Article

Latent GLM Tweedie Distribution in Butterflies Species Counts

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Abstract: Background: The diversity of butterflies relies on the accessibility of food plants and the quality of their habitat. Methods: The purpose of this study was to evaluate the diversity butterfly based on latent GLM in 3 different Habitat. At the same time, we perform the step construction of Tweedie Distribution both in species levels and individual level. Results: Our finding can be shown by accuracy AIC, AICc, and BIC. Conclusions: In modelling with latent glm tweedie it can conclude that the our model is suitable for use at the species or individual level.

Keywords: tweedie; GLM; species counts; butterfly

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1. Introduction

Research on ecology is always interesting to study, especially in species modelling. The scope of the most essential Ecological studies is ideally about changes in the population of a species at different time vulnerable, the transfer of energy and matter of living things to one another, as well as the factors that influence and the occurrence of interrelationships between living things (animals, plants, and microorganisms, and The environment is a unity of space with all objects, power, conditions, and living things, as well as behaviours that affect the survival and well-being of humans and other living things. Ecology has a variety of levels, ranging from the smallest organisation or cell to large scale such as biosphere.Based on the composition of the types of organisms studied, Ecology can be divided into autecology and synecology. Aukelogi discusses the study of individual organisms or individual species whose emphasis is on the histories of life and behaviour in adjusting to the environment, for example, studying the life history of a species, and its adaptation to the environment. Meanwhile, Synecology discusses the study of groups or groups of organisms as a unit. For example, studying the structure and composition of plant species in swamp forests, studying the distribution patterns of wild animals in natural forests, tourist forests, or national parks.

Ecosystems are dynamic, continually changing, can be fast, or can be for thousands of years. The area of the ecosystem varies significantly from small to large and large. The diversity of animals in Indonesia is high so that it is also known as Megabiodiversity. Insect is the most dominant fauna group in almost every habitat type, both in terms of diversity, abundance, and its role in the ecosystem. One member of Insecta who is very diverse and has an important role in the ecosystem is the butterfly. Butterflies are diurnal insects belonging to the Order Lepidoptera. To date, there are at least 28,000 species of butterflies that have been described worldwide and nearly 80% are found in the tropics [1] . Indonesia as a mega-biodiversity country has a high level of endemic species of butterflies. The number of Indonesian butterfly species is estimated at 1,600 species. This number is only less than Brazil and Peru which have approximately 3,000 species [2].

Butterflies have a very important role in the ecosystem. This group is one of the important pollinators that help the process of pollinating various species of flowering plants. In addition to helping pollination, butterflies also play a role in increasing plant genetic variation. This is because butterflies can carry pollen from one individual plant to another so that cross-pollination can occur. In the food network, butterflies are a source of food for various predatory fauna located at higher trophic levels such as birds, reptiles and amphibians. Butterflies also have important economic value. Larvae from several species of butterflies can produce high economic value silk. Many species of butterflies have beautiful colors and shapes so that many are used as a tourist attraction. Besides having important ecological and economic functions, butterflies are also a bio-indicator of the balance of an ecosystem. Butterflies are very sensitive to changing environmental conditions so they are often used as key indicators in monitoring changes in ecosystems. In addition, butterflies can also be used as indicators to assess the success of ecosystem restoration [3].

The existence of butterflies is greatly influenced by the condition of the habitat where they live. In general, the diversity and abundance of butterflies tend to be high in locations with diverse vegetation structures. Butterflies also tend to prefer open spaces that have water sources [4].

One of the diversity that is classified as high is a butterfly. The existence of butterflies is strongly influenced by the carrying capacity of existing habitats including physical and biotic components. This causes the butterfly is one of the insects of the order Lepidoptera which has a beautiful shape and colour pattern with wings covered with varying fine scales. Butterflies are one type of insect that has essential value as pollinators and prey for insectivorous animals [5]. Butterflies are one of the pollinators in the process of flower fertilisation. Ecologically this has contributed to maintaining the balance of the ecosystem so that changes in diversity and population density can be used as an indicator of environmental quality [6]. Butterflies are fascinating insects, colourful, and present everywhere. The larvae are clustered on a host and the transformation of their larvae into butterflies is very easily observed.

