

Introduction to USDA Integrated Pathogen Modeling Program – Dynamic Prediction

(IPMP-Dynamic Prediction)

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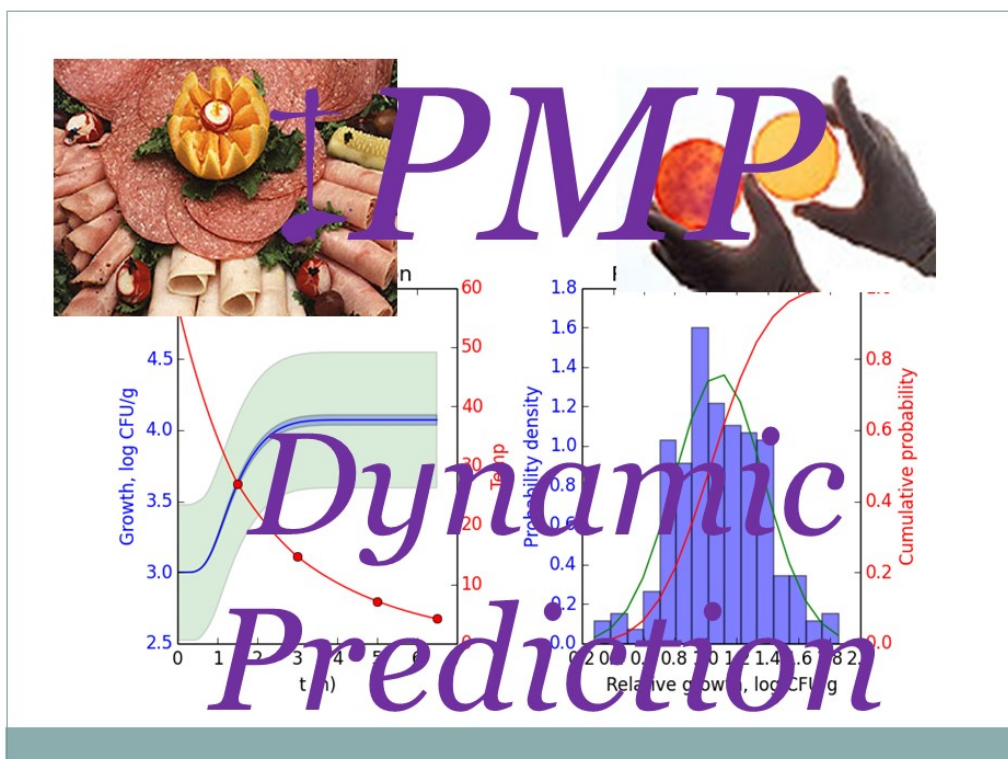
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INTRODUCTION

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 inactivation under dynamic conditions. It differs from IPMP, which is design to analyze individual growth or inactivation curves. IPMP- Dynamic Prediction is to use kinetic parameters and predict the growth and inactivation of microorganisms exposed dynamically-changing temperature and other environmental conditions.

What is required to use IPMP-Dynamic Prediction?

IPMP-Dynamic Prediction can be run under Microsoft Operating Systems (32 or 64 bit).

What models are included in IPMP-Dynamic Prediction?

IPMP-Dynamic Prediction has one model now, and will be expanded gradually to include more models.

STRUCTURE of IPMP-Dynamic Prediction

IPMP-Dynamic Prediction is based on IPMP. So 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.

DATA WINDOW

Components

The data window contains a spreadsheet-style input area and output area (Figure 1). The data input area contains three columns and 5000 rows. The data table can be scrolled to examine the data.

Data Window

Data Input F C Data Output

	t (h)	Temp		t (h)	Growth	95% LP	95% UP
1	0	57		1	0.00	3.00	2.52 3.48
2	1.5	26.95461822		2	0.01	3.00	2.52 3.48
3	3	14.66921832		3	0.02	3.00	2.52 3.48
4	5	7.157845614		4	0.03	3.00	2.52 3.48
5	6.5	4.178917939		5	0.04	3.00	2.52 3.48
6				6	0.05	3.00	2.52 3.48
7				7	0.06	3.00	2.52 3.48
8				8	0.07	3.00	2.52 3.48
9				9	0.08	3.00	2.52 3.48
10				10	0.09	3.00	2.52 3.48
11				11	0.10	3.00	2.52 3.48
12				12	0.11	3.00	2.52 3.48
13				13	0.12	3.00	2.52 3.48
14				14	0.13	3.00	2.52 3.48
15				15	0.14	3.00	2.52 3.48
16				16	0.15	3.00	2.52 3.48
17				17	0.16	3.00	2.52 3.48
18				18	0.17	3.00	2.52 3.48
19				19	0.18	3.00	2.52 3.48
20				20	0.19	3.00	2.52 3.48
21				21	0.20	3.00	2.52 3.48
22				22	0.21	3.00	2.52 3.48
23				23	0.22	3.00	2.52 3.48
24				24	0.23	3.00	2.52 3.48
25				25	0.24	3.00	2.52 3.48
26				26	0.25	3.00	2.52 3.48

Initial load (log CFU/g) Submit raw data Clear data

Figure 1. Data table

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). The data can be growth or survival data. Raw data can be edited by right-clicking the mouse. The edit operations include “cut”, “copy”, “paste”, and “clear”. The data can be saved to “csv” format by clicking the “save” option. If necessary, click “Clear data” to erase the data from the input area. Clear data before entering new data.

