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# Possiamo prevedere il comportamento delle muffe?

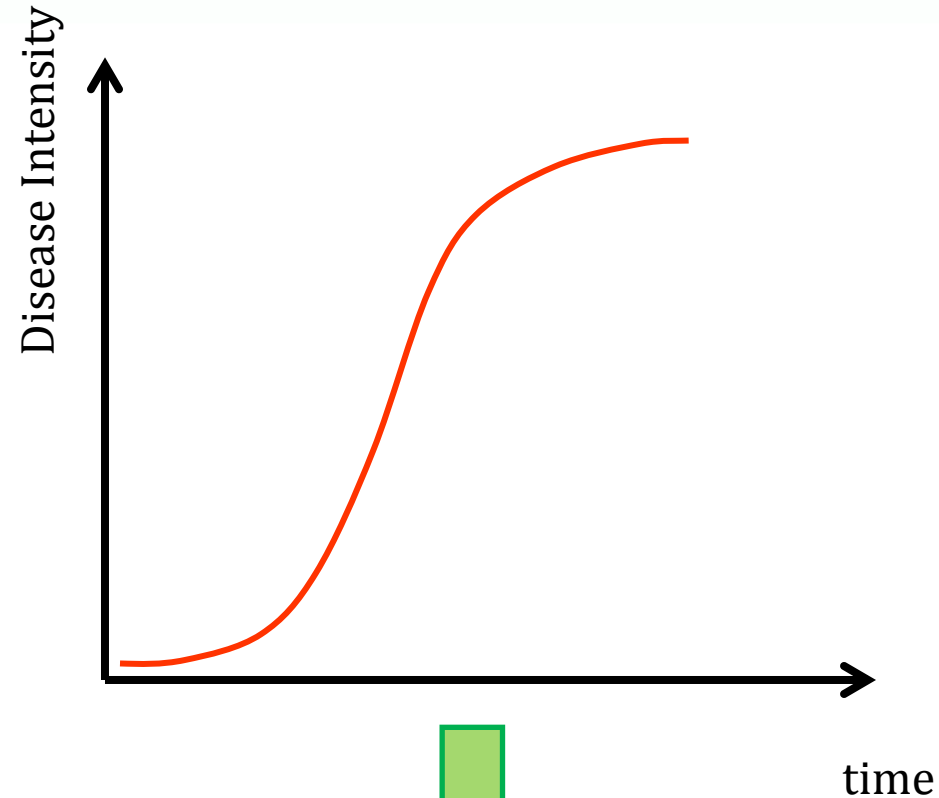
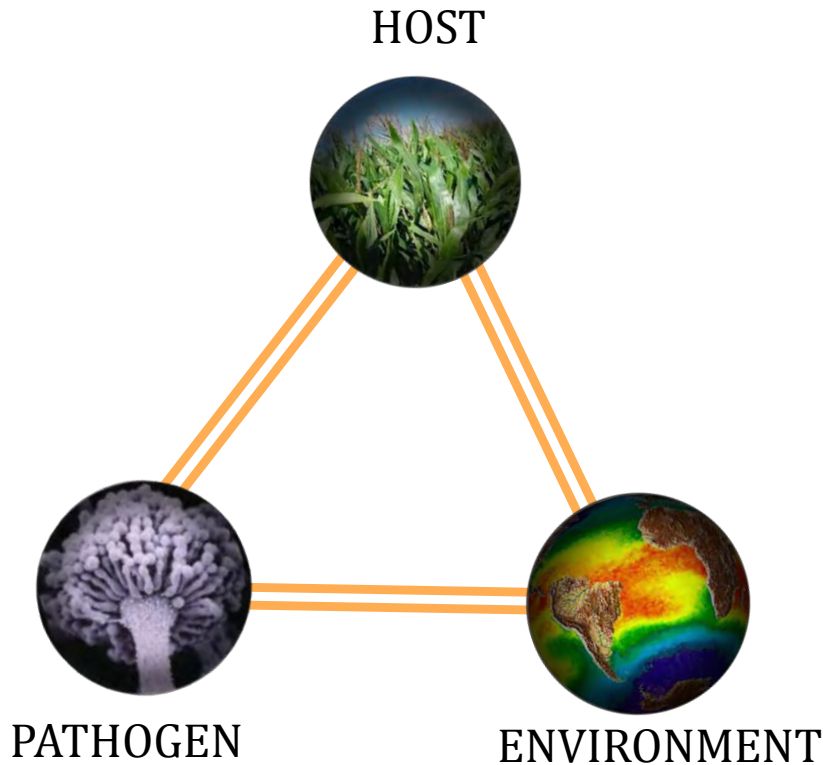
*Cenni riguardo ai modelli previsionali per lo  
sviluppo dei funghi e la produzione di  
micotossine*

Marco CAMARDO LEGGIERI



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# General Introduction: Epidemiology



MODEL



*“A model is a simplified representation of reality.”*

In fungal epidemiology, possible objectives are:

- Predicting the time and the scale of an event
- Predicting the probability of an event
- Comparing the performance of different management strategies



# General Introduction: Model

## Modelling approaches

### Empirical

Predictor variables ———→ Response variables

**STATISTICAL PRINCIPLES**

Empiric rule



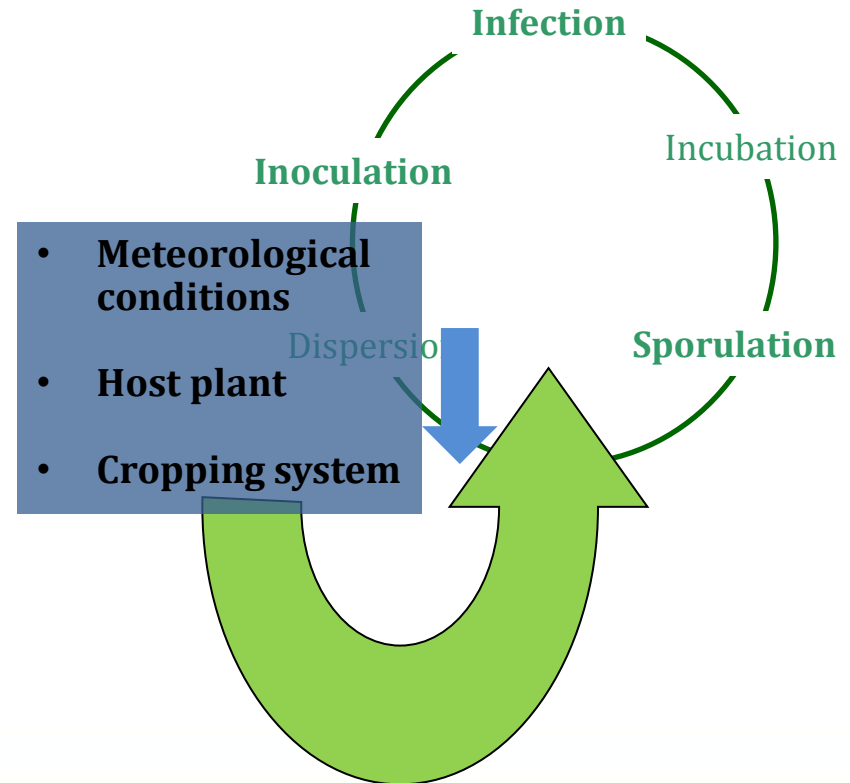
Regression analysis

Non parametric analysis

Stochastic model

Neural network

### Mechanistic





***A posteriori* analysis of the variations of epidemics according to changes on the affecting factors.**

Analysis of the quantitative relation which links *epidemics* with *influencing variables*

