MODEL FOR BIONOMY OF PRIVET SAWFLY (*Macrophya punctumalbum* L.) (Hymenoptera, Tenthredinidae)

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Abstract. The aim of the paper is to construct a model which describes the life expectancy of privet sawfly females (*Macrophya punctumalbum* L.), including additional information on the number of eggs. The data on life expectancy of females and their fertility were obtained in the course of research on the bionomy of the privet sawfly. A variety of discrete distributions to modelling the lengths of life was provided, namely: the Poisson Distribution, the Negative Binomial Distribution and the Poisson-inverse Gaussian Distribution. The analysis the above distributions were applied along with the GAMLSS (Generalized Additive Models for Location, Scale and Shape) and the resulting models were compared with the use of the Global Deviance criterion, the Akaike information criterion and the Schwarz Bayesian criterion. For the best model the expected value and the standard deviation were defined. The profile deviance plot of this parameters, analysis of the residuals, kernel density and Q-Q plot are presented, too. All analyses were performed in R with the GAMLSS package.

Key words. *Macrophya punctumalbum* L., modelling, Negative Binomial Distribution, Poisson Distribution, Poisson Inverse Gaussian Distribution

INTRODUCTION

The privet sawfly (*Macrophya punctumalbum* L.) is a phytophagous species which frequently infests urban greenery. Its larvae feed on various ornamental trees and bushes of the olive family (Oleacea). The species can also cause damage in nurseries of lilacs (*Syrynga* spp.) and privet (*Ligustrum vulgare* L.). The privet sawfly harms plants in the following manner: larvae initially scrape off the pulp, and then bite out round holes in leaves, often leaving damages, consequently severely reducing the aesthetic value of urban greenery. Adult insects bite into leaves, leaving short trails behind and damaging their upper cuticle and mesophyll. The information on the bionomy and harmfulness of this species was presented eg. in the publications by Schwenke [1982], Hoop [1983],

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Pniak [1998] and Piekarska-Boniecka et al. [2008]. The size of damage caused by macrophya is closely related to the number of the larvae feeding there. Their abundance in turn depends on the number of eggs deposited by females. On the other hand, the fertility of females closely correlates with the length of their imaginal life [Piekarska-Boniecka et al., 2008].

The next section describes the data and methods used, as well as provides a more formal definition of the distributions.

The major aim of this paper was developing a model describing the life expectancy of privet sawfly females (*Macrophya punctumalbum* L.).

MATERIAL AND METHODS

The model was developed on the basis of the data on life expectancy of females and the number of their eggs, obtained as a result of studies on the bionomy of this species. The methods and results of those studies can be found in Piekarska-Boniecka et al. [2008]. Research on the life of females and their fertility was conducted in 1982 in the habitat of Poznań, Poland. The experiment involved 30 females which after reaching sexual maturity (it usually lasts 8–9 days) started laying eggs. The fertility of females ranged from 1 to 122 eggs. In total they laid 1652 eggs during the period, with the average fertility 55 eggs per female, and the standard deviation 30.32. The females lived from 4 to 36 days, with 73.3% females' between 7 and 14 days. On the other hand, the mean life expectancy of females was 11 days and the standard deviation was 5.69. The estimation of a model for binomy of the privet sawfly *Macrophya punctumalbum* L. adopted the number of days of life as the observed data (responses), while the number of eggs laid was treated as additional information, the so-called weight.

In this research the Generalized Additive Models for Location, Scale and Shape (GAMLSS) are applied [Rigby and Stasinopoulos 2005)]. The GAMLSS model assumes independent observations y_i for $i = 0,1,2,...n$ with the probability (density) function $p_Y(y_i|\mu_i,\sigma_i,\nu_i,\tau_i)$ conditional on $(\mu_i,\sigma_i,\nu_i,\tau_i)$, a vector of four distribution parameters, each of which is related to the explanatory variables. Further $(\mu_i,\sigma_i,\nu_i,\tau_i)$ are assumed to be the distributional parameters. The first two population distributional parameters μ and σ are usually characterized as location and scale parameters, while the remaining parameters, if any, are characterized as shape parameters, e.g. skewness and kurtosis parameters.