On the other hand, some species species that are rarely found actually prefer dense forest habitat that has not been disturbed. This pattern of population distribution makes butterflies very interesting to be used as statistical object modeling species counts. One of the main problems in modeling species counts is that there are often quite a lot of data with zero values and there are also latent variables outside the observation that also influence so that the statistical method that can be used is very limited. In this work we will perform latent glm with laplace approximation [7] and tweedie distribution to see the diversity of butterfly in three different habitat.

2. Materials and Methods

Tweedie Latent GLM

In general, statistical modelling is abstract which is a simple concept from a theory that is generally used in the scientific family, research technology on the relationship between real phenomena is the basis of the goals of science and plays a vital role in everyday life. Nowadays regression analysis is a popular tool for finding out these relationships. Regression analysis is one method for determining the causal relationship between one variable and another. The cause variable is called the independent variable, the explanatory variable or the X variable [8]. While the affected variable is known as the affected variable, the dependent variable, the dependent variable, the response variable or the Y variable. Estimated regression curves are used to explain the relationship between explanatory variables and response variables. The most commonly used approach is the parametric approach. The assumption underlying this approach is that the regression curve can be represented by a parametric model [9].

In parametric regression, it is assumed that the shape of the regression curve is known based on theory, previous information, or other sources that can provide detailed knowledge. If the model of the parametric approach is assumed to be correct, then the parametric estimation will be very efficient. However, if it is wrong, it will lead to misleading data interpretations. In addition, parametric models have limitations in predicting unexpected data patterns. If the assumptions of the parametric curve are not met, then the regression curve can be assumed using a regression model from the nonparametric approach. The nonparametric approach is a model estimation method which is based on an approach that is not bound by certain assumptions of the regression curve shape. The classical regression analysis has the requirement to fulfil linearity assumptions and the assumption of normally distributed data. This analysis aims to determine the direction of the relationship between the independent variable with the dependent variable whether positive or negative as well as to predict the value of the dependent variable if the value of the independent variable has increased or decreased. The data used is usually interval or ratio scale. If the number of independent variables is more than one, multiple linear regression analysis is used. In practice in the field, the data found often does not meet the assumptions required by classical linear regression. The generalized linear model (GLM) is an extension of the linear regression model assuming the predictor has a linear effect but does not assume a certain distribution of the response variable and is used when the response variable is a member of an exponential family.

Natural exponential families (NEFs) are an essential part of theoretical statistics. For several decades, they have been studied and classified.. Many authors then looked at their classification according to the form of their variance function (i.e. the writing of their variance as a function of the mean parameter). For example, [10], [11], [12] who gave a complete description of all the NEFs of R d of quadratic variance function. A very particular case of these families, when they generate an exponential dispersion model, are those of Tweedie models. These laws, introduced by Tweedie (1984) [13] [14] The variance function is very specific and is given by equation (1):

$$V(m) = m^p \tag{1}$$

With $p \in]-\infty, 0] \cup [1, +\infty$ [.Tweedie laws are involved in a significant number of fields of application. They are indeed linked, by the relation (1.1), to the law of Taylor's power. The latter appears in both biology and physics and states that the power of the average gives the empirical variance. In particular, the links between Tweedie models and Taylor's power law in physical science are brought to light [15]. To make these laws accessible to practitioners, [16]) proposed a package for the R software [17] who proposed a method for estimating the densities of Tweedie laws, which are not explicable for the most part, by Fourier inversion.

We will now introduce the family of Tweedie laws. This family contains some well-known laws such as the normal law, the gamma law, the law of Poisson or the inverse Gaussian law. To begin, put *d = 1*. We recall that for $\lambda > 0$, the NEFs ($\mu\lambda$) generates the family of laws $ED^*(\theta, \lambda)$ called the exponential dispersion model and whose elements are written

$$exp[\theta x - \lambda k_\mu(\theta)]\mu_\lambda d(x) \tag{2}$$

This family of laws is called additive. Indeed, it is easy to see that for every $\lambda_1, \lambda_2, \ldots, \lambda_n$ of Λ_μ

$$ED^*\left(\theta, \sum_{i=1}^{n} \lambda_i\right) \overset{\iota}{=} \sum_{i=1}^{n} ED^*(\theta, \lambda_i), \tag{3}$$

where $\overset{\iota}{=}$ = designates equality in law. The corresponding family $ED(m, \sigma^2) \overset{\iota}{=} \frac{1}{ED^*(\theta.\lambda_i)}$ with m = τ (θ) and $\sigma^2 = \frac{1}{\lambda}$ is called the exponential reproductive dispersion model.

