全国农产品质量安全风险评估学术研讨会
风险评估方法模型及应用分会场

“农田至餐桌”黄羽肉鸡沙门氏菌定量风险评估模型

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汇报内容

一 背景和目的

二 内容和方法

三 结　果

四 结论与展望

Part 1

背景和目的

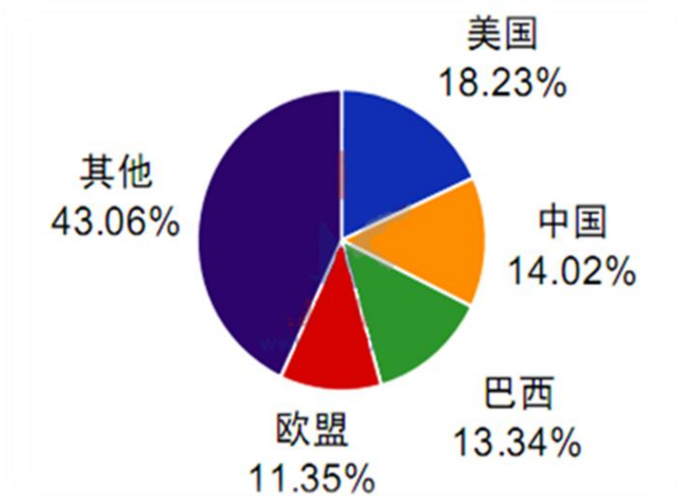


图1.1 2016年世界主要鸡肉消费国鸡肉消费占比

