

# Risk Management Tool for the Control of *Campylobacter* and *Salmonella* spp. in Chicken Meat

(Version 1.0)

## User Guide

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## Overview

This web site provides access to a risk management simulation tool based on the Codex Guidelines for the Control of *Campylobacter* and *Salmonella* in Chicken Meat available at:

[http://www.codexalimentarius.net/download/standards/11780/CXG\\_078e.pdf](http://www.codexalimentarius.net/download/standards/11780/CXG_078e.pdf).

The tool can model the complete production-to-consumption process flow described in the Guidelines. These models are referred to as process flows. Users may investigate one or both pathogens and determine which steps to include in the process flow.

The tool is designed to compute the residual risk between a baseline process flow and a process flow applying selected interventions as outlined in the Guidelines. The residual risk measure may be used to evaluate the overall effectiveness of the applied interventions.

Users define the process flow in terms of stages that change the concentration and/or prevalence of broiler carcasses as they move through the process flow. These stages are parameterized by a mix of fixed values and distributions (e.g. a growth stage may result in an increase in concentration characterized by a Normal distribution of  $2 \log_{10}$  with a standard deviation of 0.4). The tool uses Monte Carlo simulation to calculate the net effect of the entire process flow and to calculate the residual risk measure.

Users should be familiar with poultry processing and statistics in general, as well as Monte Carlo simulation and the Guidelines in particular. Reviewing the Guidelines before continuing with this document is strongly recommended. Links to several additional background documents are also provided on the tool's web site for reference, including a tutorial illustrating the creation of a process flow.

Please also review the disclaimer and privacy policy provided on the web site.

There are several steps required to use the tool and build process flow scenarios.

- Step 1: Register your account
- Step 2: Login
- Step 3: Navigate using the main tool bar
- Step 4: Load an existing process flow or create a new process flow
- Step 5: Navigate using the process flow tool bar
- Step 6: Edit the process flow name and description
- Step 7: Edit the process flow model for one or both pathogens
- Step 8: Review the process flow model for one or both pathogens
- Step 9: Run the models and review results

## Glossary

Term	Definition
Carcass	A single bird (prior to slaughter) or carcass (post-slaughter). The carcass is the unit used when computing changes in concentration.
Flock	A collection of carcasses processed as a group.
Contaminated	The presence of one or more pathogens on one or more carcasses in a flock.
Within Broiler Flock Prevalence	The fraction of carcasses that are contaminated in a flock, as defined above.
Between Broiler Flock Prevalence	The fraction of flocks, as defined above, which contain contaminated carcasses.
Process Type	The tool provides several process types to model stages. These include types such as growth, decrease and prevalence changes.
Stage	A single process step in the overall process flow (e.g. defeathering, inside/outside wash). Each stage is modeled using a process type.
Intervention	A process added to the process flow with the intention of reducing contamination and/or prevalence, and therefore reducing risk compared to the baseline scenario.
Process Flow	A sequence of stages and interventions describing the flow of carcasses through production, processing and consumption.
Baseline Scenario	The process flow as described, excluding any interventions.
Path	A process flow may be split into one or more paths to model distinctly different processes (e.g. some carcasses are stored fresh while others frozen)
Residual Risk	Residual risk is the ratio of the mean risk of illness per serving of the pathways including interventions to the mean risk of illness per serving of the baseline scenario (no interventions). A value of one indicates no change. Values greater than one indicate an increase in risk while values less than one indicate a decrease in risk relative to the baseline scenario. For example, if the interventions reduce the risk by half, the residual risk will be 0.5.
Weighted Residual Risk	The weighted residual risk of all paths is the sum of the residual risk of each path weighted by the probability of that path.

## Step 1: Register your account

Before using the tool, each user must create an account. This account will allow users to maintain a private workspace for their process flow models, and store them for subsequent use.

The registration page may be accessed from the home page.

Please [login](#) or [register](#). ←

To create an account, fill in the email address, password and confirmation textboxes for the account, and then click the "Register" button.

### Register

The purpose of registration is to allow the user to save process models for subsequent use. These models will not be available to other users.

Please complete the following form to register. Email address and password are required.

**Email Address:**  (will act as user ID)

**Confirm Email:**

**Password (show):**

**Confirm Password:**

To simplify verification of the password, click the "show" link beside the "Password" label. If "show" is clicked, the password is no longer hidden and the "show" link is replaced by a "hide" link. Clicking the "hide" link hides the password again.

If the account already exists, the user will receive a warning message with a link to the password reminder page. In this case, use the password reminder page to have the application send a reminder email with the account password.

The password reminder feature only works if a valid email address was entered when registering.

## Step 2: Login

To login, go to the login page. Enter the email address and password used to create the account and click the "Login" button. Users must check the "I have reviewed the disclaimer" checkbox each time they log in. Please review the disclaimer.

### Login

**Email Address:**

**Password:**

I have reviewed the [disclaimer](#).

([password reminder](#))

If you do not currently have an account, please [register](#) to use the tool.

A link is provided on the login page for a password reminder. The password reminder will send the account password to the provided email address, assuming the email address corresponds to a valid user account. If no match is found, register a new account.

### Password Reminder

Please enter your email address to receive a password reminder.

**Email Address:**

The login page will redirect the user to the Process Flow List page by default.

### Step 3: Navigate using the main toolbar

The main toolbar at the top of the web page provides quick links to the following site features:

- Home
- Process Flow List
- Documents
- User Guide
- Tutorial
- Send Comments
- Login/Logout

#### **Risk Management Tool for the Control of *Campylobacter* and *Salmonella* spp. in Chicken Meat** (Version 1.0)

[Home](#) | [Process Flow List](#) | [Documents](#) | [User Guide](#) | [Tutorial](#) | [Send Comments](#) | [Logout](#)  
(username@mramodels.org)

#### **Home**

This link opens the home page for the application.

#### **Process Flow List**

This link opens the list of process flows for the current account.

#### **Documents**

This link opens a new window with links to supporting documents, including the Guidelines.

#### **User Guide**

This link opens a new window with a PDF copy of the current user guide.

#### **Tutorial**

This link opens a new window with a PDF copy of the current tutorial.

#### **Send Comments**

This link opens a form with which to send comments on the application.

#### **Login/Logout**

When the user is logged in, clicking on this link will logout the current account. When the user is not logged in, it provides a link to the login page.

When logged in, the email address of the current account is displayed to the right of this link, or below the toolbar as in the above example.



## Step 4: Load an existing process flow or create a new process flow

From the Process Flow List page, the user may choose to view/edit, copy or delete an existing process flow, or create a new process flow.

### Process Flows

Select an existing process flow from the list below and click View/Edit to work with that process flow, click Copy to make a copy, Delete to delete the process flow, or click New Flow to create a new process flow.

Please review the [Guidelines](#) and [user guide](#) before using this tool.

Existing Flows			New Flow		
Name	Description	Created On			
Process Flow 1		28-Nov-2011 20:47:00 EST	<a href="#">View/Edit</a>	<a href="#">Copy</a>	<a href="#">Delete</a>
Process Flow 2		28-Nov-2011 20:47:08 EST	<a href="#">View/Edit</a>	<a href="#">Copy</a>	<a href="#">Delete</a>

Each of the user's existing process flows will be listed alphabetically in the table. Click on the View/Edit link to view/edit the process flow, the Copy link to make a copy, or the Delete link to delete the flow.

When first accessing this page after creating an account, the list will be empty and the user must click on New Flow to create a new process flow.

Clicking the Copy link creates a copy of the selected Process Flow and then opens the edit page for the new Process Flow.

If the Delete link is clicked, the user will be prompted to confirm or cancel the deletion.

### Delete Process Flows

Please confirm the deletion of the process flow below. Note that this process is permanent and the data cannot be recovered. You may wish to print the model and result pages first as a permanent reference.

**Name:** Process Flow 1

**Description:**

**Created On:** 30-Nov-2011 09:22:22

Deletion is irreversible.

## Step 5: Navigate using the process flow tool bar

When viewing or editing a Process Flow, the Process Flow toolbar is added to the top of the page.

---

**Name and Description** | [Campylobacter Model](#) | [Campylobacter Results](#) | [Salmonella Model](#) | [Salmonella Results](#)

---

Using this toolbar, the user can access the following forms for the current process flow:

- Name and Description
- *Campylobacter* Model
- *Campylobacter* Results
- *Salmonella* Model
- *Salmonella* Results

These forms are described in more detail in the subsequent sections.

## Step 6: Edit the process flow name and description

When the user opens a process flow or clicks on the Name and Description link in the process flow toolbar, the Name and Description form is presented.

---

**Name and Description** | [Campylobacter Model](#) | [Campylobacter Results](#) | [Salmonella Model](#) | [Salmonella Results](#)

---

### Name and Description

Please define the name and description for this process flow. Click "Save" to save the changes. Click on the appropriate model or result links in the toolbar above to edit or run the models for each pathogen. Models for each pathogen are constructed separately.

Please see [Page Help](#) for details on this page.

