AN ASSESSMENT OF SAMPLING DETECTABILITY FOR GLOBAL BIODIVERSITY MONITORING: RESULTS FROM SAMPLING GRIDS IN DIFFERENT CLIMATIC REGIONS

Master thesis

by

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Abstract

This thesis provides important input for the development of a cost-effective global biodiversity assessment and monitoring system. The study is embedded in a larger project to evaluate possibilities of multiple-species surveys using biodiversity GRIDs. As a pilot study six GRIDs in diverse ecosystem settings are sampled. Sampling methods used for animal species are point transects for birds and trapping webs for arthropods; additionally a line transects add-on protocol is used at some study areas for amphibians, reptiles and butterflies. Within this framework the task is taken over to develop predictive models for sampled animal species with Random Forests. Additionally the data is analyzed to derive abundance estimates with multiple covariate DISTANCE sampling and occupancy estimates through the software PRESENCE.

A total of 5,007 observations from six study areas from all over the world are analyzed in detail. Total sampling time is about 12 weeks. High quality non-random predictive models with a ROC value > 0.5 are gained with Random Forests analysis for 116 described animal narratives. Half of these observations origin from point transect sampling, the other half from trapping web catches. The line transects add-on protocol results in another 3 predictive models. Abundance and occupancy estimates are derived from the data for 46 animal narratives, 23 of those for point transect data, 22 for trapping web data, and 1 for line transect data. Predictive modeling with Random Forests proves to be a very powerful tool. DISTANCE sampling estimates from this study show large confidence interval ranges, but are extremely cost-efficient to gather initial information for multiple species rapidly. PRESENCE estimates are partly unsatisfying because of a large portion of animal narratives with perfect occupancy estimates (Psi = 1.0). It is assumed that this is an effect of small sampling size which will not be problematic for larger amounts of data. This has to be kept in mind when comparing DISTANCE and PRESENCE results. Correlation between DISTANCE and PRESENCE detection probability estimates is negative, while correlation between DISTANCE abundance estimates and PRESENCE occupancy estimates is positive for all but one study area. It is recommended to repeat the comparison when data from more plots is available. On one hand the results, the cost-effectiveness of the study, and possibilities opened by this kind of multiple-species multi-method sampling are promising, on the other hand funding for this visionary approach was not available.

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List of Abbreviations

1CR	1st GRID in Costa Rica
2Ni	2nd GRID in Nicaragua
3AK	3rd GRID in Fairbanks, Alaska
4Ru	4th GRID in Russia
5PG	5th GRID in Papua New-Guinea
6Ba	6th GRID in Barrow, Alaska
ABMP	Alberta Biodiversity Monitoring Program
AIC	Akaike Information Criterion
all	all available data (pooled)
aur	only data aurally detected
Bi	Bird
CBD	Convention on Biological Diversity
CDS	Conventional DISTANCE Sampling
Covariates	one of three Random Forests model definitions
DIWPA	Diversitas in Western Pacific and Asia
D	Density
DS	DISTANCE Sampling
DT	DISTANCE Sampling Line Transect
GBIF	Global Biodiversity Information Facility
GEO	Group on Earth Observations
GEOSS	Global Earth Observation System of Systems
GIS	Geographic Information Systems
GLM	Generalized Linear Models
IBOY	International Biodiversity Observation Year
Interspecies	one of three Random Forests model definitions
IPY	International Polar Year
ITIS	Integrated Taxonomic Information System
MCDS	Multiple Covariate DISTANCE Sampling
MSIM	Multiple Species Inventory and Monitoring Protocol
p	Probability of Detection
Plot	one of three Random Forests model definitions
PR	PRESENCE
Psi	Occupancy estimate
ran	only data from randomly selected Plots
RF	Random Forests
ROC	Receiver Operating Characteristic
sys	only data from systematically selected Plots
TW	Trapping Web
vis	only data visually detected

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1 Introduction

1.1 Global Biodiversity Crisis and Biodiversity Monitoring

Biodiversity loss is widely recognized as a crucial survival issue in society, at the latest since most countries of the international community signed the Convention on Biological Diversity at the Earth Summit in Rio de Janeiro in 1992 (Brooks et al. 2002; CBD 2006; McKee et al. 2004). There is vast evidence that the loss of biodiversity is not only an ethical problem, but also substantially financial because important ecosystem services are lost on a global level (Mainka et al. 2005; Millennium Ecosystem Assessment, ongoing). Many countries have recognized these facts and have implemented national biodiversity monitoring strategies to detect changes in biodiversity, usually substituted by monitoring of species richness (Nakashizuka & Stork 2002; Wilson 1992). More and more of these protocols accept a loss of precision for single species by assessing multiple species at the same time, because resources to implement one monitoring system per species are simply not available and multiple-species monitoring on a landscape level is much more resource-efficient (Franklin 1993; Manley et al. 2005; Manley et al. 2004). These systems are also more resilient against sudden changes in the focus of research interest, which may render more specific monitoring systems useless before they are fully implemented (Watson & Novelly 2004). Some regional examples of such monitoring systems are the Multiple Species Inventory and Monitoring Protocol (MSIM) for National Forest System Lands in the United States (Manley & van Horne 2006); the Alberta Biodiversity Monitoring Program (ABMP) in Canada (ABMP 2006; Stadt et al. 2006); Biodiversity Monitoring Switzerland (Küttel 2007); or International Biodiversity Observation Year in Western Pacific and Asia (IBOY-DIWPA, Nakashizuka & Stork 2002).

The use of these systems presents a major step forward to make biodiversity research more relevant, rigorous, compelling and thus more tangible and usable for political planning and implementation processes (Marzluff et al. 2001). But they can have two problems: firstly they are highly specialized for the area within the borders of the country they were developed for. Very often these protocols can only be used in specific environments, for example temperate forests and mountainous areas, but are usually not applicable to ecosystems which do not occur in the country of origin. Political borders are (usually) clear and precise, while changes of biodiversity respectively of nature in general are subtle and gradient. Most of today’s threats to biodiversity, for example global climate change, have influences which do not stop at political and administrative borders, neither do migrating animals nor ecological processes. Secondly, even if the ecosystems in different countries are similar enough, very often the details of data collection and/or processing methods differ too much to compare monitoring results from different countries. As a result they are not allowing for proper generalizations. Green et al. (2005) "*argue that there is a shortage of standardized, regularly repeated measurements of the state of biomes and their biota that could be used to monitor progress toward this goal*". In the long-term view the intention behind the project is to develop a globally valid biodiversity monitoring system which delivers comparable results at achievable costs in every ecosystem and every country of the world. "*Global conservation assessments require information on the distribution of biodiversity across the planet*" (Ferrier et al. 2004). Achieving this global perspective is obviously a very ambitious goal and might not be completely attained in the very near future. To this date most habitats have not even been assessed once and there is a considerable shortage of biodiversity monitoring on a global scale (Dobson 2005; Green et al. 2005).

Another intention for this project is to work with low-cost methods. The budget available for biodiversity monitoring on a global scale is unfortunately very low. As the method to develop is supposed to be used in many areas of the world which can not or are not willing to afford to invest large amounts of money and resources into the implementation of such a monitoring method, the intention is to work on a "shoestring budget". "*I've become convinced that design for I&M programs must be predicated on the idea that funds are ephemeral and so the core of a monitoring program should be very lean (and relatively inexpensive). Around that core, you can develop add-on protocols and additional sampling that are only implemented when funds are available*" (Morton 2007, pers. comm.). Sampling is therefore primarily conducted for taxonomic groups that are potentially living in almost every terrestrial ecosystem: birds and ground-living insects. One possible add-on protocol for butterflies, amphibians and reptiles is developed for this study; further add-on protocols for other animal groups can be developed at a later stage.

In short, the project idea is to develop a relatively simple low-cost rapid biodiversity assessment and monitoring system, which aims at multiple species and offers multiple ways of analysis. Furthermore this system is supposed to be globally applicable and compatible with current data standards, so that data from this project may contribute to ongoing global biodiversity initiatives (Global Earth Observation System of Systems (GEOSS) 2008; Group on Earth Observations (GEO) 2008; International Polar Year (IPY) 2008). As a pilot study data was collected with different methods from six diverse regions in the world in form of a biodiversity GRID (as explained in chapter 2.2.1). The study at hand is a partial assessment of some of the most important possibilities to analyze these GRIDs offer for the estimation of animal populations. The results will provide a valuable starting point for more detailed taxonomic studies and provide crucially needed information for setting up sampling schemes with higher accuracy. For that reason data are made fully available to the public and investigators for their own assessment. Full Metadata for the datasets will be uploaded to NBII Clearinghouse website and found online at http://mercdev3.ornl.gov/nbii/ . In the long-term such data is expected to be easily visualized and connectable to other data sets in public domains (Guralnick et al. 2007).

1.2 Goals of the Study

This thesis supports the overall biodiversity GRID project by analyzing wildlife data from the project at three different analysis levels: prediction, abundance and occupancy. A short overview is given in this introduction; detailed information is available from the methods section.

The first analysis goal, prediction respectively predictive modeling, was in the past in practice limited to Generalized Linear Models (GLMs) by lack of computing power, in spite of ecological data often being non-linear, interactive and multi-dimensional in nature. Recent developments in computer technology and steep price declines of equipment and communication are relaxing these limitations (Bauldock et al. 2001). First studies using machine learning algorithms in ecology are promising and seem to clearly outweigh the traditional GLMs in convenience, speed and accuracy (e.g. Huettmann 1999; Magness et al. 2008; Prasad et al. 2006). Predictive modeling is a tool to achieve global information about biodiversity distribution conveniently (Elith et al. 2006). It has the ability to process all available environmental data to analyze the effect on general biodiversity patterns (Faith 2005). It has also been shown in numerous cases that well-constructed models often show a much better performance and higher consistency in population estimations and habitat modeling than do expert opinions (Pearce et al. 2001; Yamada et al. 2003). Predictive modeling using data mining can also handle a large variety of data since there are no requirements of parametric assumptions to be met. Additionally these machine learning algorithms have less problems interpreting noisy or sparse information (Elith et al. 2006), partly because interactions between variables are included in analysis (Craig & Huettmann 2008; Magness et al. 2008). The predictions have the advantage that they can be tested for generalizations.

Abundance and population density are probably the most important basic parameters in population dynamics (Krebs 2001). This makes abundance a very valid second analysis goal. Whenever possible it is intended to get true abundance estimates for each species, corrected for imperfect detection of individuals with different methods (Buckland et al. 2001; MacKenzie 2005a). However, with a standardized multiple-species protocol this is not always possible. Especially species with large territories are often difficult to monitor on an eco-regional scale (Manley & van Horne 2006). Therefore as a third point the probability that an area is occupied by a species, known as occupancy or Psi, is also estimated. Occupancy is the simplest level of interest (Hill et al. 2006), which gives much less information than abundance or density, but still has implications for wildlife management. At the same level of precision it can usually be obtained at lower costs than abundance estimates (Bailey et al. 2007; MacKenzie 2005b). Clearly, occupancy is not the prime goal in this project, but it is accepted as better-than-nothing baseline information. It also allows matching up with studies underway elsewhere worldwide. Results of abundance and occupancy estimates will also be directly compared to each other.

2 Methods

2.1 Study Area

Data from six different study areas from all over the globe was used for this thesis. The data was collected in:

(1) Costa Rica, lowland tropical rainforest, data collection from 10th to 22nd June 2007 (data collected by Falk Huettmann and Dirk Nemitz)

(2) Nicaragua, tropical dryforest, data collection from 22nd June to 5th July 2007 (data collected by Falk Huettmann, Dirk Nemitz and Andre Breton)

(3) Central Alaska (USA), boreal forest, data collection from 14th July to 3rd August 2007 (data collected by Dirk Nemitz and Andre Breton)

(4) Sakhalin Island (Russia), data collection from 6th to 24th August 2007 (data collected by Falk Huettmann)

(5) Papua New-Guinea, data collection from 22nd to 28th December 2007 (data collected by Falk Huettmann)

(6) Northern Alaska (USA), arctic tundra, data collection from 29th June to 4th July 2008 (data collected by Falk Huettmann)

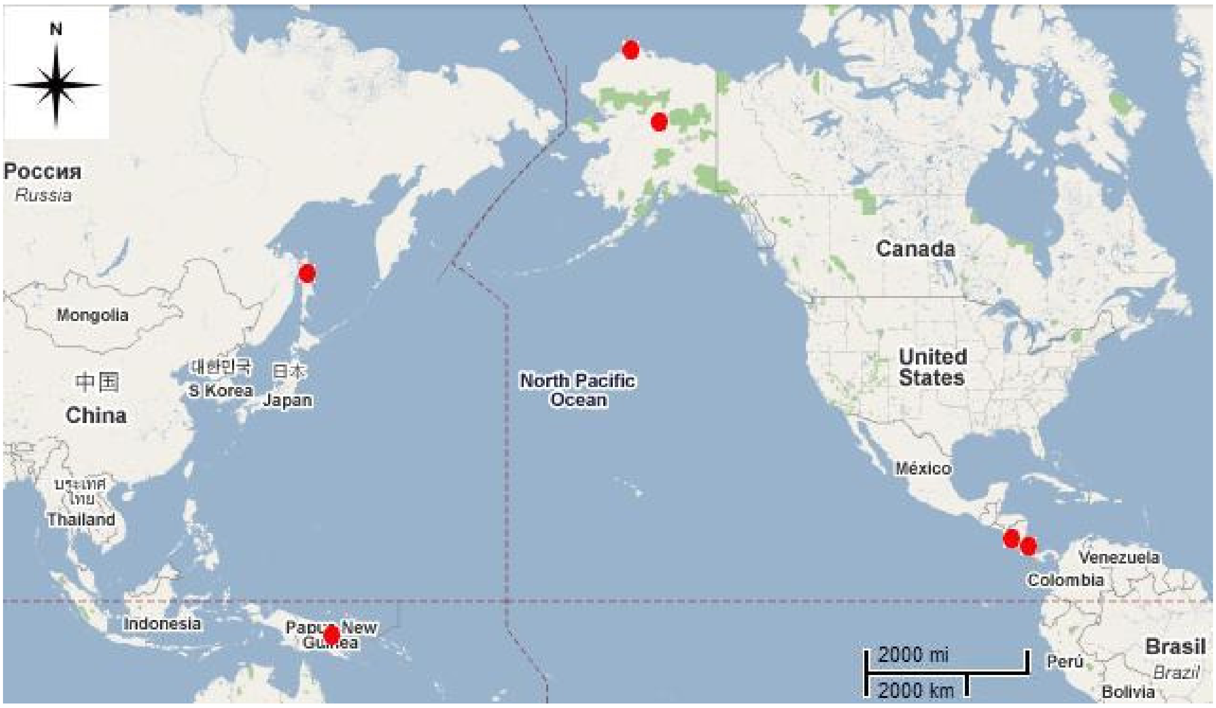

Figure 1: Location of study sites (Google Maps, adjusted)

2.1.1 Study Area 1CR: La Suerte Station, Costa Rica

Figure 2: Location of study area 1CR in Costa Rica (Google Maps, adjusted)

The studied lowland tropical rainforest is located at La Suerte Biological Station at the Río Suerte in north-eastern Costa Rica (Janzen 1983). The station is a teaching and research facility with ca. 20 ha advanced secondary tropical rainforest. It is located about 50 m above sea level, and one of the sites carrying highest biodiversity in the world. According to the owners of the Biological Station it is "*home to thousands of plant and insect species as well as hundreds of species of amphibians, reptiles, birds and mammals*" (Molina 2007). The area receives about 3800 mm annual rainfall on average. It is well known for studies on neo-tropical primates, especially mantled howling monkeys (*Alouatta palliata*), black-handed spider monkeys (*Ateles geoffroyi*) and white-faced capuchins (*Cebus capucinus*) (Garber & Rehg 1999). According to hand-held GPS measurements the study GRID extends from about 10.26573 to 10.26805 north and from 83.46704 to 83.46919 west.

2.1.2 Study Area 2Ni: Ometepe Island, Nicaragua

Figure 3: Location of study area 2Ni in Nicaragua (Google Maps, adjusted)

The second area where data was collected is a tropical dryforest close to Point San Ramon Village on Ometepe Island in Lake Nicaragua. Ometepe Island encompasses about 276 km² and is the biggest volcanic island in the world that is located in a freshwater lake. The island is dominated by the two volcanoes Concepción and Maderas. Almost the entire flat land is used agriculturally, while secondary tropical dry forest grows on the slopes of the volcanoes. With higher altitude the forest gradually changes into undisturbed virgin tropical cloud forest. Volcanic rocks from former eruptions are scattered all over the island. The island receives about 1,600 mm average annual rainfall and has a medium daily temperature between 26° and 29° Celsius (Steck 1997). The area is especially known for studies on the easily observable mantled howling monkeys (*Alouatta palliata*) population (Garber et al. 1999; Huettmann 1999; Popp et al. 2007). According to hand-held GPS measurements the study GRID extends from about 11.25120 to 11.25388 north and from 85.31858 to 85.32143 west.

2.1.3 Study Area 3AK: Fairbanks, Alaska

Figure 4: Location of study area 3AK in Alaska, USA (Google Maps, adjusted)

The third data collection area is a boreal forest located on the campus of the University of Alaska, Fairbanks, USA. Fairbanks is located in the centre of interior Alaska. The climate is rather continental because of the surrounding mountain ranges, resulting in cold winters as well as warm and dry summers. The temperature ranges from -50° Celsius in January to over 30° Celsius in July. The average annual precipitation is 287 mm (Chapin et al. 2006). Frequent forest fires influence all boreal forests in this eco-region (Kasischke et al. 2006). According to hand-held GPS measurements the study GRID extends from about 64.520482 to 64.521789 north and from 147.512596 to 147.515652 west.

2.1.4 Study Area 4Ru: Verengery Sakhalin Island, Russia

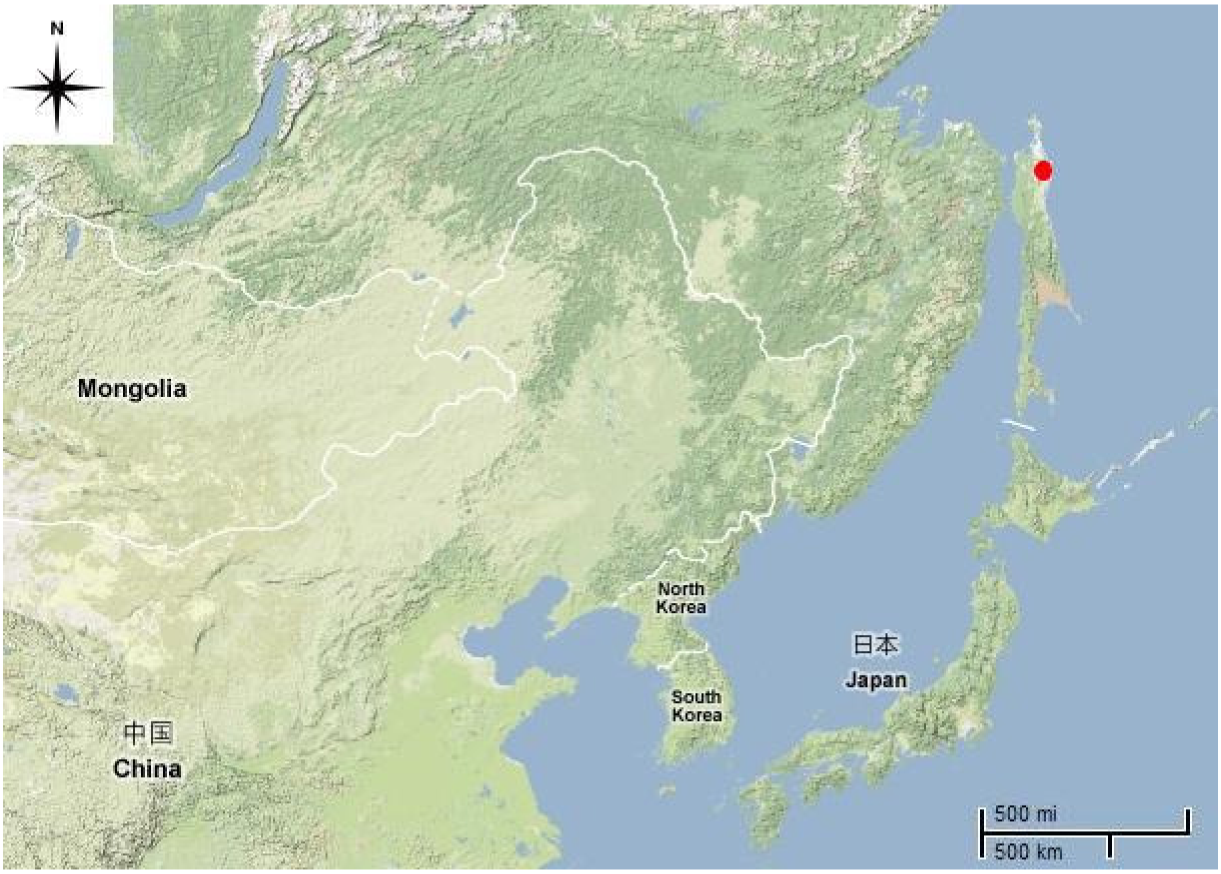

Figure 5: Location of study area 4Ru in Russia (Google Maps, adjusted)

The fourth study area is located in the Russian Far East, on Sakhalin Island in the North Pacific. With about 78,000 km² Sakhalin Island is the largest Russian island. Its climate is rather cold and usually considered to be sub-arctic. Much of the Sea of Okhotsk between the island and the mainland is usually covered by ice during the long winters. The area is regarded as extremely important for conservation of arctic and sub-arctic migratory shorebirds. Despite holding large amounts of oil and gas resources, most of the island's hinterland is relatively undisturbed (Huettmann & Gerasimov 2006). According to hand-held GPS measurements the study GRID extends from about 50.59892 to 50.60234 north and from 143.69052 to 143.69526 east.

2.1.5 Study Area 5PG: Bismarck Range, Papua New-Guinea

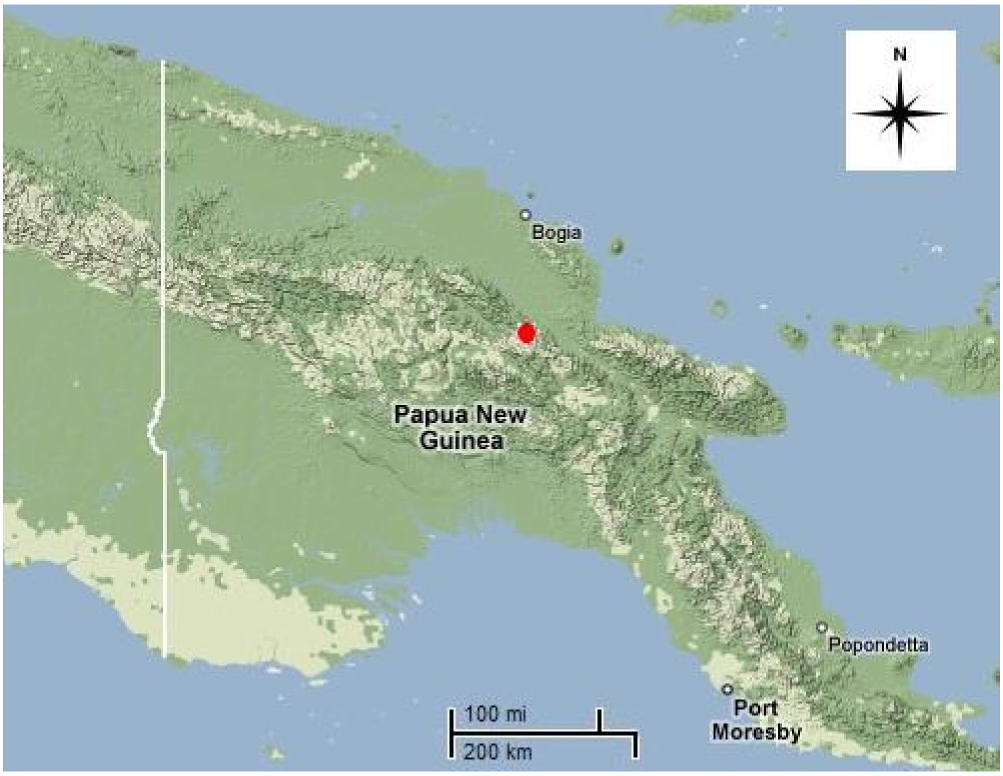

Figure 6: Location of study area 5PG in Papua New-Guinea (Google Maps, adjusted)

The location of the fourth study area is in the Bismarck range in Papua New Guinea. Papua New Guinea is the world's third largest insular state. It is especially known for its enormous scenic, cultural and biological diversity. Papua New Guinea has a high variation in rainfall, altitude, soil, and history of disturbances, resulting in high biodiversity (Miller et al. 1994b). It is estimated that about 5 % of the world's total biodiversity is located in the country, while exact information about species details and taxonomy is very sparse (Miller et al. 1994a). The area covered by the study GRID is located in the Bismarck range at an altitude of ca 850 m, typically being classified as Lowland Humid Forest with an average annual rainfall between 2,500 mm and 3,500 mm (Miller et al. 1994b). The GRID covers prime forest, an adjacent garden and a forest trail.

2.1.6 Study Area 6Ba: Barrow, Alaska

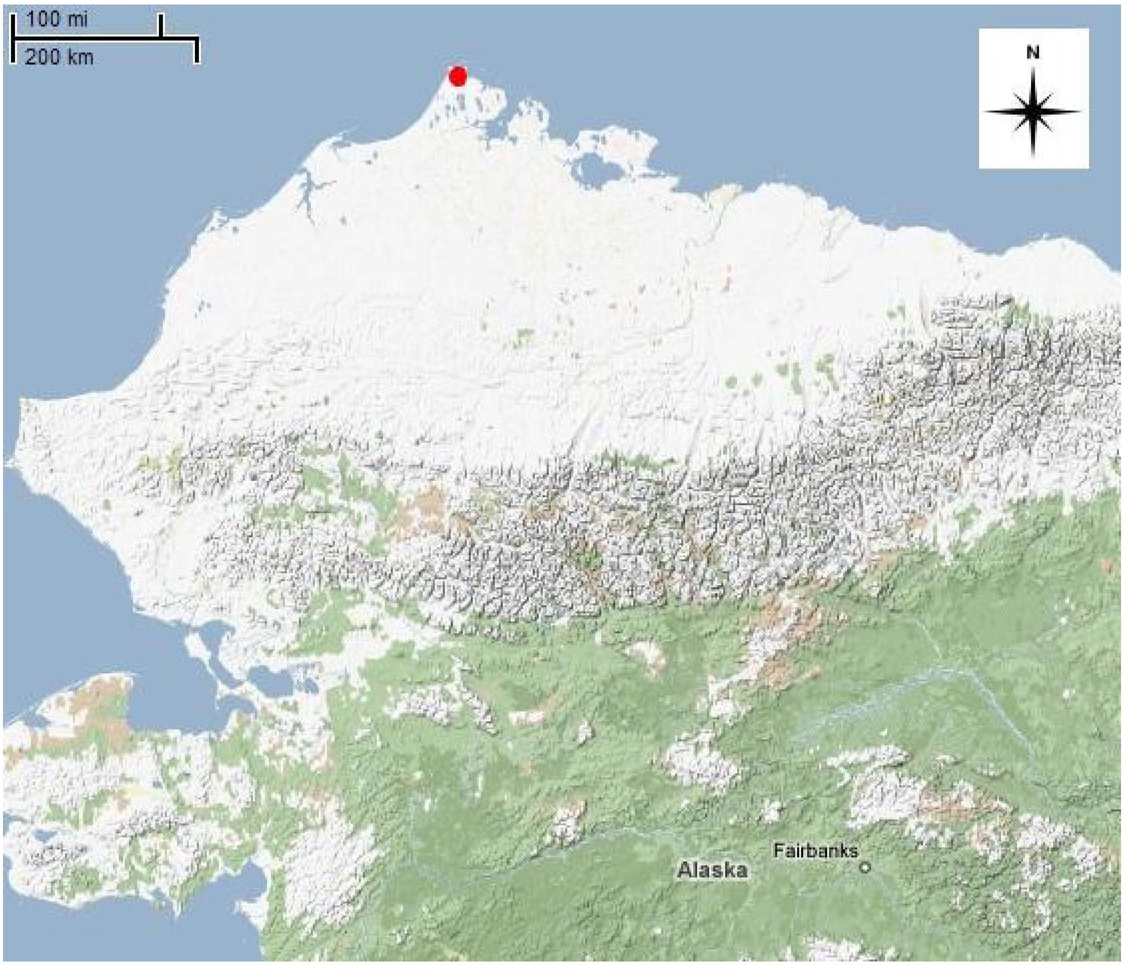

Figure 7: Location of study area 6Ba in Alaska, USA (Google Maps, adjusted)

The sixth study area is Barrow, located in the North of Alaska. It is the northernmost settlement of the United States. The climate is polar, very cold, with less than four months exceeding a mean temperature of 0° Celsius. Because of its dryness the area is classified as desert. Barrow and the surrounding area are extremely important bird habitat (Pitelka 1974). This study area differs from the other five in two main ways. Firstly it contains only one habitat type: arctic tundra without major vegetation and trees. Secondly there was midnight sun during the time the sampling took place, so it was not determinable if the time of sampling relative to the time of sunrise has an effect on the results. According to hand-held GPS measurements the study GRID extends from about 71.24034 to 71.24467 north and from 156.56546 to 156.57717 west.

2.2 *Sampling Methods*

2.2.1 Biodiversity GRID

For efficiency reasons a systematic sampling approach was chosen (Cochran 1946; Olea 1984). First of all an equally spaced GRID was implemented: 25 points were arranged in five rows and five columns in order to cover a consistent area but also to have a known spatial neighbor relationship among all plots, which is consistent with recommendations given by Ricklefs (2004). The distance between plots was 100 m, resulting in a total GRID size of 500 m x 500 m. While the final GRID system ideally covers the globe systematically without intentional placement, for these initial studies the GRIDs were placed in a way that roughly half to two thirds of the plots fell inside a forested area, the remaining plots at the forest edge or inside the cultural landscape. This survey setup enables other studies on the same data set to make realistic and representative statements about fragmentation effects. The only exception is GRID 6Ba in northern Alaska, where naturally only one habitat type, arctic tundra, occurs. Additionally, five points were randomly placed within the GRID to be able to model the influence of random patterns on the results and their spatial relations (Figure 8).

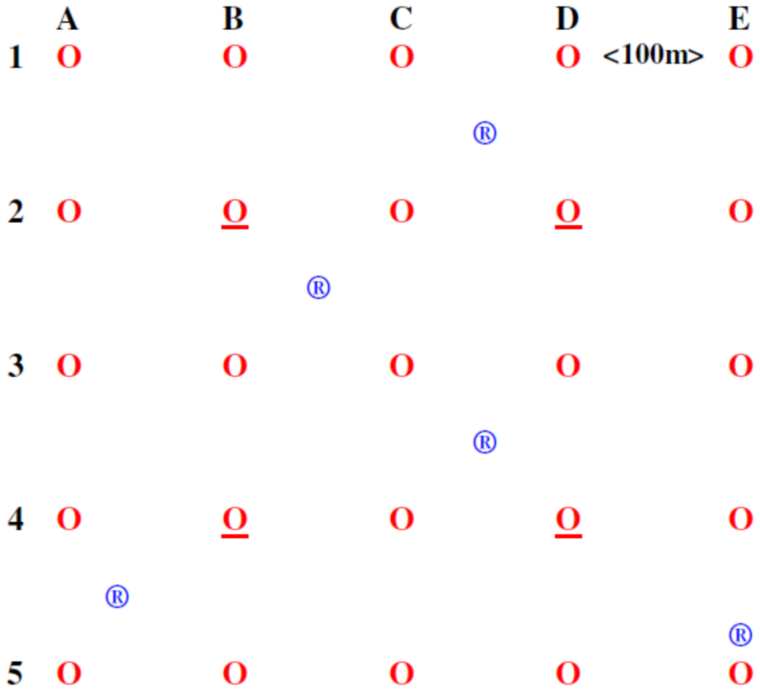

Figure 8: Structure of the biodiversity GRID with 25 systematically selected plots, 5 randomly selected plots, and trapping webs installed at 4 plots (underlined)

The coordinates of each plot were obtained from a regular hand-held GPS receiver and re-visited by using the "Go to" function. All plots as well as the path between them were marked with decomposing flagging tape to make recognition in the field easier. A simple schematic map was drawn by hand for each field work participant to ensure that plots are found when the GPS does not receive signals, as was often the case in dense forest settings.

2.2.2 Budget Constraints

The biodiversity GRID is meant as a method for cost-efficient rapid biodiversity assessment that allows for an analysis of spatial relations as well. All methods involved have to work in relatively short time, with low costs and little demand of technological equipment. There is no objection to include more sophisticated methods in add-on protocols, but they are discouraged for the main protocol to keep the inhibition threshold for decision makers low.

Trained taxonomists were not available, as they rarely are for many ecosystems. All notes regarding the observed species were made as precisely as possible, although most of the observers were not trained especially in tropical ornithology or entomology. Data collection followed the motto the more detail the better, but it was not intended to refuse data because of lacking taxonomic details. If the observer did not readily know the correct scientific name of a specimen, a common name or, in lack of knowledge of a common name, a short description was noted. This original field note is referred to as the "narrative name" of an observation respectively of a species. Such process is common when dealing with large numbers of species and in largely unexplored environments, where huge fractions of the biodiversity remains still unknown, or where appropriate taxonomic guide books are missing.

This resulted in good abundance and occupancy estimates, but in less detailed taxonomic data. Such is the characteristic in rapid biodiversity assessments on shoestring budgets, which allow for a first impression and provide detailed information for deeper investigation if desired. This type of rapid assessment additionally serves as a pilot study for further assessments. In the present study the focus lies on spatial global coverage, instead of local detail.

2.2.3 Animal Species Data Collection

In the ideal case, the protocol should result not only in information about the presence or absence of species, but also in an estimate of population size. The DISTANCE sampling approach uses the concept of a detection function based on distance of the observed object from the observer to estimate population density (Buckland et al. 1993; Buckland et al. 2001). It plays a central role in this study and is used in a number of ways.

At each of the 30 plots (25 systematic and 5 random), five minute point transect DISTANCE sampling counts for birds were conducted within 360 degrees (Buckland et al. 2008). A short settle-in period of one minute was granted prior to counting to allow for the snapshot character of DISTANCE sampling, especially meeting the assumption that presence of the observer does not introduce bias by causing responsive movements of animals. Following common practice the point counts took place only in the morning between 5:30 and 10 am. Birds are known to show higher activity at this time, which generally increases detectability and maximizes inventory accuracy. Each bird seen or heard was noted, including an estimate of the radial distance from the observer. Double counts were avoided by the observer's attention and the relatively short counting period.

Observers decided to make two adjustments:

- in study area 4Ru seabird observations were excluded from plot A1;
- in study area 6Ba the survey time was reduced from five to four minutes.

The second method of DISTANCE sampling used was a trapping web (Parmenter & MacMahon 1989). 17 pitfall traps with a diameter of 9 cm each were arranged in a DISTANCE sampling trapping web design to estimate ground-living insects (as described in Buckland et al. 2001, p.216ff). This sampling method is very labor-intensive and could not be implemented at all 30 plots given the short time period available. Thus, four of the plots were systematically selected to capture the general patterns of species and abundances within the GRID: B2, D2, B4 and D4 (underlined in Figure 8) to gather at least some information about ground-living insects. Trapping webs were usually checked every 24 hours; and records were taken every 48 hours. In between check dates the cups were emptied without recording to avoid correlation in time between trapping events, and obtain spatially independent results.

Because of the low number of traps and more available work force it was decided to add a third circle of traps at 3 m from the centre in study areas 4Ru, 5PG and 6Ba. This increased the total number of pitfall traps in these areas to 25.

The third application of DISTANCE sampling was an add-on sampling protocol using DISTANCE sampling line transects, conducted at each of the 30 plots. Transects with a length of 10 m and traversing the plot at its centre were surveyed to estimate numbers of butterflies, amphibians and reptiles.

DISTANCE sampling point counts for birds and trapping webs for ground living insects were repeated three times. These repetitive visits further allow for an analysis with the software PRESENCE, which gives an estimate of general occurrence of a species in the area in a point-based sense. PRESENCE generates a detection function based on multiple visits under the assumption that the population is closed, meaning that no animals leave or enter the area of interest between several visits. Repetitions were not realized for the add-on protocol for DISTANCE sampling line transects.

2.2.4 Vegetation & Environment

Additionally, basic data about the plot environment was collected. If at all possible, the GPS coordinates were noted. A plot picture and a canopy picture were taken with a digital camera to give a general impression of the area and also allow for an analysis of light conditions in other studies on the same data set, e.g. remote sensing investigations (Figure 9). All pictures are available in the raw data file of the digital appendix on the accompanying DVD.

Figure 9: Sample pictures (habitat picture plot D3 in 1CR; canopy picture plot D3 in 3AK)

A short description of the ecosystem was noted as well (for example: pasture, forest interior, forest edge). Height and diameter at breast height were recorded for all trees within 5 m of plot centre. Estimates were noted regarding canopy cover percentage, understory cover percentage, shrub cover percentage (at 1.35 m height), bare soil percentage, duff coverage percentage, leaf browsing percentage, and number of flowers visible. The thickness of epiphytes, hemi-epiphytes, mosses and lichen was noted in categories (none, low, medium, high). Presence/absence of identified plant species or plant families was noted, as well as remarkable animal tracks (e.g. land crab holes, large mammal tracks, etc). Those are referred to as “Covariates 1 to32” in all six study areas, but the actual meaning is different in each. Detailed lists are attached for each study area (page 123). The full protocol is attached in the appendix (page 117 ff). The covariates can have one of four effects:

1. affecting habitat quality (presence/ absence of a species)
2. affecting detectability (detection/ non-detection of a species that is present)
3. affecting both of the above
4. affecting none of the above.

2.3 Analysis Methods

All observations were sorted by plot label and visit number; and marked with an individual observation ID. The data was then cleaned according to the following protocol:

- missing distances were replaced with ‘5000 m’ to be discarded due to data truncation as described by Thomas et al. (2006);
- fields for plots with no observations were emptied, lines with no observations were uniformly marked as ‘none’;
- narrative names assigned during observations were cleaned and summarized to avoid duplicates (“small ant” and “ant, small” are the same narrative, while “tiny ant” is a new one);
- type of identification during observation was standardized to aural/visual;
- habitat type was standardized to 3-5 classes in each region (cp. Table 1);
- sunrise time for each day and region was added, as well as the calculated amount of time between sunrise and observation;
- effective survey effort was calculated for trapping webs;
- comments were worked through and additional information was integrated into the data as far as possible.

Table 1: List of habitat types by study area

1CR	2Ni	3AK	4Ru	5PG	6Ba
Forest edge	Forest edge	Forest edge	Forest trail	Forest edge	Arctic tundra
Forest gap	Forest trail	Forest trail	Interior forest	Forest trail	
Forest trail	Interior forest	Interior forest	Scrubs	Interior forest	
Pasture	Pasture	Pasture		Pasture	
Wetland	Plantation	Wetland			

One table each for observations, plot information and visit information was prepared and imported into MS Access database (Microsoft Office Access 2003 SP3). Additionally, an attempt was made to derive as much taxonomic information about the narrative names noted in the field as possible. All information was cross-checked and taxonomic validity was verified with online information provided by ITIS (Integrated Taxonomic Information System (ITIS), www.itis.gov) and imported into the same Access project database. The full database (DB_MINC.mdb) is available on the digital appendix DVD for this thesis, as well as all raw data sheets (in file “RawData”).

All files for data analysis with other software were derived through individual queries from this central project database. According to the method of plot selection the bird count and DISTANCE transect data was separated into a systematic set (25 plots) and a random set (5 plots). The random set was run as a test set for the systematic set, although small sample sizes were expected to increase standard errors. To increase the number of observations for analysis these two sets were also pooled and additionally analyzed together. Bird count data was further split into aural and visual detections as the form of detection is known to greatly influence detection probability (Marques et al. 2007). If an observation was detected both visually and aurally, then it was allocated to the visual data set. This resulted in a total of nine data sets for each of the six study areas:

- five bird count data sets (systematic, random, pooled, visual detection, aural detection);
- three DISTANCE transect data sets (systematic, random, pooled);
- one trapping web data set.

The exception is the GRID in 6Ba, where all bird detections were visual. In this case there are only three bird count data sets (systematic, random, and pooled).

Usually, each analysis was run using the narrative name given to the specific observation in the field. If further information was expected by summarizing different observation narratives and running the analysis on a higher taxonomic level, especially biological order and biological family, additional analysis targeted those levels. These have been found to be valid surrogates for rapid assessment and monitoring of species diversity (e.g. Negi & Gadgil 2002). Pooling decisions were made on a case-by-case basis (detailed lists are provided under 0 in the appendix).

2.3.1 Random Forests

Each data set was analyzed with Salford Systems Random Forests, version 1.0 (Breiman & Cutler 2005). Random Forests is a machine learning algorithm using sets of classification and regression trees for data mining and to build powerful predictive models (Breiman 2001). The value of such analysis methods for numerous ecological applications is increasingly recognized.

Three different models were built: the first one used only plot data plus detection/non-detection of narratives at each plot to find patterns in the data and make predictions per plot by given spatial covariates. It is called '*Plot*', targets were all narrative names detected at least at five different plots. Because trapping webs were implemented at four plots only, this model was not applied to trapping web data.