Generalized Linear Models (GLM) aims to determine the causal relationship, the effect of independent variables on the dependent variable ([18], [19]). The superiority of GLM compared to ordinary linear regression lies in the distribution (curve shape) of dependent variables [20]. Variable dependent on GLM is not socialized with a normal distribution (symmetrical bell curve), but distributions that belong to an exponential family, namely; Binomial, Poisson, Negative Binomial, Normal, Gamma, Gaussian Inverse. In GLMs, the distribution of responses can be of various types, which are included in the Exponential Family. A random variable Y, included in the distribution that is incorporated in the Exponential Family, if it has a form

$$f_Y(y: \theta, \phi) = \exp\{(y\theta - b(\theta))/a(\phi) + c(y, \phi)\} \tag{4}$$

with certain functions $a(.)$, $b(.)$ and $c(.)$. If ϕ is known, then the form of equation (4) is an Exponential Family with canonical parameters θ.

The GLLVM model is generally used to model the type of data where the response variable is large enough [21], $p > n$ where p is the number of respondent variables and n is the number of observations [22]. If we assume that the response variables are independent of each other, then we can do the glm analysis as usual individually or can jointly use the manyglm () function available in the mvabund package [23]. So that the regression equation will be obtained as many as p pieces. However, the fact is in ecology that these response variables are not mutually exclusive. To be able to model the types of correlated responses we need a combined model and one of them is to introduce random effects into the model [24], [25],[26]. In general, the GLLVM model is defined as follows:

$$g(\mu_{ij}) = \eta_{ij} = \tau_i + \beta_{0j} + \mathbf{x}^\mathbf{T}\boldsymbol{\beta}_j + u_i^T \lambda_j \tag{5}$$

Each butterfly goes through four phases in its life cycle which starts from the egg, caterpillar, pupa and imago stages. The change from caterpillar to cocoon and into butterfly involves a major change in the appearance of the butterfly called metamorphosis [27]. Butterfly classification and diversity, namely:

- Order: Lepidoptera
- Suborder: Rhopalocera
- Superfamily: Hesperioidea and Papilionoidea
- Family Hesperioidea: Hesperidae
- Family Papilionoidea: Papilionidae, Pieridae, Lycanidae, Nymphalidae

The data obtained are secondary data from the Cangkringan Resort Mount Merapi National Park area. The main focus of this paper is for modeling using the tweedie distribution.

Table 1. Species Counts

Habitat A (Flowing Water)		**N**	**Habitat B (Puddle)**		**N**	**Habitat C (No Watter)**		**N**
Lampides boeticus	Lycanidae	3	*Jamides tiglath*	Lycanidae	4	Leptosia Nina	Lycanidae	1
Jamides tiglath	Lycanidae	1	*Lampides boeticus*	Lycanidae	4	Euplea Eunice	Nymphalidae	2
Jamides celeno	Lycanidae	3	Danaus chrysippus	Nymphalidae	1	Junonia Hedonia	Nymphalidae	5
Neptis clinioides	Nymphalidae	1	Euploea Mulciber	Nymphalidae	5	Hypolimnas Bolina	Nymphalidae	3
Junonia almana	Nymphalidae	20	Hypolimnas Bolina	Nymphalidae	5	Ideopsis Vulgaris	Nymphalidae	1
Athyina nefre	Nymphalidae	1	Ideopsis Vulgaris	Nymphalidae	1	Troides Helena	Papilionidae	1
Euploea eunice	Nymphalidae	2	Junonia orithya	Nymphalidae	4	Calopsilia pomona	Pieridae	43
Ideopsis vulgaris	Nymphalidae	1	Catopsilia pomona	Pieridae	61	Eurema sp.	Pieridae	36
Euploea climena	Nymphalidae	5	Eurema sp.	Pieridae	17			
Danaus chrysippus	Nymphalidae	3						
Neptis hylas	Nymphalidae	5						
Euploea mulciber	Nymphalidae	1						
Papilio helenus	Papilionidae	2						
Pachliopta aristolochiae	Papilionidae	1						
Papilio memnon	Papilionidae	1						
Graphium sarpedon	Papilionidae	1						
Papilio demoleus	Papilionidae	1						
Graphium agamemnon	Papilionidae	1						
Papilio polytes	Papilionidae	1						
Eurema sp.	Pieridae	54						
Catopsilia pomona	Pieridae	63						

