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

(Version 1.0)

Quick Start Tutorial

Overview

Please note: All the values input in the course of this tutorial are used solely for the purpose of demonstrating how the tool works and in no way represent any recommended or proposed default values.

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.

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.

This document provides a quick start tutorial on creating a sample model. It is intended to give an overview of the major steps involved. All parameters values are for illustrative purposes only. For a more complete understanding of the tool, please review the Guidelines, user guide, supporting documents and disclaimer from the links available on the tool's web site.

The quick start tutorial assumes you have already registered your account and are currently logged into the application. Please see the user guide for details on registering your account.

Step 1: Create a new process flow

Please note: All the values input in the course of this tutorial are being used solely for the purpose of demonstrating how the tool works and in no way represent any recommended or proposed default values.

Step 1A: Click "New Flow"

After registering and logging into the tool, click on the **New Flow** link to 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		23-Mar-2011 16:12:02 EST	View/Edit	Copy	Delete

Step 2: Enter a process flow name and description

The **Name and Description** form gives the user the option to provide a meaningful name and short description of the process flow to help describe and identify the process flow on the **Process Flow List** page.

Step 2A: Modify fields values

Enter "Tutorial" for the process flow name and "This is a tutorial process flow" as the description, and then click **Save Changes**:

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.

See the User Guide and Tutorial for additional details.

Process Flow Name: Tutorial

Description: This is a tutorial process flow

Save Changes | Save And Close | Close

Step 2B: Switch to the model view

Click on the *Campylobacter* Model link to move to the model page:

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

Name and Description

Step 3: Edit the initial contamination parameters

Users enter initial values for between flock prevalence, within flock prevalence, and carcass concentration on the **Initial Contamination** page. Note that all values apply to the broiler flock (i.e. during processing) and not parent or grandparent flocks. Values entered in the production stages must reflect those eventually observed on the flock arriving for processing.

The initial concentration defined here will be applied at the first model stage which changes concentration and must be the concentration for that stage. For example, if concentration data are only available after defeathering, then all stages prior must only modify prevalence. A text box is provided to record the stage at which concentration first applies for reference purposes.

Step 3A: Open the edit form

Click on the **IC** link in the **Initial Contamination** node on the model page to open its edit form:

Step 3B: Modify the parameter values

Change the Initial Concentration Normal distribution's mean to 6 $\log_{10}$ cfu/carcass and the Standard Deviation to 1.2. Note that this concentration is **per carcass** and not per gram or per milliliter.

Enter "At Receipt" for the Specified for text box.

Change the Within Broiler Flock Prevalence to 0.65, and Between Broiler Flock distribution to 0.6.

Then click Save Changes to save the changes.

Click on the Show Chart button to view a chart of the Initial Concentration distribution.

Step 3C: Save changes and close the form

Click **Save and Close** to return to the model view.

Step 4: Edit the consumer practices parameters

The **Consumer Practices** form allows the user to change parameters related to consumer cooking and optionally for consumer cross contamination and undercooking.

Step 4A: Open the edit form

Click on the **CP** link in the **Consumer Practices** node to open its edit form:

Step 4B: Modify parameters and save changes

Change the Cooking Log Reduction to use a Normal distribution with a Mean of 6 and a Standard Deviation of 1.

Set the Frequency of cross contamination to 0.01.

Change the proportion of pathogens consumed uncooked from a Fixed Value distribution to a Uniform distribution (please allow the page to reload). Change the Minimum to 0.001 and the Maximum to 0.004.

Leave the Frequency Undercooked at 0.

Click Save and Close.

Consumer Practices Page - *Campylobacter*

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

Consumer Cooking

Specify the $\log_{10}$ reduction achieved through the cooking process.

