

Introduction to USDA Integrated Pathogen Modeling Program – Dynamic Prediction

(IPMP-Dynamic Prediction)

Lihan Huang, Ph.D.

Microbial and Chemical Food Safety (MCFS) Research Unit

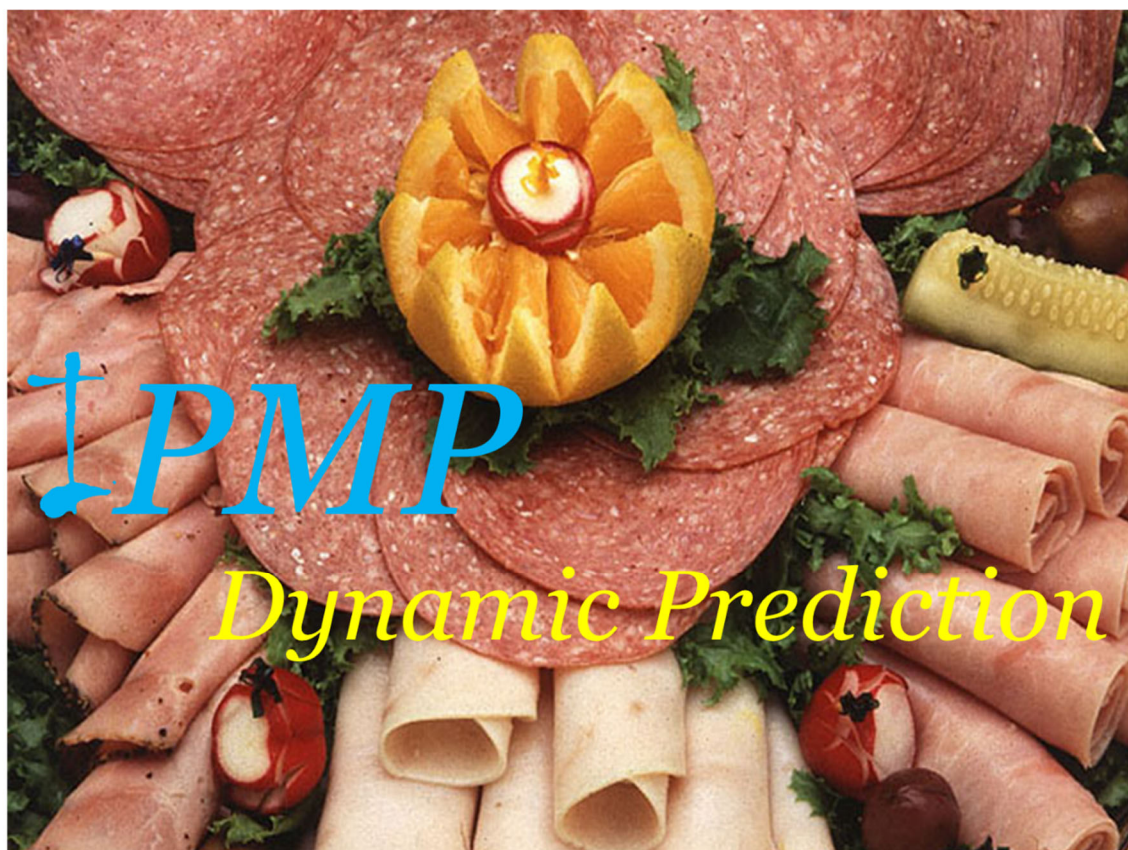
Eastern Regional Research Center

USDA Agricultural Research Service

600 E. Mermaid Lane

Wyndmoor, PA 19038

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Please contact Dr. Lihan Huang (Lihan.Huang@usda.gov) for technical questions.

INTRODUCTION

What is IPMP-Dynamic Prediction?

IPMP-Dynamic Prediction is an extension of the USDA Integrated Pathogen Modeling Program (IPMP). It is designed to simulate and predict microbial growth and survival under suitable temperature conditions using previously determined and validated kinetic parameters and predictive models. It can be used to predict the growth of foodborne pathogens in foods exposed to dynamically changing or isothermal temperature conditions. It has been redesigned and programmed with Python 3.10 (64 bit).

