## User Guide for the Share Table Model for *Listeria monocytogenes* in Milk

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### Model Background

The share table model in the present study is an adapted version of the share table model originally published by our group (Reyes et al., 2022). The original work presented a quantitative microbial risk assessment of norovirus transmission in school cafeteria systems with a share table.

We later revised the model to study milk spoilage, specifically for a common, fast-growing psychrotrophic bacteria, *Pseudomonas poae* (Pinto et al., 2024). We utilized the same sharing dynamics as the original model, and additionally tracked the initial level of spoilage bacteria in milks and microbial growth over simulated cafeteria service(s), using the Buchanan 3-phase linear model (Buchanan et al., 1997) and parameters from Lau et al. (2022). Microbial growth was measured for each milk until it was consumed, discarded, or donated. We utilized the empirical temperature data collected during our experimental study of *P. poae* growth as an input to the milk spoilage growth model, and evaluated at what point (if any) contaminated milks in the system exceed our defined spoilage threshold of 6.0 Log10 CFU/ml. We modeled a single scenario, representing our experimental share table: two 50-minute lunch services with a 25-minute break between the services each day (5 days/week, repeated over 1,000 weeks) with no temperature management implemented from the start to the end of the lunch services and overnight refrigeration between days of service. A further adaption of the milk spoilage model was made to evaluate 25 realistic school cafeteria scenarios (Corea et al., 2024). Most scenarios included manipulation of single variables at a time, including length of meal services and breaks, initial spoilage contamination, ambient temperature of the cafeteria, overnight refrigeration temperature, share table storage conditions, and toggling the share table off. We also evaluated scenarios manipulating share table conditions (adding a tray with ice or ice packs) for long and very long meal service lengths. A full description of the scenarios and values input to the model can be found in Table 1 and the supplemental materials of Corea et al. (2024).

This study presents an adaptation of the model from Corea et al. (2024) to assess the safety of milk on share tables by studying: (i) time to 1-Log10 *Listeria monocytogenes* growth, (ii) *L. monocytogenes* concentration at consumption, and (iii) listeriosis risk from milk consumption under 22 scenarios. The initial spoilage contamination scenarios were omitted from this model as the initial contamination of *L. monocytogenes* in pasteurized milk is extremely low. Here, we simulate milk in a cafeteria system with a share table over a 5-day school week (37 weeks/school year, repeated over 50 school years).

### User Guide Overview

This document contains information on input and output datasets, brief descriptions of files needed for a user to run this model, and detailed information and how-to-use for main analysis.

### Input and output datasets

#### Input datasets

* Time and temperature profiles: In the “Pedicted Time and Temp Profiles” folder, there are 21 Df\_RT\_MT\_xxx.csv files created for 22 different time and temperature abuse scenarios (Note: the “no share table” scenario uses the same file as baseline share table scenario).
* Datasets generated for this manuscript: In the “Input Data” folder, there are 22 RDS files that contains the saved data files generated for this manuscript from running this model. These files contain the information used to calculate the (i) time to 1-Log10 *L. monocytogenes* growth, (ii) *L. monocytogenes* growth, and (iii) listeriosis risk from milk consumption under school share table scenarios. You can reproduce the same results if you input these RDS files**. If you rerun the model and generate new main datasets for analysis, you would obtain similar results, but these would vary slightly from what is presented in the manuscript. Thus, these RDS files are saved to this GitHub.**

#### Output datasets

All output datasets saved in “Output Data” folder:

* Time\_to\_1log\_22\_Scenarios.xlsx: save the results of time to 1-Log10 *L. monocytogenes* growth.
* Growth\_during\_d1.xlsx: save the results of *L. monocytogenes* growth on Day 1.
* DR\_Output\_for\_22\_Scenarios.xlsx: save the results of listeriosis risk from milk consumption under school share table scenarios.

### Files needed to run this model

The following are the files needed to run this model. Most of the files do not need to be modified to run the model. For those that need to be changed, the how-to-use and detailed information are described below.

#### Analysis Pinto et al 2025.Rmd

The main analysis file. This file runs the model and generates the results: (i) time to 1-Log10 *L. monocytogenes* growth, (ii) *L. monocytogenes* growth, and (iii) listeriosis risk from milk consumption under school share table scenarios.

#### Calc\_FeedingItems.R

Restock the service line if items ran out for a given day.

#### Calc\_StudentContamination.R

Calculate initial contamination of pathogen or allergen in students.