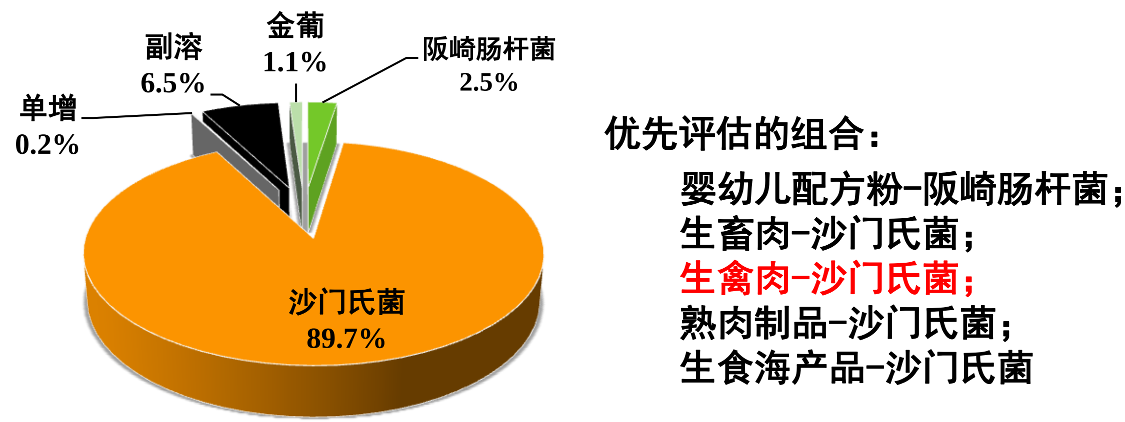


图1.2 国家食品安全风险评估中心发布致病菌归因和优先评估组合

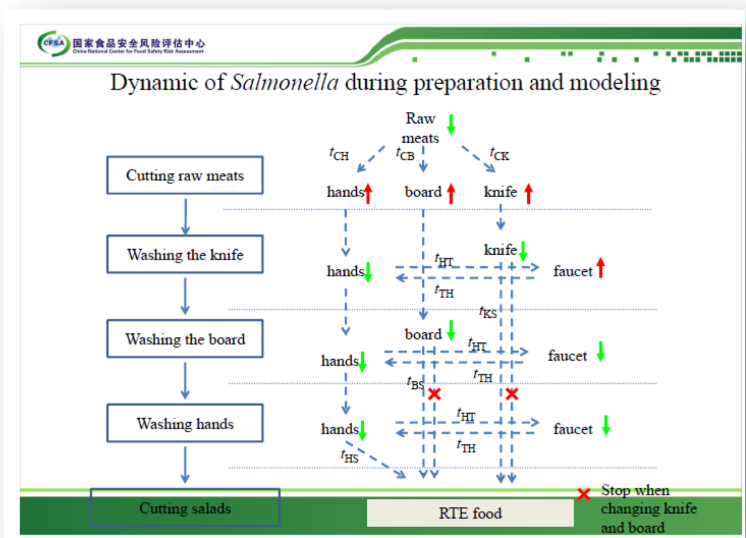


图1.3 国家食品安全风险评估中心
零售鸡肉沙门氏菌风险评估研究

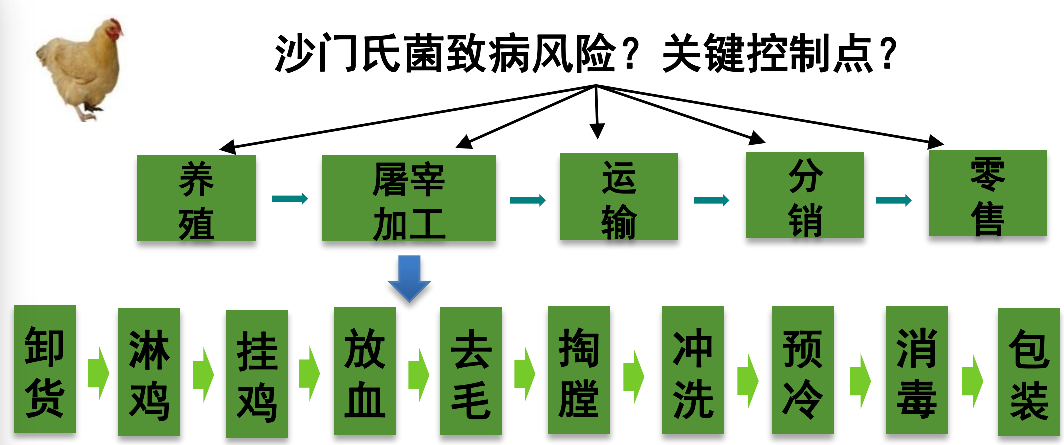
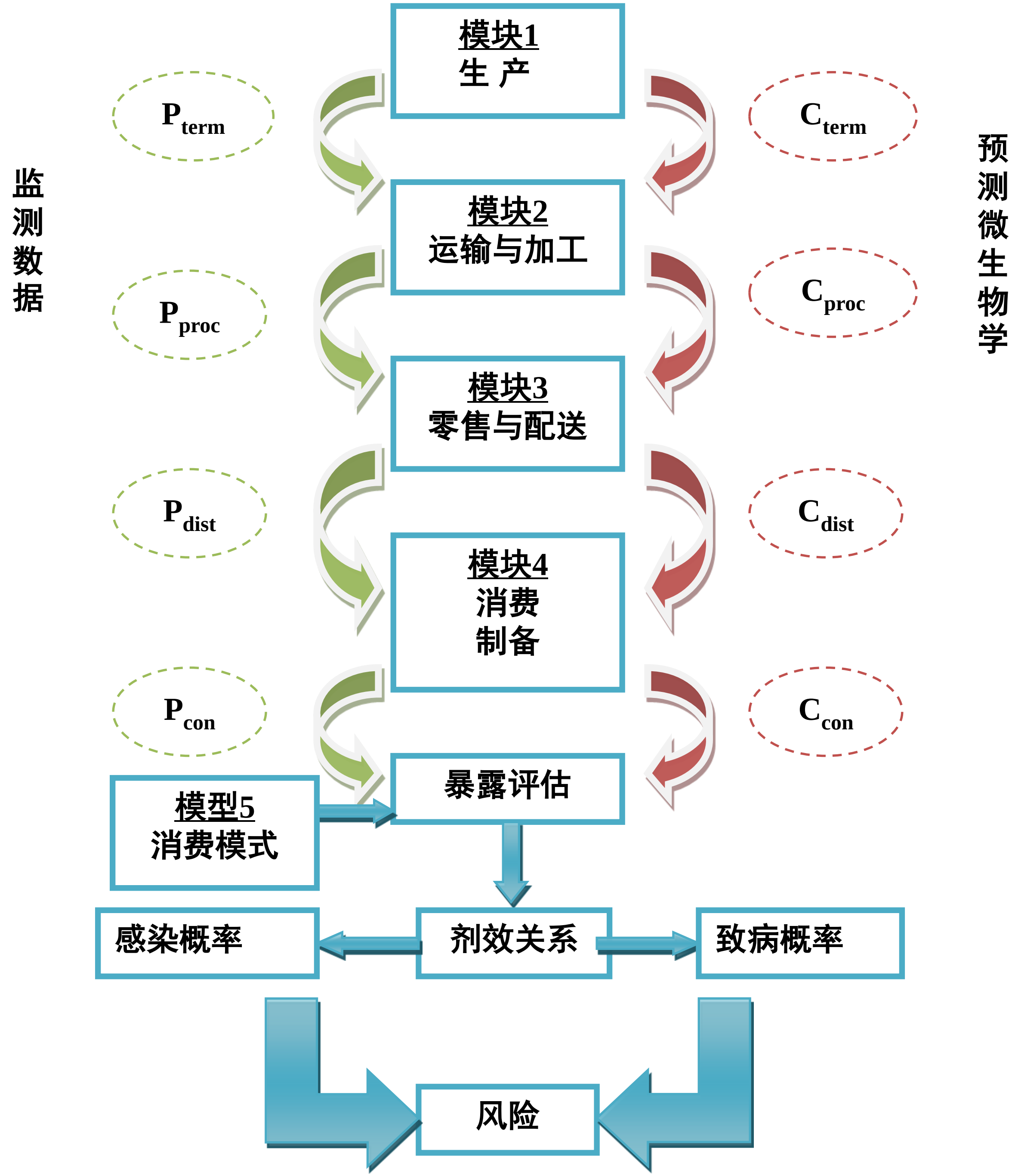