According to statistical analyses

Empiric rule

Regression analysis

Non parametric analysis

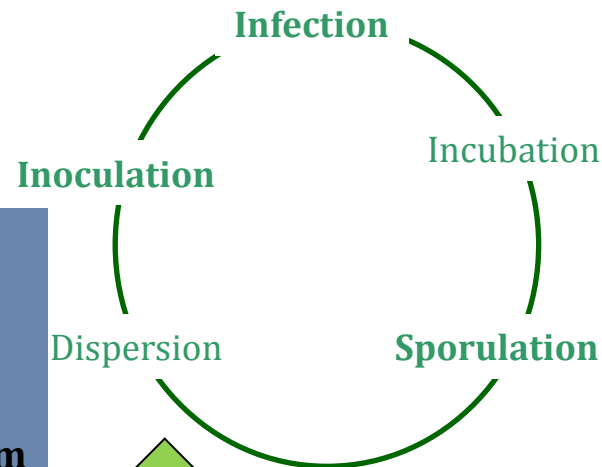
Stochastic model

Neural network



***A priori* analysis of the variations of epidemics according to changes in the affecting factors.**

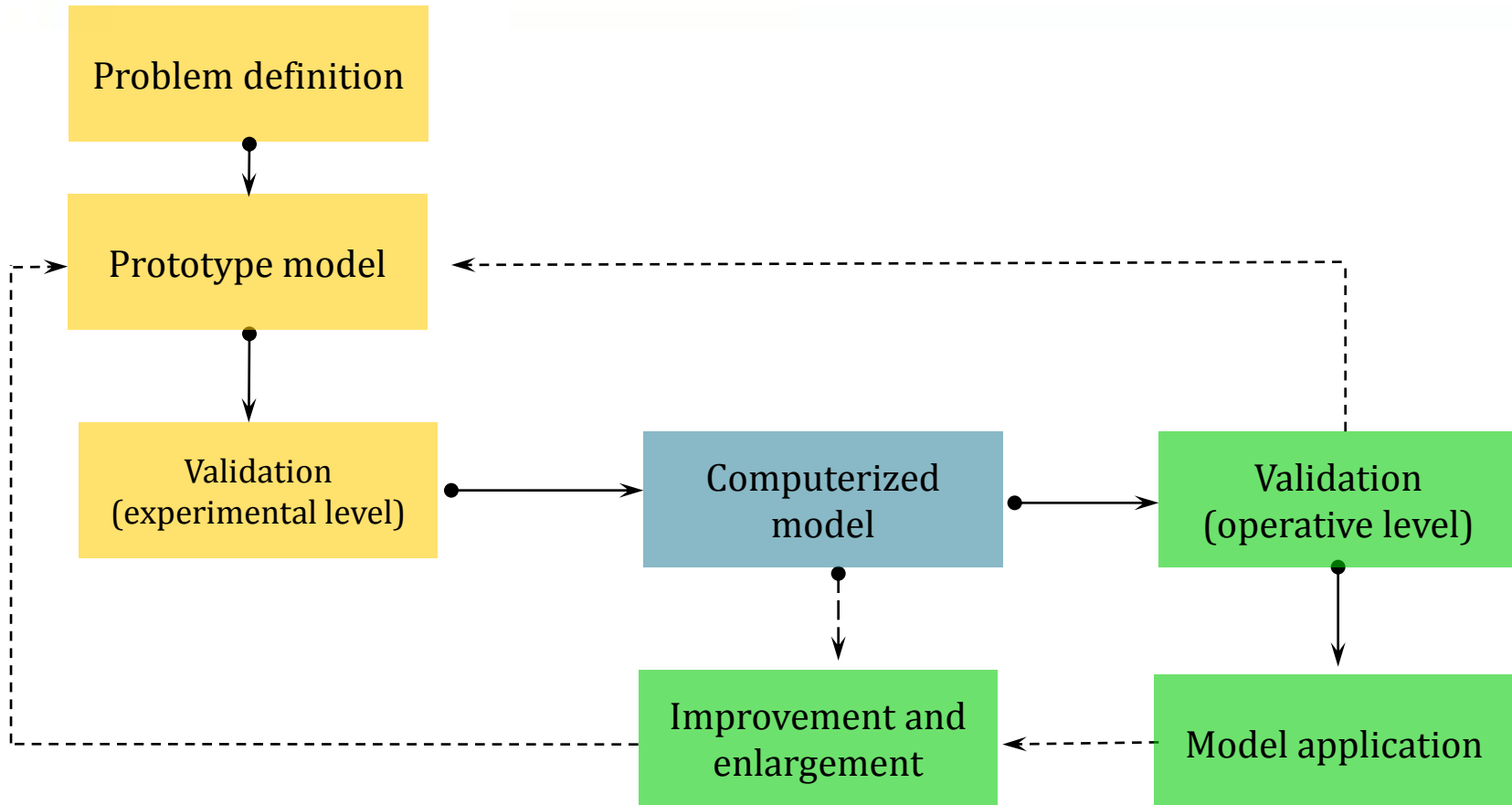
Analysis of each steps of pathogen infection cycles, influencing variables and change



- Meteorological conditions
- Host plant
- Cropping system



# General Introduction: model development





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# Possiamo prevedere il comportamento delle muffe?

*Sviluppo di modelli previsionali, base di dati,  
elaborazioni matematiche e validazioni dei  
risultati.*

Marco CAMARDO LEGGIERI





***A posteriori* analysis of the variations of epidemics according to changes in the factors affecting it**

Analysis of the quantitative relation which links *epidemics* with *influencing variables*

According to statistical analyses

Empiric rule

Regression analysis

Non parametric analysis

Stochastic model

Neural network



# Steps to built empirical models based on regression analysis

1. Collection of experimental data about disease and biological/meteorological influencing factors
2. Creation of a correlation matrix between variables
3. Elaboration of statistical regression model with the most effective variables
4. Model outputs evaluation



$$Y = a + bX_1 + cX_2 + \dots + nX_n$$

where: Y = level disease

X<sub>1</sub> ... X<sub>n</sub> = independent variables

Air temperature

Relative humidity

Rain

Leaf wetness

Condition of pathogen

Phenological host stage

Host susceptibility



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# Empirical model

## Principle drawback:

Based on a numerical relation between collected data in specific experimental condition without any *a priori* defined relation cause-effect between variables

## Therefore:

*Problems with data out of the experimental range*



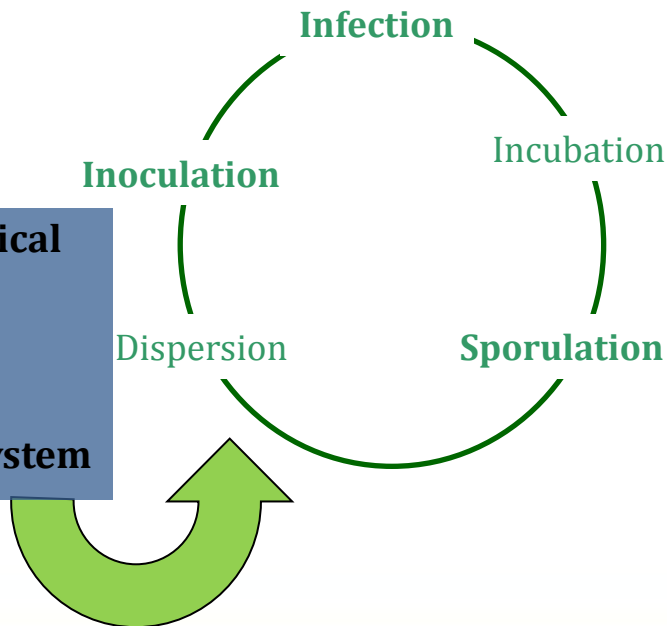
**Care validation and re-calibration**



## ***A priori* analysis of the variations of epidemics according to changes in the factors affecting it**

Analysis of each steps of pathogen infection cycles, influencing variables and change

- Meteorological conditions
- Host plant
- Cropping system





# Steps to built a mechanistic model

1. Definition of influencing variables on the patho system, and relations between (logical model)
2. Experimental design to determine quantitative relation between variables /data collection in literature
3. Development of mathematical equation to describe these relations (operative models)

