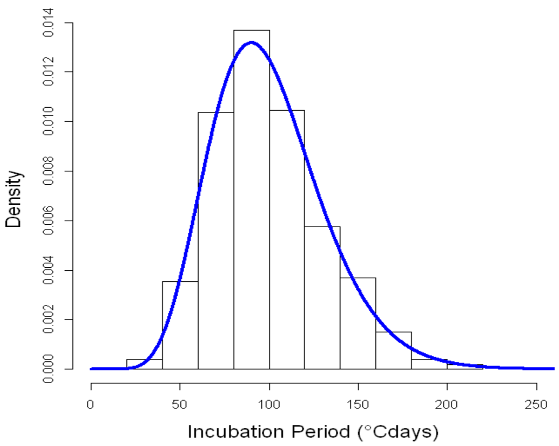
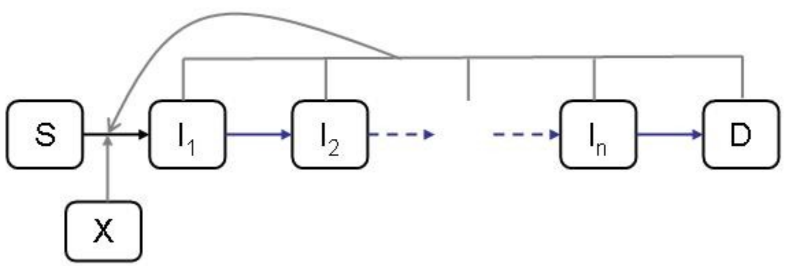
Estimating the delay between host infection and disease (incubation period) and assessing its significance to the epidemiology of plant diseases