Cooking $\log_{10}$ Reduction: | Normal ▼ | (Should range between 0 and 15)

Mean: 6 ←

Standard deviation: 1 ←

[Show Chart]

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: 0.01 (0-1) ←

Proportion of Pathogens Consumed Uncooked: | Uniform ▼ | (Should range between 0 and 1) ←

Minimum: 0.001 ←

Maximum: 0.004 ←

[Show Chart]

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 (0-1) ←

$\log_{10}$ Reduction when Undercooked: | Fixed Value ▼ | (Should range between 0 and 15)

Value: 0

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Step 5: Review the dose response model

The **Dose Response** form allows the user to review the default dose response model and create a custom model if required.

Step 5A: Open the edit form

Click on the **DR** link in the **Dose Response** node to open its edit form:

DR	**Dose Response**
Beta-Poisson (alpha:0.21 beta:59.95; probability of illness given infection=33; fraction consumed=0.25)	

Step 5B: Review the dose-response model chart and close the form

Click Show Chart to see the chart, and then Close to close without saving:

Show Chart

Fraction of Carcass Consumed: 0.25 (>0-1)

Save Changes   Save And Close   Close

Step 6: Planning the process flow

There are three types of elements the user may add to the process flow: stages, interventions and paths.

Stages

Stages describe the baseline process flow as it currently exists. These include elements such as defeathering, inside/outside wash, and storage.

Interventions

Interventions are designed to model changes to the existing process flow intended to reduce the risk from contamination. Interventions may include elements such as fly traps or additional washing steps.

Paths

Paths are used when portions of the flock may be processed differently, such as a small percentage held before processing or a split between storing fresh and frozen.

The resulting process flow will be computed twice. The first pass uses only the stages to determine the baseline scenario risk. The second pass applies the interventions to compute the risk considering interventions. The tool compares the risk between these two scenarios to produce a residual risk value intended to help evaluate the effectiveness of the specified interventions.

It is important to note that the term intervention refers to planned interventions or interventions under consideration. If an intervention is already part of the existing process, it should be included as a stage to form part of the baseline scenario.

Step 7: Insert the manage chickens stage

The process flow starts with the first stage.

Step 7A: Insert the stage

To add a stage at a specific point, click on the Insert Stage link where the stage should be inserted. In this case, under the Initial Path node:
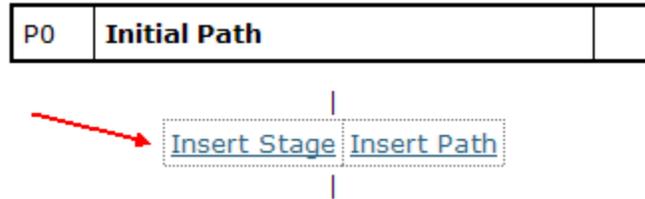
Step 7B: Select the stage type

The tool will then provide a list of stage (step) types based on the Guidelines document. By default, each stage is set to the process type of no significant change. The user must modify the process type and parameters based on their knowledge of the system under study.

Select **9. Manage Chickens** from the drop down list on the **Add Stage** form and click **Continue**:

Step 7C: Review the parameter settings

Review the items on the page. The Path-Sequence shows that this stage is in the default path (Path 0) and is the first item in that path (0-1).

It displays the name of the step, as well as the pathogen for which this process flow applies. It also displays the Step Type (9), which refers to the step definitions in the Guidelines.

There is also a text box where the user may change the default stage name.

Note the process type is set to No Significant Change and, as such, this stage will not modify concentration or prevalence values.

Path-Sequence: 0-1

Step: Manage chickens (No change) - *Campylobacter*

Step Type: 9

Stage Name: No change

Process Type: No significant change

Step 7D: Save changes and close the form

Click **Save and Close**.

Step 8: Add an intervention to this stage

Interventions are used to model interventions under consideration. If an intervention already exists as part of the baseline process, it should be included as a stage instead. Only add items as interventions to determine their possible impact on the risk as compared to the baseline scenario.