Since there was a maximum of 30 plots at each region and 30 is a low number of samples for machine learning applications, two additional models were run on the complete number of observations, allowing spatial repeats. The first model used only environmental and vegetation covariates collected in the field; it is referred to as '*Covariates*'. The second one additionally used detection/non-detection of other animal species at the same plot as covariates to account for interactions between species; it is referred to as '*Interspecies*'. Table 2 gives an overview about differences between the used models. When aiming at the biological order or biological family level, all narrative names/species belonging to this particular order/family were excluded as covariates. Narratives observed through point or line transect sampling were taken into account when targeting trapping web narratives, because this data was equally available for all four trapping web plots. The only exception was study area 5PG, where the combined number of all point transect and trapping web observations exceeded the software limit for queries, so that only point count observations were used as additional covariates. On the other hand, narratives observed through trapping webs were not taken into account for *Interspecies* models for point and line transect narratives; this data was available for only four of the 30 plots. Targeted was the detection/non-detection of each narrative name with at least five observations. Random Forests settings all remained as 'default' (500 decision trees), only the number of predictors considered for each node was set to the square root of the number of used covariates (rounded up), as indicated in the accompanying software handbook. The best model was selected by highest ROC integral (Fawcett 2006).

All Random Forests import files and project files are available in the accompanying digital appendix DVD (under "ProjectFiles/RandomForests").

Table 2: Random Forests model overview

Model name	Set of predictors	Response Variable	Spatial Repeats
Plot	Environmental covariates	Presence/ absence of target (Narrative, Order, Family)	No
Covariates	Environmental covariates	Presence/ absence of target (Narrative, Order, Family)	Yes
Interspecies	Environmental covariates and presence of other species	Presence/ absence of target (Narrative, Order, Family)	Yes

2.3.2 DISTANCE Sampling

A full DISTANCE sampling analysis was run for all narrative names with at least 20 observations using DISTANCE 5.0 Release 2 (Thomas et al. 2006). This is considerably lower than the 60-80 observations usually recommended, so inconsistencies resulting from small sample size have to be considered especially for those narratives with less than 60 observations. All of the following model key functions and model series expansion combinations were used (as in Buckland et al. 2001, p. 47):

1. Half-normal/ Cosine
2. Half-normal/ Hermite polynomial
3. Uniform/ Cosine
4. Uniform/ Simple polynomial
5. Hazard-rate/ Cosine
6. Hazard-rate/ Simple polynomial

Additionally, the two Half-normal and two Hazard-rate key function combinations were also analyzed with multiple covariate DISTANCE sampling (MCDS) in combination with each of the ten covariates identified as the most important by Random Forests for point and line transect data (Table 9 to

Table 11 in the results section). For trapping web data only the five most important covariates were used (Table 12 to Table 14 in the results section). All model definitions are listed in detail in the appendix under 7.3. Multiple covariate DISTANCE sampling is especially useful in situations were not enough detections are achieved to stratify the data by habitat and analyze each stratum separately (Alldredge et al. 2007; Marques et al. 2007). Among all models for a narrative name, the best ones for conventional DISTANCE sampling and multiple covariate DISTANCE sampling were selected by visual assessment of model fit and Akaike information criterion (AIC).

All DISTANCE sampling import files and project files are available for investigation in the accompanying digital appendix DVD (under "ProjectFiles/DISTANCE").

2.3.3 PRESENCE / Occupancy

Occupancy estimations were derived by the software PRESENCE (Hines 2006) for the same narrative names as selected for DISTANCE analysis. For each narrative name one model was run assuming constant detection probability and second assuming different detection probabilities for each visit. Additional runs were conducted adding each of the site and visit specific covariates used in DISTANCE. Observation specific covariates were left out because of the different structure of analysis in PRESENCE, which takes only site and visit specific covariates into account. Categorical and continuous covariates were standardized in MS Excel according to common standards before importing into PRESENCE software (Donovan & Hines 2007). All models are listed in the appendix in chapter 7.4. The best model was selected using AIC.

All PRESENCE import files and project files are available for investigation in the accompanying digital appendix DVD (file "ProjectFiles/PRESENCE").

3 Results

3.1 General Overview

Statistically there are two totally different estimations of biodiversity at each GRID: a systematic sampling design using 25 plots (respectively four for ground-living insects), and a random sampling design using five plots. They are lumped together for analysis to increase sample size for this initial method evaluation, despite losing the possibility to generalize the results to a larger region. Added together from all 180 plots at six study areas the three data collection routines resulted in a total of 5,007 animal observations (Table 3). 496 different narrative names are registered; Table 4 allocates the narrative names to the study areas in different regions. The add-on protocol for butterflies, amphibians and reptiles yields results in two out of the six study areas. Detailed species lists are given in the appendix (page 146 ff.). These also show the level to which taxonomic identification is possible. The number following some narrative names refers to the title of the picture taken of this particular narrative in the field. This is especially the case for trapping web narratives caught at 2Ni. All of these pictures are available from the digital appendix DVD (under RawData).

Table 3: Number of observations by region

Study area	Number of bird observations	Number of trapping web observations	Number of line transect observations
1CR	646	195	18
2Ni	361	480	61
3AK	692	237	-
4Ru	509	231	-
5PG	440	238	-
6Ba	419	480	-
Total	3067	1861	79

Table 4: Number of narratives by region

Study area	Number of bird narrative names	Number of trapping web narrative names	Number of line transect narrative names
1CR	49	11	5
2Ni	33	58	11
3AK	17	20	-
4Ru	45	34	-
5PG	86	66	-
6Ba	22	39	-
Total	252	228	16

Figure 10 shows a comparison of the number of observations in different regions, divided by point transect bird observations; trapping web catches and line transect observations. The GRID in 1CR for example yielded 21.1 % of bird observations, but only 10.5 % of ground insect observations, while having the same survey effort as the GRID in 2Ni with 11.8% of bird observations, but 25.8% of trapping web observations. These figures are raw count data and not corrected for detectability.

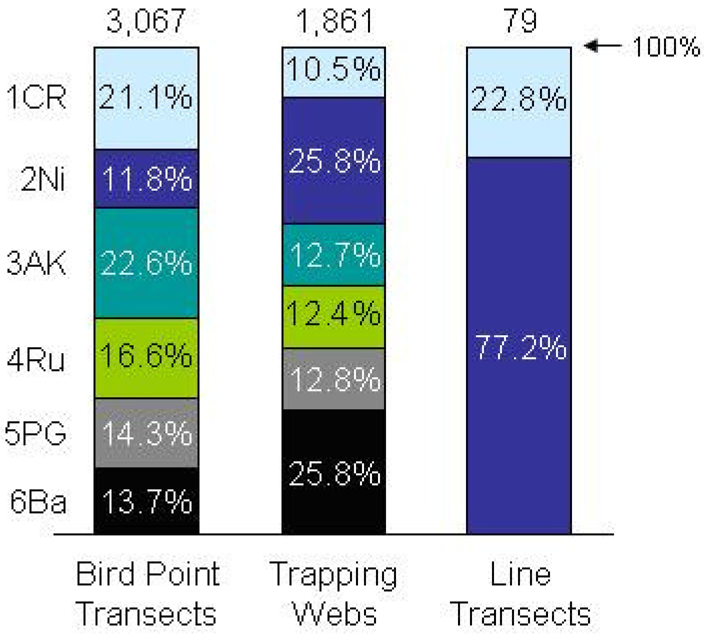

Figure 10: Percent of observations by region and type of survey

Figure 11 divides the number of narrative names into percent by region. This can be seen as a very simple estimate of species richness. For example, the GRID 3AK resulted in 22% of total bird observations (Figure 10), but yielded only 7% of bird species richness (Figure 11).

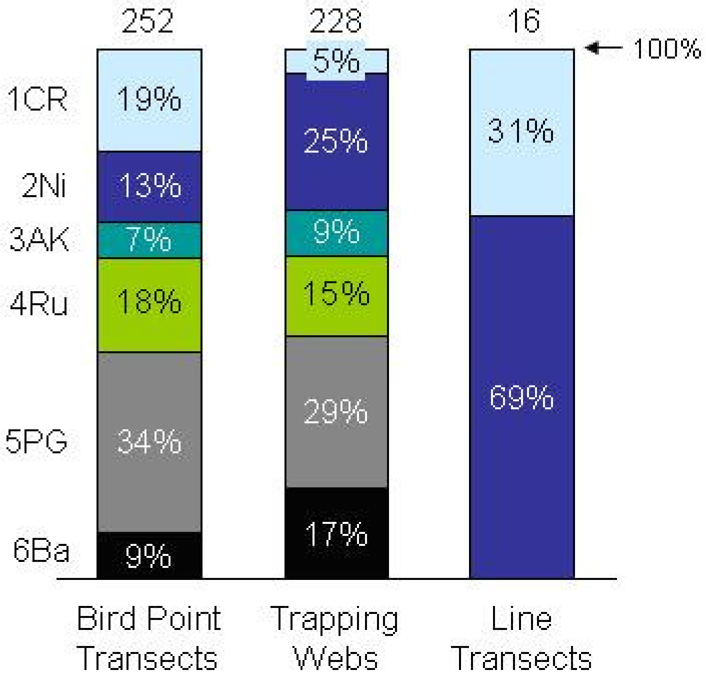

Figure 11: Percent of narrative names by region and type of survey

Despite all efforts to have equal survey effort in all 6 regions this goal was not reached and differences in survey effort have to be kept in mind when interpreting these figures. Table 5 gives an overview over survey effort by sampling method and region. Line transect survey effort was consistent in 1CR and 2Ni, while this sampling method was abandoned in the other regions.

Table 5: Survey effort by region and sampling method

	Bird point transects	Trapping web: number of traps	Trapping web: area covered	Trapping web: total time
1CR	3x 5 min/ plot	17/ plot	4x 19.63 m²	311 h
2Ni	3x 5 min/ plot	17/ plot	4x 19.63 m²	299 h
3AK	3x 5 min/ plot	17/ plot	4x 19.63 m²	296 h
4Ru	3x 5 min/ plot	25/ plot	4x 38.48 m²	216 h
5PG	3x 5 min/ plot	25/ plot	4x 38.48 m²	192 h
6Ba	3x 4 min/ plot	25/ plot	4x 38.48 m²	279 h

There is no visible trend connecting greater survey effort with higher species richness. For example, the trapping webs in 1CR yielded only 5 % of observed species in spite of having the greatest total survey effort, while the trapping webs in 5PG with the lowest survey effort yielded 29 % of all species catches.

The data from systematic plots is expected to contribute about 80 % of observations, the data from random plots 20 %. Figure 12 shows the distribution of raw count data not corrected for detectability between random and systematic plots for all point transect detections, Figure 13 provides the same information for data collected through line transects. Trapping webs are not shown because they were installed at four systematic plots only. With the exception of bird point transect data at GRID 1CR, the proportion of observations from random plots is generally a little lower than expected. At this point this phenomenon can only be explained with a relatively small sample size because there were no obvious differences between random and systematic plots.

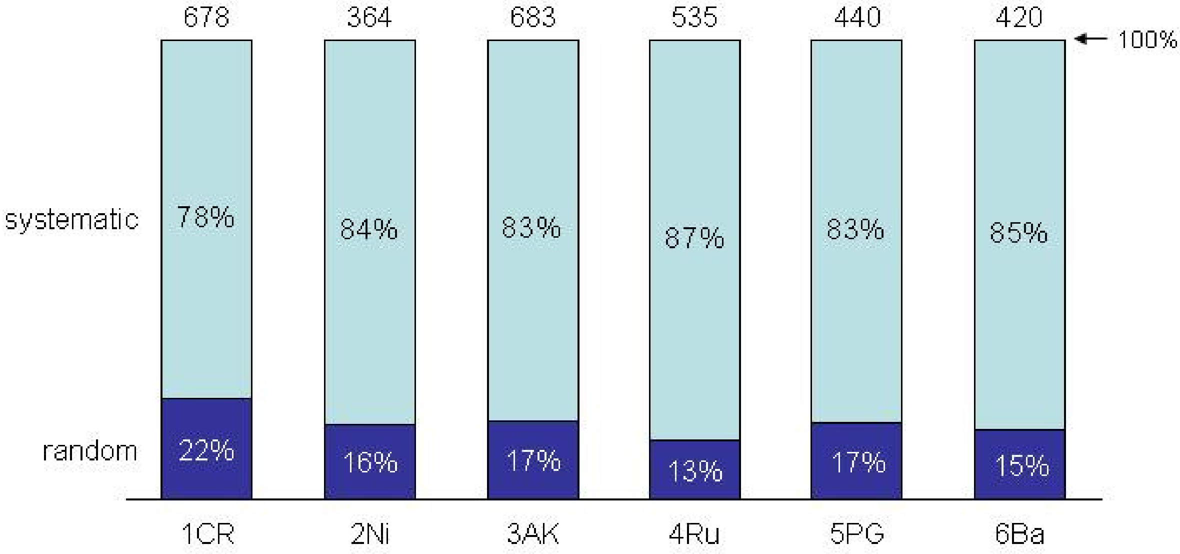

Figure 12: Distribution of point transect observations by plot type (random/systematic)

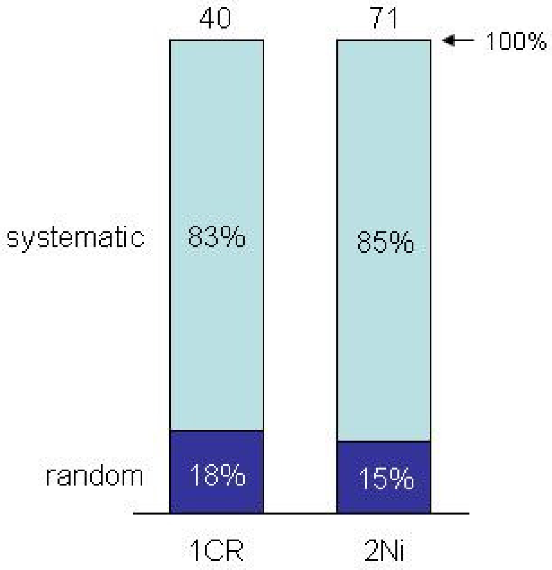

Figure 13: Distribution of line transect observations by plot type (random/systematic)

Figure 12 shows all observations made from all plots. For analysis using plot features the data has to be spatially tied to a plot, meaning observations further away than 50 m are discarded because they possibly are spatially closer to the neighboring plot and its features. Since information of the direction of observations from the observer was not collected, the observations at greater distances than 50 m could not be assigned to one of the neighboring plots. The 50 m border is not relevant for trapping web and line transect data because there were no observations at distances greater than 50 m. Figure 14 shows the distribution for bird point count data, for further analysis only observations within 50 m of the observer is used. The percentage of observed distances greater than 50 m at 3AK is obviously high, while the percentage at 6Ba seems to be low considering that there was no vegetation blocking view in any direction. There is no readily available explanation for these points.

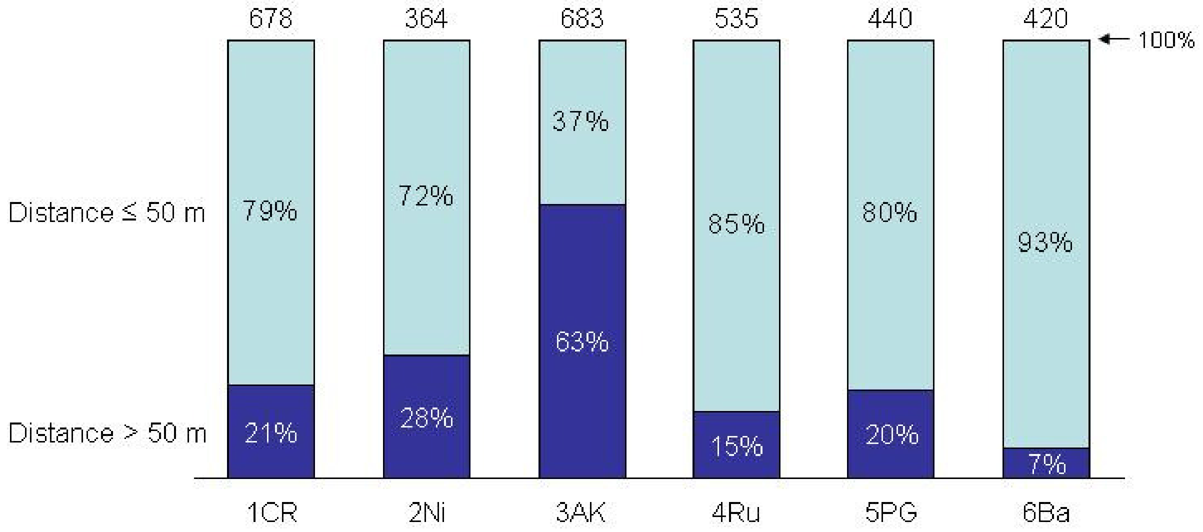

Figure 14: Percent of observations spatially belonging to plot (within 50 m radius)

The last split is between aural and visual detections for point transects (Figure 15). Observations for which information about the form of detection was lacking were disregarded for this analysis. All observations that were detected aurally as well as visually were noted as 'visual' and are used only in the assessment of visual detections.

Figure 15: Proportion of aural and visual point transect observations

3.2 Predictive Modeling with Random Forests

Any Random Forests model with a ROC value greater than 0.5 is considered non-random, and therefore a valid predictive model. Complete tables with best ROC values for each data set can be found in the appendix (page 150 ff), while all ROC values are available from the digital appendix DVD. Here only the key results will be displayed. Analysis is run on the pooled data from random and systematic plots and from aural as well as visual detections, unless stated otherwise.

Figure 16 shows the relationship between ROC value and number of observations. An overview about which narrative names are summarized together and analyzed at the biological family and/or biological order level is given in the appendix starting at page 166.

Generally there are many valid models for narrative names with less than 20 observations, but there are also many random models. All models with at least 80 observations, which is recommended as a minimum for DISTANCE sampling analysis, result in valid non-random models in Random Forests. This picture is less clear for analysis at the biological order or family level, in both of these cases there are random models (ROC <= 0.5) or models with a ROC only slightly higher than 0.5 which build on 200 or more observations. This might be an indicator that pooling in taxonomic classes is not a valid way to receive bigger datasets, especially since differences on the biological level, like habitat requirements, can be huge between two species belonging to the same taxonomic tree.

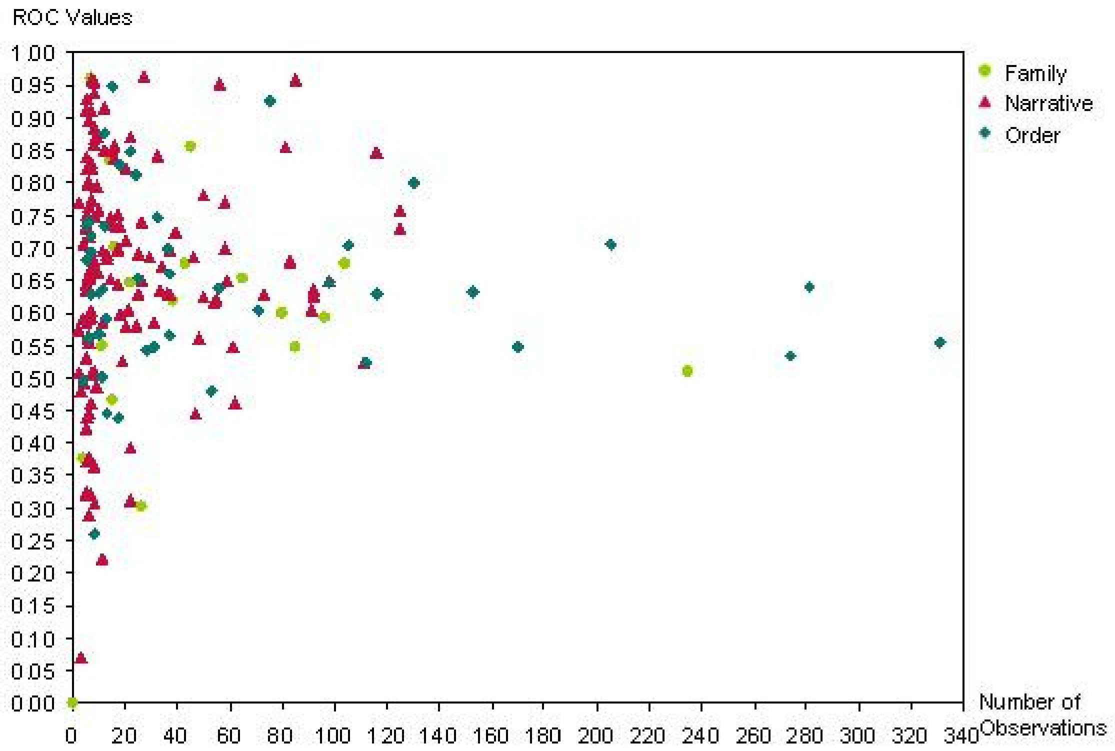

Figure 16: Correlation between number of observations and ROC values of model

3.2.1 ROC Values by Region and Model

Three different models are used for predictive modeling with Random Forests: *Plot*, *Covariates*, and *Interspecies*. *Plot* uses only detection/ non-detection data for each plot, combined with this plot's covariates. *Covariates* uses all detections at a plot combined with its covariates, allowing for spatial repeats. *Interspecies* is basically the same model as *Covariates*, but adds detection/ non-detection of other species as additional covariates to the analysis. Naturally, the *Plot* model was possible for fewer narratives than the other two (cp. chapter 2.3.1).

The following figures from Figure 17 to Figure 28 compare the ROC values from these different models for each narrative name. For each study area there are two figures, one comparing all narratives analyzed with three models (including *Plot*), the second comparing all narratives analyzed with only two models because the number of plots where the narrative was detected was below five and thus not sufficient to run the *Plot* analysis. This affects especially all trapping web data, because it was collected at four plots only. Narrative names from point and line transects are capitalized to be able to discern them from trapping web narratives.

Of 22 narrative names observed at study area 1CR predictive modeling results in valid models for all but two of them (Dove and Spider), for both of them analysis with *Plot* model is not possible. The *Plot* model failed to result in valid models for three more narrative names (Mealy Parrot, Oropendula, and Parrot). ROC value results from the different models usually are very close together (Figure 17 and Figure 18). The *Plot* model slightly outperforms the other two models in three cases (Parrot large, Toucan, and Woodpecker). *Covariates* proofed to be the best model for 11 narrative names and *Interspecies* for 9 narrative names, but both usually yield close results.

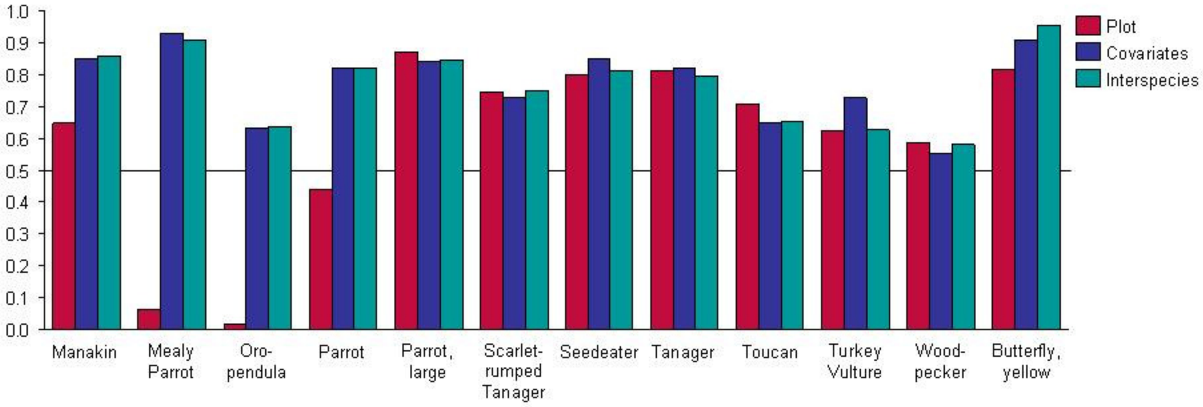

Figure 17: ROC values for narratives at 1CR (analysis with three different models)

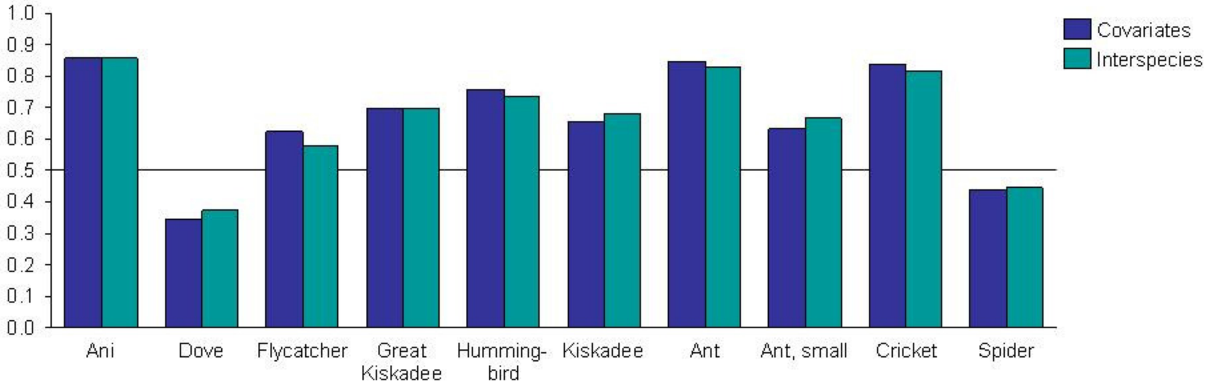

Figure 18: ROC values for narratives at 1CR (analysis with two different models)

30 narrative names are analyzed with Random Forests at study area 2Ni (Figure 19 and Figure 20). Valid models with ROC values > 0.5 are retrieved for 25 of those narratives, the lacking

five were Parakeet, Swallow, Beetle ground, Bristletail, and Caterpillar 877. *Plot* outperforms the other models only for Hawk. Adding species data to the modeling process does not increase ROC values in most cases, *Interspecies* is the best model only in four cases, and only in one of them it is actually better than *Covariates* (Butterfly, yellow), in the other three cases the results are equal. *Covariates* outperforms the other two models in 20 out of all valid models (ROC > 0.5).

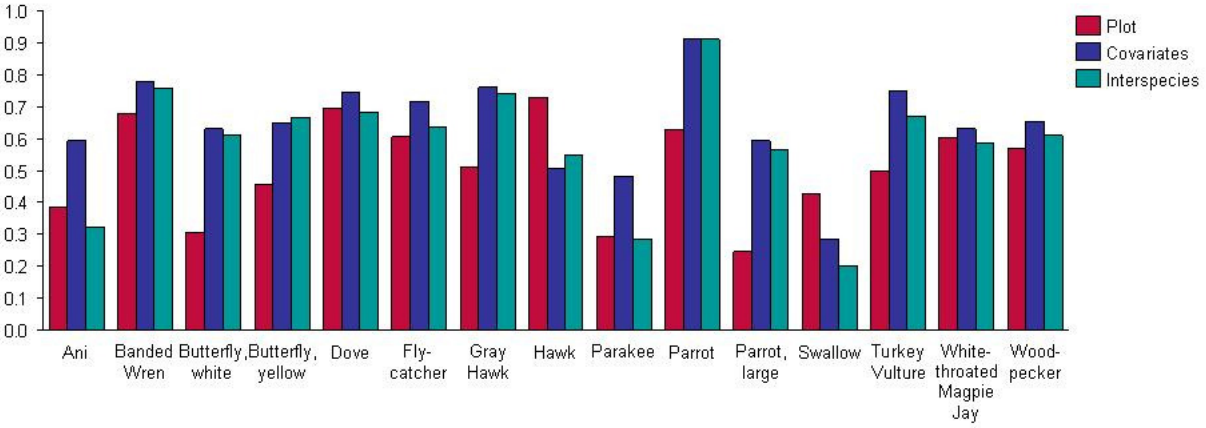

Figure 19: ROC values for narratives at 2Ni (analysis with three different models)

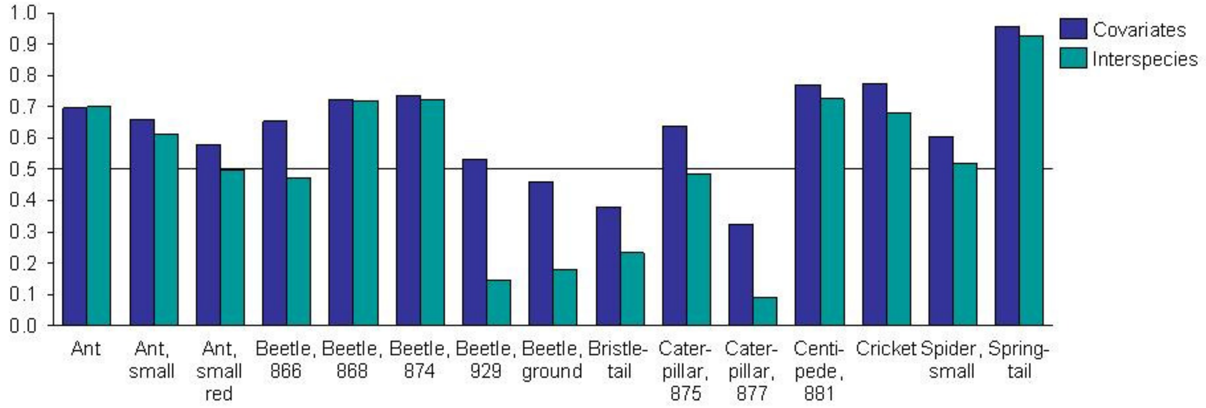

Figure 20: ROC values for narratives at 2Ni (analysis with two different models)

11 Narratives are analyzed from the observations at 3AK, 10 of which result in non-random models (Figure 21 and Figure 22). The only case in which the *Plot* model outperforms the other two is for Squirrel, but there the difference is very clear (ROC 0.86 against ROC 0.56). In all other cases the models *Covariates* and *Interspecies* are again very close, with a maximum ROC value difference of only 0.05 (for Spider, tiny).

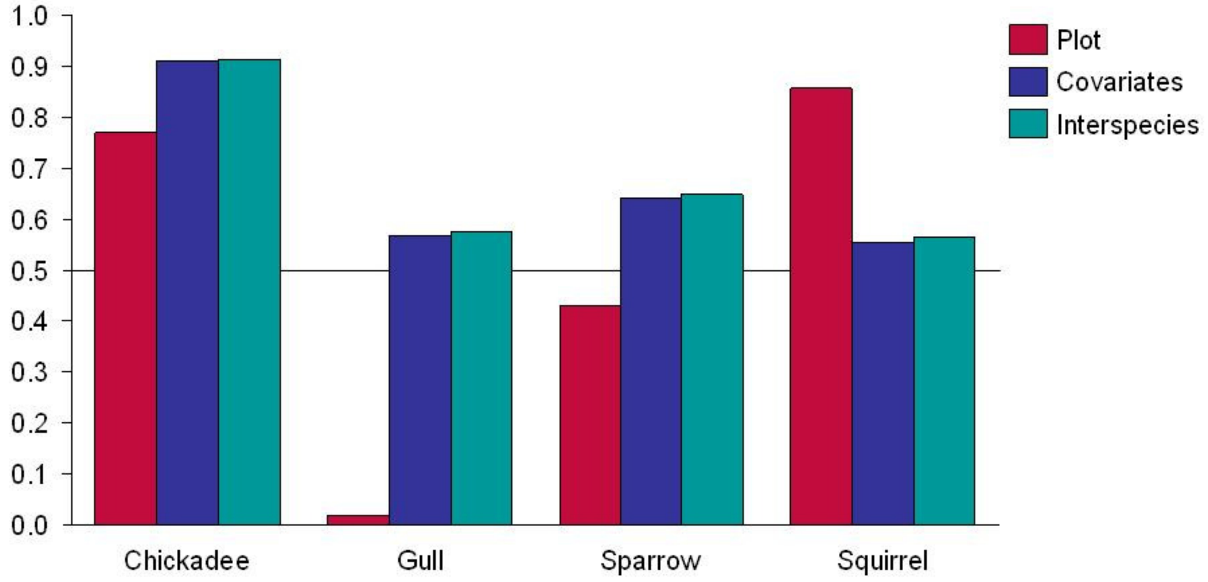

Figure 21: ROC Values for narratives at 3AK (analysis with three different models)

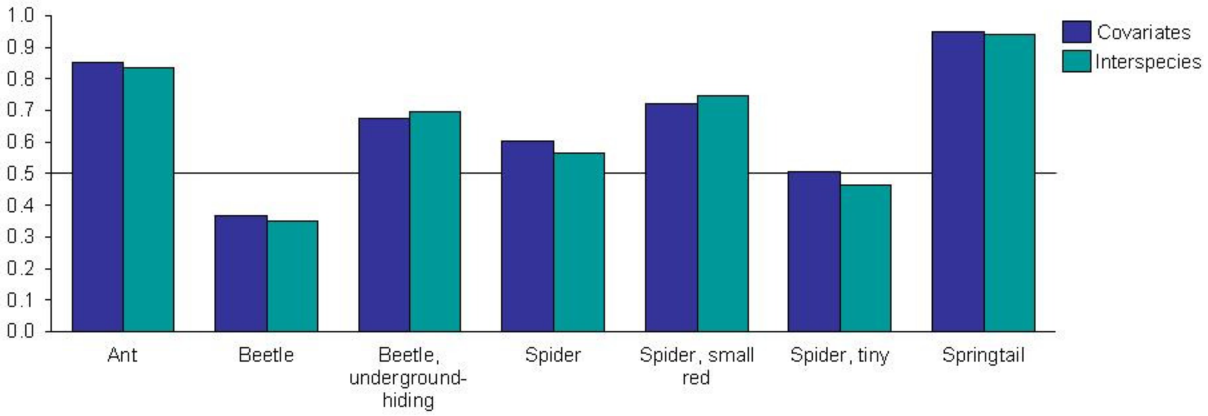

Figure 22: ROC values for narratives at 3AK (analysis with two different models)

23 out of the 27 narratives analyzed from 4Ru result in valid models, no predictive model is gained for Oriental Dove, Oriental Greenfinch, Beetle, and Spider (Figure 23 and Figure 24). The *Plot* model gains the same ROC value as the best other model for Chickadee and Woodpecker, but does not outperform any of the other models. *Covariates* and *Interspecies* results are again very close to each other, in five cases exactly the same ROC values are received. If those are disregarded the *Covariates* model outperforms the other two in 12 cases, the *Interspecies* model in 5 cases.

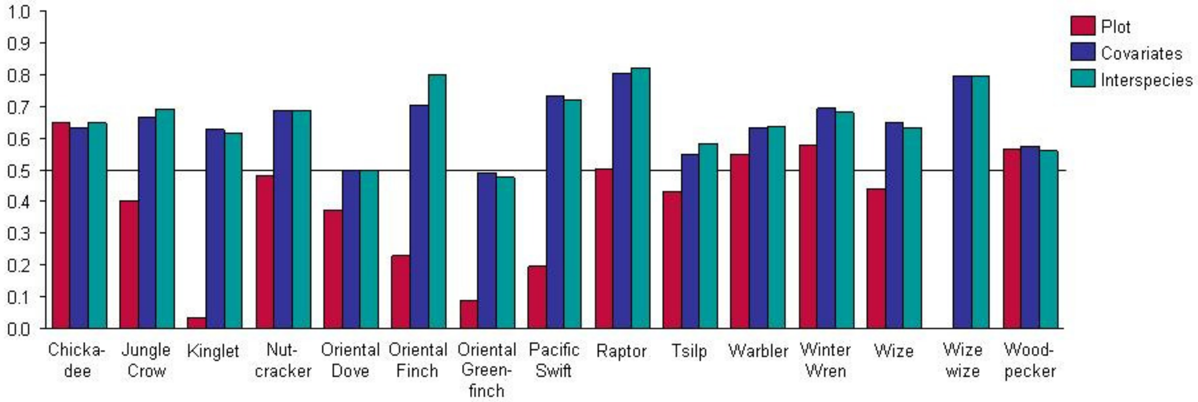

Figure 23: ROC values for narratives at 4Ru (analysis with three different models)

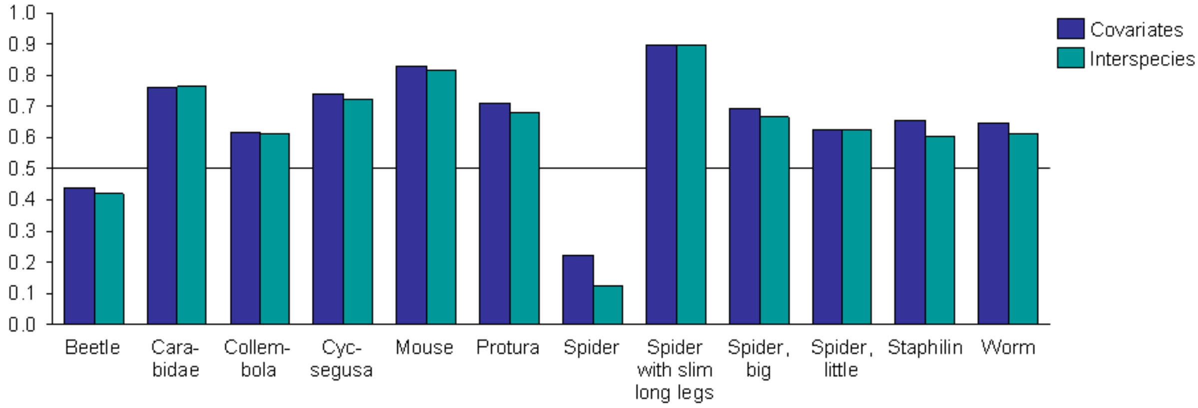

Figure 24: ROC values for narratives at 4Ru (analysis with two different models)

At study area 5PG 31 narratives are analyzed, of which only 23 result in valid models (Figure 25 and Figure 26). The eight narratives not adequately modeled are Parrot, Wize Wize, Woodpecker, tiny black Ant, Balu, Hawk, Hornbill, and Melodious Song. *Plot* outperforms other models for narrative Wiz Wiz, *Interspecies* is the best model for predictive modeling of Swallow. In the other 21 cases *Covariates* outperforms the other models.

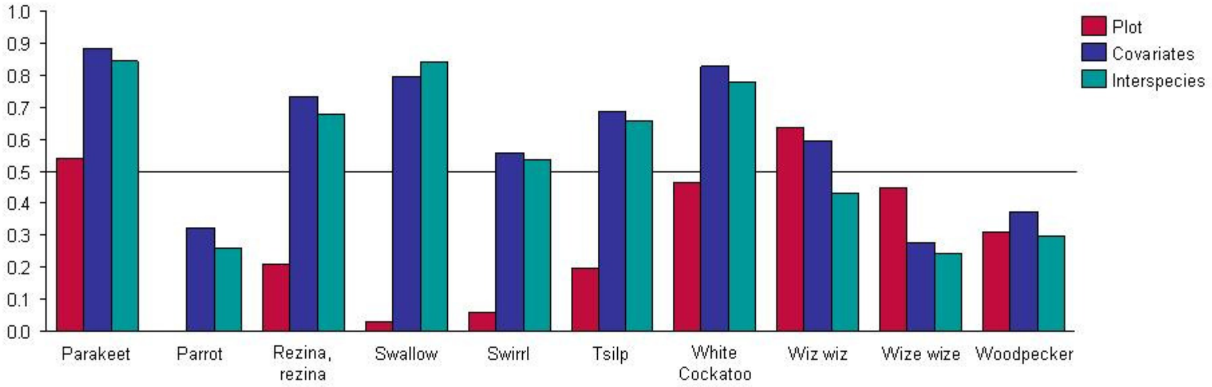

Figure 25: ROC values for narratives at 5PG (analysis with three different models)

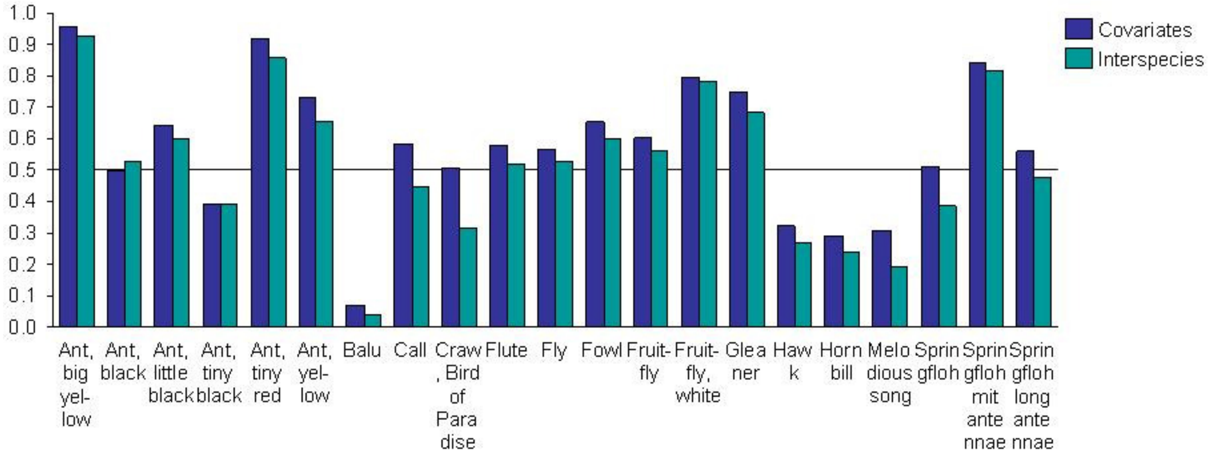

Figure 26: ROC values for narratives at 5PG (analysis with two different models)

Two out of the 20 narratives at study area 6Ba do not result in valid models: Semipalmated Sandpiper and Schuster. The other 18 gain ROC values > 0.5 (Figure 27 and Figure 28). The *Plot* model outperformsd the others in two cases: Dunlin and Red Phalarope. The *Interspecies* model delivers best results for Red-necked Phalarope and Pectoral Sandpiper, while having equally good results as *Covariates* for three more narratives (Longbilled Dowitcher, Lapland Bunting, and Pomarine Jaeger). *Covariates* is the best model for all 11 trapping web narratives as shown in Figure 28.

