Impact of some model misspecification in multi-response HSMM - application to fruit tree.

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Outline of presentation

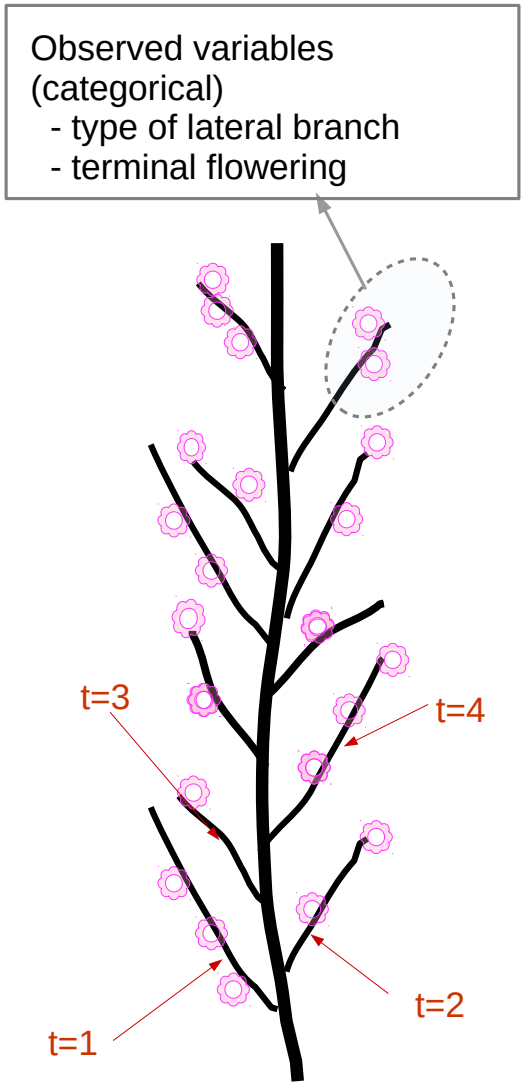
Biological model, motivation and problem statement