Step 8A: Add the intervention

To add an intervention, click on **Add Intervention** in the **Manage Chickens** node:
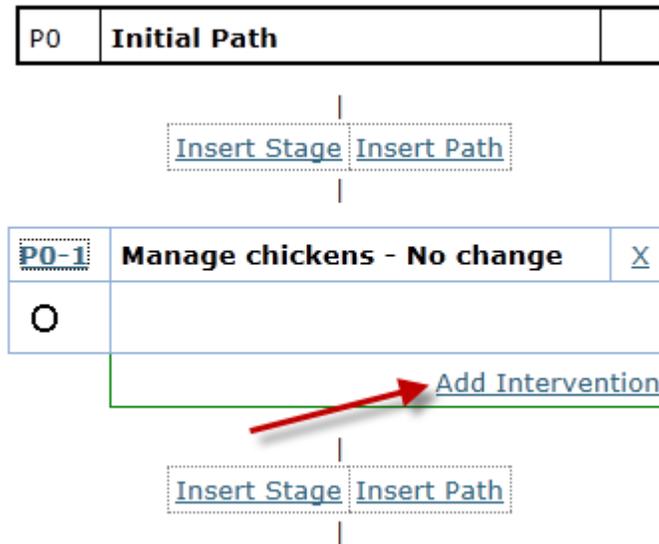
Step 8B: Select the intervention type

Select **9. Manage chickens – Fly screens** from the list of interventions and click **Continue**:

Step 8C: Review the parameter settings

Note the intervention will be applied after the stage.

Applied At: After Stage

Note the description of the intervention from the Guidelines.

Change the process type from No Significant Change to Between Flock Prevalence Decrease and allow the page to reload.

Review the instructions for this process type and set the fixed value to 0.7.

Process Type: Between Flock Prevalence Decrease ◄━━━━

Instructions: Decreases the current prevalence by the factor provided. E.g. a value of 0.2 resuts in a 20% reduction. The value must be less than 1. **Warning:** this process only modifies prevalence and does not modify concentration. Some processes achieve a prevalence reduction as a result of a concentration reduction sufficient to eliminate all pathogens on some carcasses. In these cases, a decrease model would be a better choice if data are available to assign the log reduction.

Distribution: Fixed Value (Should be greater than or equal to 0 and less than 1)

Value: 0.7 ◄━━━━

Note that this prevalence decrease process type will only change the prevalence value and not the concentration value.

Step 8D: Save changes and close the form

Click **Save and Close**.

Step 9: Add receive at slaughter house stage

The remainder of this tutorial will add additional stages and interventions to complete the basic process flow model.

Step 9A: Insert the stage

Click on **insert stage** after the **Manage Chickens** node:

Step 9B: Select the stage type and review defaults

Select **12. Receive at slaughterhouse – Receipt** from the dropdown list and click **Continue**:

Leave the process as No Significant Change and click **Save and Close.**

Step 10: Add a path split to the model

Paths are used to model different physical pathways that a flock might take though a process flow. For example, paths may be used if some of the broilers are stored fresh while others are stored frozen. Each path is assigned a probability indicating the fraction of the broilers that follow that path.

In this tutorial, we will use paths to show that some flocks are held prior to further processing.

Step 10A: Insert the path

To insert a path, click on **Insert Path** after the **Receive at Slaughterhouse** node:
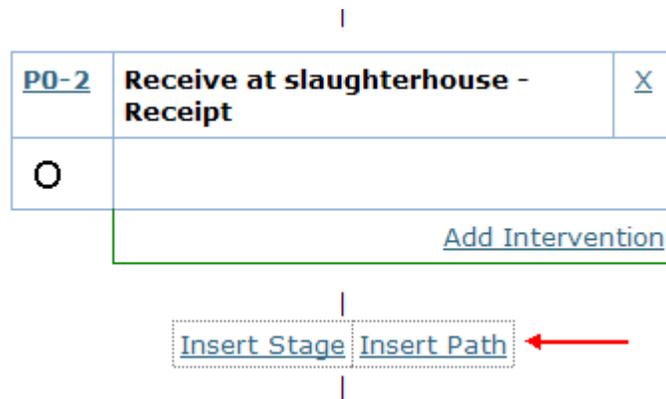
Step 10B: Assign path probabilities

Assign a probability of 0.01 to path 1 and a probability of 0.99 to path2, then click **continue** (note, clicking continue will close the form and return to the model view):

