Modelling of the leaf appearance process or *phyllochron* with interval censored measurements

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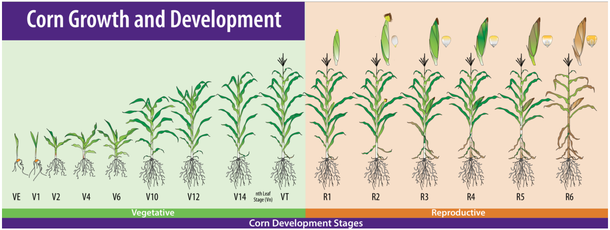
Plant growth and development

- Growth and development : synchronized processes



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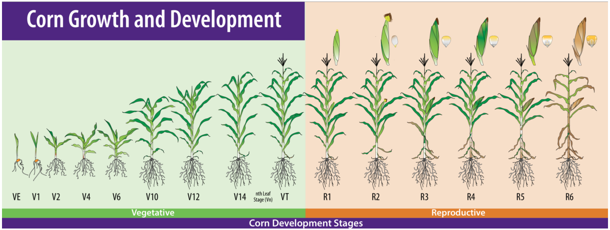

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  - Plot/field level
  - Plant level
  - Organ level
  - Cellular level

↪ Stochastic and deterministic model

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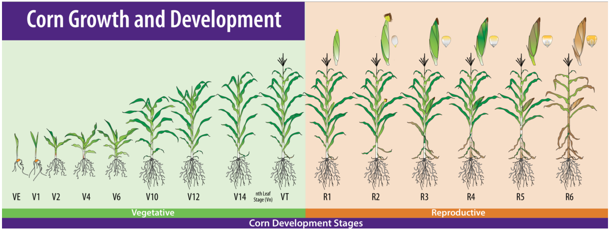

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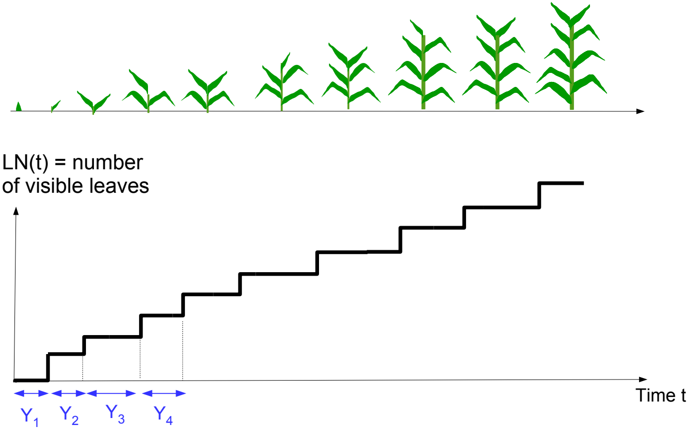
↪ **Stochastic** and deterministic model

↪ Our model : **single phenotype**

Process of leaf appearance or *phyllochron*

- Phyllochron : times of leaf appearance on the plant/ interval of time between successive leaves



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► Good indicator of plant development

► Easy measurements

► Non destructive observations

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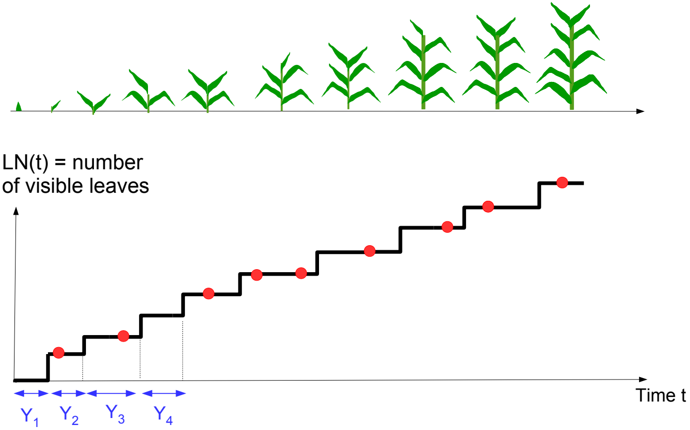