All analyses were performed with R [R Development Core Team 2009] with the GAMLSS package [Rigby and Stasinopoulos 2005].

DISTRIBUTIONS

For this experiment discrete distributions were implemented: the Poisson Distribution, the Negative Binomial Distribution and the Poisson-inverse Gaussian Distribution.

Poisson Distribution. The probability function of the random variable *Y,* which follows the Poisson distribution denoted here as PO(μ) is given by

$$p_Y(y|\mu) = P(Y = y|\mu) = \frac{e^{-\mu}\mu^y}{y!}$$

where $y = 0,1,2,...,\infty$, $\mu > 0$, with $E(Y) = \mu$ [Johnson et al. 2005].

Poisson Inverse Gaussian. The probability function of the Poisson inverse Gaussian distribution, denoted here as PIG(μ,σ), is given by

$$p_Y(y|\mu,\sigma) = \left(\frac{2\alpha}{\pi}\right)^{1/2} \frac{\mu^y e^{1/\sigma} K_{y-1/2}(\alpha)}{(\alpha\sigma)^y y!}$$

where $\alpha^2 = \dfrac{1}{\sigma^2} + \dfrac{2\mu}{\sigma}$, $K_\lambda(t) = \dfrac{1}{2}\int_0^\infty x^{\lambda-1} exp\left\{-\dfrac{1}{2}t(x+x^{-1})\right\}dx$ is the modified Bessel

function of the third kind, $y = 0,1,2,...,\infty$, $\mu > 0$ and $\sigma > 0$. Here $E(Y) = \omega^{1/2}e^\mu$ and $Var(Y) = \omega(\omega - 1)e^{2\mu}$, where $\omega = exp(\sigma^2)$ [Johnson et al., 2005].

Negative Binomial Distribution. The probability function of the Negative Binomial distribution, denoted here as NBI(μ,σ) is given by

$$p_Y(y|\mu,\sigma) = \frac{\Gamma(y+1/\sigma)}{\Gamma(1/\sigma)\Gamma(y+1)}\left(\frac{\mu\sigma}{1+\mu\sigma}\right)^y\left(\frac{1}{1+\mu\sigma}\right)^{1/\sigma}$$

for $y = 0,1,2,...,\infty$, where $\mu > 0$, $\sigma > 0$ with $E(Y) = \mu$ and $Var(Y) = \mu(1 + \mu\sigma)$ [Johnson et al., 2005].

RESULTS AND DISCUSSION

At the first stage of the analysis the above probability distributions were applied along with the GAMLSS and the resulting models were compared with the use of the Global Deviance criterion [Spiegelhalter et al. 2002], the Akaike information criterion [Akaike 1974] and the Schwarz Bayesian criterion [Schwarz 1978]. The results are presented in table 1.

Table 1 shows that the best fit was achieved with the Poisson Inverse Gaussian distribution.

Therefore, for this model thus created the expected value and the standard deviation were then defined (tab. 2). Hence the fitted Poisson Inverse Gaussian model for *Macrophya* data is given by $y \sim$ PIG($\hat{\mu},\hat{\sigma}$) where $\hat{\mu} = exp(2.62157) = 13.75731$ and $\hat{\sigma} = exp(-2.00146) = 0.13514$.