Step 10C: Review the changes to the model flow chart

There will now be two paths on the model page:

PO-2	Receive at slaughterhouse - Receipt	X
O		

Add Intervention

Insert Stage | Insert Path

P1	Path Probability: 0.01	X

Insert Stage | Insert Path

Merge with P2

P2	Path Probability: 0.99	X

Insert Stage | Insert Path

Merge with P1
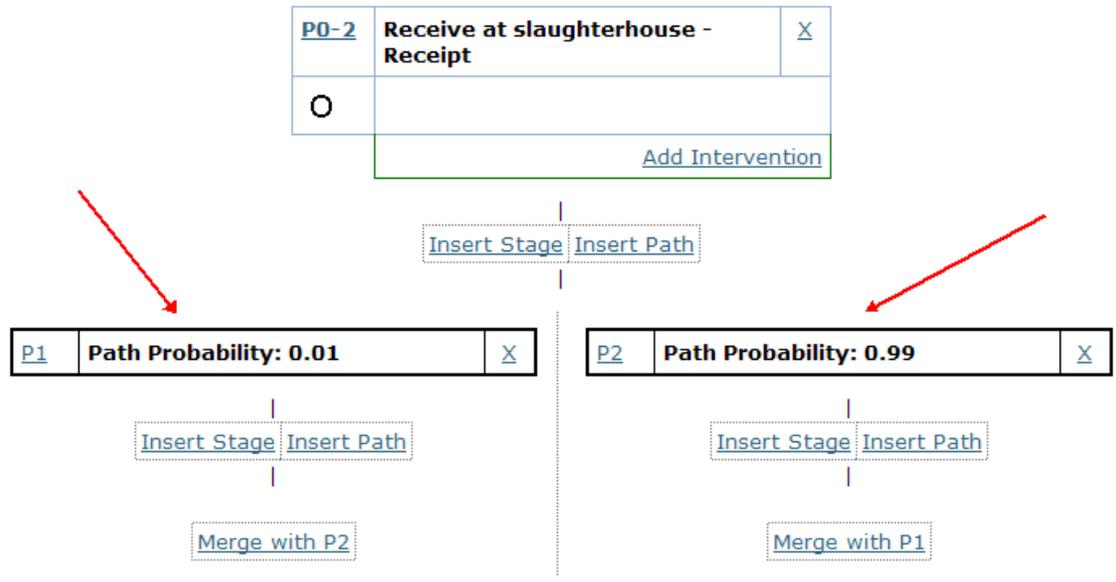
Step 11: Add a holding stage to path 1

Now that model contains two paths, each path may follow a different structure and include different stages and interventions. In this tutorial, we will add a holding stage to the first path.

Step 11A: Insert the stage

Click on **Insert Stage** after **Path 1**:
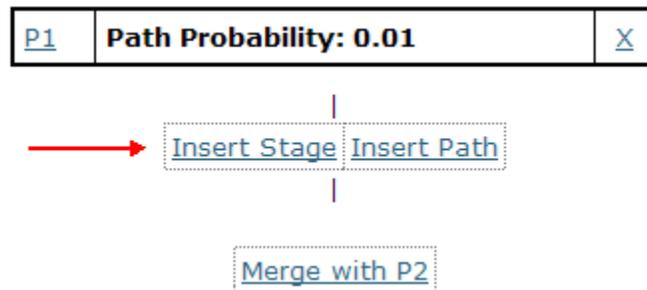
Step 11B: Select the stage type

On the **Add a Stage** form, select **12. Receive at slaughterhouse – Holding** from the list and click **Continue**.

Step 11C: Review and modify the parameters and save changes

Change the process type from No Significant Change to Increase (growth). Allow the page to reload

Change the distribution from Fixed to Triangular. Allow the page to reload. Note that there are now three parameter values. Change the **Mode** to 0.5 and the **Maximum** parameter value to 1:

Click **Save and Close.**

Step 12: Merge the paths

Once the necessary stages have been added to describe the differences between the paths, the user may optionally merge the paths again to complete the model. Merging the paths will reduce the number of duplicate entries required to complete the model.

