LARCH BUDMOTH STATE-SPACE MODEL

AAK, ELI, SPE, KBN

- Three state variables, Q_t (measure of food quality on $[0,1]$), N_t (budmoth density) and S_t (fraction of budmoth larvae infected with parasitoids).
- Three observations, $\hat{Q}_t$ (needle length), $\hat{N}_t$ and $\hat{S}_t$.

1. STATE PROCESS

Uncorrelated random effects, for $t = 1, \ldots, T$:

$$\alpha_t \sim \text{LogitNormal}(\text{logit}(\alpha), \sigma_\alpha^2) \tag{1}$$

$$\lambda_t \sim \text{Gamma}(\lambda, \sigma_\lambda^2) \tag{2}$$

$$a_t \sim \text{LogNormal}(\log(a), \sigma_a^2) \tag{3}$$

Note: X is LogitNormal(μ, σ^2) if logit(X) is Normal(μ, σ^2).

The inverse of logit is expit. R functions `logit`, `expit`, `rlogitnorm`, `dlogitnorm` are part of `pompExamples`.

The state process, for $t = 1, \ldots, T$:

$$Q_t = (1 - \alpha_t)\frac{\gamma}{\gamma + N_{t-1}} + \alpha_t Q_{t-1} \tag{4}$$

$$N_t = \lambda_t N_{t-1}(1 - S_{t-1})\exp\left\{-gN_{t-1} - \delta(1 - Q_{t-1})\right\} \tag{5}$$

$$S_t = 1 - \exp\left(\frac{-a_t S_{t-1} N_{t-1}}{1 + a_t w S_{t-1} N_{t-1}}\right) \tag{6}$$

2. MEASUREMENT PROCESS

For $t = 1, \ldots, T$:

$$\hat{Q}_t \sim \text{LogNormal}(\log(\beta_0 + \beta_1 Q_t), \sigma_Q^2) \tag{7}$$

$$\hat{N}_t \sim \text{LogNormal}(\log(N_t), \sigma_N^2) \tag{8}$$

$$\hat{S}_t \sim \text{LogitNormal}(\text{logit}(uS_t), \sigma_S^2) \tag{9}$$

3. IDENTIFIABILITY AND CONSTRAINTS

One may wish to set $\beta_0 = 0$. The logic is as follows: the steady state value of Q_t is $\bar{Q} = \gamma/(\gamma + \bar{N})$. If Q_t is in practice close to this value then $\bar{Q}$ identifies the mean of $\hat{Q}_t$ in (7), leaving only the scale parameter β_1 to be determined. Thus, the combination of γ, β_0 and β_1 is only weakly identifiable when Q_t varies over only a fraction of its full range of $[0, 1]$.

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4. The budmoth example implemented

This model is implemented in the package and can be loaded with the command

```
data(budmoth.sim)
```

The object thereby loaded contains a named, length-4 list of pomp objects

```
names(budmoth.sim)
```

```
[1] "tri"   "para1" "food"  "para2"
```

There are three parameter regimes ("food", "para", and "tri" representing a food-quality-dominated, a parasitoid-dominated, and true tritrophic dynamics, respectively). In total, there are 4 imulated data sets of length 61 years.

The process model is implemented using the `euler.simulate` plugin with step function `budmoth_map` defined in `src/budmoth.c` in the package source. The log likelihood of any state transition is given by the native routine `budmoth_density`. The measurement model is simulated using `budmoth_rmeasure` and the likelihood is computed via `budmoth_dmeasure`. Finally, the state process is initialized by

```
function (params, t0, ...)
{
    x <- c(params[c("Q.0", "N.0", "S.0")], c(0, 0, 0))
    names(x) <- c("Q", "N", "S", "Alpha", "Lambda", "A")
    x
}
```

The parameters at which the simulated data are generated can be extracted via

```
true.pars <- sapply(budmoth.sim[c("food","para1","para2","tri")],coef)
```

and are displayed in Table 1.

We can get a benchmark for likelihood-based fitting methods by computing the true likelihood at the true parameter values. To do this, we run the `pfilter` particle filtering code.

Table 2 shows these likelihoods.

To get some sense of the shape of the likelihood surface, we can construct slices through each of the true parameter points. These likelihood slices are shown in Fig. 2.

These calculations took 49.2 CPU secs on inexpensive processors.