Illustration of errors of interpretation in case of model misspecification

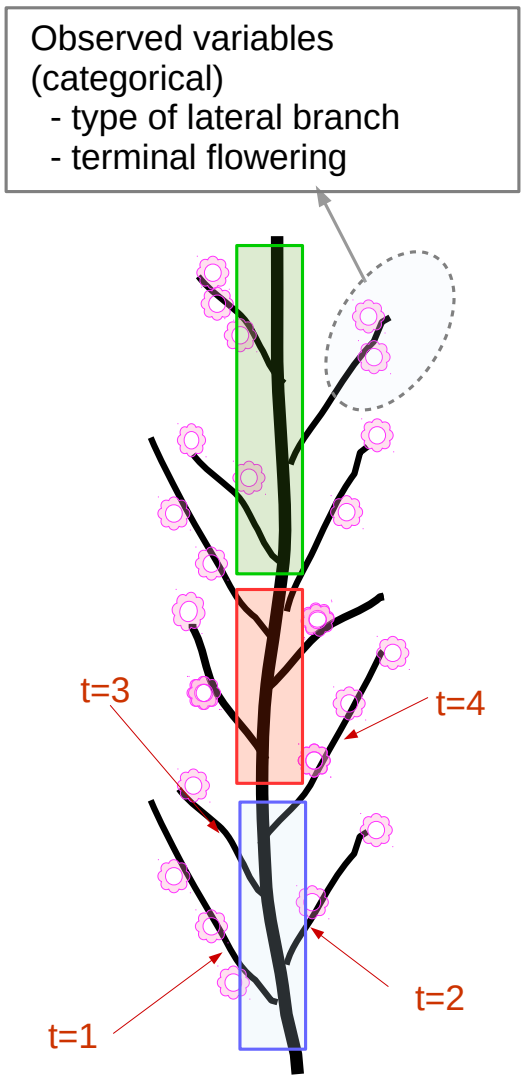
Model selection by BIC

Biological model of apple tree flowering

- Nodes on trunk $\Leftrightarrow$ discrete index process



Biological model of apple tree flowering



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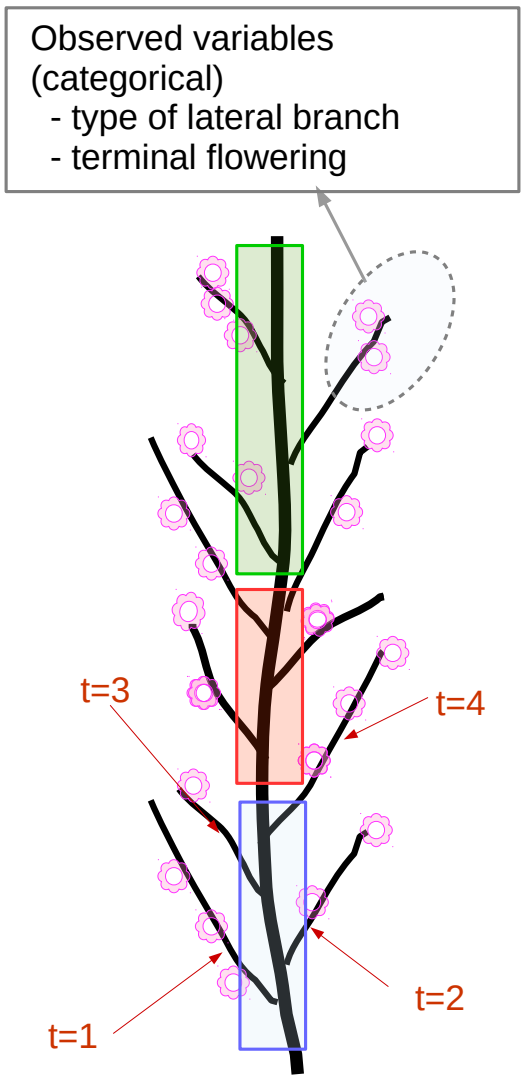
- Biological assumption: phases of growth that impact simultaneously all observed variables

Biological model of apple tree flowering



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- Mathematical model: multi-response HSMM (mHSMM) with
  - hidden states = growth phases
  - observations = categorical variables
- Question: effect of cultivar (among 2) on growth phase lengths and/or compositions in terms of observations.

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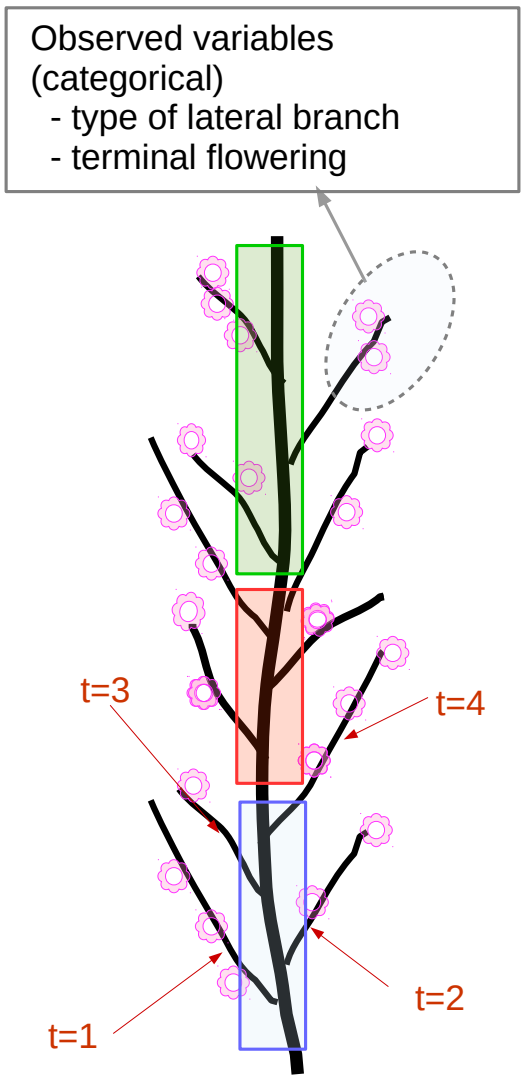

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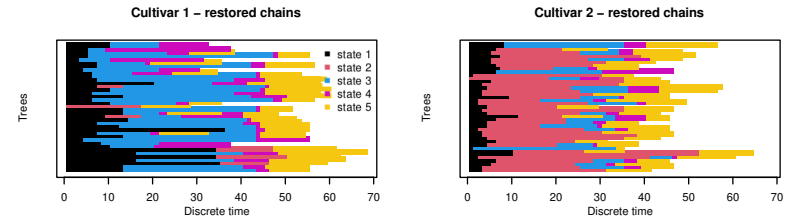
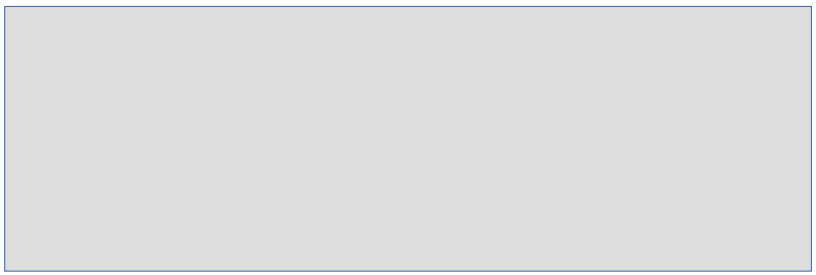
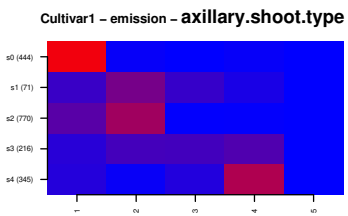
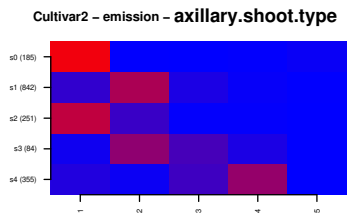
- Question: effect of cultivar (among 2) on growth phase lengths and/or compositions in terms of observations.
- Approximate inference
  - Inference of mHSMM parameters regardless of cultivar (several trajectories)
  - Restoration of hidden chains (Viterbi)
  - Estimation of emission and state duration distributions: empirical distribution given restored hidden states (counts)