**Process Flow Name:**

**Description:**

On this page, the user may update the Process Flow name and description.

Click "Save Changes" to save the changes. Click "Save And Close" to save the changes and return to the process flow list page. Click on "Close" to return to the process flow list page without saving.

A user may also return to the process list page without saving by clicking on the Process Flow List link in the main toolbar.

## Step 7: Edit the process flow model for one or both pathogens

In this application, models for *Campylobacter* and *Salmonella* are constructed and run separately. Users may choose to implement models for one or both pathogens in each process flow.

Users assemble a process flow model using a flowchart style of interface. When a new model is first opened, the user will see the following form:

**Elements Common to All Paths**

<table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="text-align: center; width: 30px;"><u>IC</u></td> <td><b>Initial Contamination</b></td> </tr> <tr> <td colspan="2">Not defined Specified for: First Step Within Prevalence: Fixed Value (Value: 0) Between Prevalence: 0</td> </tr> </table>	<u>IC</u>	<b>Initial Contamination</b>	Not defined Specified for: First Step Within Prevalence: Fixed Value (Value: 0) Between Prevalence: 0		<table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="text-align: center; width: 30px;"><u>DR</u></td> <td><b>Dose Response</b></td> </tr> <tr> <td colspan="2">Beta-Poisson (alpha:0.21 beta:59.95; probability of illness given infection=0.33; fraction consumed=0.25)</td> </tr> </table>	<u>DR</u>	<b>Dose Response</b>	Beta-Poisson (alpha:0.21 beta:59.95; probability of illness given infection=0.33; fraction consumed=0.25)	
<u>IC</u>	<b>Initial Contamination</b>								
Not defined Specified for: First Step Within Prevalence: Fixed Value (Value: 0) Between Prevalence: 0									
<u>DR</u>	<b>Dose Response</b>								
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<table border="1" style="width: 100%; border-collapse: collapse;"> <tr> <td style="text-align: center; width: 30px;"><u>CP</u></td> <td><b>Consumer Practices</b></td> </tr> <tr> <td colspan="2">Cooking log reduction: Fixed Value (Value: 0); Frequency of cross contamination: 0; Proportion consumed uncooked: N/A; Frequency undercooked: 0; Log reduction when undercooked: N/A</td> </tr> </table>		<u>CP</u>	<b>Consumer Practices</b>	Cooking log reduction: Fixed Value (Value: 0); Frequency of cross contamination: 0; Proportion consumed uncooked: N/A; Frequency undercooked: 0; Log reduction when undercooked: N/A					
<u>CP</u>	<b>Consumer Practices</b>								
Cooking log reduction: Fixed Value (Value: 0); Frequency of cross contamination: 0; Proportion consumed uncooked: N/A; Frequency undercooked: 0; Log reduction when undercooked: N/A									

**Process Flow**

**Process Types**

No significant change	Increase (growth)	Increase (addition - within flock)
Decrease	Cross-contamination (within flock)	Within Flock Prevalence Decrease
Between Flock Prevalence Decrease	Within Flock Prevalence Increase	Between Flock Prevalence Increase

P0	<b>Initial Path</b>
----	---------------------

Insert Stage | Insert Path

The nodes Initial Contamination (IC), Dose Response (DR), Consumer Practices (CP) and Path 0 (P0) are included by default and cannot be deleted. However, Initial Contamination, Dose Response, and Consumer Practices may be edited. In addition, users may add stages, interventions and paths to complete the process flow model. Each model requires at least one path and this is represented by Path 0 (P0).

**PLEASE NOTE: The user must review and modify the Initial Contamination and Consumer Practices node to set the values based on their data.** While the user may edit the Dose Response model, it is expected that most users will use the default provided.

### ***A Note about Numerical Values***

The user will be required to enter many parameter values in the model. Numerical parameter values may be entered in either decimal notation (e.g. 3) or scientific notation (e.g. 2E-2).

## Initial Contamination

To review and edit the Initial Contamination parameters for the model, the user clicks on the IC link in the top left box of the Initial contamination node on the Model page.

**Elements Common to All Paths**

<u>IC</u>	<b>Initial Contamination</b>	<u>DR</u>	<b>Dose Response</b>
	Not defined Specified for: First Step Within Prevalence: Fixed Value (Value: 0) Between Prevalence: 0		Beta-Poisson (alpha:0.21 beta:59.95; probability of illness given infection=0.33; fraction consumed=0.25)

<u>CP</u>	<b>Consumer Practices</b>
	Cooking log reduction: Fixed Value (Value: 0); Frequency of cross contamination: 0; Proportion consumed uncooked: N/A; Frequency undercooked: 0; Log reduction when undercooked: N/A

This opens the Initial Contamination form:

Initial concentration must be between 0 and 15 log<sub>10</sub> cfu/carcass. Note that this is per carcass and not per g or per ml. Initial prevalence values must be greater than 0 and less than or equal to 1. Distributions are permitted for Initial Concentration and Within Flock Prevalence, but not for Between Flock Prevalence.

**Initial Concentration (0-15 log<sub>10</sub> cfu/carcass)**  
Distribution:   
Mean:   
Standard deviation:   
Specified for:

**Within Flock Prevalence (0-1)**  
Prevalence: Distribution:   
Value:

**Between Flock Prevalence (0-1)**  
Prevalence:

**Comments:**

Please note that when a process flow is created, the initial concentration is set to 0 log<sub>10</sub> cfu/carcass, and the initial prevalence values are set to 0. The user must assign appropriate values for the new model based on their data or research.

Prevalence is specified as a value between 0 and 1. Please note that the prevalence is for the broiler flock (i.e. during processing). For example, if the step "Manage grandparent flocks" was included in the model, the user would enter prevalence values here that would be observed in the broiler flock due to management techniques and not in the grandparent flock itself.

This also applies to concentration, which is specified in log<sub>10</sub> cfu/carcass in the broiler flock. While the user may elect to define their process flow starting from the very first stage (e.g. Manage Grandparent Flocks), the user should carefully select the point at which the process flow starts modeling concentration (and prevalence) based on available data and research (e.g. after defeathering).

Note that the concentration is **per carcass** and not per gram or per milliliter. Please refer to Appendix A for a discussion of converting from cfu/g and cfu/ml to cfu/carcass.

When defining the initial concentration values, the user may select from the following distributions:

- Beta PERT
- Cumulative
- Fixed Value (no distribution)
- Normal
- Triangular
- Uniform

When changing the distribution, allow the page to reload before modifying the parameter values as each distribution has different parameter requirements. In particular, review the on screen instructions for specifying the Cumulative Empirical distribution.

Note that the parameters are on the  $\log_{10}$  scale when selecting the appropriate distribution. To aid in properly parameterizing the distributions, users may click on the Show Chart button for all distributions except Fixed Value. Please note that this does not save changes.

Caution should be exercised when using the Normal distribution. Some combinations of mean and standard deviation may result in the simulation generating values outside the specified range for parameters. If the mean +/- four standard deviations falls outside the range for the parameter, a warning message will be displayed. Users may elect to ignore the message, but are strongly encouraged to adjust the parameters or select a bounded distribution such as the Beta PERT instead.

While the user may note the step at which the initial concentration is first applied in the "Specified for" textbox, the user determines which stages modify concentration by selecting appropriate process types (see the Add a Stage section). This textbox is provided for notation only and the user must exercise caution that changes to concentration are not applied before intended.

The user may also specify within flock prevalence as a distribution. In this case, however, the Normal distribution is not an option as prevalence must be bounded between 0 and 1.

Between lot prevalence may only be specified as a fixed value.

The Save Changes and Save And Close buttons will both save changes. The Save and Close and Close buttons will return the user to the model page. The Close button does not save changes.



## Consumer Practices

Consumer practice models the in-kitchen practices in consumer homes. It allows the user to define an expected log reduction resulting from cooking.

The user may optional specify parameters for cross contamination and undercooking as well.

To edit the consumer practices parameters for the model, the user clicks on the CP link in the top left box of the Consumer Practices node.

<a href="#">CP</a>	<b>Consumer Practices</b>
Cooking log reduction: Fixed Value (Value: 0); Frequency of cross contamination: 0; Proportion consumed uncooked: N/A; Frequency undercooked: 0; Log reduction when undercooked: N/A	

This will open the consumer practices form, as shown on the next two screenshots:

### Consumer Practices Page - *Campylobacter*

Consumer practices consists of cooking and two optional elements: cross contamination and undercooking.

<b>Consumer Cooking</b>
Specify the log <sub>10</sub> reduction achieved through the cooking process.
<b>Cooking Log<sub>10</sub> Reduction:</b> <input type="text" value="Fixed Value"/> (Should range between 0 and 15)
<b>Value:</b> <input type="text" value="0"/>

### Cross Contamination

Optionally specify the mean frequency that cross contamination events occur as well as the proportion of pathogens that will be consumed uncooked through transfer to surfaces and other foods. This proportion is assumed removed from the carcass prior to cooking. To exclude cross contamination, set the frequency value to 0.