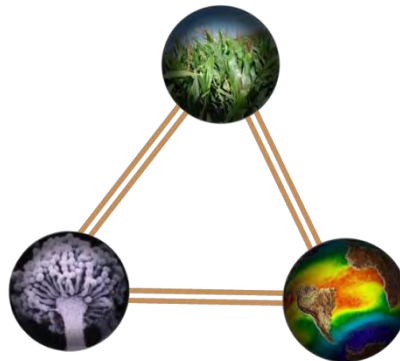


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# Steps to build a mechanistic model – SYSTEMS ANALYSIS

System = limited part of reality which contain element in relation between them (de Wit, 1993)

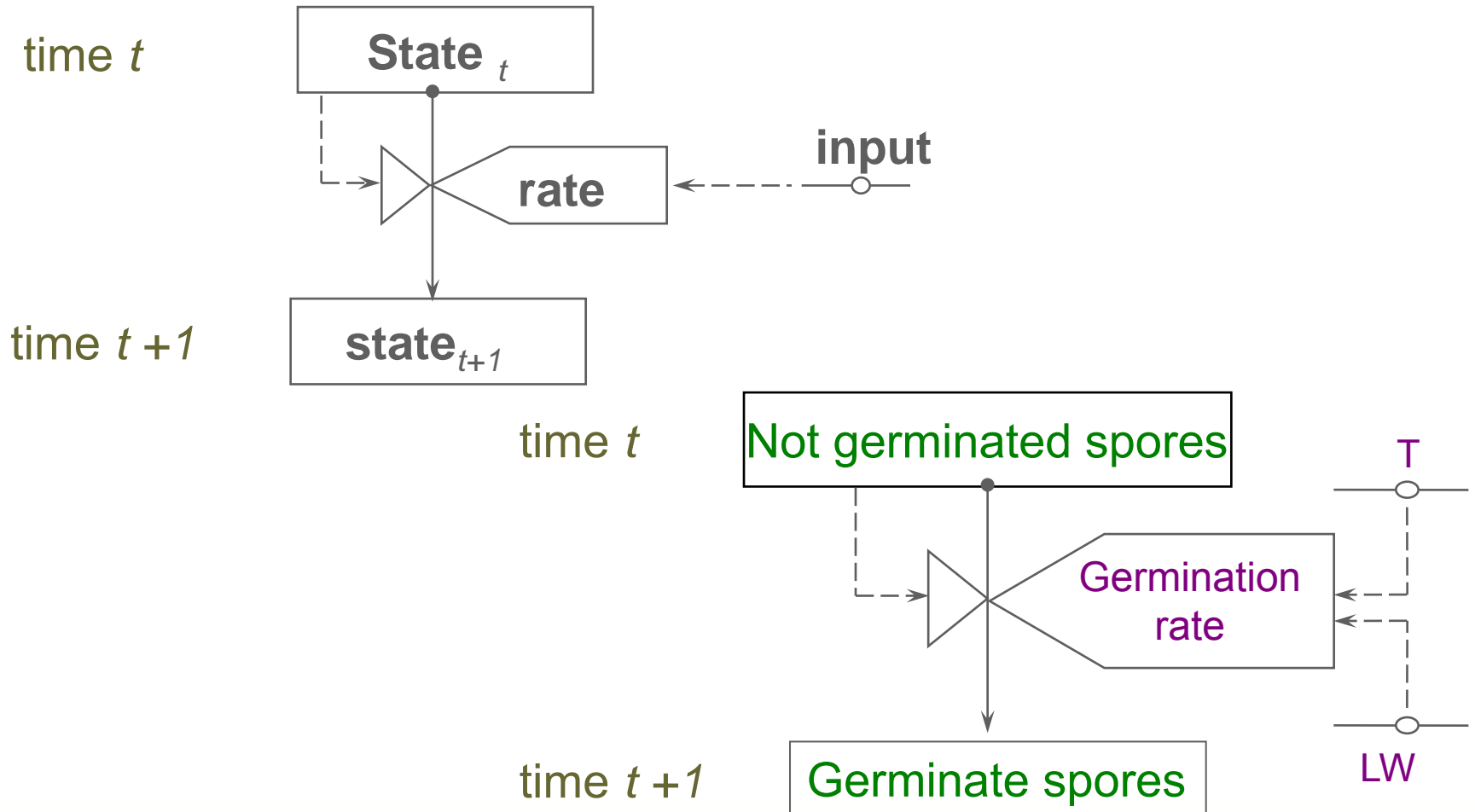
System's sctructure = all the relation in the system analysed



Patho system



# Mechanistic model RELATIONAL DIAGRAM







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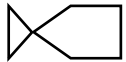
# Mechanistic model RELATIONAL DIAGRAM



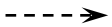
State variable



Direction flow; links two state variables



Rate; are always mathematical equations



Information flow



Constant or parameter (*driving variable*)



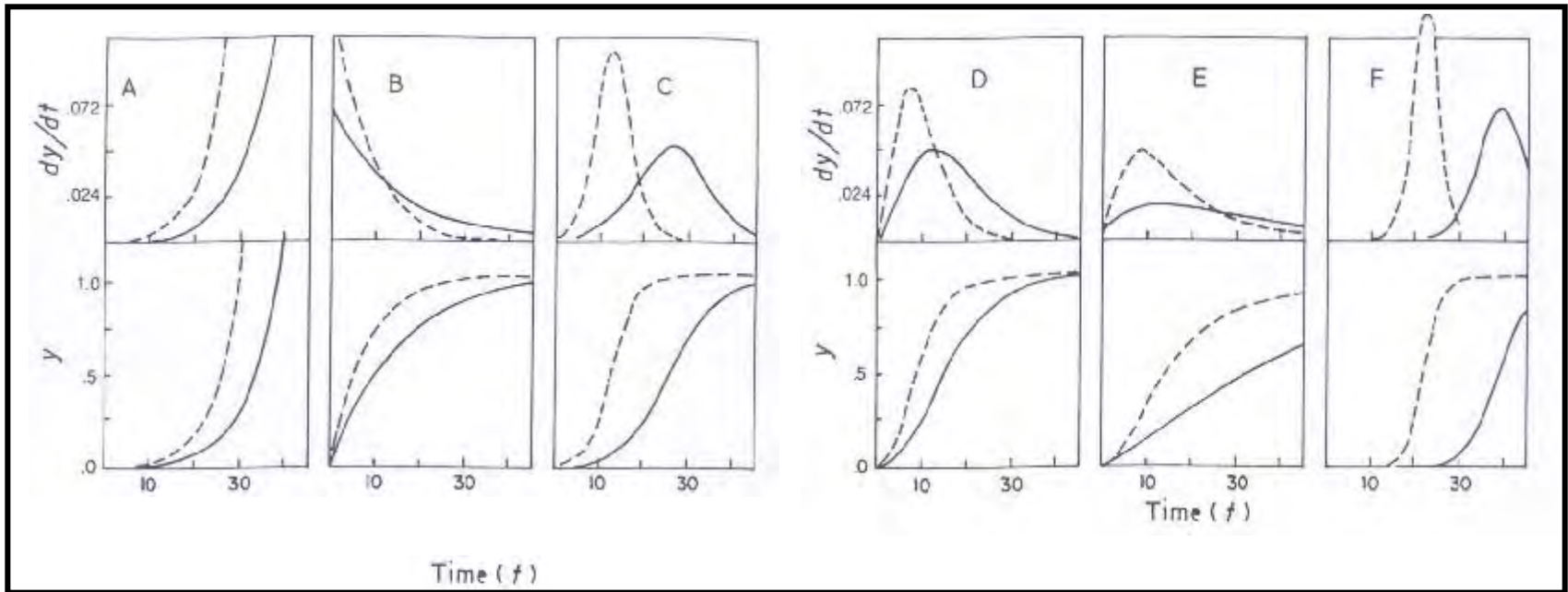
Intermediate variable



Not quantifiable variable



# Suitable library of equation for fitting



A. Exponential

B. Monomolecular

C. Logistic

D. Gompertz

E. Log-logistic

F. Richards



# Suitable library of equation for fitting

## Exponential

$$Y = b \cdot \exp(aX)$$

## Logarithmic

$$Y = \ln(aX^b)$$

## Power

$$Y = aX^b$$

## Asintotic

$$Y = a - b \cdot c^X$$

## BETE

$$Y = [a \cdot X^b \cdot (1-X)]^c$$

## Logistic

$$Y = c / [1 + a \cdot \exp(-bX)]$$

## Monomolecular

$$Y = 1 - b \cdot \exp(-aX)$$

## Gompertz

$$Y = \exp[-b \cdot \exp(-aX)]$$

## Richards

$$Y = [1 - b \cdot \exp(-aX)]^{1/(1-c)}$$

## Weibull

$$Y = 1 - \exp\{-[(X-a)/b]^c\}$$

Y = dependent variable  
X = independent variable  
a, b, c = parameters



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# Mechanistic model CASE STUDY