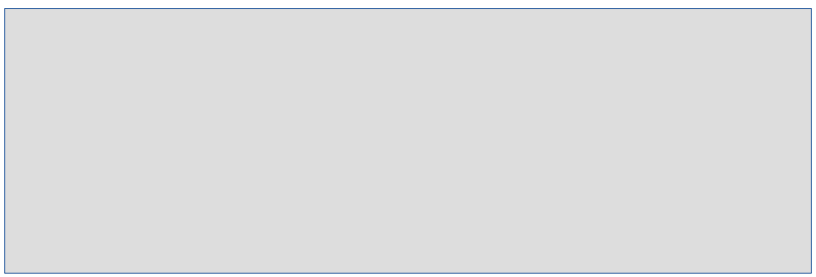
Data analysis based on the mHSMM model

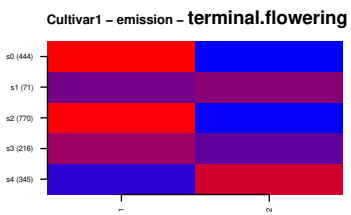


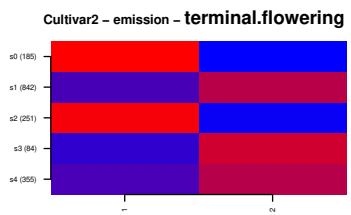










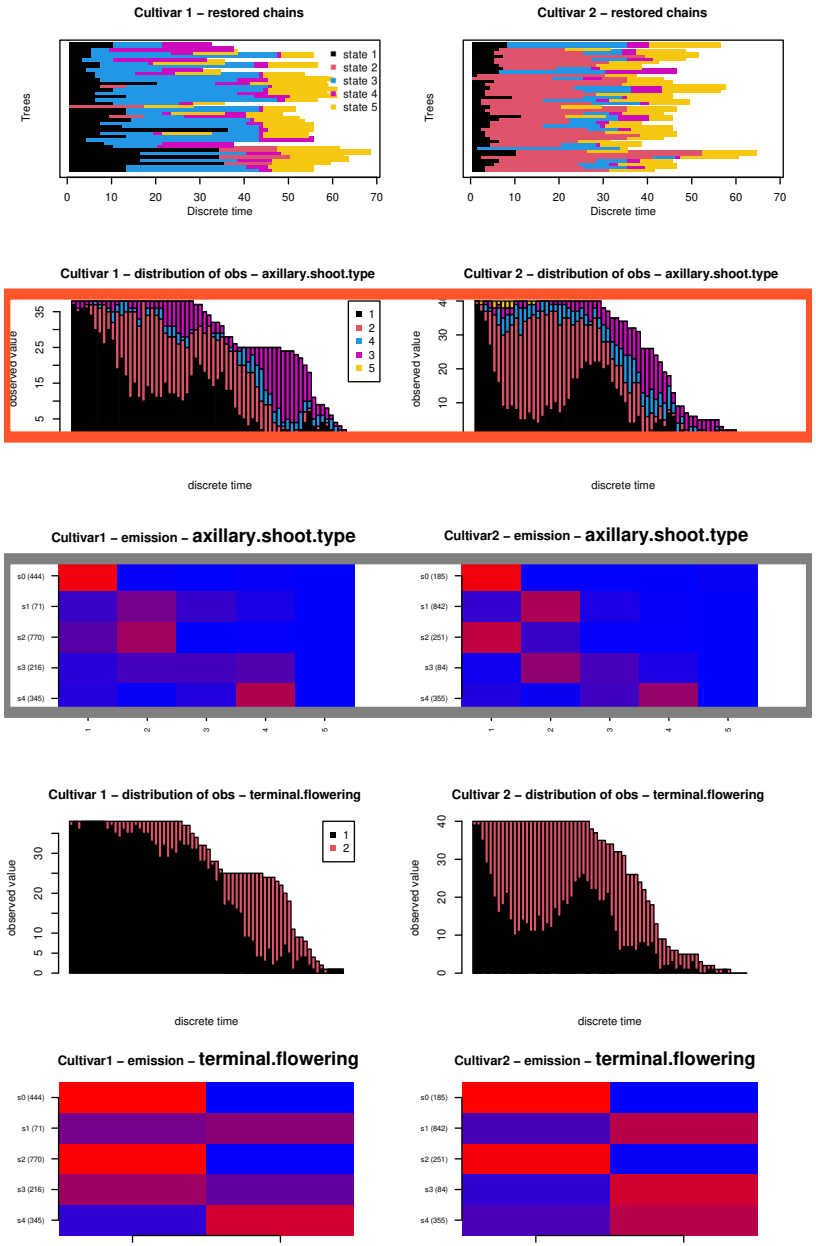


Conclusion

- Cultivar effect on hidden chains (state durations)
- Cultivar effect on "terminal flowering"
- Cultivar effect on "shoot type"

[2]: M. Mészáros, Y. Guédon, B. Krška and E. Costes, 'Modelling the bearing and branching behaviors of1-year-old shoots in apricot genotypes,' PLoS ONE, Public Library of Science, 2020.

