

# bumbl: An R package for modeling growth-switchpoint-decline in bumblebee colony size

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## Software

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## Statement of Need

Bumble bees (*Bombus* spp.) are important pollinators of wild plants and agricultural systems, and many species of bumble bees are in decline (D. Goulson et al., 2008). Bumble bees are social bees, but unlike honeybees their colonies are annual. In early spring, queens emerge, establish nests, and produce offspring that function as workers. Colony size (e.g. number of workers) increases exponentially until the colony switches from growth to reproduction, when males and new queens are produced (Dave Goulson, 2010). After this, the colony size declines as workers die and new queens and males disperse. At the population level, standard generalized linear models (GLMs) are commonly used to estimate and forecast population growth, but these methods are unable to capture the sharp switch point from growth to reproduction of individual colonies. However, the timing of this switch point for individual colonies, as well as growth and decline rates before and after it, has important consequences for population dynamics. Crone & Williams (2016) developed a method to estimate the switch from growth to reproduction by fitting a modified GLM with a switchpoint included. Their method required repeated creation of dummy variables in the data for many values of the switchpoint in order to choose the value of the switchpoint that maximized the likelihood of the modified GLM. This package automates the model fitting process and uses optimization for a more precise estimate of the switchpoint. `bumbl` aims to make this method broadly accessible to bumble bee biologists, and others who are interested in similar growth-switchpoint-decline phenomena.

## Background

Crone & Williams (2016) describe a mathematical model for bumblebee colony growth, switch to reproduction, and decline.

$$W_t = \begin{cases} \lambda^t W_0 & t \leq \tau \\ \lambda^\tau W_0 \delta^{t-\tau} & t > \tau \end{cases}$$

It defines the expected colony weight (or other proxies for size such as counts of workers) over time as having an initial size ( $W_0$ ), a growth rate ( $\lambda$ ), a switch from growth to decline at time  $t = \tau$ , and a rate of decline ( $\delta$ ) after the switch to reproduction. This can be then be log-linearized and fit as a single model by creating a variable  $x$  that is 0 when  $t \leq \tau$  and equal to  $t - \tau$  when  $t > \tau$

$$\ln(W_t) = \ln(W_0) + \tau \ln(\lambda) + x \ln(\delta)$$

**Table 1:** Data frame output by the `bumb1()` function showing estimates of switchpoint ( $\tau$ , in weeks), estimated initial size ( $\log N_0$ ), growth rate ( $\log \lambda$ ), decay rate (decay), and maximum size ( $\log N_{\max}$ )

colony	converged	tau	logN0	logLam	decay	logNmax
104	TRUE	6.42	3.44	0.380	-0.541	5.78
17	TRUE	6.36	3.39	0.407	-0.662	5.83
20	TRUE	7.27	2.79	0.194	-0.345	4.14
24	TRUE	6.23	4.06	0.167	-0.391	5.06

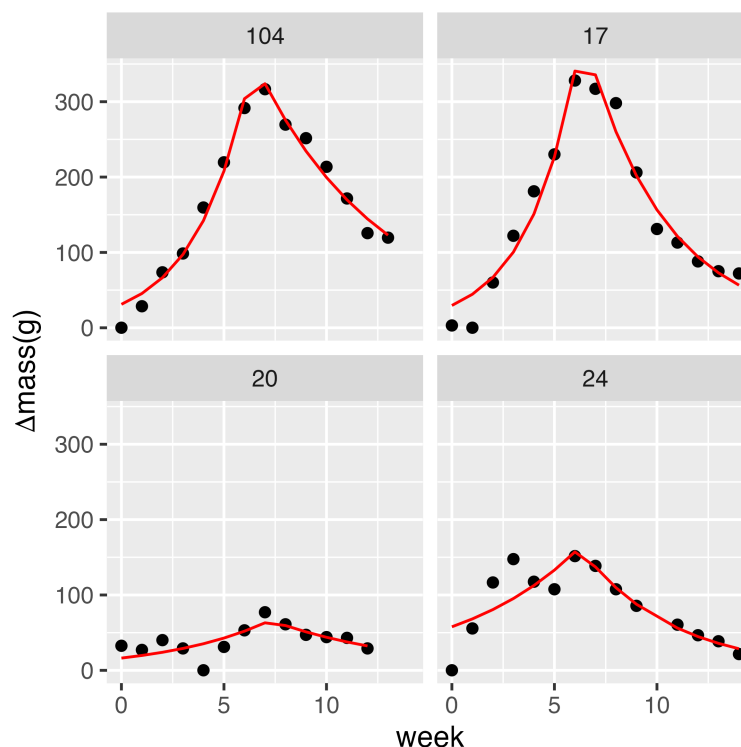
The `bumb1()` function finds a value for  $\tau$  that maximizes the likelihood of this model, then returns the maximum likelihood estimate for  $\tau$  ( $\tau$ ), the estimated initial colony weight on a log scale ( $\ln(W_0)$ ,  $\log N_0$ ), the average colony growth rate on a log scale ( $\ln(\lambda)$ ,  $\log \lambda$ ), the rate of decline after  $\tau$  ( $\ln(\delta - \lambda)$ , decay), and the estimated maximum weight of each colony, on a log scale ( $\log N_{\max}$ ).

The object created by `bumb1()` has methods for both `plot()` and the `autoplot()` function from the `ggplot2` package (Wickham, 2016) to plot the fitted models.

## Example

The package includes a built-in dataset, `bombus`, that contains weekly weights of *Bombus vosnesenskii* colonies originally published in Crone & Williams (2016). Here is an example analysis using just four colonies from this dataset. The output from the `bumb1()` function is a `tibble` with one row for each colony and columns for parameters calculated from the models (Table 1).

Using the `autoplot()` function from the `ggplot2` package on the output object generates a faceted plot with raw data and best fit lines (Figure 1).



**Figure 1:** Results of analysis by the `bumbl()` function as visualized by `ggplot2::autoplot()`. Each facet represents one of the four colonies. Raw data are plotted as points with the red line representing the fitted values for those points.

## Acknowledgments

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