RESULTS AND DISCUSSION

Species Level

The highest abundance of individuals and species of butterflies in Habitat A (flowing water) is thought to be due to the suitable location for life, in addition to that available sunlight, so the amount of vegetation that grows is different. That the number of species is sufficiently affected by the canopy cover and intensity of sunlight. Variation of canopy cover provides a suitable place for butterflies so that species of butterflies in locations that have water become more diverse. At the same time, in order to survive, the butterfly must drink. Flower nectar is a drink that butterflies like because it contains sugar which can be used as an energy source. In addition to nectar, some butterflies also like to drink water vapour from sand and water vapour from rotted fruit. To form a latent model in this paper using the Gaussian inverse. However, in other studies using the Poisson distribution. One assumption in the Poisson distribution is that the mean and variance have the same value (equidispersion) [28]. The mean and variance of a data count are often not the same whether the mean is higher than the variance (overdispersion) or the mean is smaller than the variance (underdispersion). In other words, the assumption of equidispersion is often violated. Chopped data often shows a quite large variance because it contains a lot of zero values (extra zeros) or a distribution that is greater than the values in the data or both. Overdispersion cases if ignored can lead to underestimation of the estimated standard error, which can result in errors in decision making some hypothesis testing. For example, a predictor variable has a significant effect, but in reality it has no significant effect. Based on Table 2, the intercept, theta latent values and parameters of the dispersion are obtained.

In this paper, we will use the tweedie distribution or also said that the Gaussian inverse distribution is a continuous distribution and is a family of exponential distributions. This distribution has one mode and has curves that tilt to the right, sometimes even the right tail curve of this distribution is very long. The opportunity density function is as follows:

$$f(v;\delta,\tau) = (2\pi\tau v^3)^{-\frac{1}{2}} \exp -\frac{(\delta v-1)^2}{2\tau v}, v \geq 0, \delta > 0, \tau > 0 \quad (6)$$

The parameters δ and τ are known as shape parameters. The expected value and variance of the Gaussian inverse distribution are $E(V) = \frac{1}{\delta}$and $Var(V) = \frac{\tau}{\delta^3}$.. Skewness and kurtosis of the Gaussian inverse distribution are $3\sqrt{\frac{\tau}{\delta}}$ and $\frac{15\tau}{\delta}$, respectively. This distribution is named Gaussian inverse by Tweedie because its cumulative generating function is the opposite of the Gaussian distribution. To evaluate the models we use AIC, AICc, and BIC The AIC is defined as

$$AIC = 2k - 2\ln(l) \quad (7)$$

and its corrected form for small sample sizes,

$$AIC_c = AIC + \frac{2k(k+1)}{N-k-1} \quad (8)$$

as well as its Bayesian alternative,

$$BIC = -2\ln(l) + \ln(N) * k \quad (9)$$

where l denotes the number of parameters and k denotes the maximized value of the likelihood function. For model comparison, the model with the lowest AIC score is preferred. The *absolute* values of the AIC scores do not matter. These scores can be negative or positive.

Table 2. Parameter Estimation GLLVM

	Intercept	theta.LV1	Dispersion parameters
Lycanidae	1.562320	-0.4909974	6.893565e-01
Nymphalidae	2.877803	-0.6032400	3.188624e-06
Pieridae	4.498928	-0.1745962	5.485229e-02
Papilionidae	0.513864	-1.0766610	1.871521e+00

Then also obtained values from species ordination based on habitats A, B, and C. It can be seen clearly in Table 3 and Figure 1 that the difference in the number of species in this habitat for habitat A has negative ordinance compared to B and C. It can be assumed that statistically clear differences the number of butterflies at location A with B and C.

