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SUGGESTED CITATION

Huang, L. 2015. USDA Integrated Pathogen Modeling Program – Global Fit. USDA Agricultural Research Service, Eastern Regional Research Center, Wyndmoor, PA.

INTRODUCTION

What is IPMP - Global Fit?

IPMP-Global Fit is an extension of the USDA Integrated Pathogen Modeling Program (IPMP). It is designed to analyze and fit the entire experimental data set of growth and inactivation curves commonly encountered in predictive microbiology to growth and inactivation models by minimizing the global errors. It differs from IPMP, which is designed to analyze individual growth or inactivation curves. IPMP-Global Fit is to analyze all growth or inactivation curves obtained under different conditions together, and try to derive kinetic parameters that are optimized for the entire data set.

Why IPMP-Global Fit?

The development of primary models in predictive microbiology usually involves a two-step process. The first step is to analyze each individual growth or inactivation curve obtained under a constant environmental condition (temperature, for example). The kinetic parameters (growth rate or lag time) from different conditions are then used to derive a secondary model. For some growth or inactivation curves, one or more common parameters are shared under different conditions. Some examples of shared parameters may include the exponent of the Weibull model, h_0 of the Baranyi model, z value of linear inactivation model, and maximum cell concentration for growth curves. Under normal circumstances, a mean value of these parameters is taken from different curves and conditions. This value is used as a common parameter for the microorganisms under the experimental conditions.

IPMP-Global Fit takes a different approach. It is designed to analyze the entire data set at the same time in search for the common parameters for each condition and for the entire model. IPMP-Global Fit tries to optimize the fit between the data and model by minimizing the global error, producing estimates for each parameter.

What is difference between IPMP and IPMP-Global Fit?

IPMP analyzes each individual curves, and IPMP-Global Fit works on the entire data.

What is required to use IPMP-Global Fit?

All the statistical analysis and model development are handled seamlessly behind the scenes. No programming knowledge is needed. The user only needs to enter the data and click a few buttons on the screen to complete any data analysis. The only requirement is that the users have a basic knowledge of predictive microbiology to allow for the selection of suitable models for data analysis.

What models are included in IPMP-Global Fit?

The development of IPMP-Global Fit was inspired by the need to solve for a common exponent of different curves of the Weibull model. It contains only one model now, but it will be incrementally expanded to include more models

STRUCTURE of IPMP-Global Fit

IPMP-Global is based on IPMP. So they share similar components and design. If you are familiar with IPMP, you should be able to use IPMP-Global Fit. 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.

Independent variable
Treatment or condition Dependent variable

	Treatment	x	y
1	70	0	0.00
2	70	1	-0.22
3	70	2	-0.32
4	70	0	0.00
5	70	1	-0.21
6	70	2	-0.30
7	80	0	0.00
8	80	1	-0.26
9	80	2	-0.37
10	80	3	-0.45
11	80	0	0.00
12	80	1	-0.25
13	80	2	-0.35
14	80	3	-0.43
15	80	4	-0.50
16	80	5	-0.56
17	90	0	0.00
18	90	1	-0.32
19	90	2	-0.45
20	90	3	-0.55
21	90	4	-0.63
22	90	5	-0.71
23	90	0	0.00
24	90	1	-0.29
25	90	2	-0.41
26	90	3	-0.50

Submit or Clear Data
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

The first column is reserved for “treatment” or “conditions” of experiment. The secondary column is reserved for the independent variables. The third column is reserved for dependent variable. It is recommended that the data of the same treatment are grouped together (Figure 1) before assembling the entire data set.

MATHEMATICAL MODELS IN IPMP-Global Fit

1 – Weibull- Mafart model (Mafart, Couvert, Gaillard, and Leguerinel, 2002)

$$y(t) - y_0 = - \left(\frac{t}{D} \right)^\alpha$$

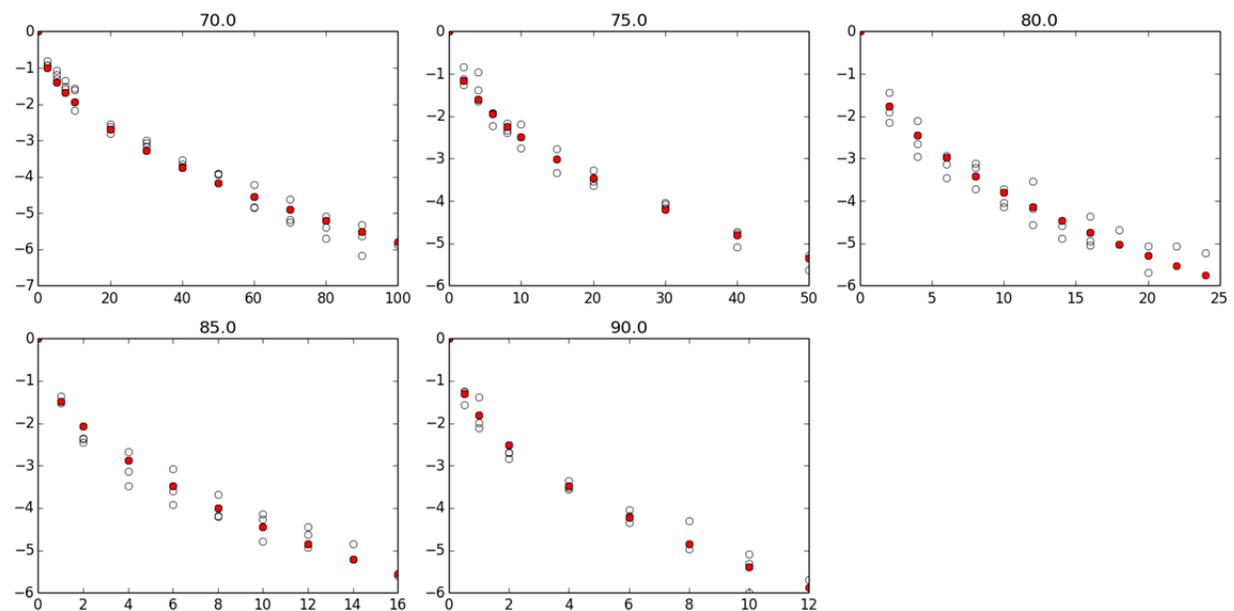


Figure 2. Multiple survival curves are analyzed simultaneously

To use IPMP-Global Fit for Weibull model, the dependent variable is $y - y_0$. This transformation is needed for each survival curve.

References

Mafart, P., Couvert, O., Gaillard, S., and Leguerinel. 2002. On calculating sterility in thermal preservation methods: application of the Weibull frequency distribution model. *International Journal of Food Microbiology*, 72: 107 – 113.