MATHEMATICAL MODELS IN IPMP-Dynamic Prediction

1. Growth of *C. perfringens* in cooked beef

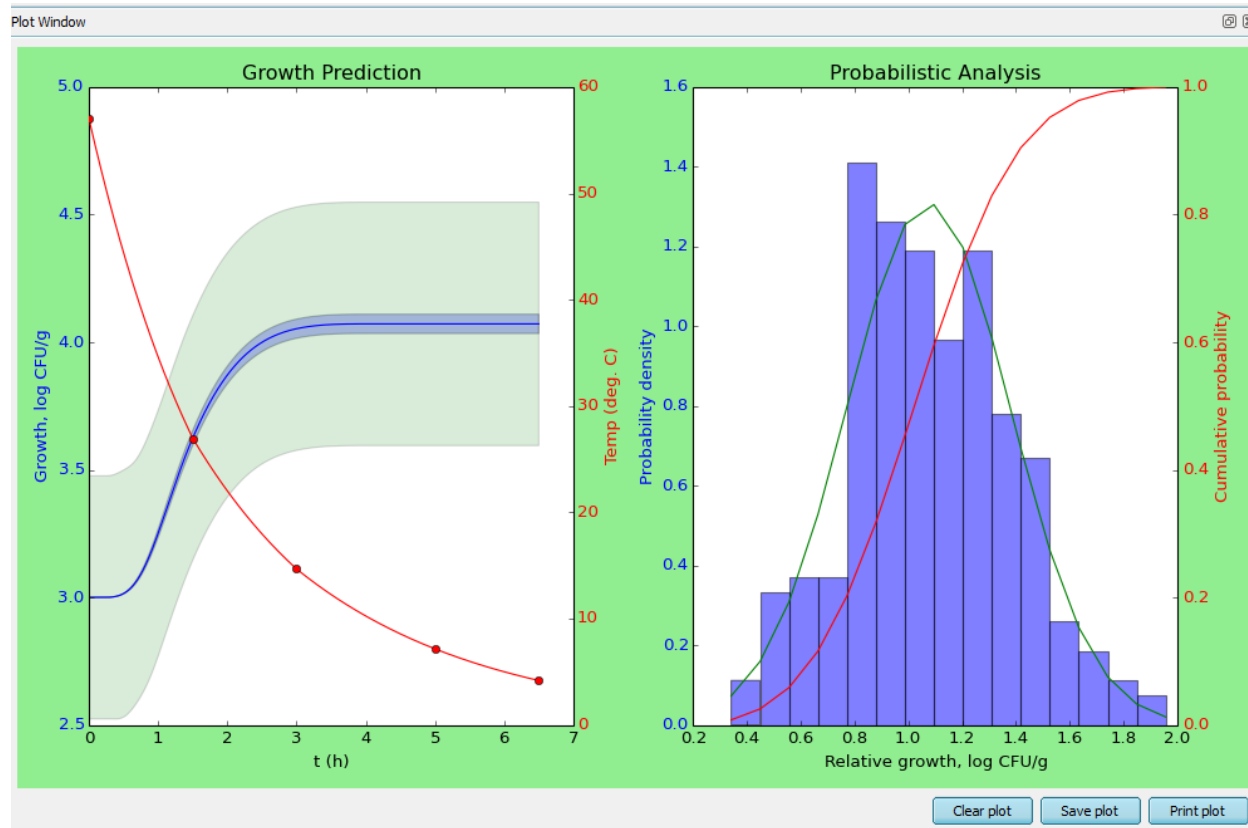


Figure 2. Output of simulation

This model is based on research reported by Huang (2015), entitled Dynamic determination of kinetic parameters, computer simulation, and probabilistic analysis of growth of *Clostridium perfringens* in cooked beef during cooling. International Journal of Food Microbiology, 195: 20-29. This model can be used to predict the growth of *Clostridium perfringens* during cooling or under constant (static) temperature conditions.

General description:

1.1 Raw Data Entry

- 1.1.1 Enter or copy temperature history to the Data Input area
- 1.1.2 The time must be in hours.
- 1.1.3 At least two data points are needed for simulation.
- 1.1.4 Choose the unit of the temperature (Celsius or Fahrenheit).

1.2 Click Submit Data Button to start simulation

Interpretation of results:

Model

$$y_i = f(t_i) + \epsilon_i$$

The model is based on Huang (2015).

t_i : cooling time, h.

y_i : the predicted growth of *C. perfringens* in cooked at time t_i , log CFU/g.

ϵ_i : the error term at t_i , which may include both experimental errors and model errors.

The blue-colored curve in the left chart is the growth predicted by the model.

Probability of >1 log CFU/g relative growth

This is the probability of seeing a > a 1-log CFU/g growth at the end of cooling or incubation.

Probability of >2 log CFU/g relative growth

This is the probability of seeing a > a 2-log CFU/g growth at the end of cooling or incubation.

95 percentile of relative growth

A statistical term for relative growth that 95% of simulation results will be equal to or below this value.

Shaded areas in the left chart

There are two shaded areas in the left chart. The outer shaded area represents lower and upper 95% prediction intervals. The smaller shaded area is the lower and upper 95% confidence intervals of simulation.

Interpretation of 95% Prediction intervals - anticipated single experiment observations:

If you conduct a random experiment using the initial level of inoculum in the chart, 95% of your observations are likely fall within this region.

Interpretation of 95% confidence level of simulation

Monte Carlo simulation is used to estimate growth. Under of the condition of simulation, 95% of the simulated results will fall within this shaded area.

References

Huang, L. 2015. Dynamic determination of kinetic parameters, computer simulation, and probabilistic analysis of growth of *Clostridium perfringens* in cooked beef during cooling. *International Journal of Food Microbiology*, 195: 20-29.