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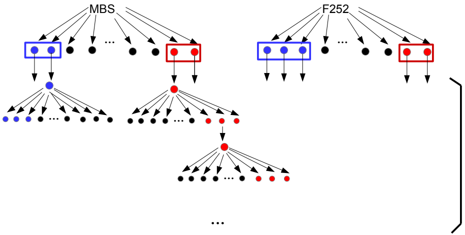
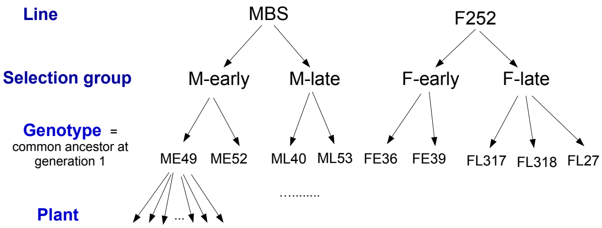
- ► Non destructive observations

- Divergent selection of early/late flowering plants



⇒ hierarchical grouping



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- Linear phyllochron : $\text{Leaf Number}_p(t) = \alpha_p TT_t + \varepsilon_{p,t}$
  - Inference of α_p by linear regression
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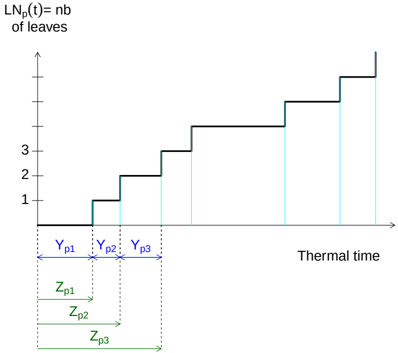
- More flexible models : $LN_p(t) = f(TT_t) + \varepsilon_{p,t}, \quad \varepsilon_{p,t} \quad i.i.d.$
  - bi/tri-linear, splines
  - Descriptive analysis
  - Statistical analysis (confidence interval, tests)
    $\hookrightarrow$ auto-correlation $\Rightarrow$ bias

Independent waiting times model

Consider a given genotype and a given year.



- Realistic biological assumption : $(Y_{p,f})_{f=1,\dots,F}$ independent

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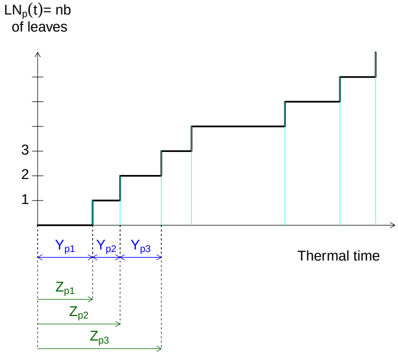

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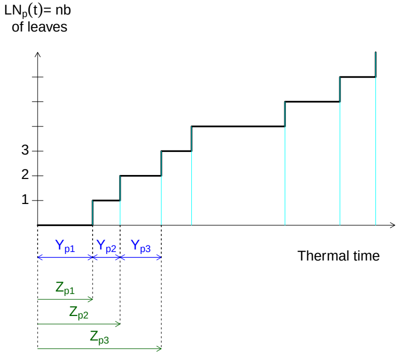

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- More generally

$$Y_{p,f} \sim \mathcal{D}(\theta_f)$$

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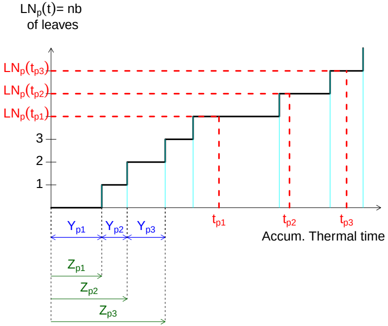

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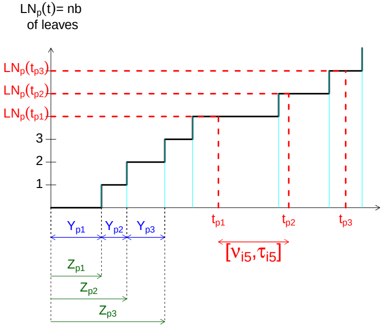

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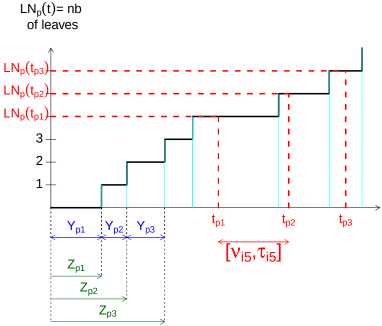