**OTA-Grapes: a prototype model to  
predict ochratoxin A risk in grapes**



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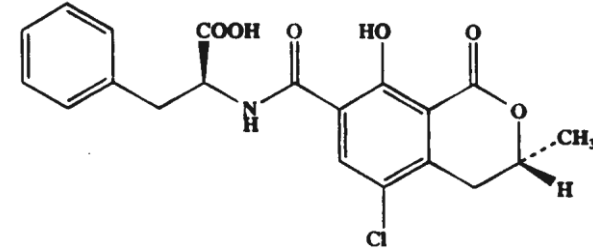
# Introduction

*Grape*

**PREDICTION**

*Environment*

*A. carbonarius*



*Reg. EC. N  
1881/2006  
2µg/kg*

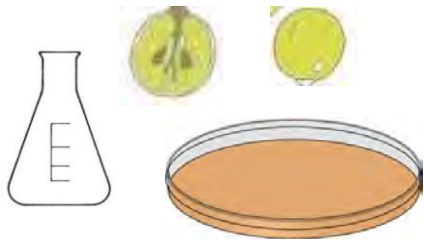




# Germination rate

Experimental conditions:

**Temperature** 15 - 40°C, **Relative humidity** 85 - 100%, **Incubation time** 3 - 36hrs



Spore suspension of *A. carbonarius* ( $10^6$  / ml) inoculated onto **skin** and **flesh** of berries of white organic **grapes** and **artificial grape juice** medium (SGM)

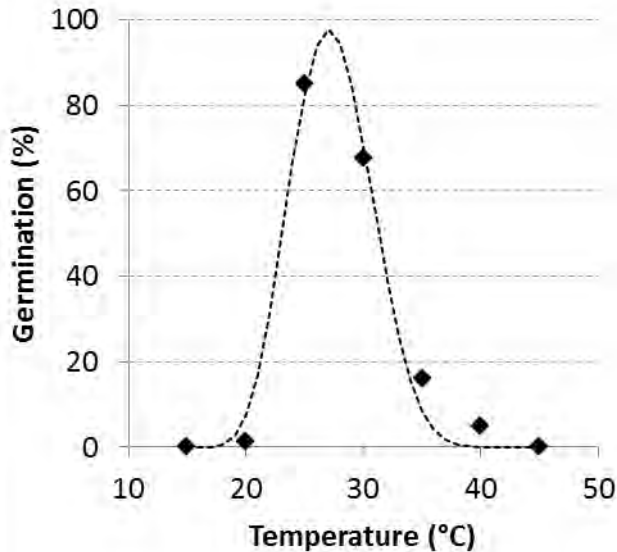
50 single spores were examined (x 3 replicates), temporal observations every 3 hours

**Germination rate:** non-linear regression models were fitted to the observed data using the statistical package PASW statistics 21

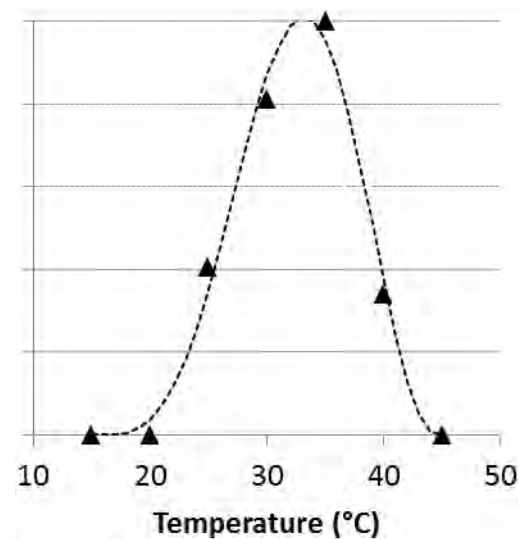


# Germination rate: results

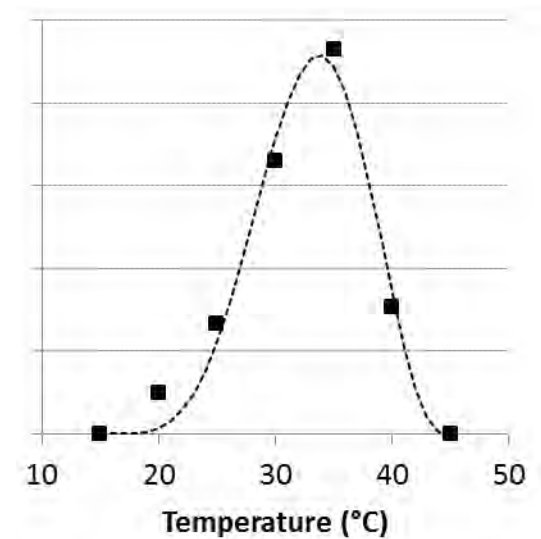
SKIN



FLESH



SGM



The dynamics of spore germination in different T regimes (GeRT) was fitted using a Bete equation (Teq is the equivalent of temperature)

$$\text{GeR}_T = \left( a * (\text{Teq})^b * (1 - \text{Teq}) \right)^c$$

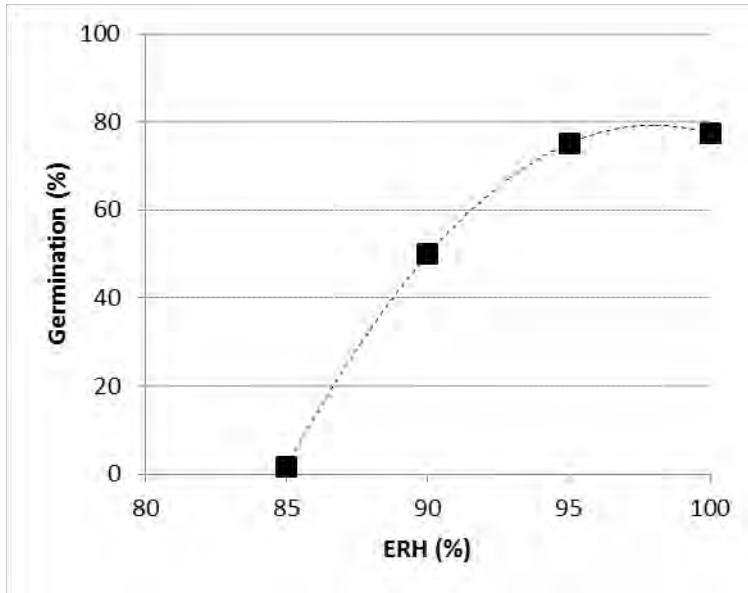
$$\text{Teq} = \left( \frac{T - T_{\min}}{T_{\max} - T_{\min}} \right)$$

(T is the daily mean temperature, T<sub>min</sub> = 5°C and T<sub>max</sub> = 45°C)