**Frequency of Cross Contamination:**  (0-1)

**Proportion of Pathogens Consumed Uncooked:**  (Should range between 0 and 1)

**Value:**

### Undercooking

Optionally specify a frequency that carcasses are undercooked and the  $\log_{10}$  reduction achieved when the carcass is undercooked. To exclude undercooking, set the frequency value to 0.

**Frequency Undercooked:**  (0-1)

**Log<sub>10</sub> Reduction when Undercooked:**  (Should range between 0 and 15)

**Value:**

The user should first specify a standard  $\log_{10}$  reduction from consumer cooking.

Optionally, the user may include cross contamination by specifying the expected frequency of cross contamination events and the proportion of pathogens consumed uncooked (as a fraction of the total count available on the carcass). To exclude cross contamination, the user must leave or set the frequency to 0.

As well, the user may also include undercooking by specifying a frequency at which carcasses are undercooked and the reduced cooking log reduction experiences by those carcasses. To exclude undercooking, the user must leave or set the frequency to 0.


Frequencies are specified as fixed values between 0 and 1, while the proportion and cooking log reductions may be specified as distributions or fixed values.

By default, all values on this page are set to 0 for new process flows and the user must define appropriate parameter values based on their data and research.

It is important for the user to remember to save changes for these modifications to take effect. The Save Changes and Save And Close buttons will both save changes. The Save and Close and Close buttons will return the user to the model page. The Close button does not save changes.

## Dose Response

To review and edit the Dose Response model and parameters, the user clicks on the DR link in the top left box of the Dose Response node.

<a href="#">DR</a>	<b>Dose Response</b>
	Beta-Poisson (alpha:0.21 beta:59.95; probability of illness given infection=0.33; fraction consumed=0.25)

This opens the Dose Response Model form.

## Default Models

By default, the model will use the JEMRA dose response model for each pathogen, as specified on the form. By default, the model also assumes a serving size of ¼ (0.25) of a carcass.

E.g. Model for *Campylobacter*:

**Model Type:** Beta-Poisson  
**alpha:** 0.21 (No units)  
**beta:** 59.95 (No units)  
**Probability of adverse effect given response:** 0.33 (0-1, use 1 when dose response is for effect)  
[Show Chart](#)  
**Fraction of Carcass Consumed:** 0.25 (>0-1)

For more information on the default dose response models, please refer to the risk assessments carried out by FAO/WHO of *Campylobacter* and *Salmonella* in broiler chickens:

Risk assessment of *Salmonella* in eggs and broiler chickens. 2002. Microbiological Risk Assessment Series 2. Available at <ftp://ftp.fao.org/docrep/fao/005/y4392e/y4392e00.pdf>

Risk assessment of *Campylobacter* spp. in broiler chickens: Technical Report. 2002. Microbiological Risk Assessment Series 12. Available at <http://www.fao.org/ag/agn/agns/JEMRA/MRA%2012%20final%20for%20web.pdf>

## Custom Models

The user may choose to implement a custom dose response model instead and change the serving size. To do this, the user clicks on the "Use Custom Model" option.

- Use Default Model  
 Use Custom Model

This will cause the page to reload and present the user with editable fields with which to specify the model and serving size.

**Model Type:**

**alpha:**  (No units)

**beta:**  (No units)

**Probability of adverse effect given response:**  (0-1, use 1 when dose response is for effect)

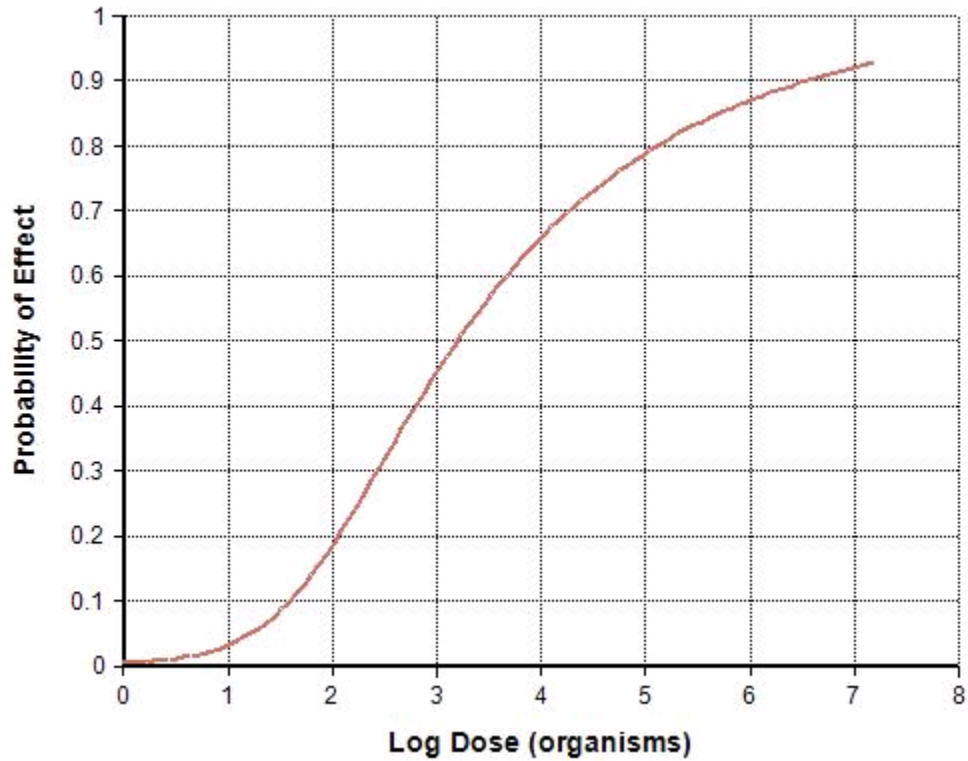
**Fraction of Carcass Consumed:**  (>0-1)

Users have the choice of the following dose response model forms:

- Beta-Poisson
- Exponential
- Linear

If the model type is changed, the user must allow the page to reload before specifying the parameters.

Users can review the current dose response model by clicking on the "Show Chart" button. This chart shows the probability of effect given the dose. The Probability of Adverse Effect Given Response is used to denote the percentage of responses that result in an adverse effect.



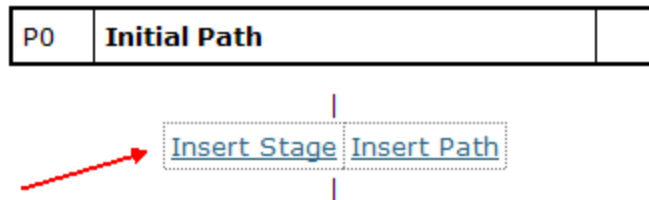
The user can at any time revert back to the default model by clicking on the "Use Default Model" radio button.

It is important for the user to remember to save changes for these modifications to take effect. The Save Changes and Save And Close buttons will both save changes. The Save and Close and Close buttons will return the user to the model page. The Close button does not save changes.

## Adding a Stage

Once the fixed elements of the model are reviewed and revised, the user then constructs the process flow model itself by adding stages, interventions and paths.

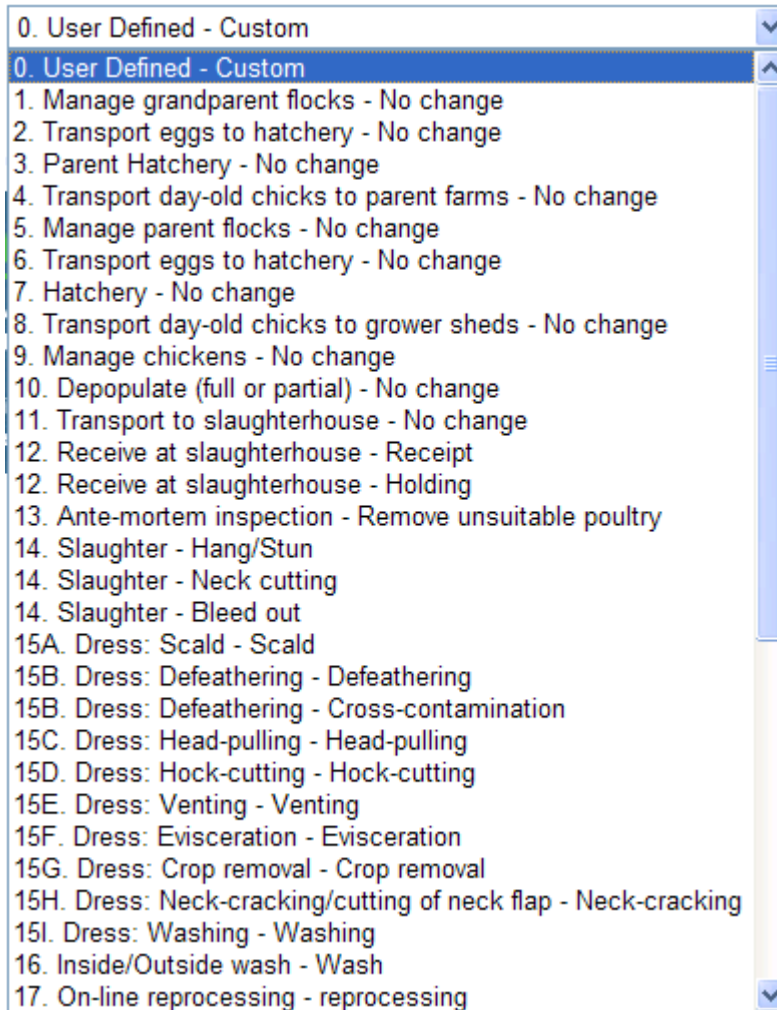
When the process flow model is first opened, no stages are provided. To add a stage, the user clicks on the Insert Stage link below the Initial Path node.