What is required to use IPMP-Dynamic Prediction?

IPMP-Dynamic Prediction can be run under Microsoft Operating Systems (64 bit).

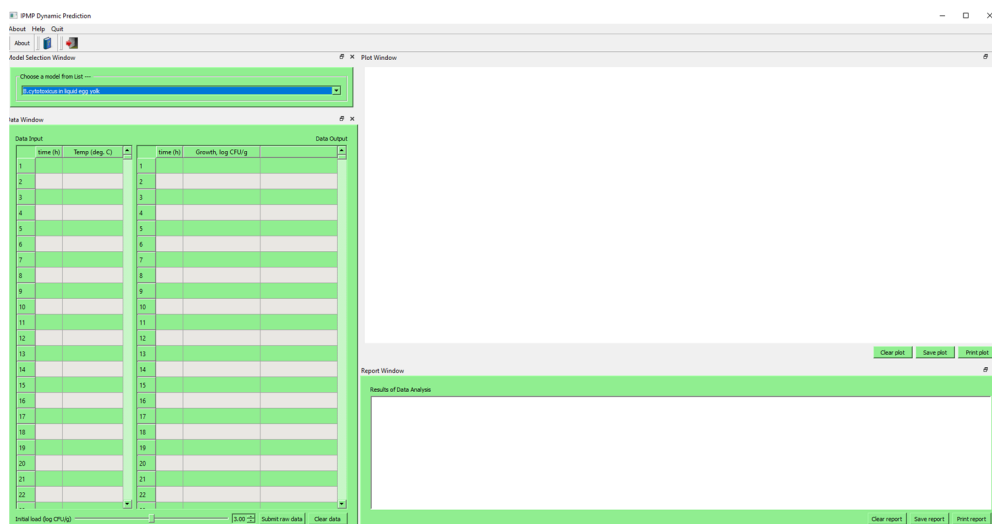
What models are included in IPMP-Dynamic Prediction?

IPMP-Dynamic Prediction has included 24 growth models and will be expanded gradually to include more as new ones are developed and validated.

STRUCTURE of IPMP-Dynamic Prediction

IPMP-Dynamic Prediction is based on IPMP (Figure 1). They share similar components and design. If you are familiar with IPMP, you should be able to use IPMP-Dynamic Prediction. The major difference is in the data window, which is explained in the Data Window Section.

Figure 1. IPMP-Dynamic Prediction



DATA WINDOW

The data window contains a spreadsheet-style input area and output area (Figure 2). The data input area contains three columns and 5000 rows. The data table can be scrolled to examine the data.

Figure 2. Data table

The screenshot shows a window titled "Data Window" with a tab labeled "Data Input". The window contains two tables side-by-side. The left table has columns for "time (h)" and "Temp (deg. C)". The right table has columns for "time (h)" and "Growth, log CFU/g". Both tables have 23 rows visible, numbered 1 to 23. The rows alternate between light green and light gray. At the bottom of the window, there is a control bar with a label "Initial load (log CFU/g)" followed by a text input field containing "3.00", a "Submit raw data" button, and a "Clear data" button.

Data Input		Data Output	
time (h)	Temp (deg. C)	time (h)	Growth, log CFU/g
1		1	
2		2	
3		3	
4		4	
5		5	
6		6	
7		7	
8		8	
9		9	
10		10	
11		11	
12		12	
13		13	
14		14	
15		15	
16		16	
17		17	
18		18	
19		19	
20		20	
21		21	
22		22	
23		23	

Initial load (log CFU/g)

Raw Data Entry

Raw data must be entered in the data input area. The raw data can be directly entered from the keyboard or copied/pasted from a text editor or a spreadsheet (Excel®, for example). Raw data can be edited by right clicking the mouse. The data edit can include “cut”, “copy”, “paste”, and “clear”. If necessary, click “Clear data” to erase the data from the input area. Clear data before entering new data.