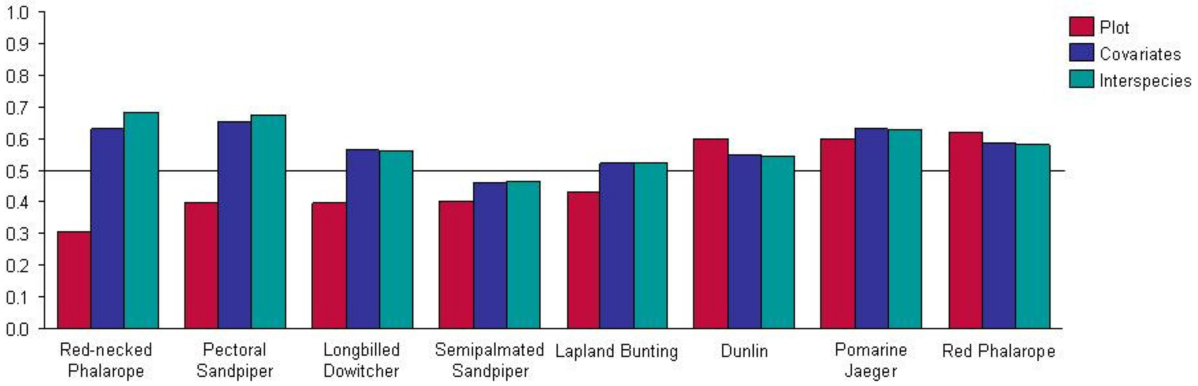

Figure 27: ROC values for narratives at 6Ba (analysis with three different models)

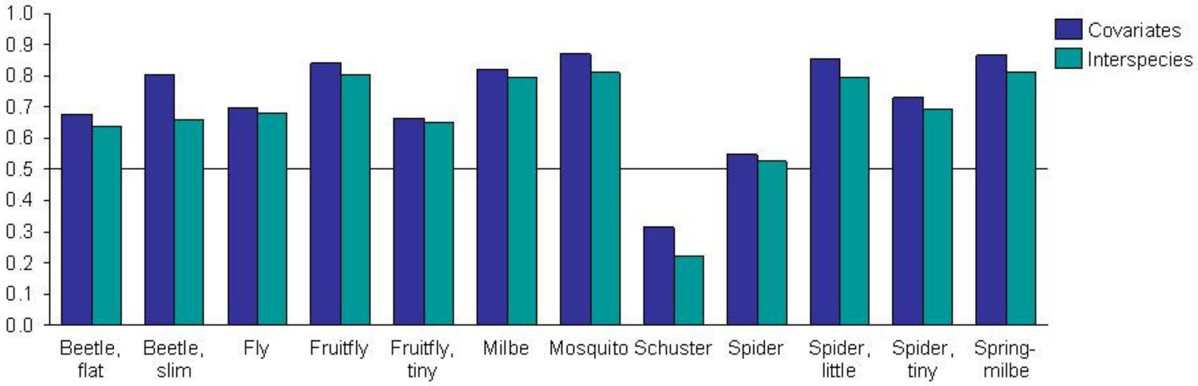

Figure 28: ROC values for narratives at 6Ba (analysis with two different models)

Table 6 shows the total number of models for each study area and the number of valid models with ROC values > 0.5 derived for this particular area. It also summarizes how often each of the models is the best valid model with the highest ROC value. If two models gain the same ROC value, both are regarded as best models, thus adding all best models together results in a number larger than the number of valid models (140 compared to 119). In about 67 % of all cases *Covariates* is the best model to predict a narrative, in 25 % it is *Interspecies*, and in 8 % the *Plot* model.

Table 6: Overview of models with best ROC values by region

	Total no of models	**No of models with ROC>0.5**	**Best model: *Plot***	**Best model: *Covariates***	**Best model: *Interspecies***
1CR	22	20	4	11	9
2Ni	30	25	1	24	4
3AK	11	10	1	6	5
4Ru	27	23	2	18	11
5PG	31	23	1	21	1
6Ba	20	18	2	14	5
Total	141	119	11	94	35

3.2.2 Randomly Selected vs. Systematically Selected Plots

For Random Forests analysis all observations from randomly selected and systematically selected plots are added together. Statistically this approach can be further stratified and fine-tuned. The pooling is done to increase sample size and it is based on the assumption that biology, occupancy, abundance, and all other attributes of a population do not differ between random and systematic plots for the GRID area. To check this assumption the data from random and systematic plots is analyzed separately and the best ROC value results compared with the results from the pooled data set. This is also set in relation to the number of observations gained from each of the two plot types. Since 25 plots are systematically selected at each GRID and only five are randomly selected the assumption would be that the random plots yield about 20 % of all observations, the systematic plots about 80 %. Since trapping webs have only been run at systematic plots this analysis is aiming at point and line transect data only.

Figure 29 and Figure 30 show these comparisons for narratives from 1CR and 2Ni. Generally the observations at random plots have a share of between 16 % and 23 % of total observations, coming close to the expected 20 % (Figure 30). Exceptions are Flycatcher at 1CR with only 10% and Banded Wren at 2Ni with 11 %. In effect, Flycatcher is the only narrative for which the data from randomly selected plots does not result in a non-random model, while there is no obvious effect at Banded Wren models. Surprisingly, the small amount of observations at random plots results in better models for Woodpecker and white Butterfly than the systematic or pooled data sets. For all other narratives either the systematic or the pooled data results in better models, with both values usually being close together. In three of these cases the pooled data delivers slightly higher ROC values than the systematic data, in two cases the ROC values of both are equal, and in the case of Banded Wren the ROC value for systematic data is 0.01 higher than the one for pooled data.

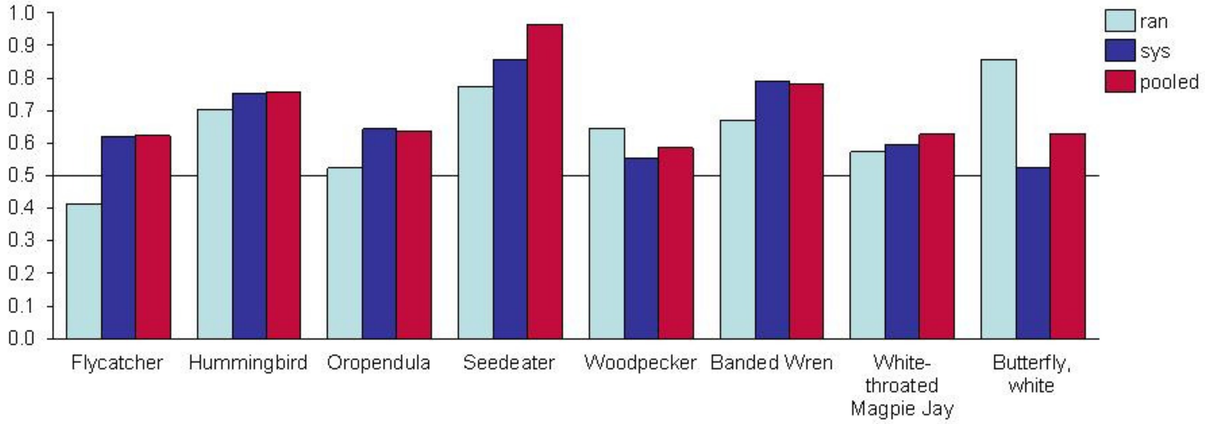

Figure 29: Best ROC values by plot type (1CR & 2Ni)

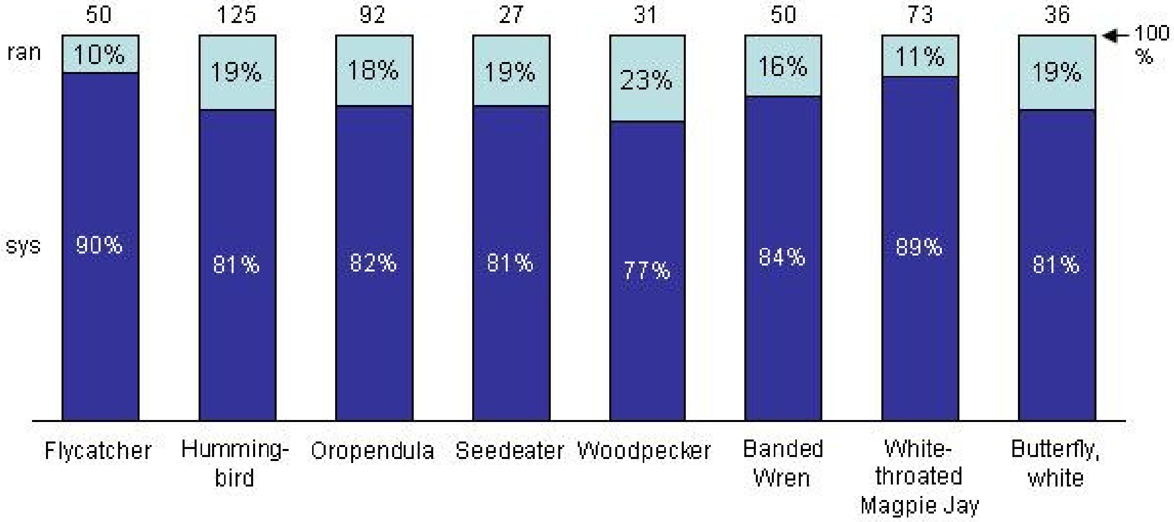

Figure 30: Distribution of observations by plot type (1CR & 2Ni)

ROC values for the different data sets from 3AK and 4Ru are shown in Figure 31, the distribution of observations between plot types in Figure 32. It is remarkable that only two species generate close to 20 % of observations from random plots: Squirrel at 3AK (16 %) and Kinglet at 4Ru (25 %). Proportions of observations from random plots for Sparrow at 3AK and for Chickadee and Wize at 4Ru are all quite low (12 %). Even lower is this proportion for Nutcracker at 4Ru (7 %), while all Warbler and Winter Wren observations at 4Ru stem from systematic plots. Only in the latter two cases an effect on the ROC values derived through the random data sets is visible because the modeling is impossible without input observations. Nutcracker with only 7 % of observations from random plots even has the highest ROC value from a random data set among all narratives. At 3AK pooling of the data for Squirrel results by far in the best model, while pooled data set and the random data set have the same ROC values for Sparrow, which is only slightly better than the one from systematic data set. At 4Ru the random data set results in the best model for Nutcracker, the systematic data set in the best model for Chickadee, and the pooled data set in the best model for the other four narratives.

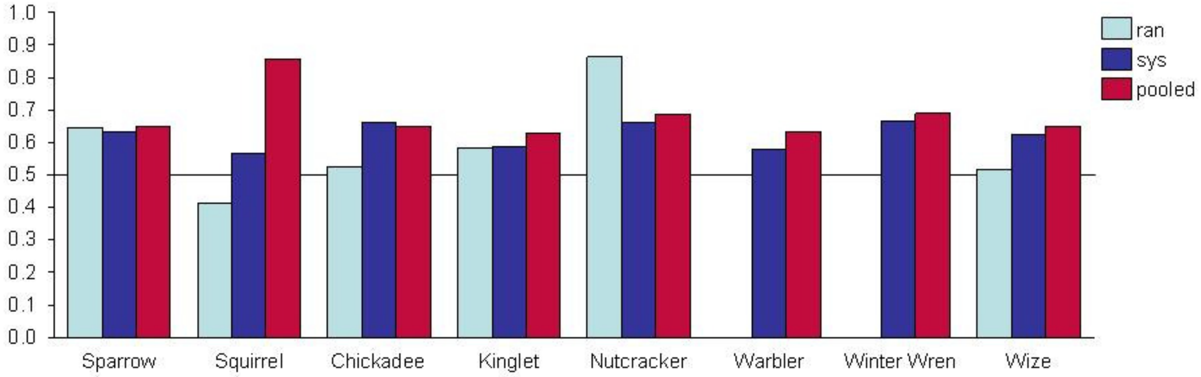

Figure 31: Best ROC values by plot type (3AK & 4Ru)

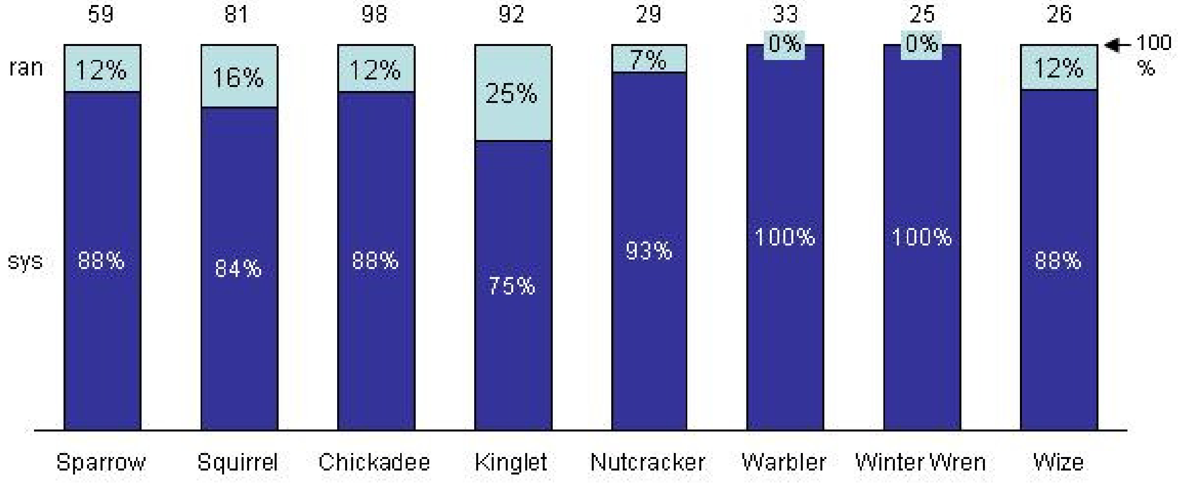

Figure 32: Distribution of observations by plot type (3AK & 4Ru)

At 5PG exactly 20% of observations are made from random plots, while for four of the six narratives from 6Ba the proportion of observations from random plots falls between 15 % and 19 % (Figure 34). Only 11 % of Red Phalarope observations are made from random plots, while Pectoral Sandpiper observations are only made from systematic plots. As a result, the random data set for Pectoral Sandpiper can not be modeled (Figure 33). The random data set for Red Phalarope results in a poor model with ROC = 0.39, but compared to the other models this does not seem to be a result of the relatively small proportion of observations from random plots. For both Flute and Tsilp from 5PG the highest ROC value is derived for analysis of the pooled data set. At 6Ba the models for Lapland Bunting and Semipalmated Sandpiper based on the random data set have the highest ROC value, for Pomarine Jaeger the one based on the systematic data set, and for the other three narratives based on the pooled data set.

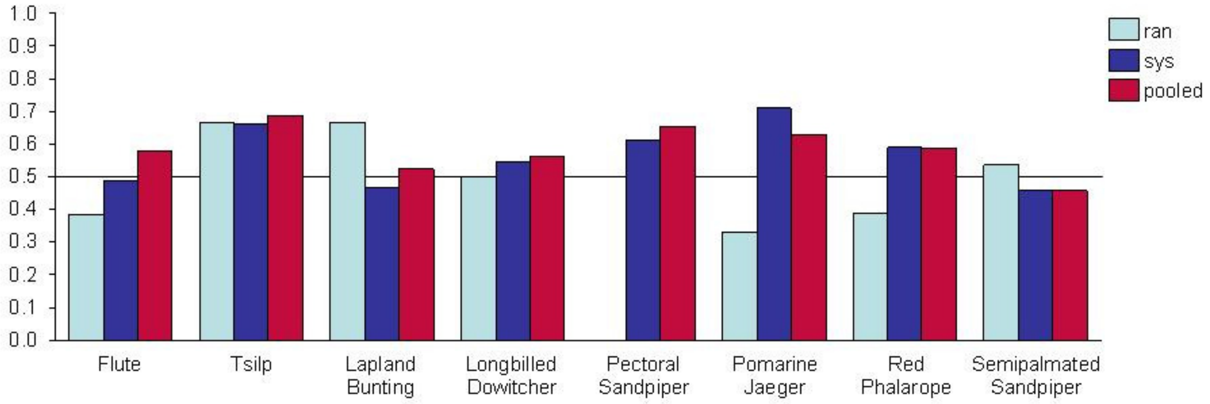

Figure 33: Best ROC values by plot type (5PG & 6Ba)

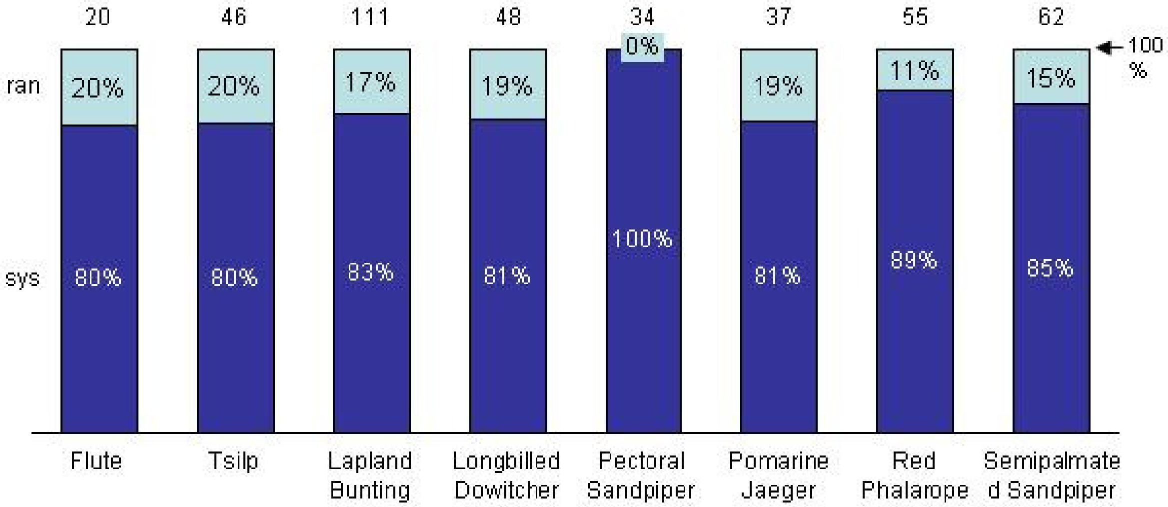

Figure 34: Distribution of observations by plot type (5PG & 6Ba)

Table 7 gives an overview about analysis of which data set resulted in the best model for the narratives analyzed. If two models gain the same ROC value, both are regarded as best models. Thus adding all best models together results in a number larger than the number of valid models (24 compared to 27). Differences between ROC values from systematic and from pooled data sets are relatively small, but usually the pooled data set performs slightly better (resulting in the low number of best models derived through systematic data sets). Sometimes the few observations at random plots analyzed separately result in surprisingly strong models.

Table 7: Best models for data sets from different plot types (random, systematic, pooled)

	Total no of models	No of models with ROC>0.5	Best model: random	Best model: systematic	Best model: pooled
1CR	5	5	1	2	4
2Ni	3	3	2	0	1
3AK	2	2	1	0	2
4Ru	6	6	1	1	4
5PG	2	2	0	0	2
6Ba	6	6	2	1	3
Total	24	24	7	4	16

3.2.3 Aural vs. Visual Bird Detections

It is common knowledge in bird surveys that visual detectability differs from aural detectability (Buckland et al. 2008). Birds can not be seen, but often be heard and identified by their song. To check the effect of pooling these two kinds of detections together the data is analyzed separately and the best ROC value results compared with the best results from the pooled data set. This is also set in relation to the number of observations gained from each of the two kinds of observation. This analysis is only done for the first five study areas. At the 6th study area 6Ba all detections are obtained visually, because the tundra is an open habitat hardly without visual distractions.

Figure 35 compares the ROC values of point transect detections from 1CR, 2Ni and 3AK; while Figure 36 shows the percentages of aural and visual detections. The proportion of visual detections ranges from 89 % for Seedeater in 1CR to only 4 % for Banded Wren in 2Ni and Squirrel in 3AK. The overall effect on ROC values seems to be rather low. For example, although 89 % of Seedeater observations are visual, the model built on the visual data set has almost the same ROC value as the one using the remaining 11 % of aural detections (0.73

compared to 0.72). The 4 % of Banded Wren detections which are visual result in a poorer model than the 96 % of aural detections (0.40 compared to 0.54), but the 4 % of Squirrel detections which are visual actually gain a much better model than the 96 % of aural detections (0.92 compared to 0.48).

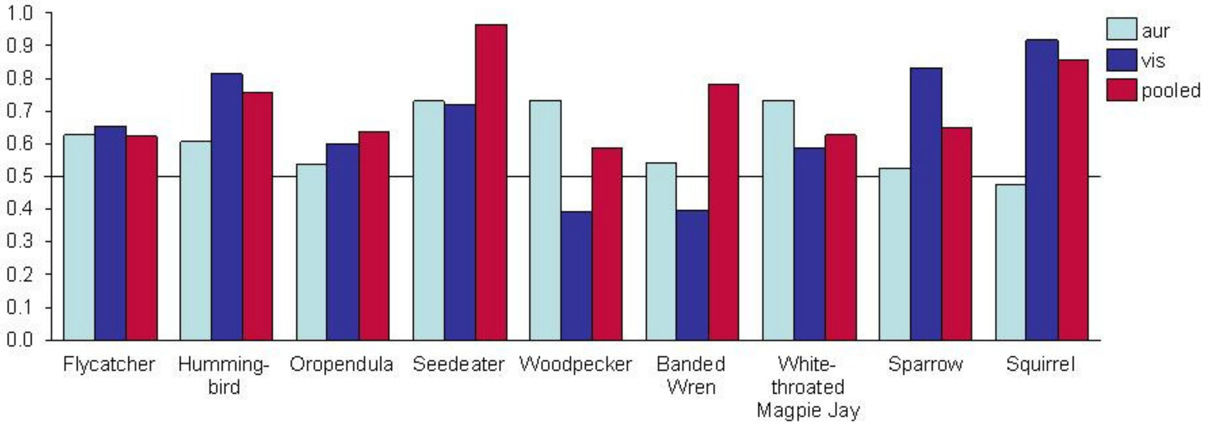

Figure 35: Best ROC values by type of observation (1CR-3AK)

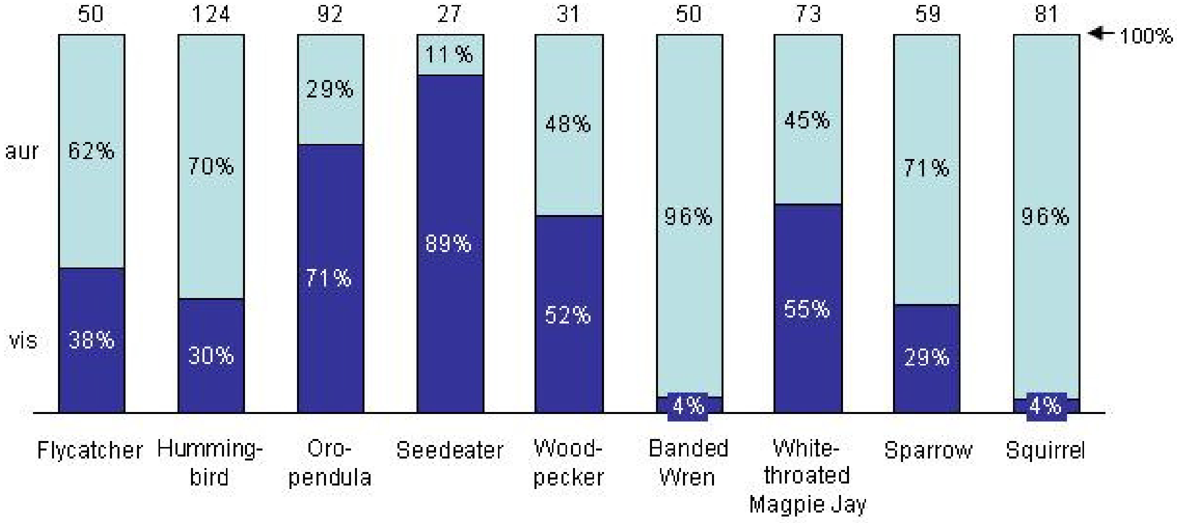

Figure 36: Distribution of observations by type of observation (1CR-3AK)

Figure 38 shows the distribution of detections between aural and visual in 4Ru and 5PG. Clearly most observations in these areas are aural, with percentages between 72 % and 100 %. Chickadee, Kinglet and Nutcracker with between 72 % and 75 % of observations being aural receive good ROC values from these data sets, while ROC values of this data set for narratives with more than 90 % aural detections are relatively poor (Figure 35).

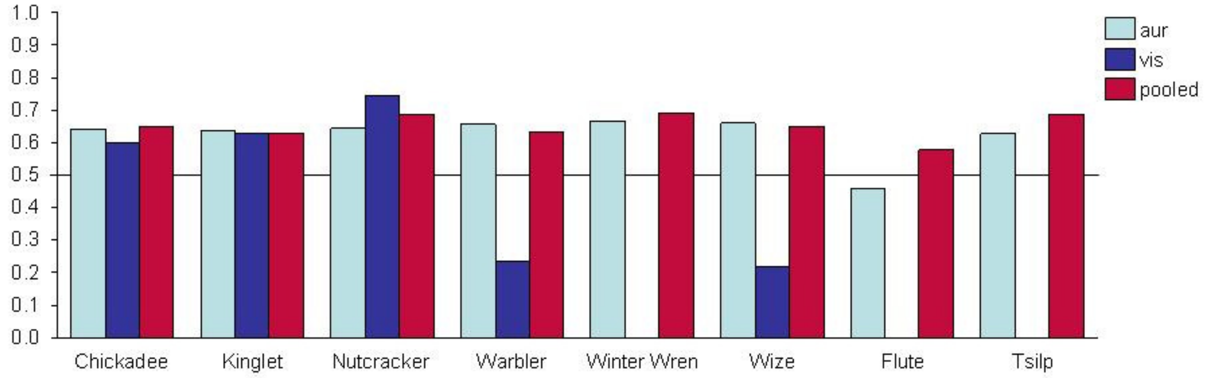

Figure 37: Best ROC values by type of observation (4Ru & 5PG)

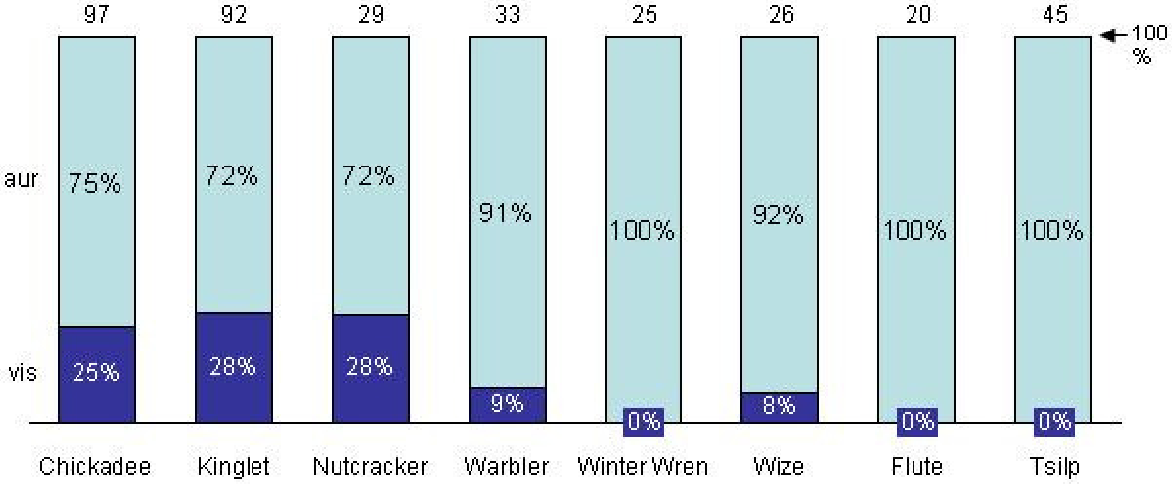

Figure 38: Distribution of observations by type of observation (4Ru & 5PG)

An overview about which data set results in the highest ROC value for a narrative is given in Table 8. The overall distribution is quite even between aural, visual and pooled data sets.

Table 8: Best models for data sets from different types of detection (aural, visual, pooled)

	Total no of models	No of models with ROC>0.5	Best model: aural	Best model: visual	Best model: pooled
1CR	5	5	1	2	2
2Ni	2	2	1	0	1
3AK	2	2	0	2	0
4Ru	6	6	3	1	2
5PG	2	2	0	0	2
6Ba	-	-	-	-	-
Total	17	17	5	5	7

3.2.4 Biological Family and Order as Analysis Targets

The main unit of interest for any biodiversity assessment is the biological species. But in many cases identification to species level is not possible, or the number of observations is too small for analysis at species level. To make use of this data, predictions at the biological family and biological order level are made in this section, detailed tables showing which narratives are summarized under which family and/or order name can be found in the appendix (page 166 ff). This chapter gives a short overview about analysis trends when moving up the taxonomic tree.

Figure 39 shows the best ROC values for analysis at biological family level, while Figure 40 gives an overview about how many observations the model was built on. A clear trend is not visible, for example 44 observations of Paradisaeidae from 5PG reached a higher ROC than 470 observations of Scolopacidae from 6Ba (0.65 compared to 0.51). Only the model for Tipulidae from 6Ba did not achieve a ROC value > 0.5. The highest ROC value achieved is 0.86 for Thraupidae from 1CR, building on 90 observations.

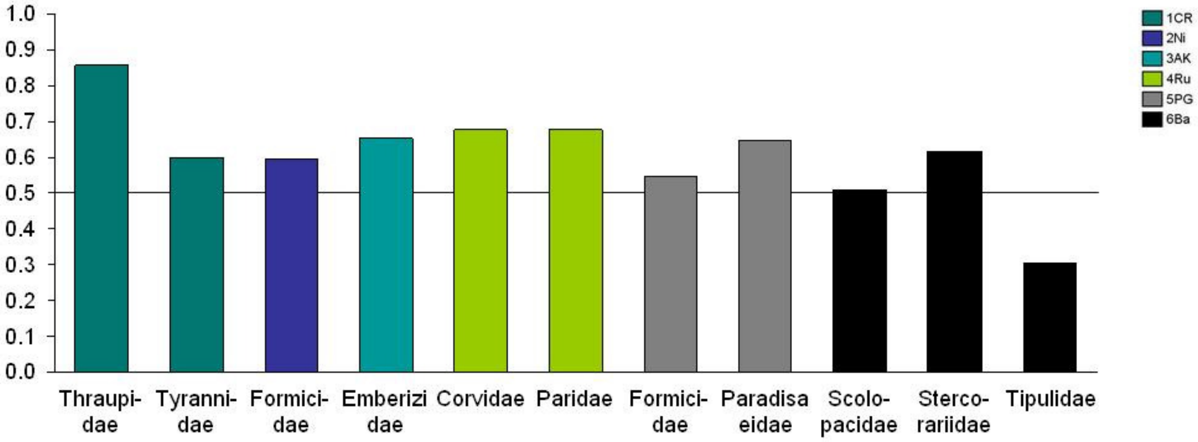

Figure 39: Best ROC values for analysis at biological family level

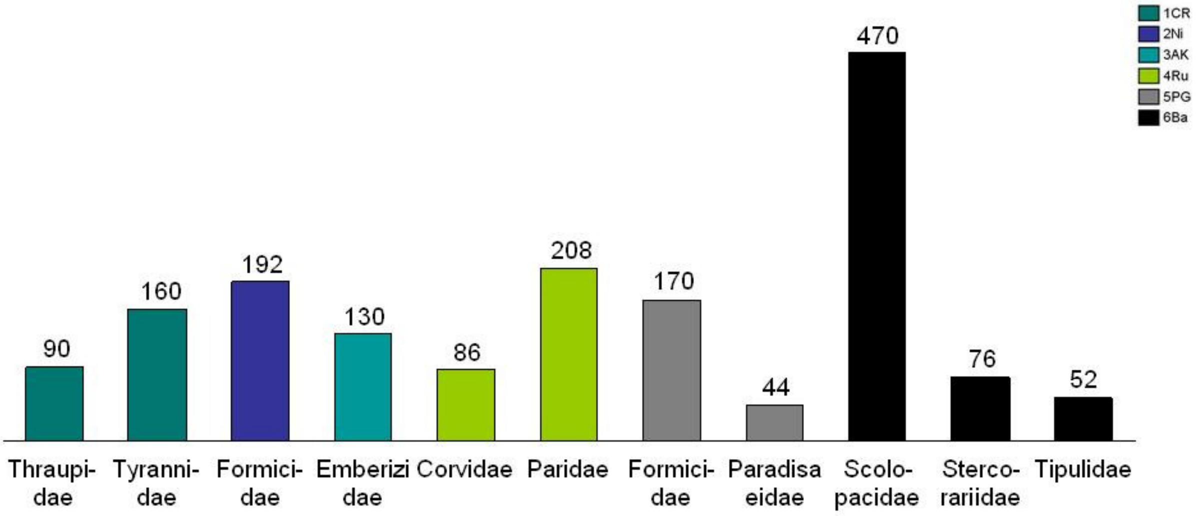

Figure 40: Number of observations pooled by biological family

The second biological level analyzed is the biological order. Results are shown in Figure 41 and Figure 42 for the study areas 1CR, 2Ni and 3AK. Also here larger numbers of detections do not automatically result in higher ROC values. Psittaciformes from 1CR built on the lowest number of observations received a ROC value of 0.85, while Passeriformes from the same study area built on the largest number of observations received a ROC value of 0.64. In this set ROC values > 0.5 indicate valid models for all runs at the biological order level.

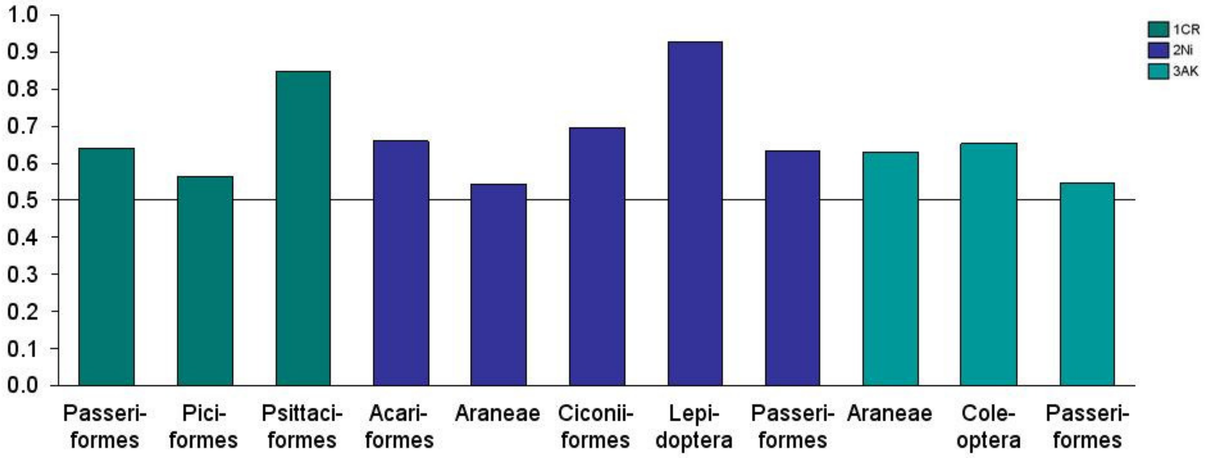

Figure 41: Best ROC values for analysis at biological order level (1CR-3AK)

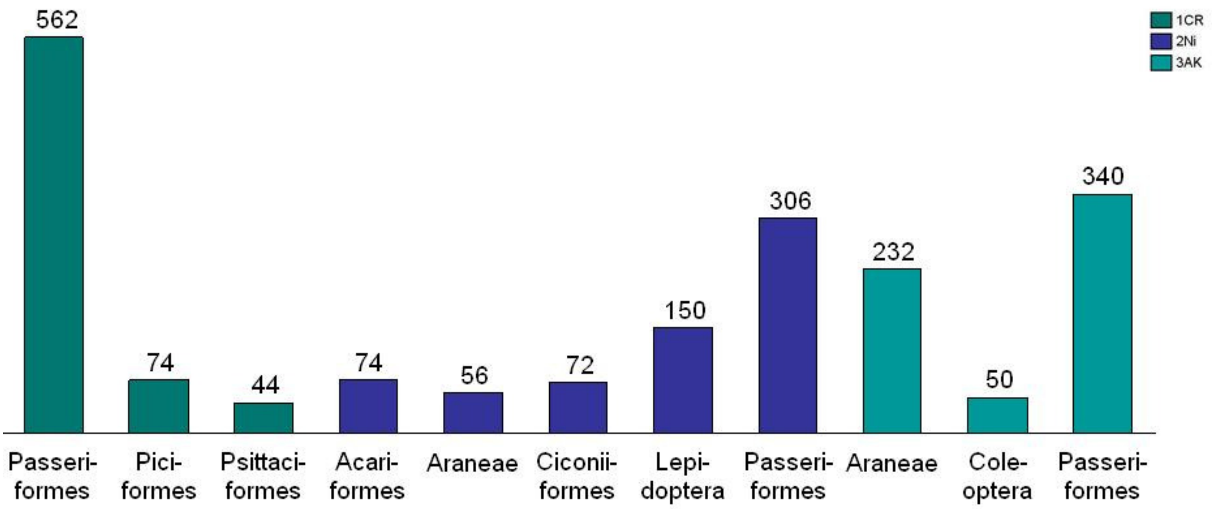

Figure 42: Number of observations pooled by biological order (1CR-3AK)

Figure 43 and Figure 44 illustrate the best ROC values and number of observations for the remaining study areas 4Ru, 5PG and 6Ba. Only one of the orders does not result in higher quality non-random model (ROC of 0.48 for collembola at 5PG). The lowest number of observations compared within this set leads again to the best available model (ROC = 0.81 for Psittaciformes at 5PG), while the highest number of observations resulted in a relatively poor ROC of 0.56 (Passeriformes at 4Ru).

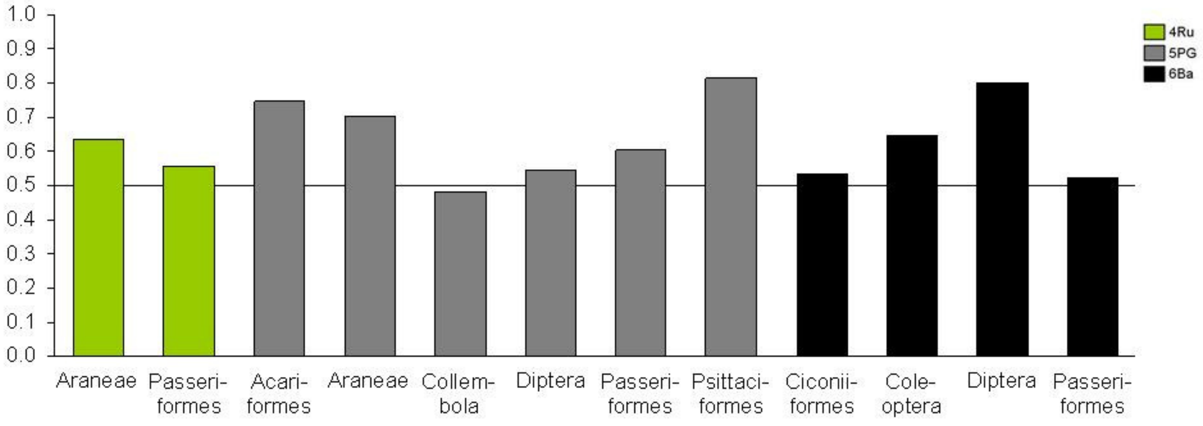

Figure 43: Best ROC values for analysis at biological order level (4Ru-6Ba)

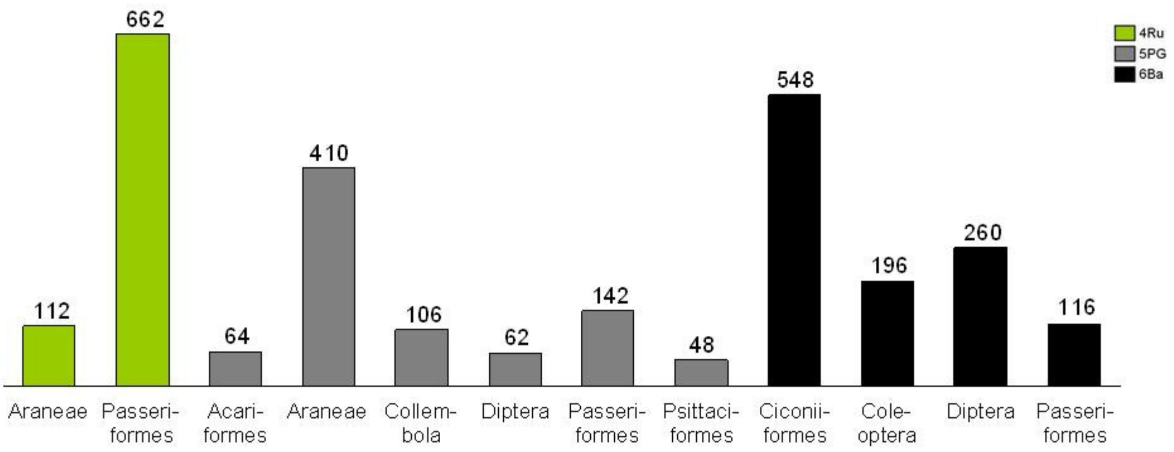

Figure 44: Number of observations pooled by biological order (4Ru-6Ba)

3.2.5 Covariates Identified as Important

Random Forests assigns importance values to each covariate used in a model, the ones identified as most important are used for further analysis. Table 9 to

Table 11 show the ten most important covariates for each narrative in the different study areas for point and line transect data, Table 12 to Table 14 illustrate the five most important covariates for trapping web data. Additionally the model resulting in the best ROC values, the ROC value, and the number of observations are shown for each narrative. Full results can be found in the project files in the digital appendix. Generally speaking all environmental covariates that are spatially tied to a plot, like habitat type, height of highest tree or presence/absence of key plant species, are ‘good’ results, those can easily used for prediction when the spatial data is available. Other covariates that are survey-specific are rather difficult as input variables, because they area unknown prior to sampling (e.g. cluster size, aural or visual identification). Some of them are even indicators that there could have been a problem with survey circumstances, when they should not have an effect but do (e.g. minutes since sunrise, number of visit). A detailed species-based biological discussion of covariate influence is beyond the scope of this thesis.