Melen Leclerc, Thierry Doré, Christopher Gilligan, Philippe Lucas, João Filipe

ModStatSP Meeting – 16th December 2013 - Paris

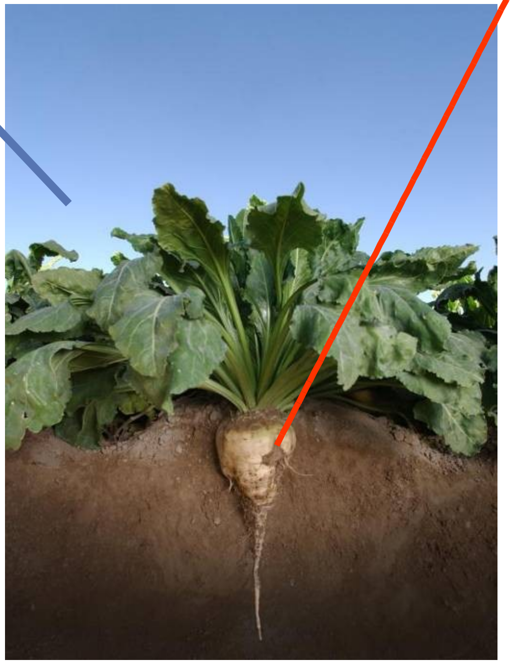




Our problem : link hidden infections and observable symptoms

Visible epidemic

Symptomatic plants



Hidden epidemic

Cryptic infections

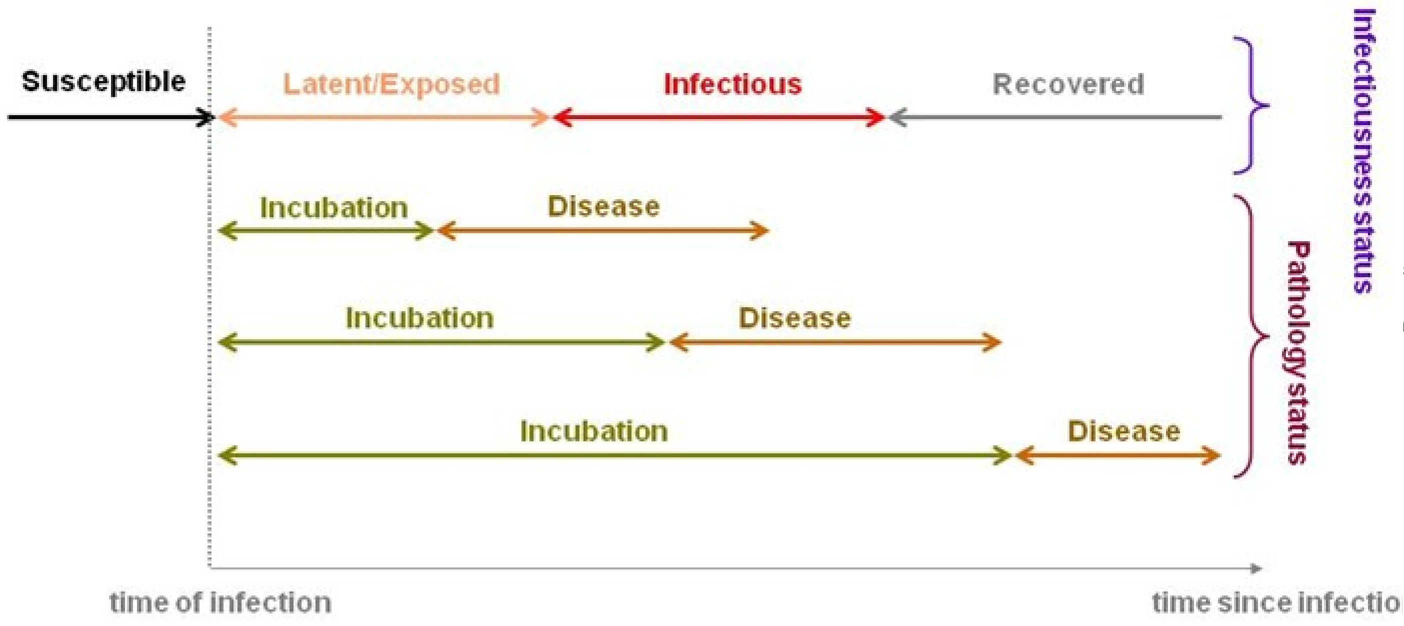
The incubation period

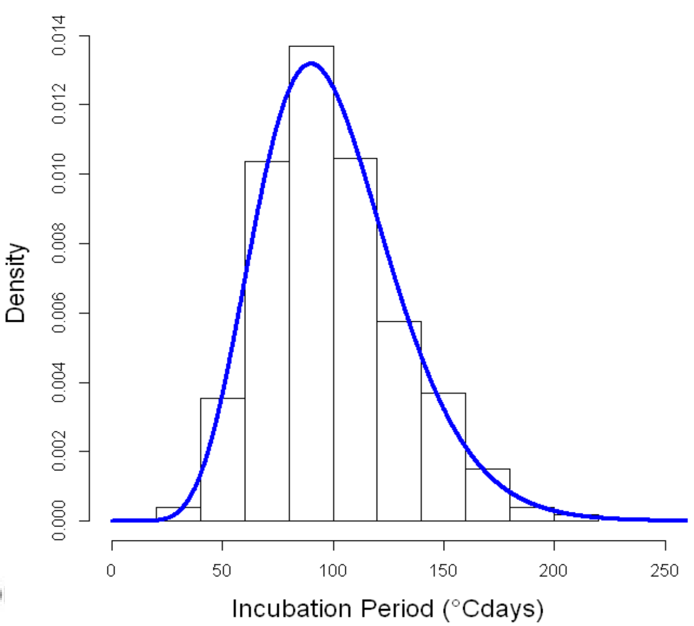
- Time between hidden infection and appearance of detectable symptoms of pathology (Kern, 1956 ; Keeling & Rohani, 2008)

- Specificity of each disease

- Incubation period distrubutions are generally described by **non-negative probability distributions** with a **pronounced mode** (Keeling & Rohani, 2008 ; Chan & Johansson, 2012)

- In general, **incubation period data are rare**...(nonexistent in the case of soilborne plant diseases)





Patho-system, working hypothesis and methodology

- Patho-system : *Rhizoctonia solani* in sugar beet
- Hypothesis : **age-specificity** of the incubation period

