New confidence interval methods for Shannon index

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Abstract

1. Several factors affect the structure of communities, including biological, physical and chemical phenomena, impacting the quantification of biodiversity, measured by diversity indexes such as Shannon’s entropy. Then, once a point estimate is obtained, confidence intervals methods such as the bootstrap ones are often used. These methods, however, can have different performances, which many authors have revealed in the last decade. Furthermore, problems such as the asymmetry of the distribution of estimates and the possibility of Shannon’s diversity index estimator bias can lead to incorrect recommendations to the research community. Thus, we propose two methods and compare them with seven others using their performances to face these problems.

2. The first idea uses the credible interval (CI) method to build a bootstrap confidence interval. The second one starts by correcting the bias and then uses an asymptotic approach. We considered 27 community structures representing scenarios with high dominance, high codominance or moderate dominance, the number of species equal to 4, 20 or 80 and 10, 50 or 500 individuals to compare their performances. Then, we generated 1000 samples, built 95% confidence intervals, and calculated the percentage of times they included the
community diversity index (coverage percentage) for each community structure.

3. Our results showed the feasibility of both proposed methods to estimate Shannon’s diversity. The simulation study revealed the bootstrap-t technique had the best performance, i.e., best coverage percentage, compared with the other methods. Finally, we illustrate the methodology by applying it to an original aphid and parasitoid species dataset.

4. We recommend the bootstrap-t when the community structure analysed is similar to the simulated ones. Also, the methods provided high performance for the high dominance scenarios.

**Keywords**: Diversity, statistical inference and bootstrap methods.

1 **Introduction**

The study of biodiversity involves interdisciplinary approaches aiming to understand the variety of life (Noss, 1990; O’Connor et al., 2020). These studies resulted in several applications including biological control and pollination in agriculture to a clear notion of the ecosystem services that biodiversity promotes (Altieri, 1999; Godfray, 1994; Goodell, 2009; Mitchell and Onstad, 2014; Williams et al., 1996). Another aspect that highlights the importance of biodiversity is the comparison of impacts on natural communities, such as human impacts and others (Gotelli and Colwell, 2001; Magurran, 2004, 2005, 2010; McGlinn et al., 2019). Researchers can also obtain measures of biodiversity in different scales depending on the study. For example, a local scale (α diversity) comprehends a community in a specific habitat (Gotelli and Colwell, 2001; Magurran, 2004). Also, a regional scale (β diversity) comprise the variety of species in different geographic areas. Finally, the landscape scale (γ diversity) aim to obtain an overall species diversity within geographic areas (Levin, 2013; Magurran, 2004; Ricklefs, 2016).

The most common indexes used in these different scales comprise Shannon’s, Simpson’s, and Chao’s index (Magurran, 2004), which appears in many studies as measures of biodiversity. Among these methods, to study local diversity (α), Shannon’s and Pielou’s indices are the
most popular ones to obtain information about the diversity and evenness of natural communities (Magurran, 2004). A single index focuses on some aspects of biodiversity. For example, Shannon’s entropy and Pielou’s index helps to understand some components of a community related to dominance, richness, diversity and evenness (Levin, 2013; Magurran, 2004; Zar, 2009). However, simply computing these statistics based on a sample is not enough to obtain accurate information in a location.

For that, several methods aim to estimate such indices varying in scope from points to interval estimates. Among the literature of biodiversity, the usage of interval estimation is a common task including different methods, such as parametric or non-parametric techniques (Carvalho et al., 2019; Davison and Hinkley, 1997; Kamiyama et al., 2020; Naranjo-Guevara et al., 2020; St Laurent et al., 2020; Willett et al., 2020). On the non-parametric approach, the bootstrap techniques are the most used for this task comprehending multiple confidence interval methods such as bootstrap t, bias corrected-accelerated, bias-corrected percentile, percentile, standard percentile and empirical corrected methods (Fritsch and Hsu, 2000; McDonald et al., 2010; Pesenti et al., 2016; Pla, 2004; Scherer et al., 2013). Previous studies evaluated the performance of the bootstrap confidence interval methods to suggest a recommendation, mainly to estimate Shannon’s diversity, for biologists that aim the use a quantitative approach to study biodiversity (Pesenti et al., 2016; Pla, 2004).