A time-temperature history of a product is needed for using IPMP-Dynamic Prediction and must be entered in the Data Input Table, starting from Row 1 (Figure 3). In the Data Input Table, the time (“time (h)”) must be consecutive time in hours. The temperature must be Celsius (°C). The temperature history can be dynamic, i.e., changing with time (Figure 3, Left), or isothermal (constant) (Figure 3, Right).

A minimum of two time-temperature points is needed. For a constant temperature, two time points are needed, but the temperature entry is the same (Figure 3, Right).

The time-temperature history must be numerical values and cannot contain any non-numerical characters or missing values. The program is designed with a data checking algorithm to validate the data and warn the users if it finds any non-numerical entries or missing data once the data are submitted for analysis (Figure 3). If an error is found, the users must click the “OK” button and then correct the error item(s) in the Data Input Table. The error must be corrected before a prediction can be made.

Figure 3. Data entry to IPMP-Dynamic Prediction. The temperature history may be dynamic or isothermal.

The figure displays two side-by-side screenshots of the IPMP-Dynamic Prediction software interface, showing data entry tables for dynamic and isothermal conditions.

Left Window (Dynamic Temperature History):

time (h)	Temp (deg. C)	time (h)	Growth, log CFU/g
1	0	20.8	
2	0.5	10	
3	1	5	
4	5	30.5	
5	30	15.6	
6			
7			
8			
9			
10			
11			
12			
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18			
19			
20			
21			
22			
23			

Right Window (Isothermal Temperature History):

time (h)	Temp (deg. C)	time (h)	Growth, log CFU/g
1	0	20.5	
2	30	20.5	
3			
4			
5			
6			
7			
8			
9			
10			
11			
12			
13			
14			
15			
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23			

Both windows feature a control panel at the bottom with an 'Initial load (log CFU/g)' field set to 3.00 and buttons for 'Submit raw data' and 'Clear data'.

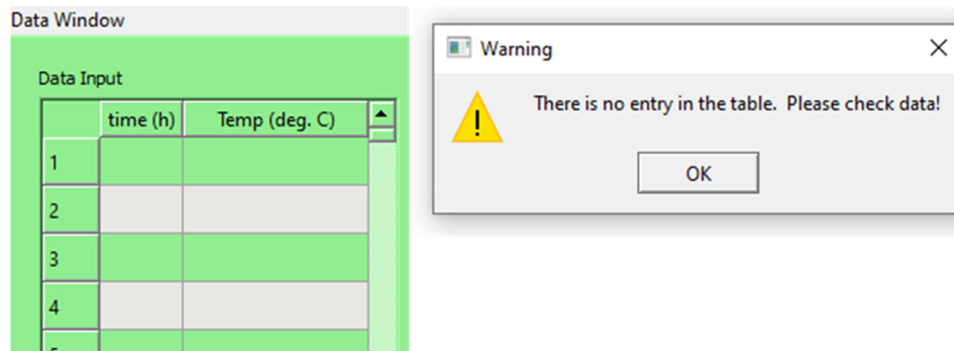
Data validation and error checking

The program contains a basic algorithm for validating the input data. If an error is found, it must be corrected before the program can proceed. The errors may include one of the following categories:

- 1) No data (Figure 4)

If the program detects no data in the input data, a warning will appear (Figure 4)

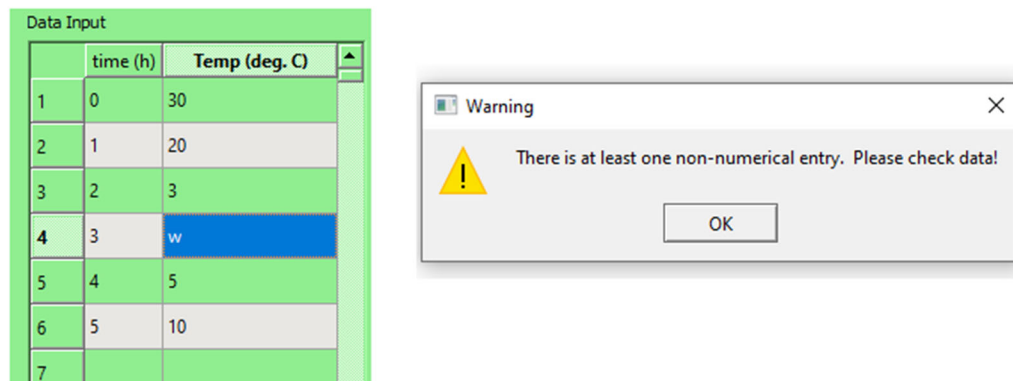
Figure 4. No data entry error.