Contradiction with observations on raw data



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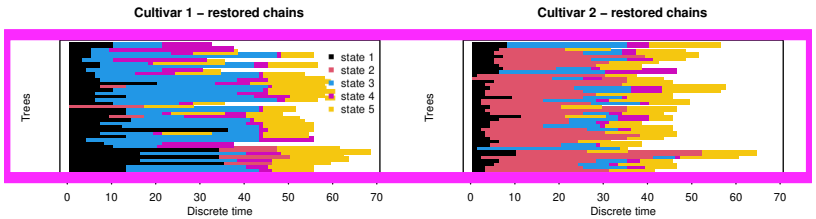

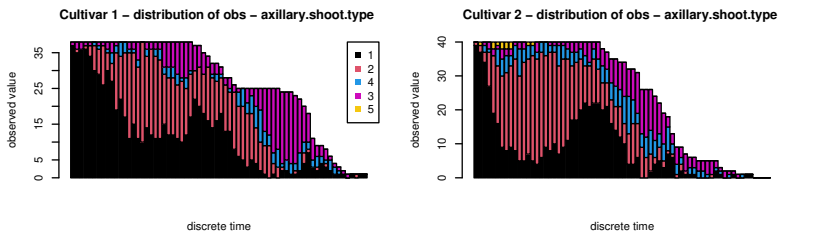

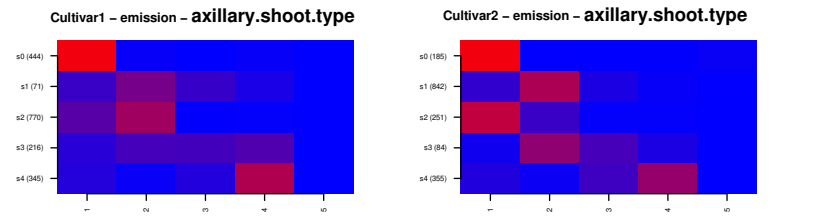

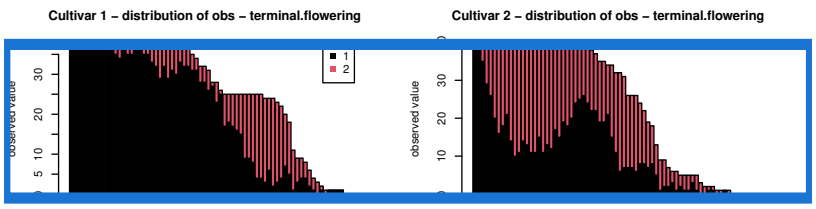

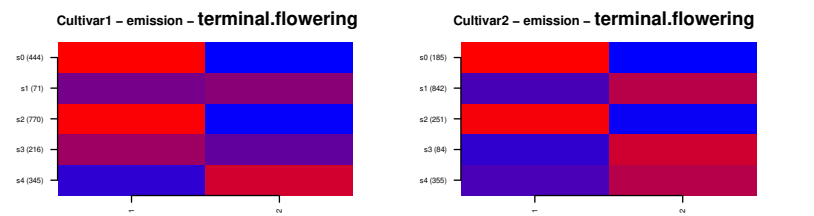

- Consistency between observations and parameters on "terminal flowering"
- Contradiction on "shoot type"
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- Heuristical justification
  - Variable "terminal flowering" different between cultivars $\Rightarrow$ generate different semi-Markov chains.