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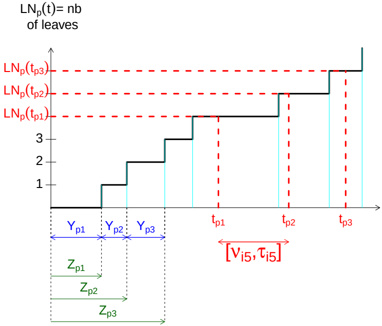

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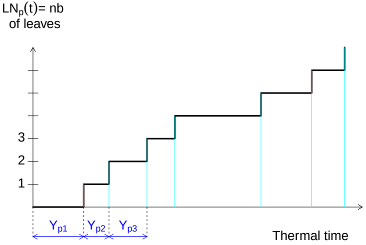
Issue : estimation of the model from discrete measurements/ interval censored observations

The model

Consider a given genotype and a given year, for each plant p

$$\mathbf{Y}_p = (Y_{p,f})_{f=1,\ldots,F_p} \sim \mathcal{N}_{F_p}(\mu, D), \quad D = \mathrm{diag}(\sigma^2)$$



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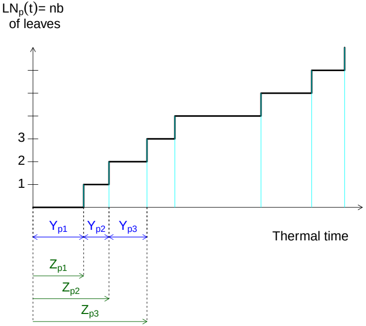

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$\Rightarrow$ Leaf appearance times $\mathbf{Z}_p \sim \mathcal{N}(\overline{\mu}, \Sigma))$ with Σ not diagonal

Monte Carlo EM algorithm

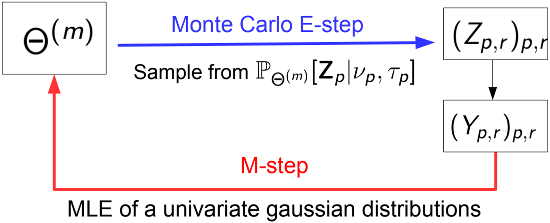
- Latent variables :

$$(\mathbf{Y}_p)_p \Leftrightarrow (\mathbf{Z}_p)_p$$

- Observed variables :

$$((\nu_{p,f}, \tau_{p,f})_f)_p$$

- $\Theta = (\mu, \sigma)$



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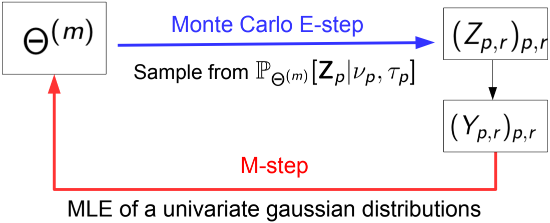

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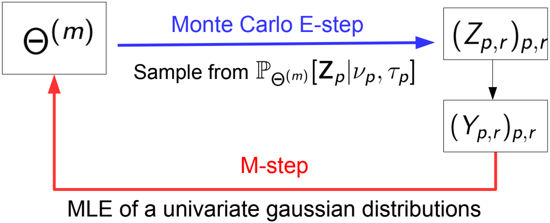

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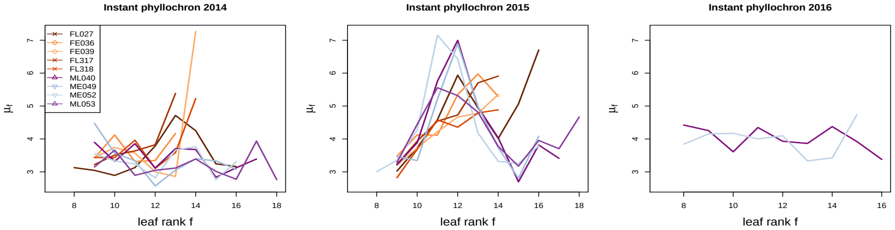
  $\hookrightarrow$ Basic rejection methods fail when dimension increases
- Various methods for gaussian distribution
  $\hookrightarrow$ Package `truncatedNormal`, Botev (2016)