Table 9: Covariates identified as important for point and line transect observations (1CR-3AK)

Region	1CR	1CR	1CR	1CR	1CR	2Ni	2Ni	2Ni	3AK	3AK
Model	Covariates	Covariates	Interspecies	Interspecies	Covariates	Covariates	Covariates	Covariate	Interspecies	Interspecies
Target Variable	Flycatcher	Hummingbird	Oropendula	Seedeater	Woodpecker	Banded Wren	White-throated Magpie Jay	Butterfly, white	Sparrow	Squirrel
ROC Integral	0.623	0.756	0.635	0.812	0.585	0.78	0.628	0.629	0.649	0.564
Observations	50	125	92	27	31	50	73	36	59	81
VarImp01	Visit No	Duff	Ident	Habitat	Habitat	Ident	Cluster Size	Distance	High. Tree	Duff
VarImp02	Distance	Habitat	Moss/Lichen	Duff	Moss/Lichen	Habitat	Epiphytes	Min_Sunrise	Habitat	Ident
VarImp03	Min_Sunrise	Epiphytes	High. DBH	Moss/Lichen	Canopy	Moss/Lichen	Habitat	Bare Soil	Duff	Min_Sunrise
VarImp04	Habitat	Moss/Lichen	High. Tree	Epiphytes	Epiphytes	Understory	Min_Sunrise	Duff	Moss/Lichen	Cov13
VarImp05	Shrubs	Canopy	Habitat	Cov05	Visit No	Duff	Moss/Lichen	High. DBH	Min_Sunrise	Cov14
VarImp06	Epiphytes	Understory	Epiphytes	Shrubs	Cov04	Distance	High. DBH	Habitat	Canopy Trees	High. Tree
VarImp07	Plot Type	High. Tree	Distance	Understory	High. DBH	Epiphytes	Ident	Canopy	Canopy	Cov12
VarImp08	Moss/Lichen	Distance	Canopy Trees	High. Tree	Bare Soil	High. Tree	Distance	Canopy Trees	Squirrel	Cov11
VarImp09	Ident	Ident	Bare Soil	Canopy	Min_Sunrise	Shrubs	High. Tree	Epiphytes	Cov19	Moss/Lichen
VarImp10	Cov05	Cov05	Flowers	Turkey Vulture	High. Tree	Cluster Size	Shrubs	High. Tree	Cov01	High. DBH

Table 10: Covariates identified as important for point and line transect observations (4Ru-5PG)

Region	**4Ru**	**4Ru**	**4Ru**	**4Ru**	**4Ru**	**4Ru**	**5PG**	**5PG**
Model	Interspecies	Covariates	Covariates	Interspecies	Covariates	Covariates	Covariates	Covariates
Target Variable	Chickadee	Kinglet	Nutcracker	Warbler	Winter Wren	Wize	Flute	Tsilp
ROC Integral	0.647	0.625	0.685	0.634	0.691	0.65	0.578	0.686
Observations	98	92	29	33	25	26	20	46
VarImp01	Moss %	Moss %	Moss %	Moss %	Moss %	Moss %	Habitat	Visit No
VarImp02	High. DBH	Distance	Cov01	Cov16	Cov01	Lichen %	Cov12	Ident
VarImp03	Lichen %	High. Tree	Cov21	Lichen %	Habitat	Cov20	Ident	Min_Sunrise
VarImp04	Cluster Size	Lichen %	Cov12	High. DBH	Shrubs	Cov18	Visit No	Habitat
VarImp05	High. Tree	Visit No	Cov05	Plot Type	Cov21	Visit No	Cov11	Canopy
VarImp06	Cov16	Plot Type	Habitat	Cov31	Plot Type	Cov30	Duff	Bare Soil
VarImp07	Understory	Min_Sunrise	Cov20	Cov15	Duff	Cov31	High. Tree	Epiphytes
VarImp08	Wize	Canopy Trees	Understory	Understory	Canopy	Cov28	Min_Sunrise	Distance
VarImp09	Duff	Understory	Cov15	Cov20	Lichen %	Cov16	Bare Soil	Cov01
VarImp10	Distance	Shrubs	Cov23	Canopy	Distance	Understory	Distance	High. Tree

Table 11: Covariates identified as important for point and line transect observations (6Ba)

Region	6Ba	6Ba	6Ba	6Ba	6Ba	6Ba
Model	Covariates	Covariates	Interspecies	Covariates	Covariates	Interspecies
Target Variable	Lapland Bunting	Longbilled Dowitcher	Pectoral Sandpiper	Pomarine Jaeger	Red Phalarope	Semipalmated Sandpiper
ROC Integral	0.523	0.561	0.671	0.629	0.585	0.463
Observations	111	48	34	37	55	62
VarImp01	Moss %	Grass %	Grass %	Grass %	Moss %	Grass %
VarImp02	Grass %	Moss %	Moss %	Moss %	Grass %	Moss %
VarImp03	Visit No	Lichen %	Diam. Lake	Dist. Lake	Leafs	Diam. Lake
VarImp04	Diam. Lake	Diam. Lake	Leafs	Leafs	Diam. Lake	Dist. Lake
VarImp05	Leafs	Dist. Lake	Dist. Lake	Cov06	Dist. Lake	Leafs
VarImp06	Dist. Lake	Cov03	Plot Type	Diam. Lake	Lichen %	Lichen %
VarImp07	Distance	Leafs	Lichen %	Flowers	Cov02	Visit No
VarImp08	Flowers	Flowers	Cov08	Lichen %	Flowers	Flowers
VarImp09	Cluster Size	Cov08	Cov01	Cluster Size	Visit No	Distance
VarImp10	Cov07	Cov07	Cov02	Cov05	Cov07	Cov10

Table 12: Covariates identified as important for trapping web catches (1CR-2Ni)

Region	1CR	1CR	2Ni	2Ni	2Ni	2Ni	2Ni	2Ni
Model	Interspecies	Interspecies	Interspecies	Covariate	Covariate	Covariate	Covariate	Covariate
Target Variable	Ant	Spider	Ant	Ant, small red	Beetle, 868	Centipede, 881	Spider, small	Springtail
ROC Integral	0.831	0.446	0.699	0.581	0.724	0.77	0.604	0.958
Observations	116	47	58	24	39	58	21	85
VarImp01	Epiphytes	Min Sunrise	Habitat	Cuplabel	Epiphytes	Status	Visit	Cluster Size
VarImp02	Habitat	Visit	Bug, other red	Visit	Understory	Habitat	Cuplabel	Status
VarImp03	Shrubs	Status	Visit Effort	Habitat	Habitat	Epiphytes	Min Sunrise	Visit
VarImp04	Bare Soil	Moss Lichen	Bug, 870	Epiphytes	Shrubs	Visit Effort	Cluster Size	Epiphytes
VarImp05	Understory	High DBH	Toad	Visit Effort	Visit Effort	Visit	Epiphytes	Visit Effort

Table 13: Covariates identified as important for trapping web catches (3AK-5PG)

Region	3AK	3AK	4Ru	4Ru	4Ru	4Ru	5PG
Model	Covariate	Covariate	Covariate	Covariate	Covariate	Covariate	Interspecies
Target Variable	Spider	Springtail	Collembola	Cycsegusa	Protura	Spider, little	Ant, tiny black
ROC Integral	0.604	0.951	0.616	0.74	0.709	0.628	0.393
Observations	91	56	54	26	20	25	22
VarImp01	Cov18	Cov13	Moss %	Cov21	Cov11	Cuplabel	Habitat
VarImp02	Cov14	Cluster Size	Lichen %	Habitat	Lichen %	Visit	Cov01
VarImp03	Cov11	Cov12	Cov01	Moss %	Cov19	Cluster Size	Cov06
VarImp04	Cov08	Moss Lichen	High. Tree	Cov11	Moss %	Lichen %	Cov08
VarImp05	Cov04	Habitat	Habitat	Lichen %	Habitat	Cov05	Cov05

Table 14: Covariates identified as important for trapping web catches (6Ba)

Region	6Ba	6Ba	6Ba	6Ba	6Ba	6Ba	6Ba	6Ba
Model	Covariate	Covariate	Covariate	Covariate	Covariate	Covariate	Covariate	Covariate
Target Variable	Beetle, flat	Fly	Fruitfly	Milbe	Mosquito	Schuster	Spider	Spider, tiny
ROC Integral	0.678	0.696	0.841	0.821	0.871	0.313	0.548	0.729
Observations	83	37	32	20	22	22	61	125
VarImp01	Moss %	Status	Status	Lichen %	Status	Visit	Status	Lichen %
VarImp02	Lichen %	Moss %	Moss %	Cov10	Visit	Status	Lichen %	Cov10
VarImp03	Grass %	Lichen %	Lichen %	Visit Effort	Cuplabel	Cuplabel	Cov10	Grass %
VarImp04	Status	Cov10	Cov10	Moss %	Grass %	Lichen %	Moss %	Cov01
VarImp05	Cov02	Grass %	Grass %	Grass %	Moss %	Cov10	Cov01	Cov08

3.3 DISTANCE Sampling

46 different models are used for DISTANCE analysis to estimate abundance of each narrative; the different model definitions for each study area are given in the appendix (page 123 ff). Models 1-6 are standard models without covariates; models 7 and higher are covariate DISTANCE models using one covariate each. For each study area and sampling method the actual population densities as well as upper and lower confidence level are shown in this analysis, followed by DISTANCE detection function graphs for each narrative. Missing indicators for confidence levels indicate that they have not been calculated by the software.

3.3.1 DISTANCE Sampling Results: Bird Point Transects

Density estimates by the best available DISTANCE sampling model for narratives at 1CR range from 17 individuals per km² for Flycatcher to 2,908 individuals per km² for Hummingbird, mostly with relatively large confidence intervals (Figure 45). Figure 46, Figure 47 and Figure 48 show the model fit in detection function graphs for these narratives. Only in case of Oropendula the best model is one without covariate use (conventional DISTANCE sampling). In two cases adding plot related covariates results in the best model: Habitat for Flycatcher (model 26) and Duff cover % for Seedeater (model 39). For Hummingbird using the type of identification (aural/ visual) results in the best model fit (model 16), indicating that split of the data in two sets could be beneficial (resulting in much smaller population estimates of 302 or 662 individuals per km², compare chapter 3.3.5:

DISTANCE Sampling Results: Aural vs. Visual Bird Detections). Cluster size as a covariate is found to result in the best model fit for Woodpecker (model 11).

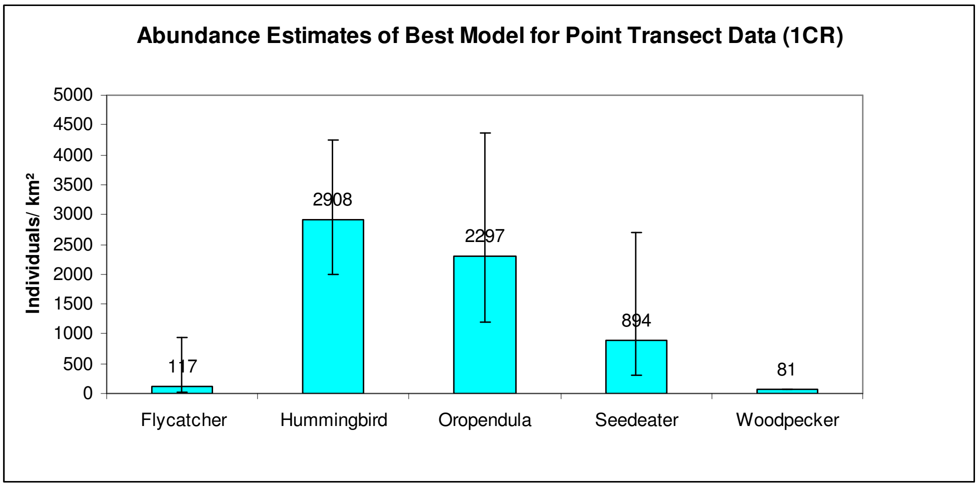

Figure 45: Abundance estimates and confidence intervals of best model for point transect data (1CR)

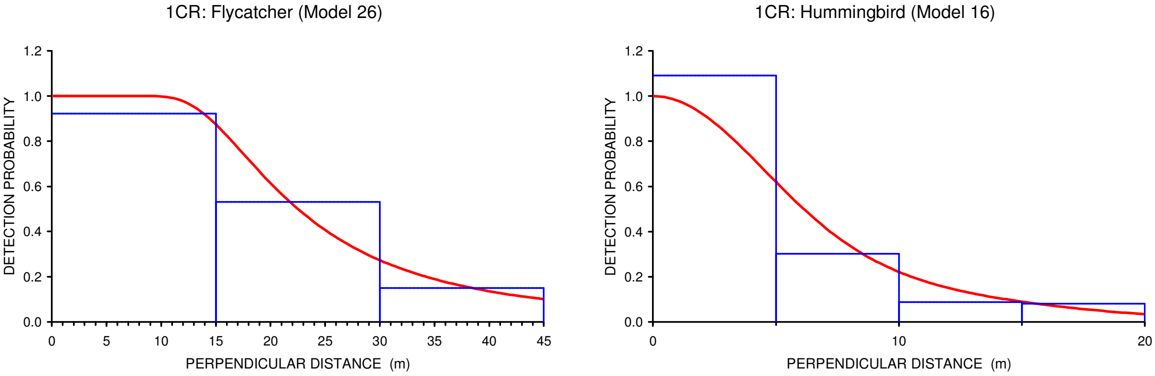

Figure 46: DISTANCE detection functions for Flycatcher and Hummingbird (1CR)

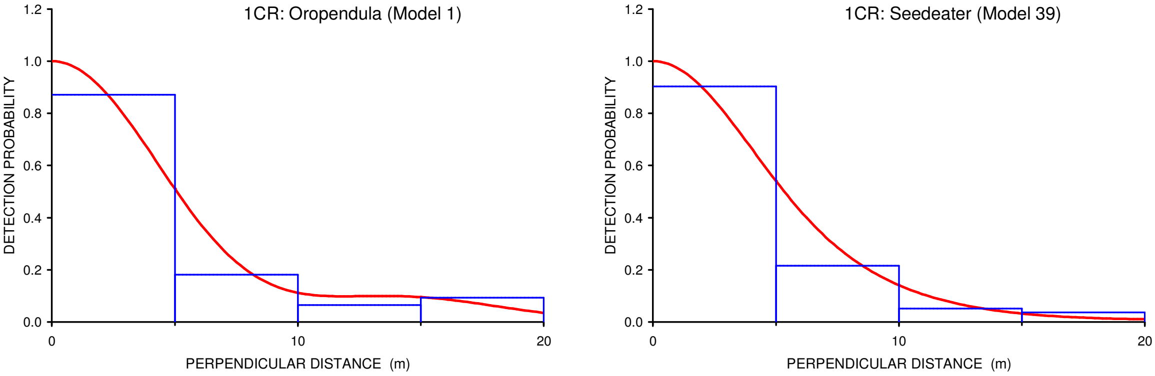

Figure 47: DISTANCE detection functions for Oropendula and Seedeater (1CR)

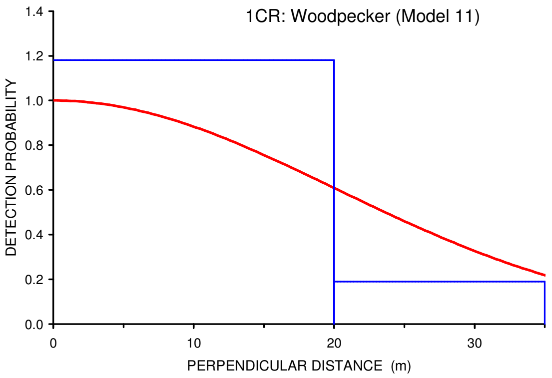

Figure 48: DISTANCE detection function for Woodpecker (1CR)

At study area 2Ni density is estimated for two narratives: White-throated Magpie Jay (152 individuals/ km²) and Banded Wren (160 individuals/ km²). Confidence intervals are relatively high, ranging from 93 to 277 individuals/ km² for Banded Wren and from 88 to 264 individuals/ km² for White-throated Magpie Jay (Figure 49). Both narratives receive best model fit adding Shrub cover % as covariate (Figure 50).

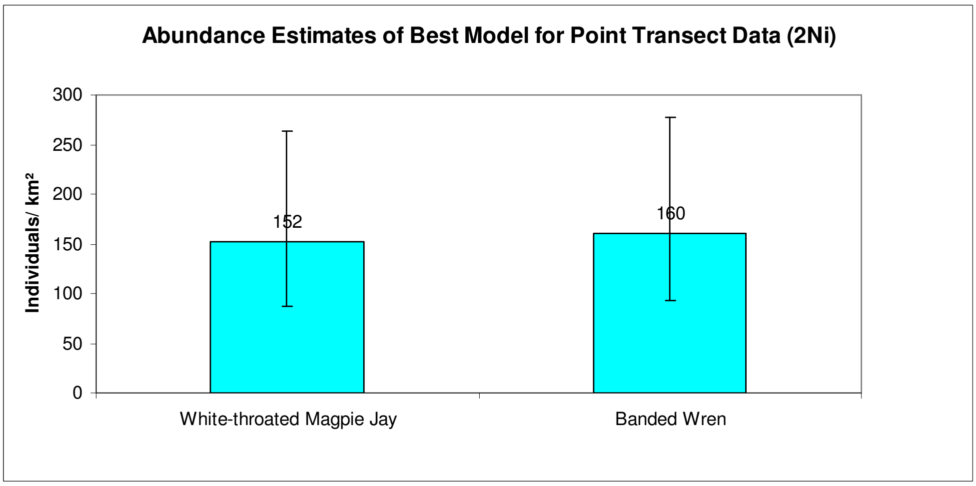

Figure 49: Abundance estimates and confidence intervals of best model for point transect data (2Ni)

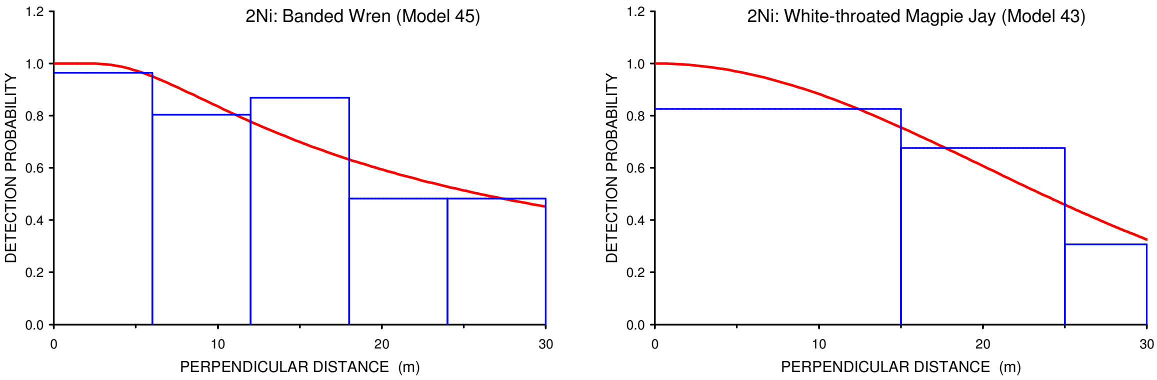

Figure 50: DISTANCE detection functions for Banded Wren and White-throated Magpie Jay (2Ni)

From study area 3AK densities for Sparrow and Squirrel are estimated (Figure 51). The Sparrow population is estimated to have 16 individuals/ km² with confidence interval ranging from 10 to 26 individuals/ km²; the Squirrel population has a very similar estimate of 17 individuals/ km² with confidence interval ranging from 11 to 26 individuals/ km². The best model fit for Sparrow is achieved using minutes since sunrise as covariate (model 12), while the best model fit for Squirrel uses Habitat type as covariate (model 15). Both detection functions are shown in Figure 52. In both cases there were no observations within 5 m of the observer and the number of observations was generally not decreasing smoothly with growing distance.

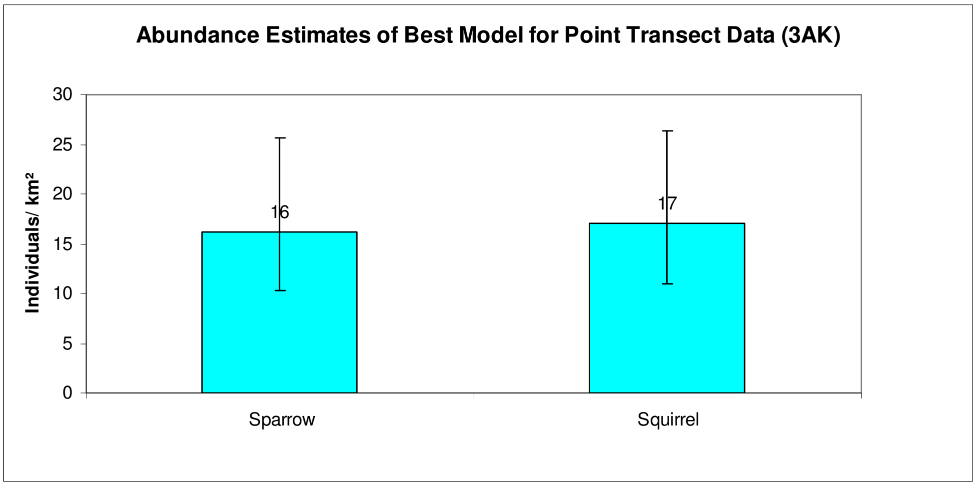

Figure 51: Abundance estimates and confidence intervals of best model for point transect data (3AK)

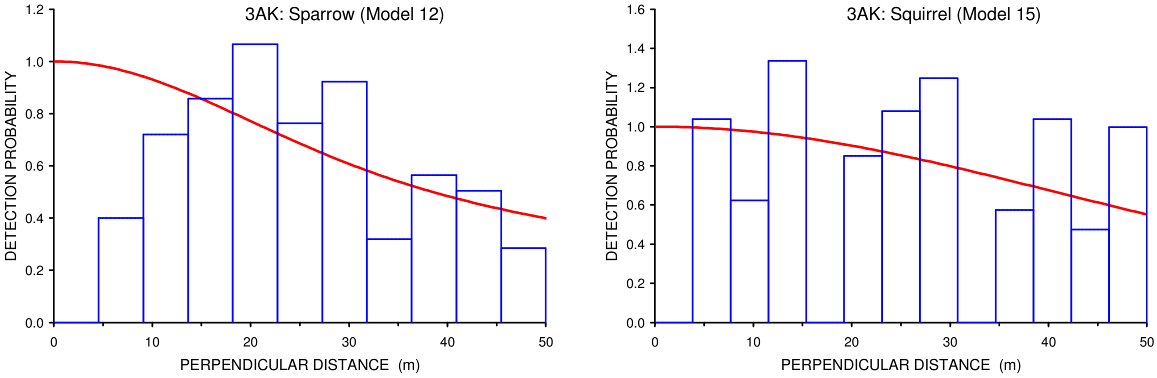

Figure 52: DISTANCE detection functions for Sparrow and Squirrel (3AK)

Density estimates for narratives from study area 4Ru range from 17 individuals/ km² for Winter Wren and Wize to 572 individuals/ km² for Chickadee (Figure 53). Confidence intervals are again relatively large; reaching up to almost 100 % (upper confidence interval for Chickadee is 1077 individuals/ km²). DISTANCE detection functions for the six narratives from 4Ru are shown in Figure 54, Figure 55 and Figure 56. Many of those graphs show problematic trends in the data, like the highest number of observations being at greater distance from the observer (Kinglet and Warbler) or like having no observations within 5 m of the observer (Wize). The latter could possibly be explained by the fact that Wize is an aural identification and most birds closer to the observer will usually be identified aurally as well as visually (it is unknown to which bird species the sound belongs). The model for Chickadee was best with conventional DISTANCE sampling; all other models had a better model fit using plot related covariates. These covariates were Number of flowers (model 43 for Kinglet and model 44 for Nutcracker), Habitat type (model 20 for Warbler), Lichen % (model 67 for Winter Wren), and Covariate 23 (model 111 for Wize). Covariate 23 at study area 4Ru is *Rhodococcum vitis-idaea* (see chapter 7.2: Covariates by Study Area).

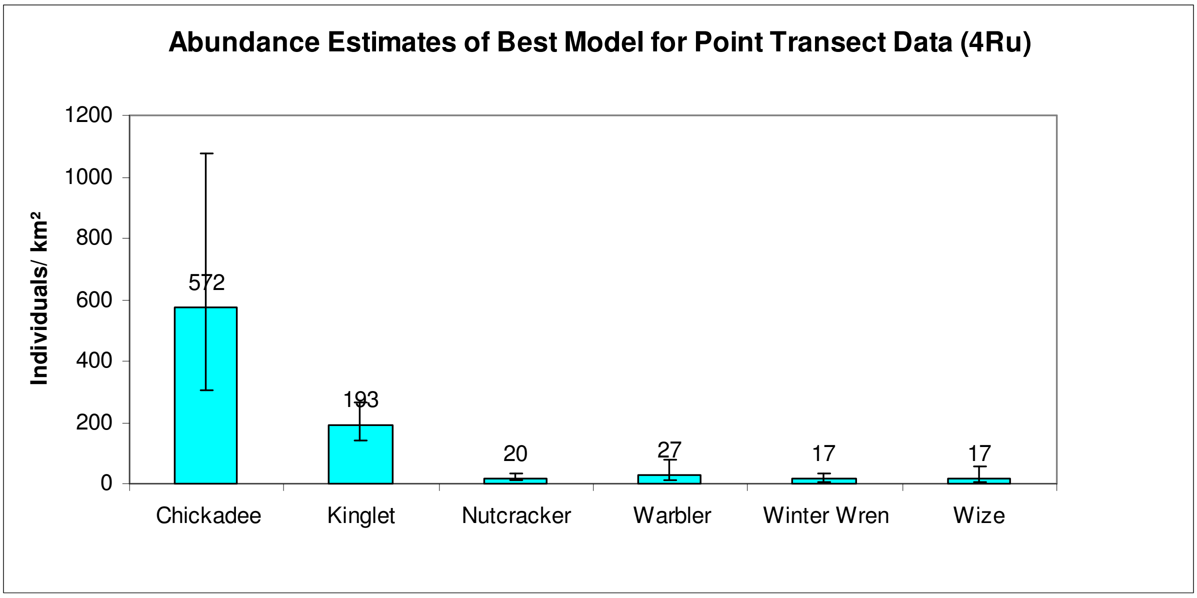

Figure 53: Abundance estimates and confidence intervals of best model for point transect data (4Ru)

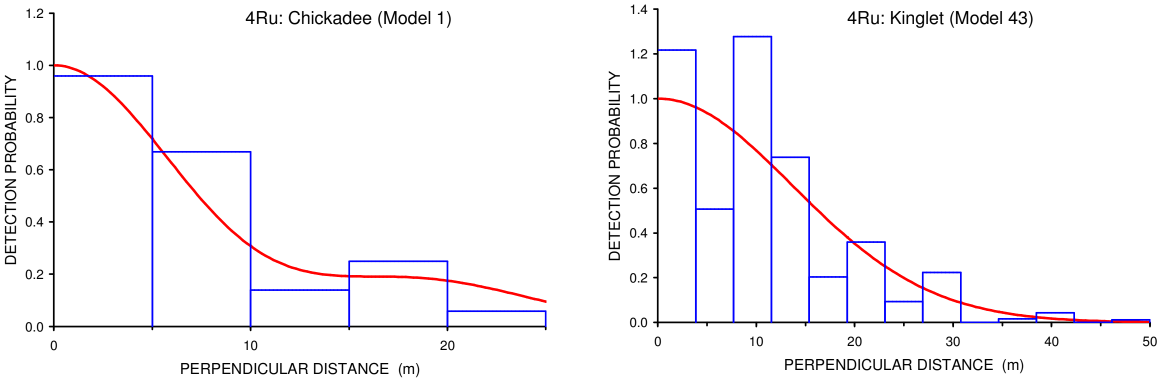

Figure 54: DISTANCE detection functions for Chickadee and Kinglet (4Ru)

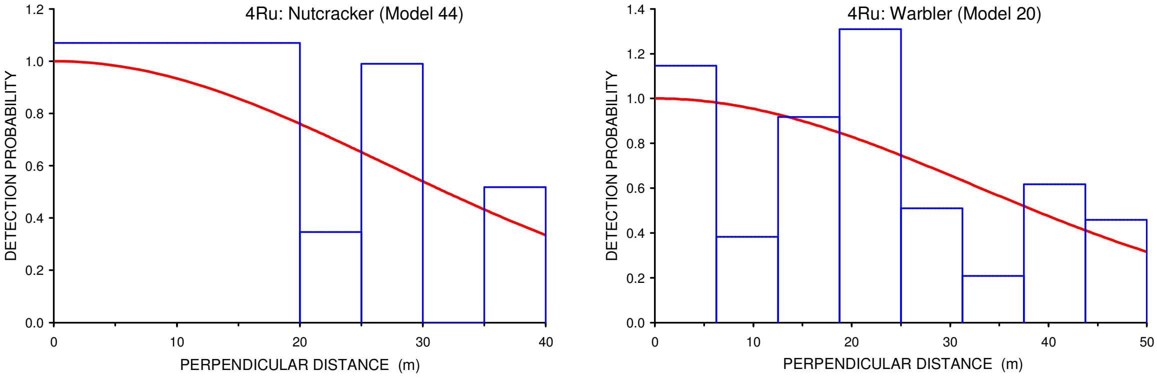

Figure 55: DISTANCE detection functions for Nutcracker and Warbler (4Ru)

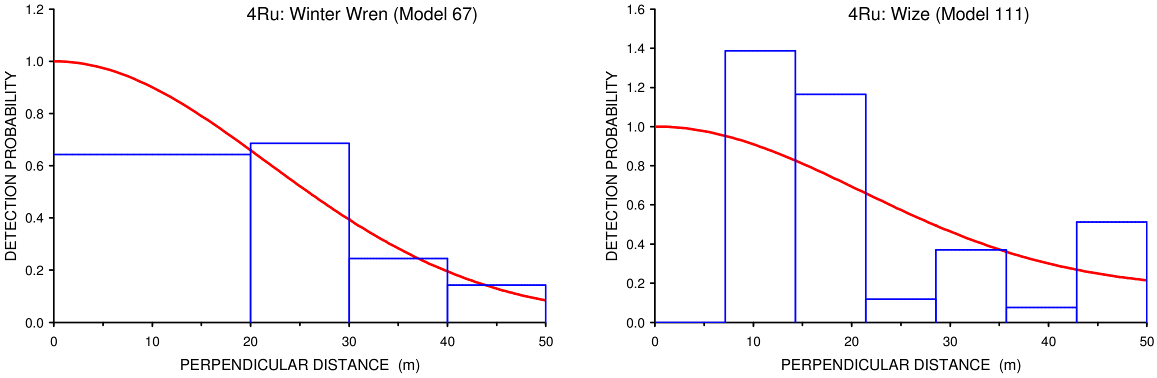

Figure 56: DISTANCE detection functions for Winter Wren and Wize (4Ru)

Abundance estimates are derived for Flute and Tsilp from study area 5PG, both being phonetic descriptions of bird songs (Figure 57). The best estimate for Flute is 17 individuals/ km² (confidence interval from 10 to 27 individuals/ km²), the best one for Tsilp is 67 individuals/ km² (confidence interval not available). The best detection function fit for Flute is achieved without covariates (model 1), while the best one for Tsilp is model 11 using Cluster size as a covariate (Figure 58).

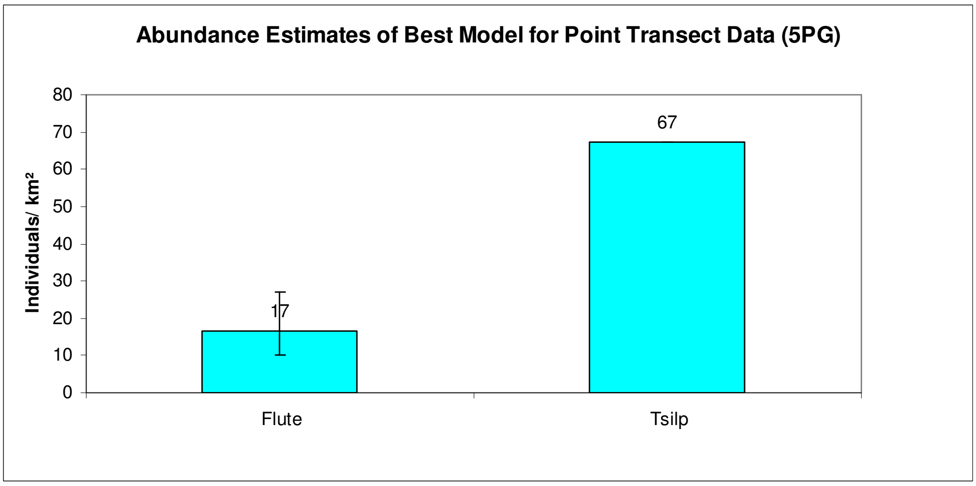

Figure 57: Abundance estimates and confidence intervals of best model for point transect data (5PG)

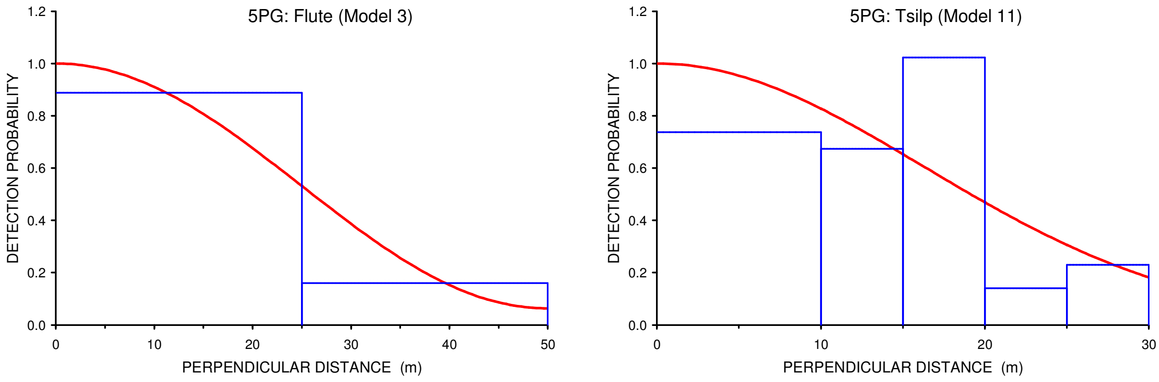

Figure 58: DISTANCE detection functions for Flute and Tsilp (5PG)

Densities between 6 and 70 individuals per km² are estimated for six narratives at study area 6Ba (Figure 59). Confidence intervals are relatively large, ranging up to four times the initial estimate (252 individuals/ km² as upper confidence interval for Pomarine Jaeger). For Lapland Bunting, Longbilled Dowitcher, Pectoral Sandpiper and Semipalmated Sandpiper the Diameter of the nearest lake is the covariate resulting in best model fit with MCDS (models 35-37, with detection functions as shown in Figure 60, Figure 61 and Figure 62). For Pomarine Jaeger model 18 using number of flowers as covariate has the best model fit, for Red Phalarope it is model 52 using detection/ non-detection of coltsfoot as covariate.

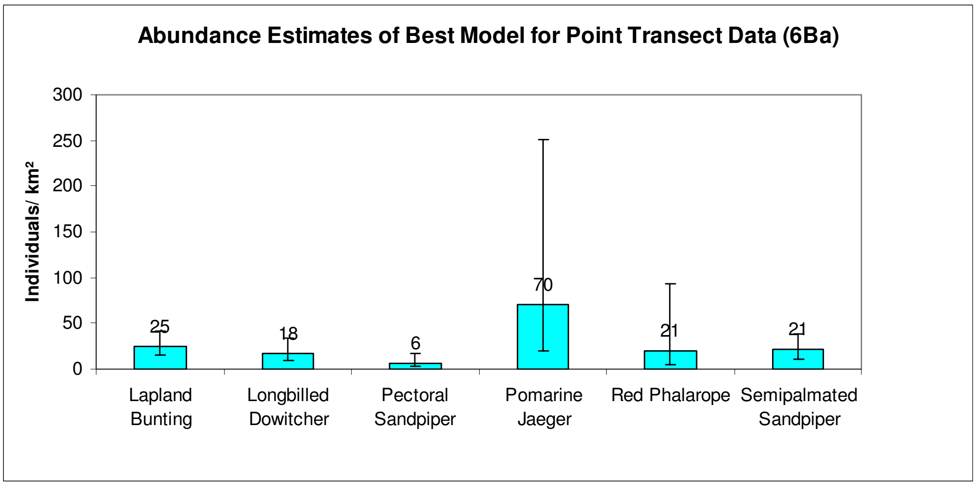

Figure 59: Abundance estimates and confidence intervals of best model for point transect data (6Ba)

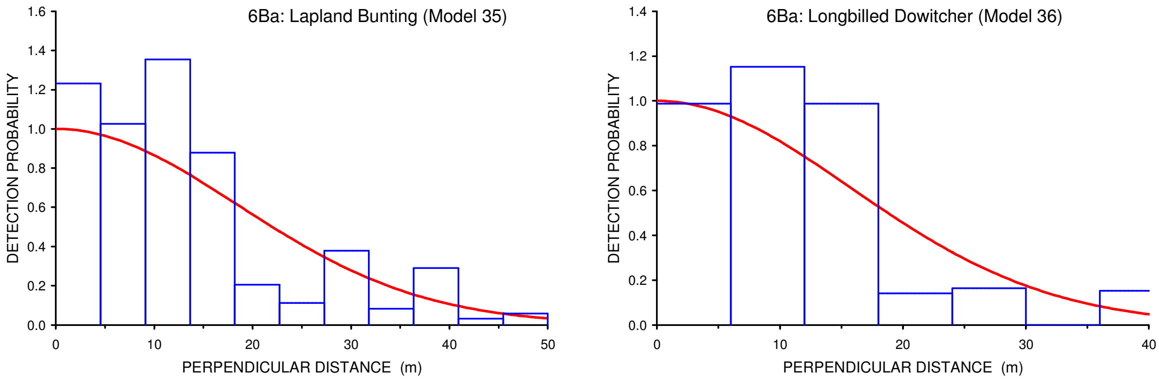

Figure 60: DISTANCE detection functions for Lapland Bunting and Longbilled Dowitcher (6Ba)

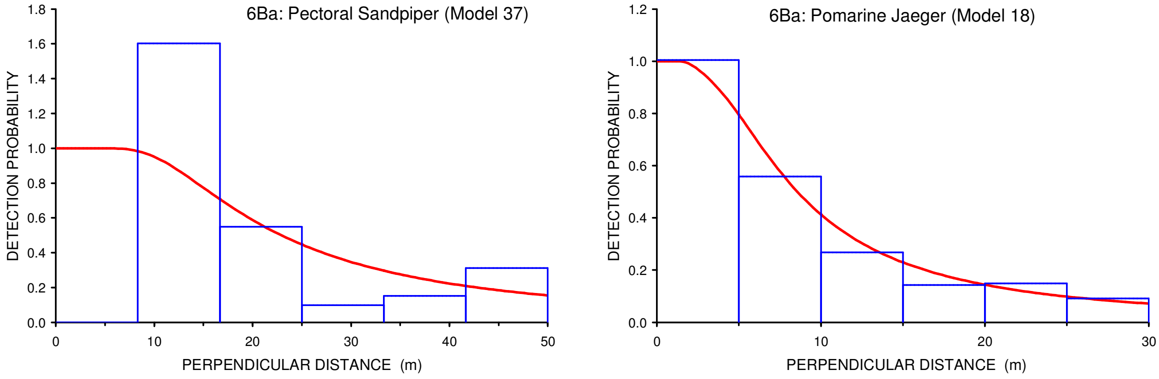

Figure 61: DISTANCE detection functions for Pectoral Sandpiper and Pomarine Jaeger (6Ba)

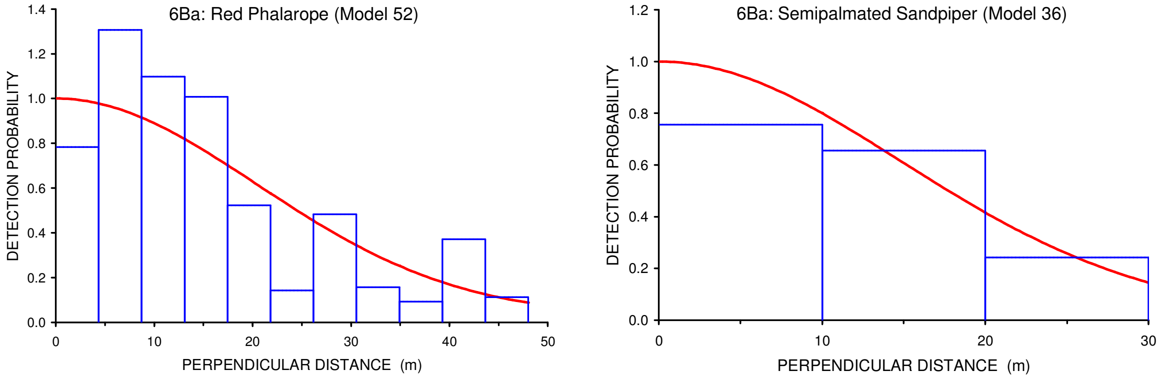

Figure 62: DISTANCE detection functions for Red Phalarope and Semipalmated Sandpiper (6Ba)

Table 15 gives an overview of density estimates and confidence intervals for all narratives. In most cases the relatively large range covered by the confidence interval indicates relatively low precision of the estimates. The last column adds an estimate of the narrative density per

GRID. For each study area the total number of birds per GRID is calculated. Bird totals range from 4 per GRID in 3AK to 1,574 per GRID in 1CR. This calculation disregards all observations which could not be analyzed with DISTANCE because of low sample size.