This will open a new page where the user must select the type of stage to add and confirm the addition.

**Select stage:**

The default is a user defined custom stage. However, the user may select from a list of predefined stages based on the guidelines. Please note that these stages, at present, do not have any associated parameters and are included primarily to allow the user to construct a flow based on the terms and sequence described in the Guidelines.



When the user clicks Continue, the stage is added to the model and the Stage Edit form is opened.

**Path-Sequence: 0-1**

**Step:** **User Defined (Custom) - *Campylobacter***

**Step Type:** **0**

**Stage Name:**

**Process Type:**

**Instructions:** No change in prevalence or concentration.

**Distribution:** Not applicable (Should be greater than or equal to 0 and less than or equal to 0)

This form has several important elements.

## **Path-Sequence**

The Path-Sequence shows the current path number for the stage, and the sequence of this stage in that path.

## **Step Type**

Step Type corresponds to the step number from the guidelines and is included for cross referencing.

## **Stage Name**

Users may change the stage name to better describe the stage.

## **Process Type**

Users must select the process type for this stage. There are nine process types:

- No significant change
- Increase (growth)
- Increase (addition – within flock)
- Decrease
- Cross-contamination (within flock)
- Within Flock Prevalence Decrease
- Between Flock Prevalence Decrease
- Within Flock Prevalence Increase
- Between Flock Prevalence Increase

By default, No significant change is selected.

Each process type has its own parameter requirements. Users may find it necessary to create two stages in sequence to completely characterize a process step. For example, a washing step might require both a decrease and cross-contamination process. The user needs to decide the sequence in which the two processes would occur. The order selected may have implications for the net prevalence and concentration values at the end of both processes.

## **List of Process Types**

### **No significant change**

- This process type will not change concentration or prevalence values. It is used primarily to indicate the user has considered the stage and determined that it results in no significant change.

### **Increase (growth)**





This process type will increase the current concentration, on the  $\log_{10}$  scale, by the amount specified (on the  $\log_{10}$  scale).

Prevalence values remain unchanged.

### **Increase (addition – within flock)**



This process type may or may not add the amount specified (on the  $\log_{10}$  scale) to each carcass in the flock based on the likelihood (0-1). The amount may be added to currently contaminated carcasses or currently uncontaminated carcasses. Also, currently contaminated carcasses may not have any amount added. For example, if 30% of carcasses are currently contaminated and the likelihood of addition is 0.4 (40%), then 12% of the previously contaminated carcasses will have this amount added while 18% will not. In addition, 40% of the 70% uncontaminated carcasses will now be contaminated with the amount specified at this stage.

Within flock prevalence is adjusted (increased) to reflect the increase in the number of carcasses in the flock that are contaminated after this stage. Between flock prevalence remains unchanged.

With the current version, rare-event additions cannot be modeled in the tool. The lower limit on the likelihood is set to 0.002 (0.2%).

### **Decrease**



This process type will reduce the current contamination by the amount specified, on the  $\log_{10}$  scale. As the tool models only contaminated carcasses with their associated prevalence, if this reduction results in the complete elimination of pathogens on some carcasses then the concentration for those carcasses is set to 1 cfu/carcass (0  $\log_{10}$  cfu/carcass). However, the within flock prevalence is reduced appropriately to reflect the reduced likelihood of any carcass being contaminated.

### **Cross-contamination (within flock)**



This process type will add the specified  $\log_{10}$  increase values to the current concentration. Prevalence values remain unchanged.

### **Within Flock Prevalence Decrease**



This process type reduces the within flock prevalence by the amount specified. For example, a value of 0.2 will result in a 20% reduction in within flock prevalence.

Between flock prevalence and concentration are not modified.

### Between Flock Prevalence Decrease



This process type reduces the between flock prevalence by the amount specified. For example, a value of 0.2 will result in a 20% reduction in between flock prevalence.

Within flock prevalence and concentration are not modified.

### Within Flock Prevalence Increase



This process type increases the within flock prevalence by the amount specified. For example, a value of 0.2 will result in a 20% increase in within flock prevalence.

Between flock prevalence and concentration are not modified.

### Between Flock Prevalence Increase



This process type increases the between flock prevalence by the amount specified. For example, a value of 0.2 will result in a 20% increase in between flock prevalence.

Within flock prevalence and concentration are not modified.

As with other forms, if the user changes the process type or the distribution for the current process type, the page must reload before the parameter values are modified. For example, if the user selects Increase (growth), the following will appear:

<b>Process Type:</b>	<input type="text" value="Increase (growth)"/>
<b>Instructions:</b>	Increase in concentration. Select a distribution for the magnitude of growth (log <sub>10</sub> ).
<b>Distribution:</b>	<input type="text" value="Fixed Value"/>
Value:	<input type="text" value="0"/>

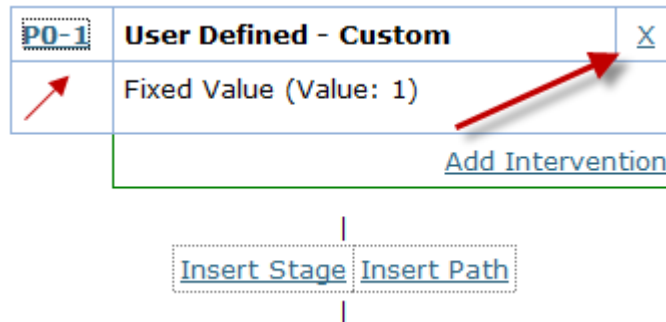
## Comments

Users may also add comments in the comment field for this stage for future reference:

### Comments:

## Deleting a Stage

Users can delete an existing stage by clicking on the X in the top right box of the stage node.



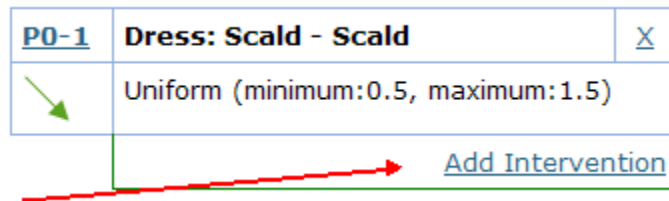
A confirmation screen will open. Deleting a stage is permanent, though the user could recreate the stage using the Insert Stage link and completing the relevant forms again.

The Insert Stage link will always insert the stage at the selected location in the model flow chart.

## Adding an Intervention

This simulation model is designed to compute the residual risk between a baseline scenario and a scenario including interventions. The user should therefore specify at least one intervention in the model. An intervention is defined for specific stages in the process flow model. The user indicates whether the intervention is applied before, after or replaces the stage. Only one "replaces" intervention type can be applied to each stage.

To add an intervention, the user clicks on the Add Intervention link in an existing stage node.



This will open the Add Intervention form:

**Select intervention:** 0. User Defined - Custom

This page functions in the same way as the Add Stage form, but the list of available intervention type is limited to either just Custom or a list of known interventions for that stage. For most stages, only custom is available.

If the user clicks on continue, the intervention is added and the edit intervention form opens. As with stages, the user must define the process type and parameters for the intervention.

**Intervention:** Custom

**Applied At:** After Stage  (Please note only one "Replaces Stage" is permitted per stage.)

**Description:** User-defined intervention

**Process Type:** No significant change

**Instructions:** No change in prevalence or concentration.

**Distribution:** Not applicable

### Intervention Name

Users may specify the name of the intervention.

### Applied At

Users may also specify whether the intervention is applied before, after or in place of the existing stage process. Only one "Replaces Stage" intervention type can be applied to a specific stage.

### Description

This field provides a description of the intervention.

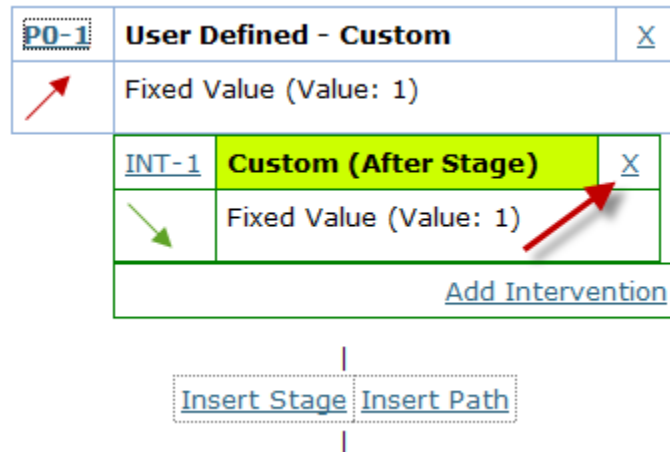
### Process Type

The user then specifies the process type much like they would for a process stage. All process types are included to allow the user to create a Replacement type of intervention.

