

# Package ‘pompExamples’

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**Type** Package

**Title** Additional POMP Examples

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**URL** <http://github.com/kingaa/pompExamples>

**Description** Provides more 'pomp' examples.

**Depends** R(>= 3.1.0), stats, graphics, pomp(>= 1.5.3)

**Suggests** plyr, reshape2, magrittr, ggplot2

**LinkingTo** pomp

**License** GPL (>= 2)

**LazyData** true

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**BugReports** <http://github.com/kingaa/pompExamples/issues>

**Collate** attach.R

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budmoth

*Larch budmoth model POMP with real and simulated data.***Description**

`pompExample(budmoth.sim)` constructs a `pomp` object containing the larch budmoth model and simulated budmoth density, parasitism rate, and food quality (needle-length) data. Four datasets, representing four distinct parameter regimes, are available.

The model has three state variables:

1.  $Q_t$  (measure of food quality on  $[0, 1]$ )
2.  $N_t$  (budmoth density)
3.  $S_t$  (fraction of budmoth larvae infected with parasitoids)

There are three observables:

1.  $\hat{Q}_t$  (needle length)
2.  $\hat{N}_t$
3.  $\hat{S}_t$

**State process**

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

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

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

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

Note:  $X$  is  $\text{LogitNormal}(\mu, \sigma)$  if  $\text{logit}(X)$  is  $\text{Normal}(\mu, \sigma)$ .

The inverse of logit is `expit`. **R** functions `logit`, `expit`, `rlogitnorm`, `dlogitnorm` are defined in **pompExamples**.

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

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

$$N_t = \lambda_t N_{t-1} (1 - S_{t-1}) \exp \{ -g N_{t-1} - \delta (1 - Q_{t-1}) \}$$

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

**Measurement process**

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

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

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

$$\hat{S}_t \sim \text{LogitNormal}(\text{logit}(u S_t), \sigma_S)$$

**Examples**

```
## three regimes, high and low noise regimes for parasitism and tritrophic
bm <- pompExample(budmoth,envir=NULL)
plot(bm$food)
plot(bm$para1)
plot(bm$para2)
plot(bm$tri)
```

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lavine2013*POMP model for pertussis in Copenhagen*

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**Description**

A pomp object encoding the model and data from the Lavine et al. (2013) paper on pertussis in Copenhagen.

The data consist of weekly pertussis case reports from 1900 through 1937.

The model is the “SIRW” model described in the paper. The pomp object includes parameters at the maximum likelihood point estimate.

**Author(s)**

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**References**

J.S. Lavine, A.A. King, V. Andreasen, and O.N. Bjørnstad, Immune Boosting Explains Regime-Shifts in Prevaccine-Era Pertussis Dynamics, PLoS ONE, 8:e72086, 2013. DOI: 10.1371/journal.pone.0072086

**See Also**

[pomp-class](#)

**Examples**

```
library(ggplot2)
library(reshape2)
library(magrittr)

pompExample(lavine2013)

plot(lavine2013)
plot(simulate(lavine2013))
```

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parus	<i>POMPs for time series of Parus major population counts from Wytham Wood</i>
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### Description

pompExample(parus) constructs a function that constructs pomp objects implementing each of several population-dynamics models and abundance data from Parus major in Wytham Wood.

The model has one state variable,  $N_t$ , the true abundance. There is one observable,  $\text{pop}_t$ .

The function defined is:

```
parus(proc = c("Gompertz", "Ricker"),
      meas = c("lognormal", "Poisson", "negbin"))
```

### State process

If proc="Gompertz", the state process is the stochastic Gompertz model

$$N_t = K^{1-S} N_{t-1}^S \epsilon_t,$$

where  $S = e^r$  and  $\epsilon_t \sim \text{Lognormal}(0, \sigma)$  i.i.d.

If proc="Ricker", the state process is the stochastic Ricker model

$$N_t = N_{t-1} \exp \left( r \left( 1 - \frac{N_{t-1}}{K} \right) \right) \epsilon_t,$$

where, again,  $\epsilon_t \sim \text{Lognormal}(0, \sigma)$  i.i.d.

### Measurement process

There are three alternative measurement models.

If meas="Poisson", the measurement process is

$$\text{pop}_t \sim \text{Poisson}(N_t).$$

If meas="negbin", the measurement process is

$$\text{pop}_t \sim \text{Negbin}(N_t, \theta),$$

i.e.,  $\text{pop}_t$  has mean  $N_t$  and variance  $N_t + \frac{N_t^2}{\theta}$ .

If meas="lognormal", the measurement process is

$$\text{pop}_t \sim \text{Lognormal}(\log(N_t), \theta).$$

### See Also

vignette("parus")

**Examples**

```
pompExample(parus)
p1 <- parus(proc="Ricker",meas="negbin")
plot(p1)
plot(simulate(p1))

p2 <- parus(proc="Gompertz",meas="lognormal")
plot(simulate(p2))
pf <- pfilter(p2,Np=1000)
```

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