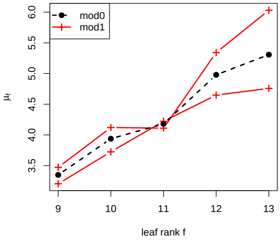
Implementation on ITEMAIZE data



- Test genotypic group effect
- Test assumption of *linear phyllochron* i.e. $\mu_f = constant$
- Imput of climatic variables

Genotypic group effects

- Model comparison



- (mod1) $(\mu_f, \sigma_f)_{f=f^{\mathbf{min}},\dots,f^{\mathbf{max}}}$ depend on genotype
- (mod0) $(\mu_f, \sigma_f)_{f=f^{\mathbf{min}},\dots,f^{\mathbf{max}}}$ same for all genotypes in the selection group

- Criteria based on likelihood : AIC, χ^2-likelihood ratio test
  - Almost all tests are significant (some strongly)
  - Permutation test on one comparison

    $\hookrightarrow$ Results reliable even slightly over-estimated

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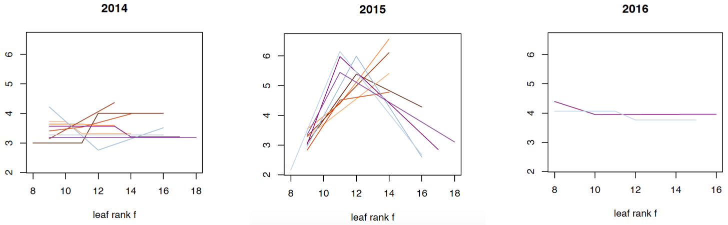

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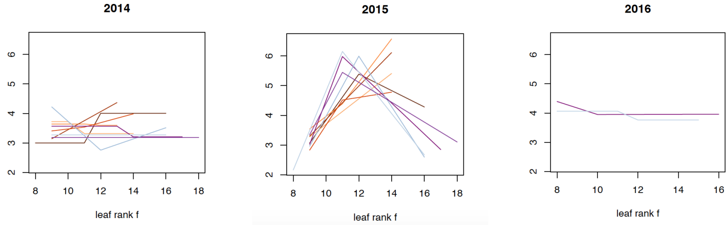

$\hookrightarrow$ Constant μ selected only once

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- Results : in progress

Strengths of the model

- Less biased modelling

Classic approach

Leaf number :

$$LN(t) = f(TT_t) + \varepsilon_t$$

with $(\varepsilon_t)_t$ independent

$\hookrightarrow$ No account for auto-correlation

Our model

Interval between successive leaves

$$Y_f \sim \mathcal{D}(\theta_f)$$

with $(Y_f)_f$ independent.

$\hookrightarrow$ Independence : realistic

- More flexible modelling
- Allows to
  - Test conditions/genotypic effects
  - Select parametric models for μ
  - Evaluate climate effect

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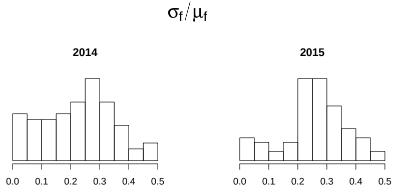

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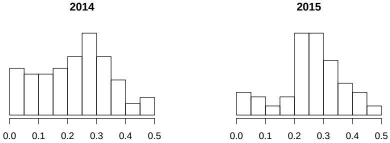

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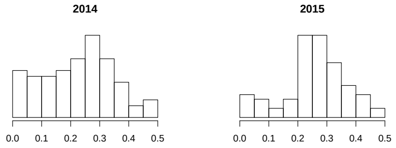

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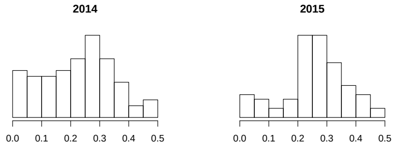

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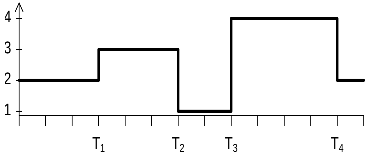
$(S_t)_{t\in\mathbb{N}^*}$ a discrete time process with $S_t \in \{1,\dots,J\}$



- Semi Markov property : State and sojourn duration depends only on previous state and sojourn duration

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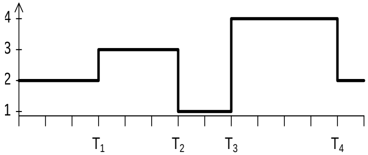