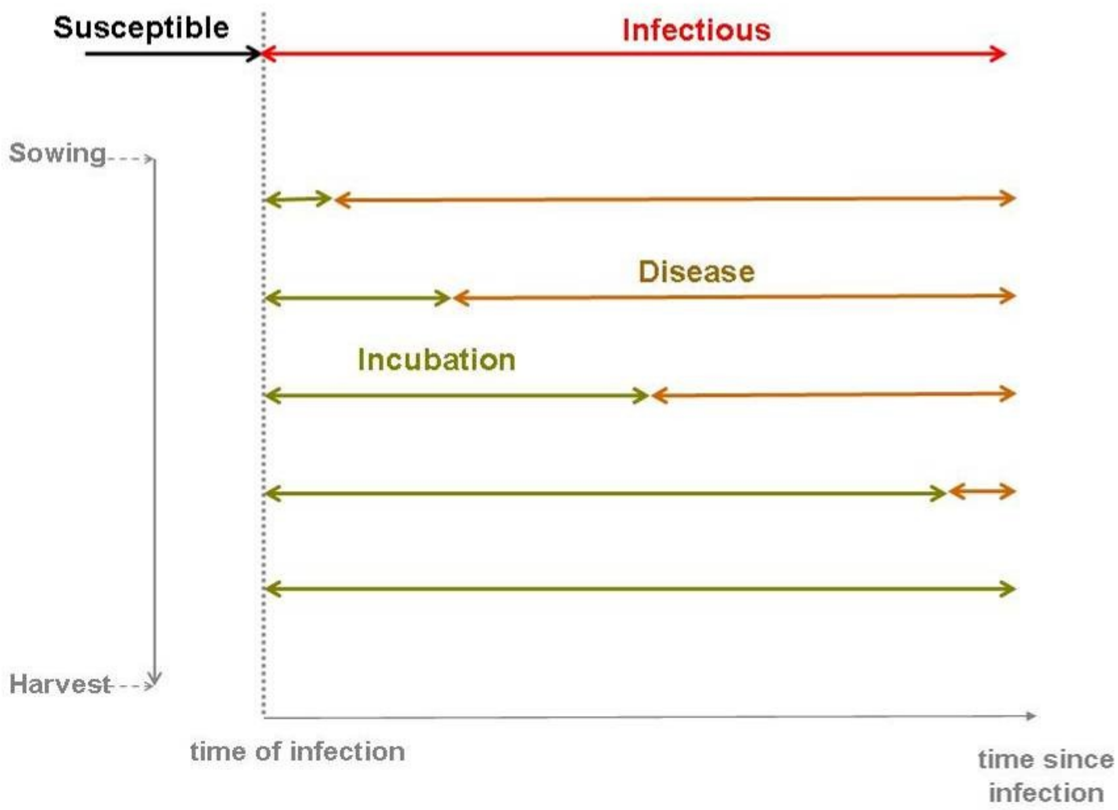
- Methodology :

Experimental measurements of the incubation period

Age-specific incubation period analysis

Build an age-varying model of the incubation period distribution

Assess the importance of using suitable distribution through simulations of a compartmental markovian model

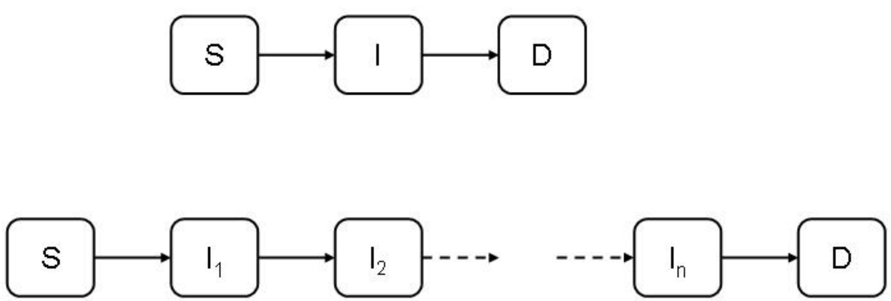


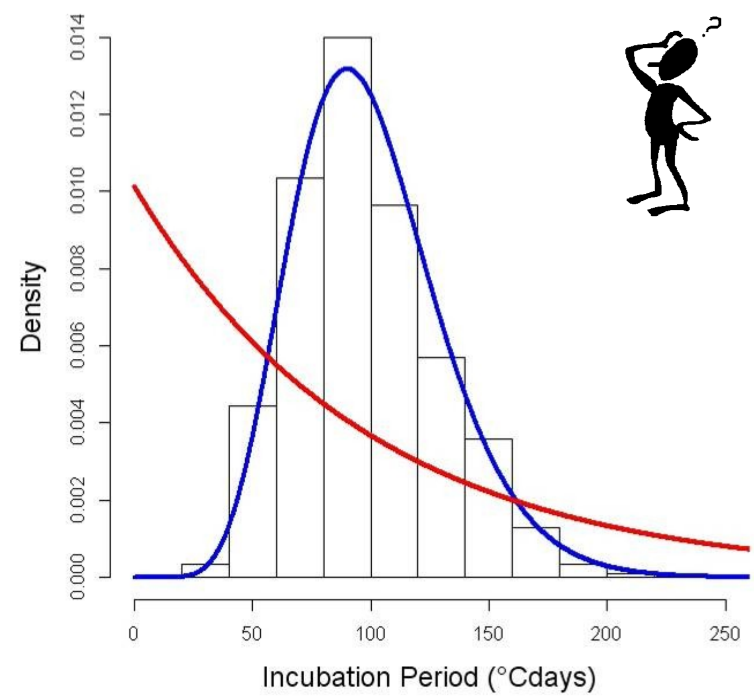
Probability distributions and epidemiological periods

- In compartmental Markovian models the time spent in each state is **exponentially distributed**

→ in a simple SID model the incubation period is exponentially distributed (no mode)