- 2) No-numeric entry

If the program detects a non-numerical entry in the input table, Figure 5 will appear.

Figure 5. Non-numerical error

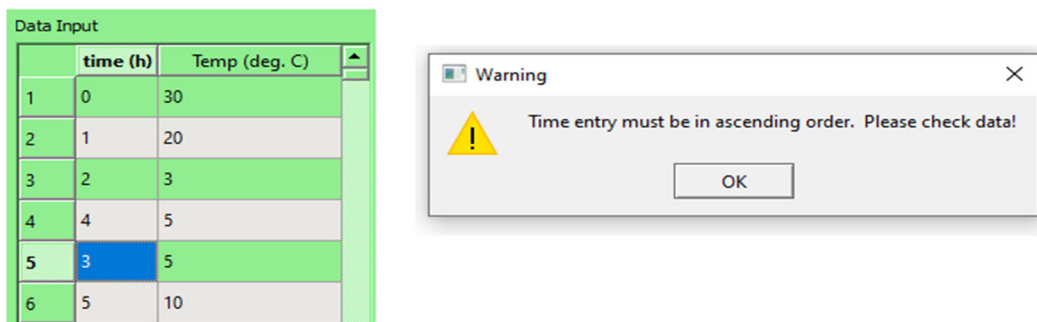


The non-numerical entry error can occur when the users reuse the data input after making a prediction, but the length of the data is shorter than previous one. If this is the case, the users can click the "Clear Data" button next to the "Submit Button" to refresh the data input table.

3) Unsorted time data

If the time data are not in an ascending order, a time entry error will appear (Figure 6).

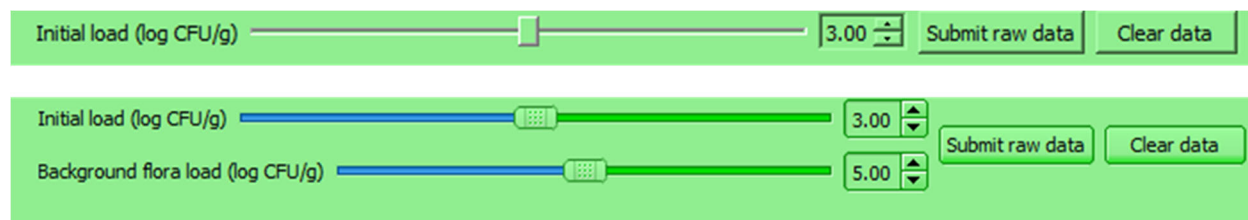
Figure 6. Time entry error



INITIAL BACTERIAL LOAD ADJUSTMENT

Under the Data Input Table, the users can adjust the initial bacterial load by adjusting the slider or the spinner next to it (Figures 2 and 7). Most models contain only one microorganism. So, only the initial load of that microorganism is needed (Figure 6, Top). The users can adjust the initial load using the slider or the spinner box to make the adjustment. Some models may also predict the growth of background microorganisms. If a model contains a model for background microorganisms, another slider and spinner will appear to allow the users adjust the initial load of the background microorganisms (Figure 7, Bottom). The GUI for the background microorganisms (background flora load or other microorganisms) will automatically appear when it is needed.

