Modèle SEIR de Zadoks
Application à la rouille brune

+ document guide du TP

François Brun, Jean-Noël Aubertot

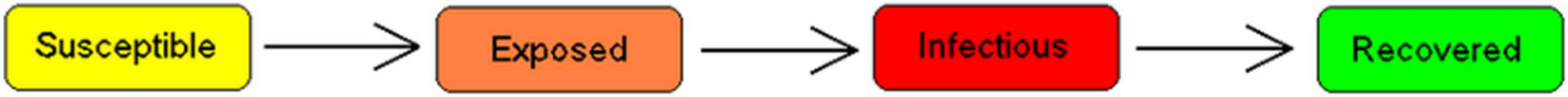
Formation Introduction à la modélisation pour la protection intégrée des cultures.

30 novembre au 4 décembre 2015

Principes d'un modèle SEIR

- Susceptible-Exposed-Infectious-Removed (SEIR).
- Modèle à compartiment fréquemment utilisé en épidémiologie (humaine, animale, végétale,…) épidémiologie (humaine, animale, végétale)

From http://en.wikipedia.org/wiki/Compartmental_models_in_epidemiology



  - Pour des infections présentant un délais significatif entre l'infection (contamination) et l'état infectieux
  - Pendant cette période de latence, on dans le compartiment « Exposed »
  - Basé sur les concepts épidémiologique de « période de latence », de « période infectieuse » et "coefficient de multiplication »

Publication d'origine

- Zadoks (1971). Systems Analysis and the dynamics of Epidemics. Phytopathology, 61:441-598

Systems Analysis and the Dynamics of Epidemics

J. C. Zadoks

Laboratory of Phytopathology, Agricultural University, Wageningen, The Netherlands.

I thank C. T. De Wit for technical advice, and Mrs. F. M. Daendels for linguistic assistance.

A system is a limited section of the real world. The limits are chosen in such a way that the environment of the system does not materially influence the system. Within a system, the variables show a variety of mutual interactions. In botanical epidemiology, the main components of the system are the host crop, the parasite (sometimes also the vector), and the microclimate.

Systems analysis is a method by which complex situations can be understood and described quantitatively. A systems analysis contains some of the following elements: measurement, analysis, and simulation. The variables of the system must be measured. The quantitative relations between the variables must be analyzed. Prior to or during the measurement and analysis phases, the basic concepts evolve which are to be applied in a model that embraces all variables and their interrelationships. Simulation is the construction of the model and the study of its behavior.

The aim of systems analysis is to describe a system as a whole, the holistic approach. Advances have been made in the fields of business administration research (4), ecology (1, 16), and recently in phytopathology (15). The present contribution is mainly inspired by the author's studies on cereal rusts.