- More realistic **Erlang** (or Gamma) -distributed periods can be introduced into compartmental models by subdividing compartments (i.e. **introducing transient states**) (Cairns, 1990 ; Lloyd, 2001, Wearing et al., 2005 ; Cunniffe et al., 2012)





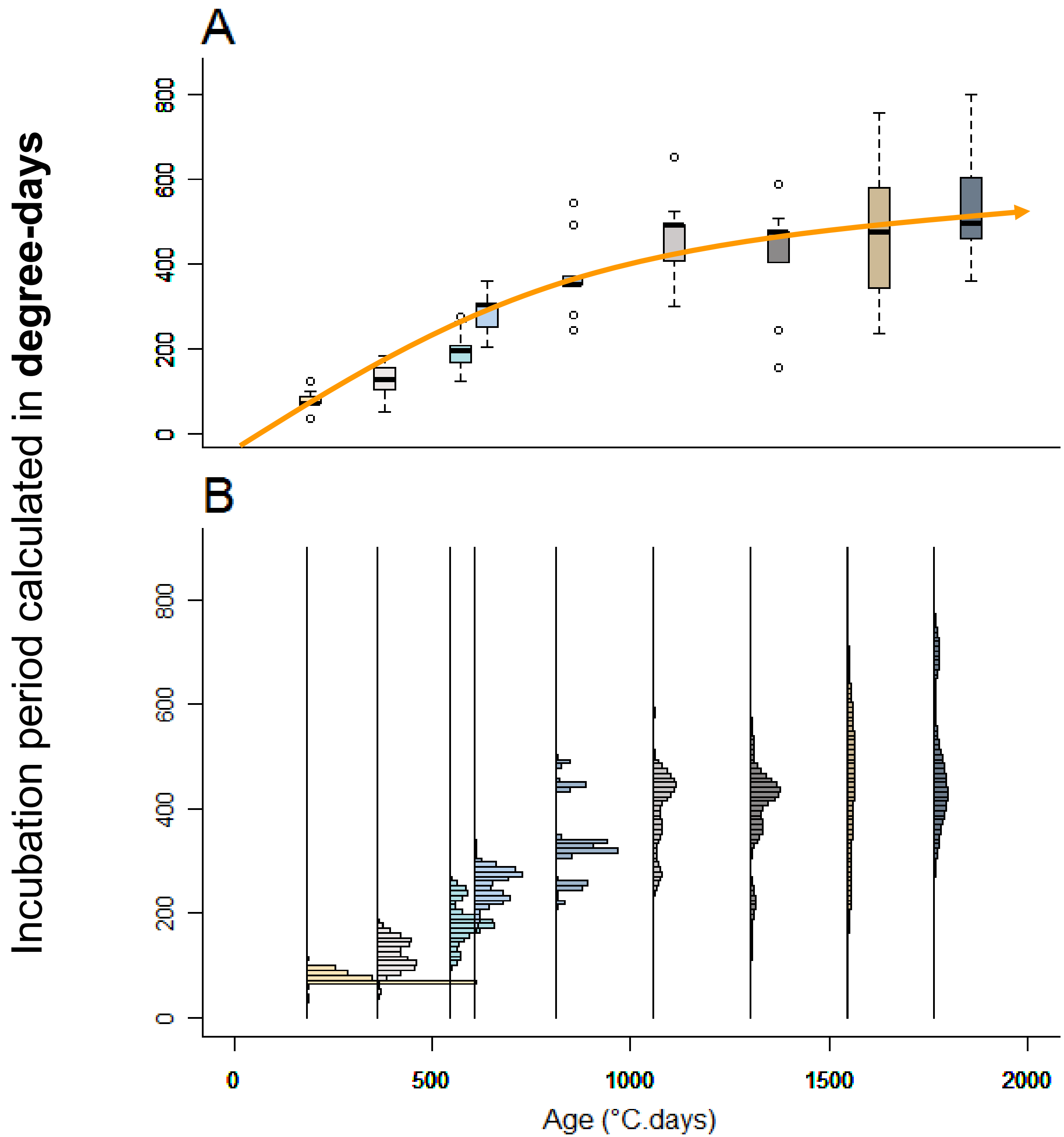
- Can we use the <u>Erlang</u> distribution for our specific system ?