图1.4 黄羽肉鸡农田至餐桌生产过程

Part 2

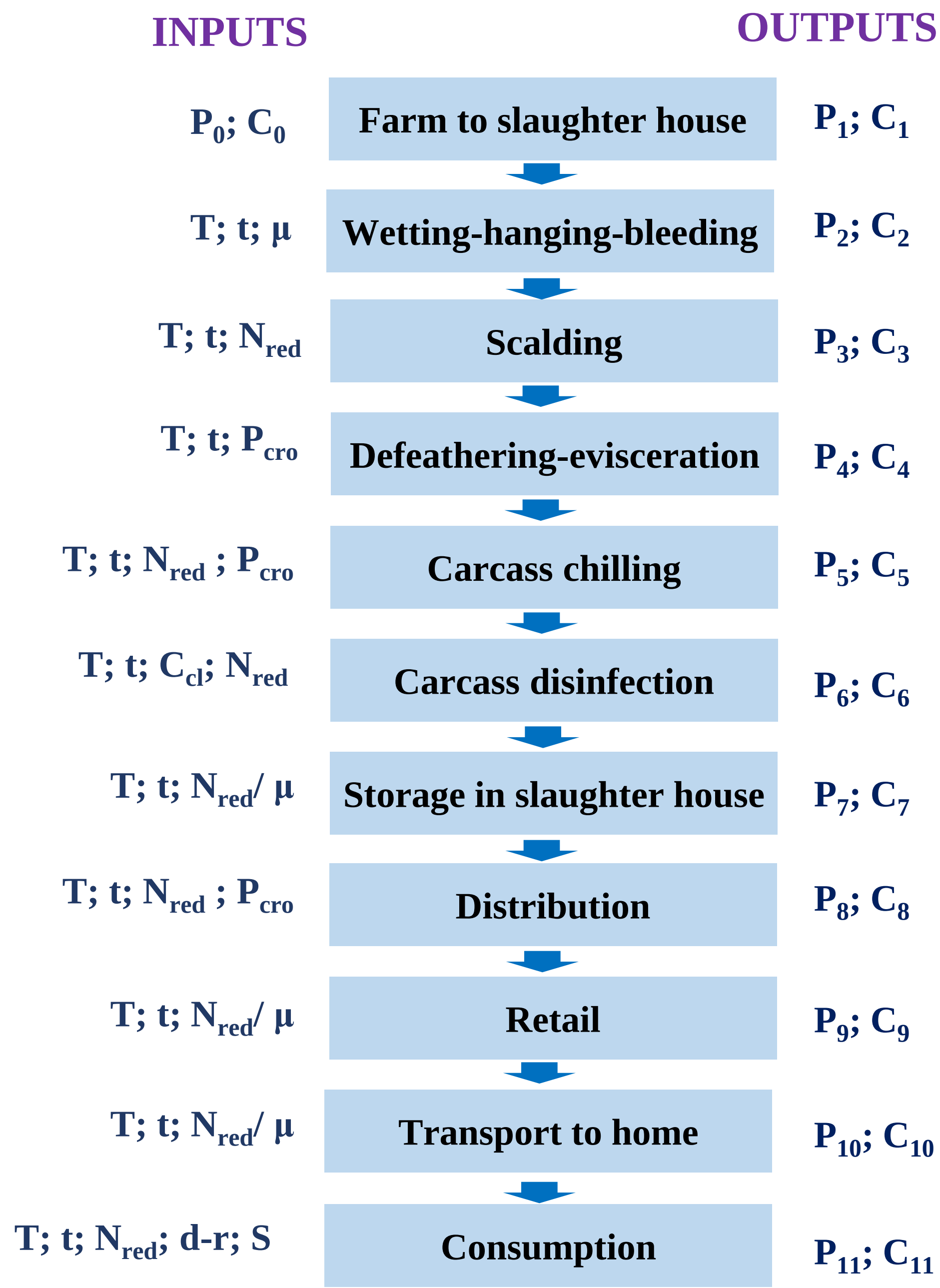
内容和方法



农田-餐桌评估模型框架（WHO）

- 收集各环节参数数据
  - 温度
  - 时间
  - 污染率和污染水平
  - 干预措施参数
  - …
- 分布拟合和预测模型构建
  - 温度、时间等参数分布
  - 不同温度下生长/衰亡预测模型
  - 干预措施细菌致死模型
  - 交叉污染分布/模型
- 暴露评估模型构建和风险拟合

$$P(ill) = prob \times cont \times (dose - response)$$



➢ 预测模型构建-以生长/衰亡模型（分布）为例

1. 接种

Stanley BYC12, Indiana HZC10, Typhimurium YXC1, Thompson LWC10, Kentucky CBC2

2. 不同温度下培养

衰亡温度：2-8 ℃
生长温度：10-38 ℃

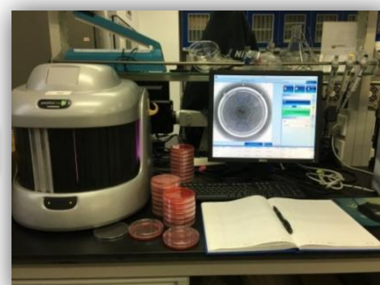
3. 均质

130rpm；1min

4. 螺旋涂布

5. 细菌培养，37 ℃

6. 细菌计数



7. 模型构建/分布拟合

一级模型
- Gompertz
- Huang
- Buchanan
- Baranyi

二级模型
- Arrhenius
- Ratkowsky平方根
- Huang平方根

模型比较参数：AIC

OriginLab 8.0 Pro/ @risk

8. 模型验证

RMSE、R^2 等内验因子

精确度 因子
（Accuracy factor, A_f）
偏差度因子
（Bias factor，B_f）

OriginLab 8.0 Pro
Combase

➢ 评估模型

Description	Variable	Language	Value	Unit	Source
1.Farm to Slaughter house					
Input	Prevalence in fraction contaminated	P1(in)=Lognorm(0.05,0.04)	0.072	percent	SCAU
Input	Contamination level in fraction contaminated	C1(in)=Pert(3,3.5,4)	3.50	log CFU/g	literature
Output	Prevalence	P1(out)=P1(in)	0.072	percent	calculated
Output	Initial level	C1(out)=(C1(in))	3.50	log CFU/g	calculated
2.Wetting-hanging-bleeding					
Input	Prevalence	P2(in)=P1(out)	0.072	percent	calculated
Input	Bacterial level	C2(in)=C1(out)	3.50	log CFU/g	calculated
Input	Temp	T2=Normal (22,7)	26.87	℃	investigation
Input	Time	t2=Pert (0.33,0.67,1)	0.57	h	investigation
Input	Bacterial growth	D=0.002*(T2+273.15)*exp{-[(2424.900)/(8.134(T2+273.15))]^(49.767) }*t2	1.13E-22	log CFU/g	this study
Output	Prevalence after	P2(out)=P2(in)	0.072	percent	calculated
Output	Bacterial level after	C2(out)=C2(in)+D	3.50	log CFU/g	calculated
3.Scalding					
Input	Prevalence	P3(in)=P2(out)	0.072	percent	calculated
Input	Bacterial level	C3(in)=C2(out)	3.50	log CFU/g	calculated
Input	Temp	T3=Pert(50,60,70)	61.53	℃	investigation
Input	Time	t3=Normal (1.2,0.17)	1.11	min	investigation
Input	Bacterial reduction in scalding at 50 and 60 C	N''_{red}=Lognorm(0.10,0.045,RiskShift(0.13))	0.26	log CFU/g	calculated
Input	Bacterial reduction in scalding at 70 ℃	N_{red}=[(-1.46+0.03T3)^2]*t3^[(2.49-0.018T3)^2]	0.18	log CFU/g	this study
Output	Prevalence after	P3(out)=P3(in)	0.07	percent	calculated
Output	Bacterial level after	C3(out)=IF(T3< 60,C3(in)- $N''_{red,}$C3(in)-N_{red})	3.24	log CFU/g	calculated
4.Defeathering-evisceration					
Input	Prevalence	P4(in)=P3(out)	0.07	percent	calculated
Input	Bacterial level	C4(in)=C3(out)	3.24	log CFU/g	calculated
Input	Prevalence in cross-contamination in Evisceration	P(Eviisceration)=Triang(-0.25,0,0.15)	0.08	percent	calculated
Output	Prevalence after	P4(out)=P4(in)+P(Eviisceration)	0.15	percent	calculated
Output	Bacterial level after	C4(out)=C4(in)	3.24	log CFU/g	calculated
5.Carcass chilling					
Input	Prevalence	P5(in)=P4(out)	0.15	percent	calculated
Input	Bacterial level	C5(in)=C4(out)	3.24	log CFU/g	calculated
Input	Initial level (Transform unit)	C_{IL}=C5(in)*22/30	2.38	log CFU/ml	investigation
Input	Log reduction	D=Normal (0.2,0.05)	0.21	log CFU/g	this study
Output	Prevalence in cross-contamination in carcass chilling	P5(out)=-24.8+15.5*C_{IL}+0.74*P5(in)	0.23	percent	calculated
Output	Bacterial level	C5(out)=C4(out)-D	3.03	log CFU/g	calculated