To simulate ignorance, we will assume that we are uncertain about the values of some of the parameters. In particular, we will suppose that we wish to estimate the parameters that distinguish the regimes.

We will assume a hypercube within which we are uniformly uncertain as to the parameter values. The upper and lower limits for each of the parameters we will estimate are given in Table 3.

Table 1. Parameters of the larch budmoth model, and the values corresponding to the simulated data.

| parameter	R name	food	para1	para2	tri
α	alpha	0.50	0.50	0.50	0.50
σ_α	sig.alpha	0.10	0.10	0.10	0.10
γ	gam	20.00	50.00	50.00	50.00
λ	lambda	5.00	22.00	10.00	22.00
σ_λ	sig.lambda	0.25	0.25	5.00	0.25
g	g	0.02	0.08	0.08	0.08
δ	delta	10.00	0.50	0.50	10.00
a	a	1.00	1.70	1.70	1.70
σ_a	sig.a	0.10	0.10	1.00	0.10
w	w	0.00	0.15	0.15	0.15
β_0	beta0	0.00	0.00	0.00	0.00
β_1	beta1	35.00	35.00	35.00	35.00
u	u	0.90	0.90	0.90	0.90
σ_Q	sigQobs	0.03	0.03	0.03	0.03
σ_N	sigNobs	0.50	0.50	0.50	0.50
σ_S	sigSobs	0.10	0.10	0.10	0.10
Q_0	Q.0	0.96	0.96	0.96	0.96
N_0	N.0	0.02	0.02	0.02	0.02
S_0	S.0	0.22	0.22	0.22	0.22
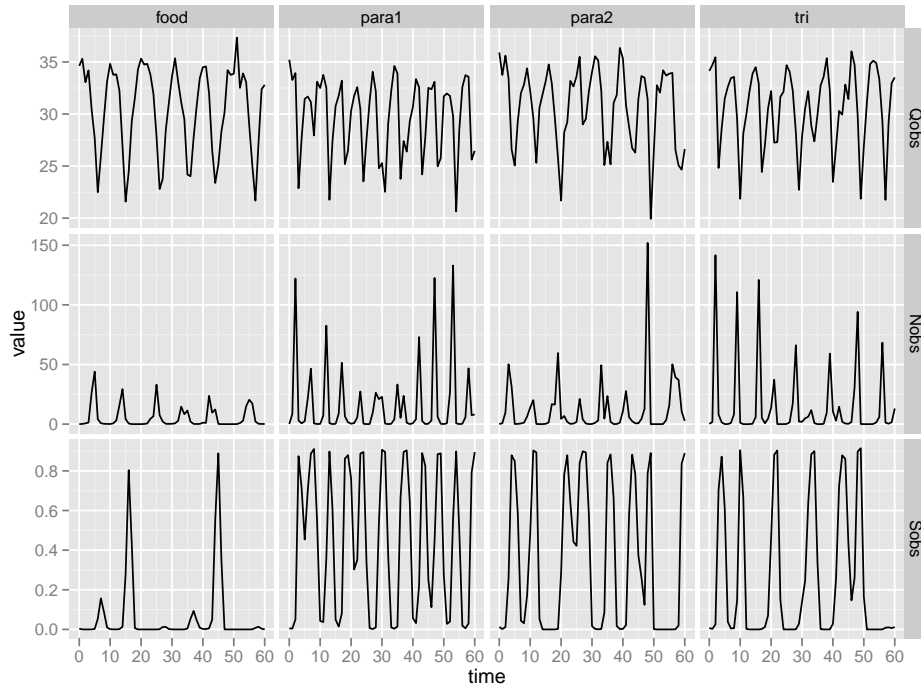
Figure 1. Plot of the simulated budmoth data.