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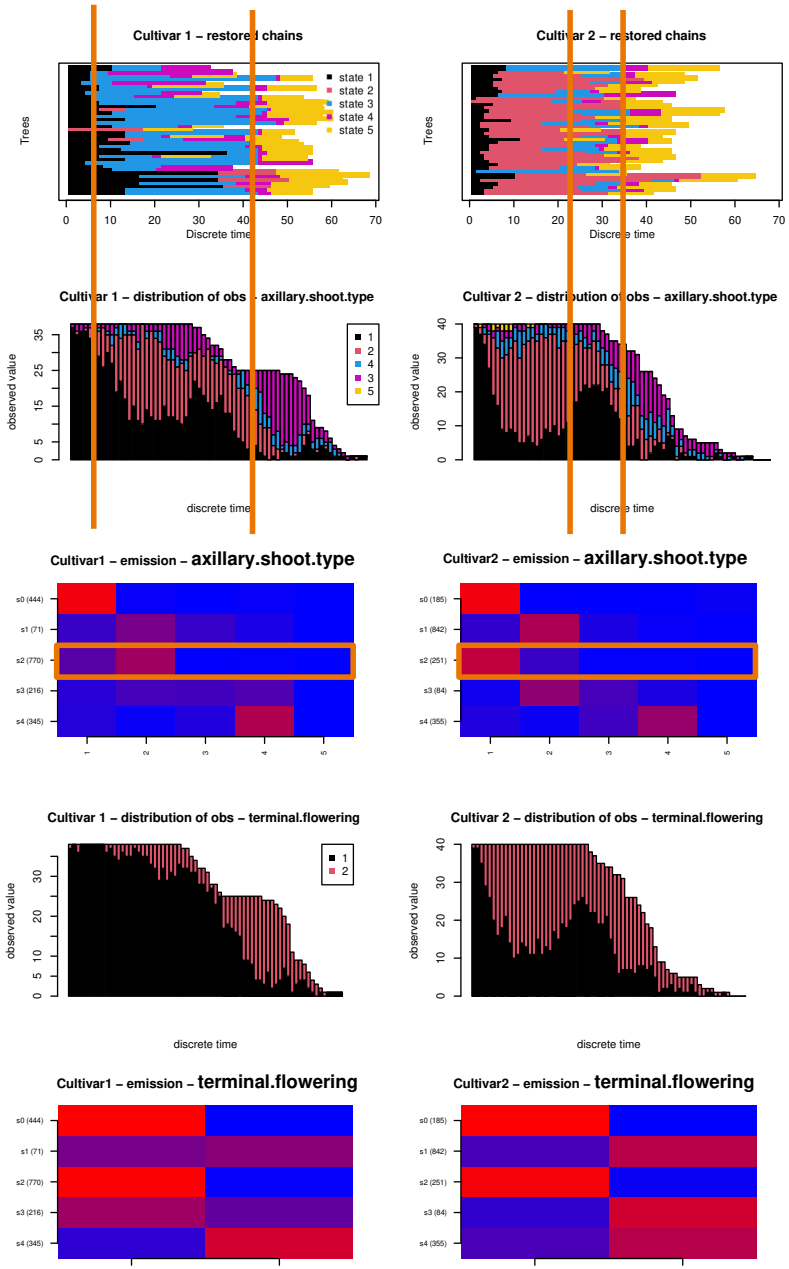

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- Heuristical justification
  - Variable "terminal flowering" different between cultivars $\Rightarrow$ generate different semi-Markov chains.
  - Different semi-Markov chains $\Rightarrow$ Different time frame for a given state $\Rightarrow$ Difference in variable distribution given state

Two potential classes of models

State $S_{i,t}$, observation $O_{i,t}^{(c)}$, covariate z_i for sequence (tree) i.

(mHSMM)
- (1) $(S_{i,t})_t$ unidirectional (Left-right) SMM with state duration potentially dependent on z_i : $\mathbb{P}[S_{i,[t+1:t+d]} = s|z_i] := f(d|s, z_i)$
- (2) $(O_{i,t}^{(1)})_t$ independent given $(S_{i,t})_t$ with emission distribution potentially dependent on z_i : $\mathbb{P}[O_{i,t}^{(1)} = x|S_{i,t} = s, z_i] = g_1(x|s, z_i)$
- (3) $(O_{i,t}^{(2)})_t$ independent given $(S_{i,t})_t$ with emission distribution potentially dependent on z_i : $\mathbb{P}[O_{i,t}^{(2)} = x|S_{i,t} = s, z_i] = g_2(x|s, z_i)$

(reg-HSMM)
- (1) $(S_{i,t})_t$ unidirectional SMM with state duration potentially dependent on z_i : $\mathbb{P}[S_{i,[t+1:t+d]} = s|z_i] := f(d|s, z_i)$
- (2) $(O_{i,t}^{(1)})_t$ independent given $(S_{i,t})_t$ with emission distribution potentially dependent on z_i : $\mathbb{P}[O_{i,t}^{(1)} = x|S_{i,t} = s, z_i] = g(x|s, z_i)$
- (3) $(O_{i,t}^{(2)})_t$ follows a regression model on time, does not depend on $(S_{i,t})_t$ and may depends on z_i : $O_{i,t}^{(2)} \sim \mathcal{D}(\theta(t))$