Step 12A: Merge the paths

Click on **Merge with P2** under the **Holding** stage:

P1	Path Probability: 0.01	X

Insert Stage Insert Path

P1-1	Receive at slaughterhouse – Holding	X
↗	Triangular (Minimum: 0, Mode: .5, Maximum: 1)	
	Add Intervention	

Insert Stage Insert Path

Merge with P2 ←

P2	Path Probability: 0.99	X

Insert Stage Insert Path

Merge with P1
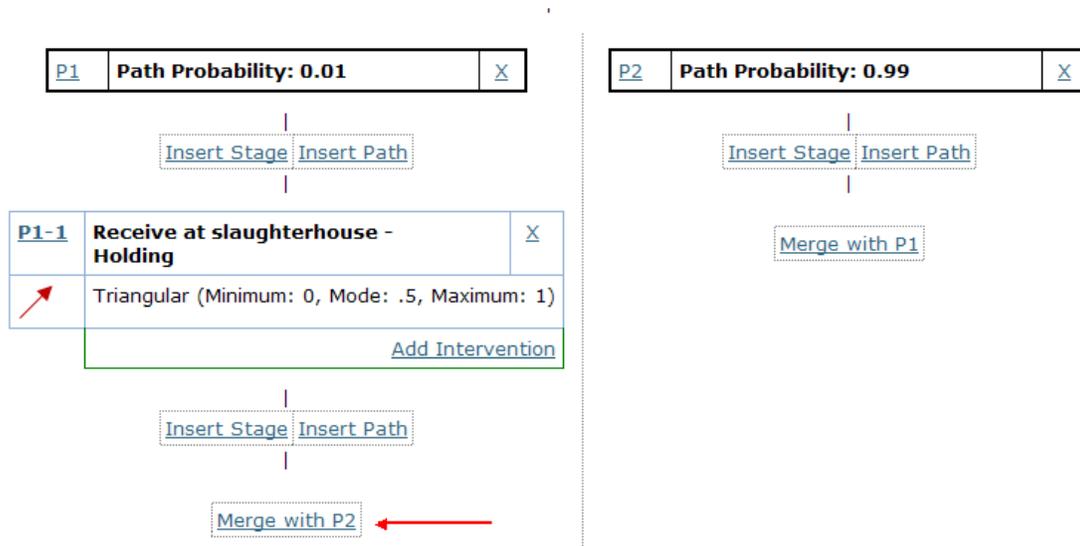
The model page will reload and now indicate the paths are merged:
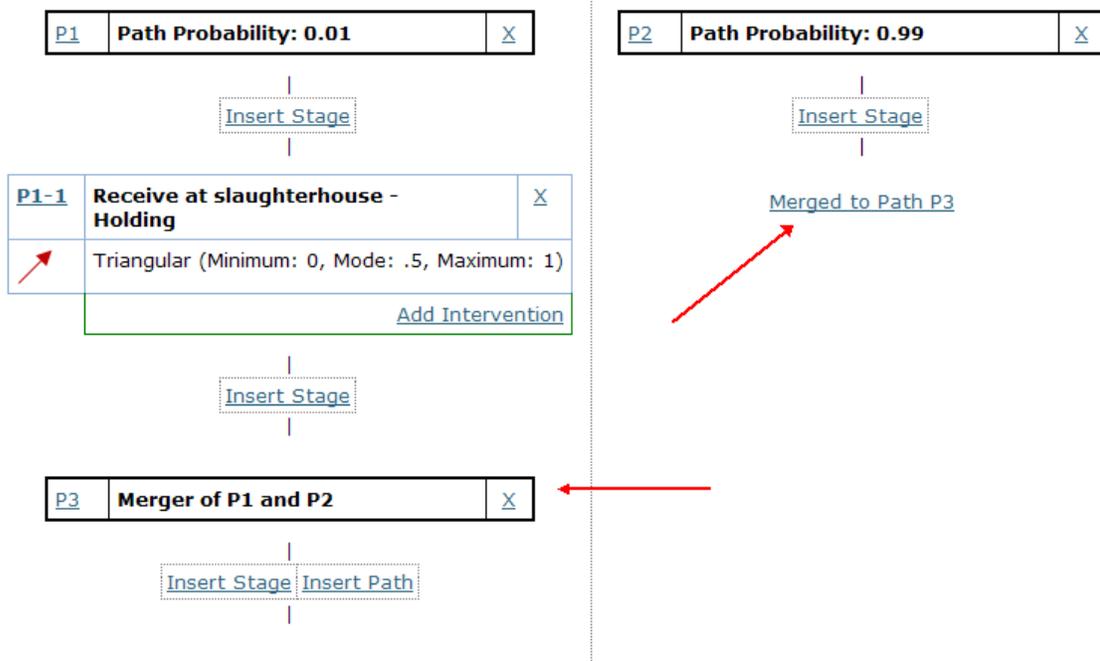
Note that while you can continue to add stages in each path, you may not add new paths until after the merge point.