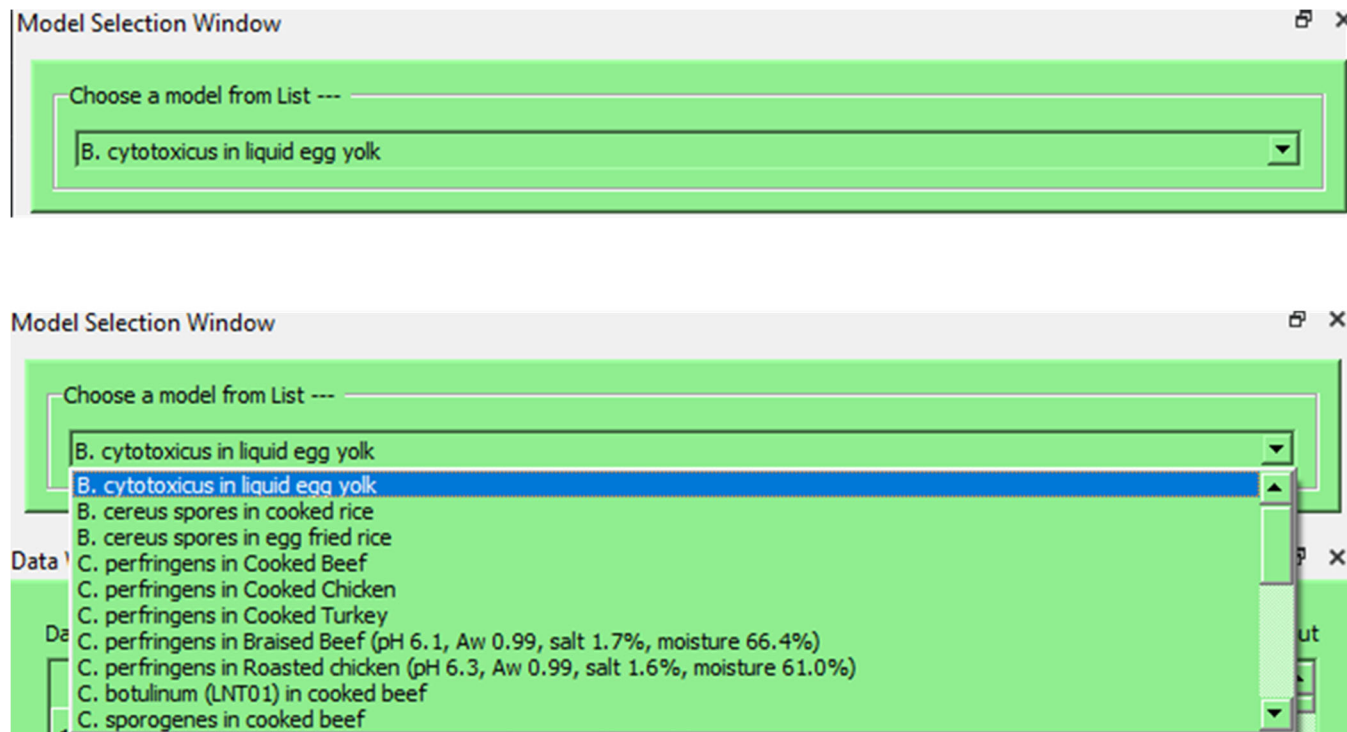
Figure 7. Adjustment of initial loads



SELECTION OF A PREDICTIVE MODEL

The users can choose from the Model Selection Window (Figure 8, Top). Once it is clicked, a list will appear (Figure 8, Bottom). The users can scroll down the list to the available models. Once a model is selected, it is ready for prediction if the time-temperature history is available in the Data Input Table. Model selection can be done at any time, before or after data entry. Only one model can be selected at a time, the users can choose another anytime during data analysis.

Figure 8. Model selection.