State transitions are necessarily $s \to s + 1$

Goals

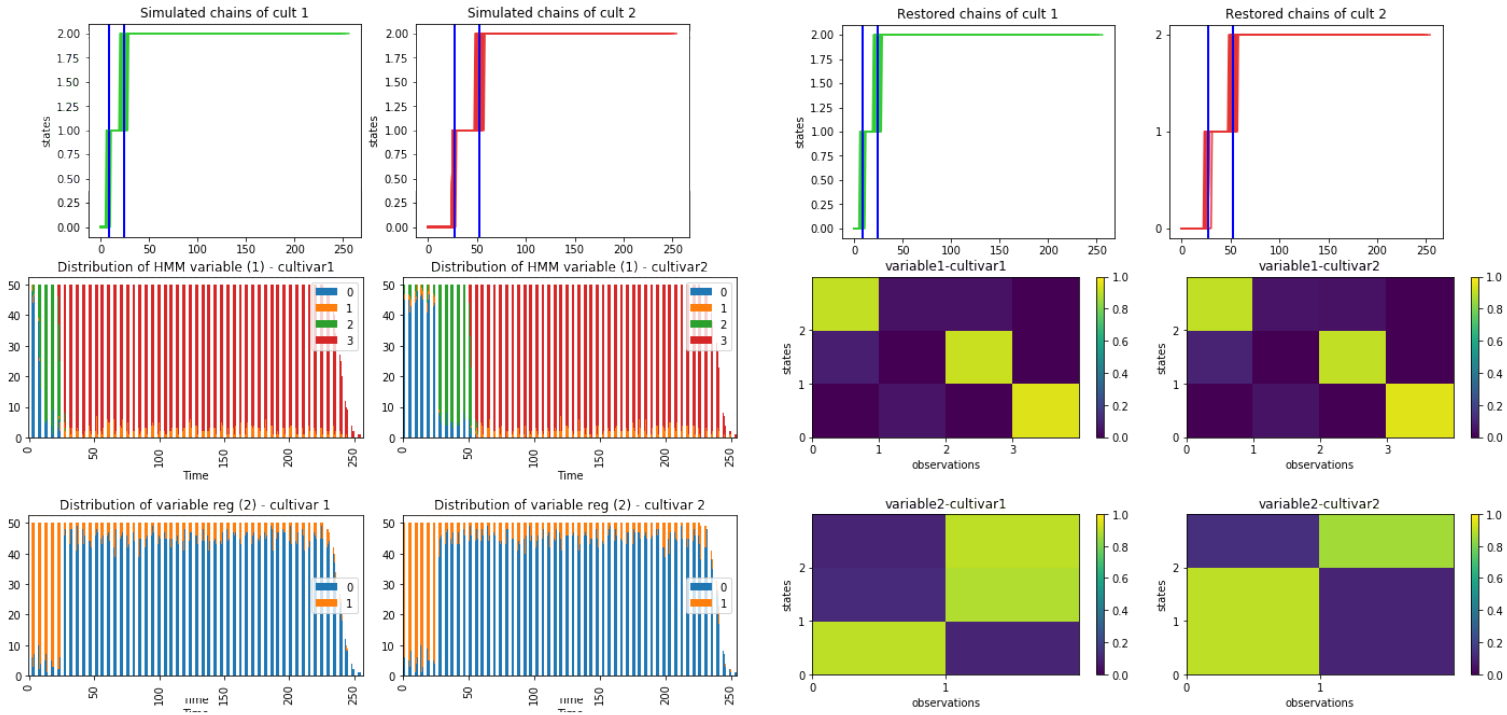
- To emphasize using simulations that considering wrong models may lead to wrong interpretation.
- Illustrate that BIC may select the correct model
- Application to our true data set

Remark

In (reg-HSMM) we will consider a simple parametric regression model: two-piece "histogram" (Bernoulli single change-point model).

Simulations under true (reg-HSMM) and estimation based on (mHSMM)