➢ 评估模型

Description	Variable	Language	Value	Unit	Souce
11.Consumption					
Input	Prevalence in home	P11(in)=P10(out)	0.26	percent	calculated
Input	Bacterial level in home	C11(in)=C10(out)	2.05	log CFU/g	calculated
Input	Prevalence in cross-contamination	P(CC)=0.1	0.1	percent	literature
Input	Prevalence after cross-contamination	P11(out)==P11(in)+P(CC)	0.36	percent	calculated
Input	cooking time	t11=pert (20,30,40)	31.98	min	investigation
Input	Bacterial reduction after cooking	N_{red11}=2.02t11-44.095	20.50	log CFU/g	calculated
Input	Serving size	S=27.39	28.16	g	literature
Input	non-log level after disinfection step	C11(out)=10^(C11(in)-N_{red11})	1.12E-05	CFU/g	calculated
Input	Dose-response alpha	A=0.175	0.175	no-unit	qmrawiki
Input	Dose-response N50	B=1110000	1.11E+06	no-unit	qmrawiki
Output	P(response)	P=1-POWER(1+(S*C11(out)*(POWER(2,1/A)-1)/B),-A)	2.55E-09	percent	calculated
Output	Probability of illness	P(illness)=P(response)*P11(out)	9.31E-10	percent	calculated

➢ 风险拟合

基于拉丁方抽样的一维蒙特卡洛模拟

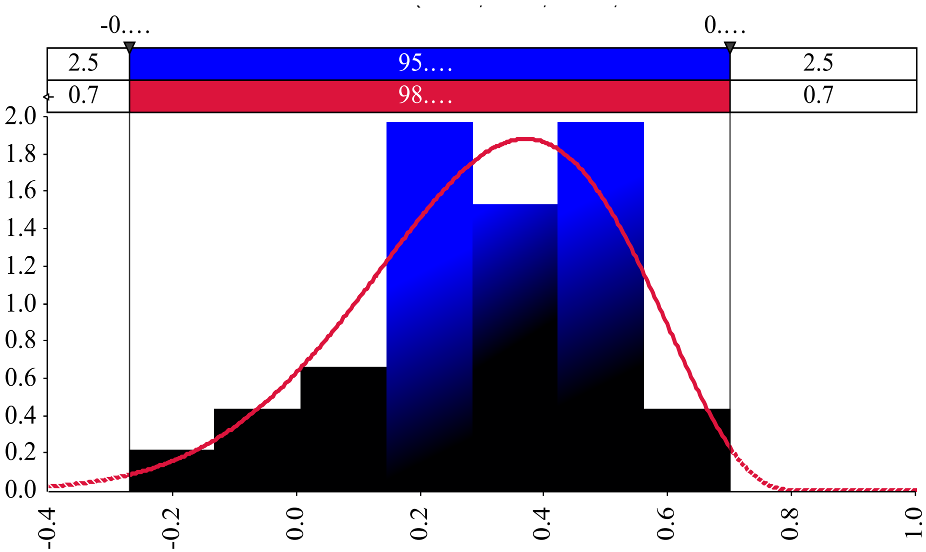
工具：@risk 6.3

Part 3

结 果

不同温度下沙门氏菌生长/衰亡分布和模型

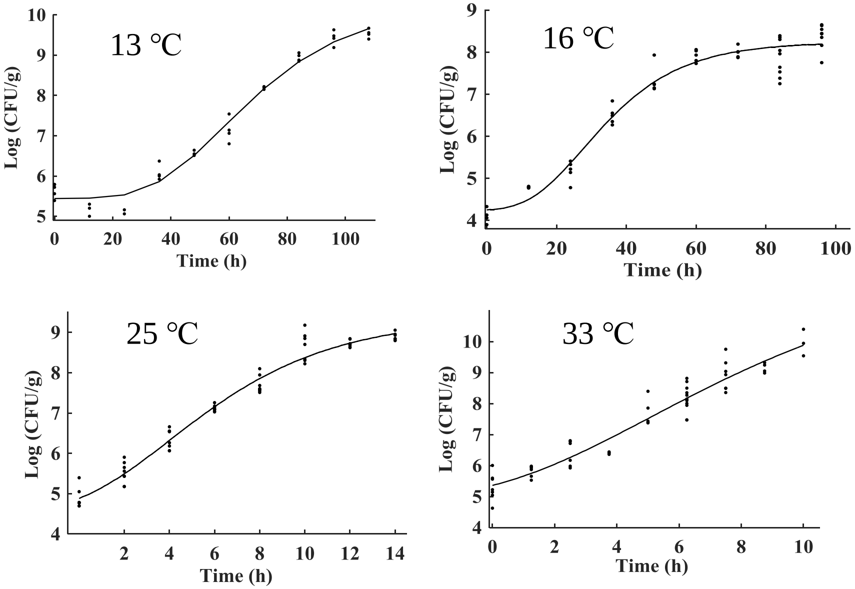
低温 (2 – 8 °C)