Table 15: Overview of density estimates and confidence intervals for point transect data

Study area	Target Narrative	Density (individuals per km²)	Lower confidence interval	Upper confidence interval	Density (individuals per GRID)
1CR	Flycatcher	117	15	930	29
1CR	Hummingbird	2908	1992	4244	727
1CR	Oropendula	2297	1209	4365	574
1CR	Seedeater	894	296	2696	224
1CR	Woodpecker	81	0	0	20
1CR	**Bird Total:**	**6297**	**-**	**-**	**1574**
2Ni	Banded Wren	160	93	277	40
2Ni	White-throated Magpie Jay	152	88	264	38
2Ni	**Bird Total:**	**312**	**-**	**-**	**78**
3AK	Sparrow	16	10	26	4
3AK	Squirrel	17	11	26	4
3AK	**Bird Total:**	**16**	**10-**	**26**	**4**
4Ru	Chickadee	572	304	1077	143
4Ru	Kinglet	193	140	266	48
4Ru	Nutcracker	20	12	33	5
4Ru	Warbler	27	9	79	7
4Ru	Winter Wren	17	8	34	4
4Ru	Wize	17	5	58	4
4Ru	**Bird Total:**	**846**	**-**	**-**	**212**
5PG	Flute	17	10	27	4
5PG	Tsilp	67	0	0	17
5PG	**Bird Total:**	**84**	**-**	**-**	**21**
6Ba	Lapland Bunting	25	15	41	6
6Ba	Longbilled Dowitcher	18	9	33	5
6Ba	Pectoral Sandpiper	6	2	17	2
6Ba	Pomarine Jaeger	70	19	252	18
6Ba	Red Phalarope	21	5	93	5
6Ba	Semipalmated Sandpiper	21	11	39	5
6Ba	**Bird Total:**	**161**	**-**	**-**	**40**

3.3.2 DISTANCE Sampling Results: Trapping Web Catches

From study area 1CR abundance estimates for Ant and Spider are calculated (Figure 63). The estimate for ant is 2,741 individuals/ km², while the confidence interval ranges from 656 to 11,448 individuals/ km². The estimate for spider is 702 individuals with a confidence interval from 403 to 1,225 individuals/ km². Both detection functions are shown in Figure 64. For both narratives model 32 with Shrubs % resulted in best model fit.

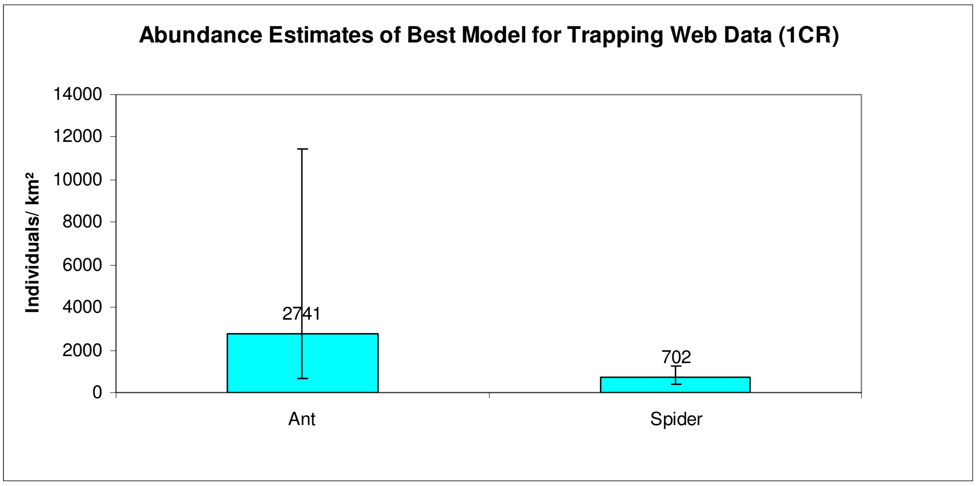

Figure 63: Abundance estimates and confidence intervals of best model for trapping web data (1CR)

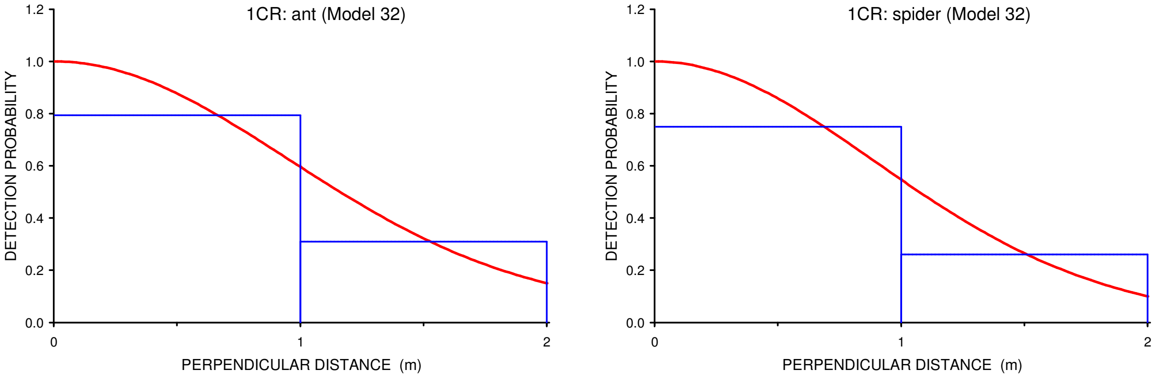

Figure 64: DISTANCE detection functions for Ant and Spider (1CR)

Density estimations at 2Ni range from 271 individuals/ km² for Spider, small to 2,091 individuals/ km² for ant (Figure 65). The estimated density of Springtail was 47,207 individuals/ km², which made the use of a second scale on the right side of the graph necessary. Confidence intervals have a relatively large range, for springtail for example the lower confidence interval is 25,775 individuals/ km² and the upper confidence interval is 86,463 individuals/ km². Five out of the six narratives reach best model fit with the standard models 1-6, without use of covariates (from Figure 66 to Figure 68). Adding a covariate increased model fit only for ant, for which Habitat was used as covariate in MCDS analysis.

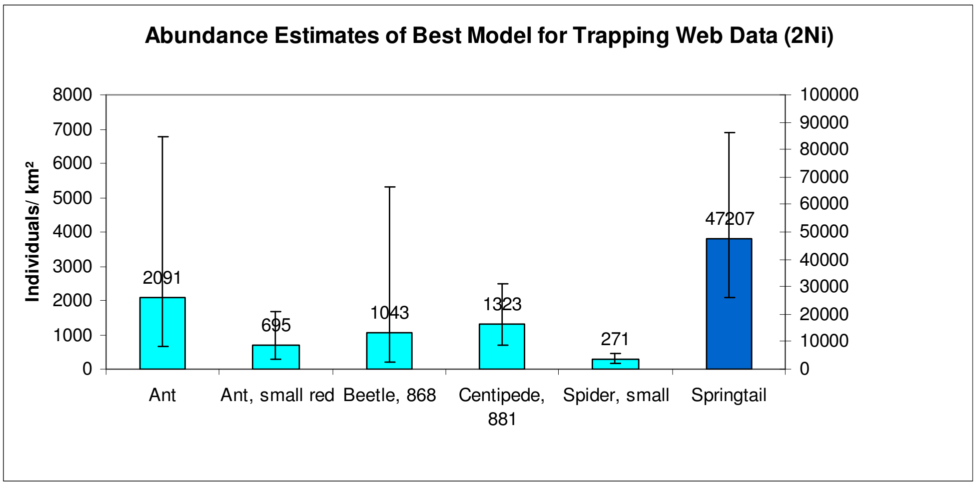

Figure 65: Abundance estimates and confidence intervals of best model for trapping web data (2Ni)

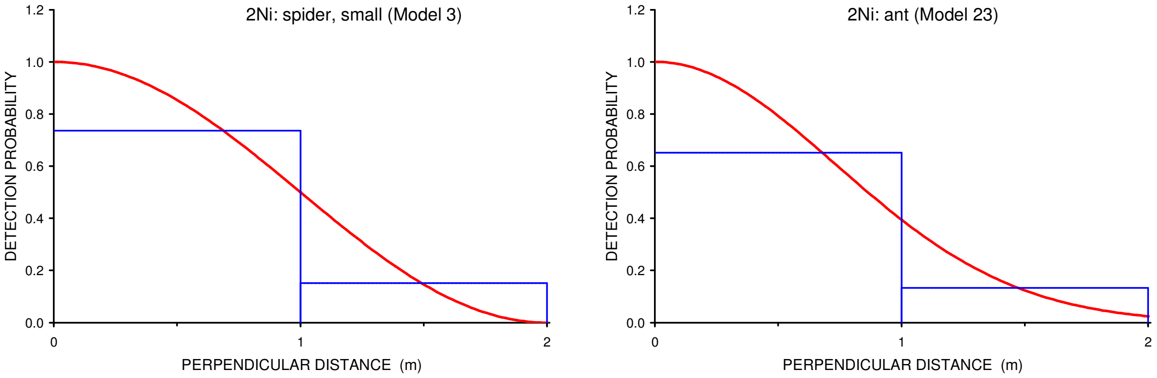

Figure 66: DISTANCE detection functions for Spider, small and Ant (2Ni)

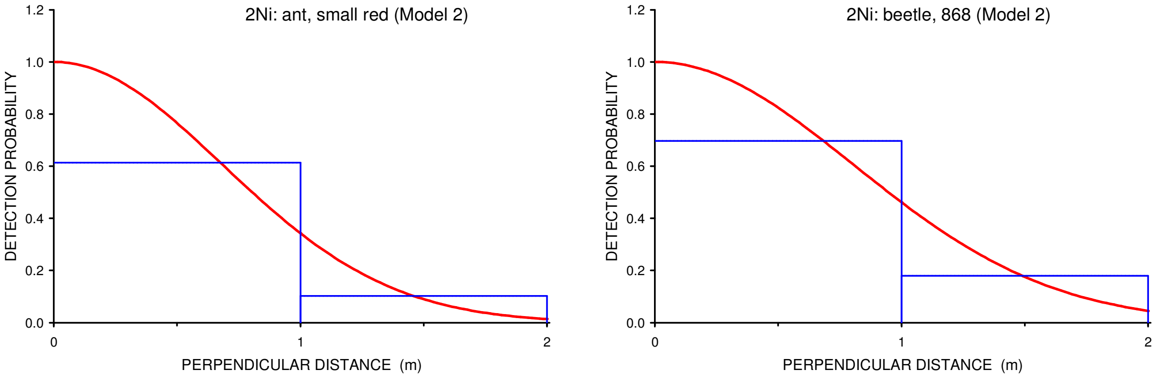

Figure 67: DISTANCE detection functions for Ant, small red and Beetle, 868 (2Ni)

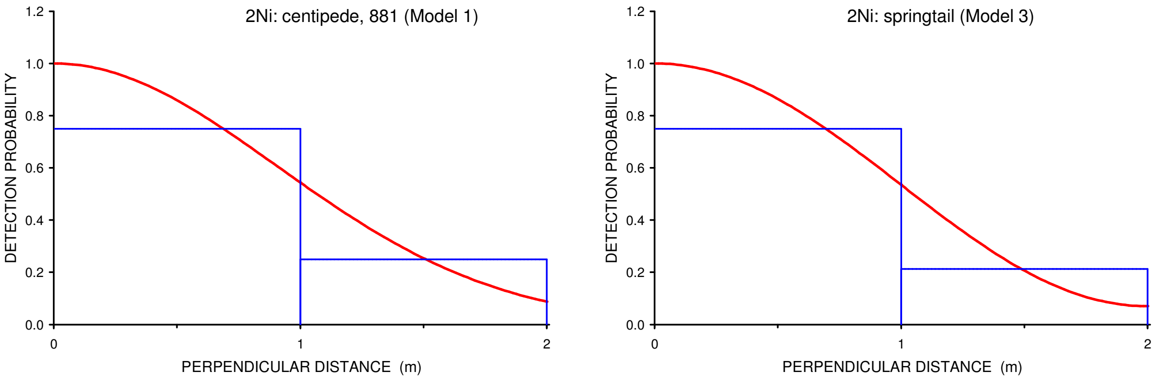

Figure 68: DISTANCE detection functions for Centipede, 881 and Springtail (2Ni)

Sufficient trapping web data for DISTANCE analysis at study area 3AK was collected for Spider and Springtail (Figure 69). Density estimate for Spider is 970 individuals per km² with a confidence interval range from 476 to 1,976 individuals/ km². Density estimate for Springtail is 39,238 individuals/ km² with a confidence interval range from 7,950 to 193,674 individuals/ km². For both narratives the best model fit is achieved with MCDS analysis, best model fits are shown in Figure 70. Model 20 used for Spider has habitat type as covariate, model 71 for springtail uses Covariate 18 for study area 3AK as a covariate (Covariate 18 refers to an unidentified plant species, detailed pictures are available in the digital appendix).

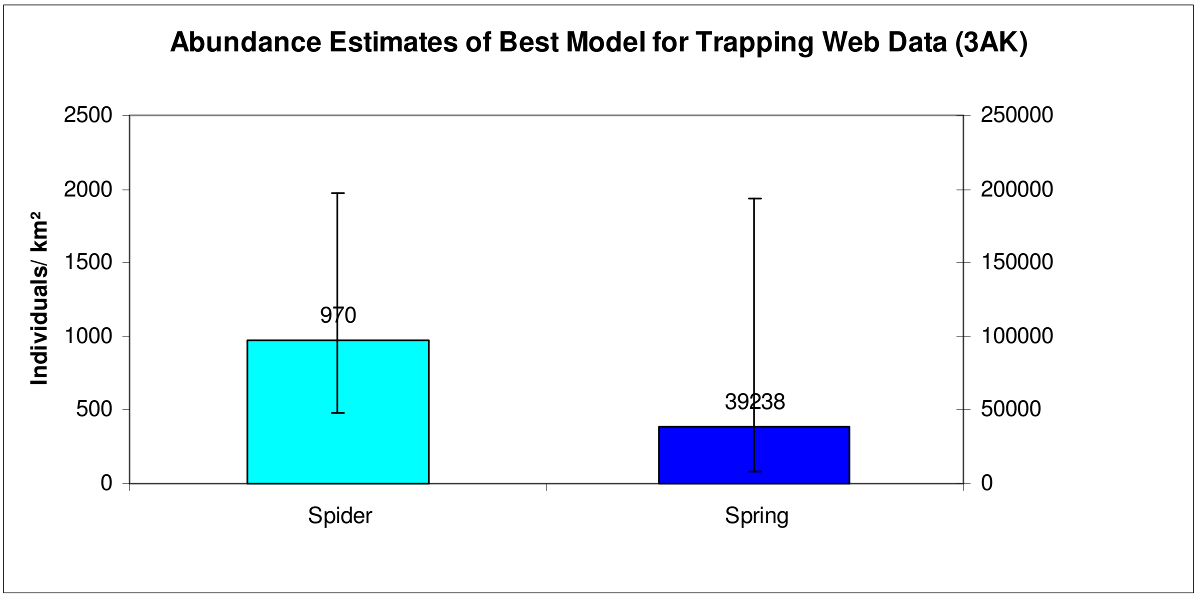

Figure 69: Abundance estimates and confidence intervals of best model for trapping web data (3AK)

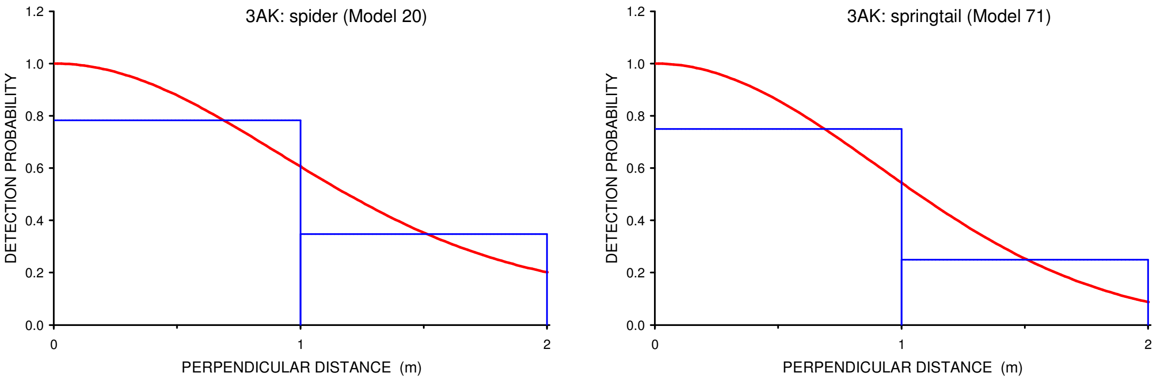

Figure 70: DISTANCE detection functions for Spider and Springtail (3AK)

Abundance at 4Ru is estimated for Cycsegusa, Protura, and Spider, little (Figure 71). Estimates are relatively close together and reach from 163 individuals/ km² for Protura to 281 individuals/ km² for Cycsegusa. Upper confidence interval is up to more than four times the estimate (1,171 individuals/ km² for Cycsegusa). Best model fits for Cycsegusa and Spider little are achieved without use of covariates (model 1 respectively model 2), as shown in Figure 72 and Figure 73. For the analysis of Protura adding *Betula ermanii* as a covariate resulted in best model fit (model 44).

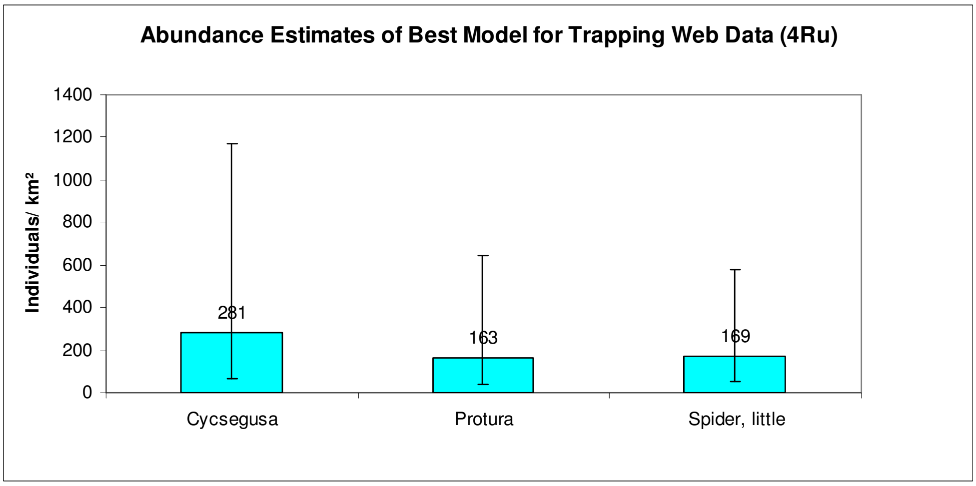

Figure 71: Abundance estimates and confidence intervals of best model for trapping web data (4Ru)

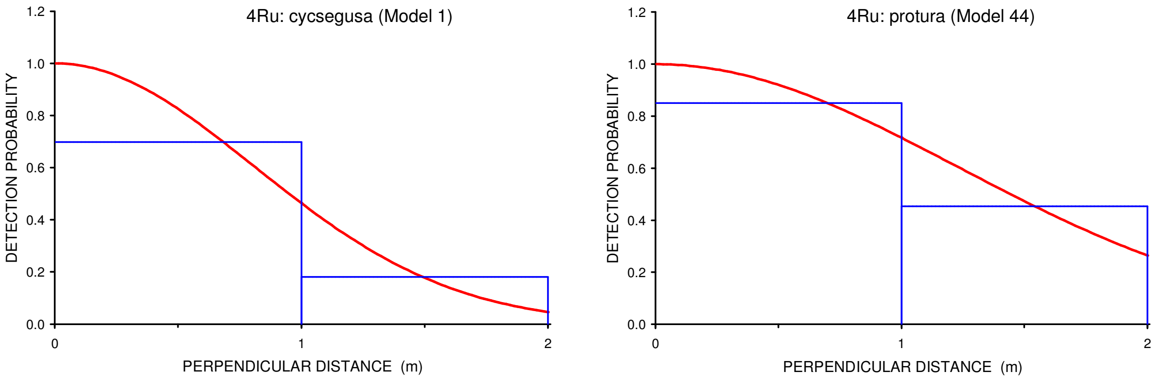

Figure 72: DISTANCE detection functions for Cycsegusa and Protura (4Ru)

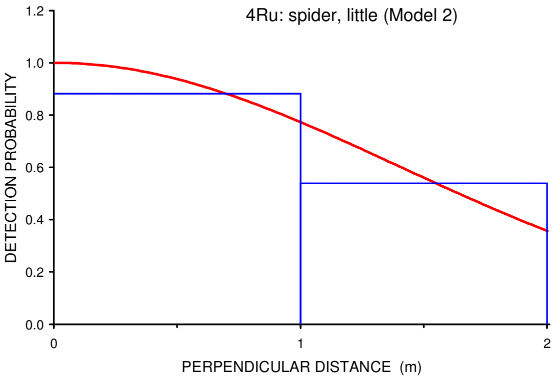

Figure 73: DISTANCE detection function for Spider, little (4Ru)

At 5PG the data allow to calculate density estimates only for tiny black Ant (Figure 74). The actual estimate is 199 individuals/ km²; confidence interval covers a range from 67 to 592 individuals/ km². The best model fit is shown in Figure 75 (model 3, without covariate use).

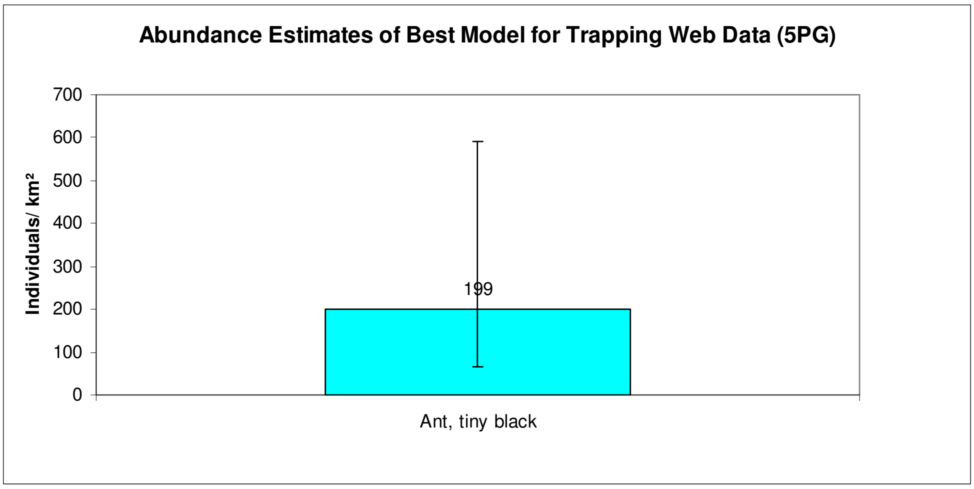

Figure 74: Abundance estimates and confidence intervals of best model for trapping web data (5PG)

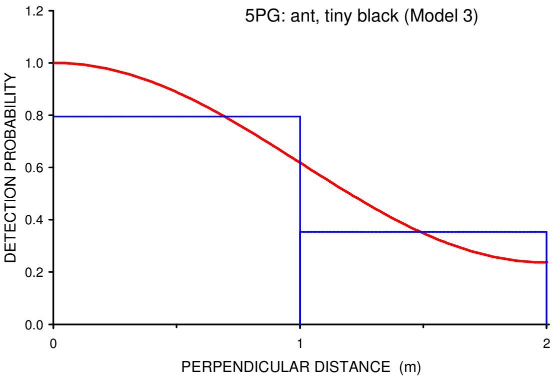

Figure 75: DISTANCE detection functions for Ant, tiny black (5PG)

Figure 76 shows abundance estimates and confidence intervals for eight narratives from 6Ba. Because of the comparably high estimates for flat Beetle and tiny Spider a different scaling is used to display results for these two. DISTANCE detection functions are displayed from Figure 77 to Figure 80. For seven narratives the best model fit is achieved without covariate use, only the model for Spider gained from adding the covariate Cluster size.

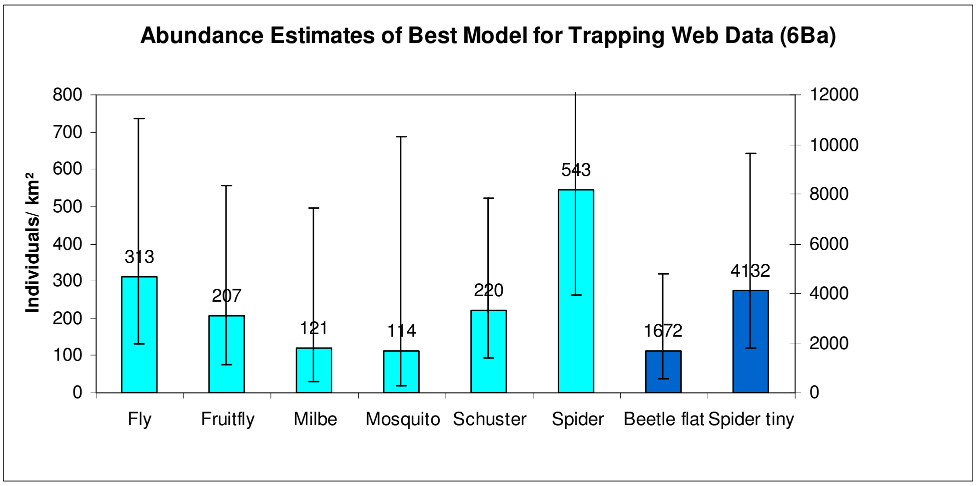

Figure 76: Abundance estimates and confidence intervals of best model for trapping web data (6Ba)

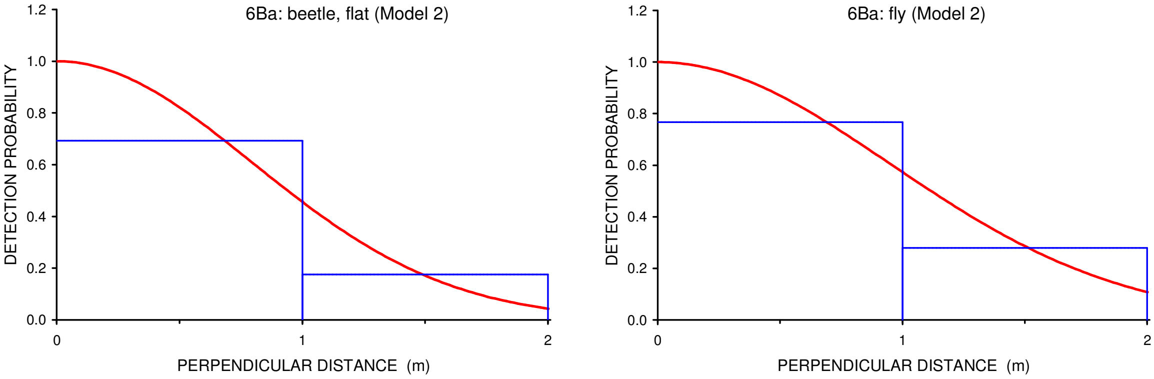

Figure 77: DISTANCE detection functions for Beetle, flat and Fly (6Ba)

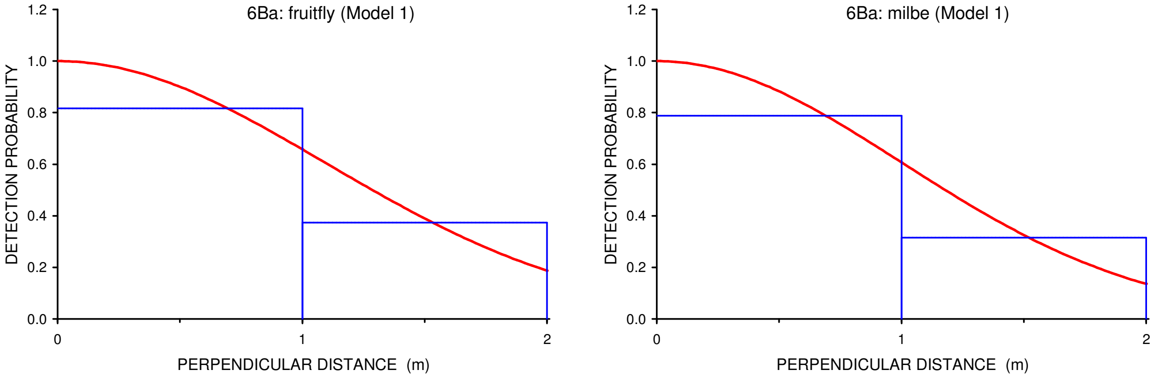

Figure 78: DISTANCE detection functions for Fruitfly and Milbe (6Ba)

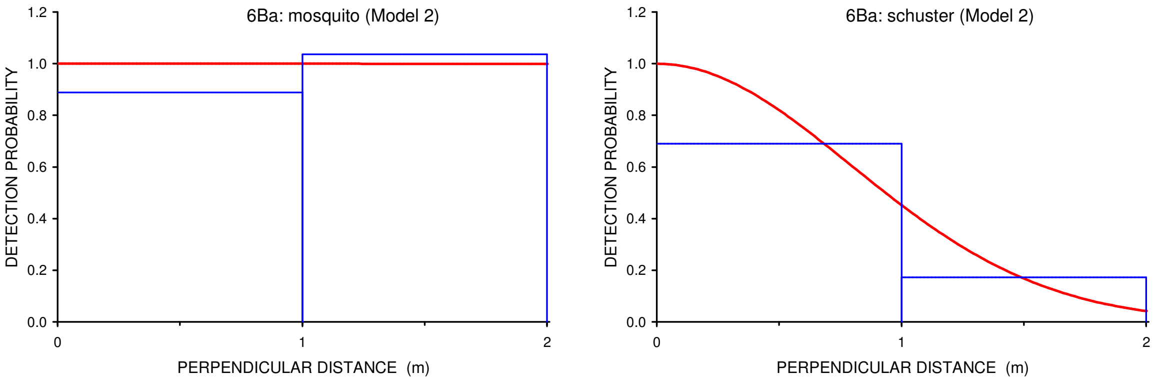

Figure 79: DISTANCE detection functions for Mosquito and Schuster (6Ba)

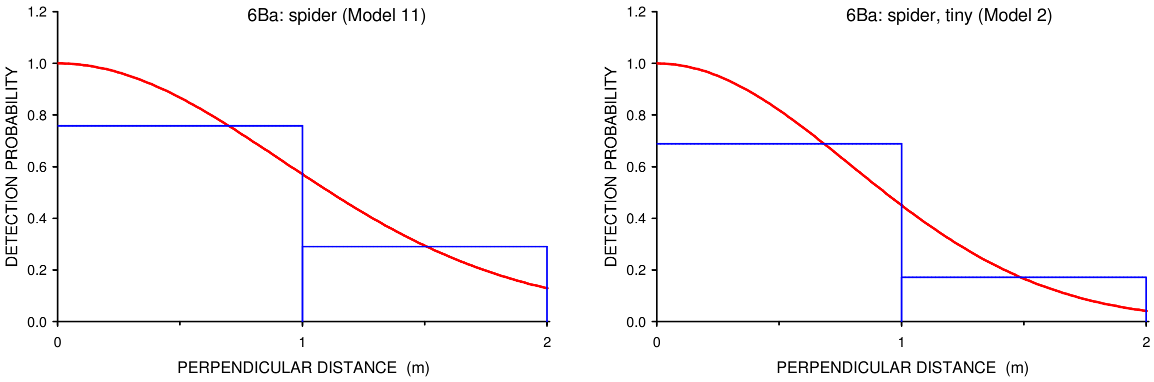

Figure 80: DISTANCE detection functions for Spider and Spider, tiny (6Ba)

Density estimates per km² and per GRID as well as confidence intervals for all narratives are summarized in Table 16. In most cases the range of the confidence interval is relatively large compared to the original estimates. For each study area the total number of arthropods per GRID is calculated. This number can be seen as a simple estimate of arthropod biomass, although it is limited because mean mass per animal is unknown. Arthropod totals range from 50 per GRID in 5PG to 13,158 per GRID in 1CR. This calculation disregards all observations which could not be analyzed with DISTANCE because of low sample size.

Table 16: Overview of density estimates and confidence intervals for trapping web data

Study area	Target Narrative	Density (individuals per km²)	Lower confidence interval	Upper confidence interval	Density (individuals per GRID)
1CR	Ant	2741	656	11448	685
1CR	Spider	702	403	1225	176
1CR	**Arthropods Total:**	**3443**	**-**	**-**	**861**
2Ni	Spider, small	271	170	432	68
2Ni	Ant	2091	644	6787	523
2Ni	Ant, small red	695	289	1673	174
2Ni	Beetle, 868	1043	206	5290	261
2Ni	Centipede, 881	1323	700	2501	331
2Ni	Springtail	47207	25775	86463	11802
2Ni	**Arthropods Total:**	**52630**	**-**	**-**	**13158**
3AK	Spider	970	476	1976	243
3AK	springtail	39238	7950	193674	9810
3AK	**Arthropods Total:**	**40208**	**-**	**-**	**10052**
4Ru	Cycsegusa	281	67	1171	70
4Ru	Protura	163	41	642	41
4Ru	Spider, little	169	50	578	42
4Ru	**Arthropods Total:**	**613**	**-**	**-**	**153**
5PG	Ant, tiny black	199	67	592	50
5PG	**Arthropods Total:**	**199**	**67**	**592**	**50**
6Ba	Beetle, flat	1672	584	4781	418
6Ba	Fly	313	133	738	78
6Ba	Fruitfly	207	77	556	52
6Ba	Milbe	121	29	497	30
6Ba	Mosquito	114	19	686	29
6Ba	Schuster	220	93	522	55
6Ba	Spider	543	263	1119	136
6Ba	Spider, tiny	4132	1776	9614	1033
6Ba	**Arthropods Total:**	**7322**	**-**	**-**	**1831**

3.3.3 DISTANCE Sampling Results: Line Transect Counts

Enough data to model abundance with DISTANCE was collected for only one narrative through the line transects add-on protocol: white Butterfly at 2Ni. The abundance estimate of 98,778 individuals/ km² was high compared to other insects from trapping web data (Figure 81). Model 4 without covariate use showed the best fit (Figure 82).

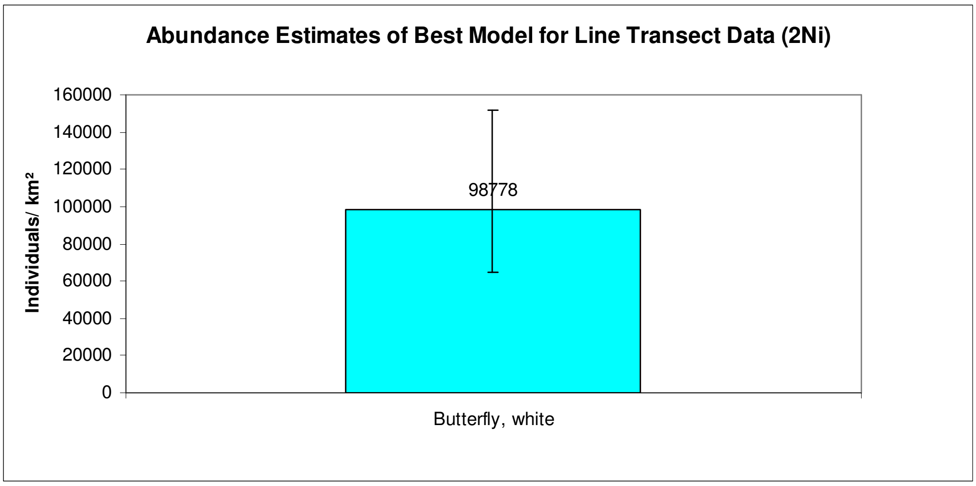

Figure 81: Abundance estimates and confidence intervals of best model for line transect data (2Ni)

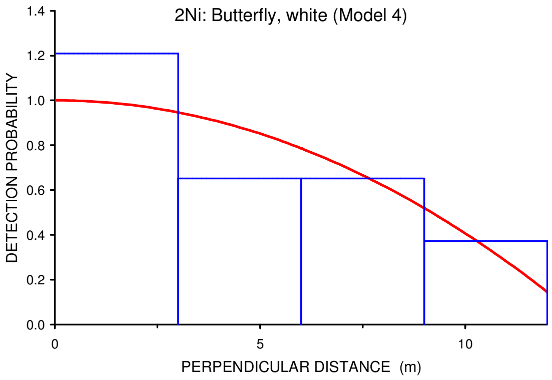

Figure 82: DISTANCE detection function for Butterfly, white (2Ni)

3.3.4 DISTANCE Sampling Results: Randomly vs. Systematically Selected Plots

DISTANCE analysis in above chapters uses pooled data sets under the assumption that true densities are relatively constant between randomly and systematically selected plots. Figure 83, Figure 84 and Figure 85 show comparisons of density estimates for point transect data; for clarity the confidence intervals are not shown in the graphs of this section, but they are available from the digital appendix. Keeping in mind the high confidence intervals shown in the former section some variance between the three data sets (all, ran, sys) is expected. The tendency is that narratives from 1CR and 2Ni have considerably higher estimates for the pooled data set than for the other two. The exception is the Hummingbird estimate, where the random data set as well as the pooled data set results in extremely high estimates compared to the systematic data set. Estimates from 3AK seem to be relatively balanced.

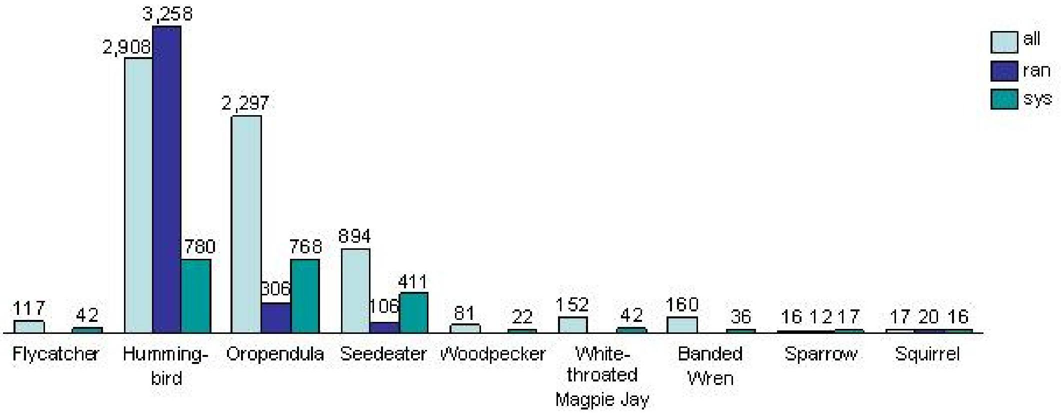

Figure 83: Comparison of abundance estimates for point transect data from random and systematic plots (1CR-3AK)

Abundance estimates for 4Ru and 5PG are also relatively balanced (Figure 84). The most obvious exception is Chickadee at 4Ru, where the estimate based on the random data set is lower compared to the other two.

Figure 84: Comparison of abundance estimates for point transect data from random and systematic plots (4Ru-5PG)

Figure 85 shows estimates of best models for narratives from study area 6Ba. All of them seem to be quite balanced; a larger variance in estimates from the random data set is expected because of the considerably lower sample size.