To evaluate the performance of confidence interval methods these studies performed simulations using different community structures. These structures have distinct species abundance distributions, number of species, and individuals in a certain location. Thus, they consider the index calculated on these communities as the parameters target of estimation. Moreover, by taking samples from them, it is possible to obtain statistics, such as width and coverage percentage showing the performance of each confidence interval method. The first statistic is the difference between upper and lower interval limits and the other is the number of times that the interval contains the parameter divided by the total number of samples. However, the restricted number of community structures simulated, can affect the method recommendations because, as
Hutcheson (1970), Shenton et al. (1969), Pla (2004) and Zhang and Zhang (2012) mentioned, the species abundance distribution affect the bias of Shannon’s index.

Among these studies, there are several results suggesting gaps in the literature that requires attention. These gaps include the creation of simulation studies with communities biologically meaningful. Also, more studies focused on the bias of Shannon’s index (Hutcheson, 1970; Pla, 2004; Shenton et al., 1969; Zhang and Zhang, 2012), and alternative methods that deal with the fact that bootstrap confidence interval methods are inadequate for situations where there is asymmetry and multimodality in the distribution of estimates.

Therefore, we propose two new confidence interval methods for Shannon’s index. The basis of the first one is a bootstrap approach, and the second is an asymptotic approach. They deal with, respectively, asymmetry (i.e. a distribution skewed for the right or left) and Shannon’s index bias (i.e. Point estimation error of the parameter $H$). Also, we aim to compare it with bootstrap t (t), bias corrected-accelerated (BCA), bias-corrected percentile (BC), percentile (Perc), standard percentile (SPerc) and empirical corrected (EC) methods using a simulation study with biological meaningful community structures. Given that high dominance, moderate dominance and codominance patterns are commonly encountered in community structures restricted to a local scale, the simulated scenarios were based on a degree of dominance according to the codominance and evenness indices (Gray et al., 2021; Pielou, 1966). Finally, to support our recommendation, we presented a case study of an aphid monitoring system emphasising the scenarios presented in the simulation study.

2 Methods

In this section we describe the proposed confidence interval methods and compare them with some traditional bootstrap methods. Let

\[
x = \begin{pmatrix}
  S_{p_1} & S_{p_2} & \ldots & S_{p_k} \\
  n_1 & n_2 & \ldots & n_k
\end{pmatrix}
\]
be the observed species frequency distribution in a sample, where: $k$ is the number of species; $n_j$ ($j = 1, \ldots, k$) is the frequency of individuals of species $S_{p_j}$ and $n = \sum_{j=1}^{k} n_j$ is the total number of individuals. Consider that $H$ is the parameter of interest and $\hat{H} = -\sum_{j=1}^{k} \frac{n_j}{n} \log \frac{n_j}{n}$ ($n_j \neq 0$) its estimator. Then, as an example, the 7 individuals sample

$$x = \{S_{p_1}, S_{p_2}, S_{p_2}, S_{p_4}, S_{p_3}, S_{p_2}, S_{p_3}\} = \begin{pmatrix}
S_{p_1} & S_{p_2} & S_{p_3} & S_{p_4} \\
1 & 3 & 2 & 1
\end{pmatrix} \tag{2}$$

will give the estimate $\hat{H} = -\left(\frac{1}{7} \log \frac{1}{7} + \frac{3}{7} \log \frac{3}{7} + \frac{2}{7} \log \frac{2}{7} + \frac{1}{7} \log \frac{1}{7}\right) = 1.2770$.

Despite its frequent use, the estimator $\hat{H}$ generally underestimates $H$ (Pla, 2004), but, taking into account the 2-nd order series expansion expressions for the expected bias of $\hat{H}$ and variance of $\hat{H}$, $\overline{\text{Var}}(\hat{H})$, presented by Hutcheson (1970), Shenton et al. (1969), Pla (2004) and Zhang and Zhang (2012), an approximately unbiased estimator of $H$ will be

$$\hat{H}' = \hat{H} + \frac{k - 1}{2n} - \frac{1}{12n^2} \left(1 - \sum_{j=1}^{k} \frac{n_j}{n} \right), \tag{3}$$

with approximate variance

$$\overline{\text{Var}}(\hat{H}') \approx \frac{1}{n} \left( \sum_{j=1}^{k} \frac{n_j}{n} \left( \log \frac{n_j}{n} \right)^2 - \hat{H}'^2 \right) + \frac{k - 1}{2n^2}.$$ 