Table 3. Habitat Ordination

Habitat	Ordination
Habitat A (Flowing Water)	-1.3025632
Habitat B (Puddle)	0.1744208
Habitat C (No Watter)	1.1281974

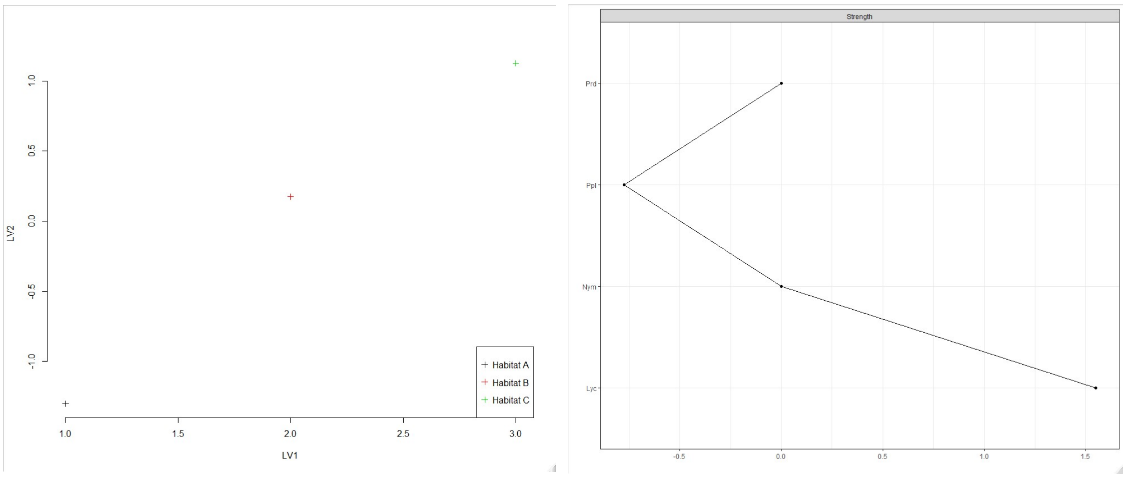

Figure 1. Ordination Habitat (left), Strength Species (right)

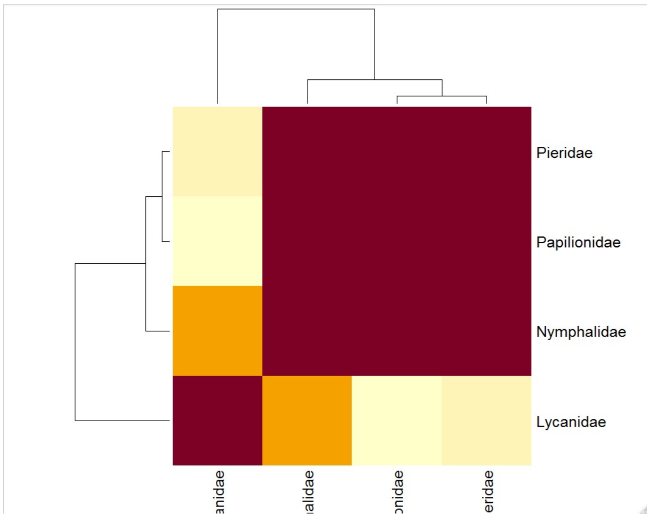

Figure 2. Heatmap Based on Species

In Figure 1 the right can be seen the centrality of this species and can be seen that *Lycanidae* is more dominant than *Papilionidae*. *Lycanidae* can be found in all habitats A, B, and C. While *Papilionidae* is only found in specific habitats. To evaluate the model, log-likelihood is obtained, AIC 92.22747, AICc 61.02747, BIC 81.41082.