→ comparison against <u>exponential</u>, <u>Gamma</u> (free shape parameter), <u>Weibull</u> and <u>Lognormal</u> distributions

Experimental measurements of the incubation period

- Plant inoculated with 3 infested barley seeds (inoculum)
- 9 ages of plants (14, 32, 46, 60, 74, 88, 102, 116, 130 days)
- For each individual the time-to-disease (above-ground symptom) was recorded
- At least 45 individual observations for each age → **distribution of the incubation period**

Results of the experiments (raw data)



Age-specific distribution analysis

	Gamma			Weibull			Lognormal		
Total AIC	**4998.06**			**4994.65**			**5017.56**		
Age in days (°C.days)	AIC(*)	shape	rate	AIC(*)	shape	rate	AIC(*)	meanlog(**)	sdlog(**)
18 (182.35)	**604.40**	47.88	0.600	620.73	6.47	0.0119	**607.52**	4.36	0.15
32 (359.25)	**512.60**	15.30	0.120	**507.04**	4.83	0.0071	517.00	4.82	0.27
46 (542.00)	**552.50**	20.84	0.100	**552.70**	5.18	0.0046	**554.21**	5.27	0.22
60 (607.05)	**488.00**	67.72	0.240	**484.18**	9.90	0.0034	489.35	5.63	0.12
74 (811.15)	**536.11**	21.68	0.060	542.85	4.74	0.0025	**535.20**	5.90	0.21
88 (1053.95)	**582.90**	24.39	0.050	**580.60**	5.78	0.0021	**584.89**	6.10	0.21
102 (1303.35)	548.21	18.00	0.040	**527.12**	6.83	0.0021	555.82	6.06	0.26
116 (1545.00)	**595.53**	9.83	0.020	**592.74**	3.76	0.0018	597.83	6.14	0.33
130 (1764.85)	**577.81**	19.19	0.030	586.69	4.19	0.0017	**575.74**	6.26	0.23

	Erlang			Exponential	
Total AIC	**4996.8**			**6084.6**	
Age in days (°C.days)	AIC(*)	shape	rate	AIC	rate
18 (182.35)	**604.50**	48	0.610	840.01	0.013
32 (359.25)	**513.00**	15	0.120	611.20	0.008
46 (542.00)	**552.55**	21	0.110	669.00	0.005
60 (607.05)	**488.05**	68	0.240	652.04	0.004
74 (811.15)	**535.11**	22	0.060	638.52	0.003
88 (1053.95)	**583.00**	24	0.050	697.81	0.002
102 (1303.35)	548.24	18	0.040	640.31	0.002
116 (1545.00)	**595.54**	10	0.020	663.30	0.002
130 (1764.85)	**576.81**	18	0.030	672.41	0.002

(*) Bold indicates lowest or within 5 units from the lowest AIC score.

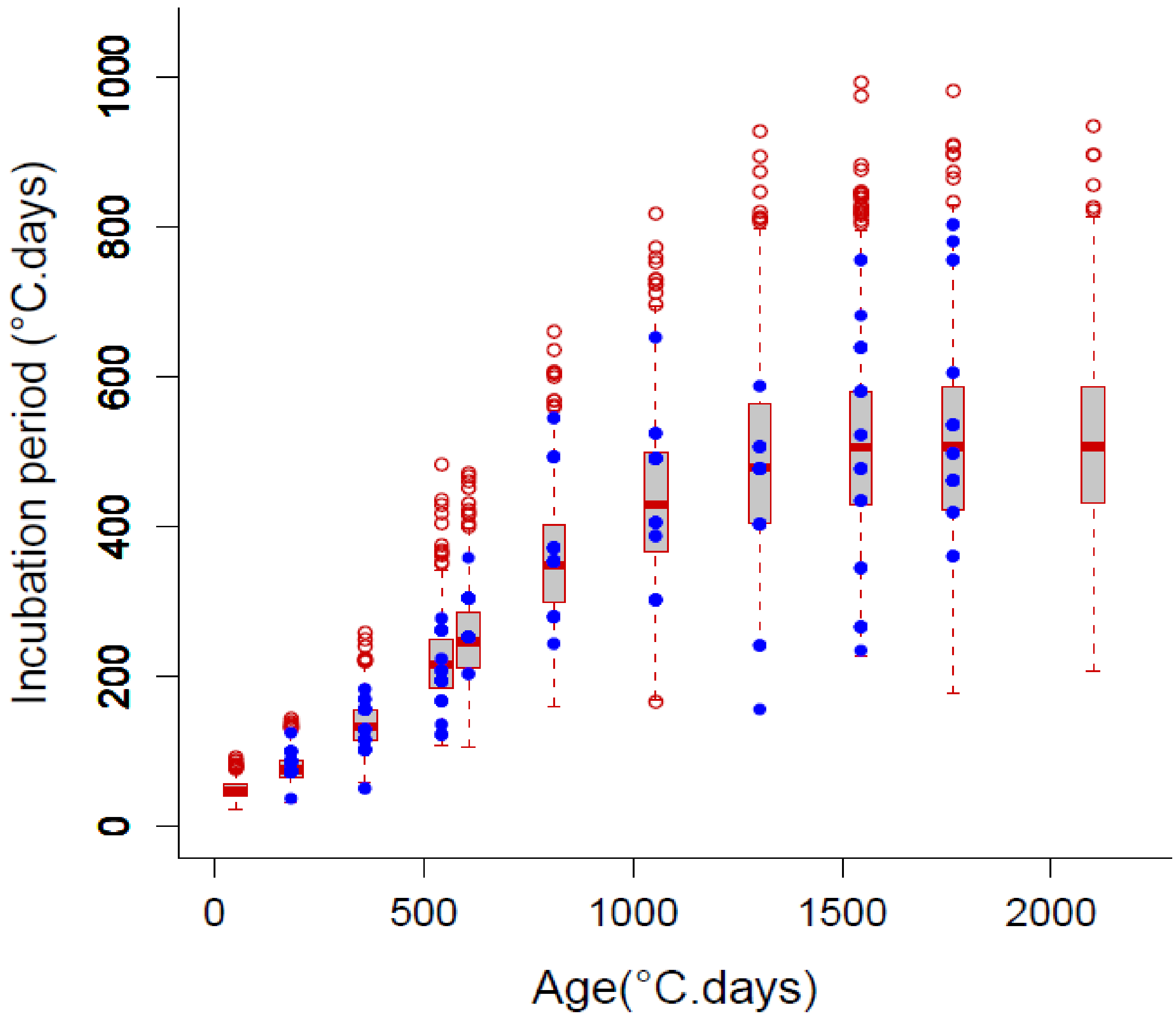
(**) Mean and standard deviation of the log transformed variable

