

Continuous Development Models for Greenup Phenology

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This document explains how the two-stage and three-stage phenology models are set up and structured.

Two-Stage Phenology Model

The two-stage model is based on only a single transition point: **Onset**. And therefore, the two stages are 1) pre-onset and 2) post-onset. Here, I explain the theoretical framework for a Hierarchical Bayesian model that can simulate the process.

We first define a latent development state where the greenup continuously develops:

$$h_{p,y,d+1} = h_{p,y,d} + \delta h_{p,y,d} \quad (1)$$

where $h_{p,y,d}$ is the latent state for pixel p , in year y and day d . $\delta h_{p,y,d}$ is the latent state increment. We use an exponential increment function that

$$\delta h_{p,y,d} = e^{X_{p,y,d}\beta + \epsilon} (1 - h_{p,y,d}/h_{max}) [T_{p,y,d} - T_{base}] \quad (2)$$

where $X_{p,y,d}$ is the matrix of predictors and ϵ is the process error, defined as:

$$\epsilon \sim Normal(0, \sigma^2) \quad (3)$$

We set $h_{p,y,1} = 0$, and $h_{max} = 1$. To link the discrete observations (pre-onset/post-onset or True/False) to the continuous scale that the development happens, we use a logit transformation:

$$logit(P_{p,y,d}) = \kappa + \lambda * h_{p,y,d} \quad (4)$$

where κ and λ are the intercept and slope of the transformation and $P_{p,y,d}$ is the probability that the onset occurs at pixel P in year y and day d . $P_{p,y,d}$ has the Bernoulli distribution:

$$Y_{p,y,d} \sim Bernoulli(P_{p,y,d}) \quad (5)$$

where $Y_{p,y,d}$ is the observed phenological stage for pixel p in year y and day d .

Three-Stage Phenology Model

The three-stage model is based on two transition points: **Onset** and **Maturity**. And therefore, the three stages are 1) pre-greenup and 2) greenup and 3) post-greenup. Here, I explain the theoretical framework for a Hierarchical Bayesian model that can simulate the process.

The process level of the three-stage model is the same as the two-stage phenology model. However the link function level would be slightly different

Similar to two-stage model, the latent states are defined as:

$$h_{p,y,d+1} = h_{p,y,d} + \delta h_{p,y,d} \quad (6)$$

$$\delta h_{p,y,d} = e^{X_{p,y,d}\beta + \epsilon} (1 - h_{p,y,d}/h_{max}) [T_{p,y,d} - T_{base}] \quad (7)$$

$$\epsilon \sim Normal(0, \sigma^2) \quad (8)$$

$$h_{p,y,1} = 0 \quad (9)$$

$$h_{max} = 1 \quad (10)$$

Since the latent state continuously increases over different phenology stages, we define $\theta_{p,y,d,m}$ as the probability that pixel p is in stage m in year y and day d , while $P_{p,y,d,m}$ is the the probability that pixel p is in any of stage 1 to m in year y and day d . The cumulative probability accounts for the compatibility with the development function.

The observations and the latent states are linked with the Multinomial distribution:

$$Y_{p,y,d} \sim Multinomial(1, \Theta_{p,y,d}) \quad (11)$$

where $\Theta_{p,y,d}$ is the probabililty that pixel p in year y and day d is in any of the stages 1 to M (in this case $M = 3$) and

$$\theta_{p,y,d,1} = P_{p,y,d,1} \quad (12)$$

$$\theta_{p,y,d,2} = P_{p,y,d,2} - P_{p,y,d,1} \quad (13)$$

$$\theta_{p,y,d,3} = 1 - P_{p,y,d,2} \quad (14)$$

To link the discrete observations (pre-onset/post-onset or True/False) to the continuous scale that the development happens, we use a logit transformation:

$$\text{logit}(P_{p,y,d,1}) = \kappa_1 + \lambda_1 * h_{p,y,d} \quad (15)$$

$$\text{logit}(P_{p,y,d,2}) = \kappa_2 + \lambda_2 * h_{p,y,d} \quad (16)$$

$$P_{p,y,d,3} = 1 \tag{17}$$

where κ_m and λ_m are the intercept and slope of the transformation for stage m .