Furthermore, according to the authors $\hat{H}$ is asymptotically normal distributed and thus, so will be $\hat{H}'$. Then, the proposed $(1 - \alpha)100\%$ asymptotically corrected confidence interval for $H$ will be

$$CI_{(1-\alpha)100\%}(H) = \hat{H}' \pm \sqrt{\overline{\text{Var}}(\hat{H}')} \cdot t_{\{1-\frac{\alpha}{2},n-1\}}, \tag{4}$$

where $t_{\{1-\frac{\alpha}{2},n-1\}}$ is the $(1 - \frac{\alpha}{2})$-th quantile of the $t$ distribution with $n - 1$ degrees of freedom.

Now, considering the dataset (2), we will have $\hat{H}' = 1.5233$, $\overline{\text{Var}}(\hat{H}') = 0.06020$, $t_{\{0.975,6\}} = 2.4469$ and $CI_{95\%}(H) = (0.9230, 2.1237)$, noticing that for small samples like in this case ($n = 7$), the expression (4) gives only an approximate interval.

Hereinafter, we describe the fundamental idea of bootstrap methodology and how to use it to build a percentile confidence interval for $H$. The first step is to extract $B$ random samples with replacement of (1), known as bootstrap samples (Davison and Hinkley, 1997; Efron and Tibshirani, [1993]).
Let the \( b \)-th bootstrap sample \((b = 1, \ldots, B)\) be

\[
x^{(b)} = \begin{pmatrix} S_{p_1} & S_{p_2} & \cdots & S_{p_k} \\ n_1^{(b)} & n_2^{(b)} & \cdots & n_k^{(b)} \end{pmatrix},
\]

where \( n_j^{(b)} \) is the frequency of species \( S_{p_j} \) \((j = 1, \ldots, k)\) in the sample. The following step is to compute the statistic of interest, \( \hat{H} \), in our case, for each bootstrap sample, named \( \hat{H}^{(b)} \), forming the set

\[
(\hat{H}^{(1)}, \hat{H}^{(2)}, \ldots, \hat{H}^{(B)}).
\]

(5)

As an example, the 5-th bootstrap sample extracted from (2) could be

\[
x^{(5)} = \{S_{p_3}, S_{p_2}, S_{p_2}, S_{p_3}, S_{p_2}, S_{p_2}, S_{p_3}\} = \begin{pmatrix} S_{p_1} & S_{p_2} & S_{p_3} & S_{p_4} \\ 0 & 4 & 3 & 0 \end{pmatrix},
\]

leading to the estimate \( \hat{H}^{(5)} = -\left(\frac{4}{6} \log \frac{4}{6} + \frac{3}{6} \log \frac{3}{6}\right) = 0.6829 \). Now, given the set of bootstrap estimates (5), the percentile bootstrap 100\((1 - \alpha)\)% confidence interval for \( H \) is

\[
CI(H)_{100(1 - \alpha)\%} = (P_{\frac{x}{2}}, P_{1 - \frac{x}{2}}),
\]

where \( P_{\frac{x}{2}} \) and \( P_{1 - \frac{x}{2}} \) are the \( \frac{x}{2} \)-th and \((1 - \frac{x}{2})\)-th percentiles of (5), respectively.

However, despite the popularity of this and other bootstrap methods in building confidence intervals, when the distribution of bootstrap estimates is skewed, the use of credible intervals shall be more appropriate. Essentially, a one mode \((1 - \alpha)100\%\) credible interval (CrI) is the interval with the smallest width such that the percentage of values of (5) pertaining to it is greater than or equal to \((1 - \alpha)100\%\).

From this point on, we describe the simulation methodology to compare the performance of the proposed methods, credible interval (CrI) and asymptotically corrected (AC), with the methods: bootstrap t (t); bias corrected-accelerated (BCA); bias-corrected percentile (BC); percentile (Perc); standard percentile (SPerc) and empirical corrected (EC).