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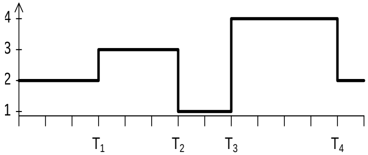

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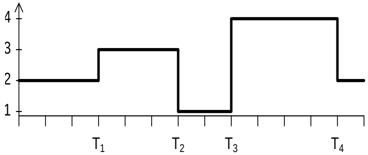

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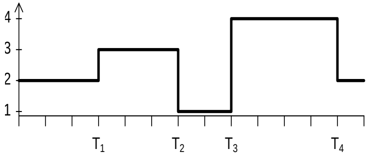

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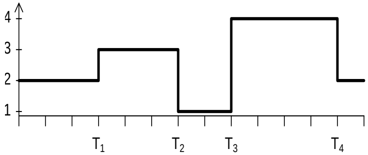
- *Unidirectional* SMM $=$ transition only from i to $i+1$
- Phyllochron : sojourn time independent of time in previous state :

$$a_{(i,d)(j,d')} = \mathbb{1}_{i=j+1} f_i(d) \quad \text{with} \quad f_i(d) = \mathbb{P}[Y_i = d].$$

(Discrete time) Semi-Markov models

$(S_t)_{t\in\mathbb{N}^*}$ a discrete time process with $S_t \in \{1, \dots, J\}$



- Semi Markov property : State and sojourn duration depends only on previous state and sojourn duration

$$\mathbb{P}[S_{[t+1:t+d]} = i | (S_{t'})_{t' \leq t}] = \mathbb{P}[S_{[t+1:t+d]} = i | S_{[t-d'+1:t]} = j] := a_{(i,d)(j,d')}$$

with $\{S_{[t+1:t']} = i\} = \{S_{t+1} = \dots = S_{t'} = i, S_t \neq i, S_{t'+1} \neq i\}$

- *Unidirectional* SMM = transition only from i to $i+1$
- Phyllochron : sojourn time independent of time in previous state :

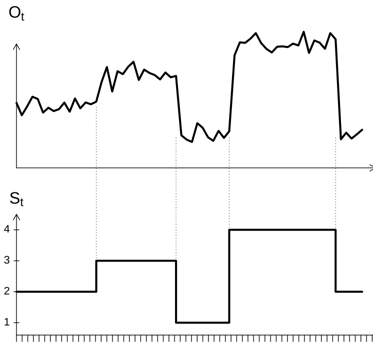
$$a_{(i,d)(j,d')} = 1\!\!1_{i=j+1} f_i(d) \quad \text{with} \quad f_i(d) = \mathbb{P}[Y_i = d].$$

$\hookrightarrow$ If f_i geometric : Poisson point process

SMM with interval censoring : analogy with HSMM

Hidden SMM

- $(S_t)_{t=1,\ldots,T_{\max}}$ unobserved SMM



SMM with interval censoring : analogy with HSMM

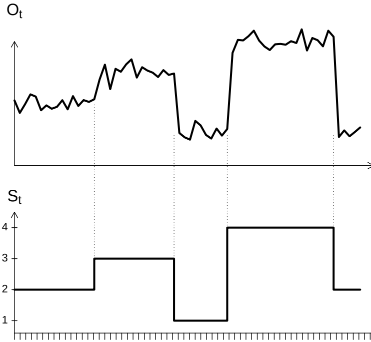
Hidden SMM

- $(S_t)_{t=1,\ldots,T_{\max}}$ unobserved SMM
- $(O_t)_{t=1,\ldots,T_{\max}}$ observed process with

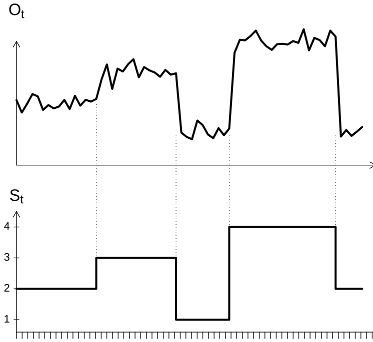
$$\mathbb{P}[O_t = x | (S_{t'})_{t'}, (O_{t'})_{t' \neq t}]$$

$$= \mathbb{P}[O_t = x | S_t = j] = b_j(x)$$

$\hookrightarrow b_j(\cdot) =$ emission proba in state j.