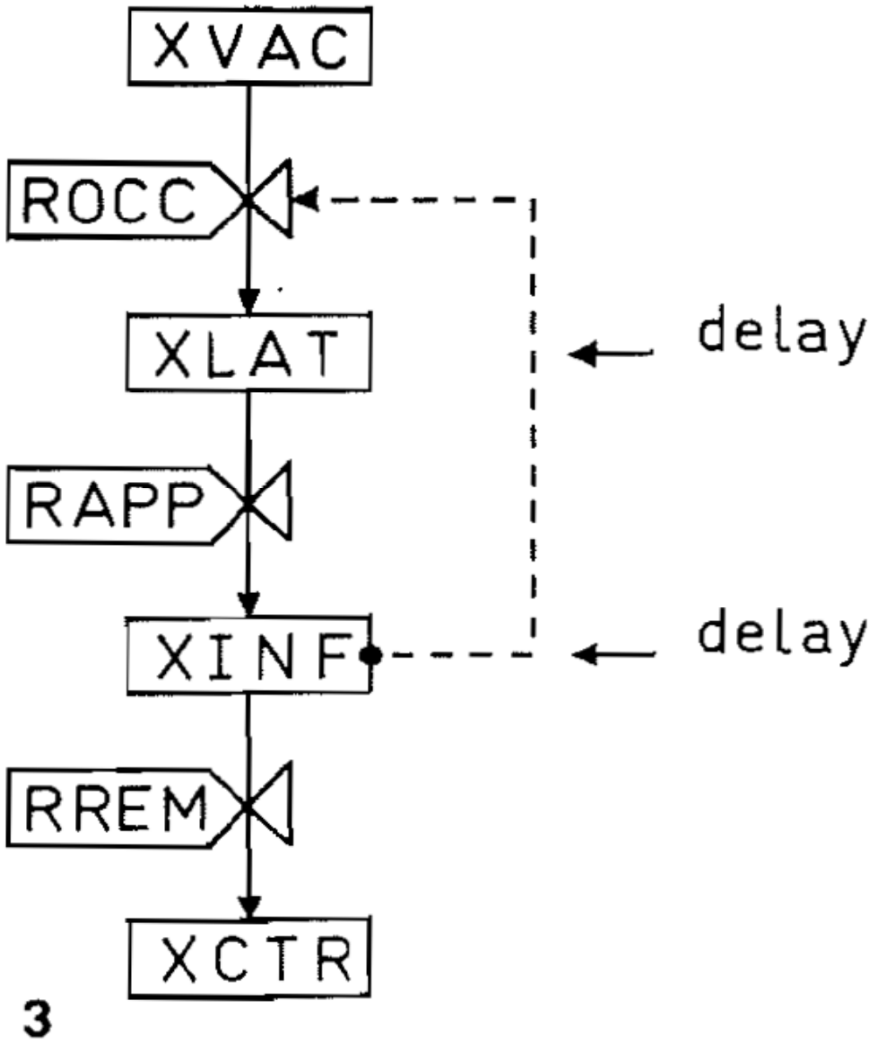
Systems analysis.—Measurement and analysis.—This paper is a theoretical study. It is not concerned with the techniques of measuring. The measurements referred to are taken from the literature. Only two

PHYTOPATHOLOGY for May (61:441-598) was issued 19 May 1971

Objectifs

- Comprendre le fonctionnement d'un modèle simple SEIR existant dans la littérature.
- Ecrire le simulateur correspondant sous R.
- Utiliser le modèle pour prendre en compte différentes pratiques et comparer des scénarios.