RiskNormal (0.30,0.21)

生长温度(10 –38 °C)

Primary model: Modified Gompertz model



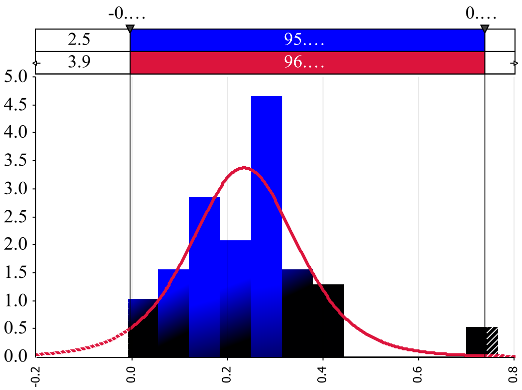
Secondary model: Arrhenius Model

$$\mu_{max} = 0.002 * (T + 273.15) * exp - [(2424.9) / (8.134(T + 273.15))]^{(49.767)}$$

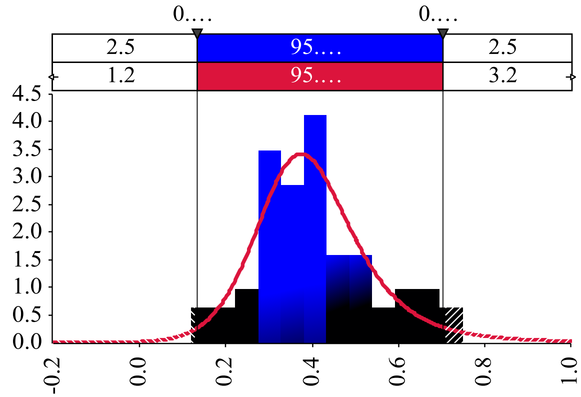
干预措施下的细菌致死分布和模型

Scalding (50 – 70 °C)

Distributions for bacterial survival at 50 and 60 ℃

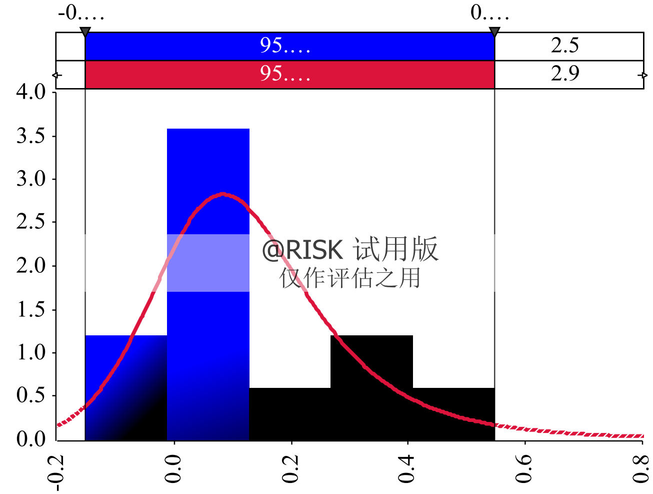


RiskLogistic(0.23, 0.074)



RiskLogLogistic(-0.25, 0.64, 8 .67)

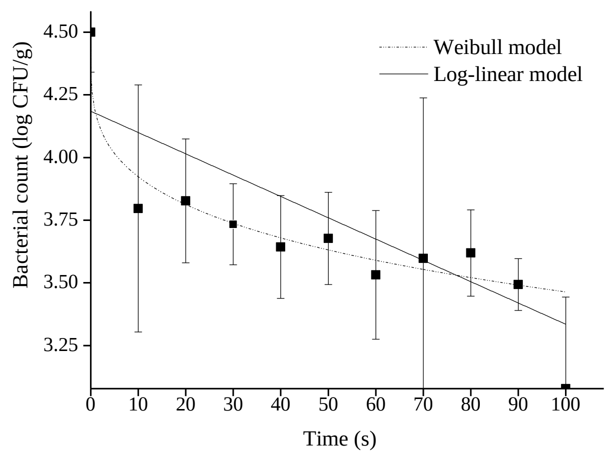
Chlorine water washing (20-100 ppm)



RiskLogLogistic(-0.44,0.55,6.06)

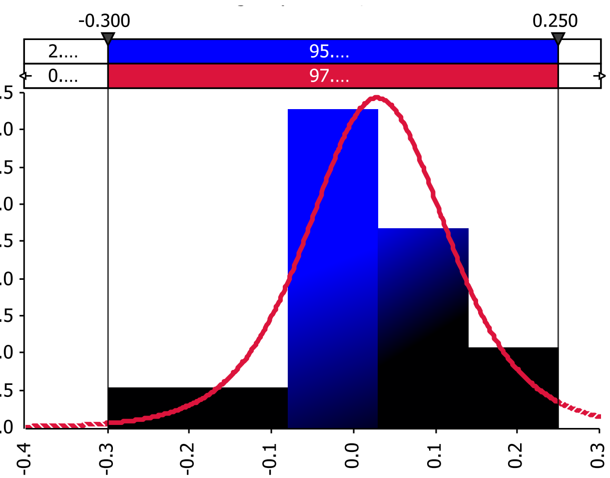
Weibull model showed a satisfied fitness at 70 °C.