As with stages, the user must allow the page to reload after the process type is changed to see the new parameter fields.

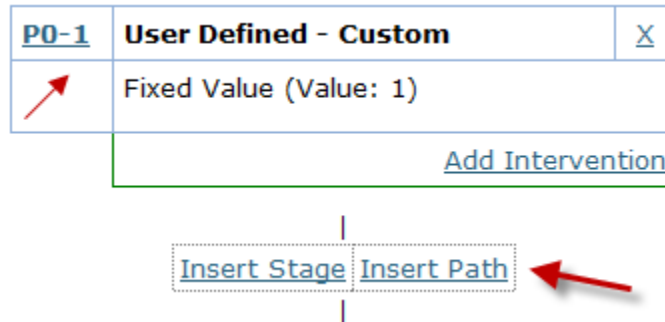
## Deleting an Intervention

Users may delete an intervention by clicking on the X in the top right box of the intervention node within the stage node on the process model page.



## Adding a Path

If the user decides that at a point in the process flow broilers may follow two distinctly different processes, the user may elect to add a path to the model. To do so, the user clicks the Insert Path link after the stage where the split is to occur.

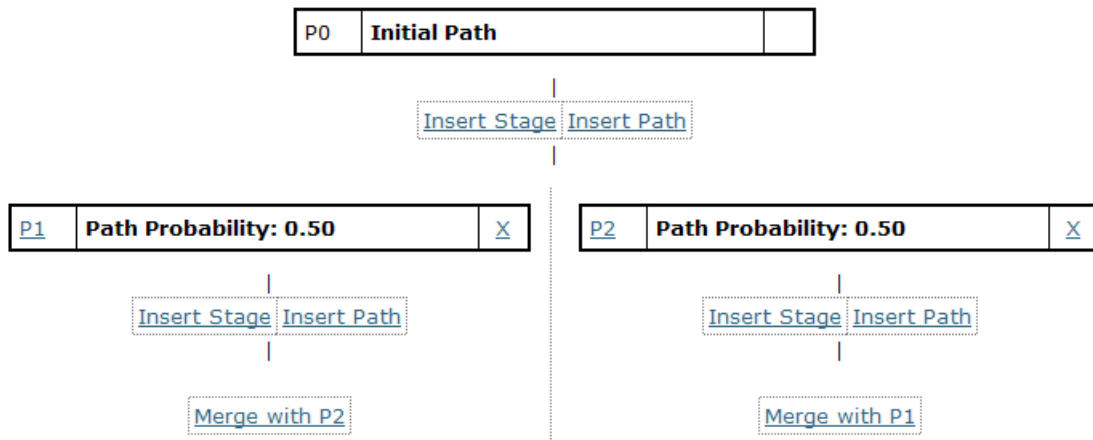


This will open the Add Path form where the user may specify the relative weights of the two paths. The weights must sum to 1.

**Path 1 Probability:**  (0-1)

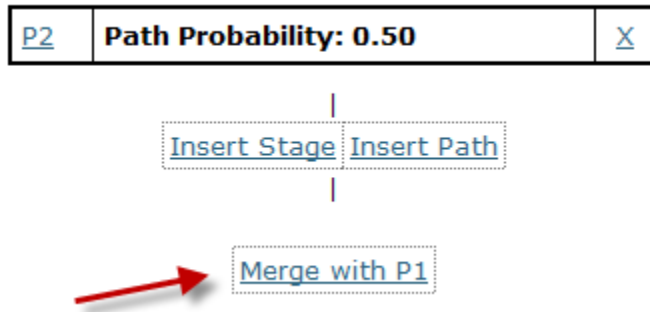
**Path 2 Probability:**  (0-1)

Clicking the Continue button will insert two paths starting after the stage.



If any stages were defined after this point, they will be assigned to the first path. The user may then add stages to each path individually. If, after one or more

stages, the process converges again, the user may click on one of the Merge With links to merge the two paths together.



## Step 8: Review the process flow model for one or both pathogens

At any time, the user may click on the appropriate Results link in the toolbar to review the model and run results for the selected pathogen.

When the results page loads, the application scans the process flow model defined for that pathogen and assembles all the distinct paths required to fully describe the process flow from initial contamination, through all the stages and interventions, and ending with consumer practices and dose response. At the top of each result path is the computed probability of that path based on the path probabilities entered by the user.

The user may use this view to confirm that the process flow is structured as intended by checking that individual stages are present as expected in each of the paths. If not, the user may edit the model to make adjustments. Clicking on any of the links in the flow chart will return the user to the model page at that point.

Please note that the link names will reflect the original path as displayed on the edit page, and not the current result path. For example, in the image below, result path 1 contains links with the following path-sequence identifiers: P0-1, P0-2, P1-1 and P3-1.

Result Path 1 (Probability:0.0100)		Result Path 2 (Probability:0.990)	
<a href="#">IC</a>	<b>Initial Contamination</b> Normal (Mean: 6, Standard deviation: 1.2) Specified for: At receipt Within Prevalence: Fixed Value (Value: 0.65) Between Prevalence: 0.6	<a href="#">IC</a>	<b>Initial Contamination</b> Normal (Mean: 6, Standard deviation: 1.2) Specified for: At receipt Within Prevalence: Fixed Value (Value: 0.65) Between Prevalence: 0.6
<a href="#">P0-1</a>	<b>Manage chickens - No change</b> ○	<a href="#">P0-1</a>	<b>Manage chickens - No change</b> ○
<a href="#">INT-1</a>	<b>Fly screens</b> B↓ Fixed Value (Value: 0.7)	<a href="#">INT-1</a>	<b>Fly screens</b> B↓ Fixed Value (Value: 0.7)
<a href="#">P0-2</a>	<b>Receive at slaughterhouse - Receipt</b> ○	<a href="#">P0-2</a>	<b>Receive at slaughterhouse - Receipt</b> ○
<a href="#">P1-1</a>	<b>Receive at slaughterhouse - Holding</b> ↗ Triangular (Minimum: 0, Mode: 0.5, Maximum: 1)	<a href="#">P3-1</a>	<b>Dress: Scald - Scald</b> ↘ Uniform (Minimum: 0.5, Maximum: 1.5)
<a href="#">P3-1</a>	<b>Dress: Scald - Scald</b> ↘ Uniform (Minimum: 0.5, Maximum: 1.5)	<a href="#">P3-2</a>	<b>Dress: Defeathering - Defeathering</b> ↘ Uniform (Minimum: 1, Maximum: 3)



<b>CP</b>	<b>Consumer Practices</b>	<b>CP</b>	<b>Consumer Practices</b>
Frequency of cross contamination: 0.01; Proportion consumed uncooked: Uniform (Minimum: 0.001, Maximum: 0.004); Cooking log reduction: Normal (Mean: 6, Standard deviation: 1); Frequency undercooked: 0; Log reduction when undercooked: N/A		Frequency of cross contamination: 0.01; Proportion consumed uncooked: Uniform (Minimum: 0.001, Maximum: 0.004); Cooking log reduction: Normal (Mean: 6, Standard deviation: 1); Frequency undercooked: 0; Log reduction when undercooked: N/A	
<b>DR</b>	<b>Dose Response</b>	<b>DR</b>	<b>Dose Response</b>
Beta-Poisson (alpha:0.21 beta:59.95; probability of illness given infection=0.33; fraction consumed=0.25)		Beta-Poisson (alpha:0.21 beta:59.95; probability of illness given infection=0.33; fraction consumed=0.25)	

The user can choose to hide any stages with a process type of No Significant Change by clearing the checkbox and clicking Reload Paths.

Include stages set to no significant change


If the user has not used paths, then only one path will be present on this page.

When the user is satisfied with the application's interpretation of the model, the user may click the Run Model button.