Description du modèle



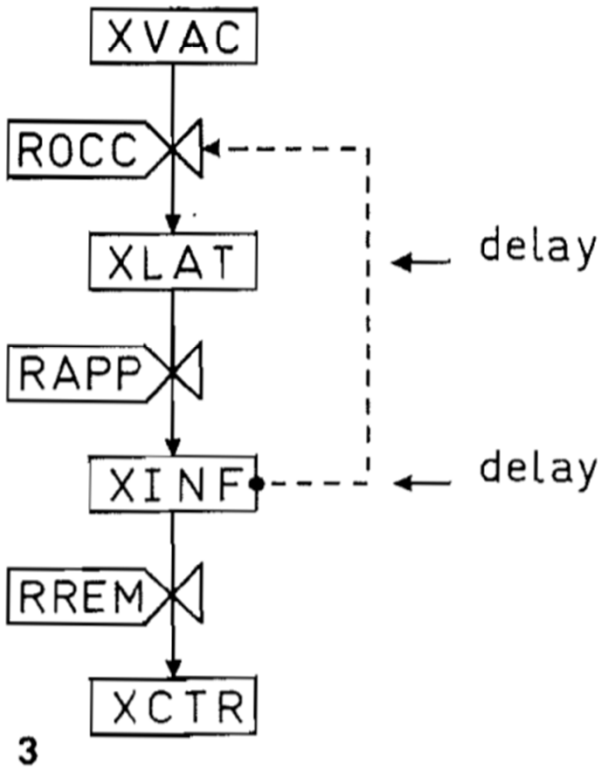
4 state variables

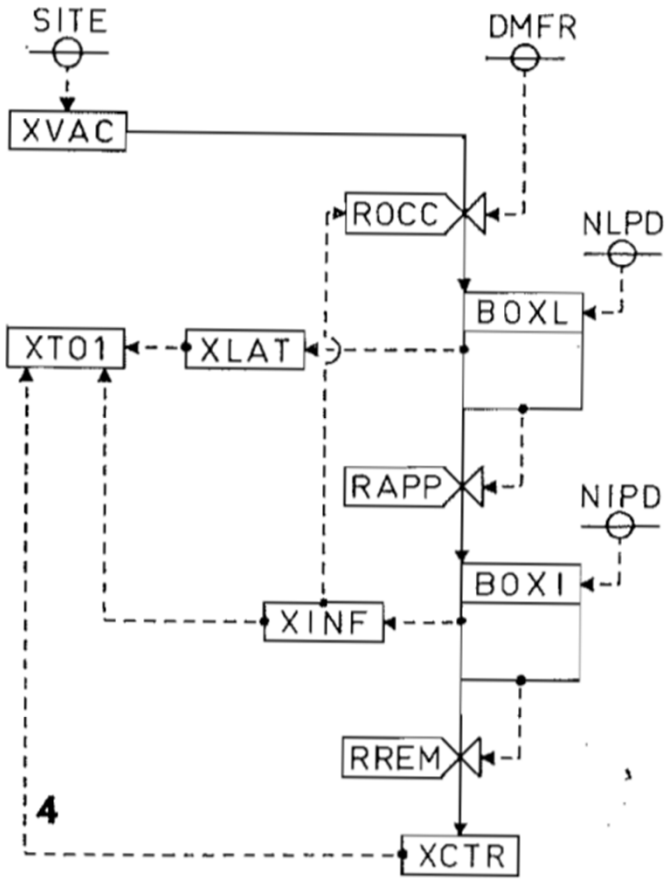
- **XVAC** : vacant (healthy) sites
- **XLAT** for latent site
- **XINF** for infectant sites
- **XCTR** for the cumulative total of removal (post infectious) sites

Fluxes (rates)

- **rocc**: rate of occupation
- **rapp**: rate of apparition
- **rrem**: rate of removal

Versions plus détaillées de la publication





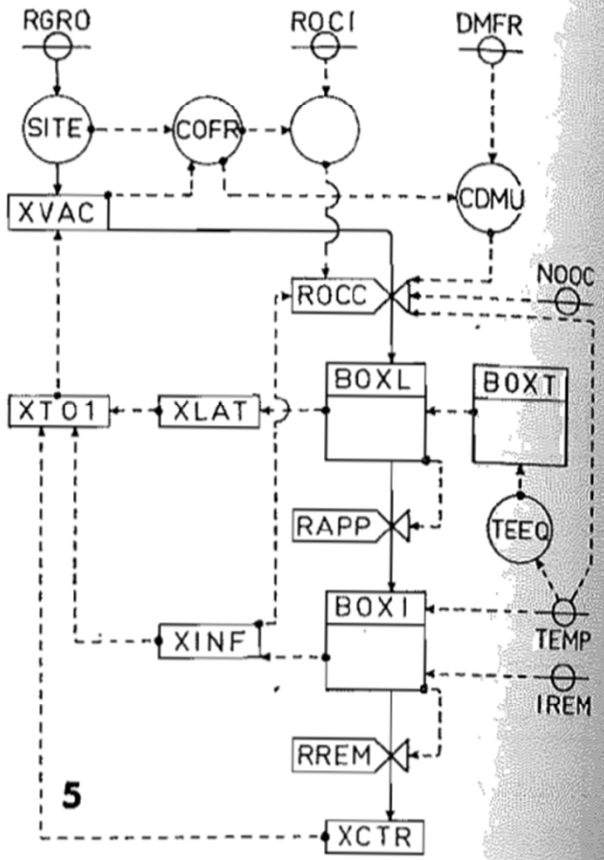


Fig. 3-5. Models of epidemics: **3)** a simple model, elementary flow diagram; **4)** a simple model, detailed flow diagram; and **5)** advanced model, detailed flow diagram.

Equations of the SEIR model for plant disease of Zadoks (1971)

Definition of the model structure as difference equations.

XVAC(day+1) = XVAC(day)-rocc

XLAT(day + 1) = XLAT(day) +rocc - rapp

XINF(day+1) = XINF(day) + rapp - rrem

XCTR(day+1) = XCTR(day) + rrem

Delays for latency and infectiousness

In order to represent the delay processes of latency and infectiousness, both XLAT and XINF state variables are defined as boxcar trains BOXL (latent) and BOXI (infectant). For example, the structure BOXL stores information on each cohort, ie number of sites that enter latency on each day, and determines when the cohort finishes the latency period (nlpd).