The first step is to set the number of species in the community, \( K \), considered here, equal to 4, 20, or 80. Low numbers of species \((K < 30)\) are common in community structures of agricultural landscapes, which exhibits low number of pests in response to poor diversity of host plants.
(Guo et al., 2019). In larger areas with an heterogeneity old-growth rainforest, though, a larger number of species, e.g. \( K = 80 \), are more likely to occur (Mulder et al., 2004; Ojo and Ola-Adams, 1996; Vanclay, 1989; Wubs and Bezemer, 2018).

Given \( K \), the following step is to set the relative abundance of species, \( S_p_j (j = 1, 2, \ldots, K) \), in these community structures, given by

\[
p_j = \frac{1}{100K} + \frac{99}{100 \sum_{j=1}^{K} j^{-\nu}} (j = 1, \ldots, K),
\]

where \( \nu \geq 0 \) is a parameter that is related to the level of dominance and codominance in the community (Table I). Note that \( p_1 > p_2 > \cdots > p_{K-1} > p_K > \frac{1}{100K} \), \( \sum_{j=1}^{K} p_j = 1 \) and \( \frac{1}{100K} \) is the minimum detection probability of any species. The choice of \( \nu \) was set for three different scenarios: 1. high dominance; 2. high codominance and 3. moderate dominance. Given \( K \), the values of \( \nu \) for the first and third scenarios were the ones that the Pielou’s evenness index, \( J = \frac{H}{\log K} \), where 0.15 and 0.9, respectively. On the other hand, given \( K \), the chosen \( \nu \) value for the second scenario was the one that maximized the codominance index by Gray et al. (2021),

\[
C_{k_c} = \frac{k_c}{\sum_{j=1}^{k_c} p_j} - p_{k_c+1}
\]

where \( 2 \leq k_c < K \) is the number of codominance species, considered here equal to 2, that is

\[
C_{k_c} = C_2 = \frac{2}{p_1 + p_2} - p_3.
\]

\( C_2 \) is, then, the difference between the harmonic mean of \( p_1 \) and \( p_2 \), and \( p_3 \).

For each community structure, i.e., combination of scenario and value of \( K \), presented on Table I, we extracted \( N = 1000 \) random samples with size \( n = 10, 50 \) or 500 individuals and for each generated sample, 95% confidence intervals for \( H \) were built based on the described methods. Note that for bootstrap methods, we used \( B = 1000 \) bootstrap samples. Also, we assumed that missing species in samples of community structures and bootstrap samples are not considered for computing Shannon’s index. The equation shows an example of it.
Table 1: Chosen values of $\nu$ and values of Pielou’s evenness index, $J$, Shannon’s diversity index, $H$ and codominance index, $C_2$, for three different scenarios: 1. high dominance; 2. high codominance and 3. moderate dominance, given the number of species in the community, $K$.

| Parameters       | Scenarios          | $K$  | $\nu$  | $J$  | $H$  | $C_2$  |
|------------------|-------------------|------|--------|------|------|--------|
|                  | 1. High dominance | 4    | 4.9618 | 0.15 | 0.21 | 0.0574 |
|                  |                   | 20   | 3.7901 | 0.15 | 0.45 | 0.1079 |
|                  |                   | 80   | 3.2263 | 0.15 | 0.66 | 0.1399 |
|                  | 2. High codominance| 4    | 1.8480 | 0.69 | 0.96 | 0.2029 |
|                  |                   | 20   | 2.1700 | 0.42 | 1.27 | 0.1811 |
|                  |                   | 80   | 2.2250 | 0.30 | 1.34 | 0.1788 |
|                  | 3. Moderate dominance| 4   | 0.9913 | 0.90 | 1.25 | 0.1577 |
|                  |                   | 20   | 0.8210 | 0.90 | 2.70 | 0.0687 |
|                  |                   | 80   | 0.7612 | 0.90 | 3.94 | 0.0367 |

Then, in order to compare their performances, for each set of $N = 1000$ confidence intervals, we computed the coverage percentage, i.e., the percentage of times that $H$ belongs to the confidence interval and the average width, i.e., the mean of the widths of the 1000 confidence intervals. It is expected that a good method will produce a coverage percentage close to 95% and a narrow average width.