#### Functions\_Full\_Analysis.R

Create the main data frame for running the share table model.

#### Input\_Functions.R

Create functions for adding time to main data frame.

#### Input\_Random.R

Create functions for generating probabilities of touching food items and other student behaviors (sharing food, picking an additional item from share table, and eating share table items).

#### Input\_RandomWeeks.R

Track the weekly random input of wash hand or hand sanitizer method.

#### Input\_Static.R (Input\_Static\_xxxx.R)

Static inputs in the model, including student data, number and length of services, days and weeks, service line information (number of items and size of selection table), inputs for calculation if student is contaminated, inputs for allergen contamination, inputs behavioral probabilities. Multiple files created for different number and length of services.

#### Main\_Loop.R

Create the Main\_Loop function that runs the model simulation for one food item (whether be touched, whether be contaminated, is there enough in selection table, whether get consumed).

#### Main\_Loops2.R

Create the loops to iterate for students, services, days per week, and weeks per school year.

#### Output\_Days.R

For items left over from one day of service, add the overnight time, growth during overnight time, and return to reservice in next day of service.

#### Output\_Services.R

For items left over from selection table or share table during one day of service, add the growth of *L. monocytogenes* between every service and the turnaround growth.

#### Util\_CCFunctions2.R

Create functions for touching items, picking items (from selection table and share table), eating items, sharing items, and cross contamination.

#### Util\_Counter&Lists.R

Create the empty lists and counters.

#### Util\_DataFrames.R

Add contamination and time to the main data frame.

#### Util\_DFFunctions.R

Create functions for creating data frames for items in one service in the first day, data frames for items in the reservice, and data frame for items that are restocked to service line when run out.

#### Util\_DFWeekCreation.R

Create data frames for sensitivity analysis.

#### Util\_Functions.R

Create functions for searching data frames, log reduction, adding time, unit conversion, etc.

#### Util\_Library.R

Load/library the packages for running the model.

#### Util\_Output\_Functions.R

Create functions for assigning not consumed items (discarded/donated), adding number of services to total, and getting leftover items.

### Detailed description for main analysis files

#### Analysis Pinto et al 2025.Rmd

|  |  |  |
| --- | --- | --- |
| **Function name** | **Description** | **Notes** |
| new\_growth\_rate | Calculate the growth rate at different temperature based on the baseline growth rate at reference temperature in °C | Allow to change the reference temperature (oldTemp) and minimum growth temperature (T0). In this model, oldTemp=5 and T0=-2. |
| new\_lag\_time | Calculate the lag time at different temperature based on the lag time at reference temperature | Allow to change the reference temperature (oldTemp) and minimum growth temperature (T0). In this model, oldTemp=5 and T0=-2. |
| Func\_Growth\_LagCon | Function to calculate *L. monocytogenes* growth (using growth rate, lag time, and maximum growth) based on a time and temperature profile for one milk | Input total lag time consumed (In\_Lag\_Consumed), time and temperature profile (Time\_Temp\_df), time interval in hours in the time and temperature profile (Interval), and adjusting factor (AF). In this model, In\_Lag\_Consumed = 0 and AF = 1. The Time\_Temp\_df is the input data frame (CSV) for each condition. Interval = 1/60. |
| LMO\_Function\_Single\_Milk | Function to calculate *L. monocytogenes* growth over time under Buchanan three phrase (lag, log, and stationary) | Use the Func\_Growth\_LagCon function output, as well as initial concentration (Cont) before growth and maximum growth population (Pop\_Max) for a time and temperature profile. Cont = 0 and Pop\_Max = 8.5. |
| Appling\_Changes | Calculate the *L. monocytogenes* growth over time in the system (by the time consumed, discarded, or donated) for one milk | Input the main data frame generated from the model simulation (df) and the *L. monocytogenes* growth over time generated from LMO\_Function\_Sinlge\_Milk (Changes\_Over\_Time). |
| Obtaining\_LMO\_Milks\_DFs | Run the share table model with N\_Years of simulations | Input number of years for simulations (N\_Years), length of the service (Service\_Length), and length of the turnaround (TurningT\_Length). In this model, N\_Years = 50. For baseline, Service\_Length = 50 and TurningT\_Length = 50; for other lengths of service, Service\_Length and TurningT\_Length need to be changed accordingly. |
| dose\_response\_listeria | Calculate the probability of illness per serving of milk based on the *L. monocytogenes* concentration in the milk carton at the point of consumption | Input the data frame contained information about *L. monocytogenes* concentration at consumption (df), exponential dose-response parameter (r\_mean, r\_sd), the serving size used to calculate the total dose of *L. monocytogenes* at the point of consumption (serving\_size), and indicator created to note which scenarios (scenario). In this model, we choose the dose-response parameter from Pouillot et al., 2024 for a virulent strain of *L. monocytogenes* in 5 to 14-year-old females, r\_mean = -12.582, r\_sd = 0.836. |
| LMO\_for\_1log\_change | Calculate the time for *L. monocytogenes* 1log change based on a time and temperature profile | Like LMO\_Function\_Single\_Milk, but one indicator was added to calculate the time for *L. monocytogenes* growth over 1log using the same input variables. |
| Cat\_Time\_1log | Calculate number and percentage of milks consumed with 1log change of *L. monocytogenes* and maximum *L. monocytogenes* log change per day in the system | Input the data frame contained information about *L. monocytogenes* concentration at consumption (df) and the length of total service time (bell\_schedule). For baseline, bell\_schedule = 125, which calculated as 1440 minus total overnight time, 1315; for other lengths of service, bell\_schedule is calculated accordingly. |
| delta\_d1 | Calculate the growth of *L. monocytogenes* (median, 5th and 95th percentiles) for milk (by consumed, discarded, and donated) on the first day of service | Input the data frame contained information about *L. monocytogenes* concentration at consumption (df) and the length of total service time (bell\_schedule). For baseline, bell\_schedule = 125, which calculated as 1440 minus total overnight time, 1315; for other lengths of service, bell\_schedule is calculated accordingly. |