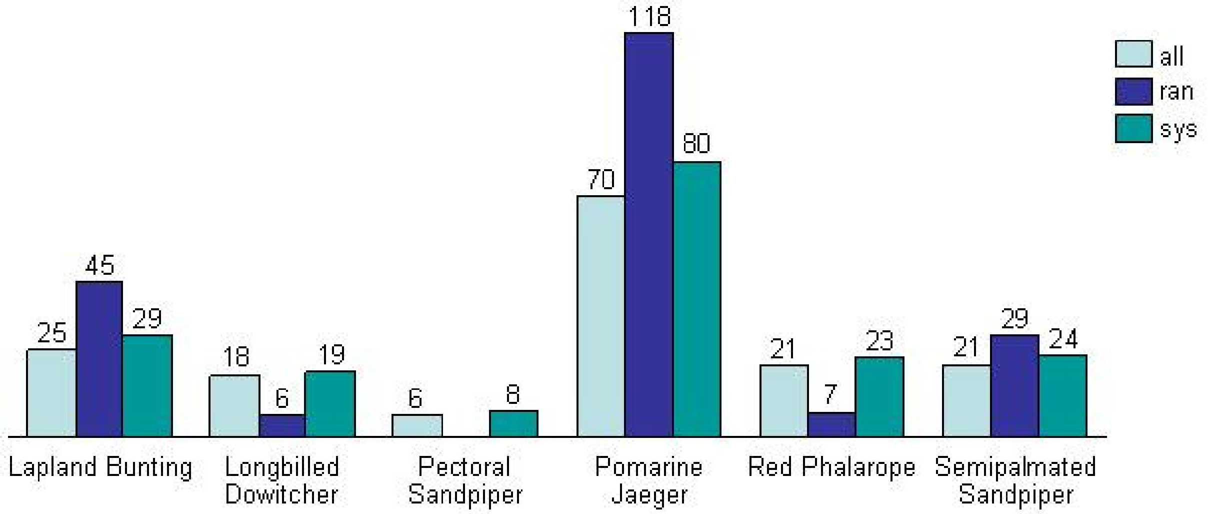

Figure 85: Comparison of abundance estimates for point transect data from random and systematic plots (6Ba)

The only estimate for line transect data shows almost identical values for the systematic and the pooled data set, while the random data set results in a much lower estimate (Figure 86). Trapping web data has not been analyzed this way because it was only collected at systematically selected plots.

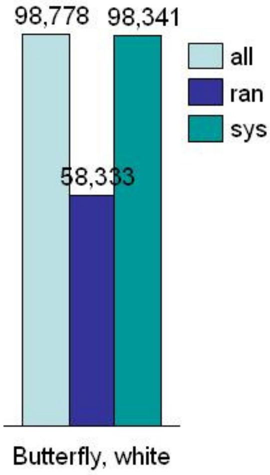

Figure 86: Comparison of abundance estimates for line transect data from random and systematic plots (2Ni)

3.3.5 DISTANCE Sampling Results: Aural vs. Visual Bird Detections

In this section the best model results for pooled data set from point transects at the first five study areas are compared with the ones for aural and visual data sets to check validity of pooling. The results are very different from narrative to narrative, as are the shares of visual and aural detections (compare Figure 36 and Figure 38 above). Figure 87 shows results for the different data sets from 1CR, 2Ni and 3AK. Some of the narratives have relatively close estimates from random and systematic data sets, but much higher values for the pooled estimate (Flycatcher, Hummingbird, White-throated Magpie Jay, Banded Wren). The same applies for Chickadee from 4Ru (Figure 88). This is an indicator that in theses cases the pooling may result in too high estimates.

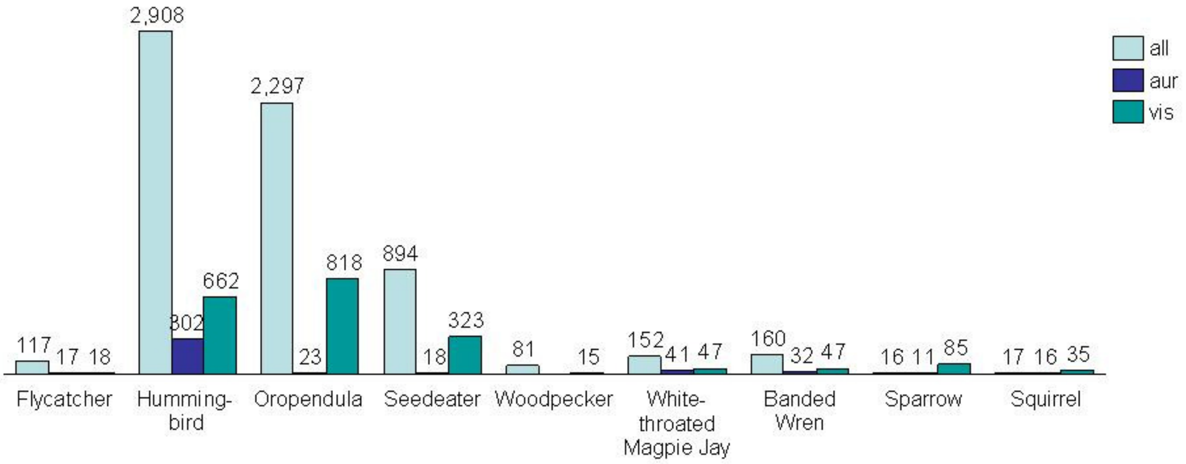

Figure 87: Comparison of abundance estimates for point transect data from aural and visual observations (1CR-3AK)

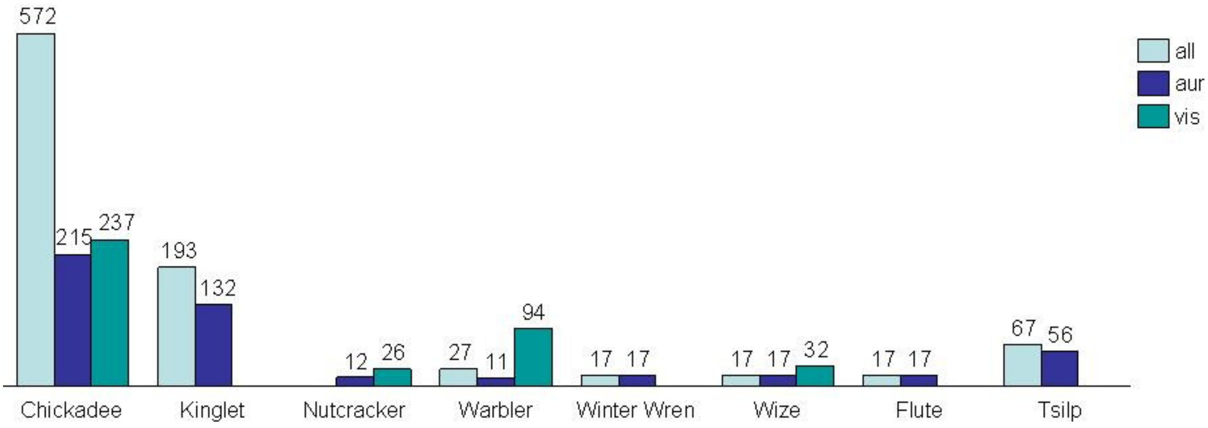

Figure 88: Comparison of abundance estimates for point transect data from aural and visual observations (4Ru-5PG)

3.3.6 DISTANCE Sampling Results: Biological Family and Order

Figure 89 and Figure 90 show estimates for data pooled by biological order, separately for point count data and trapping web data. In both graphs two different scaling are used. Whenever possible the range of confidence interval is indicated. The larger sample size generated through pooling of data does not result in smaller confidence intervals compared to single narrative analysis. Estimates for the same biological order can be compared between study regions. Density for Ciconniiformes for example is relatively similar at 2Ni and 6Ba, despite the first being close to the equator and the second being at the northernmost point of the American continent. Density for Passeriformes for example is below 100 individuals/ km² at 3AK, 6Ba and 5PG, but reaches 1,000 individuals/ km² and higher at 2Ni, 4Ru and 1CR. Explanations for these differences are not readily available because both groups, the one with low estimates and the one with high estimates, include study areas from arctic as well as tropical zones.

The only order analyzed from line transect data was Lepidoptera from 2Ni with an estimated density of 228,394 individuals/ km² (confidence interval between 161,618 and 322,760 individuals/ km²).

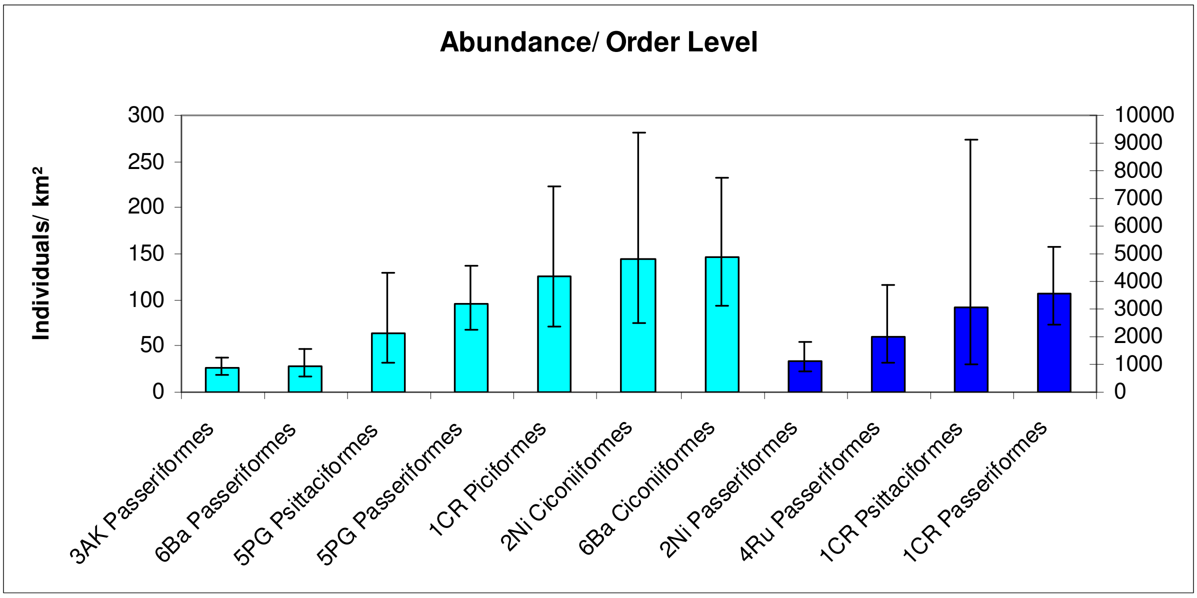

Figure 89: Abundance estimates for point transect data at biological order level

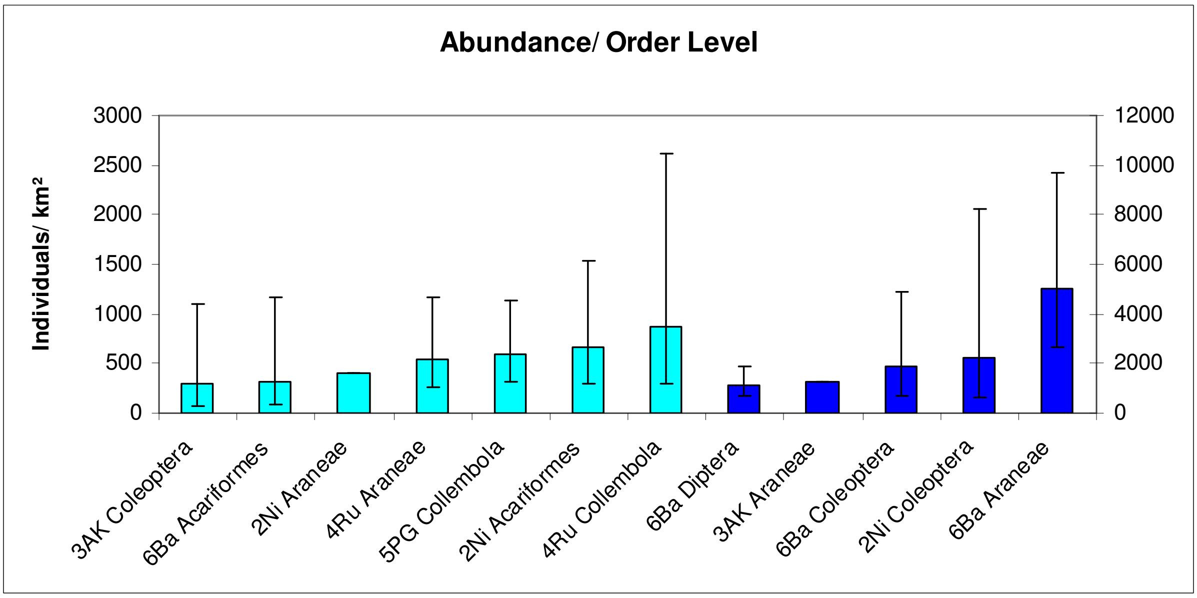

Figure 90: Abundance estimates for trapping web data at biological order level

The same information as above is shown by Figure 91 and Figure 92 for data pooled at the biological family level. Again the confidence interval range is so large that it is safe to assume that pooling does not result in precision gain. Biological family is more specific than order, so aside from Formicidae there are no biological families which are estimated at different study regions. The most interesting point about Formicidae might be that at study area 5PG the abundance estimate of tiny black Ant looks very small (199 individuals/ km²), but the overall ant density is much larger and corrects this first impression (950 individuals/ km²). However, reasons for the dominance of particular ant species can not be found without a much more detailed survey.

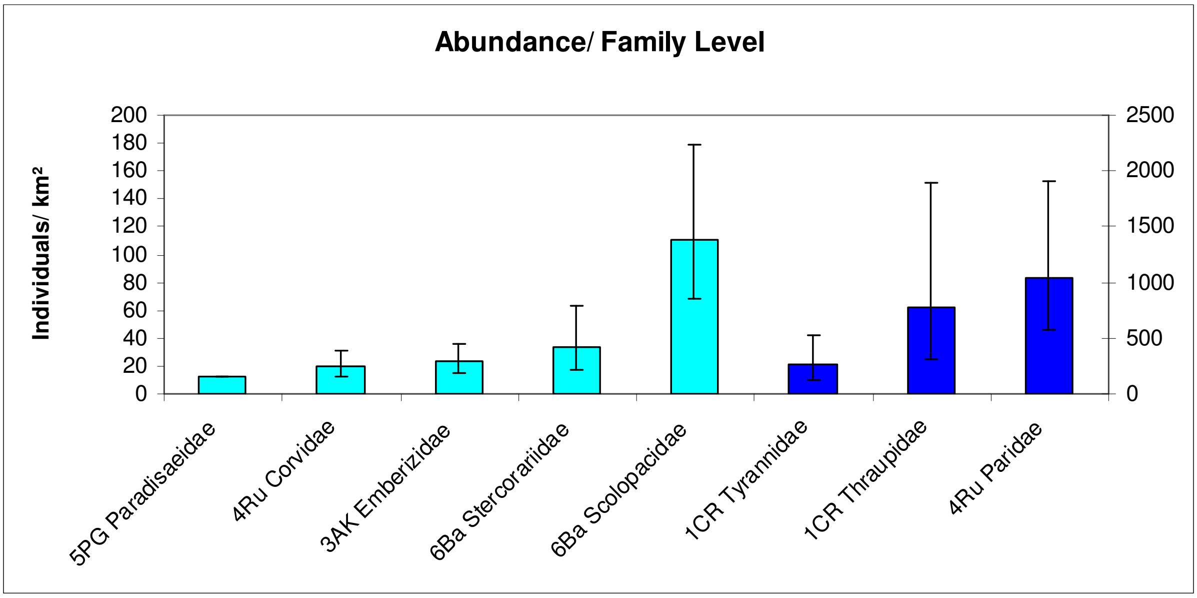

Figure 91: Abundance estimates for point transect data at biological family level

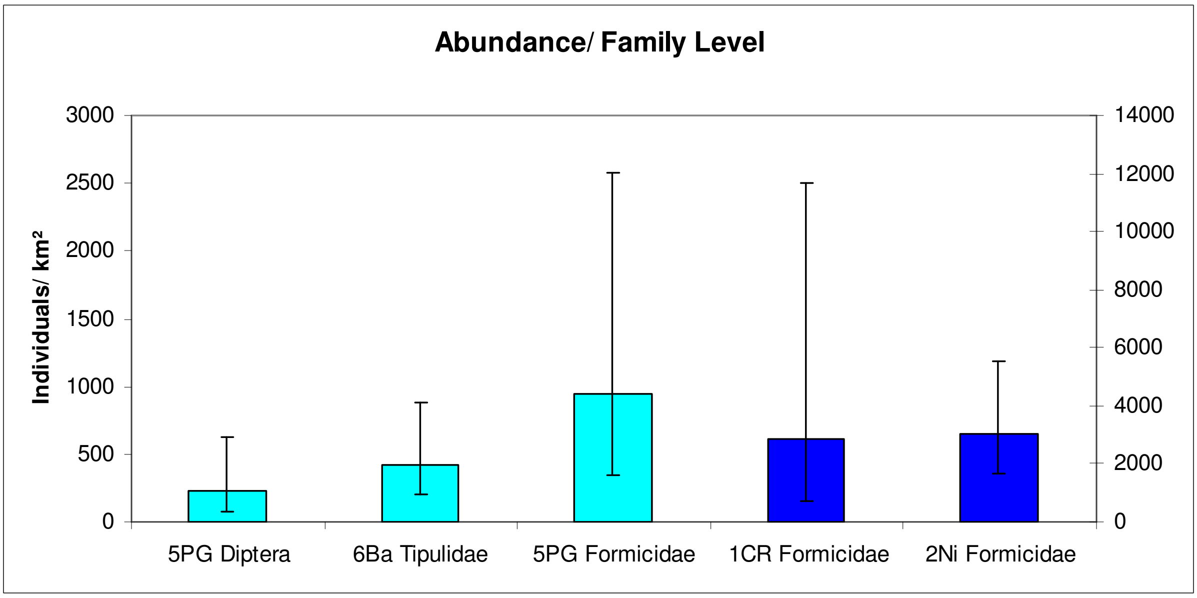

Figure 92: Abundance estimates for trapping web data at biological family level

3.4 PRESENCE / Occupancy

Probability of occupancy (Psi) at a plot is estimated with up to 12 different models for the same species respectively narrative names for which DISTANCE analysis is run (model overview by study area in appendix, starting at page 124). Estimates and standard errors for a study area are only readily available for models 1 and 2 because of PRESENCE results structure. When covariates are used PRESENCE gives single Psi values for each of the 30 plots. For brevity it is decided not to display all 30 plot results for each narrative from all six study areas. Calculating Psi estimates and confidence intervals for each study area considering the covariate values was of a mathematical complexity beyond the limits of this thesis. Detailed results are available for each individual plot from each study area from the PRESENCE project files in the digital appendix. Thus, in this section only results from model 1 (assuming constant probability of detection for all three visits) and model 2 (calculating survey-specific probabilities of detection for each visit) are shown. A table showing best models selected by AIC is given in the appendix (from page 189).

3.4.1 PRESENCE Results: Occupancy Estimates

Occupancy estimates for point transect data is shown in Figure 93 and Figure 94. Both models give relatively constant results for all narratives, model 1 with constant p sometimes having slightly higher estimates. Differences between confidence intervals ranges are also small.

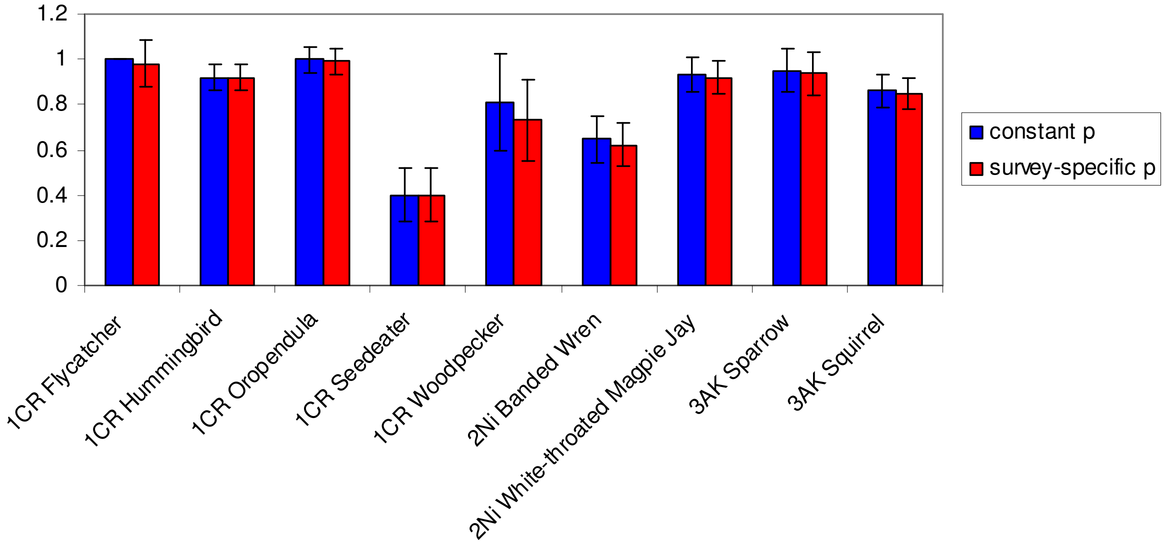

Figure 93: Occupancy estimates and confidence intervals of two models for point transect data (1CR-3AK)

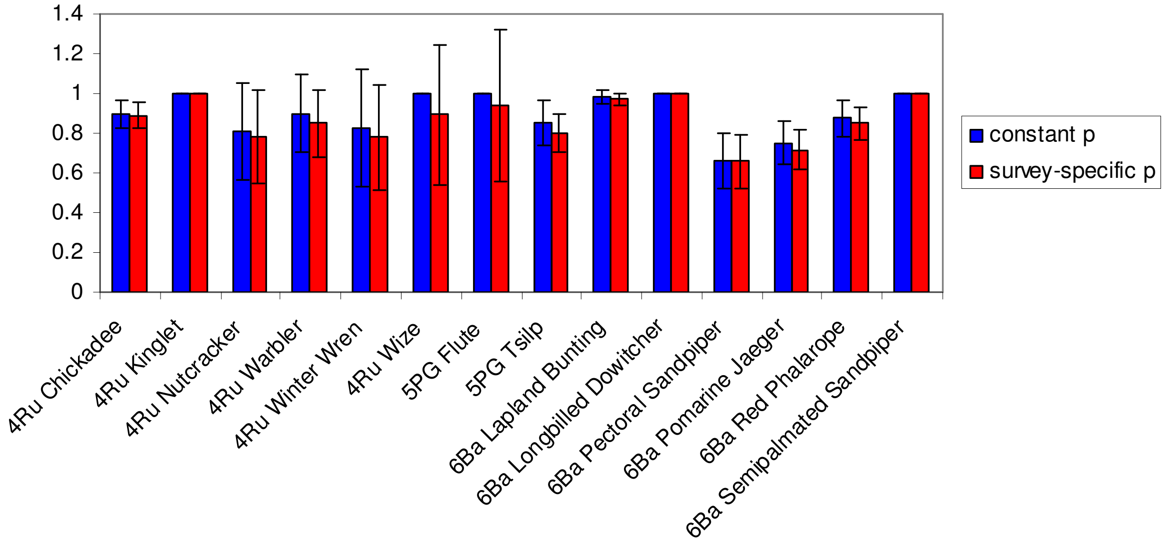

Figure 94: Occupancy estimates and confidence intervals of two models for point transect data (4Ru-6Ba)

Figure 95 and Figure 96 display occupancy estimates for model 1 and model 2 for trapping web data. All but three narratives reach occupancy estimates of 1.0 without confidence interval, meaning that the animals the narratives refer to occupy the plots in the study area with certainty. The three narratives with Psi estimates < 1.0 are Springtail from 3AK, Cycsegusa from 4Ru, and Milbe from 6Ba. There is no immediate explanation why these three narratives differ from the others. The large number of trapping web narratives with perfect occupancy estimates of 1.0 is probably the result of two phenomena: small number of trapping webs, and small size of each web. The small number of trapping webs leads to relatively little variation in habitat types. Combined with the small size of each web it also leads to low numbers of catches for common and rare species, so that these can not be analyzed properly. On the other hand, abundant species are caught at each plot and reach the necessary number of observations, but also naturally reach very high to perfect occupancy estimates.

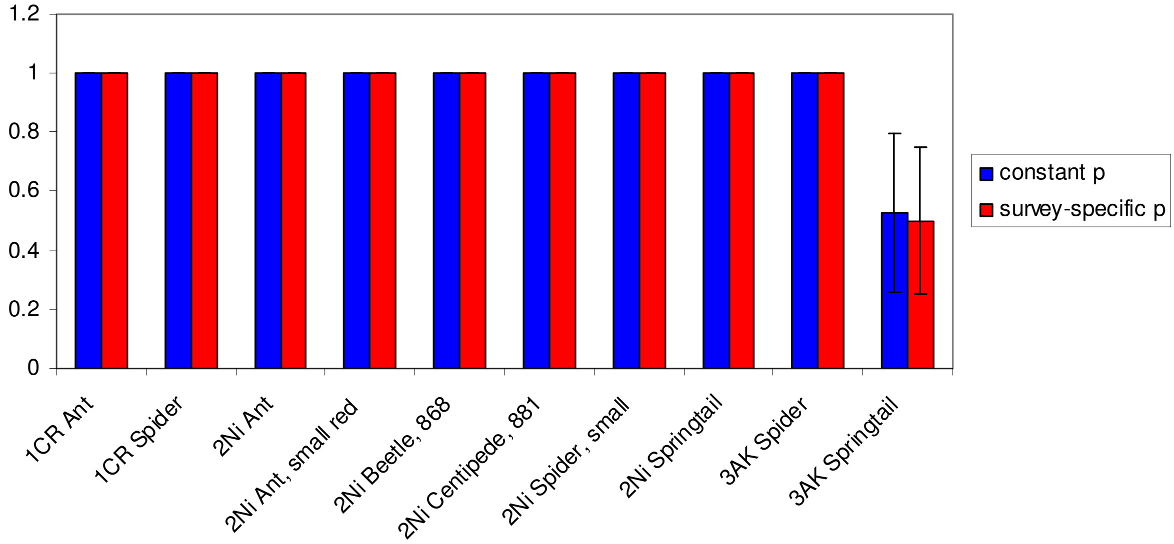

Figure 95: Occupancy estimates and confidence intervals of two models for trapping web data (1CR-3AK)

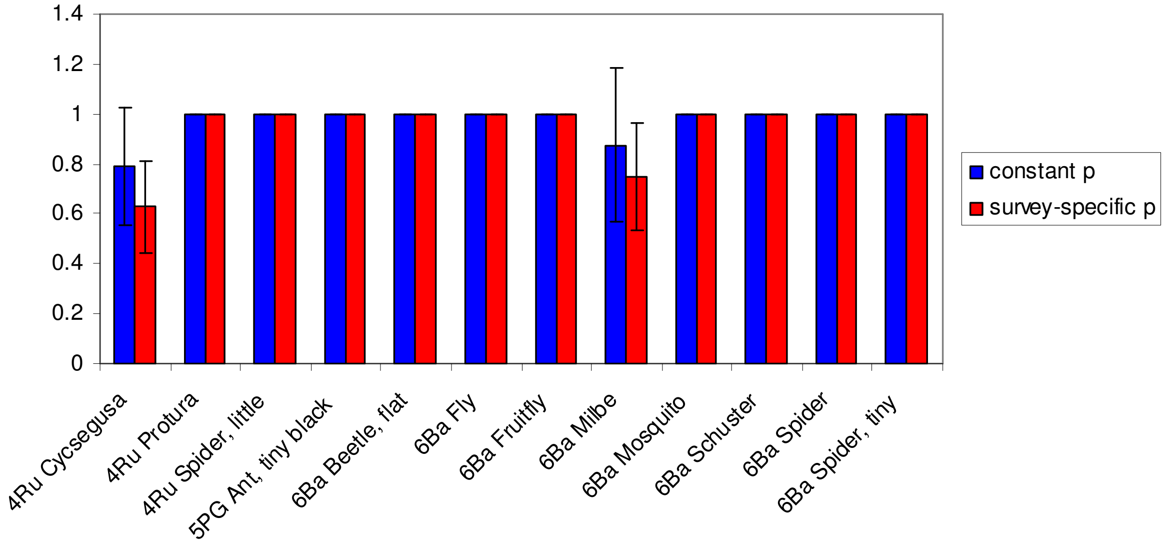

Figure 96: Occupancy estimates and confidence intervals of two models for trapping web data (4Ru-6Ba)

3.4.2 PRESENCE Results: Randomly vs. Systematically Selected Plots

The comparison of analysis for pooled, random and systematic data sets for point transect data shows that differences in occupancy estimates are much smaller than for density estimates in former chapters (Figure 97 and Figure 98). The main exceptions are Seedeater at 1CR and Pomarine Jaeger at 6Ba, which both have comparably high occupancy estimates for the random data set.

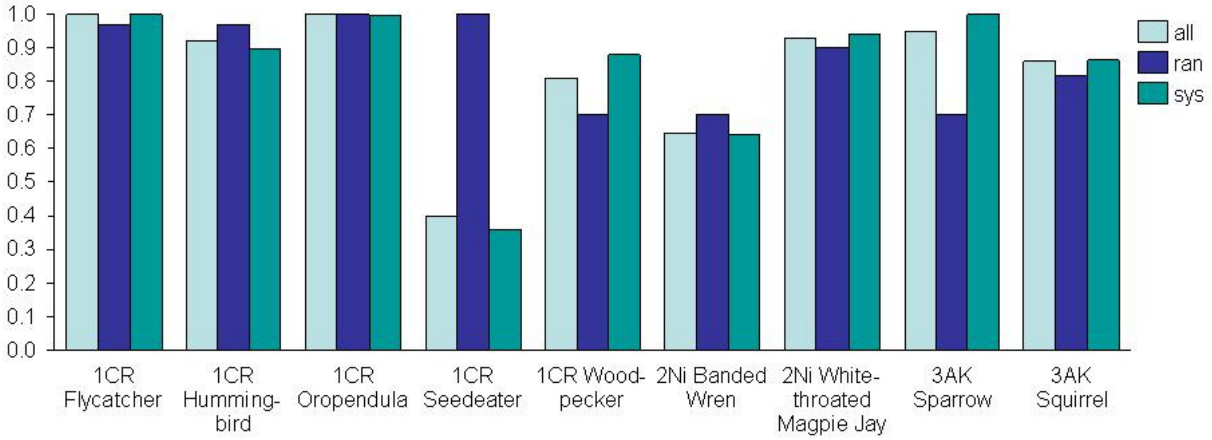

Figure 97: Comparison of occupancy estimates for point transect data from random and systematic plots (1CR-3AK)

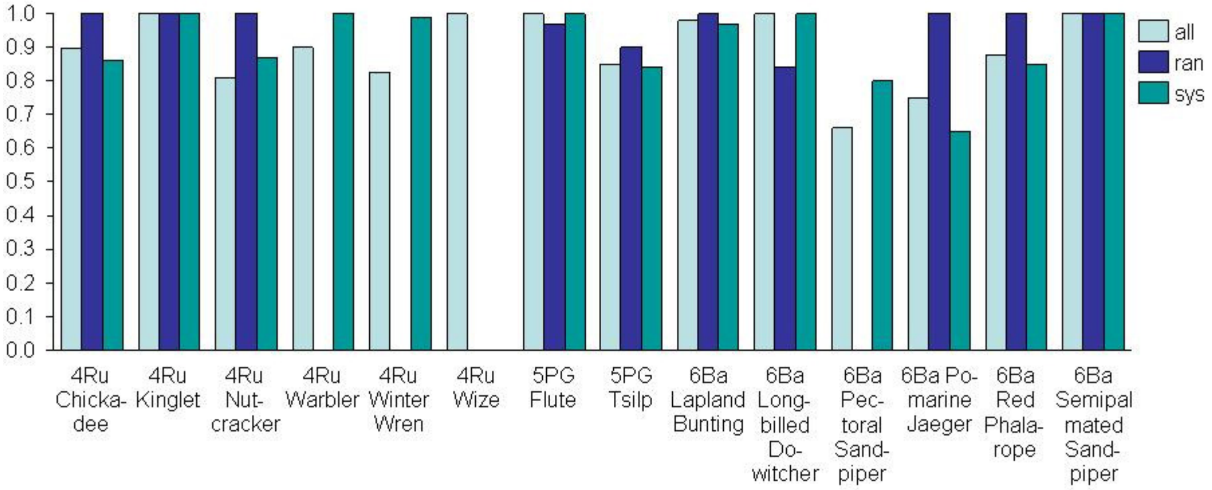

Figure 98: Comparison of occupancy estimates for point transect data from random and systematic plots (4Ru-6Ba)

3.4.3 PRESENCE Results: Aural vs. Visual Bird Detections

Figure 99 and Figure 100 compare occupancy estimates for point transect data from pooled data set with data sets including only aural and only visual detections. Some narratives have relatively close estimates for all three data sets (e.g. Hummingbird at 1CR or Warbler at 4Ru), indicating that there was no problem in pooling two kinds of detection together. Especially in study areas 4Ru and 5PG some narratives are detected only aurally, resulting in missing estimates for visual data set and equal or very close estimates for the aural and the pooled data set. In many cases one kind of detection results in a considerably higher estimate, for example Seedeater at 1CR or Banded Wren at 2Ni. This strongly suggests that at least for those narratives where this is the case the pooling may negatively affect estimates and analysis should be separated by type of detection.

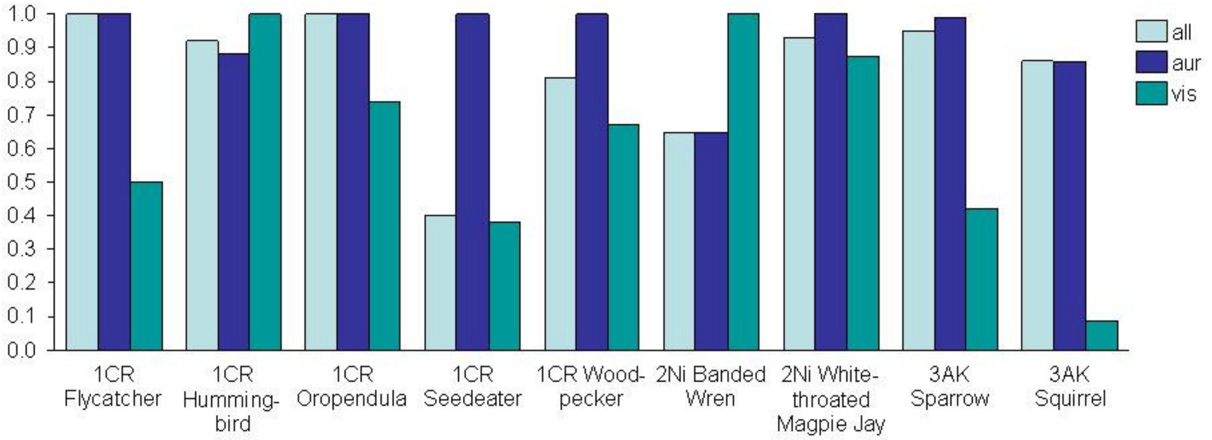

Figure 99: Comparison of occupancy estimates for point transect data from aural and visual detections (1CR-3AK)

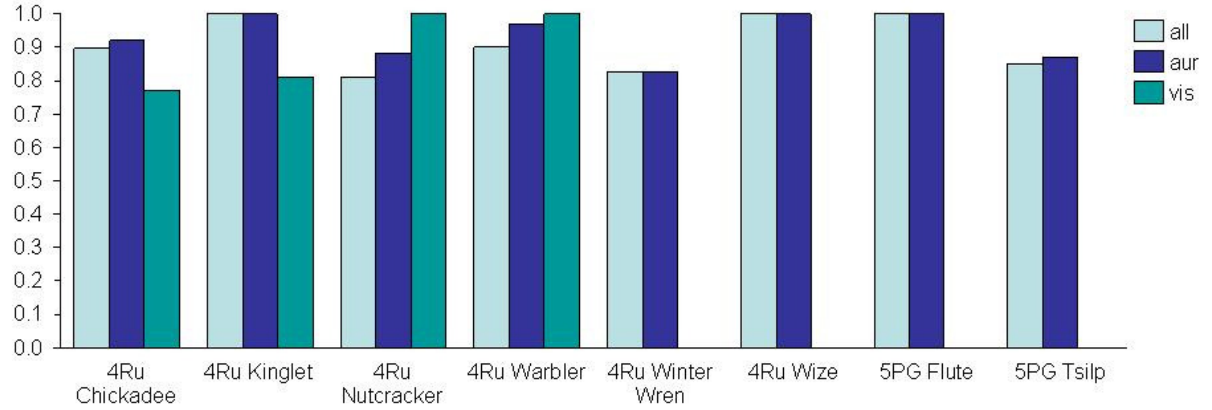

Figure 100: Comparison of occupancy estimates for point transect data from aural and visual detections (4Ru-5PG)

3.4.4 PRESENCE Results: Biological Family and Order

At the biological order level the results and confidence intervals calculated through the two PRESENCE models are relatively close together (Figure 101 and Figure 102). The only exception is Passeriformes from 4Ru, for which the constant detection probability (model 1) results in considerably lower occupancy estimate. Trapping web estimates are all at 1.0 and show no differences for different biological orders, which is difficult to analyze (see also chapter 3.4.1). The same tendency can be seen for point transect data, where only two of eleven biological orders show occupancy estimates lower than 1.0.

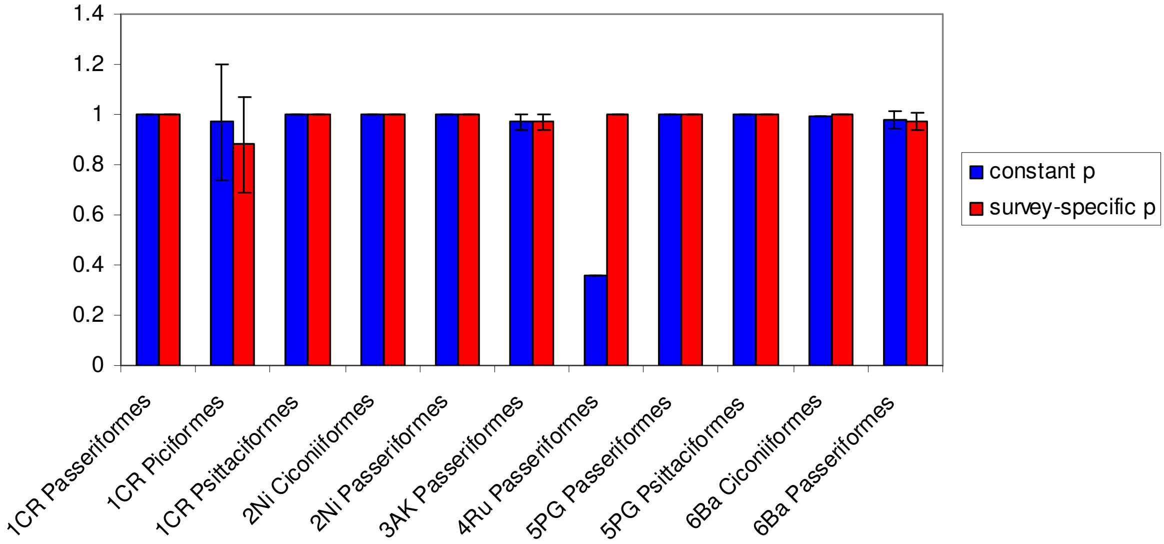

Figure 101: Occupancy estimates and confidence intervals of two models for point transect data at biological order level

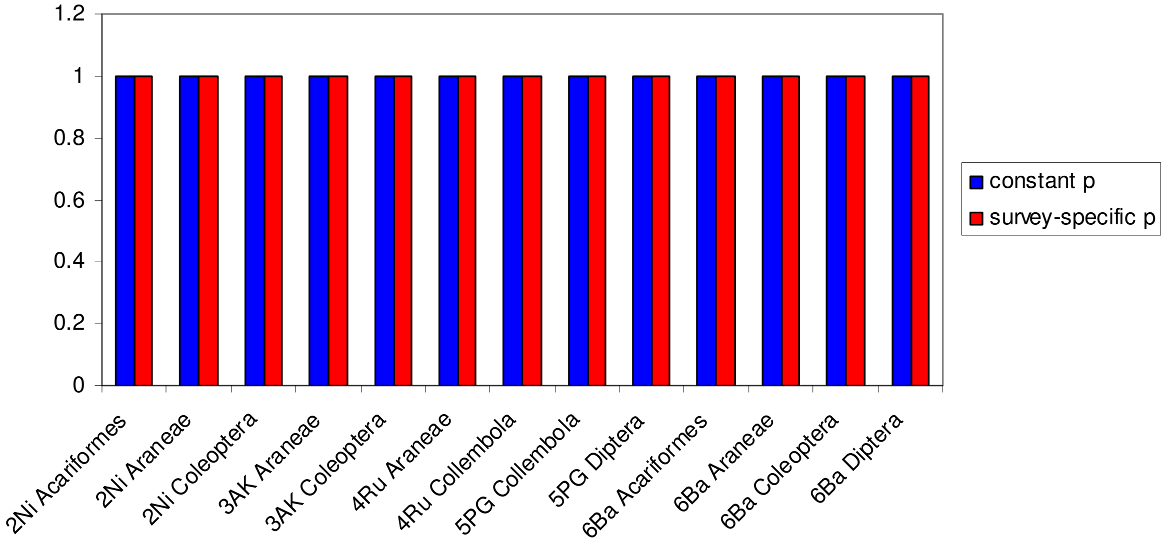

Figure 102: Occupancy estimates and confidence intervals of two models for trapping web data at biological order level

Results at biological family level for point transect data are more diverse (Figure 103), while for trapping web data all estimates show certain occupancy (Psi = 1.0, Figure 104). Results of both models are close together, with the exception being Paradisaeidae from 5PG. Here model 1 results in an occupancy estimate of 1.0 and model 2 comes close to this estimate, but shows an exceptionally large confidence interval. Explanation for this exception can not be offered.