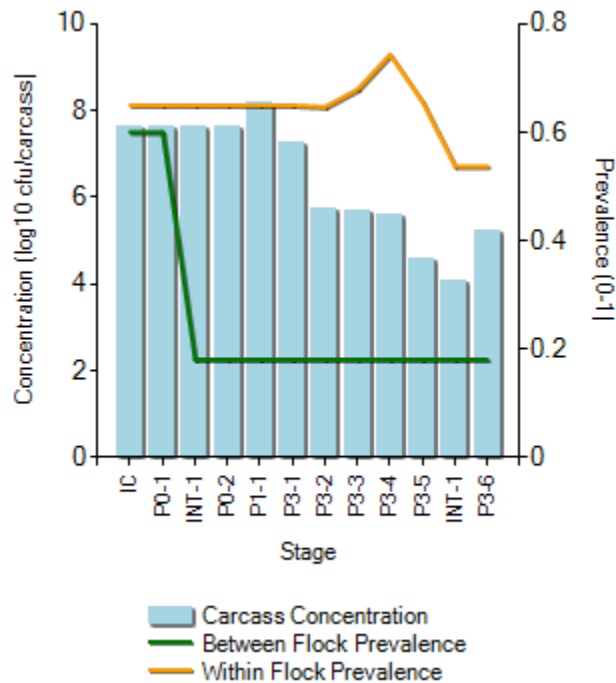
## Step 9: Run the models and review results

When the user clicks on the Run Model button, the results page reloads and includes the computed values for mean between flock prevalence, mean within flock prevalence,  $\log_{10}$  of the arithmetic mean carcass concentration, and residual risk.

Each of the flowchart boxes will now include the results for each stage:

<a href="#">P3-1</a>	<b>Dress: Scald - Scald</b>	
	Uniform (Minimum: 0.5, Maximum: 1.5)	
B: 0.18	W: 0.65	C: 6.7

In addition, before the first stage, a chart is included showing the change in these values over the path:



Finally, residual risk results are included at the bottom of the page along with the weighted residual risk of the combined pathways:

RR	Residual Risk
	Residual risk of pathway after interventions: 0.25

RR	Residual Risk
	Residual risk of pathway after interventions: 0.22

**Weighted Residual Risk of all Paths:** 0.22

Residual risk is the ratio of the mean risk of illness per serving of the pathways including interventions to the mean risk of illness per serving of the baseline scenario (no interventions). If no interventions are included, it will have a value of 1, meaning no change. If the interventions reduce the risk by half, the residual risk will be 0.5.

The weighted residual risk of all paths is the sum of the residual risk of each path weighted by the probability of that path.

The risk for a scenario is determined by computing the final concentration distribution and within flock prevalence values for that scenario. These are passed to the consumer practices and dose response models to determine a risk value which is further adjusted by the between lot prevalence.

## Appendix A: Factors Affecting Count Conversions in Determining Microbial Contamination of Poultry Carcasses

### Conversion of cfu / g to cfu / carcass

The need to make this conversion stems from the fact that the decision-support tool requires microbial counts to be expressed as cfu / carcass. However, some countries prefer to sample carcasses by macerating portions of neck skin, which yields cfu / g. In contrast, counts obtained from rinse-sampling of whole carcasses are usually expressed as cfu / mL of rinse fluid and are more readily converted to cfu / carcass (see below).

It is known that microbial contamination of carcasses is unevenly distributed over internal and external surfaces, and several studies have compared counts obtained from different sampling sites on individual carcasses. Unfortunately, no publication has been found that compares counts from neck skin with those from other sites, although it is recognised that neck skin is likely to be more heavily contaminated because carcasses are suspended from the processing line by their legs and drain down into the neck region.

Conversion of cfu / g requires the following manipulations. Firstly, it can be assumed from previous experience that 1 g of skin is equivalent to an area of 10 cm<sup>2</sup>. Then, it is necessary to calculate the total surface area of the carcass, as described by Thomas (1978). This is given by the equation:

$$A = 637 + 0.87 w$$

where A is the total surface area in cm<sup>2</sup> and w is the carcass weight in grams. Thus, the weight of neck skin taken (or skin from another region) will be known and therefore cfu / g is easily converted to cfu / carcass by multiplying by A/10. The equation differs from that described by Schmidt-Nielson (1984) which does not take account of the carcass cavity.

If the neck skin is, in fact, more heavily contaminated than other carcass sites, expressing the count obtained as cfu / carcass may yield a figure that is disproportionately high. To test this possibility, some data from Cox *et al.* (2010) for levels of *Escherichia coli* on pre-chill carcasses were utilised. Results of the conversion are as follows and all counts are expressed as cfu / carcass for a mean of 60 carcasses in each case:

Sample type	Plant A	Plant B	Plant C
Neck skin	6.14	6.04	5.00
Carcass rinse	5.45	5.08	5.92
Note: carcass weight not given and assumed to be 1.5 kg			

The results show that, for two of the processing plants studied, counts were higher from neck skin. At the third plant, the situation was reversed but, in all three cases, mean counts from the two sampling methods differed by no more than one log<sub>10</sub>

unit, and less in two cases.

It is concluded that taking skin samples and converting cfu / g to cfu / carcass yields counts for the latter with the right order of magnitude and does not appear to require any correction factor (which would equal the quotient of mean carcass contamination and neck skin contamination). Moreover, when the impact of a processing intervention is being determined, it is reasonable to assume that the same sampling method will have been used before and after the intervention has been applied.

### **Conversion of cfu / mL to cfu / carcass**

Rinse sampling is a common sampling method for collecting microbial data. However, rinse sampling only removes a portion of the microbes on the carcass. An estimate of the total number of microbes on a carcass requires that counts obtained from rinse sampling are scaled up.

Few studies have focused on the proportion of microbes removed by carcass rinsing. Lillard (1988) estimated approximately 14.1% of Enterobacteriaceae and 10.0% of aerobic bacteria are removed using a 100 mL rinse volume. Jorgensen *et al.*, (2002) show limited data for rinse sampling with a 300 mL volume. While no estimates of the removal rate are provided in that study, fitting an exponential decay function to their summary data suggests a removal rate of roughly 34% per minute of agitation.

To estimate carcass levels from rinse data, the following equation can be used:

$$\text{bacteria / carcass} = \frac{\text{cfu / mL} \times \text{rinse volume}}{\text{recovery rate}}$$

where cfu / mL is obtained by either direct plating or from most probable number estimates of the number of cells in the rinsate, rinse volume is the volume of rinsate in mL originally added to the rinse bag, and recovery rate is the efficiency by which the rinse volume used can remove bacteria from the carcass.

Estimating bacterial removal rates for rinse sampling usually requires sampling the same carcass multiple times. The counts thus obtained are fitted to an exponential decay model to determine the recovery rate.

To estimate the recovery rate for a 400 mL rinse volume, the following data were used. In one study, 300 chicken carcass rinse samples were collected at a single facility (unpublished). During the study, rinse sampling was performed with either a 100 or 400 mL rinsate volume. Summary statistics and simple tests of equivalence did not demonstrate the notion of equivalence and suggest that rinse sampling with the 400 mL rinsate volume removed a higher proportion of bacteria.

To estimate the 400 mL recovery rate parameter using the data from this study, a stochastic model was developed that describes the process of rinsing a carcass and sampling the rinsate to obtain a count of the number of bacteria present. The model uses Bayesian inference, information from previous studies, and the available

data to determine the effect of rinse volume on the proportion of bacteria removed through rinsing (Williams *et al.*, 2010). This study found a 70% removal efficiency, 0.7 recovery rate, suggesting that 400 mL is superior to 100 mL.

## References

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- Jorgensen F, Bailey R, Williams S, Henderson P, Wareing D R A, Bolton F J, Frost J A, Ward L and Humprey T J (2002). Prevalence and numbers of *Salmonella* and *Campylobacter* spp. on raw, whole chickens in relation to sampling methods. *Int. J. Food Microbiol.*, **76**: 151 – 164.
- Lillard H S (1988). Comparison of sampling methods and implications for bacterial decontamination of poultry carcasses by rinsing. *J. Food Prot.* **51**: 405 – 408.
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- Thomas N L (1978). Observations of the relationship between the surface area and weight of eviscerated carcasses of chickens, ducks and turkeys. *J. Food Technol.* **13**: 81 – 86.
- Williams M S, Ebel E D, Golden N J, Berrang M E, Bailey J S, Hartnett E (2010). Estimating removal rates of bacteria from poultry carcasses using two whole-carcass rinse volumes. *Int. J. Food Microbiol.* **139**: 1140 – 1146.

## Appendix B: Technical Description (including Glossary)

The mathematics and algorithms presented in this paper set out to characterize a typical process flow as defined by the user. Please refer to the main User Guide for a description of how to create a process flow using the tool.

A process flow is modeled using six main elements:

- initial concentration and prevalence parameters
- a set of sequential processes that may or may not modify concentration and/or prevalence values
- consumer practices
- dose response
- the calculation of relative risk reduction between the baseline and intervention scenarios.

Monte Carlo simulation is used to produce a stochastic model of the process flow based on the fixed and distribution parameters for the process flow provided by the user.

Please refer to the glossary for definitions of key terms.