3 Results

The simulation results are presented in Table 2. We expected that the coverage percentages would be close to 95% and considered here, as acceptable, values greater or equal to 80%. Following
this consideration, the bootstrap t, AC, bootstrap BCA, bootstrap EC, bootstrap Perc, bootstrap S Perc and Crl methods have acceptable coverage percentages in 89, 74, 63, 59, 41, 41 and 37% of the 27 considered community structures, respectively. Based on these results, we recommend the bootstrap t.

Now, considering communities with a high dominance scenario, though, the best two methods were the bootstrap t and BCA (100 and 89% of the 9 simulated community structures with acceptable coverage percentages, respectively). Moreover, for the communities with a high codominance scenario, the best two were bootstrap t and AC (100 and 89% of the 9 simulated community structures with acceptable coverage percentages, respectively). Finally, for the moderate dominance scenario, the bootstrap t and the AC (both with 67% of the 9 simulated community structures with acceptable coverage percentages) were the best two methods.

As an example, we will now calculate the confidence intervals of $H$ for a community of parasitoids and wheat crop aphids presented in Table 3. As the statistics, $k$, $\hat{H}$, $\hat{J}$ and $\hat{C}_2$, calculated for the samples collected during the three periods were similar to the ones presented in the simulation study, the bootstrap t method was selected. The first period shows a high codominance of species *Rhopalosiphum padi* and *Aphidius rhopalosiphi* and $CI_{95\%}(H) = (0.73, 2.32)$. The second, a high dominance of *Rhopalosiphum padi* and $CI_{95\%}(H) = (0.09, 0.25)$. The last, a moderate dominance and $CI_{95\%}(H) = (1.12, 3.12)$.

## 4 Discussion

We proposed the credible interval (Crl) and an asymptotically corrected (AC) method to estimate confidence intervals for Shannon’s index. Also, we compared them with commonly used methods for interval estimation of this diversity index. Therefore, the recommended method was the bootstrap-t.

The example presented showed how to use the results obtained from the simulated scenarios in real-world data. These scenarios reflect real conditions of aphids exploring wheat culture.
because our simulation uses the degree of dominance as conditions to generate community structures. It is emphasised by the fact that environments with lower resource heterogeneity tend to present community structure with high dominance or codominance (Chaves and Smith, 2021; Tsakalakis et al., 2020; Wilsey and Polley, 2002). These patterns are not restricted to the presented taxa, and they could be observed in other insect orders, such as Fruit Flyes and Dung insect communities (de Araujo et al., 2021; Hanski, 2014).

Now, by analysing papers similar to ours, we found that Pesenti et al. (2016) have used the average width and computational speed as a criterion of method selection. They concluded that the bootstrap percentile must be recommended based on their simulation study. Table 2 shows that if we use their criteria and compare the bootstrap percentile, bias-corrected, bias-corrected accelerated and t, we agree with their conclusions. However, by introducing the other methods in the comparison, the proposed asymptotic corrected method has better performance because it is 4053 times faster than the bootstrap percentile.

Moreover, wide or fewer intervals are not necessarily the best ones as they may not contain the community index. Is more important than the produced intervals contain most of the times this index, which is evaluated through the percentage of coverage. Given that said, table 2 shows a clear example of it considering the second scenario with $n = 10$. The methods with higher average width contain Shannon’s index in the community more times than the ones with wide intervals.

Finally, our findings also suggest that the community structure can influence the selection of methods for the construction of confidence intervals for Shannon’s index. Our main contribution is an innovative approach to provide recommendations for naturalists studying local diversity. Also, our simulation study helps the selection of appropriate confidence interval methods to estimate Shannon’s index, and this approach can be extended to any diversity index. However, the limitations of our work rely on the restricted simulated scenarios leading us to produce limited recommendations for community structures. So, in future work, we will explore more biological scenarios.
5 Conclusion

The simulation study showed that the bootstrap-t method produced a superior performance for 88% of the simulated dataset for Shannon’s diversity, $H$, indicating its superior overall performance as compared to the others and, thus, we recommend it when the community structure analysed is similar to the ones that we simulated. Finally, the methods provided more accurate estimations of Shannon’s diversity for the high dominance scenario.