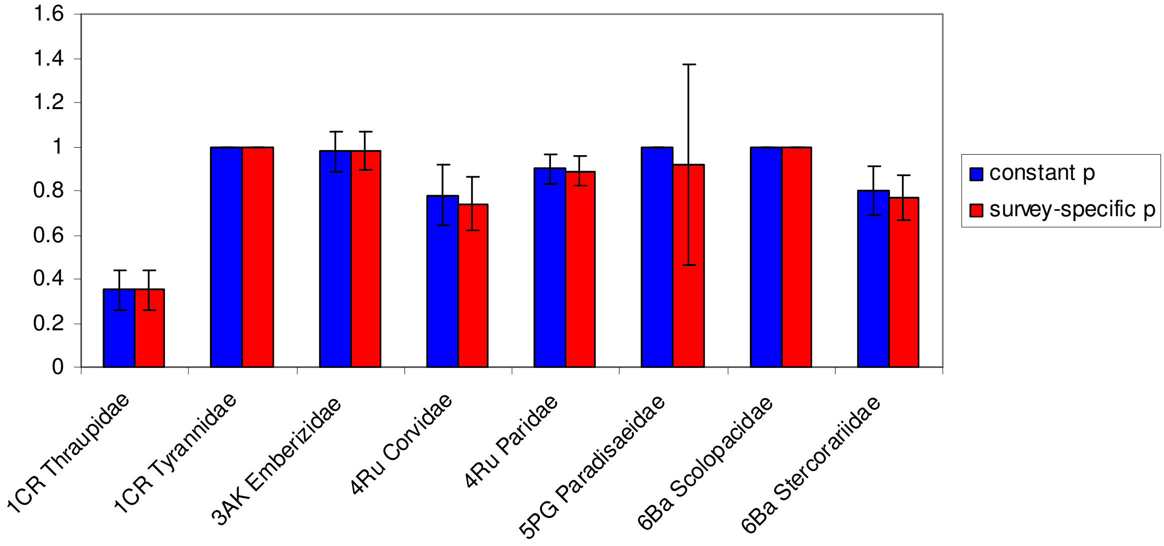

Figure 103: Occupancy estimates and confidence intervals of two models for point transect data at biological family level

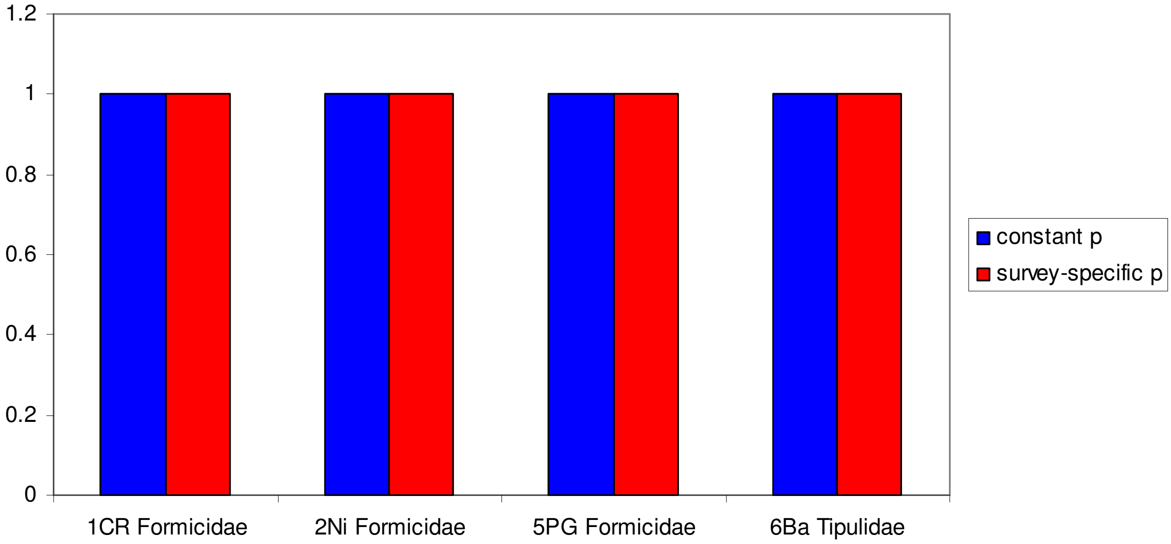

Figure 104: Occupancy estimates and confidence intervals of two models for trapping web data at biological family level

3.5 Comparing DISTANCE and PRESENCE Results

Abundance as estimated by DISTANCE is a direct estimate of population size. Occupancy estimates as derived by PRESENCE are expected to correlate with population size and are seen as indicator for population trends by many wildlife biologists. Following this assumption the estimates of DISTANCE and PRESENCE can be expected to correlate. In this chapter this assumption is analyzed in two parts, separately for point transect and trapping web results:

1. correlation between p estimated by DISTANCE and p estimated by PRESENCE
2. correlation between d estimated by DISTANCE and Psi estimated by PRESENCE.

For this analysis only data from systematic plots is used to avoid any differences between the analysis methods and their ability to handle the combined data, although real differences in the data from the two types of plot would not be expected.

3.5.1 Comparing Point Transect Results

The correlation graph for DISTANCE detection probabilities and PRESENCE detection probabilities from point transect data shows a slightly negative correlation (Figure 105). There is no immediate explanation for this phenomenon, and more detailed analysis did not bring much different results. Both detection probabilities seem to be not directly comparable.

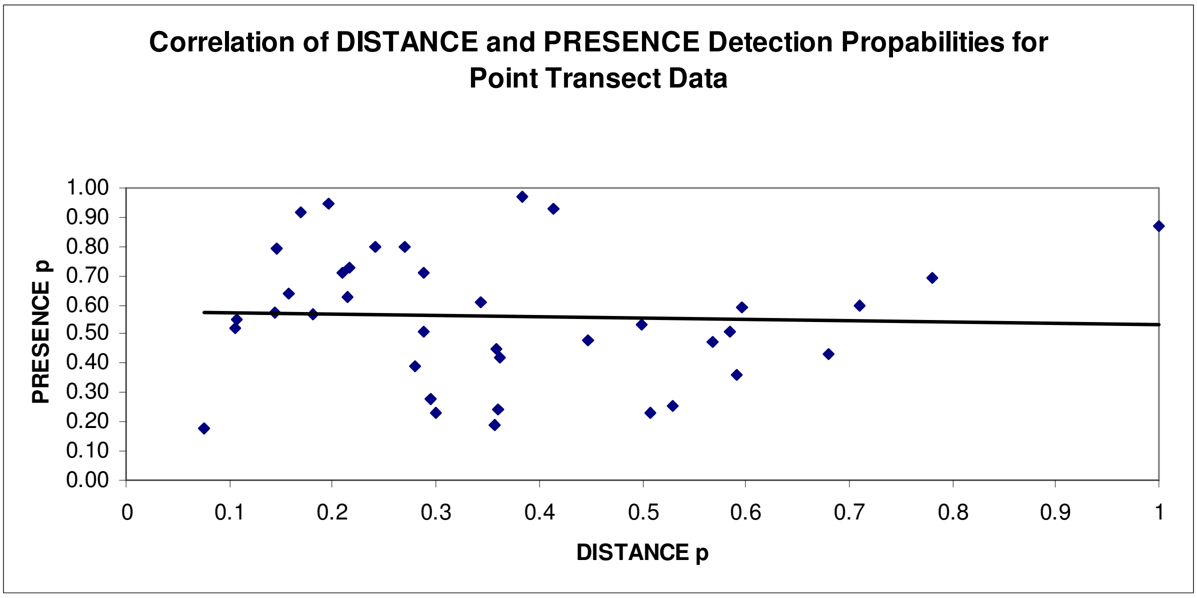

Figure 105: Correlation of DISTANCE and PRESENCE detection probabilities for point transect data (all study sites)

Abundance and occupancy estimates correlate weakly positive (Figure 106). For brevity reasons only those estimates are analyzed in more detail.

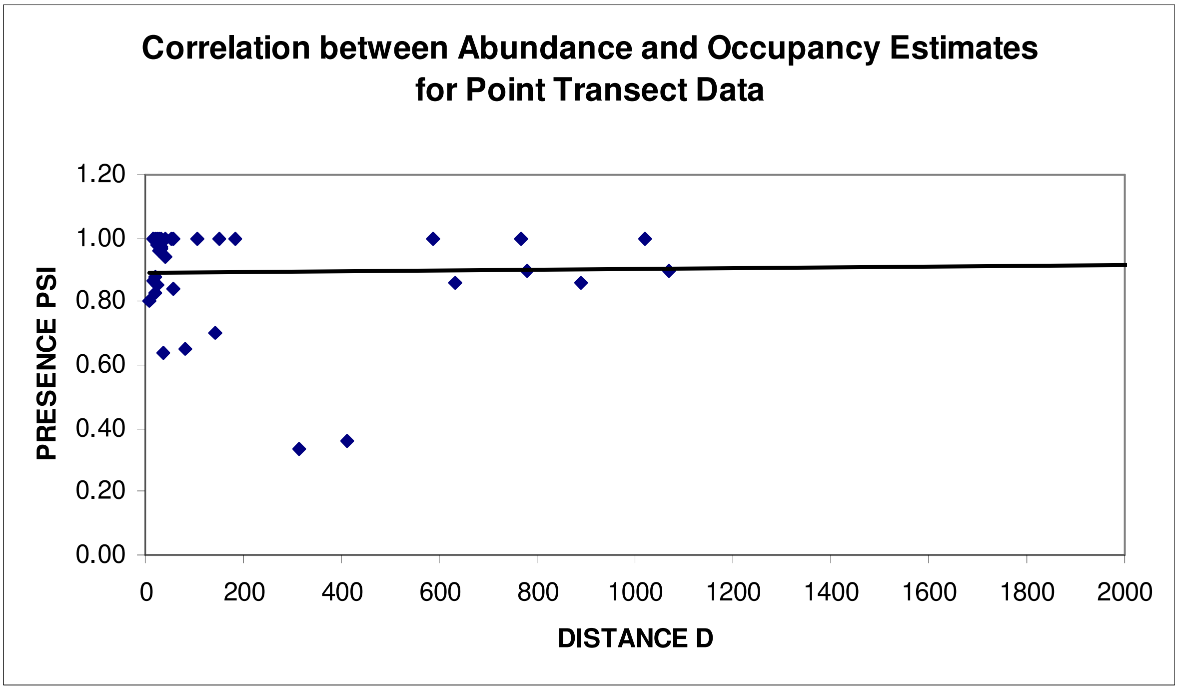

Figure 106: Correlation between abundance and occupancy estimates for point transect data (all study sites)

Correlation for point transects data differs substantially between study areas (Figure 107 to Figure 109). For most study areas relatively low positive correlation can be observed (1CR, 2Ni, 4Ru, and 5PG). The graph for study area 3AK shows a rather steep positive correlation. There is no immediately available explanation why this study site differs so clearly from the other four. The results for study area 6Ba are sticking out even more; there a negative correlation between the two estimates is observed (Figure 109).

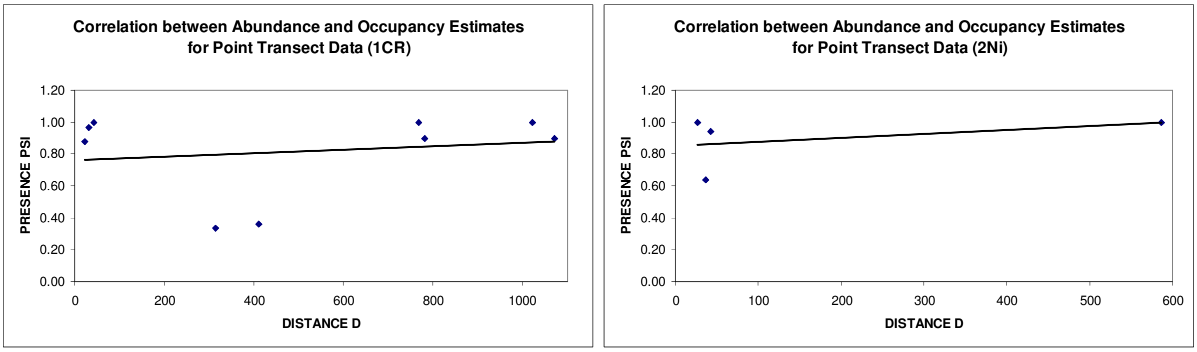

Figure 107: Correlation between abundance and occupancy estimates for point transect data (study sites 1CR and 2Ni)

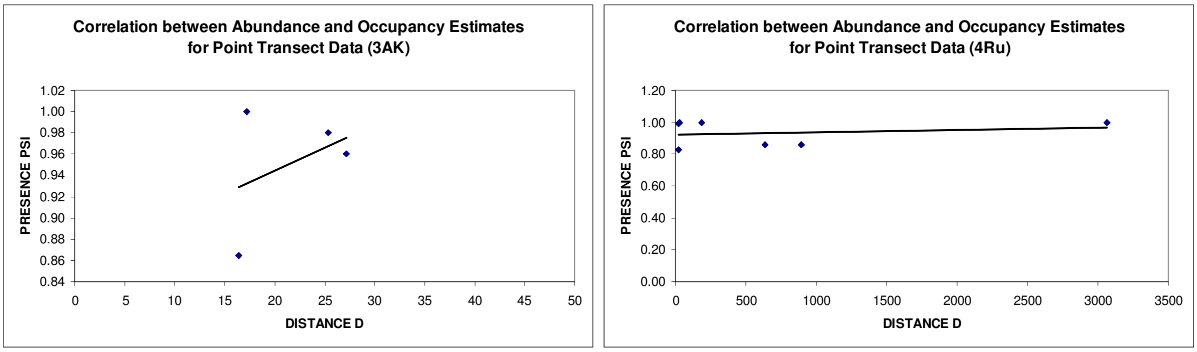

Figure 108: Correlation between abundance and occupancy estimates for point transect data (study sites 3AK and 4Ru)

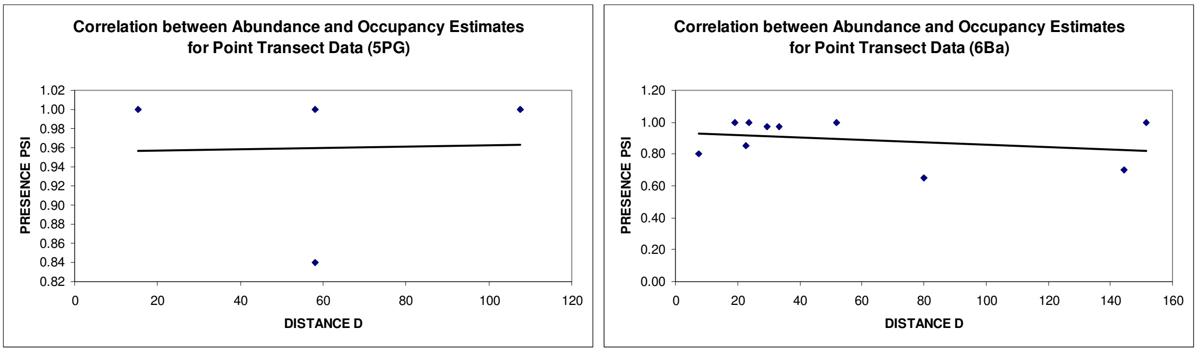

Figure 109: Correlation between abundance and occupancy estimates for point transect data (study sites 5PG and 6Ba)

3.5.2 Comparing Trapping Web Results

Detection probability as estimated by PRESENCE compared to the one estimated by DISTANCE are negatively correlated also for trapping web data (Figure 110). This underlines the impression from the former chapter that both estimates are possibly not directly comparable, despite having the same label.

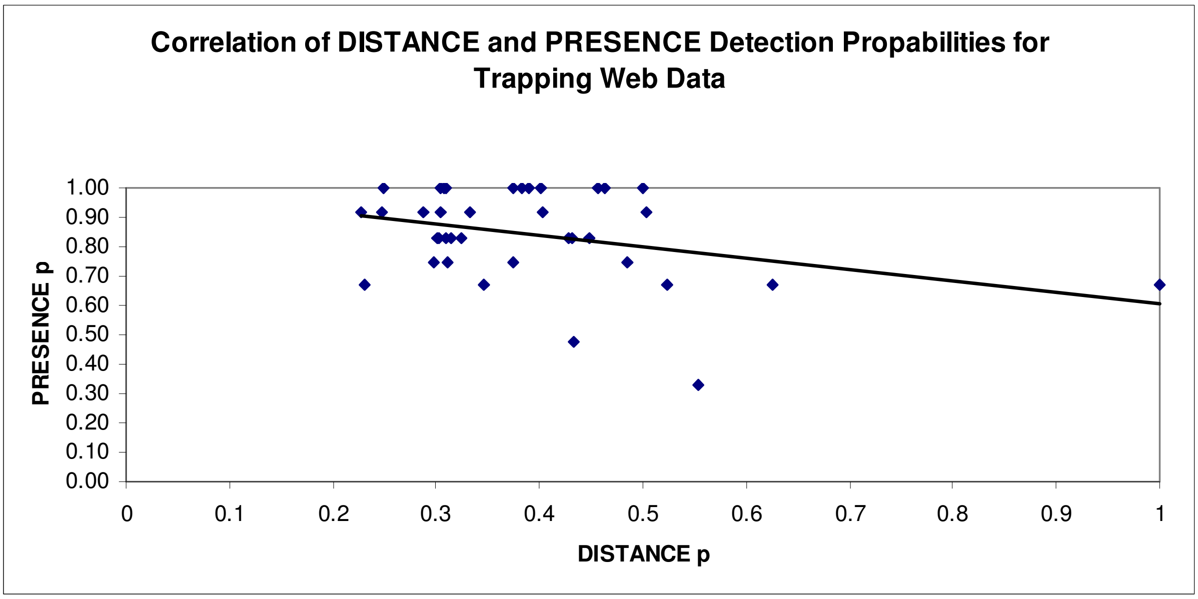

Figure 110: Correlation of DISTANCE and PRESENCE detection probabilities for trapping web data

Figure 111 shows the trend for correlations between occupancy and density estimates: the constantly high occupancy estimates for trapping web data result in a simple horizontal line with no variation for higher density estimates. The same trend can be seen in the separated figures for study areas 1CR and 2Ni (Figure 112), figures for study areas 3AK and 5PG are not displayed because they basically have the same outlook. The large numbers of narratives with perfect occupancy result probably from small number and size of trapping webs (as formerly discussed in chapter 3.4.1).

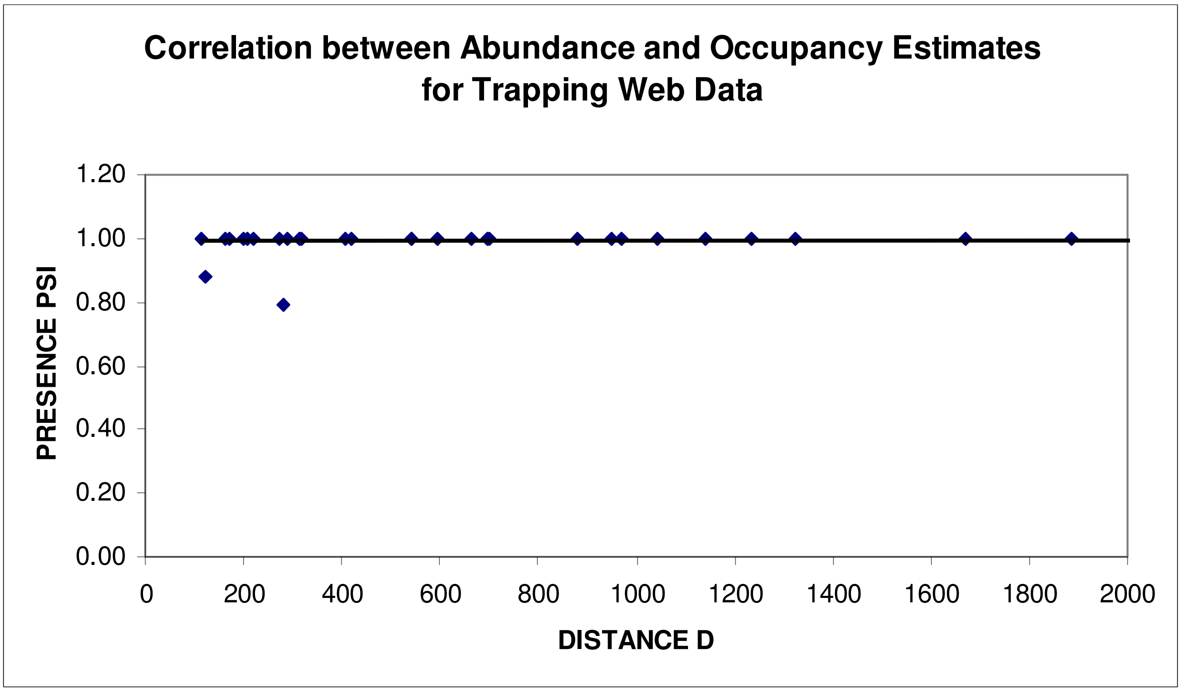

Figure 111: Correlation between abundance and occupancy estimates for trapping web data (all Study Sites)

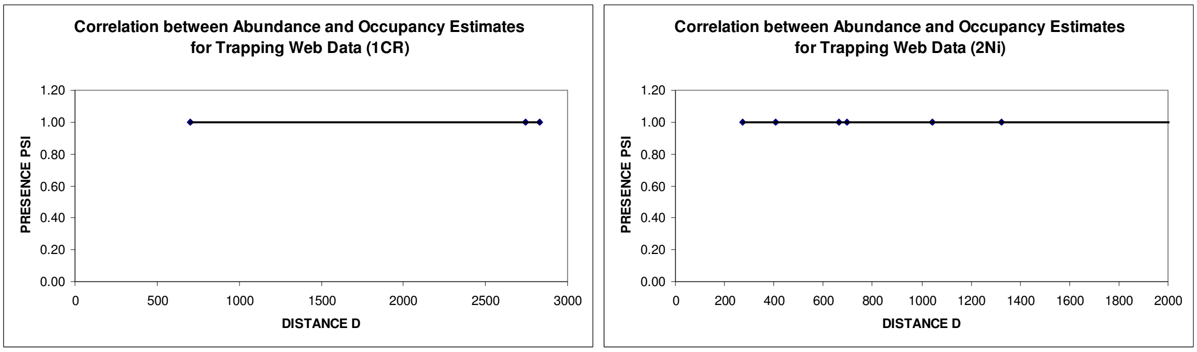

Figure 112: Correlation between abundance and occupancy estimates for trapping web data (study sites 1CR and 2Ni)

At study sites 4Ru and 6Ba a slightly positive correlation can be observed (Figure 113). A closer look reveals that this is in both cases the result of one data point with low DISTANCE density estimate being off the 1.0-occupancy line, while all other data points are exactly on this horizontal line (as for the other study areas). It is also at least questionable if a valid correlation can be built on only four data points.

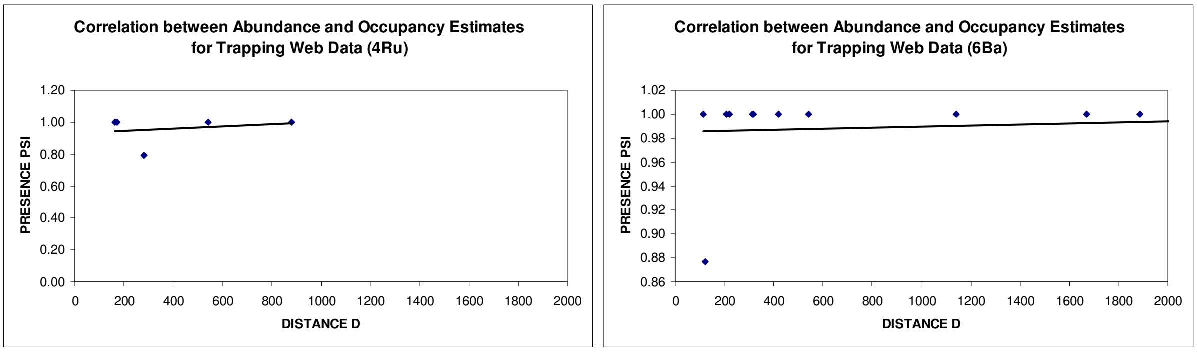

Figure 113: Correlation between abundance and occupancy estimates for trapping web data (study sites 4Ru and 6Ba)

4 Discussion

4.1 Discussion of Results

The amount of information gathered through each GRID was enormous given the relatively short sampling time of 10-14 days. Table 17 displays the number of narratives for which valid predictive models were retained through Random Forests analysis (ROC value > 0.5); as well as the number of narratives for which abundance estimates through DISTANCE sampling and occupancy estimates through PRESENCE analysis were gained. The line transects add-on protocol added another three narratives to Random Forests analysis for 1CR and 2Ni and one narrative to DISTANCE/ PRESENCE analysis for 2Ni (not included in Table 17). In short, 116 valid predictive models were gained through only 12 weeks of sampling! 45 of those also delivered abundance and occupancy estimates. In Random Forests analysis each of the three constructed models (*Plot*, *Covariates*, *Interspecies*) proved to be the best model for some of the narratives analyzed, thus each of them was ultimately useful. A consideration built on this observation is the construction of more model definitions, especially if additional spatially assigned covariate data becomes available from other sources. The quality of the data was in some cases not very good; especially confidence interval ranges for DISTANCE sampling were relatively large. It is assumed that larger data sets will enable stratification of analysis by habitat and solve this problem. Larger amounts of data would also open the possibility to split the data in different sets and analyze those separately if this is assumed to be beneficial for analysis precision, as is probably the case for aural and visual detection of some narratives (chapter 3.3.5). PRESENCE analysis showed a high tendency for perfect probability of occupancy (Psi = 1.0), especially for trapping web results. It is expected that this problem can be solved with larger data sets, especially larger numbers of plots respectively more GRIDs per study area. The effective PRESENCE sampling size for each narrative in each study area was 30 per visit, because this is the number of plots and detection/ non-detection is entering the analysis only once per plot and species (similar to the *Plot* model in Random Forests). DISTANCE analysis on the other hand benefited from spatial repeats, because all distances of all narrative detections at each plot were used for the modeling of the detection function (similar to the *Covariates* and *Interspecies* models in Random Forests).

Table 17: Total number of narratives analyzed by study area, sampling method and analysis method

	Random Forests			DISTANCE / PRESENCE		
	Total	Point Transects	Trapping Webs	Total	Point Transects	Trapping Webs
1CR	19	16	3	7	5	2
2Ni	23	11	12	8	2	6
3AK	10	4	6	4	2	2
4Ru	23	13	10	9	6	3
5PG	23	7	16	3	2	1
6Ba	18	7	11	14	6	8
Total:	116	58	58	45	23	22

The comparison of ROC values for data from systematic and random plots showed relatively small differences (chapter 3.2.2). In most cases the ROC values for data from systematic plots were very close to the pooled ones, which is to be expected as survey effort for this data had a share of roughly 80 % at each study site (25 plots compared to 5 plots). In a few cases the ROC values of data from random plots were surprisingly high. In these cases the most likely explanation is that the input data was very clean, allowing for very strong models. Random Forests has no tendency to overfit data with larger numbers of covariates for small sample sizes (Breiman 2001). In DISTANCE and PRESENCE analysis the differences between the estimates from random and systematic plots were generally low, results usually were very close. Few exceptions stand out, where the difference between estimates from random and systematic plots was rather large (e.g. Hummingbird at 1CR and Chickadee at 4Ru).

The comparison of results from visual and aural data sets implied that for a detailed analysis the individual species' biology has to be taken into account. In many cases the analysis results were similar, but there were also many narratives for which the proportion of observations by one of the two means of detection (aural/ visual) as well as the gained results differed considerably. In some cases the larger number of observations was of one type of detection, while the ROC value derived through Random Forests analysis was larger using the other type of detection. There were also a number of narratives for which the pooled data resulted in considerably higher DISTANCE abundance estimates than the separated data sets, which seems to be implausible (e.g. Oropendula at 1CR and Chickadee at 4Ru). A multitude of biological reasons can explain such differences, for example gender dimorphism in singing behavior (affecting aural detectability), gender dimorphism in coloration of plumage (affecting visual detectability), differences in general behavior/ secrecy by age or gender, different effect of environmental covariates on (especially visual) detectability etc. It is highly recommended to separate between aurally and visually collected data, although this was not possible continuously in the study at hand because of relatively low sample size.

There was a considerable difference between analysis at the narrative level and analysis at higher taxonomic levels. Figure 16 for example shows that 80 and more observations for a narrative generally resulted in valid Random Forests models with ROC > 0.5 (page 37). For higher taxonomic levels there were some with more than 200 observations which did not or only barely result in valid models, and generally a high number of observations did not automatically imply a high ROC value (chapter 3.2.4). This indicates that pooling by taxonomic classes like family or order is not a recommended way to receive bigger datasets. Differences on the biological level, like habitat requirements, can be huge between two species belonging to the same taxonomic class, especially when looking at such diverse ones as Passeriformes. The benefits gained through the analysis of higher taxonomic classes were rather low; the range of DISTANCE confidence intervals was not reduced. In PRESENCE analysis the pooling caused similar problems for point transect data as did the small number of plots for trapping web data: low variance between plots, because some bird belonging to the order Passeriformes was detected at almost every plot, and therefore universally high occupancy estimates (Psi = 1.0 for all analyses at the biological order level). The assumption that higher taxonomic categories can be used as valid surrogates for rapid assessment and monitoring of species diversity gains no support from this study.

Generally both PRESENCE and DISTANCE analysis are supposed to estimate trends in animal populations. Joseph et al. (2006) for example directly compare the two methods and give a recommendation for which types of species which type of sampling can be used. They come to the conclusion that "*Abundance surveys were best if the species was expected to be recorded more than 16 times/year; otherwise, presence-absence surveys were best*" (Joseph et al. 2006). Support in the study at hand for interchangeability of these two methods is ambiguous. Probability of detection as estimated by DISTANCE correlated slightly negative with probability of detection as estimated by PRESENCE. The two might be mathematically different in fundamental ways while only sharing the same label, but this hypothesis was untested. Detailed comparison of these two different p estimates and their methodological differences is beyond the scope of this thesis. The main results, DISTANCE density estimates and PRESENCE occupancy estimates, showed in all but one study area positive correlations for point transects (chapter 3.5.1). Correlations for trapping web data were basically not analyzable because of the large number of perfect or near perfect occupancy estimates (Psi = 1.0, cp. chapter 3.5.2). It is also imaginable that the strict GRID design, which is not tailored to gain high precision results for any of the two methods, does in fact work in favor for one of the two.

4.2 Discussion of the GRID Approach

This section discusses problems with the biodiversity GRID in general and the six study sites specifically. Despite the global relevance and scope of the project it was not funded by relevant funding bodies. This resulted in very few sampling sites which in addition had been selected opportunistically: GRIDs were installed in areas of ongoing other research. The coverage and diversity was still extremely high so that problems of this way of selecting are not expected, but with better funding a more careful design could have been implemented. Probably more important would be a higher number of study sites, since effectively the sample size for the whole globe is six study areas. Another very important area definitely needing attention is the development of a similar approach for aquatic or partly aquatic ecosystems, which have been ignored completely in this work despite their importance for biodiversity.

One reason for the lack of funding could be the visionary approach taken. The intention to have a globally applicable multiple-species monitoring and rapid biodiversity assessment scheme is contrary to the recommendation of many scientists to aim for maximum precision by designing each survey individually for each species of interest (Bailey et al. 2007; MacKenzie & Royle 2005; Pollock et al. 2002). The argument against this point of view is that it is ultimately more cost-effective and useful to aim for several dozens of species estimates with a precision of plus-minus 80 % (or similar) than to aim for only 1 species estimate with a precision of plus-minus 5 %. It has also been shown that the assumption that information of single species can serve as surrogate information for biodiversity in general is often not valid (cp. also van Jaarsveld et al. 1998). Manley et al. (2004) make a point that history of ecological research is rather dubious in some cases, which can also result in favoring multiple-species surveys: "*Any effort that relies solely on a small set of indicator* *species will be subject to skepticism given the history of misuse, overuse, and poor performance of the indicator concept*".

In addition, the large data set produced through this type of survey resulted in a treasure for data mining approaches and pilot study data for more detailed study of species of special interest, for which pilot studies would have to be conducted anyway. A promising idea that to the author's knowledge has not been tested would be to use predictive modeling to identify study sites for adaptive sampling of species of special interest, optimizing precision per study effort (as described by Pollard & Buckland 2004). This could prove especially useful for the monitoring of endemic species with small regional distributions, which might be sampled inadequately by a global biodiversity GRID system, depending on plot density. Distances of 100 m between plots seem to be ideal, but can probably not be achieved on a global scale. Assuming a land area of about 130 million km² (without Antarctica) this would result in roughly 13 billion plots. Increasing the distance to 500 m would still add up to 2.6 billion plots; while 5 km distances as have been used by Magness et al. (2008) in Alaska would result in 260 million plots. This sounds huge at first, but political will built on economic and social considerations clearly decided to protect biodiversity, while so far the necessary actions to do so are lacking. Information is essential for conservation and protection, while "*the extent of global data gathering underway is inadequate to meet the challenge set out at the WSSD in Johannesburg*" (Green et al. 2005). To act accordingly is certainly costly but so is the cost of restoration, with the latter one often being even higher than combined costs of monitoring and conservation (Dobson 2005). The decision ultimately boils down to one question: how valuable is reliable knowledge? (MacKenzie 2005b).

4.3 Discussion of Sampling Methods

The overall biodiversity GRID approach has some promising aspects, especially global coverage and avoidance of bias common in many population studies (e.g. roadside bias, Kadmon et al. 2004). However, some aspects of the sampling methods can be discussed, one being differences in taxonomic knowledge and identification skills between different observers. This was already observable in this relatively small pilot study and will probably grow to a major challenge for a truly global GRID system. The low number of identified species in study area 3AK for example could partly be an effect of less ornithological experience of the observer compared to the observers at the other study sites, qualifying especially the simple species richness estimates from chapter 3.1 (Figure 10 and Figure 11). Generally speaking many biological aspects can hinder identification when observers are lacking specific experience, for example species' gender and age dimorphism in appearance and behavior (the latter one also affecting detectability). On the other hand it is well known also for more traditional survey approaches that "*misidentifications at the species level are common*" (Guralnick et al. 2007). It can be argued that lower precision in taxonomic identification is a minor issue compared to the analysis methods and results offered by the GRID, much as lower estimate precision discussed above. In addition it has been found that a feedback system to integrate observers experience with the sampling methods in different ecosystems is essential. Observers sometimes decided to make immediate adjustments in the field, like exclusion of seabirds from plot A1 in study area 4Ru. A communication system has to be implemented to ensure that this information will be taken into account when analyzing the data sets. It also has to be checked whether it would make sense to include the adjustment in the general survey protocol.

A major issue with the data as collected for this pilot study is the large number of observations with subjective descriptions. An observation noted as "tiny ant" may be a "small ant" for the next observer, thus real monitoring of trends in time by visiting the same plot several times might prove difficult, especially when different observers are surveying. There is no immediate solution for this problem, because even if time and financial resources allowed for an extensive training period prior to sampling, for many regions and ecosystems qualified trainers and literature would still not be available, especially not for more than one taxonomic group. However, when considering that no other relevant data exist, such approaches will help to further fine-tune sampling efforts in the future. And at least for aural detections of bird species automated identification methods are under development (Brandes 2008). These add other technological and financial challenges, but those are expected to be smaller than those from providing adequate training for a large number of observers. It is far easier and more reliable to teach a bird song to a computer and multiply digitally than to train human observers one by one. Thus it would still be costly technology; but it is also expected to be a cost-effective method. Similarly automated approaches for identification of insect species and visual bird detections would be extremely helpful for further development of the biodiversity GRID approach, but are to the author's knowledge not (yet) in sight.

Another important question is the importance of time of the year when the survey is carried out. Buckland et al. (2008) recommend the breeding season for bird surveys. The opportunistically selected study sites in this project were not ideal to meet this criterion. Especially at study area 3AK most aural bird detections were by single call, no bird song melodies were detected, indicating that surveys took place in the last phase of or maybe even after the breeding phase. To conduct studies exactly at the best time of the year will provide a considerable planning challenge in a global project.

Three other issues have been observed which mainly affect trapping webs. The first is survey effort. Despite all endeavor to keep survey effort constant between all study plots and visits, this goal was already not achievable for only 24 sampled plots at 6 study areas. It can be assumed that the differences are not very important because all trapping events took place over night (at least 12 hours trapping time) and differences in trapping time were after all relatively marginal. The second issue with trapping webs is the availability of weather protection and/or a trapping fluid. For budget reasons in this study all cups were set dry and unprotected from rain and predators. Both points do not seem to cause any immediate problems, but a more sophisticated approach would be to protect the cups with small roofs and use a trapping fluid, which would also avoid predatory arthropods to eliminate each others while in trap. However, this could also exclude insects that fly into the trap. These issues require more study. The last point is that some species traits that are regarded to have important influences on precision (e.g. home range size and movement rates, Lukacs et al. 2005) can not be taken into consideration for study design when using multiple-species trapping webs. As stated before and shown in this study the gain in number of animals surveyed in combination with sophisticated modeling approaches outweighs this lack of precision.

The tested line transects add-on protocol produced observations only in the first two study areas, and enough for analysis only for butterfly species. Snakes were detected, but only when walking between the plots and not enough to run a valid analysis. For many species it is probably just the small survey effort of 300 m per GRID that is not sufficient to collect enough data. Thus, add-on protocols using line transects probably have to use longer lines, which might result in problems to assign them to spatial covariate data. Occupancy estimates for this sampling method would have been especially interesting, but the necessary three repeats were not realizable.

Violation of assumptions necessary for DISTANCE and PRESENCE analysis has not been tested explicitly in this study. Repeats of sampling at each plot have been done within few days, so that extensive movement of animals is unlikely, but not impossible. Movement of animals in and out of the sampled area would be problematic for PRESENCE analysis, which assumes a constant population. However, results did not imply that this is a problem in the study at hand. Results of models with constant detection probability were generally very close to those with survey-specific detection probability (chapter 3.4.1). DISTANCE assumptions were a bit trickier. Recent research suggests that the assumption of perfect detectability close to the observer, at a distance of 0 m ($g(0) = 1$), should be vigorously tested in each study (Bächler & Liechti 2007). This is simply impossible given the number of study sites and different ecosystems, the short time and the budget constrains. This assumption might have been violated for four of the 45 point transect DISTANCE estimates, where detection functions clearly showed no observations in the first segment from the observer (chapter 3.3.1). Another assumption crucial for DISTANCE analysis is high precision of distance estimates. In this study all distances for point and line transect observations were estimated by the observers without technical distance measurement tools, because technical devices were not available and would have failed in some of the environments anyway, especially for aural detections. Besides, the GRID system with distances of 100 m between plots and additional markers at 50 m between plots proofed to be extremely helpful for the observers to validate their estimates.

The last minor issue worth mentioning in this section is a possible effect the preparation of a GRID may have on animal behavior. Especially in dense lowland tropical rainforest as encountered in Costa Rica there is a necessity to cut trails if one wants to do intensive repetitive sampling in the area over several days or even weeks. On the one hand it would be interesting to know if these trail works actually affect the gathered observations, but on the other hand there is little one can do to investigate this issue. To count and survey animals scientists have to walk through the forest, and to do this in a lowland tropical rainforest in Costa Rica some trails have to be cut prior to sampling.

4.4 Discussion of Analysis Methods

Most of the encountered analysis problems have been mentioned in the results section already. In this section a summary of general limits of the study are given. The biggest problem for analysis is the relatively small data set. On the one hand more than 5,000 observations are available for analysis, but on the other hand these were collected in 6 study areas with three different survey methods. Strictly speaking the splitting in most cases should have gone even further to separate data collected at randomly selected plots from data collected at systematically selected plots, and aural detections from visual detections at the same time. But all analysis methods used usually profit from larger amounts of data. The decision here was to report detailed results for the pooled data sets and additionally display trends for split data sets separately. The trends indicated in many cases that a general split would have been beneficial. Additionally, the split was always only at one level, random data was separated from systematic data, but not split further in aural detections from random data and visual detections from random data, simply because the data sets became too small for analysis this way. Another option that is certainly promising and could not be used because of lacking data is stratification by habitat. In this study habitat was used in different ways of analysis only as a covariate, simply because the data set was too small to stratify by habitat. In short: the more data the better the algorithms work and the more precisely data sets can be split by important features.

To analyze the relationship between species and covariates spatially the observations have to be assigned to one particular plot, which can be difficult in open habitats where neighboring plots can be observed from a plot. The solution used for this study was to truncate all data at 50 m, half of the distance between two neighboring plots. Mathematically this way of handling cuts out some of the data: the greatest possible distance between two GRID plots is ca. 141 m measured diagonally, resulting in some data within 70 m spatially belonging to a plot. However, without indication to which direction the observations were made from the plot a clearer analysis was not possible and some data that could be used is omitted for clarity. Maybe the use of a plot form other than circle would be beneficial, but then again all other plot forms are considerably more effort to use in the field, especially combined with point transect sampling.

Another issue with the covariates is an extremely low variation at study site 6Ba. Most of the covariates gathered in the field can be expected to correlate with presence/ absence and abundance of trees (highest tree, canopy cover, duff cover, plant species presence/ absence etc.). This worked well in environments were the landscape was diverse, including pasture, wetland, and different kinds of forests. It proved to be more problematic in a relatively homogenous ecosystem like arctic tundra. Other estimates which would not be visible in dense forests, like diameter of or distance to the next lake, were added to the protocol in this case. All in all the predictive modeling still worked well at this study site, but the recommendation resulting for global monitoring is to gather additional data with higher small-scale variations at each plot, especially pedological data available in all terrestrial ecosystems. Another idea is to use data from other surveys or other publicly available geo-referenced data, for example distance to roads from available maps or slope gradient and aspect from digital elevation models. The possibilities this approach opens are amazing. The only thing to be kept in mind is the GRID spacing: a satellite picture resolution with pixel sizes of 2 km x 2 km will not provide adequate covariates for modeling of a GRID with much smaller spacing (e.g. 100 m, as in this study).