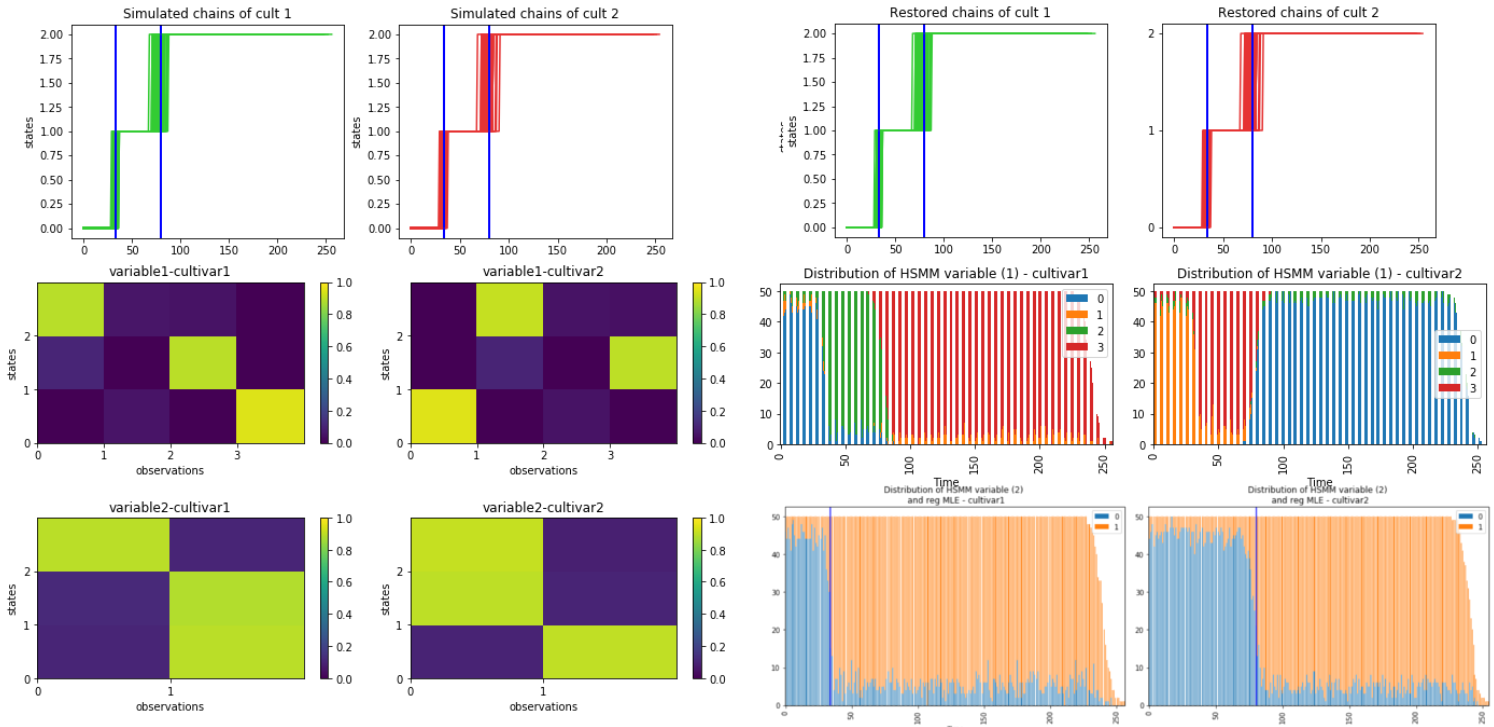
Simulations under (reg-HSMM) with	Estimation with (mHSMM) with
- SMM **depends on cultivar (duration probabilities)**	- SMM depends on cultivar (duration probabilities)
- Observed process 1 $O^{(1)}$ (HSMM variable) **independent on cultivar**	- $O^{(1)}$ (HSMM variable) depends on cultivar
- Observed process 2 $O^{(2)}$ (regression variable) **independent on cultivar**	- $O^{(2)}$ (HSMM variable) depends on cultivar



(Erroneous) conclusion: Emission distribution for $O^{(2)}$ **depends on cultivar $\Rightarrow$ cultivar effect on $O^{(2)}$.**

Simulations under true (mHSMM) and estimation based on (reg-HSMM)

Simulations under (mHSMM) with	Estimation with (reg-HSMM) with
- SMM **independent on cultivar**	- SMM depends on cultivar
- Observed process $O^{(1)}$ (HSMM variable 1) depends on cultivar	- O^1 (HSMM variable) depends on cultivar
- Observed process $O^{(2)}$ (HSMM variable 2) depends on cultivar	- O^2 (reg variable) depends on cultivar



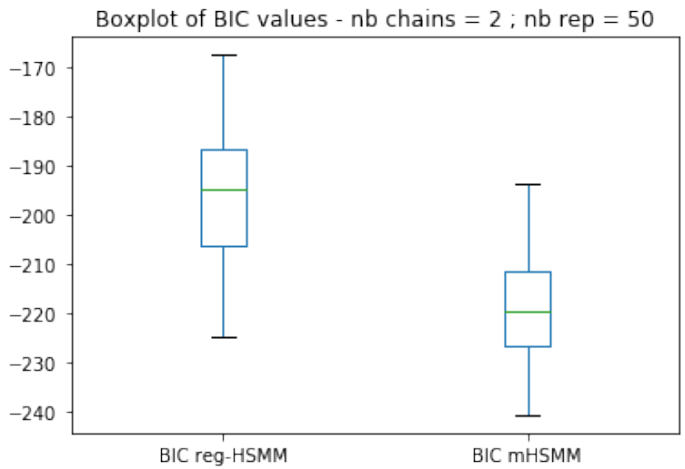
(Erroneous) conclusion: dynamics for $O^{(2)}$ **depends on cultivar** $\Rightarrow$ **cultivar effect on zone length with low flowering probability on** $O^{(2)}$

BIC for model selection

BIC = log(likelihood) - 0.5 ν log(nb obs)
(maximize over models; ν number of free parameters)

- 50 simulations of n trajectories of length T under either (mHSMM) or (reg-HSMM) (parameters as in previous examples).
- Estimate both models and compute BIC.