The next step of the analysis was examining the profile deviance plot for μ and σ from the fitted Poisson Inverse Gaussian model (fig. 1). The best estimate of the parameter μ is 13.77. The best estimate of the parameter σ is $\hat{\sigma} = 0.14$, where a 95%

H. Piekarska-Boniecka, I. Siatkowski, J. Zyprych

Table 1. Global Deviance, Akaike and Schwarz Bayesian criteria for Poisson distribution, Poisson Inverse Gaussian distribution and Negative Binomial distribution
Tabela 1. Kryteria odchylenia ogólnego, Akaike i bayesowskie Schwarza dla rozkładów Poissona, odwrotne Poissona i ujemnego binomialnego

Criteria Kryteria	Distributions – Rozkłady		
	Poisson Poissona	Poisson Inverse Gaussian odwrotny Poissona	Negative Binomial ujemny binomialny
Global Deviance Odchylenie ogólne	11390.75	9740.76	9870.43
Akaike Akaike	11392.75	9744.75	9874.43
Schwarz Bayesian Bayesowskie Schwarza	11398.10	9755.46	9885.14

Table 2. Expected value and standard error for Poisson Inverse Gaussian distribution
Tabela 2. Wartość oczekiwana i błąd standardowy dla rozkładu odwrotnego Poissona

Poisson Inverse Gaussian Rozkład odwrotny Poissona	Link function Funkcja łącząca	Estimate Estymacja	SE – Błąd	t value Wartość t
Mu (μ) – wartość oczekiwana	log	2.62157	0.02193	119.53253
Sigma (σ) – błąd standardowy	log	-2.00146	0.01062	-188.47031
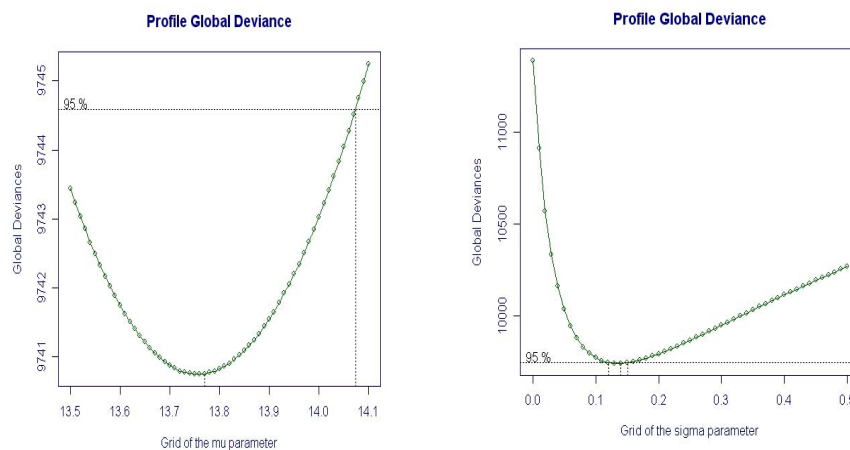
Fig. 1. The profile deviance plot for μ and σ for the fitted Poisson inverse Gaussian model
Fig. 1. Plot dopasowania μ i σ dla rozkładu odwrotnego Poissona

