

# 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.

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## 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  $\epsilon$  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  $\kappa$  and  $\lambda$  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  $d$ .

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## 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  $\kappa_m$  and  $\lambda_m$  are the intercept and slope of the transformation for stage  $m$ .

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