

HSMM driven by the observations for estimating weed dynamics

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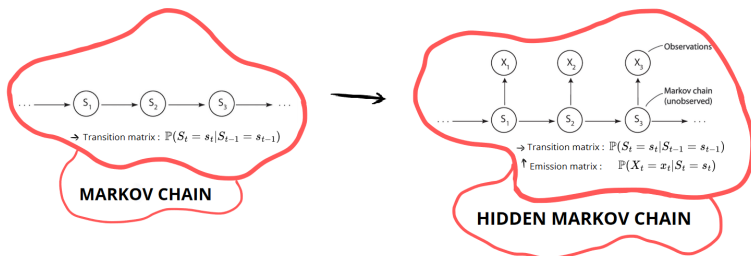
Pré-journée des doctorants, Journées des Statistiques du Sud, June 18, 2024

First step : What are Hidden Markov Models (HMM) ?

Hidden Markov Models (HMM) are used to study time series.

Example (HMM uses cases)

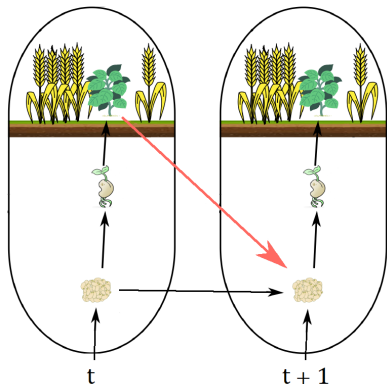
| Field of study | Uses |
|----------------|---|
| Medicine | Analyze epidemiologic surveillance data (Le Strat and Carrat 1999) |
| Ecology | Reconstruct hidden or partially observed ecological dynamics (McClintock et al. 2020) |
| Finance | Predict the regime of a monetary system thanks to the exchange rate (Engel and Hamilton 1990) |



Improve the understanding of weed dynamics

Aim of the work

Estimate key parameters of the dynamics based only on observation of standing plants.



Parameters involved in the dynamics :

- colonization
- germination
- survival
- seed production

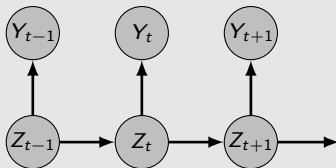
History of weed dynamics modeling

First models (Hanski and Gaggiotti 2004)

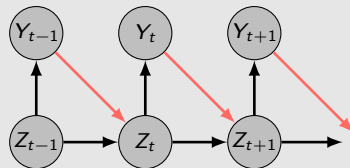
The initial models of weed dynamics assumed that the state of the seed bank was known.

Observation-Driven Hidden Markov Model (OD-HMM, Pluntz et al. 2018)

The OD-HMM is an extension of the HMM to the case where there is a **dependence** between **observations** $Y = (Y_t)_{t \in \mathbb{N}}$ and **hidden states** $Z = (Z_t)_{t \in \mathbb{N}}$.



(a) HMM.



(b) OD-HMM.

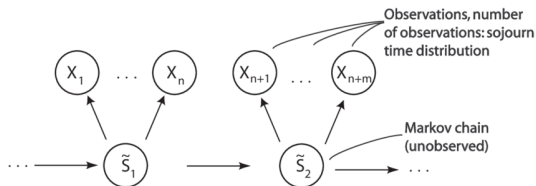
Figure: Graphical representation of conditional independencies in the chain (Z_t, Y_t) .

OD-HMM vs OD-HSMM?

Limits of the OD-HMM

Weed seeds can remain in the soil for many years, which is not modeled with HMM.

⇒ **Solution** : Hidden semi-Markov Models (HSMM).



Main difficulty of extending HSMM to the case where there is a dependence between observations and hidden states

The dependence between observations and hidden states influences the sojourn time distribution at each point in time.

⇒ **Solution** : Use the couple (state, time since entry) as the new state of a hidden Markov chain (Barbu and Limnios 2008).

Distributions defining a OD-HSMM for weed dynamics

Discrete time. State spaces : $\Omega_Z = \Omega_Y = \{0, 1\}$.

Time elapsed since the entry into the current state : $U = (U_t)_{t \in \mathbb{N}}$, with $\Omega_U = \mathbb{N}^*$.