### Parameters

Parameter	Parameter Name	Explanation
C	Contamination level	Concentration of the pathogen (cfu/carcass)
P <sub>w</sub>	Within flock prevalence	The fraction of carcasses contaminated within a broiler flock (0-1)
P <sub>B</sub>	Between flock prevalence	The fraction of all broiler flocks contaminated (0-1)
L	Likelihood	The likelihood of a process being applied (0-1).
W	Weight	The weight of a path
XC	Cross-contamination factor	A value $\geq 1$ indicating the degree of cross-contamination
RF	Reduction factor	Used in the prevalence decrease processes
IF	Increase factor	Used in the prevalence increase processes
CF	Carcass fraction consumed	The fraction of carcass consumed. Used to compute dose consumed.
D	Dose	Dose consumed (cfu)
P <sub>ill</sub>	Probability of Illness	Probability of illness from the dose consumed
R	Risk	P <sub>ill</sub> scaled by prevalence (within and between flock)
MR	Mean Risk	Mean of R for all simulation iterations for a given path. MR=R if no stochastic processes

		are used.
RR	Residual risk	The ratio of the MR for the process flow including interventions over the MR for the baseline process flow. For example, if MR is halved by the interventions, $RR=0.5$ .
WRR	Weighted residual risk	The weighted average of RR over the weights (W) of each path. If there is only one path, $WRR = RR$ .



## Assumptions

The following assumptions are made in the tool:

1. The tool models the flow of a single representative flock through the entire process.
2. While some early stages may be modelled using prevalence only, a concentration value is required to compute the residual risk.
3. Concentration values are provided as cfu/carcass or the log equivalent. Please see Appendix A on converting data from cfu/g and cfu/ml to cfu/carcass.
4. As concentrations are stored as cfu/carcass during calculations, all values are rounded to the nearest integer at the end of each stage.
5. The tool models positive only carcasses. Any process which eliminates most contamination is handled by adjusting the within flock prevalence down. As such, the minimum concentration reported will be  $0 \log_{10}$  cfu/carcass, or 1 cfu/carcass.
6. Cross-contamination and addition processes may occur within a flock but not between flocks.
7. Prevalence and concentration values entered are for the broiler flock, not necessarily the current flock. For example, if a process model begins at step 5, Manage parent flocks, any prevalence and concentration values refer to the downstream broiler flock and not to the parent flocks.
8. Likelihood is used to indicate a process may or may not happen as part of the entire process flow. It is not intended to model two or more alternate process flow options. In the current tool, likelihood is only available for the addition process type. All other situations in which flocks may follow two or more processes should be implemented using paths. See the main user guide for more details on adding paths.

### A note on paths

If the process flow uses paths, then the tool computes the path weight based on the weight values provided by the user and any previous paths. For example, if the process flow has one path, the weight is 1. If the process flow has two paths, the weights would be as entered. E.g. 0.01 and 0.99. If the first path was further split into two paths with weights 0.4 and 0.6, then the process flow would now have three paths with weights of  $0.01 \times 0.4$ ,  $0.01 \times 0.6$  and 0.99 respectively.

The process flow then models all stages on each path as required and combines the results in the weighted residual risk.

## ***Initial Concentration and Prevalence Parameters***

### *Initial Concentration*

Initial concentration is entered in units of log cfu/carcass. The user may select one of the following distributions for initial concentration: Beta PERT, Cumulative Empirical, Fixed, Normal, Triangular, Uniform.

### *Initial Within Broiler Flock Prevalence*

The user enters a value between 0 and 1 for within broiler flock prevalence using one of the following distributions: Beta PERT, Cumulative Empirical, Fixed, Triangular, Uniform. Normal is not available for parameters requiring fixed boundaries.

Please note that the prevalence is for the broiler flock. For example, if the step "Manage grandparent flocks" was included in the model, the user would enter prevalence values here that would be observed in the broiler flock due to management techniques implemented at the grandparent flock level and not the prevalence values in the grandparent flock.

### *Initial Between Broiler Flock Prevalence*

The user enters a fixed value between 0 and 1 for between broiler flock prevalence.

Please note that the prevalence is for the broiler flock. For example, if the step "Manage grandparent flocks" was included in the model, the user would enter prevalence values here that would be observed in the broiler flock due to management techniques implemented at the grandparent flock level and not the prevalence values in the grandparent flock.

## Sequential Processes

Steps as defined in the Guidelines are modeled by a set of one or more processes which may modify concentration and/or prevalence values. These processes are applied sequentially.

The following describes the implementation of each of the available process types as to their effect on concentration and prevalence values on the current stage as compared to the previous stage.

### No Significant Change

This process type has no effect on concentration or prevalence values. It is intended as a way for the user to indicate that the stage has no effect without requiring its deletion. No parameters are entered.

Variable	Effect
C	$C[\text{stage}] = C[\text{stage-1}]$
$P_W$	$P_W[\text{stage}] = P_W[\text{stage-1}]$
$P_B$	$P_B[\text{stage}] = P_B[\text{stage-1}]$

### Increase (growth)

The user enters a fixed value or distribution for the  $\log_{10}$  change, for example: 2 logs. This change will be applied to all previously contaminated carcasses. Prevalence does not change. As concentration is stored on the non-log scale, the log increase must be converted before being applied.

Variable	Effect
C	$C[\text{stage}] = C[\text{stage-1}] * 10^{\text{logChange}}$
$P_W$	$P_W[\text{stage}] = P_W[\text{stage-1}]$
$P_B$	$P_B[\text{stage}] = P_B[\text{stage-1}]$

### Increase (addition –within flock)

The user specifies the  $\log_{10}$  cfu addition to each carcass at this stage and the likelihood of the addition (L). The addition may happen to any carcass in the current flock. That carcass may be previously contaminated or not. Therefore, the current within flock prevalence is used to select randomly if the current carcass is contaminated or not. If it is, it adds the new contamination to the existing contamination. If not, it applies just the added contamination.

The new within flock prevalence integrates the previous prevalence with the likelihood of addition to reflect that a greater number of carcasses are likely now contaminated.

Variable	Effect
C	IF Bernoulli( $P_W$ [stage-1])  THEN  $C$ [stage] = $C$ [stage-1] + $10^{\text{logAdded}}$  ELSE  $C$ [stage] = $10^{\text{logAdded}}$  END IF
$P_W$	$P_W$ [stage] = $P_W$ [stage-1] + L - ( $P_W$ [stage-1] * L)
$P_B$	$P_B$ [stage] = $P_B$ [stage-1]

If the addition is less than the current contamination level, then this should reduce the mean contamination level in the flock but increase the within flock prevalence. If the addition is greater than the current contamination level, then both the mean concentration and the within flock prevalence should increase.

## Decrease

The user specifies the  $\log_{10}$  decrease expected for this stage, for example: 3 logs. This change will be applied to all previously contaminated carcasses. As concentration is stored on the non-log scale, the log decrease must be converted before being applied. In some cases, the decrease will result in a total elimination of cfu's on the carcass. This is addressed by determining the probability the log decrease would eliminate all cfu's and adjusting the within flock prevalence accordingly.

Since the tool models the contamination level of positive carcasses, if the resulting concentration is less than 1 cfu/carcass, it is set to 1 cfu/carcass.

Variable	Effect
C	$C$ [stage] = $C$ [stage-1] * $10^{(-\text{logDecrease})}$  IF $C$ [stage] < 1 THEN $C$ [stage] = 1
$P_W$	ProbDeath = $1 - (10^{(-\text{logDecrease})})$  $P_W$ [stage] = $P_W$ [stage-1] * (1 - ProbDeath <sup><math>C</math>[stage-1]</sup> )
$P_B$	$P_B$ [stage] = $P_B$ [stage-1]

## Cross-contamination

The user specifies the cross-contamination factor ( $XC \geq 1$ ) to apply to the current within flock prevalence. The tool then computes the corresponding redistribution of cfu/carcass. The tool assumes the total available concentration is sufficient to result in at least 1 cfu/carcass for the entire flock.

When applying the cross-contamination factor, the tool considers the possibility the new prevalence would be  $> 1$  and adjusts the factor accordingly. A final prevalence value of 1 implies total cross-contamination.

Variable	Effect
C	$EffectiveXC = 1 / P_W [stage-1]$  IF $(P_W [stage-1] * XC) < 1$  THEN  $C[stage] = C[stage-1] / XC$  ELSE  $C[stage] = C[stage-1] / EffectiveXC$  END IF  IF $C[stage] < 1$ THEN $C[stage] = 1$
$P_W$	$P_W [stage] = P_W [stage-1] * XC$  IF $P_W [stage] > 1$ THEN $P_W [stage] = 1$
$P_B$	$P_B [stage] = P_B [stage-1]$

## Within flock prevalence increase

The user specifies an increase factor (IF, 0-1) to apply to the current prevalence. For example, a value of 0.2 will result in a 20% increase in prevalence. Prevalence only processes should be used with caution as concentration is not affected.

Variable	Effect
C	$C[stage] = C[stage-1]$
$P_W$	$P_W [stage] = P_W [stage-1] * (1 + IF)$
$P_B$	$P_B [stage] = P_B [stage-1]$

### Within flock prevalence decrease

The user specifies a reduction factor (RF, 0-1) to apply to the current prevalence. For example, a value of 0.2 will result in a 20% reduction in prevalence. Prevalence only processes should be used with caution as concentration is not affected.