#### Input\_Static.R (Input\_Static\_xxxx.R)

Several essential objects in this file serve as inputs to the model. These are **static** inputs, meaning that these numbers will not change unless they are edited prior to the running of the model.

|  |  |  |
| --- | --- | --- |
| **Object name** | **Description** | **Notes** |
| Students\_p\_grade | Number of students per grade in the United States | The default value is 89 for this model. |
| NSLP\_rate | National School Lunch Program participation rate (%) | The default value is 0.73 for this model. |
| N\_Iterations | Number of children going through the meal service line | The value is calculated by multiplying Students\_p\_grade by NSLP\_rate |
| Service\_No | Number of meal services per day | For the baseline, it is set to 2; for different lengths of service (very short, medium, long, or very long), it is set to 1, 3, 4, or 5. |
| Food\_Days | Number of days that meal services occur per week | The default value is 5, which represents standard 5-day school week in the United States. |
| Sens\_Iterations | Number of weeks per year for each simulation (37 weeks for a school year) | The default value is 37, which represents 37 weeks for a school year in the United States. |
| Time\_Service\_Length\* | Length of time (in minutes) for one meal service | For baseline, long and very long service, it is set to 50; for different lengths of service (very short, short, or medium), it is set to 40, 30, or 31 respectively. |
| Time\_Turnaround\_Length\* | Length of time (in minutes) for break that occurs in between meal services | For baseline, it is set to 25; for different lengths of service (very short, short, medium, long, or very long), it is set to 0, 14, 16, 7, or 4 respectively. |
| Time\_Overnight\_Length\* | Length of time (in minutes) between the end of the last service on a given day and the start of services on the following day | For baseline and medium service, it is set to 1315, for different lengths of service (very short, short, long, or very long), it is set to 1400, 1366, 1219, or 1174 respectively. |
| Initial\_Pre | Number of packaged refrigerated foods stocked on the meal service line | The default value is 50 for this model. |
| Row\_Size\_Pre | Number of packaged refrigerated foods would be on the selection table | The default value is 20 for this model. |
| Pr\_touch\_Food | Probability of a student touching other line items before picking their food from the selection table | The default value is 1 for this model. |
| Pr\_touch\_Food\_ST | Probability of a student touching other line items before picking their food from the share table | The default value is 1 for this model. |
| Pr\_select\_Pre | Probability of selecting a packaged refrigerated food | The default value is 0.96 for this model. |
| Pr\_eat\_Pre | Probability of consuming a packaged refrigerated food | The default value is 0.674 for this model. |
| Milk\_Con\_Mean | The mean contamination of *L. monocytogenes* in a milk carton | The default value is -3.99 (Log10CFU/ml) for this model. |
| Milk\_Con\_SD | The standard deviation of contamination of *L. monocytogenes* in a milk carton | The default value is 0.8 (Log10CFU/ml) for this model. |
| Listeria\_Safety\_Treshold | The threshold in log CFU/ml in which milk would be considered over *L. monocytogenes* 2-log growth safety threshold | The default value is 2 (Log10CFU/ml) for this model. |
| Calculated\_Cont\_Pre | Toggle to turn on calculation for the contamination of a packaged refrigerated food (milk) in the system | The default value is 1 for this model. |
| Pre\_Mean\_area | Physical characteristics of packaged refrigerated food | The default value is 300 (cm2) for milk in this model. |
| Sim\_Pre | Toggle to turn on simulation for a packaged refrigerated food (milk). | The default value is 1 for this model. |
| Cross\_contamination | Toggle to turn on cross-contamination in the simulation | The default value is 1 for this model. |
| Ill\_Avoid\_ST | Toggle to turn off simulation for ill students avoiding share table. | The default value is 0 for this model. |
| Pr\_Ill\_Avoid\_ST | The probability of whether the ill students would avoid share table. | The default value is 0.5 for this model. |
| Growth\_Pre | Toggle to turn off usage of the growth model (and parameters) built in the Input\_Functions.R | The default value is 0 for this model since the growth model (and parameters) was built in the main analysis rmd file. |
| Share\_Table\_YN | Toggle on/off to include the share table or not in the simulation. | It is set to 0 when running a model with no share table; it is set to 1 when running a model with share table. |
| STtoReservice\_YN | Toggle on to include the reservice of share table | If the share table is on (Share\_Table\_YN=1), this value is set to 1 to turn on the reservice. |
| Milk\_Listeria\_YN | Toggle on to add the columns about *L. monocytogenes* growth to the main data frame | The default value is “TRUE” in this model. |
| Donation\_End\_Week | Toggle on to change location of any milk at the end of Day 5 that is not consumed or discarded to be donated | The default value is “TRUE” in this model. |