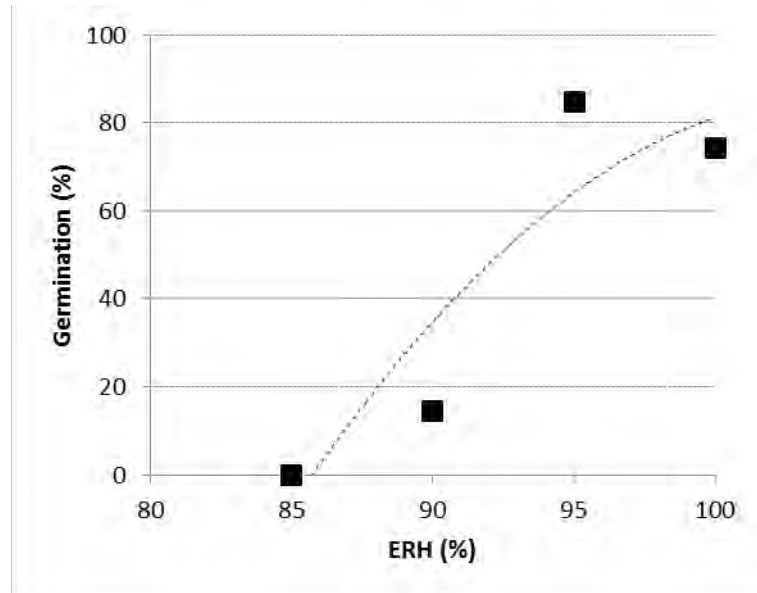


# Germination rate: results

SKIN



SGM



The dynamics of spore germination in different RH regimes (GeRRH) was fitted using a polynomial equation detailed below:

$$GeR_{RH} = a * RH^2 + b * RH + c$$

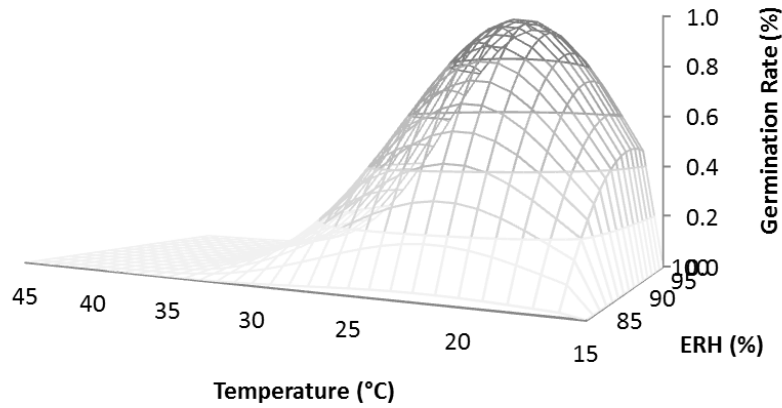
Where RH is the daily mean value.



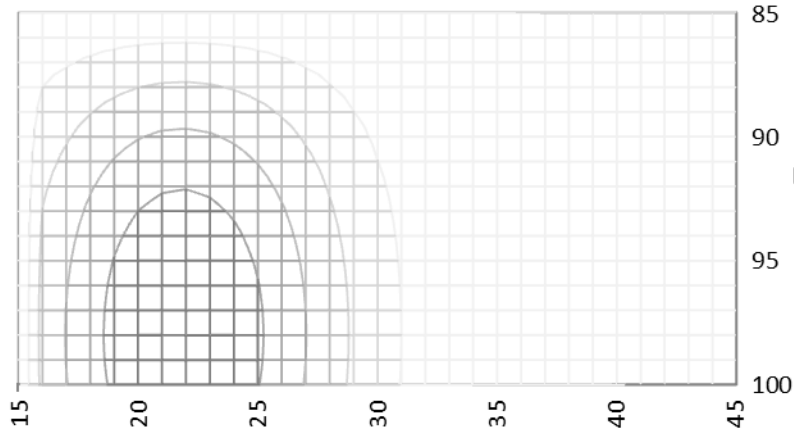


# Germination rate: results

## SKIN

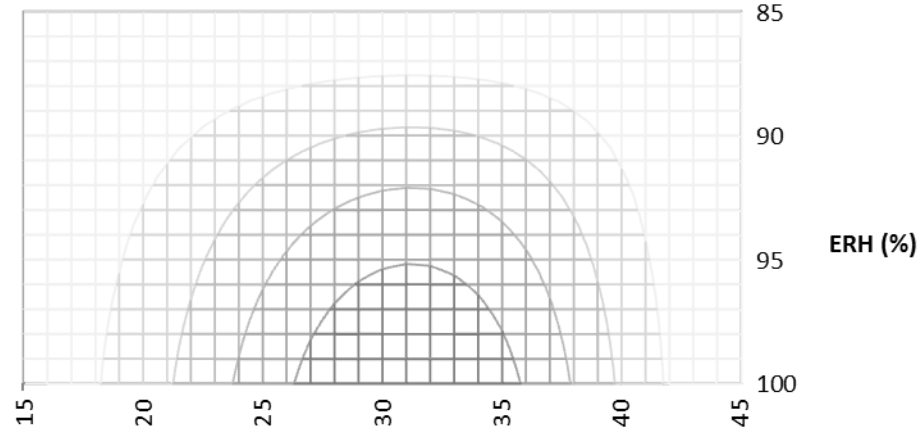
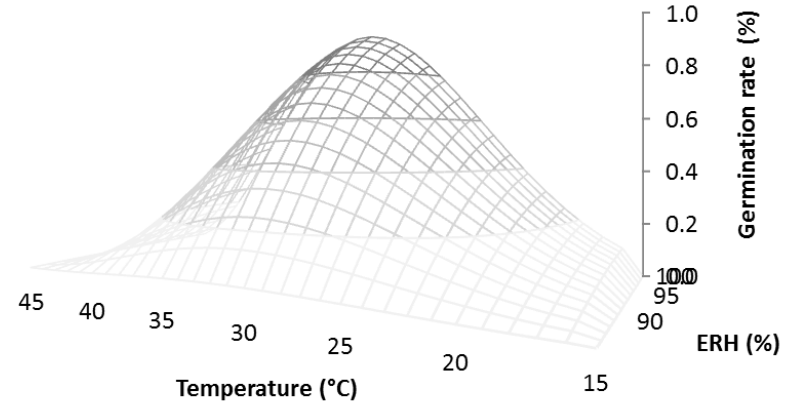