Simulation under (reg-HSMM);
$n = 50, 10, 8, 6, 4, 3, 2$; $T = 240, 50$



Boxplot of BIC values over 50 simulations ($n = 2$, $T = 50$)

nb trajectories n	4	3	2
correct selection rate (BIC)	100 %	100 %	100 %

Rate of BIC selecting (reg-HSMM)

BIC for model selection: simulation under mHSMM

BIC = log(likelihood) - 0.5 ν log(nb obs)
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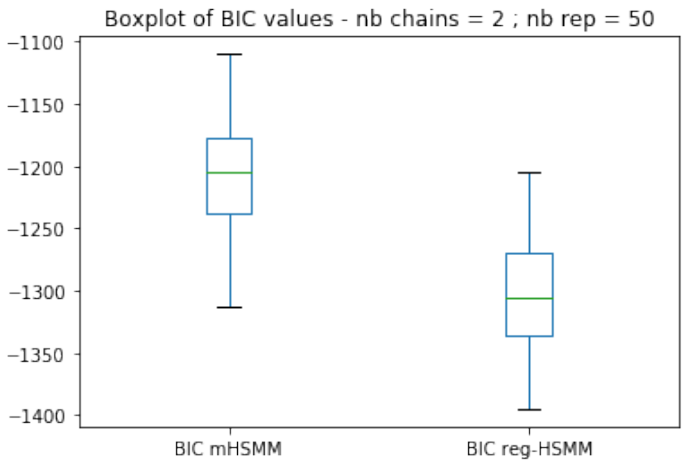

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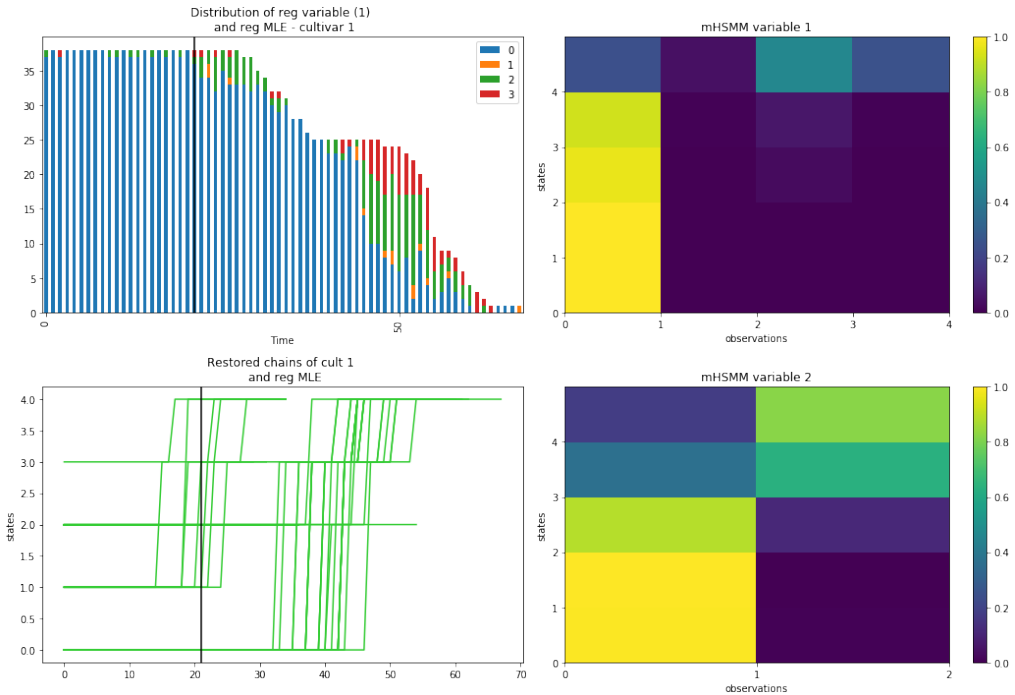
Rate of BIC selecting (mHSMM)

Results on true data set

Example: cultivar 1, variable 1 as (reg-HSMM), variables 2 and 3 as (mHSMM)

- Categorical reg variable with 5 categories, one change point.
- BIC mHSMM = -2,755 $<$ **BIC regHSMM = -2,542**
- Suggests (either?) unique, synchronous change for variable 1, independent on HSMM states
- Complicates model selection



Apple tree data set: cultivar 1. Marginal distribution of (reg) variable 1, emission distribution for mHSMM variables 2 and 3 and restored state sequences (3 states: sufficient?)

Conclusion et perspectives

- Summary
  - Classic model for fruit tree flowering (and other plant/organ development) : multi-response HSMM
  - Observations on our data: potential alternative model
  - Model misspecification can lead to erroneous biological conclusions
  - BIC for model selection has promising behaviour
- Perspectives
  - Evaluation of BIC on a realistic model (parameters estimated from data, multiple change-point models with common parameters between trajectories or other regression models)
  - Study of the consistency of BIC in model selection
  - Exploration of the combinatorics of models on true data (which variables are reg-, which ones are mHSMM and then, with how many change-points / states...?)