

“FISHMAP- PROGRAM-”

**USER MANUAL
VERSION 1.0**



“FISHMAP” version 1.0 (January, 2011)

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1. INTRODUCTION

The “FISHMAP” program is property of AZTI-TECNALIA and has been developed by the Institute of Food Research, Norwich, UK in collaboration with AZTI-TECNALIA.

The software developed “FISHMAP” allows the prediction and the visualization of growth of spoilage bacteria in fish product under modified atmosphere packed (MAP) with different concentration of carbon dioxide (CO₂) at constant and fluctuating temperatures. Moreover, the program includes the prediction of growth of spoilage bacteria under air conditions. The spoilage bacteria included in this program are:

- *Carnobacterium maltaromaticum*
- *Serratia proteamaculans*
- *Shewanella baltica*
- *Yersinia intermedia*
- *Mixed bacteria: (C. maltaromaticum, S. proteamaculans, S. baltica and Yersinia intermedia)*

Furthermore, the software allows the graphical comparison of experimental growth microbiological data with the respective microbial growth model at either constant or fluctuating temperature. Optionally, the predictions and plots can be saved as an Excel workbook. The predictive models are based on experimental data of bacterial growth obtained at AZTI-TECNALIA under different ambient conditions: temperature interval between 0-20°; under CO₂ enriched atmospheres (0-100% CO₂ v/v, balance nitrogen) and under air condition (21% O₂).

The growth kinetic parameters were estimated by fitting the model of *Baranyi and Roberts* (1994). The dependence of the maximum specific growth rate on temperature, CO₂ and O₂ was described by a cardinal model similar to that described by *Mejlholm, et al.* (2010).

1.1. Basic predictive microbiology

Predictive microbiology is the science of describing and predicting, by mathematical means, the response of microorganisms to their environments. If responses are observed under a sufficient number of combinations of the environmental factors, then it is possible to predict how the organisms would respond to any conditions of the environmental region where the observations were made.

2. HOW TO USE THE “FISHMAP”-Program

FISHMAP program is an Excel add-in, running under Windows 3.1. and Excel 5 or above.

Warning: Regional configuration/options (form Panel Control) must be set up for “English(UK)”.

2.1. The Opening Screen

Open “FISHMAP” by double clicking on the Excel file. A Welcome page will appear showing a legal advice. Click on the “GO” button for accepting those regulations and the program will be installed in Excel. **(Figure 1)**

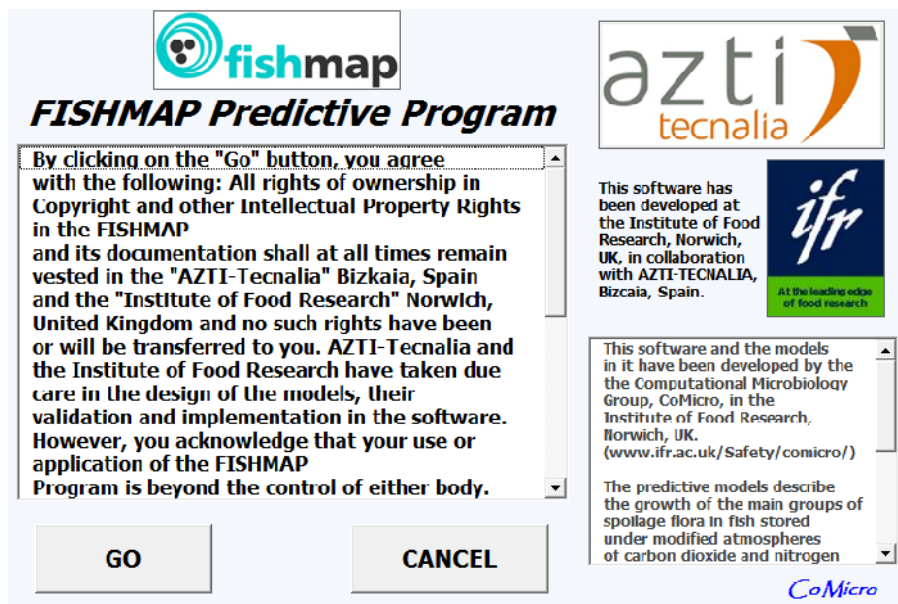


Figure 1

2.2. Generating a prediction

The first step to generate a prediction is to open a separate Excel sheet and enter time-temperature profiles (can be entered manually). Data must be organized in columns. Time (in hours) must be in the first column of the selection. The table should start at 0 time. Temperature measurements (in Celsius degrees) must be in the second column of the selection. Temperature can be entered between 0 and 20 Celsius degrees; predictions out of this range are not reliable.