Hidden SMM



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- Forward/backward algo : complexity

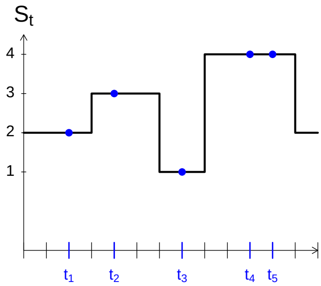
$$O((J^2 + JD^2)T_{\max}) \quad \text{with} \quad \begin{cases} J & \text{number of states} \\ D & \text{maximum sojourn time} \\ T_{\max} & \text{total time} \end{cases}$$

- For unidirectional HSMM, complexity $= O(JDT_{\max})$

SMM with interval censoring : analogy with HSMM

- Interval censoring :

$$\begin{cases} (S_t)_{t=1,dots,T_{\max}} & \text{SMM} \\ (t_1,\ldots,t_N) & \text{monitoring times} \\ (t_i, S_{t_i})_{i=1,\ldots,N} & \text{Observations} \end{cases}$$



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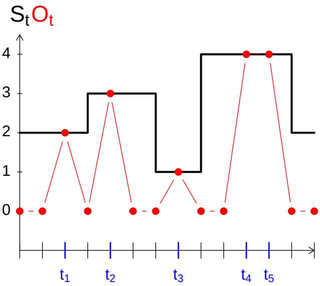
- $(O_t)_t$ observed process (determ. given $(S_t)_t$)

$$O_t = \left\{ \begin{array}{lll} S_t & \text{if} & t \in \{t_1, \ldots, t_N\} \\ 0 & & \text{otherwise} \end{array} \right.$$



SMM with interval censoring : analogy with HSMM

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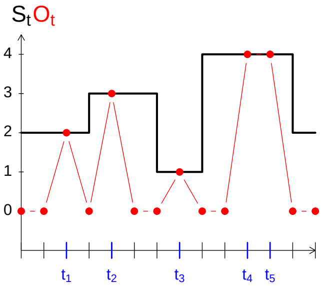
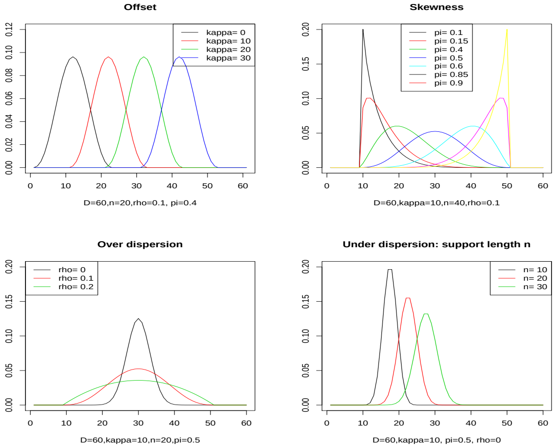


- Algorithm forward/backward : very similar to HSMM

Application to phyllochron : flexible distribution

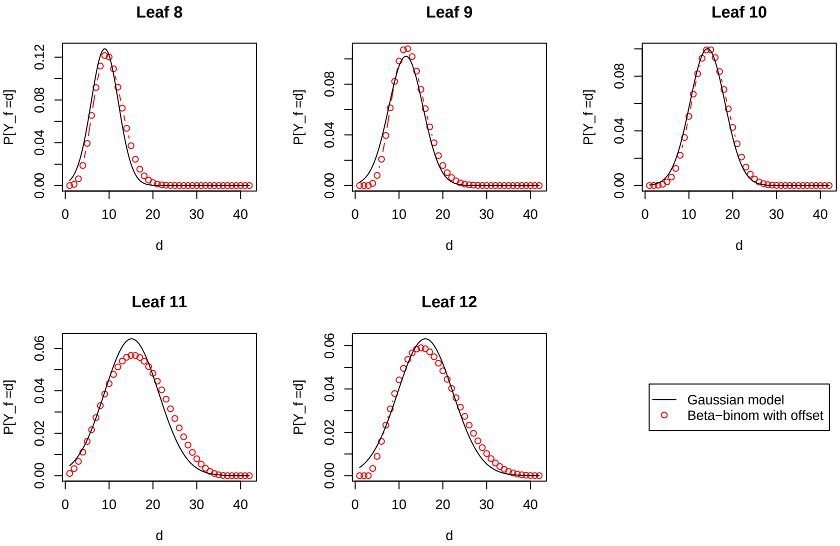
- Support $[\![1, D]\!]$
- Beta-binomiale with offset : $\kappa + \mathcal{BB}(\text{size} = n, \text{prob} = \pi, \rho)$, $n + \kappa \leq D$