\*These must add up to 1440 minutes (24 hours; 1 day)

### How to use

#### Run the analyses in the **Analysis Pinto et al 2025.Rmd**

1. Model set up
   1. Set working directory by running first chunk: 
   2. Loading all required libraries, inputs, and functions saved in R files:

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Description automatically generated

* 1. Create the functions for Listeria growth model for a single milk:

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* 1. Create the function to apply growth model based on time and temperature profile:

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* 1. Impot all time and temperature profiles:

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1. Run the model and create the main output dataframes
   1. Create the function to run the model using the inputs and functions in loaded R files:

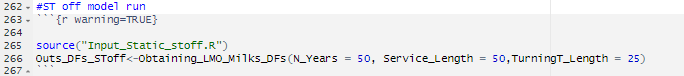
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* 1. Run the model with baseline service, as well as other conditions (typically take around 5 hours for each model run). For different length of services and toggling share table off conditions, different Input\_Static.R files are sourced and applied:

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* 1. Generate the combined dataset for each condition (run the chunks for 22 scenarios, line 303-677):

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* 1. Output the combined datasets as RDS files saved in the “Output Data” folder:

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1. Run the main analyses for this study
   1. Load the RDS files saved in the “Input Data” folder:

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* 1. Run the dose response analysis and generate the results of P(ill) from milk consumption (results for Table 4):

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* 1. Run the time to 1 log change analysis and generate the time (in days) for Listeria in milk reach 1 log increase (results for Table 2):

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* 1. Run the categorical analysis for consumed milks reached 1 log change in service days (results for Table 2):

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* 1. Calculate *the L. monocytogenes* growth in Day 1 under share table scenario compared to no share table scenario and create the comparison figure (results for Figure 1):

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### Files not in use

Some files (listed below) were created for our previous studies, but not used in this model. Thus, they were saved in the “files not in use” folder. The time and temperature profiles used in this study were generated using some of these files. You can reproduce results in this study without using the following files, but you might need these files to make more advanced modifications.

#### Bell Schedule Analysis.Rmd

#### Calc\_TimeTempProfiles.R

#### Calculations for growth rate adjustment.R

#### Time and Temperature Profiles Generator.Rmd

#### Trial Spoilage Function.R

#### Milk Internal Temperature Predictor.Rmd

#### Util\_VisualFunctions.R

#### Util\_FunctionFoodWaste.R

### References

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