Step 1. Click on **“FISHMAP”** Prediction during fluctuating temperature, and select a temperature profile in the current Excel workbook. Highlight the data only, without heading.

Step 2. Select the type of atmosphere in the fish product, packed under carbon dioxide (CO₂) or under air conditions.

Step 3. If % CO₂ is chosen, this value from 0 to 100% can be entered manually.

Step 4. Enter the initial level of each spoilage bacteria (log₁₀cfu/g) colony-forming units per gram in the text box shown.

- *Carnobacterium maltaromaticum*
- *Serratia proteamaculans*
- *Shewanella baltica*
- *Yersinia intermedia*
- *Mixed bacteria:* (*C. maltaromaticum*, *S. proteamaculans*, *S. baltica* and *Yersinia intermedia*)

Step 5. Click on the prediction button, FISHMAP will show the growth prediction graph in the same graph (Figure 2):

- (i) Time-temperature profile
- (ii) Prediction of growth of the mixed and each bacteria

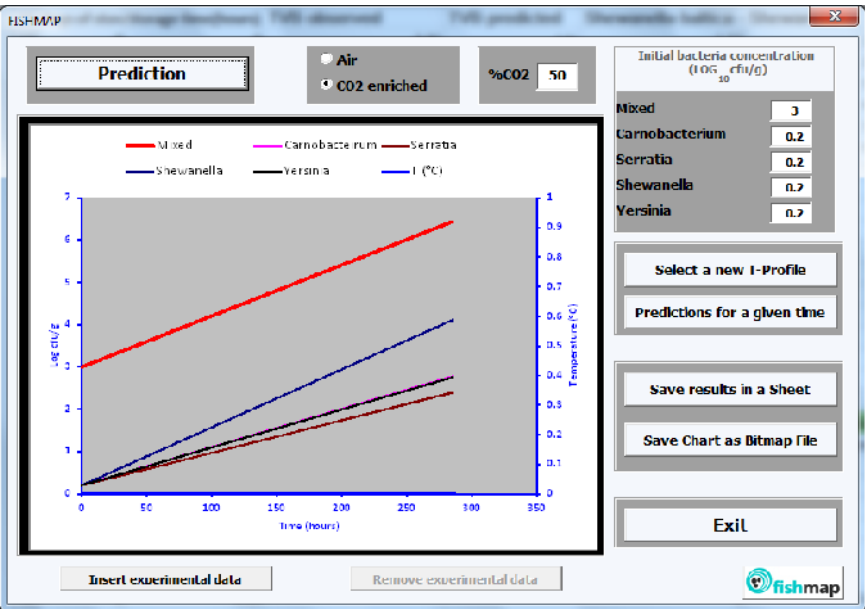


Figure 2

2.3. Prediction for a given time

Click on the “Predictions for a given time” button. Introduce the time in hours for a predictions and press “Predict”. The program shows a table with the following information:

- (i) Prediction of the each group of bacteria load at the entered time (hours)

(Figure 3)