Flexible (unimodal)

- Mode =0 / $\neq$ 0
- Skewness
- Over/under dispersion

Ex : results for group F-late



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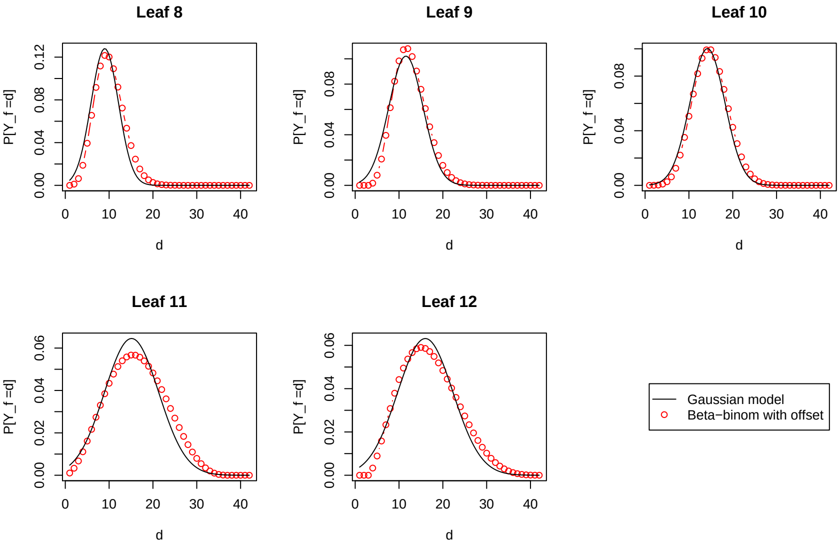
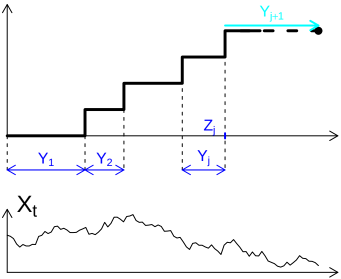


⇒ Gaussian assumption is reasonable

Longitudinal covariate in unidirectional SMM with interval censoring

- $\mathbf{X} = (X_t)_{t=1:T_{\max}}$ longitudinal covariate observed at all times



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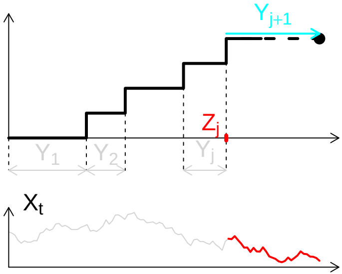

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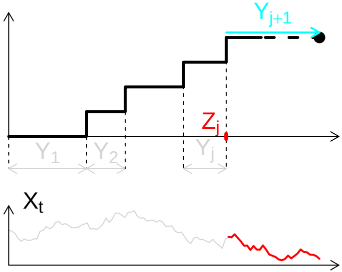

Exple. Discrete time Cox model

Perspectives

- Improve numerical implementation (general SMM w. interval censoring)

  $\hookrightarrow$ Issues similar to HSMM

- Penalized likelihood
  - Flexible distribution (splines, etc)
  - Several longitudinal covariates

- Multi-chain SMM

  $\hookrightarrow$ Application : floral transition

Conclusion

Phyllochron modelling

- Flexible average phyllochron

  ↪ Enlighten temporal trends

- Downstream analysis : less tractable than classic linear phyllochron
- Stochastic process *vs* regression models
  - Other fields e.g. plant pathogens (Nemis *et al* 2013)

Semi-Markov model with interval censoring

- More flexible framework for phyllochron
  - Any parametric distribution
  - Longitudinal covariate (unidirectional SMM)
- General interest
  - SMM with interval censoring : almost not adressed in literature
  - Application in various fields (disease progression...)
- Algorithm analogous to Hidden SMM
  - Adapt methods for HSMM to interval censored SMM