$$y = y_0 - \left(\frac{t}{85}\right)^{0.35}$$



交叉污染

Cross contamination in evisceration

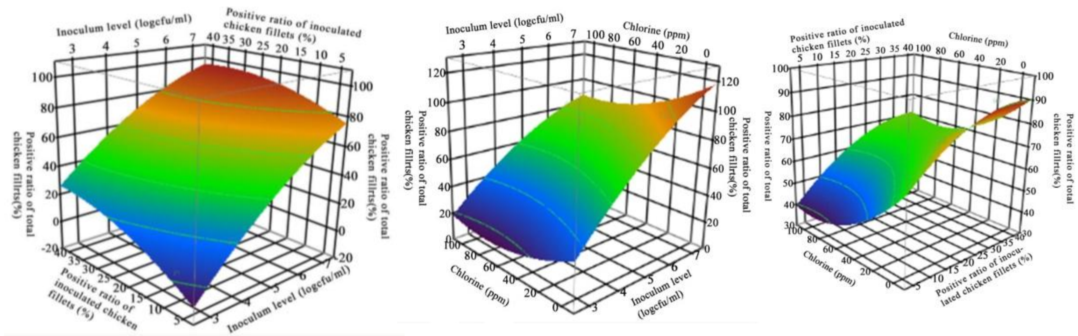


RiskLogistic(0.028, 0.056)

Cross contamination model in chilling

$$Y = -24.8 + 15.5X_1 + 0.74X_2 + 0.098X_3 - 0.003X_3^2$$

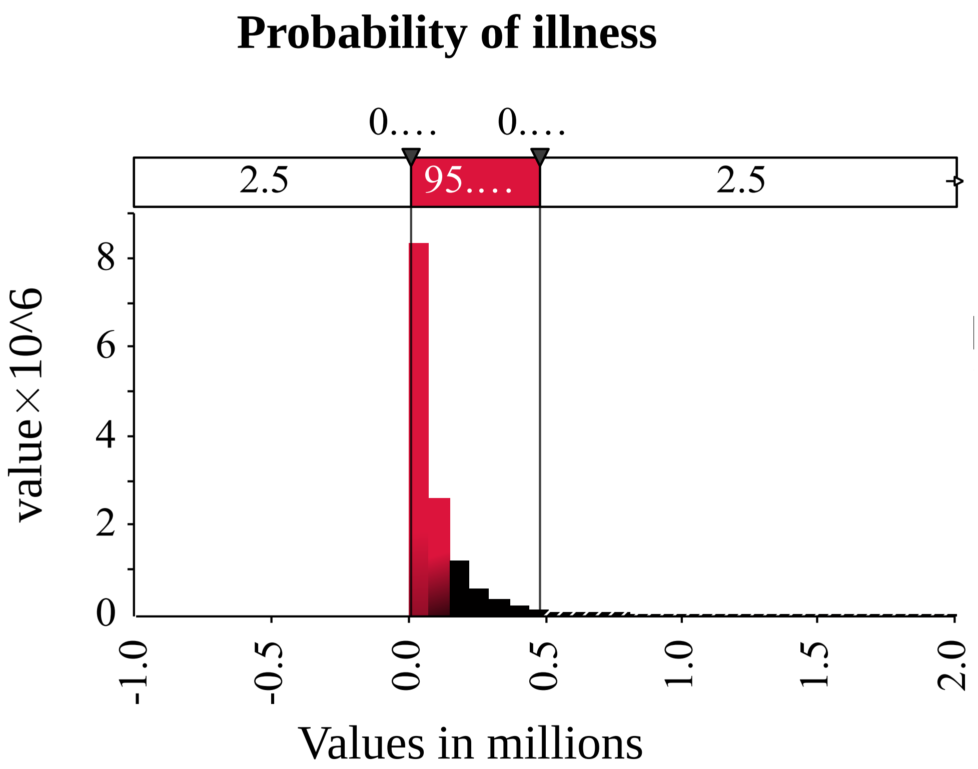
Where, Y is the predicted response (post-chill prevalence); inoculum level, pre-chill prevalence, chlorine concentration were denoted as X_1, X_2, X_3, respectively.



a b c

Response surface plots describing the effect of inoculum level and pre-chill prevalence (a); inoculum level and chlorine concentration (b); and pre-chill prevalence and chlorine concentration (c) on post-chill prevalence of *Salmonella* in chicken.

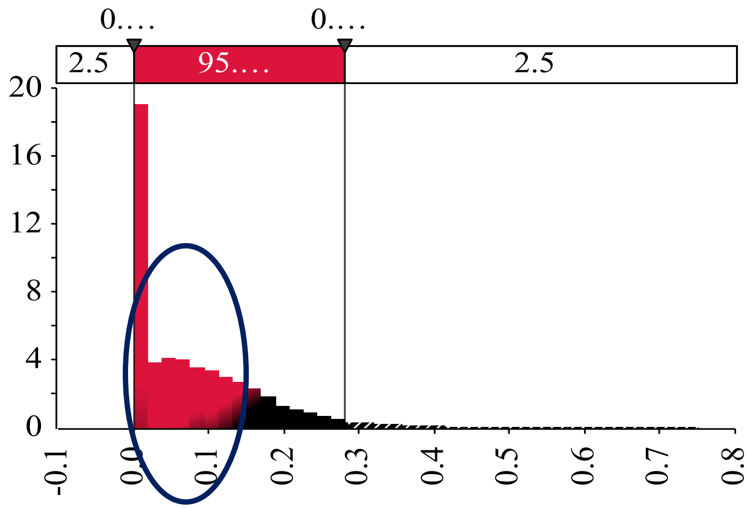
风险拟合结果



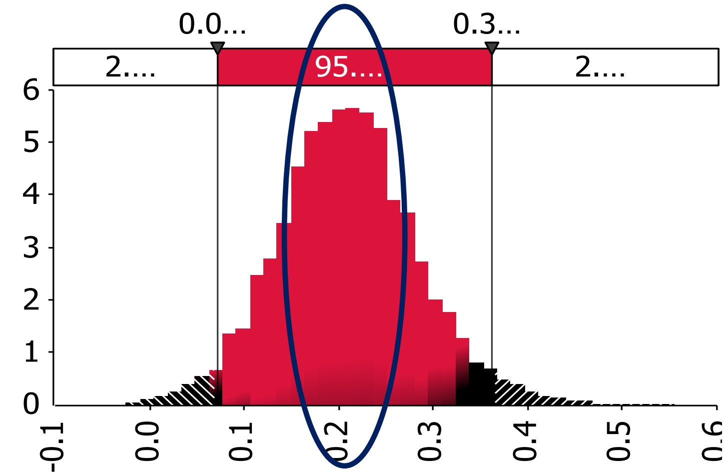
Minimum	**0.00000**
Average	**1.01E-007**
Maximum	**2.94E-006**
Standard deviation	**1.56E-007**

The average and maximum number of *Salmonellosis* cases per 10,000,000 consumer is 1 and 29, respectively.