Individual Level

Then we analysis at an individual level because this information is crucial considering the different conditions of each habitat. For example, in location C, there are a large number of *Calopsilia Pomona*, but that cannot be obtained at other locations. We also use the Tweedie distribution to get LV parameters and disperse parameters which can be seen in Table 4

Table 4. Individual Butterflies Counts

No	**Name**	**Hab A**	**Hab B**	**Hab C**	**Intercept**	**theta.LV1**	**Dispersion parameters**
1	*Lampides boeticus*	3	4	0	0.1918613	1.824132919	0.0000000
2	*Jamides tiglath*	1	4	0	0.1196806	1.390784277	0.0554530
3	*Jamides celeno*	3	0	0	-22.3256231	36.40333227	0.0000000
4	*Neptis clinioides*	1	0	0	-19.3633553	30.06868128	0.0001116
5	*Junonia almana*	20	0	0	-30.3595546	51.85249351	0.0000000
6	*Athyina nefre*	1	0	0	-20.8599137	32.40316633	0.0001140
7	*Euploea eunice*	2	0	0	-21.1510486	33.900739	0.0000000
8	**Ideopsis vulgaris**	1	1	0	-1.4365198	2.456160331	0.0000028
9	**Euploea climena**	5	0	0	-26.2246992	43.26507266	0.0000000
10	**Danaus chrysippus**	3	1	0	-3.6491945	7.324644478	0.0000000
11	*Neptis hylas*	5	0	0	-24.1491405	40.03382187	0.0000000
12	**Euploea mulciber**	1	5	0	0.2214806	1.548258021	0.2973333
13	**Papilio helenus**	2	0	0	-23.0294663	36.88284706	0.0000000
14	**Pachliopta aristolochiae**	1	0	0	-20.2489731	31.45031725	0.0001126
15	**Papilio memnon**	1	0	0	-19.6198712	30.46891488	0.0001117
16	**Graphium sarpedon**	1	0	0	-15.4576646	23.96637522	0.0001165
17	**Papilio demoleus**	1	0	0	-17.4575418	27.09332625	0.0001142
18	**Graphium agamemnon**	1	0	0	-19.9752136	31.02327873	0.0001121
19	*Papilio polytes*	1	0	0	-17.4013016	27.0054651	0.0001143
20	*Eurema sp.*	54	17	36	3.5768664	0.008946943	0.1708117
21	*Catopsilia pomona*	63	61	0	2.9489731	2.022838075	0.0029583
22	**Hypolimnas Bolina**	0	5	3	0.9453342	-0.10337632	0.4775907
23	**Junonia orithya**	0	4	0	-0.3713151	1.998601509	2.1260480
24	**Leptosia Nina**	0	0	1	-23.0476328	-12.07378698	0.0000532
25	**Euplea Eunice**	0	0	2	-22.226489	-12.0148352	0.0000000
26	**Junonia Hedonia**	0	0	5	-24.6583221	-13.77211016	0.0000000
27	**Troides Helena**	0	0	1	-24.0393129	-12.59557446	0.0000525
28	**Calopsilia pomona**	0	0	43	-33.6748127	-19.62356859	0.0000000

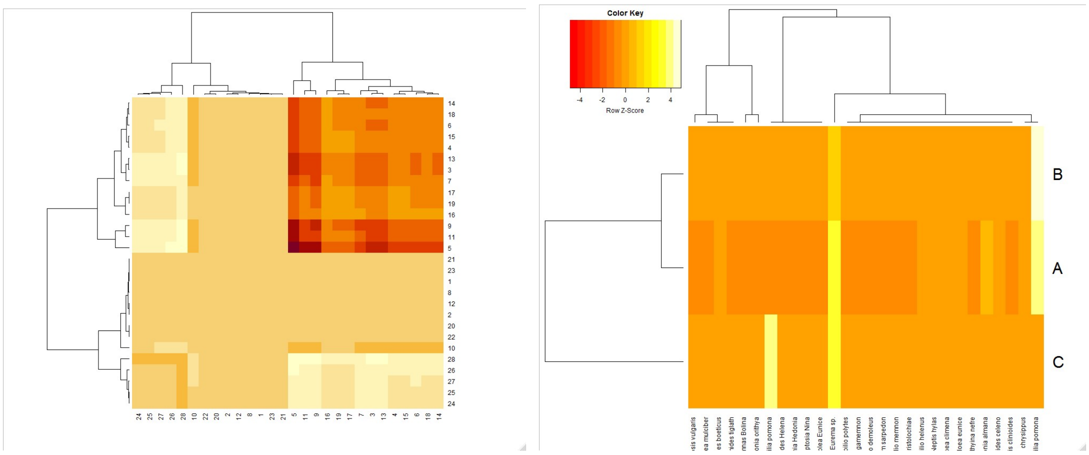

Figure 3. Heatmap Based on Individual (left) and location (right)