- **Initial probability :**

$$\pi(z_0) = \mathbb{P}(Z_0 = z_0, U_0 = 1),$$

where $p_0 = \mathbb{P}(Z_0 = 1)$;

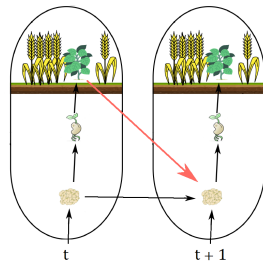
- **Emission probability :**

$$R(z_t, y_t) = \mathbb{P}(Y_t = y_t | Z_t = z_t),$$

representing the germination probability g ;

- **Transition probability :**

$P_{y_{t-1}}(z_{t-1}, u_{t-1}, z_t, u_t) = \mathbb{P}(Z_t = z_t, U_t = u_t | Z_{t-1} = z_{t-1}, U_{t-1} = u_{t-1}, Y_{t-1} = y_{t-1})$,
parameterized by probabilities of colonization c , dispersion d and survival : optimal survival s_0 + survival degeneration λ .



Example

$$P_1((1, 3), (0, 1)) = (1 - s_0 e^{-\lambda \times 2})(1 - c)(1 - d), \text{ and } R(1, 0) = 1 - g.$$

How to estimate the parameters involved in weed dynamics?

We want to estimate the parameters $\theta = (c, d, g, s_0, \lambda)$.

Approximate Bayesian Computation (ABC) algorithm - rejection method

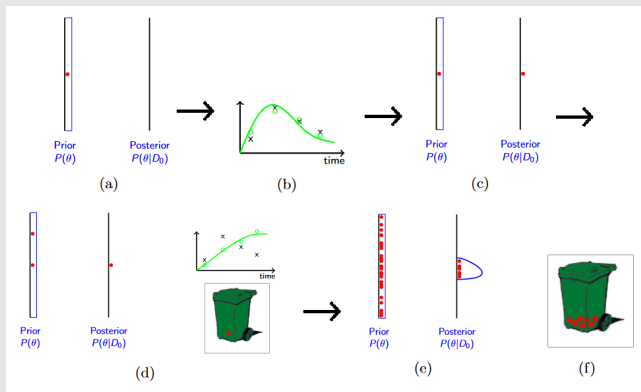


Figure: ABC tutorial taken from Toni and Stumpf 2009

We use the sequential ABC (ABC SMC) algorithm from *EasyABC* R package (Jabot et al. 2013), with the Lenormand method (Lenormand et al. 2013).

Selection of summary statistics

Example (Typical sequence of observations with $M = 10$)

$$Y_{0:M}^* = (0\ 0\ 0\ 0\ 1\ 0\ 0\ 1\ 1\ 1).$$

We consider the following summary statistics :

- 1 number of 1 ;
- 2 number of transitions from 0 to 1 ;
- 3 information about the lengths of consecutive 0's and 1's (Minimum, Maximum, Mean, Quantile at 25%, Median, Quantile at 75%) ;
- 4 mode and mode value in consecutive 0 and 1 lengths.

We consider three ways to group them :

- Group 1 : summary statistics 1, 2 and 3
- Group 2 : summary statistics 1, 2 and 4
- Group 3 : all summary statistics

Experiments on simulated data - Protocol

Protocol (repeated 30 times)

$$\begin{aligned}\theta^* &= (c^*, d^*, g^*, \lambda^*, s_0^*) \\ &= (0.5, 0.5, 0.5, 0.5, 0.5).\end{aligned}$$

- 1 Simulate a true sequence of hidden states and observations $(Z_{0:M}^*, Y_{0:M}^*)$.
- 2 For each group of summary statistics :
 - Run the ABC algorithm to estimate the distribution $\hat{\theta}$.

For each parameter, we plot the box-plot associated to the mode of the 30 estimated distributions.

Experiments on simulated data - Results for the colonization parameter c and the dispersal parameter d