Any stage added after the merge point will now be applied to both paths.

Step 13: Add remaining stages and interventions

Step 13A: Add remaining stages

To complete the model, insert the following stages after the merge point and adjust the parameters as needed:

- 15A: Dress – Scald
  - Set process type to Decrease
  - Set distribution to Uniform (Min: 0.5, Max 1.5)
- 15B: Dress – Defeathering – Defeathering
  - Set to Decrease
  - Set to Uniform (Min: 1, Max: 3)
- 15B: Dress – Defeathering – Cross-contamination
  - Set to Cross-contamination (within flock)
  - Set to Fixed (Value: 1.05)
    - Note that this example uses two stages to fully describe the defeathering process. There may be some steps in the process flow that involve two or more process types. In this situation, the user must enter each process type separately and decide on the appropriate sequence of events. This tutorial models defeathering as a decrease stage followed by a cross contamination stage.
- 15G: Dress – Evisceration – Evisceration
  - Set to Increase (addition – within flock)
  - Set Likelihood to 0.2
    - The addition process type includes an optional likelihood field which can be used to express the likelihood the addition will be applied. The tool only supports likelihoods of 0.002 and higher.
  - Set distribution to Normal (Mean: 1, Standard Deviation: 0.1)
- 16: Inside/Outside wash – Wash
  - Set to Decrease
  - Set to Fixed (value: 1)
- 30: Consumer storage
  - Set to Increase (growth)
  - Set to Triangular (Min: 0, Mode: 1, Max: 2)
  - If the growth is expected to occur less than 100% of the time, the user might consider adding a path before this stage

Step 13B: Add the final intervention

Finally, add a custom intervention to the **Inside/Outside Wash** stage.
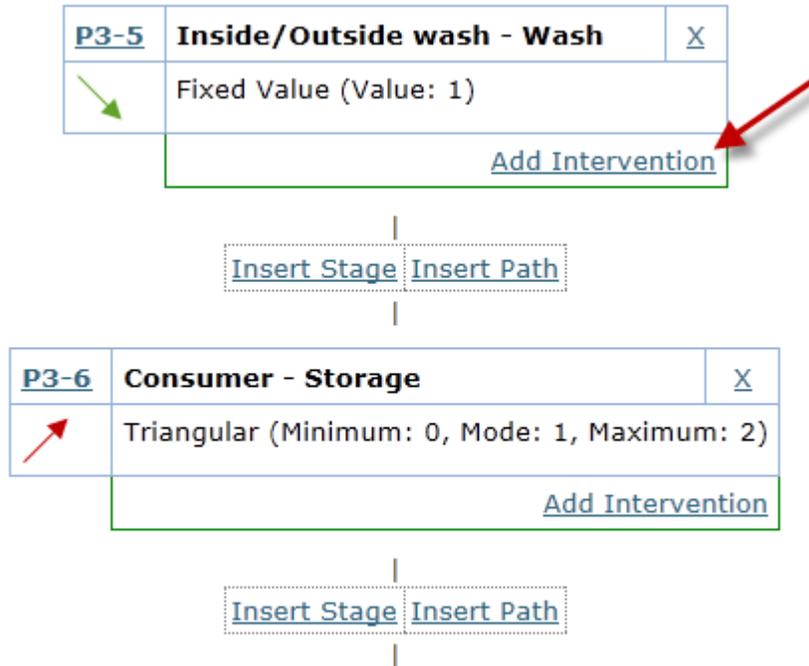
Select the intervention type of 0**. User Defined - Custom**.