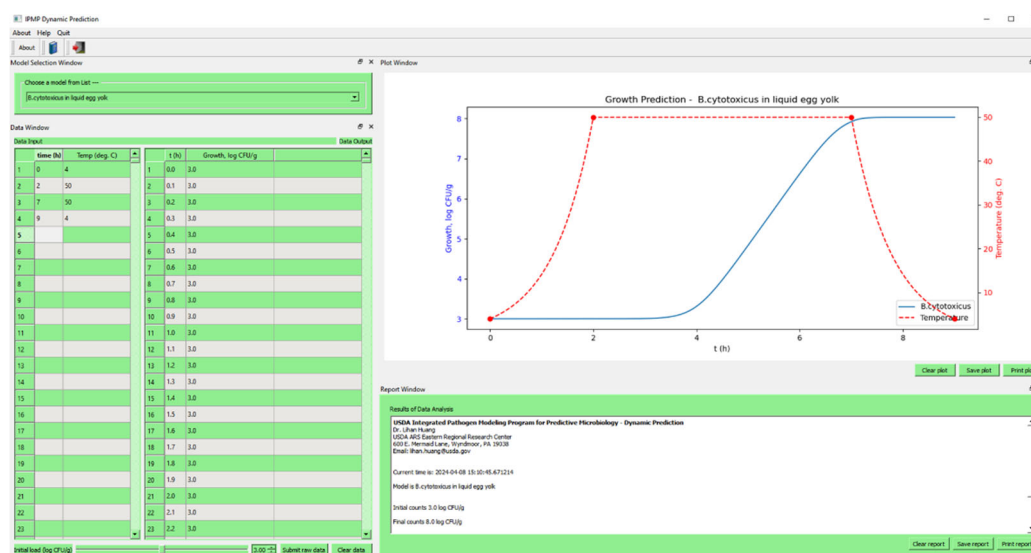
LIST OF MODELS

- 1) *B. cytotoxicus* in liquid egg yolk
- 2) *B. cereus* spores in cooked rice
- 3) *B. cereus* spores in egg fried rice
- 4) *C. perfringens* in Cooked Beef
- 5) *C. perfringens* in Cooked Chicken
- 6) *C. perfringens* in Cooked Turkey
- 7) *C. perfringens* in Braised Beef (pH 6.1, Aw 0.99, salt 1.7%, moisture 66.4%)
- 8) *C. perfringens* in Roasted chicken (pH 6.3, Aw 0.99, salt 1.6%, moisture 61.0%)
- 9) *C. botulinum* (LNT01) in cooked beef
- 10) *C. sporogenes* in cooked beef
- 11) *Cronobacter sakazakii* in Reconstituted Powdered Infant Formula
- 12) *E. coli* O157:H7 in mechanically-tenderized beef
- 13) *E. coli* non-O157 STEC in 90% lean ground beef
- 14) *E. coli* O157:H7/background microbiota in ground beef
- 15) *L. monocytogenes* in cooked pork
- 16) *L. monocytogenes* in beef hot dogs (no lactate)
- 17) *L. monocytogenes* on hard boiled eggs
- 18) *L. monocytogenes* in salmon roe
- 19) *L. monocytogenes* in fresh-cut cantaloupe
- 20) *Salmonella* spp. in raw ground beef
- 21) *Salmonella* Enteritidis in liquid egg whites
- 22) *Salmonella* Enteritidis in potato salads
- 23) *Salmonella* Enteritidis in liquid egg white and liquid yolk
- 24) *Staphylococcus aureus* in cooked potato cubes and potato salad

PREDICTION

If the data are properly entered, click the “Submit raw data” button (Figure 6) to process the data. Once the data are submitted, they will be validated and checked for any errors. If no error is found, the prediction will be calculated, and the results will be presented in the plot window and report window (Figure 9).

Figure 9. Data report



DATA DOCUMENTATION

If it is necessary to document the results of predictive modeling, the users can

- 1) Click “Save plot” button to save the figure as a Portable Network Graphic (PNG) file;
- 2) Click “Print plot” button to send the figure to a printer;
- 3) Click “Save report” button to save the report as a text (txt) file; or
- 4) Click “Print report” button to print the report.

RESETTING ENVIRONMENT

The users can click any of the “Clear data”, “Clear plot”, or “Clear report” button to clear the data. This will cause IPMP-Dynamic Prediction to reset to a blank environment.

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