- 0.8-1.0
- 0.6-0.8
- 0.4-0.6
- 0.2-0.4
- 0.0-0.2



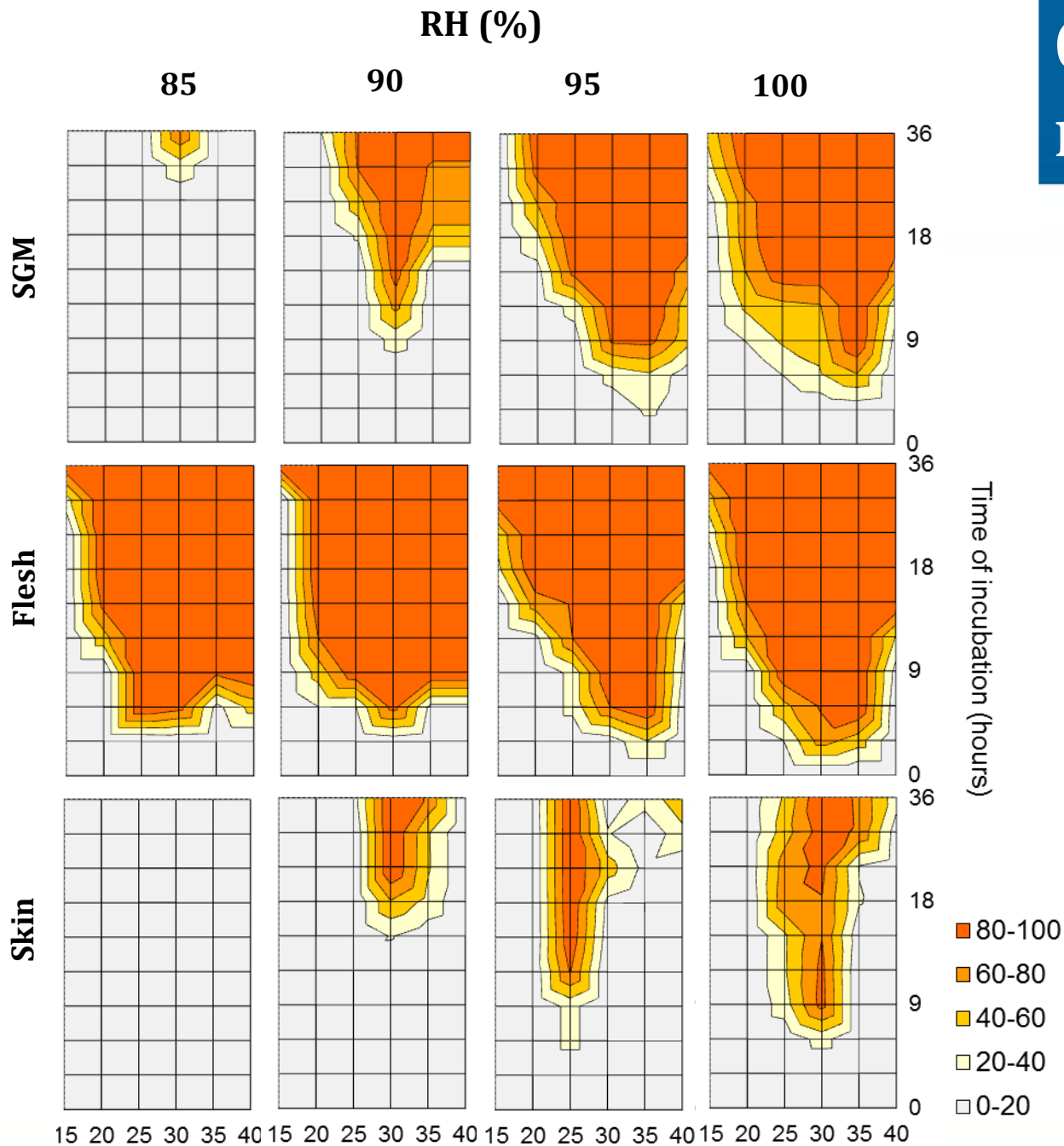
Temperature (°C)

## SGM



ERH (%)

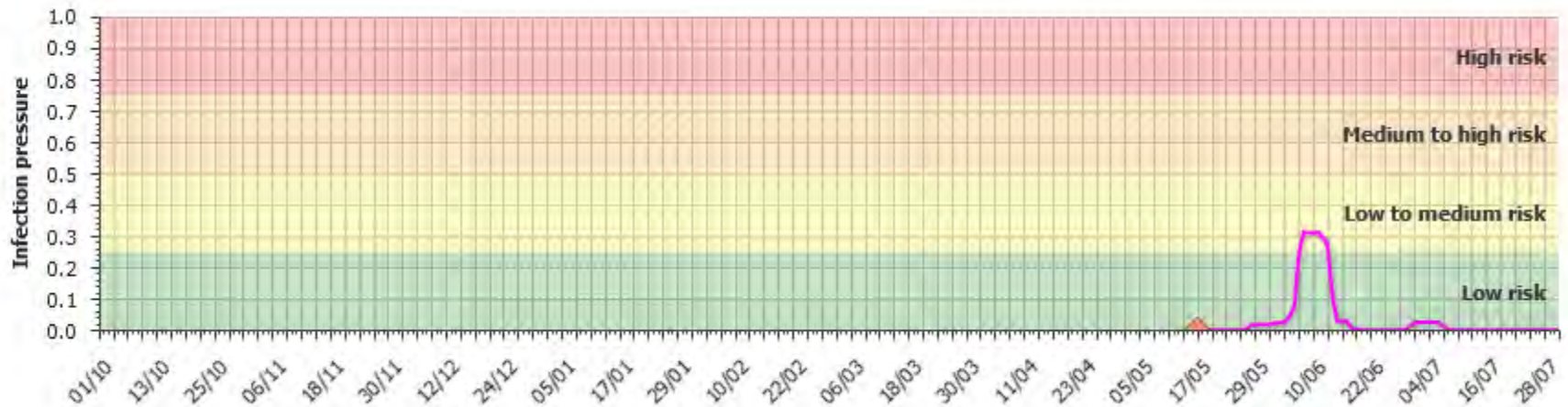
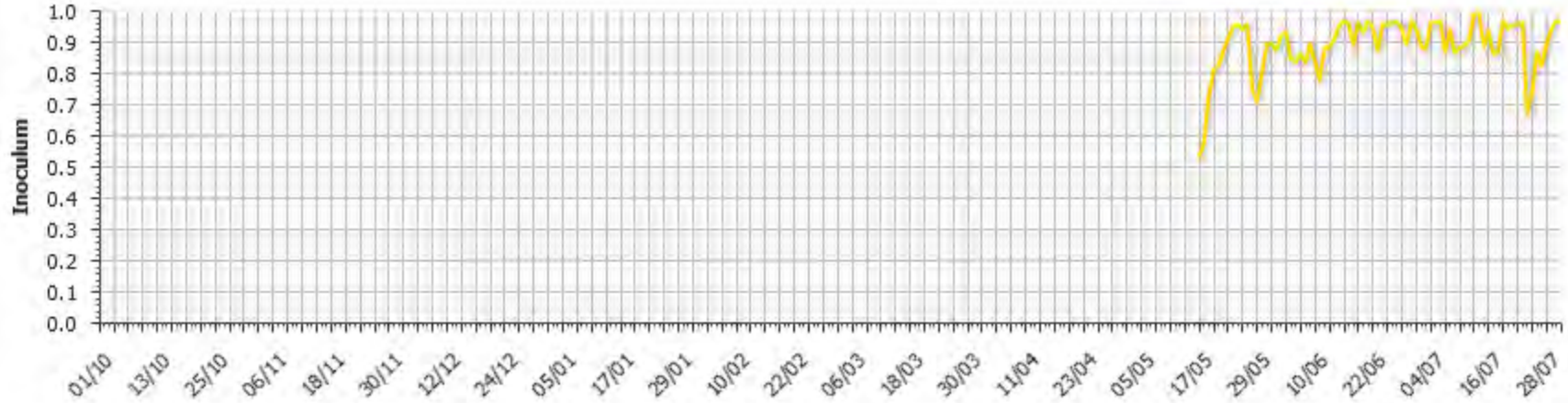
# Germination rate: result



100% germination can occur much more rapidly on grape flesh (6 hrs) followed by SGM medium (9 hrs) and then grape skin (24 hrs) under optimal condition of **30-35°C** and **100% RH**