Change the Intervention name from "Custom" to "Additional Washing"

Set the process type to Decrease and the distribution to Fixed (Value: 0.5).

Note that by default it is treated as an "**After Stage**" intervention. Alternatively, it could be modeled as "**Replaces Stage**" intervention that describes the combined log reduction of the stage and intervention.

When considering whether the intervention should come before or after the stage, note that this determines the order in which the calculations are applied.

Click on Save and Close.

The model is now complete. The next step is reviewing and running the model:

Step 14: Reviewing and running the model

Step 14A: Review the model

Click on the *Cambylobacter* **Results** link in the top tool bar:

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

This page will load and show the two paths described in the model. Scroll through the model and note the differences between the two paths, i.e. that path 2 does not include the Holding stage. Also note the path weights at the start of each path:

Result Path 1 (Probability:0.0100)

IC	**Initial Contamination**
Normal (Mean: 6, Standard deviation: 1.2) Specified for: First Step Within Prevalence: Fixed Value (Value: 0.65) Between Prevalence: 0.6	

P0-1	**Manage chickens – No change**
O	

INT-1	**Fly screens**
B↓	Fixed Value (Value: 0.7)

P0-2	**Receive at slaughterhouse – Receipt**
O	

P1-1	**Receive at slaughterhouse – Holding**
↗	Triangular (Minimum: 0, Mode: .5, Maximum: 1)

Result Path 2 (Probability:0.990)

IC	**Initial Contamination**
Normal (Mean: 6, Standard deviation: 1.2) Specified for: First Step Within Prevalence: Fixed Value (Value: 0.65) Between Prevalence: 0.6	

P0-1	**Manage chickens – No change**
O	

INT-1	**Fly screens**
B↓	Fixed Value (Value: 0.7)

P0-2	**Receive at slaughterhouse – Receipt**
O	

P3-1	**Dress: Scald - Scald**
↘	Uniform (Minimum: 0.5, Maximum: 1.5)

No results are included when the page first loads, only the definitions for each stage and intervention, as well as the initial contamination, consumer practices and dose response nodes.

Step 14B: Run the model

Click on the **Run Model** button above the key table at the top of the paths:

Reload Paths | Run Model | Create PDF | ☑ Include stages set to no significant change

Process Types

○	No significant change	↗	Increase (growth)	+	Increase (addition - within flock)
↘	Decrease	⊗	Cross-contamination (within flock)	W↓	Within Flock Prevalence Decrease
B↓	Between Flock Prevalence Decrease	W↑	Within Flock Prevalence Increase	B↑	Between Flock Prevalence Increase

The page will reload after a minute or so (please be patient) with a summary chart and the results for between flock prevalence (B), within flock prevalence (W), and the log of the arithmetic mean of the carcass concentration (C) for each node on each path:

Result Path 1 (Probability:0.0100)
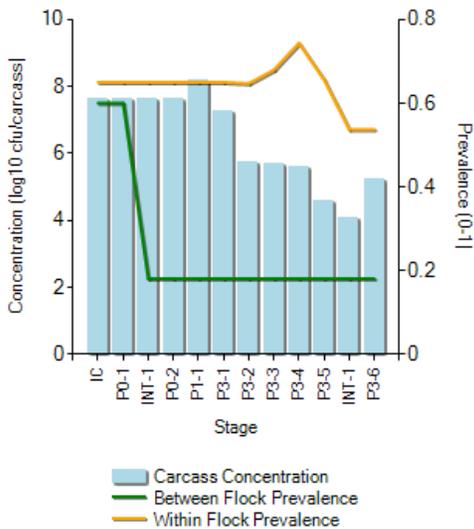
Result Path 2 (Probability:0.990)
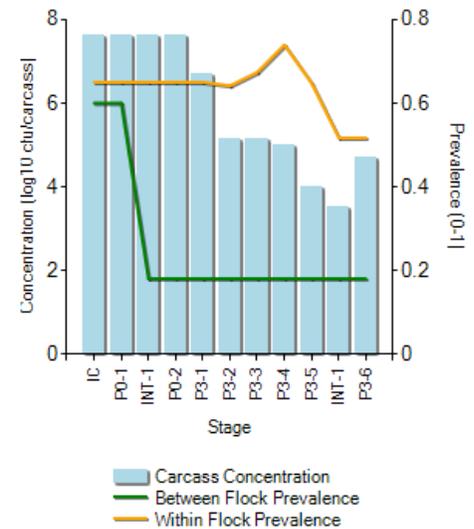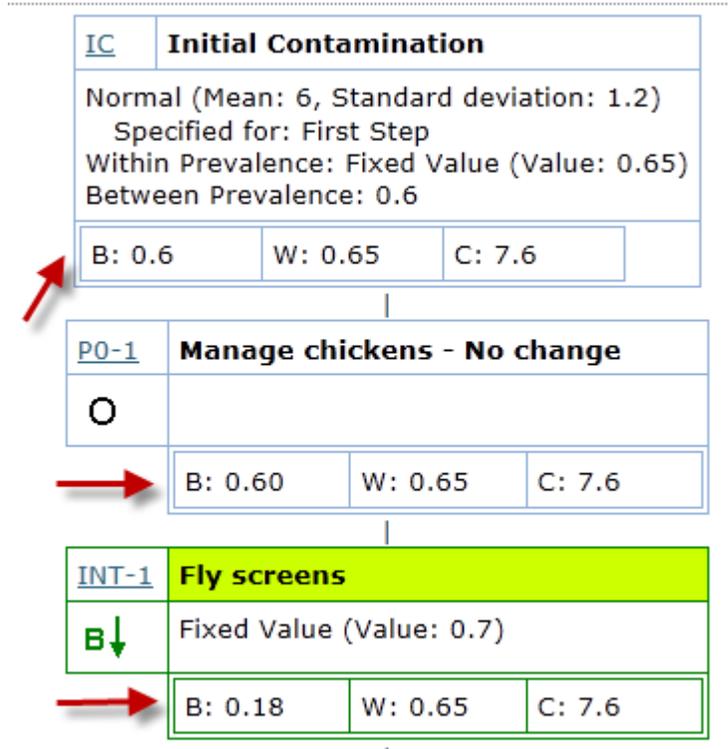
When interpreting the results, consider that the values reported are for the end of each stage and that the results are displayed for the scenario including the interventions and not the baseline scenario. They show the impact of applying the interventions to the baseline process.

Also recall that the concentration is the log of the arithmetic mean concentration in $\log_{10}$ cfu/carcass. As well, this is the concentration on positive flocks. If a process reduces the concentration of most carcasses in a flock below 0, this will be reflected in a reduced within flock prevalence. The lower bound on concentration will always be 0 $\log_{10}$ cfu/carcass, or 1 cfu/carcass on the non-log scale.

Step 14C: Interpreting residual risk

The residual risk values for each pathway as well as the weighted residual risk of all pathways, comparing the baseline scenario to that including interventions, are displayed at the very bottom of the page:

Weighted Residual Risk of all Paths: 0.22

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Residual risk is the ratio of the risk of the pathways including interventions to the risk 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.

Step 14D: Generating a PDF report

The user may also select to have a PDF report generated of the results for storing and distribution. This report differs in the layout from the web page report in that each path is presented sequentially in a text format.

For both the web page and PDF report, the user may reduce the size of the report by unchecking the "Include stages set to no significant change" checkbox prior to running the report.

This is the end of the tutorial. Please review to the user guide for additional details on using the tool and the Guidelines for background information on the process stages described in the tool.