Variable	Effect
C	$C[\text{stage}] = C[\text{stage-1}]$
$P_W$	$P_W[\text{stage}] = P_W[\text{stage-1}] * (1-\text{RF})$
$P_B$	$P_B[\text{stage}] = P_B[\text{stage-1}]$

### Between flock prevalence increase

The user specifies an increase factor (IF, 0-1) to apply to the current prevalence. For example, a value of 0.2 will result in a 20% increase in prevalence. Prevalence only processes should be used with caution as concentration is not affected.

Variable	Effect
C	$C[\text{stage}] = C[\text{stage-1}]$
$P_W$	$P_W[\text{stage}] = P_W[\text{stage-1}]$
$P_B$	$P_B[\text{stage}] = P_B[\text{stage-1}] * (1+\text{IF})$

### Between flock prevalence decrease

The user specifies a reduction factor (RF, 0-1) to apply to the current prevalence. For example, a value of 0.2 will result in a 20% reduction in prevalence. Prevalence only processes should be used with caution as concentration is not affected.

Variable	Effect
C	$C[\text{stage}] = C[\text{stage-1}]$
$P_W$	$P_W[\text{stage}] = P_W[\text{stage-1}]$
$P_B$	$P_B[\text{stage}] = P_B[\text{stage-1}] * (1-\text{RF})$

## **Dose Response**

A dose response model is used in the consumer practices node (see next section) to compute probability of illness resulting from the consumption of a contaminated serving.

The default for the model is to assume a consumption fraction (CF) of  $\frac{1}{4}$  (0.25) of the carcass per serving.

The default dose response model for *Campylobacter* is a Beta-Poisson with alpha = 0.21 and beta = 59.95. The probability of illness given infection is 0.33 (or 33%).

The default dose response model for *Salmonella* is a Beta-Poisson with alpha = 0.1324 and beta = 51.45. The probability of illness given infection is 1 (or 100%).

A user may choose to define a custom dose response model using a Beta-Poisson, exponential or linear model, and modify the fraction consumed.

The equation used to compute  $P_{ill}$  is:

$$P_{ill} = \text{DoseResponse}(C_{[final\ stage]} * CF) * (\text{Probability of Illness given Infection})$$

## Consumer Practices

Consumer practices consists of two related items: cross contamination and cooking. These are applied after all other process steps, using the final concentration and prevalence values.

### Cross contamination

The user specifies the frequency of cross contamination events (FrCC) as a value between 0 and 1.

The user specifies the proportion of pathogens consumed uncooked (though transfer to surfaces and other foods) as a value or distribution between 0 and 1 (PT).

### Consumer cooking

The user specifies the  $\log_{10}$  reduction in contamination that results from cooking (CR).

The user may also optionally specify a frequency at which carcasses are undercooked (FrUC) between 0 and 1, and an associated  $\log_{10}$  reduction (UCR).

### Consumer Practices Algorithm

The tool uses the decrease process types to determine a net concentration and prevalence from consumer practices. It also applies the dose response model to the different concentration values that result and produces a weighted mean probability of illness from all possibilities.

#### Step 1: Compute the different pathogen counts for each situation

Cross contamination may occur or not. If it does not occur, all pathogens experience cooking. If it does occur, some pathogens do not experience cooking due to transfer off the carcass while those remaining on the carcass do experience cooking. Please note in this and later steps the difference between **Uncooked** and **Undercooked**. The former refers to pathogens that experience no cooking, while the later pathogens that experience a reduced cooking level.

$$\text{countCookedNoCrossContamination} = C[\text{final stage}]$$

$$\text{countUnCookedWithCrossContamination} = C[\text{final stage}] * PT$$

$$\text{countCookedWithCrossContamination} = C[\text{final stage}] * (1 - PT)$$

#### Step 2: Compute counts after cooking



For the two situations above in which the carcass is cooked, it may be fully cooked or undercooked. This results in four new counts computed using the decrease concentration function of the decrease process type. The decrease concentration function takes as its parameters the count and the log reduction.

Additionally, each count is multiplied by the fraction of the carcass consumed (CF).

$$\text{remainingCookedNoCrossContamination} = \text{DecreaseConc}(\text{countCookedNoCrossContamination}, \text{CR}) * \text{CF}$$
$$\text{remainingUndercookedNoCrossContamination} = \text{DecreaseConc}(\text{countCookedNoCrossContamination}, \text{UCR}) * \text{CF}$$
$$\text{remainingCookedWithCrossContamination} = \text{DecreaseConc}(\text{countCookedWithCrossContamination}, \text{CR}) * \text{CF}$$
$$\text{remainingUndercookedWithCrossContamination} = \text{DecreaseConc}(\text{countCookedWithCrossContamination}, \text{UCR}) * \text{CF}$$

### Step 3: Compute the adjusted prevalence resulting from cooking

This step uses the decrease prevalence function of the decrease process type. It takes three parameters: previous prevalence, count and log reduction. Since this process is modeling only positive carcasses, a prevalence of 1 is assumed.

$$\text{prevAdjustNoCrossContam} = \text{DecreasePrev}(1, \text{countCookedNoCrossContamination}, \text{CR})$$
$$\text{prevAdjustUndercookedNoCrossContam} = \text{DecreasePrev}(1, \text{countCookedNoCrossContamination}, \text{UCR})$$
$$\text{prevAdjustWithCrossContam} = \text{DecreasePrev}(1, \text{countCookedWithCrossContamination}, \text{CR})$$
$$\text{prevAdjustUndercookedWithCrossContam} = \text{DecreasePrev}(1, \text{countCookedWithCrossContamination}, \text{UCR})$$

### Step 4: Compute the Probability of Illness for each situation

The adjusted counts above are passed to the defined dose response model to determine the probability of illness for each situation. This includes both the cooked and uncooked situations.

$$\text{pillCookedNoCrossContamination} = \text{DoseResponse}(\text{remainingCookedNoCrossContamination})$$

pillCooked**With**CrossContamination =  
DoseResponse(remainingCooked**With**CrossContamination)

pill**Under**Cooked**No**CrossContamination =  
DoseResponse(remaining**Under**cooked**No**CrossContamination)

pill**Under**Cooked**With**CrossContamination =  
DoseResponse(remainingCooked**With**CrossContamination)

pillUncooked**With**CrossContamination =  
DoseResponse(remaining**Under**cooked**With**CrossContamination)

### **Step 5: Compute the weighted average for a final probability of illness**

The weighted  $P_{ill}$  is computed by summing the following values. Each value adjusts the probability of illness by the adjusted prevalence of the situation and any associated fractions results from whether the situation involved cross contamination or undercooking.

*No cross contamination*

pillCooked**No**CrossContamination\*(1-FrCC)\* prevAdjust**No**CrossContam\*(1-FrUC)

pill**Under**cooked**No**CrossContamination\*(1-FrCC)\*  
prevAdjust**Under**cooked**No**CrossContam\*(FrUC)

*With cross contamination and cooked*

pIllCooked**With**CrossContam\*(FrCC)\* prevAdjust**With**CrossContam\*(1-FrUC)

pIll**Under**cooked**With**CrossContam\*(FrCC)\*  
prevAdjust**Under**cooked**With**CrossContam\*(FrUC)

*With cross continuation, uncooked*

pill**Un**cooked**With**CrossContami\*(FrCC)\*pillUncooked**With**CrossContamination

If the resulting weighted sum is greater than 1, it is set to 1.

## **Residual Risk**

The tool differentiates between baseline processes and intervention processes. The tool computes the process flow for both the baseline and for the baseline plus interventions. The tool compares the results of both to compute a residual risk factor (RR).

There are three steps involved to compute this factor: computing the risk (MR) per path for both the baseline scenario and scenario including interventions, computing the residual risk of each path, and then computing the weighted residual risk.

### **Computing MR from Consumer Practices**

The Consumer Practices module computes  $P_{iii}$ . This  $P_{iii}$  is scaled by the final within and between flock prevalence values to compute the risk for each iteration of the Monte Carlo simulation.

$$R = P_{iii} * P_{W[\text{final stage}]} * P_{B[\text{final stage}]}$$

The mean of all samples for each path is taken:

$$MR = \text{Mean}(R)$$

### **Compute the Residual Risk for Each Path**

The residual risk for a path is computed by taking the ratio of MR with the scenario with interventions over the MR for the baseline scenario (no interventions). A value less than 1 indicates a relative reduction in risk.

$$RR = MR(\text{interventions}) / MR(\text{baseline})$$

### **Compute the Weighted Residual Risk**

The weight for each path in the process flow is the product of all the individual weights assigned to each path.

For example, if the process flow has one path, the weight is 1. If the process flow has two paths, the weights would be as entered. E.g. 0.01 and 0.99. If the first path was further split into two paths with weights 0.4 and 0.6, then the process flow would now have three paths with weights of  $0.01 \times 0.4$ ,  $0.01 \times 0.6$  and 0.99 respectively.

The final weighted residual risk is computed using the following equation:

$$WRR = \text{SUM}(RR[\text{path}] * W[\text{path}])$$

If there is only one path, the  $WRR = RR$ .