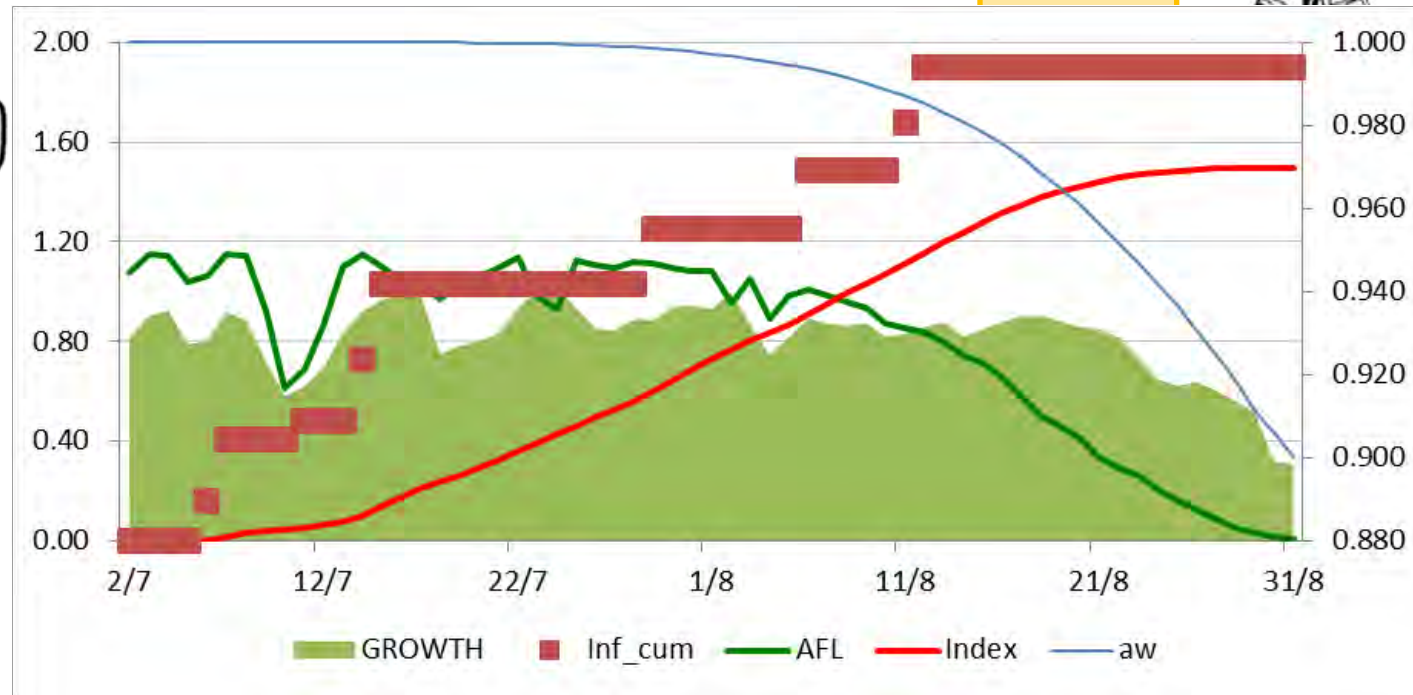
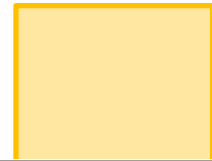
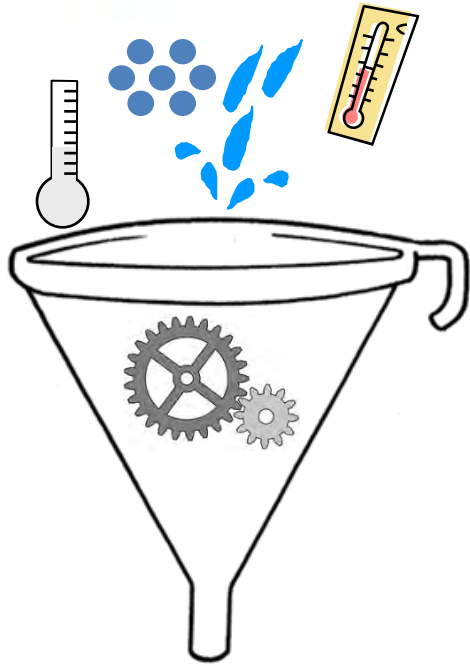
# Examples of model output: FHB-model





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# Examples of model output: AFLA model



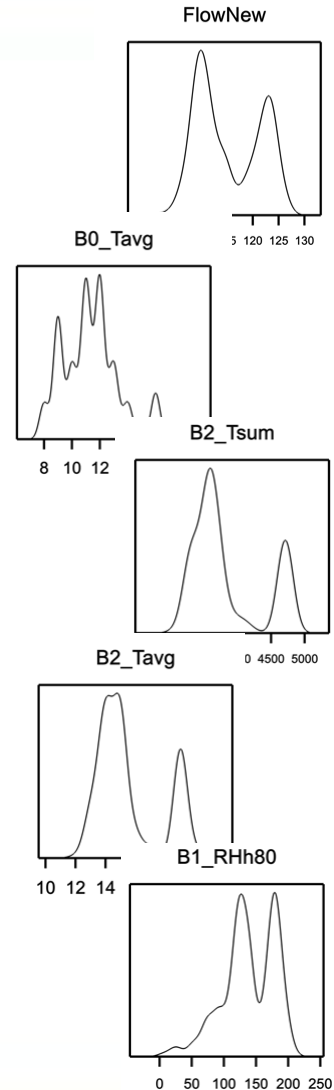
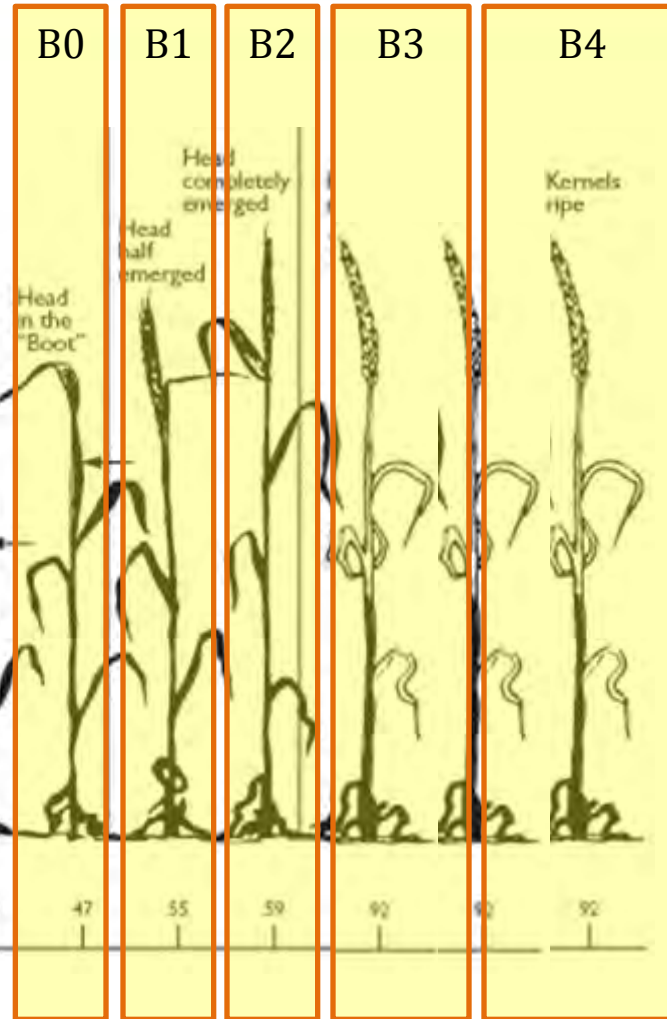
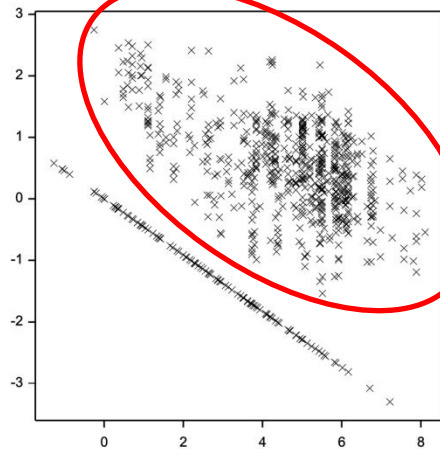
**Aflatoxin Index**