Simulated results *vs* Sampling results



Bacterial Prevalence after Evisceration



Bacterial Prevalence after Disinfection

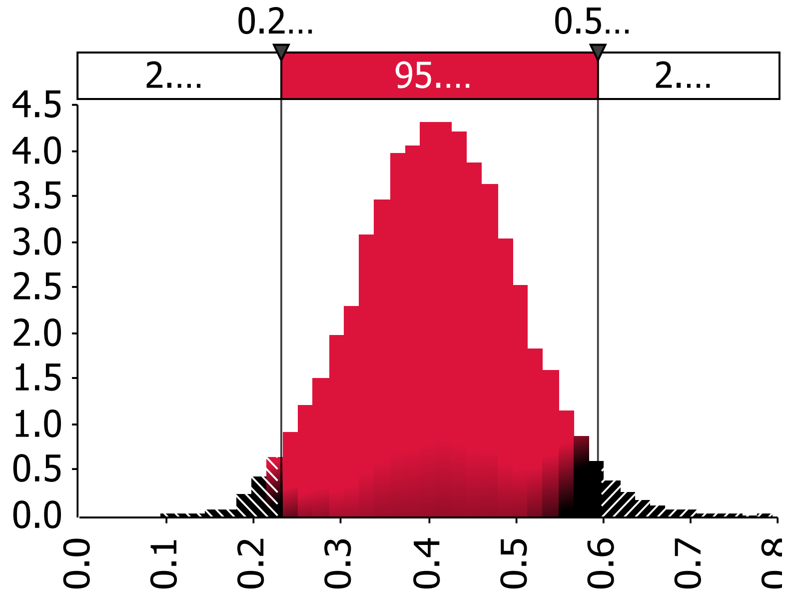
Prevalence of *Salmonella* isolated from a slaughterhouse

Sample Source	Sample Type	First Quarter	Second Quarter	Third Quarter	Fourth Quarter	Fifth Quarter	Sixth Quarter	Seventh Quarter	Pre(%)
		Pre(%)							
Evisceration	**Carcass**	15	0	3.3	3.3	10	13.3	8.3	7.6
Disinfection	**Carcass**	1.7	5	8.3	3.4	11.7	1.7	5	5.3