With this simulation we get the negative AIC: -2.2518e+16, AICc: -2.2518e+16, BIC: -2.2518e+16, and log-likelihood 1.1259e+16. This is because our likelihood is a continuous probability function, it is not uncommon for the maximum value to be greater than 1, so we calculate the logarithm of the value, we can get a positive number and (if that value is greater than *k*) get a negative AIC. At the same time, in figure 4 we can see the strength and correlation in individual level

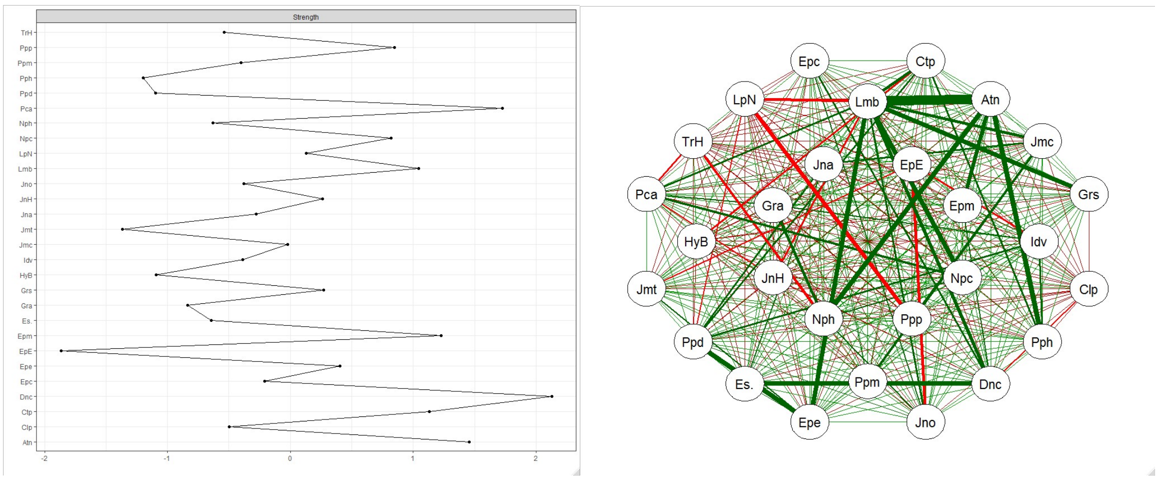

Figure 4. Strength Individual (left) and Correlation (right)

Discussion

The species richness of butterflies in habitat A is a different s when compared to Habitat b and habitat C. The high species richness in Habitat A is thought to be because the area is overgrown by nectar-producing flowering plants such as *Melastoma malabatricum*, and *C. rutidosperm, banyan (Ficus sp.), Caesalpinia pulcherrima*, and *Plumeria sp.* Habitat modification is one thing that must be considered to maintain the abundance of butterflies [29] assert that butterfly abundance will be higher in areas with moderate disturbance, where disturbance creates forest gaps. Moreover, forest encourages plant growth due to incoming sunlight, and this plant growth will provide a food source for animals. This causes the abundance of species to increase. According to [30] treated forests and grasslands are two of several habitats Which has the highest number of butterflies. The abundance of butterfly species is closely related to the abundance of plant food sources. A consistent species found in all habitat types is *Eurema sp.* However, The only species found in Habitat C are *Leptosia Nina, Euplea Eunice, Junonia Hedonia, Troides Helena,* and *Calopsilia Pomon*. In modelling with latent glm it can be seen that the model is suitable for use at the species or individual level. Butterflies increase the opening of their wings to get sunlight and increase body temperature by sunbathing in cold weather. When this cold weather the butterflies always spread their wings to dry so that they can fly lightly and easily, whereas if the body's temperature rises the butterflies will find shelter. The range of temperatures that can support the life of a butterfly is between 21°C - 34°C.

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