# Empirical model for DON in wheat

## Parameters calculated in each block:

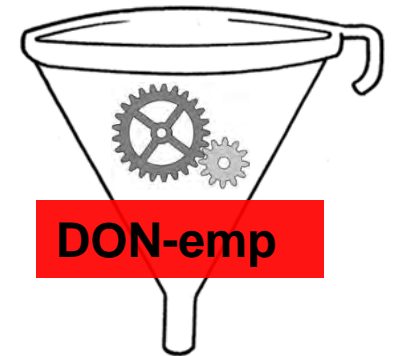
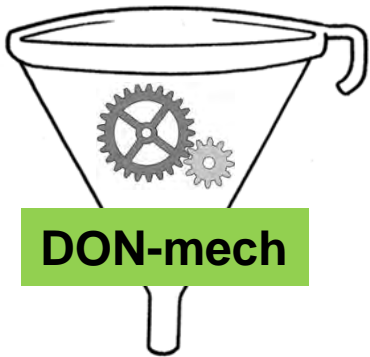
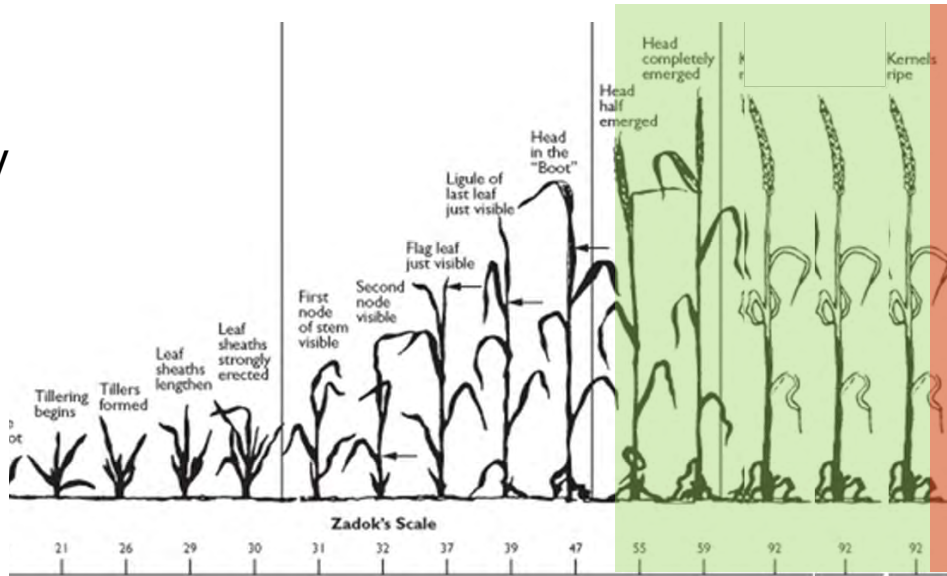
- T sum
- T avg
- Th 25
- Sum\_Rain
- RHh80





# Models input – output variables

Hourly:  
Temperature  
Relative Humidity  
Rain



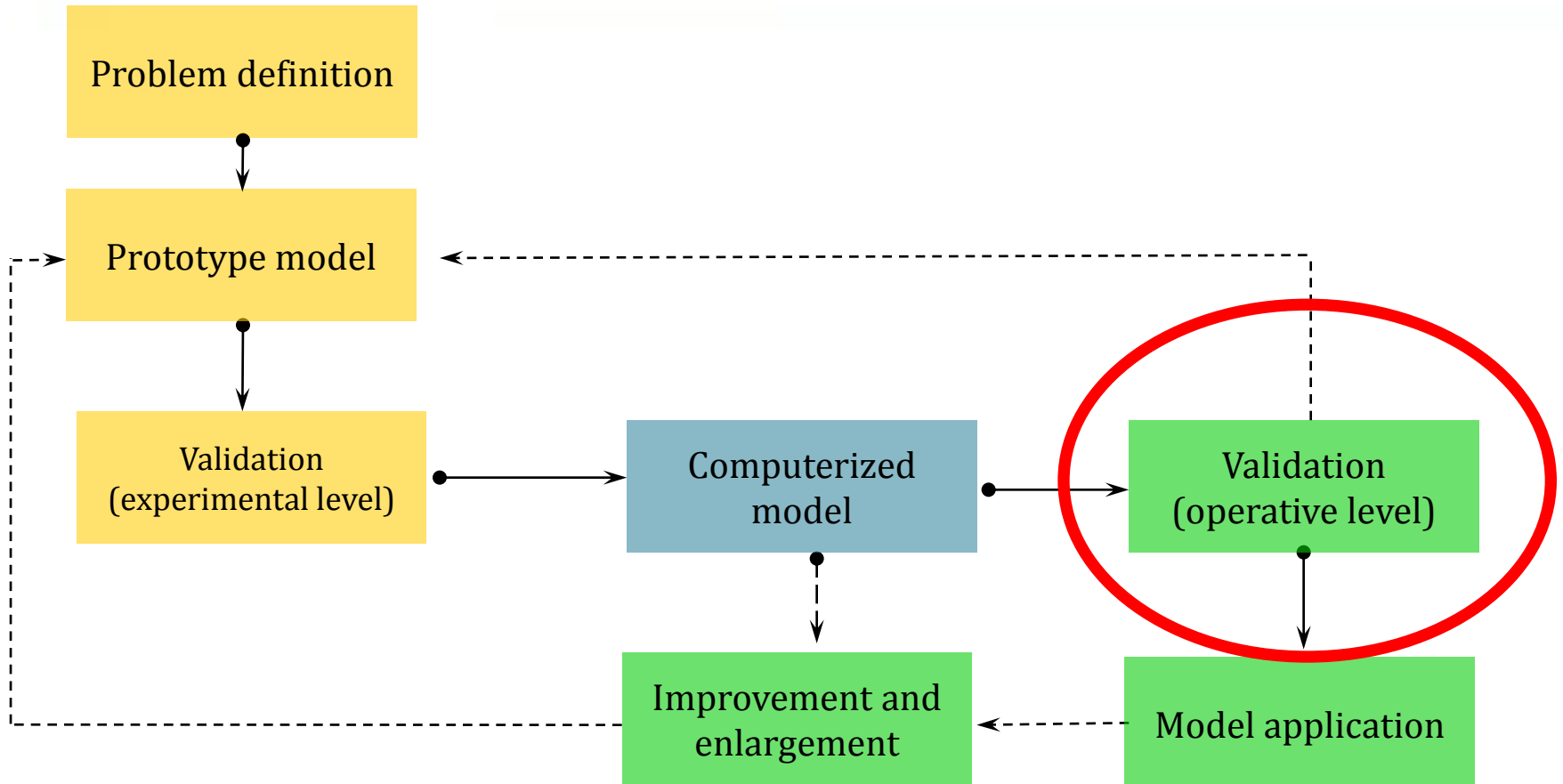
B0\_Tavg  
 B0\_Th25  
 B0\_Rain  
 B1\_Th25  
 B1\_RHh80  
 B2\_Tavg  
 B2\_Th25  
 LenFH  
 Flowering day

- FHB Index
- DON Index

- DON Index



# Last step: Model Validation





# Last step: Model Validation

Comparing model output and real observations in different epidemiological conditions (year, location, ...)

## Italian data

### PREDICTED

**OBSERVED**

	0	1
0	74	19
1	0	7

## Dutch data

### PREDICTED

	0	1
0	89	5
1	5	1



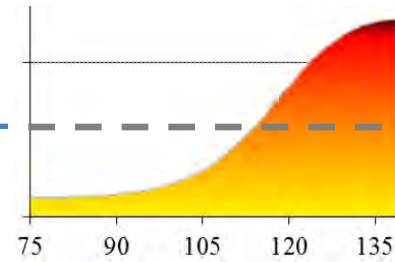
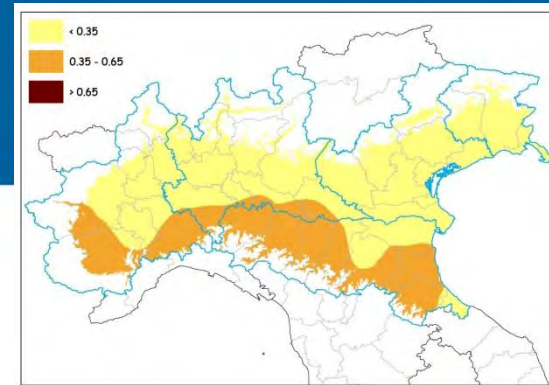


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Historic data

Actual data

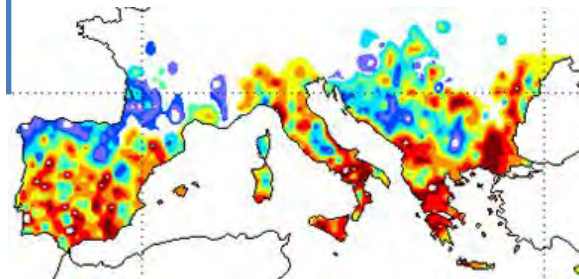
Predicted data



**ENERGY**

**FEED**

**FOOD**



Thank you for your attention!