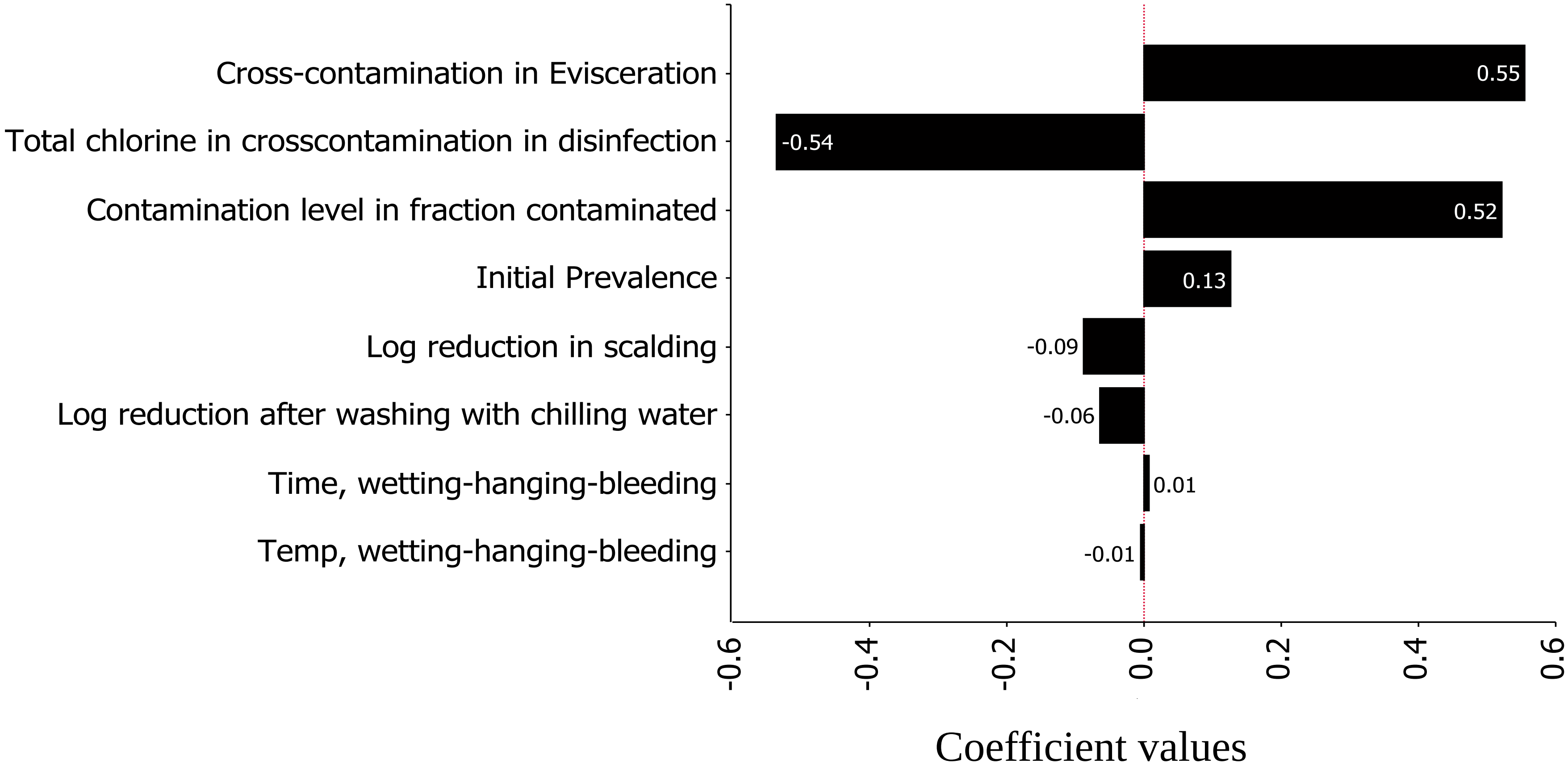
Simulated results *vs* Sampling results

Prevalence of *Salmonella* isolated from different supermarkets

Sample source	Sample type	Positive rate (%)
Jingdong Mall	chicken	30（18/60）
Su-Ning	chicken	18.8（3/16）
Wal-Mart	chicken	27.3（3/11）
Lotus	chicken	56（14/25）
Vanguard	chicken	32（8/25）

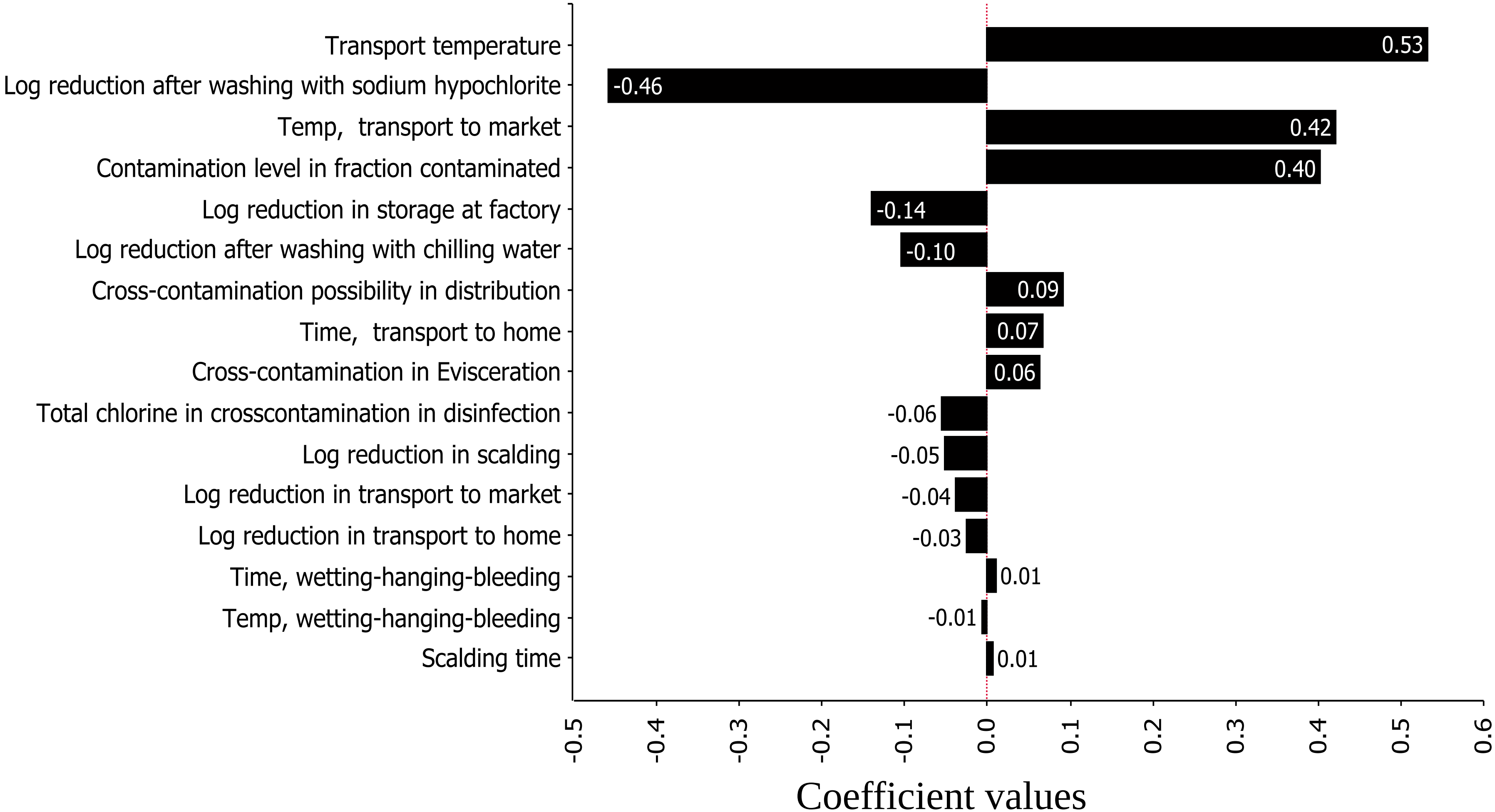


Sensitive Analysis——Critical control points



Sensitive analysis of bacterial prevalence in the end of slaughterhouse

Sensitive Analysis——Critical control points



Sensitive analysis of probability of illness

Part 4

结论与展望

- 微生物定量风险评估可用于科学确认风险关键控制点，减少养殖环节污染、冷链运输、防止交叉污染是降低黄羽肉鸡沙门氏菌污染的关键控制环节；
- 需充分结合监测数据进行模型参数优化；
- 预测模型需进行生产规模下的验证；
- 结合疾病负担研究可耐受风险水平，制定相关安全限量标准和生产操作规范；

致 谢

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