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Table 2: Coverage percentages and average widths (between parenthesis) for different 95% confidence interval methods for $H$, considering: scenarios (Scen.) with 1. high dominance, 2. high codominance or 3. moderate dominance; different sample sizes, $n = 10, 50$ or 500 and different community number of species, $K = 4, 20$ or 80. The results were based on 1000 samples, 1000 bootstrap samples (for bootstrap methods) and 25 subsamples of bootstrap samples for the $t$ method. Note: $\bar{k}$ is the average number of species in the samples.

| Scen. | $n$ | $K$ | $\bar{k}$ | Perc | BCA 95% | BCA 99% | t 95% | BC 95% | SPerc 95% | EC 95% | Crl 95% | AC 95% |
|-------|-----|-----|----------|-------|---------|---------|-------|-------|-----------|-------|--------|--------|
| 1     | 4   | 1.40| 36 (0.24)| 98 (0.65) | 99 (1.08) | 36 (0.20) | 36 (0.31) | 30 (0.31) | 36 (0.23) | 36 (0.37) |
|       | 10  | 1.78| 64 (0.45) | 99 (0.69) | 99 (0.98) | 64 (0.40) | 64 (0.55) | 60 (0.55) | 64 (0.43) | 63 (0.65) |
|       | 80  | 2.15| 44 (0.60) | 38 (0.67) | 96 (1.27) | 43 (0.54) | 78 (0.70) | 70 (0.70) | 44 (0.56) | 75 (0.82) |
| 2     | 4   | 2.25| 87 (0.31) | 99 (0.37) | 99 (0.60) | 65 (0.29) | 87 (0.33) | 85 (0.33) | 87 (0.29) | 87 (0.34) |
|       | 50  | 3.42| 80 (0.47) | 83 (0.49) | 99 (0.68) | 78 (0.47) | 84 (0.48) | 84 (0.48) | 77 (0.45) | 84 (0.49) |
|       | 80  | 4.21| 75 (0.53) | 81 (0.52) | 95 (0.70) | 78 (0.52) | 76 (0.54) | 84 (0.53) | 74 (0.51) | 85 (0.55) |
| 3     | 4   | 3.81| 93 (0.13) | 96 (0.14) | 98 (0.15) | 94 (0.13) | 93 (0.14) | 95 (0.14) | 92 (0.13) | 94 (0.14) |
|       | 500 | 8.90| 91 (0.19) | 93 (0.19) | 97 (0.21) | 93 (0.19) | 91 (0.19) | 93 (0.19) | 90 (0.18) | 93 (0.19) |
|       | 80  | 12.45| 83 (0.21) | 87 (0.21) | 94 (0.23) | 89 (0.21) | 83 (0.21) | 94 (0.21) | 82 (0.21) | 90 (0.21) |
|       | 4   | 2.92| 62 (0.78) | 72 (0.68) | 86 (1.10) | 71 (0.68) | 72 (0.84) | 77 (0.84) | 60 (0.68) | 85 (0.97) |
|       | 10  | 3.40| 43 (0.88) | 44 (0.71) | 94 (1.35) | 43 (0.71) | 45 (0.93) | 73 (0.93) | 44 (0.77) | 79 (1.09) |
|       | 80  | 3.43| 17 (0.88) | 42 (0.71) | 96 (1.37) | 37 (0.71) | 42 (0.94) | 75 (0.94) | 25 (0.79) | 80 (1.11) |
|       | 4   | 3.92| 90 (0.45) | 90 (0.44) | 95 (0.53) | 90 (0.43) | 91 (0.46) | 89 (0.46) | 90 (0.44) | 91 (0.47) |
| 2     | 50  | 7.35| 70 (0.63) | 84 (0.62) | 93 (0.78) | 80 (0.59) | 72 (0.63) | 86 (0.63) | 72 (0.62) | 85 (0.65) |
|       | 80  | 7.71| 58 (0.64) | 80 (0.63) | 90 (0.80) | 76 (0.61) | 60 (0.65) | 84 (0.65) | 58 (0.64) | 82 (0.67) |
|       | 4   | 4.00| 95 (0.15) | 96 (0.15) | 96 (0.15) | 95 (0.14) | 95 (0.15) | 95 (0.15) | 95 (0.14) | 95 (0.15) |
| 3     | 50  | 16.74| 89 (0.24) | 94 (0.24) | 96 (0.26) | 94 (0.24) | 90 (0.24) | 93 (0.24) | 88 (0.24) | 94 (0.24) |
|       | 80  | 23.80| 73 (0.26) | 89 (0.26) | 92 (0.29) | 87 (0.26) | 74 (0.26) | 92 (0.26) | 73 (0.26) | 89 (0.26) |
|       | 4   | 3.50| 54 (0.72) | 49 (0.47) | 88 (1.04) | 49 (0.49) | 56 (0.77) | 85 (0.76) | 54 (0.62) | 96 (0.88) |
|       | 10  | 7.07| 0 (0.80) | 0 (0.14) | 72 (0.96) | 0 (0.14) | 0 (0.82) | 69 (0.82) | 0 (0.74) | 60 (1.02) |
|       | 80  | 8.74| 0 (0.74) | 0 (0.03) | 0 (0.84) | 0 (0.02) | 0 (0.77) | 0 (0.77) | 0 (0.69) | 0 (1.00) |
|       | 4   | 4.00| 91 (0.31) | 92 (0.27) | 93 (0.33) | 91 (0.26) | 94 (0.31) | 89 (0.31) | 92 (0.29) | 93 (0.32) |
| 3     | 50  | 16.28| 4 (0.47) | 23 (0.20) | 91 (0.51) | 20 (0.20) | 7 (0.47) | 78 (0.47) | 6 (0.46) | 89 (0.49) |
|       | 80  | 30.53| 0 (0.45) | 0 (0.01) | 26 (0.50) | 0 (0.00) | 0 (0.46) | 70 (0.46) | 0 (0.45) | 17 (0.49) |
|       | 4   | 4.00| 94 (0.09) | 95 (0.09) | 96 (0.10) | 95 (0.09) | 95 (0.09) | 94 (0.09) | 94 (0.09) | 96 (0.09) |
| 500  | 20  | 20.00| 83 (0.14) | 94 (0.14) | 96 (0.15) | 94 (0.13) | 86 (0.15) | 90 (0.15) | 84 (0.14) | 95 (0.15) |
|       | 80  | 77.05| 3 (0.19) | 31 (0.07) | 95 (0.20) | 32 (0.07) | 4 (0.19) | 57 (0.19) | 4 (0.18) | 95 (0.19) |
Table 3: Abundances of parasitoids and wheat crop aphids in three periods in a monitoring programme at Area II (710 m altitude, 28° 11′ 42.8″ S and 52° 19′ 30.6″ W) of the Embrapa Trigo experimental station, located in Coxilha, RS, Brazil.