Weibull wins

Erlang (and Gamma) is close

Empirical age-varying model of the incubation period distribution T

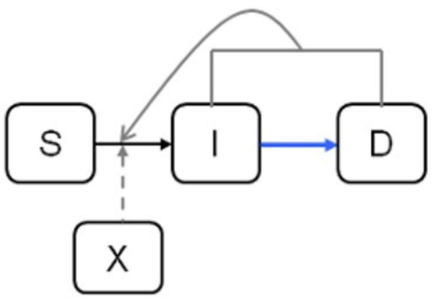
- T~ Erlang [k, λ(t)] with λ(t) = a*exp(-b*t) +c



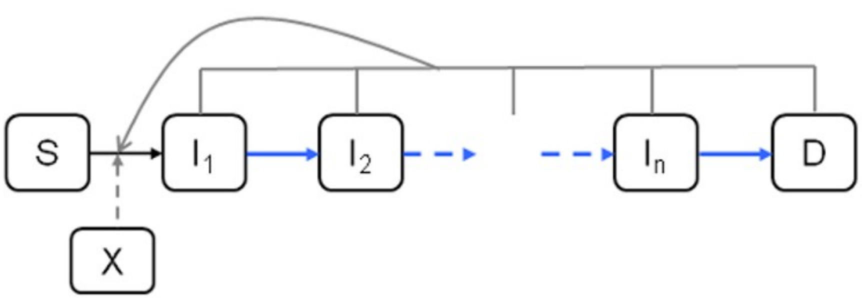
Epidemiological SID hierarchical model with differing incubation period distributions

- Spatially explicit SID model, individual-based model, discrete event Markov process
- **Exponentially** distributed vs **Erlang** distributed incubation period