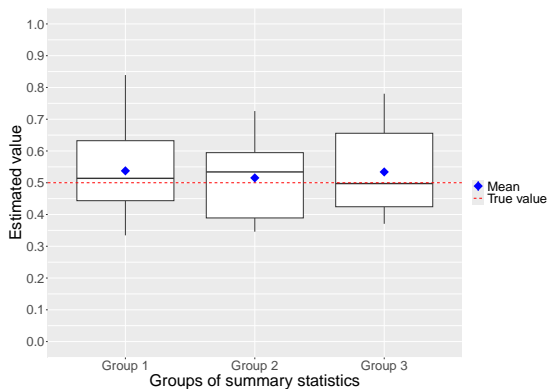


Figure: Estimation of the parameter c

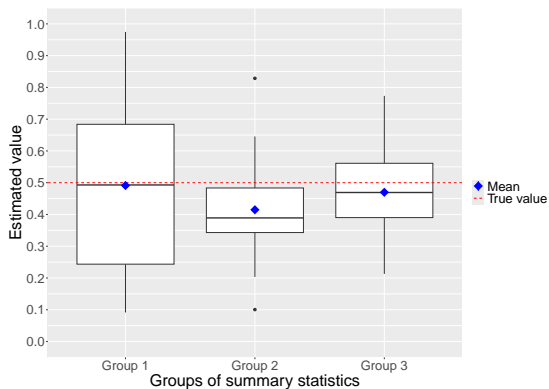


Figure: Estimation of the parameter d

Experiments on simulated data - Results for the germination parameter g and the survival parameter s_0

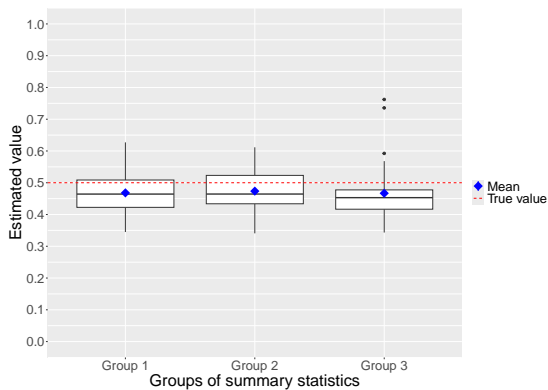


Figure: Estimation of the parameter g

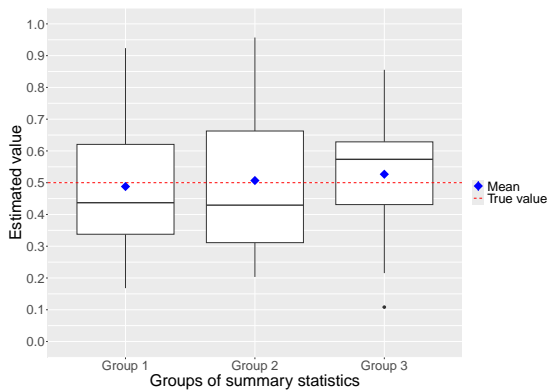


Figure: Estimation of the parameter s_0

Experiments on simulated data - Results for the survival degeneration parameter λ

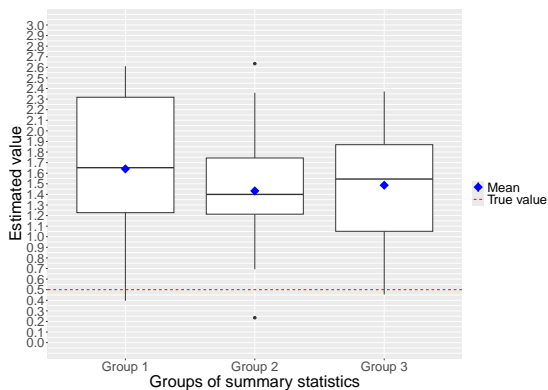


Figure: Estimation of the parameter λ

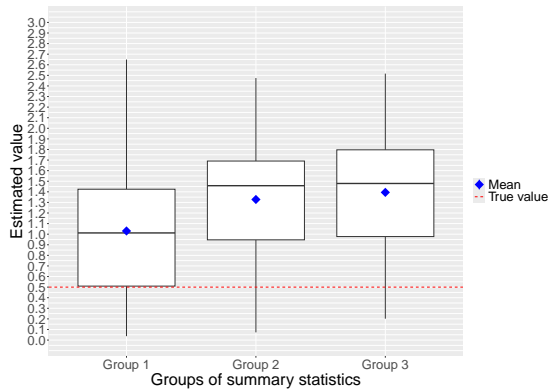


Figure: Estimation of λ with $g^* = 1$

⇒ Difficulty to estimate λ .

Conclusions

Advantage of the OD-HSMM : Realistic model taking into account the fact that the seed bank is hidden and that seeds can remain in soil for several years.

Estimation with ABC algorithm :

- Good estimation quality (except for λ).
- Difficulty to estimate $\lambda \Rightarrow$ to be explored by studying the correlations between parameters.
- Hard to choose the best group of summary statistics \Rightarrow to be chosen with weight analysis.

Perspectives

Extend OD-HSMM to the case where multiple OD-HSMMs interact in order to model colonization between multiple fields (Le Coz et al. 2019).

Main difficulties :

- How to properly define the model?
- How to aggregate data from other fields?
- ...?

Thank you for your attention !

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