.0004 – 0.0563) *for L. monocytogenes* and 0.0236 (95% CI: 0.0004 – 0.0512) for *S. aureus*.

CONCLUSIONS

Under a ZIB assumption, most of the variability in the occurrence of pathogens on chicken meat was found to lie in the process producing the extra proportion of zero counts than in the binomial probability itself. With basis on an adequate description of microbial contamination, sampling procedures of poultry meat can be effectively addressed.