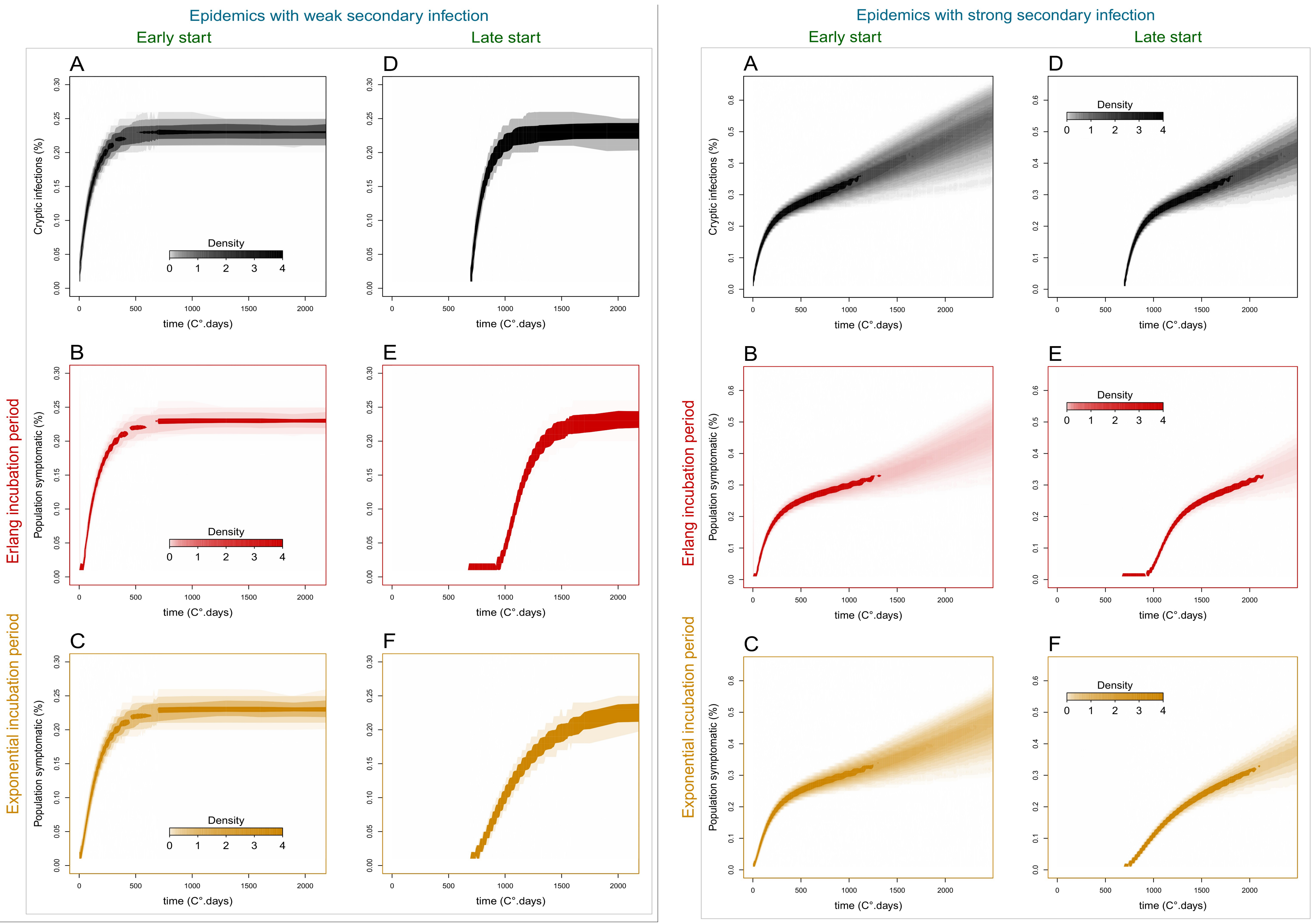
$$\begin{cases} \text{Prob}(S \to I, dt \mid S; i, t) = \left[\beta_p + \beta_s\left(n_{I,i}(t) + n_{D,i}(t)\right)\right] dt \\ \text{Prob}(I \to D, dt \mid I; i, t) = \mu \, dt \end{cases}$$



$$\begin{cases} \text{Prob}(S \to I, dt \mid S; i, t) = \left[\beta_p + \beta_s\left(\sum_{j=1}^{k} n_{I_j,i}(t) + n_{D,i}(t)\right)\right] dt \\ \text{Prob}(I_j \to I_{j+1}, dt \mid I_j; i, t) = \lambda \, dt \quad (j = 1, \dots, k-1) \\ \text{Prob}(I_k \to D, dt \mid I_k; i, t) = \lambda \, dt \end{cases}$$



- For each model, simulation of 1000 Markov chains on a 100*100 square lattice (weak/strong secondary infections ; early/late start of the hidden epidemic)