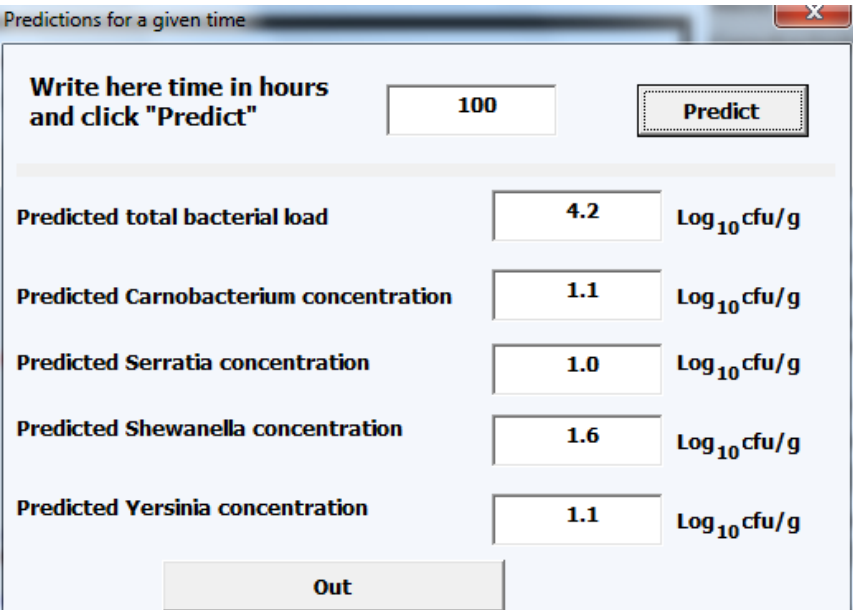


Figure 3

2.4. Comparison of observed and predicted data

The FISHMAP program allows the comparison of the predicted growth bacteria data versus experimental data.

Click on the **“Insert experimental data”** button in the bottom left corner of the screen to display prediction graphs.

Select the microbiological experimental data in an Excel sheet. Data must be organized in columns; Time (hours) in the first column and microbial counts ($\log_{10}\text{ufc/g}$) in the second column. Then press **“OK”** after selection. **(Figure 4)**

You can also remove these data by selecting **“Remove experimental data”** button.

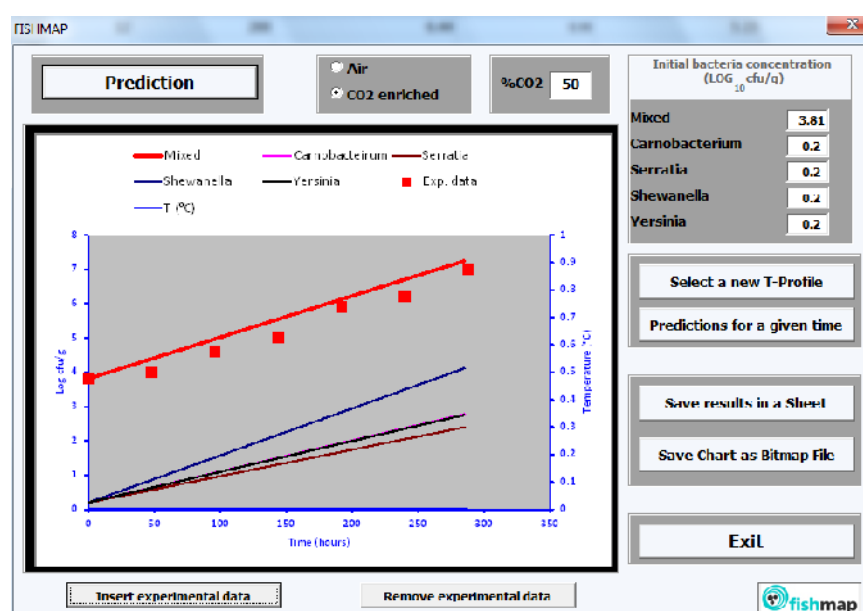


Figure 4

2.5. Saving data

Click on the bottom **“Save results in a sheet”** to save all data and graphs obtained on an excel file.

To exit the prediction window and close the program, use the **“Exit”** button.

3. REFERENCES

- Baranyi, J., Roberts, T.A., 1994. A dynamic approach to predicting bacterial growth in food. *Int J Food Microbiol* 23, 277-294.
- Mejlholm, O., Gunvig, A., Borggaard, C., Blom-Hanssen, J., Mellefont, L., Ross, T., Leroi, F., Else, T., Visser, D., Dalgaard, P., 2010. Predicting growth rates and growth boundary of *Listeria monocytogenes* - An international validation study with focus on processed and ready-to-eat meat and seafood. *Int J Food Microbiol* 141, 137-150.