| Species | 20-26/08/14 | 22-28/01/16 | 02-08/04/18 |
|---------|-------------|-------------|-------------|
| **Parasitoids** | | | |
| *Aphidius rhopalosiphi* (DeStefani, 1902) | 2 | 0 | 0 |
| *Aphidius platensis* (Brăthes, 1913) | 1 | 0 | 3 |
| *Diaeretiella rapae* (Mc’Intosh, 1855) | 1 | 0 | 1 |
| **Aphids** | | | |
| *Metapolophium dirhodum* (Walker, 1849) | 0 | 1 | 0 |
| *Rhopalosiphum padi* (Linnaeus, 1758) | 6 | 387 | 0 |
| *Rhopalosiphum maidis* (Luzhetzki, 1960) | 0 | 0 | 1 |
| *Rhopalosiphum rufiabdominalis* (Sasaki, 1899) | 0 | 1 | 0 |
| *Sitibion avenae* (Fabricius, 1775) | 0 | 10 | 1 |

\[
\hat{H} = \frac{\sum_{i=1}^{k} n_i \log n_i}{\sum_{i=1}^{k} n_i} \\
\hat{f} = \frac{\hat{H}}{\log k} \\
\hat{C}_2 = \frac{\hat{f}^2}{k(1/4)}
\]

\[
\begin{array}{ccc}
\text{n} & 10 & 399 & 6 \\
\hat{H} & 1.09 & 0.15 & 1.24 \\
\hat{f} & 0.79 & 0.11 & 0.90 \\
\hat{C}_2 & 0.20 & 0.046 & 0.083 \\
\end{array}
\]