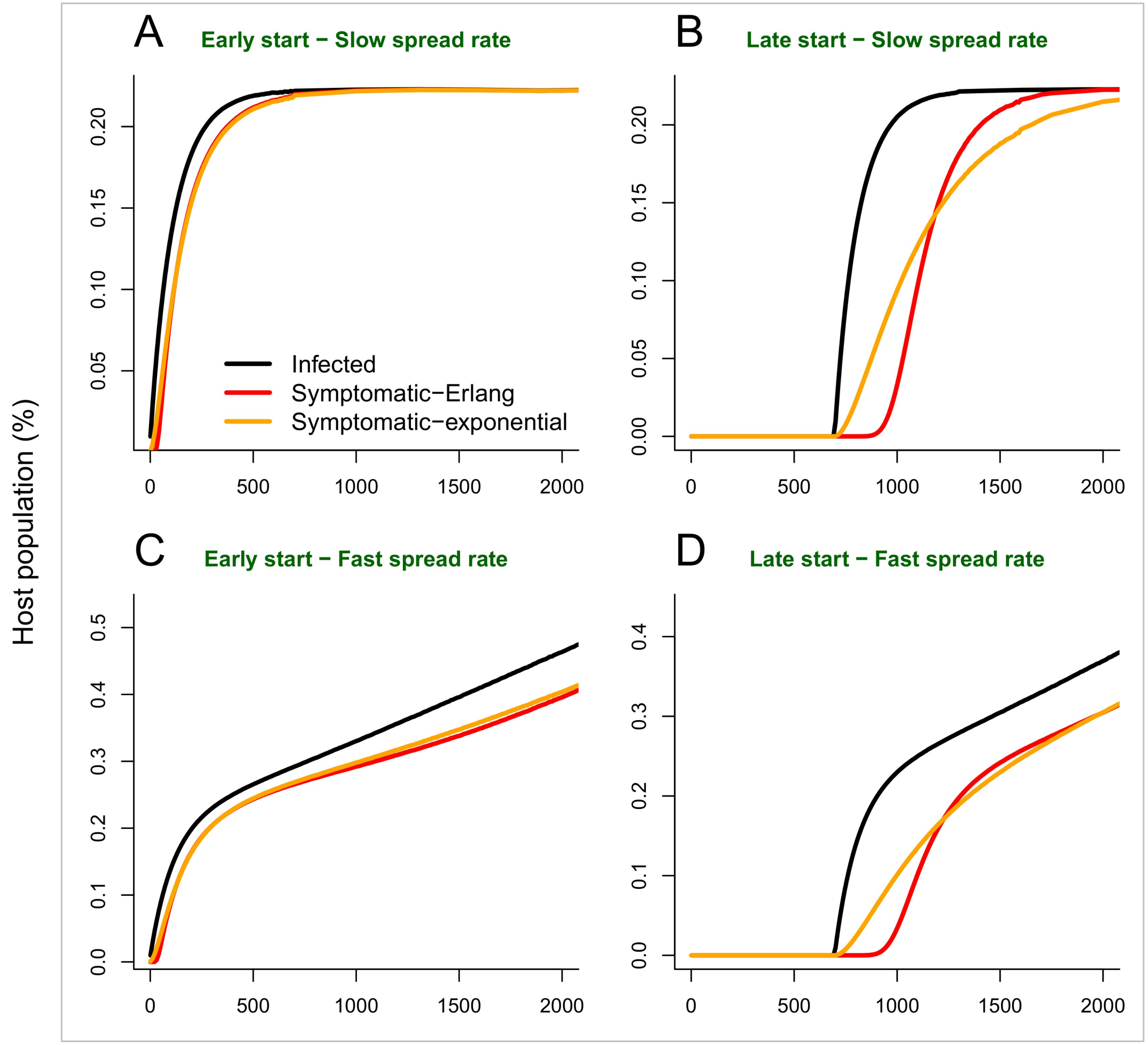

Epidemics with weak secondary infection
Early start
Late start
A
D
B
E
C
F
Cryptic infections (%)
Population symptomatic (%)
time (C°.days)
Density
0 1 2 3 4
Erlang incubation period
Exponential incubation period
Epidemics with strong secondary infection
Early start
Late start
A
D
B
E
C
F
Cryptic infections (%)
Population symptomatic (%)
time (C°.days)
Density
0 1 2 3 4
Erlang incubation period
Exponential incubation period

Simulation of the cryptic spread of infection and disease in the host population

→ considerable differences (lag) between the epidemic dynamics of cryptic infections and observable disease

→ With the exponentially distributed incubation period the lag between disease emergence and hidden infections spread is erroneously reduced

Mean epidemic dynamics



Time(°C.days)

Conclusion (1)

- First data-supported model for the incubation period (soilborne plant disease)

- Improvement of the age-varying model (multi-modal distribution, Weibull distribution) ?

- The development of observable disease epidemics can lag cryptic pathogen spread significantly

  → can mislead practitioners about the extent of infection and risk of further disease

- It is important to parameterized epidemiological models using appropriate incubation period assumptions and data to reduce errors in model prediction

Conclusion (2)

- Use the data-supported model of the incubation period to assess, through simulation, the efficacy of treatments based on the detection of above-ground symptoms of the root rot disease

- Introduce the fitted age-varying model into the observation model of a mechanistic-statistical model to infer hidden epidemiological parameters (the incubation period is related to the censoring)

- Apply the approach we had to investigate the incubation period of other patho-systems

- When experimental measurement is difficult (e.g. for perennial crops) incubation period distribution may be estimated directly from the observations of symptomatic individuals

Thank you for your attention !!!

melenleclerc@gmail.com

melen.leclerc@avignon.inra.fr