TABLE 2. Estimated log likelihood at the true parameters for the simulated budmoth data. To obtain these, 10 particle filtering runs, each with 10000 particles, were used. The column labeled "se" gives the standard error of the Monte Carlo likelihood calculation. The computation took 49 CPU secs on inexpensive processors. The last column shows the likelihood we would expect to achieve at the MLE 95% of the time when estimating 6 parameters.

dataset	loglik	se	5%
tri	215.2	0.24	216.0
para1	12.3	0.36	13.1
food	359.4	0.16	360.3
para2	36.1	1.00	36.9
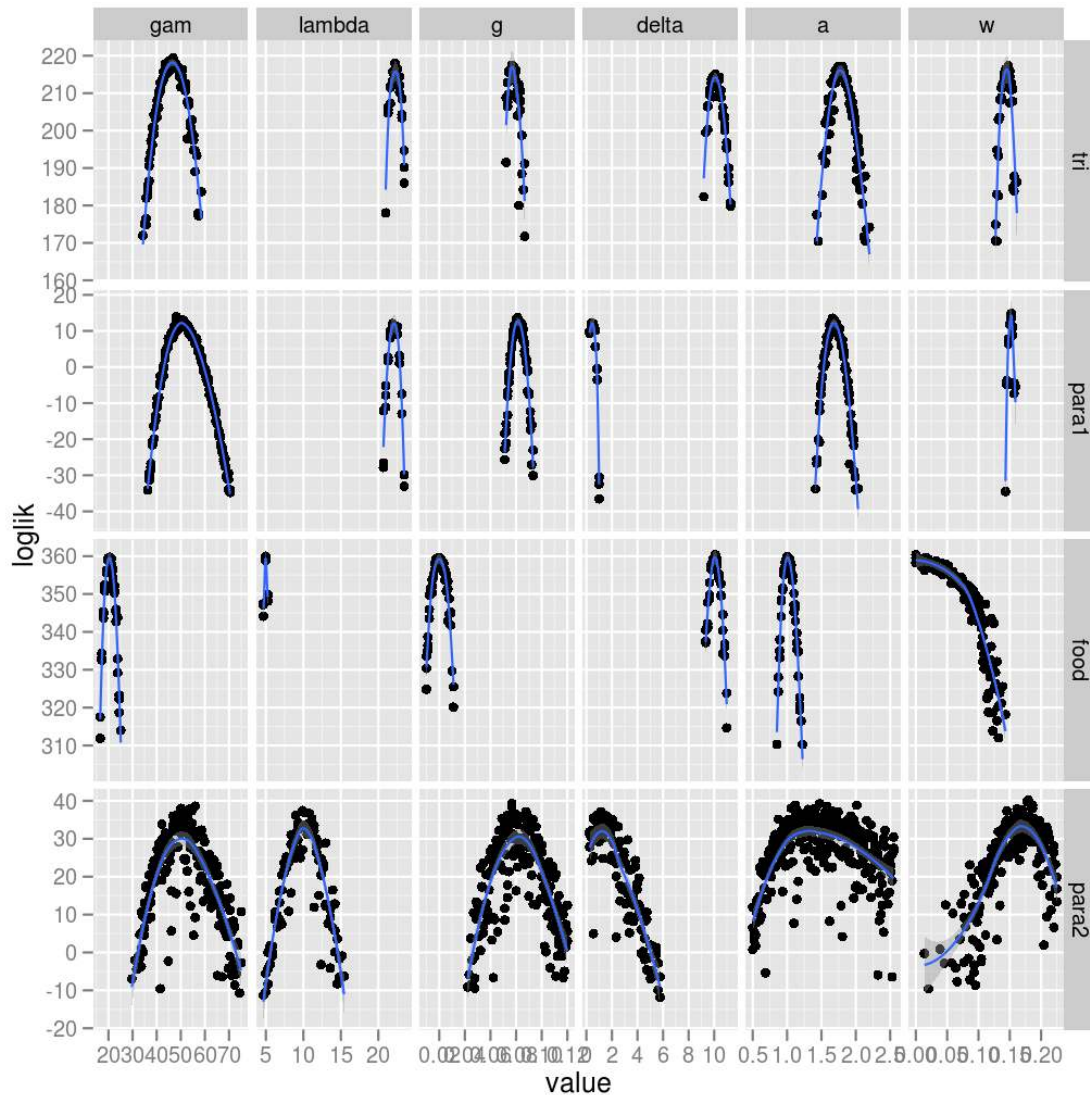
FIGURE 2. Sliced likelihood plots.

Table 3. Parameters to estimate, and limits of uncertainty.

	lower	upper
gam	10	75
lambda	2.5	33
sig.lambda	0.125	7.5
g	0.01	0.12
delta	0.25	15
a	0.5	2.55
sig.a	0.05	1.5
w	0	0.225