Definition of rates

rocc: rate of occupation : nb of sites Vacant=>Latent

rocc = cofr * DMFR * XINF

with $cofr = \max(\frac{XVAC(day)}{SITE0} ; 0)$

rapp: rate of apparition : nb of sites Latent=>Infectant

rapp= outflow(XLAT)= outflow(BOXL)

rrem: rate of removal : nb of sites Infectant=>removed

rrem= outflow(XINF) = outflow(BOXI)

Additional auxillary variables of interest are :

XTO1 = XLAT+XINF+XCTR

XSEV = XINF+XCTR

$$\text{severity} = \frac{\text{XSEV}}{\text{XLAT} + \text{XINF} + \text{XCTR} + \text{XVAC}}$$

On commence avec une version simplifiée

- Hypothèse supplémentaire :
  - Pas de fonction de délais, mais taux continu de changement d'état équivalent à la constante de temps.

(plus simple à programmer et suffisant pour comprendre le fonctionnement du modèle dynamiques SEIR)

Equations de la version simplifiée

Definition of the model structure as difference equations.

XVAC(day+1) = XVAC(day)-rocc

XLAT(day + 1) = XLAT(day) +rocc - rapp

XINF(day+1) = XINF(day) + rapp - rrem

XCTR(day+1) = XCTR(day) + rrem

Definition of rates

Note that you need to add rules to avoid having negative state variables and the order of calculation in important.

rocc: rate of occupation : nb of sites Vacant=>Latent

rocc = min(cofr*dmfr*XINF(day), XVAC(day))

with $cofr = \max(\frac{XVAC(day)}{SITE0} ; 0)$

rapp: rate of apparition : nb of sites Latent=>Infectant

rapp= min(XLAT[day]*1/nlpd, XLAT[day]+rocc)

$$rapp = \min\left(\frac{XLAT(day)}{nlpd}, XLAT(day) + rocc\right)$$

rrem: rate of removal : nb of sites Infectant=>removed

rrem: rate of removal : nb of sites Infectant=>removed

$$rrem = \min\left(\frac{XINF(day)}{nipd}, XINF(day) + rapp\right)$$

Additional auxillary variables of interest are :

XTO1 = XLAT+XINF+XCTR

XSEV = XINF+XCTR

$$\text{severity} = \frac{\text{XSEV}}{\text{XLAT} + \text{XINF} + \text{XCTR} + \text{XVAC}}$$

Sous R

Proposition d'une structure commune et vide. Copier les lines suivantes dans un script.

```
zakoks.simple.model = function (nlpd=4,nipd=1,dmfr=16,SITE0 =
5*10^9,weather=NULL, sdate = 1, ldate = 140) {

# here you will write the core of the model

return(list(sim=data.frame(day = sdate:ldate, XVAC = XVAC[sdate:ldate], XLAT =
XLAT[sdate:ldate], XINF = XINF[sdate:ldate],XCTR =
XCTR[sdate:ldate],XTO1=XTO1[sdate:ldate],  XSEV= XSEV[sdate:ldate],
severity=severity[sdate:ldate]), param=c(nlpd=nlpd,nipd=nipd,dmfr=dmfr,SITE0 =
SITE0)))
} # end of model
```

Structure du code

- creation of state variable as vector
- initialization of state variable
- Simulation loop
  - Calculate rates of change of state variables (dTT, dB, dLAI)
  - Update state variables *
- End simulation loop
- Return results

Premières simulations – paramètres par défaut

Name	**Value**	**Description**	**Unit**
nlpd	8	Duration for latency period	day
nipd	30	Duration for infectious period	day
dmfr	16	Coefficient of multiplication	-
XVAC0	1e+10	Initial number of vacant sites	sites
XLAT0	1	Initial number of latent sites (first contamination	sites

correction

Vous devriez obtenir les graphiques …

pour nipd = 8 ou 16 ou 24