The Questions
We want to use the SLIP simulator to ask questions about forest dynamics that require understanding the entire system, and not just pieces of it: 1) what demographic rates and environmental features drive species coexistence? 2) which species respond to gap dynamics and light gradients? 3) how will an increase in droughts affect forest composition?

To simulate a forest, we have broken down the problem (and the forest) into more manageable components.

The dynamics of tree species are modeled as a collection of individuals. Although seed rain, the seed bank, and yearlings are expressed as densities, once a proportion of germinants (yearlings) survive their first year, they are randomly assigned an x-y coordinate within their cell, and assigned to the individual object (which has a species designation). Finally, individuals are simulated by collecting information on their various life-history stages. We follow these individuals through their lives by identifying them as one of the life-history stages in Figure 1. We treat seeds and yearlings as densities, so it is not until stage 3, as seedlings, that the individual class truly applies.

Developing model input from data
Every arrow in the diagram of Figure 1 reflects a transition that occurs over a time step (1 yr in SLIP). Transitions include germination, growth, survival (and therefore mortality), and reproduction. All of these rates must be quantified for the model. We do this by:

1) developing a deterministic model, which mathematically posits mechanisms that drive the demographic rate. e.g. Growth in this year relates to rainfall and light.

2) use hierarchical Bayesian methods to model this process, the data that inform the process model, and the parameters that are a part of both the data and process models. (See Clark 2007)

Some of the parameters have strong analyses and experiments to estimate them, while others are built from priors. Although we estimate process, data, and parameter error, we include process error in the simulation functional forms. In some models crucially for adult growth and fecundity, we include yearly effects, individual effects in addition to the process error.

Sub-models simulate the demographic rates that are associated with specific life-history stages. All species share the form of the sub-models (the process model, but every species has its own parameters that enter the simulator.

EXAMPLE using GERMINATION: Now we get simulation parameters from data using hierarchical Bayes. This is an example, but every major demographic rate is developed in a similar manner.

By creating a process model, the core of the mechanistic relationship we believe drives the process. In the germination sub-model, Ibanez et al. (2007) point a relationship between the probability that a seed germinates and four other variables: temperature, soil moisture, light, and seed density. The function that describes this process is a logit regression model.

\[ \logit(p_{\text{germ}}) = a_0 + a_1 \text{temp} + a_2 \text{soil} + a_3 \text{light} + a_4 \text{density} + \epsilon \]

These parameters are estimated from experimental and observational data collected in Duke forest and Coveetka sites in North Carolina. We estimate joint posteriors from the process model above to get parameter. See Ibanez et al. 2007 for details.

SLIP output
Output from the SLIP model includes all information on the demographic rates, location if trees, time series, environment, etc.

These are the data that can be used to answer the questions raised in the beginning.

SLIP structure: the grid, the environment, and runs
The forest environment assigns temperature and soil moisture to each cell in the grid. The seed bank, yearlings, and seedlings are associated with those cells, but only when a seedling becomes a sapling (>5 m) it gets assigned an x-y coordinate within that cell.

The simulated forest exists on a grid with cell units of 1 x 1 and whose sides are powers of 2 (creating possible grid sizes up to 256,512 and 1024 m—the sizes we use).

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Rebuilding a forest using data-models
Rebuilding a forest using data-models

Rebuilding a forest using data-models

Seed Rain
Seed Bank
Yearling
Seedling
Sapling
Adult

Figure 1. Life-history graph of a tree. Numbers refer to life history stages. Solid lines show paths of recruitment or survival, dashed lines show mortality, and the dotted lines show the production of a seed. Each pathway reflects a potential move over the 1-year time steps.

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