confidence interval is: $\sigma \in (0.121, 0.151)$. Then figure 2 displays the residuals. Panels (a) and (b) plot the residuals against fitted values of μ and against index respectively, whereas panels (c) and (d) provide a kernel density estimate and Q-Q plot for them, respectively.
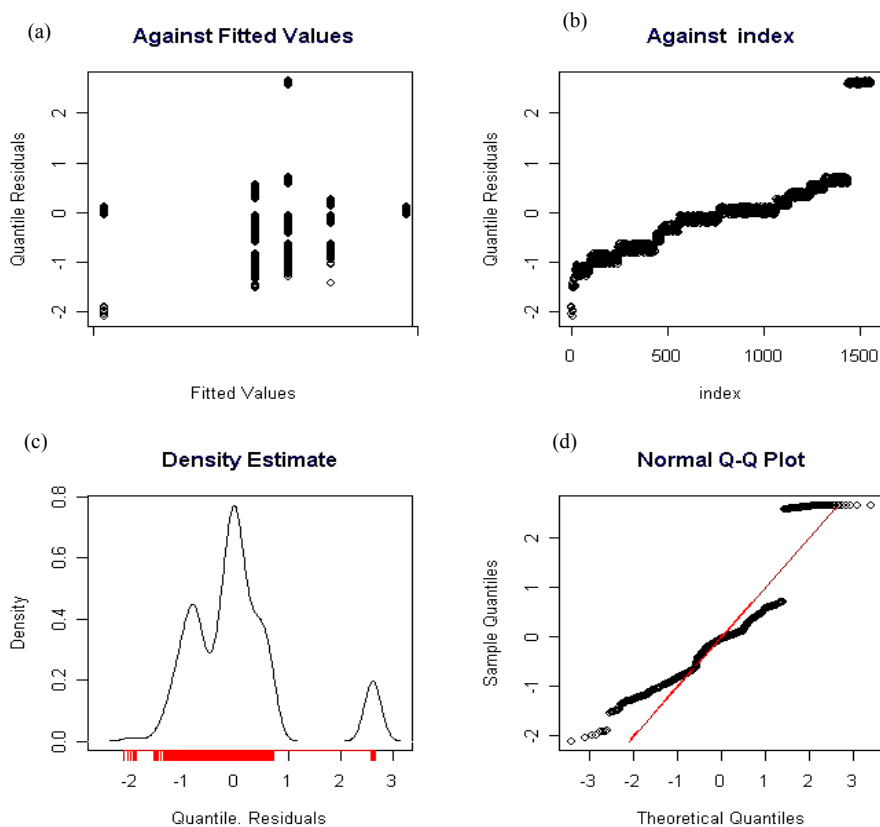
Fig. 2. For Poisson inverse Gaussian model: (a) residuals against fitted values of μ, (b) residuals against index, (c) kernel density estimate and (d) Q-Q plot

Fig. 2. Dla rozkładu odwrotnego Poissona: (a) dopasowanie dla reszt μ, (b) indeks reszt, (c) estymacja funkcji gęstości, (d) plot Q-Q

CONCLUSION

The study of the bionomy of privet sawfly (*Macrophya punctumalbum* L.), a pest of park plants, was conducted at the insectarium of the Department of Entomology, University of Life Sciences in Poznań. The aim of the paper is to define a statistical model for bionomia of the privet sawfly females. As a result of studies it was determined that the best statistical model of the life of privet sawfly females (*Macrophya punctumalbum* L.) is GAMLSS with the Poisson Inverse Gaussian distribution. Some characteristics of this distribution was presented, too.

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MODEL BIONOMII BROSZNICY JESIONÓWKI (*Macrophya punctumalbum* L.) (Hymenoptera, Tenthredinidae)

Streszczenie. Celem prezentowanej pracy jest zaproponowanie modelu statystycznego opisującego długość życia samic brosznicy jesionówki (*Macrophya punctumalbum* L.). Dane na temat długości życia samic i ich płodności zostały otrzymane w trakcie badania nad bionomią. Do modelowania długości życia z wykorzystaniem informacji o ilości składanych jaj zastosowano uogólniony addytywny model dla lokalizacji, skali i kształtu (GAMLSS) dla trzech rozkładów dyskretnych: rozkład Poissona, rozkład odwrotny Poissona oraz rozkład ujemny binomialny. Otrzymane modele porównano, stosując kryterium ogólnego odchylenia, kryterium Akaike i kryterium bayesowskie Schwarza. Uzyskano w ten sposób informacje, że najlepiej opisującym modelem badany problem jest model z rozkładem odwrotnym Poissona. Ostatnim etapem badań była estymacja wartości oczekiwanej i błędu standardowego dla najlepszego modelu oraz analiza tych wartości za pomocą wykresu dopasowania reszt dla wartości oczekiwanej, wykresu indeksów reszt, wykresu funkcji gęstości oraz wykresu typu Q-Q. Wszystkie analizy zostały wykonane za pomocą platformy obliczeniowej R z wykorzystaniem pakietu GAMLSS.

Słowa kluczowe: *Macrophya punctumalbum* L., modelowanie, rozkład Poissona, rozkład odwrotny Poissona, rozkład ujemny binomialny