Technically a problem was encountered with the MS Access database, which reached its limits already in this relatively small study. The use of point transect data for the *Interspecies* model aiming at the prediction of trapping web narratives was not possible. The combined number of trapping web and point transect data simply exceeded the limitations in the number of columns a query in MS Access can have. For biodiversity GRID studies on a larger scale a more sophisticated database application is therefore highly recommended.

5 Conclusions

This study demonstrates three of the analysis methods which carefully designed biodiversity GRIDs offer to ecological research. The available analysis options are by a magnitude more. Especially autocorrelation issues between plots and questions regarding fragmentation and change over time come to mind. Adding that all sort of spatial data, especially also those resulting from remote sensing, can be connected to the GRID data and that continuous efforts exist to make research data publicly available, the possibilities to conduct relevant analysis are enormous.

The results shown so far are more than promising. Three of the most sophisticated current methods in ecology are already involved: Random Forests as a powerful data mining tool to construct predictive models, DISTANCE sampling for the estimation of population abundance, and Occupancy estimation with PRESENCE to gain information for species with low sample sizes. Results lack in precision for each single species, but are promising regarding first snapshot assessments of multiple-species. Such an approach is urgently needed to improve cost-effectiveness of ecological research, while at the same time more precise study designs have their place in evaluation of known risk species for which more detailed population estimates are necessary. Challenges have been faced by the current study, but those are to be expected when working on a global scale. A number of recommendations could be given to improve the involved methods. The most pressing next step is to sample more study sites and build a stronger database. It is unlikely that the biodiversity GRID approach will be accepted and implemented by many country governments within a short time frame, so another urgent point of development is the connection with other data sources. Additionally the project would gain from development of a meta-software with the ability to batch several other software solutions, and from a closer investigation of the comparability of DISTANCE and PRESENCE results as well as detection probabilities estimated by those two programs.

Biodiversity GRIDs are an important step into the direction to fill holes in global biodiversity information for conservation and management in a cost-efficient way. The challenge to make this approach work is to move political decision makers to act according to their declarations of intent. The protection of biodiversity is not a selfless act of charity...

6 References

ABMP. (2006). *Terrestrial field data collection protocols, version 2.1*, Alberta Biodiversity Monitoring Program (ABMP). Accessed 2007/05/13 on World Wide Web: http://www.abmp.arc.ab.ca.

Alldredge, M. W., Pollock , K. H., Simons, T. R. & Shriner, S. A. (2007). Multiple-species analysis of point count data: a more parsimonious modelling framework. *Journal of Applied Ecology*, 44 (2): 281-290.

Bächler, E. & Liechti, F. (2007). On the importance of g(0) for estimating bird population densities with standard distance-sampling: implications from a telemetry study and a literature review. *Ibis*, 149 (4): 693-700.

Bailey, L. L., Hines, J. E., Nichols, J. D. & MacKenzie, D. I. (2007). Sampling design trade-offs in occupancy studies with imperfect detection: examples and software. *Ecological Applications*, 17 (1): 281-290.

Bauldock, B., Wicks, W. & O'Neill, J. (2001). Metadiversity II: assessing the information requirements of the biodiversity community - summary of findings. Charleston, Sponsored by the U.S. Geological Survey, Biological Informatics Office and the National Biological Information Infrastructure and the National Federation of Abstracting & Information Services (NFAIS).

Brandes, T. S. (2008). Automated sound recording and analysis techniques for bird surveys and conservation. *Bird Conservation International*, 18: 163-173.

Breiman, L. (2001). Statistical modelling: the two cultures. *Statistical Science*, 16 (3): 199-231.

Breiman, L. & Cutler, A. (2005). *Random Forests website*. Accessed on World Wide Web: http://www.salfordsystems.com/randomforests.php.

Brooks, T. M., Mittermeier, R. A., Mittermeier, C. G., da Fonseca, G. A. B., Rylands, A. B., Konstant, W. R., Flick, P., Pilgrim, J., Oldfield, S., Magin, G. & Hilton-Taylor, C. (2002). Habitat loss and extinction in the hotspots of biodiversity. *Conservation Biology*, 16 (4): 909-923.

Buckland, S. T., Anderson, D. R., Burnham, K. P. & Laake, J. L. (1993). *Distance sampling: estimating abundance of biological populations*. London, Chapman and Hall. 446 p.

Buckland, S. T., Anderson, D. R., Burnham, K. P., Laake, J. L., Borchers, D. L. & Thomas, L. (2001). *Introduction to distance sampling - estimating abundance of biological populations*. Oxford, Oxford University Press. 432 p.

Buckland, S. T., Marsden, S. J. & Green, R. E. (2008). Estimating bird abundance: making methods work. *Bird Conservation International*, 18: 91-108.

CBD. (2006). *Text of the Convention on Biological Diversity*. Montreal, Secretariat of the Convention on Biological Diversity. Accessed 2/10 2008 on World Wide Web: http://www.biodiv.org/convention/convention.shtml.

Chapin, F. S., Oswood, M. W., van Cleve, K., Viereck, L. A., Verbyla, D. L. & Chapin, M. C. (eds.). (2006). *Alaska's changing boreal forest*. New York, Oxford University Press.

Cochran, W. G. (1946). Relative accuracy of systematic and stratified random samples for a certain class of populations. *Annals of Mathematical Statistics*, 17 (2): 164-177.

Craig, E. & Huettmann, F. (2008). Using "blackbox" algorithms such as TreeNet and Random Forests for data-mining and for finding meaningful patterns, relationships, and outliers in complex ecological data: an overview, an example using golden eagle satellite data and an outlook for a promising future. In Wang, H.-F. (ed.) *Intelligent data analysis: developing new methodologies through pattern discovery and recovery*. Hershey, IGI Global.

Dobson, A. (2005). Monitoring global rates of biodiversity change: challenges that arise in meeting the Convention on Biological Diversity (CBD) 2010 goals. *Philosophical Transactions of the Royal Society B-Biological Sciences*, 360 (1454): 229-241.

Donovan, T. M. & Hines, J. E. (2007). *Exercises in occupancy modeling and estimation*. Accessed 2008/10/02 on World Wide Web: http://www.uvm.edu/envnr/vtcfwru/spreadsheets/occupancy/occupancy.htm.

Elith, J., Graham, C. H., Anderson, R. P., Dudik, M., Ferrier, S., Guisan, A., Hijmans, R. J., Huettmann, F., Leathwick, J. R., Lehmann, A., Li, J., Lohmann, L. G., Loiselle, B. A., Manion, G., Moritz, C., Nakamura, M., Nakazawa, Y., Overton, J. M., Peterson, A. T., Phillips, S. J., Richardson, K., Scachetti-Pereira, R., Schapire, R. E., Soberon, J., Williams, S., Wisz, M. S. & Zimmermann, N. E. (2006). Novel methods improve prediction of species' distributions from occurrence data. *Ecography*, 29 (2): 129-151.

Faith, D. P. (2005). Global biodiversity assessment: integrating global and local values and human dimensions. *Global Environmental Change-Human and Policy Dimensions*, 15 (1): 5-8.

Fawcett, T. (2006). An introduction to ROC analysis. *Pattern Recognition Letters*, 27: 861-874.

Ferrier, S., Powell, G. V. N., Richardson, K. S., Manion, G., Overton, J. M., Allnutt, T. F., Cameron, S. E., Mantle, K., Burgess, N. D., Faith, D. P., Lamoreux, J. F., Kier, G., Hijmans, R. J., Funk, V. A., Cassis, G. A., Fisher, B. L., Flemons, P., Lees, D., Lovett, J. C. & Van Rompaey, R. (2004). Mapping more of terrestrial biodiversity for global conservation assessment. *Bioscience*, 54 (12): 1101-1109.

Franklin, J. F. (1993). Preserving Biodiversity: Species, Ecosystems, or Landscapes? *Ecological Applications*, 3 (2): 202-205.

Garber, P. A., Pruetz, J., Lavallee, A. & Lavallee, S. (1999). A preliminary study of maneled howling monkey (Alouata palliata) ecology and conservation on Isla de Ometepe, Nicaragua. *Neotropic Primates*, 7: 113-117.

Garber, P. A. & Rehg, J. A. (1999). The ecological role of the prehensile tail in white-faced capuchins (Cebus capucinus). *American Journal of Physical Anthropology*, 110 (3): 325-339.

Global Earth Observation System of Systems (GEOSS). (2008). Global Earth Observation System of Systems (GEOSS). Accessed 09/26 2008 on World Wide Web: www.epa.gov/geoss/.

Green, R. E., Balmford, A., Crane, P. R., Mace, G. M., Reynolds, J. D. & Turner, R. K. (2005). A framework for improved monitoring of biodiversity: Responses to the World Summit on Sustainable Development. *Conservation Biology*, 19 (1): 56-65.

Group on Earth Observations (GEO). (2008). Geneva, The Group on Earth Observations Secretariat. Accessed 09/26 2008 on World Wide Web: www.earthobservations.org.

Guralnick, R. P., Hill, A. W. & Lane, M. (2007). Towards a collaborative, global infrastructure for biodiversity assessment. *Ecology Letters*, 10: 663-672.

Hill, D., Fasham, M., Tucker, G., Shewry, M. & Shaw, P. (eds.). (2006). *Handbook of biodiversity methods*. Cambridge, Cambridge University Press. 573 p.

Hines, J. E. (2006). *PRESENCE2- software to estimate patch occupancy and related parameters*, USGS-PWRC. Accessed on World Wide Web: http://www.mbr-pwrc.usgs.gov/software/presence.html.

Huettmann, F. (1999). *Abstract: interactions between mantled howling monkeys (Alouatta palliata) and neotropical birds in a fragmented forest habitat on Ometepe Island, Nicaragua.* Supplement 28 to the American Association of Physical Anthropology Annual Meeting Issue. American Journal of Anthropology.

Huettmann, F. & Gerasimov, Y. N. (2006). Conservation of migratory shorebirds and their habitats in the Sea of Okhotsk, Russian Far East, in the year 2006: state-of-the-art and an outlool. *Stilt - Journal for the East Asian - Australasian Flyway* (50): 23-33.

Integrated Taxonomic Information System (ITIS). Accessed 08/31 2008 on World Wide Web: http://www.itis.gov.

International Polar Year (IPY). (2008). Cambridge, IPY International Programme Office. Accessed 09/26 2008 on World Wide Web: www.ipy.org/.

Janzen, D. H. (ed.) (1983). *Costa Rican natural history*. Chicago, University Of Chicago Press. 823 p.

Joseph, L. N., Field, S. A., Wilcox, C. & Possingham, H. P. (2006). Presence-absence versus abundance data for monitoring threatened species. *Conservation Biology*, 20 (6): 1679-1687.

Kadmon, R., Farber, O. & Danin, A. (2004). Effect of roadside bias on the accuracy of predictive maps produced by bioclimatic models. *Ecological Applications*, 14 (2): 401-413.

Kasischke, E. S., Rupp, T. S. & Verbyla, D. L. (2006). Fire trends in the Alaskan Boreal Forest. In Chapin, F. S., Oswood, M. W., van Cleve, K., Viereck, L. A., Verbyla, D. L. &

Chapin, M. C. (eds.) *Alaska's changing boreal forest*, pp. 285-301. New York, Oxford University Press.

Krebs, C. J. (2001). *Ecology: the experimental analysis of distribution and abundance*. 5th ed. San Francisco, Cummings. 695 p.

Küttel, M. (2007). *Biodiversitäts-Monitoring Schweiz*. Bern, Bundesamt für Umwelt BAFU, Sektion Biotop- und Artenschutz. Accessed 11/23 2007 on World Wide Web: http://www.biodiversitymonitoring.ch.

Lukacs, P. M., Anderson, D. R. & Burnham, K. P. (2005). Evaluation of trapping-web designs. *Wildlife Research*, 32 (2): 103-110.

MacKenzie, D. I. (2005a). Was it there? Dealing with imperfect detection for species presence/absence data. *Australian & New Zealand Journal of Statistics*, 47 (1): 65-74.

MacKenzie, D. I. (2005b). What are the issues with presence-absence data for wildlife managers? *Journal of Wildlife Management*, 69 (3): 849-860.

MacKenzie, D. I. & Royle, J. A. (2005). Designing occupancy studies: general advice and allocating survey effort. *Journal of Applied Ecology*, 42 (6): 1105-1114.

Magness, D. R., Huettmann, F. & Morton, J. M. (2008). Using Random Forests to provide predicted species distribution maps as a metric for ecological inventory & monitoring programs. In Smolinski, T. G., Milanova, M. G. & Hassanien, A.-E. (eds.) *Applications of computational intelligence in biology: current trends and open problems*. Atlanta.

Mainka, S., McNeely, J. & Jackson, B. (2005). Depend on nature - ecosystem services supporting human livelihoods. Gland, International Union for Conservation of Nature and Natural Resouces (IUCN). 37 p.

Manley, P. N., Schlesinger, M. D., Roth, J. K. & Van Horne, B. (2005). A field-based evaluation of a presence-absence protocol for monitoring ecoregional-scale biodiversity. *Journal of Wildlife Management*, 69 (3).

Manley, P. N. & van Horne, B. (2006). *The multiple species inventory and monitoring protocol: a population, community, and biodiversity monitoring solution for national forest system lands*. USDA Forest Service Proceedings. 671-680 p.

Manley, P. N., Zielinski, W. J., Schlesinger, M. D. & Mori, S. R. (2004). Evaluation of a multiple-species approach to monitoring species at the ecoregional scale. *Ecological Applications*, 14 (1): 296-310.

Marques, T. A., Thomas, L., Fancy, S. G. & Buckland, S. T. (2007). Improving estimates of bird density using multiple-covariate distance sampling. *Auk*, 124: 1229-1243.

Marzluff, J. M., Bowman, R. & Donnelly, R. (2001). A historical perspective on urban bird research: trends, terms, and approaches. In Marzluff, J. M., Bowman, R. & Donnelly, R. (eds.) *Avian conservation and ecology in an urbanizing world*. Norwell, Kluwer.

McKee, J. K., Sciulli, P. W., Fooce, C. D. & Waite, T. A. (2004). Forecasting global biodiversity threats associated with human population growth. *Biological Conservation*, 115 (1): 161-164.

Millennium Ecosystem Assessment. Washington, D.C., World Resources Institute. Accessed 09/25 2008 on World Wide Web: www.millenniumassessment.org/.

Miller, S., Hyslop, E., Kula, G. & Burrows, J. (1994a). Status of biodiversity in Papua New Guinea. In Sekhran, N. & Miller, S. (eds.) *Papua New Guinea country study on biological diversity*, pp. 67-96. Waigani, The Department of Environment and Conservation.

Miller, S., Osborne, P., Asigau, W. & Mungkage, A. J. (1994b). Environments in Papua New Guinea. In Sekhran, N. & Miller, S. (eds.) *Papua New Guinea country study on biological diversity*, pp. 97-124. Waigani, The Department of Environment and Conservation.

Molina, R. (2007). *La Suerte Biological Field Station*. Accessed 10/25 2007 on World Wide Web: http://lasuerte.org/lasuerte.html.

Morton, J. M. (2007). *Alaska's Antarctic Treaty Article*. Nemitz, D. (ed.). Kenai.

Nakashizuka, T. & Stork, N. (eds.). (2002). *Biodiversity research methods - IBOY in Western Pacific and Asia*. Kyoto, Kyoto University Press. 216 p.

Negi, H. R. & Gadgil, M. (2002). Cross-taxon surrogacy of biodiversity in the Indian Garhwal Himalaya. *Biological Conservation*, 105 (2): 143-155.

Olea, R. A. (1984). Sampling design optimization for spatial functions. *Journal of the International Association for Mathematical Geology*, 16 (4): 369-392.

Parmenter, R. R. & MacMahon, J. A. (1989). Animal Density Estimation Using a Trapping Web Design: Field Validation Experiments. *Ecology*, 70 (1): 169-179.

Pearce, J. L., Cherry, K., Drielsma, M., Ferrier, S. & Whish, G. (2001). Incorporating expert opinion and fine-scale vegetation mapping into statistical models of faunal distribution. *Journal of Applied Ecology*, 38 (2): 412-424.

Pitelka, F. A. (1974). An avifaunal review for the Barrow region and north slope of arctic Alaska. *Arctic and Alpine Research*, 6 (2): 161-184.

Pollard, J. H. & Buckland, S. T. (2004). Adaptive distance sampling surveys. In Buckland, S. T., Anderson, D. R., Burnham, K. P., Laake, J. L., Borchers, D. L. & Thomas, L. (eds.) *Advanced distance sampling*, pp. 229-259. Oxford, Oxford University Press.

Pollock, K. H., Nichols, J. D., Simons, T. R., Farnsworth, G. L., Bailey, L. L. & Sauer, J. R. (2002). Large scale wildlife monitoring studies: statistical methods for design and analysis. *Environmetrics*, 13: 105-119.

Popp, J. N., Neubauer, D., Paciulli, L. M. & Huettmann, F. (2007). Using TreeNet for identifying management thresholds of Mantled Howling Monkey's habitat preferences on Ometepe Island, Nicaragua, on a tree and home range scale. *Journal of Medical and Biological Sciences*, 1 (1).

Prasad, A. M., Iverson, L. R. & Liaw, A. (2006). Newer classification and regression tree techniques: bagging and random forests for ecological predictions. *Ecosystems*, 9: 181-199.

Ricklefs, R. E. (2004). A comprehensive framework for global patterns in biodiversity. *Ecology Letters*, 7 (1): 1-15.

Stadt, J. J., Schieck, J. & Stelfox, H. A. (2006). Alberta biodiversity monitoring program - Monitoring effectiveness of sustainable forest management planning. *Environmental Monitoring and Assessment*, 121 (1-3): 33-46.

Steck, B. (1997). Ökotourismus: Chancen und Gefahren für den Ressourcenschutz in Mittelamerika - eine Fallstudie über die Insel Ometepe im Nicaraguasee. Eschborn, GTZ.

Thomas, L., Laake, J. L., Strindberg, S., Marques, F. F. C., Buckland, S. T., Borchers, D. L., Anderson, D. R., Burnham, K. P., Hedley, S. L., Pollard, J. H., Bishop, J. R. B. & Marques, T. A. (2006). *Distance 5.0 Release 2*. University of St. Andrews, UK, Research Unit for Wildlife Population Assessment. Accessed 08/31 2008 on World Wide Web: http://www.ruwpa.st-and.ac.uk/distance/.

van Jaarsveld, A. S., Freitag, S., Chown, S. L., Muller, C., Koch, S., Hull, H., Bellamy, C., Kruger, M., Endrody-Younga, S., Mansell, M. W. & Scholtz, C. H. (1998). Biodiversity assessment and conservation strategies. *Science*, 279 (5359): 2106-2108.

Watson, I. A. N. & Novelly, P. (2004). Making the biodiversity monitoring system sustainable: Design issues for large-scale monitoring systems. *Austral Ecology*, 29 (1): 16-30.

Wilson, E. O. (1992). *The diversity of life*. New York, Norton.

Yamada, K., Elith, J., McCarthy, M. & Zerger, A. (2003). Eliciting and integrating expert knowledge for wildlife habitat modelling. *Ecological Modelling*, 165 (2-3): 251-264.

7 Appendix

7.1 Data: Biodiversity GRID Fieldsheets

Site ID:	**Crew:**
Date:	**Latitude:**
Start time:	**Longitude:**
End time:	**Elevation:**
Trapping Web? Y/N:	**Picture taken?**

	Notes:
Canopy cover (%):	
Open soil (%):	
Open water (%):	
Groundcover veg. (%):	
Land type:	

Open soil: note main cause for open soil (e.g. cutline, trail, cattle)

Open water: note main type of water body (e.g. pond, lake, river, puddle)

Land type: note main habitat type (e.g. forest, river, lake, agriculture, rangeland)

Temperature (°C):	**Notes:**
Rainfall? Y/N	

Weather: note extraordinary weather conditions (e.g. strong wind, storm, hail)

DISTANCE sampling sheet:

Species	Distance (m)

Traces sheet:

Species	Type of sign

Species composition of ground vegetation:

Species	Count

Tree survey:

Species	DBH (cm)	Height (m)

Arthropod Trapping Web:

Species	Cup ID	Count

7.2 Covariates by Study Area

Covariate	1CR	2Ni	3AK	4Ru	5PG	6Ba
Covariate01	Melastomatacea		Spruce	Picea_jesoensis	Fern	CottonGrass
Covariate02	Costaceae		Birch	Alnus_hirsuta	TreeFern	Coltsfoot
Covariate03	Marantacea		Nothofagus	Betula_ermanii	Heliconia	WhiteKelchFlower
Covariate04	Heliconea		Equisetum	Abies_sachalinensis	Impatiens	WhiteTowerPlant
Covariate05	Palm		Salicaceae	Larix_cajanderi	Grass	Sphagnum
Covariate06	Piperaceae		Plant 01	Picea_sachalinensis	SquashFlower	Willow
Covariate07	Mimosae		Plant 02	Pinus_pumila	Pandanas	LemmingTrails
Covariate08	Fern		Plant 03	Salix_caprea	PapayaTree	HareFeces
Covariate09	Diefenbachia		Plant 04	Abies_sachalinensis	Bamboo	FoxFeces
Covariate10	Cycadaceae		Plant 05	Sorbaria_sorbifolia	BananaTree	ShorebirdFeces
Covariate11	WalkingPalm		Plant 06	Maianthemum_dilatatum	Lianas	
Covariate12	Crabholes		Plant 07	Calamagrostis_lansgdorfii	Orchids	
Covariate13			Plant 08	Daris_hexaphylla	FarmSpecies	
Covariate14			Plant 09	Spirea_betulifolia	PigTracks	
Covariate15			Plant 10	Equisetum		
Covariate16			Plant 11	Lycopodium		
Covariate17			Plant 12	Chamaepericlymenum_canadse		
Covariate18			Plant 13	Lilium		
Covariate19			Plant 14	Vaccinium_ovalifolium		
Covariate20				Dryopteris		
Covariate21				Ledum		
Covariate22				Oxyria_digyna		
Covariate23				Rhodococcum_vitis-idaea		
Covariate24				Veratrum		
Covariate25				Rubus_sachalinensis		
Covariate26				Carex		
Covariate27				Chamerion		
Covariate28				UsneaLichen		
Covariate29				AnimalBurrows		
Covariate30				BearTrail		
Covariate31				ScaleLichen		

7.3 DISTANCE Sampling Model Definitions

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
Bi	1CR	1	Half-normal	Cosine	none	none
Bi	1CR	2	Half-normal	Hermite polynomial	none	none
Bi	1CR	3	Uniform	Cosine	none	none
Bi	1CR	4	Uniform	Simple polynomial	none	none
Bi	1CR	5	Hazard-rate	Cosine	none	none
Bi	1CR	6	Hazard-rate	Simple polynomial	none	none
Bi	1CR	7	Half-normal	Cosine	VISIT	1
Bi	1CR	8	Half-normal	Hermite polynomial	VISIT	1
Bi	1CR	9	Hazard-rate	Cosine	VISIT	1
Bi	1CR	10	Hazard-rate	Simple polynomial	VISIT	1
Bi	1CR	11	Half-normal	Cosine	CLUSTER_SIZE	2
Bi	1CR	12	Half-normal	Hermite polynomial	CLUSTER_SIZE	2
Bi	1CR	13	Hazard-rate	Cosine	CLUSTER_SIZE	2
Bi	1CR	14	Hazard-rate	Simple polynomial	CLUSTER_SIZE	2
Bi	1CR	15	Half-normal	Cosine	IDENT	3
Bi	1CR	16	Half-normal	Hermite polynomial	IDENT	3
Bi	1CR	17	Hazard-rate	Cosine	IDENT	3
Bi	1CR	18	Hazard-rate	Simple polynomial	IDENT	3
Bi	1CR	19	Half-normal	Cosine	MINSINCEDAWN	4
Bi	1CR	20	Half-normal	Hermite polynomial	MINSINCEDAWN	4
Bi	1CR	21	Hazard-rate	Cosine	MINSINCEDAWN	4
Bi	1CR	22	Hazard-rate	Simple polynomial	MINSINCEDAWN	4
Bi	1CR	23	Half-normal	Cosine	HABITAT	5
Bi	1CR	24	Half-normal	Hermite polynomial	HABITAT	5
Bi	1CR	25	Hazard-rate	Cosine	HABITAT	5
Bi	1CR	26	Hazard-rate	Simple polynomial	HABITAT	5
Bi	1CR	27	Half-normal	Cosine	EPIPHYTESCAT	6
Bi	1CR	28	Half-normal	Hermite polynomial	EPIPHYTESCAT	6
Bi	1CR	29	Hazard-rate	Cosine	EPIPHYTESCAT	6
Bi	1CR	30	Hazard-rate	Simple polynomial	EPIPHYTESCAT	6
Bi	1CR	31	Half-normal	Cosine	MOSSLICHENCAT	7
Bi	1CR	32	Half-normal	Hermite polynomial	MOSSLICHENCAT	7
Bi	1CR	33	Hazard-rate	Cosine	MOSSLICHENCAT	7
Bi	1CR	34	Hazard-rate	Simple polynomial	MOSSLICHENCAT	7
Bi	1CR	35	Half-normal	Cosine	BARESOILPERC	8
Bi	1CR	36	Half-normal	Hermite polynomial	BARESOILPERC	8
Bi	1CR	37	Hazard-rate	Cosine	BARESOILPERC	8
Bi	1CR	38	Hazard-rate	Simple polynomial	BARESOILPERC	8
Bi	1CR	39	Half-normal	Cosine	DUFFCOVERPERC	9
Bi	1CR	40	Half-normal	Hermite polynomial	DUFFCOVERPERC	9

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
Bi	1CR	41	Hazard-rate	Cosine	DUFFCOVERPERC	9
Bi	1CR	42	Hazard-rate	Simple polynomial	DUFFCOVERPERC	9
Bi	1CR	43	Half-normal	Cosine	SHRUBSPERC135CM	10
Bi	1CR	44	Half-normal	Hermite polynomial	SHRUBSPERC135CM	10
Bi	1CR	45	Hazard-rate	Cosine	SHRUBSPERC135CM	10
Bi	1CR	46	Hazard-rate	Simple polynomial	SHRUBSPERC135CM	10
Bi	1CR	47	Half-normal	Cosine	CANOPYPERC	11
Bi	1CR	48	Half-normal	Hermite polynomial	CANOPYPERC	11
Bi	1CR	49	Hazard-rate	Cosine	CANOPYPERC	11
Bi	1CR	50	Hazard-rate	Simple polynomial	CANOPYPERC	11
Bi	1CR	51	Half-normal	Cosine	UNDERSTORYCOVERPE	12
Bi	1CR	52	Half-normal	Hermite polynomial	UNDERSTORYCOVERPE	12
Bi	1CR	53	Hazard-rate	Cosine	UNDERSTORYCOVERPE	12
Bi	1CR	54	Hazard-rate	Simple polynomial	UNDERSTORYCOVERPE	12
Bi	1CR	55	Half-normal	Cosine	LEAFBROWSINGPERC	13
Bi	1CR	56	Half-normal	Hermite polynomial	LEAFBROWSINGPERC	13
Bi	1CR	57	Hazard-rate	Cosine	LEAFBROWSINGPERC	13
Bi	1CR	58	Hazard-rate	Simple polynomial	LEAFBROWSINGPERC	13
Bi	1CR	59	Half-normal	Cosine	FLOWERSNO	14
Bi	1CR	60	Half-normal	Hermite polynomial	FLOWERSNO	14
Bi	1CR	61	Hazard-rate	Cosine	FLOWERSNO	14
Bi	1CR	62	Hazard-rate	Simple polynomial	FLOWERSNO	14
Bi	1CR	63	Half-normal	Cosine	CANOPYTREESNO	15
Bi	1CR	64	Half-normal	Hermite polynomial	CANOPYTREESNO	15
Bi	1CR	65	Hazard-rate	Cosine	CANOPYTREESNO	15
Bi	1CR	66	Hazard-rate	Simple polynomial	CANOPYTREESNO	15
Bi	1CR	67	Half-normal	Cosine	HIGHESTTREEM	16
Bi	1CR	68	Half-normal	Hermite polynomial	HIGHESTTREEM	16
Bi	1CR	69	Hazard-rate	Cosine	HIGHESTTREEM	16
Bi	1CR	70	Hazard-rate	Simple polynomial	HIGHESTTREEM	16
Bi	1CR	71	Half-normal	Cosine	HIGHESTDBHCM	17
Bi	1CR	72	Half-normal	Hermite polynomial	HIGHESTDBHCM	17
Bi	1CR	73	Hazard-rate	Cosine	HIGHESTDBHCM	17
Bi	1CR	74	Hazard-rate	Simple polynomial	HIGHESTDBHCM	17
Bi	1CR	75	Half-normal	Cosine	PLOT_TYPE	18
Bi	1CR	76	Half-normal	Hermite polynomial	PLOT_TYPE	18
Bi	1CR	77	Hazard-rate	Cosine	PLOT_TYPE	18
Bi	1CR	78	Hazard-rate	Simple polynomial	PLOT_TYPE	18
Bi	1CR	79	Half-normal	Cosine	COVARIATE04	28
Bi	1CR	80	Half-normal	Hermite	COVARIATE04	28

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
				polynomial		
Bi	1CR	81	Hazard-rate	Cosine	COVARIATE04	28
Bi	1CR	82	Hazard-rate	Simple polynomial	COVARIATE04	28
Bi	1CR	83	Half-normal	Cosine	COVARIATE05	29
Bi	1CR	84	Half-normal	Hermite polynomial	COVARIATE05	29
Bi	1CR	85	Hazard-rate	Cosine	COVARIATE05	29
Bi	1CR	86	Hazard-rate	Simple polynomial	COVARIATE05	29
Bi	1CR	87	Half-normal	Cosine	COVARIATE12	35
Bi	1CR	88	Half-normal	Hermite polynomial	COVARIATE12	35
Bi	1CR	89	Hazard-rate	Cosine	COVARIATE12	35
Bi	1CR	90	Hazard-rate	Simple polynomial	COVARIATE12	35
Bi	1CR	91	Half-normal	Cosine	MANAKIN	36
Bi	1CR	92	Half-normal	Hermite polynomial	MANAKIN	36
Bi	1CR	93	Hazard-rate	Cosine	MANAKIN	36
Bi	1CR	94	Hazard-rate	Simple polynomial	MANAKIN	36
Bi	1CR	95	Half-normal	Cosine	TURKEY_VULTURE	37
Bi	1CR	96	Half-normal	Hermite polynomial	TURKEY_VULTURE	37
Bi	1CR	97	Hazard-rate	Cosine	TURKEY_VULTURE	37
Bi	1CR	98	Hazard-rate	Simple polynomial	TURKEY_VULTURE	37
Bi	2Ni	1	Half-normal	Cosine	none	none
Bi	2Ni	2	Half-normal	Hermite polynomial	none	none
Bi	2Ni	3	Uniform	Cosine	none	none
Bi	2Ni	4	Uniform	Simple polynomial	none	none
Bi	2Ni	5	Hazard-rate	Cosine	none	none
Bi	2Ni	6	Hazard-rate	Simple polynomial	none	none
Bi	2Ni	7	Half-normal	Cosine	VISIT	1
Bi	2Ni	8	Half-normal	Hermite polynomial	VISIT	1
Bi	2Ni	9	Hazard-rate	Cosine	VISIT	1
Bi	2Ni	10	Hazard-rate	Simple polynomial	VISIT	1
Bi	2Ni	11	Half-normal	Cosine	CLUSTER_SIZE	2
Bi	2Ni	12	Half-normal	Hermite polynomial	CLUSTER_SIZE	2
Bi	2Ni	13	Hazard-rate	Cosine	CLUSTER_SIZE	2
Bi	2Ni	14	Hazard-rate	Simple polynomial	CLUSTER_SIZE	2
Bi	2Ni	15	Half-normal	Cosine	IDENT	3
Bi	2Ni	16	Half-normal	Hermite polynomial	IDENT	3
Bi	2Ni	17	Hazard-rate	Cosine	IDENT	3
Bi	2Ni	18	Hazard-rate	Simple polynomial	IDENT	3
Bi	2Ni	19	Half-normal	Cosine	MINSINCEDAWN	4
Bi	2Ni	20	Half-normal	Hermite polynomial	MINSINCEDAWN	4
Bi	2Ni	21	Hazard-rate	Cosine	MINSINCEDAWN	4
Bi	2Ni	22	Hazard-rate	Simple polynomial	MINSINCEDAWN	4
Bi	2Ni	23	Half-normal	Cosine	HABITAT	5
Bi	2Ni	24	Half-normal	Hermite polynomial	HABITAT	5
Bi	2Ni	25	Hazard-rate	Cosine	HABITAT	5

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
Bi	2Ni	26	Hazard-rate	Simple polynomial	HABITAT	5
Bi	2Ni	27	Half-normal	Cosine	EPIPHYTESCAT	6
Bi	2Ni	28	Half-normal	Hermite polynomial	EPIPHYTESCAT	6
Bi	2Ni	29	Hazard-rate	Cosine	EPIPHYTESCAT	6
Bi	2Ni	30	Hazard-rate	Simple polynomial	EPIPHYTESCAT	6
Bi	2Ni	31	Half-normal	Cosine	MOSSLICHENCAT	7
Bi	2Ni	32	Half-normal	Hermite polynomial	MOSSLICHENCAT	7
Bi	2Ni	33	Hazard-rate	Cosine	MOSSLICHENCAT	7
Bi	2Ni	34	Hazard-rate	Simple polynomial	MOSSLICHENCAT	7
Bi	2Ni	35	Half-normal	Cosine	BARESOILPERC	8
Bi	2Ni	36	Half-normal	Hermite polynomial	BARESOILPERC	8
Bi	2Ni	37	Hazard-rate	Cosine	BARESOILPERC	8
Bi	2Ni	38	Hazard-rate	Simple polynomial	BARESOILPERC	8
Bi	2Ni	39	Half-normal	Cosine	DUFFCOVERPERC	9
Bi	2Ni	40	Half-normal	Hermite polynomial	DUFFCOVERPERC	9
Bi	2Ni	41	Hazard-rate	Cosine	DUFFCOVERPERC	9
Bi	2Ni	42	Hazard-rate	Simple polynomial	DUFFCOVERPERC	9
Bi	2Ni	43	Half-normal	Cosine	SHRUBSPERC135CM	10
Bi	2Ni	44	Half-normal	Hermite polynomial	SHRUBSPERC135CM	10
Bi	2Ni	45	Hazard-rate	Cosine	SHRUBSPERC135CM	10
Bi	2Ni	46	Hazard-rate	Simple polynomial	SHRUBSPERC135CM	10
Bi	2Ni	47	Half-normal	Cosine	CANOPYPERC	11
Bi	2Ni	48	Half-normal	Hermite polynomial	CANOPYPERC	11
Bi	2Ni	49	Hazard-rate	Cosine	CANOPYPERC	11
Bi	2Ni	50	Hazard-rate	Simple polynomial	CANOPYPERC	11
Bi	2Ni	51	Half-normal	Cosine	UNDERSTORYCOVERPE	12
Bi	2Ni	52	Half-normal	Hermite polynomial	UNDERSTORYCOVERPE	12
Bi	2Ni	53	Hazard-rate	Cosine	UNDERSTORYCOVERPE	12
Bi	2Ni	54	Hazard-rate	Simple polynomial	UNDERSTORYCOVERPE	12
Bi	2Ni	55	Half-normal	Cosine	HIGHESTTREEM	16
Bi	2Ni	56	Half-normal	Hermite polynomial	HIGHESTTREEM	16
Bi	2Ni	57	Hazard-rate	Cosine	HIGHESTTREEM	16
Bi	2Ni	58	Hazard-rate	Simple polynomial	HIGHESTTREEM	16
Bi	2Ni	59	Half-normal	Cosine	HIGHESTDBHCM	17
Bi	2Ni	60	Half-normal	Hermite polynomial	HIGHESTDBHCM	17
Bi	2Ni	61	Hazard-rate	Cosine	HIGHESTDBHCM	17
Bi	2Ni	62	Hazard-rate	Simple polynomial	HIGHESTDBHCM	17
Bi	2Ni	63	Half-normal	Cosine	PLOT_TYPE	18
Bi	2Ni	64	Half-normal	Hermite polynomial	PLOT_TYPE	18
Bi	2Ni	65	Hazard-rate	Cosine	PLOT_TYPE	18
Bi	2Ni	66	Hazard-rate	Simple polynomial	PLOT_TYPE	18

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
Bi	2Ni	67	Half-normal	Cosine	TURKEY_VULTURE	37
Bi	2Ni	68	Half-normal	Hermite polynomial	TURKEY_VULTURE	37
Bi	2Ni	69	Hazard-rate	Cosine	TURKEY_VULTURE	37
Bi	2Ni	70	Hazard-rate	Simple polynomial	TURKEY_VULTURE	37
Bi	3AK	1	Half-normal	Cosine	none	none
Bi	3AK	2	Half-normal	Hermite polynomial	none	none
Bi	3AK	3	Uniform	Cosine	none	none
Bi	3AK	4	Uniform	Simple polynomial	none	none
Bi	3AK	5	Hazard-rate	Cosine	none	none
Bi	3AK	6	Hazard-rate	Simple polynomial	none	none
Bi	3AK	7	Half-normal	Cosine	IDENT	3
Bi	3AK	8	Half-normal	Hermite polynomial	IDENT	3
Bi	3AK	9	Hazard-rate	Cosine	IDENT	3
Bi	3AK	10	Hazard-rate	Simple polynomial	IDENT	3
Bi	3AK	11	Half-normal	Cosine	MINSINCEDAWN	4
Bi	3AK	12	Half-normal	Hermite polynomial	MINSINCEDAWN	4
Bi	3AK	13	Hazard-rate	Cosine	MINSINCEDAWN	4
Bi	3AK	14	Hazard-rate	Simple polynomial	MINSINCEDAWN	4
Bi	3AK	15	Half-normal	Cosine	HABITAT	5
Bi	3AK	16	Half-normal	Hermite polynomial	HABITAT	5
Bi	3AK	17	Hazard-rate	Cosine	HABITAT	5
Bi	3AK	18	Hazard-rate	Simple polynomial	HABITAT	5
Bi	3AK	19	Half-normal	Cosine	MOSSLICHENCAT	7
Bi	3AK	20	Half-normal	Hermite polynomial	MOSSLICHENCAT	7
Bi	3AK	21	Hazard-rate	Cosine	MOSSLICHENCAT	7
Bi	3AK	22	Hazard-rate	Simple polynomial	MOSSLICHENCAT	7
Bi	3AK	23	Half-normal	Cosine	DUFFCOVERPERC	9
Bi	3AK	24	Half-normal	Hermite polynomial	DUFFCOVERPERC	9
Bi	3AK	25	Hazard-rate	Cosine	DUFFCOVERPERC	9
Bi	3AK	26	Hazard-rate	Simple polynomial	DUFFCOVERPERC	9
Bi	3AK	27	Half-normal	Cosine	CANOPYPERC	11
Bi	3AK	28	Half-normal	Hermite polynomial	CANOPYPERC	11
Bi	3AK	29	Hazard-rate	Cosine	CANOPYPERC	11
Bi	3AK	30	Hazard-rate	Simple polynomial	CANOPYPERC	11
Bi	3AK	31	Half-normal	Cosine	CANOPYTREESNO	15
Bi	3AK	32	Half-normal	Hermite polynomial	CANOPYTREESNO	15
Bi	3AK	33	Hazard-rate	Cosine	CANOPYTREESNO	15
Bi	3AK	34	Hazard-rate	Simple polynomial	CANOPYTREESNO	15
Bi	3AK	35	Half-normal	Cosine	HIGHESTTREEM	16
Bi	3AK	36	Half-normal	Hermite polynomial	HIGHESTTREEM	16
Bi	3AK	37	Hazard-rate	Cosine	HIGHESTTREEM	16
Bi	3AK	38	Hazard-rate	Simple polynomial	HIGHESTTREEM	16
Bi	3AK	39	Half-normal	Cosine	HIGHESTDBHCM	17
Bi	3AK	40	Half-normal	Hermite	HIGHESTDBHCM	17

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
				polynomial		
Bi	3AK	41	Hazard-rate	Cosine	HIGHESTDBHCM	17
Bi	3AK	42	Hazard-rate	Simple polynomial	HIGHESTDBHCM	17
Bi	3AK	43	Half-normal	Cosine	COVARIATE01	25
Bi	3AK	44	Half-normal	Hermite polynomial	COVARIATE01	25
Bi	3AK	45	Hazard-rate	Cosine	COVARIATE01	25
Bi	3AK	46	Hazard-rate	Simple polynomial	COVARIATE01	25
Bi	3AK	47	Half-normal	Cosine	COVARIATE07	31
Bi	3AK	48	Half-normal	Hermite polynomial	COVARIATE07	31
Bi	3AK	49	Hazard-rate	Cosine	COVARIATE07	31
Bi	3AK	50	Hazard-rate	Simple polynomial	COVARIATE07	31
Bi	3AK	51	Half-normal	Cosine	COVARIATE11	34
Bi	3AK	52	Half-normal	Hermite polynomial	COVARIATE11	34
Bi	3AK	53	Hazard-rate	Cosine	COVARIATE11	34
Bi	3AK	54	Hazard-rate	Simple polynomial	COVARIATE11	34
Bi	3AK	55	Half-normal	Cosine	COVARIATE12	35
Bi	3AK	56	Half-normal	Hermite polynomial	COVARIATE12	35
Bi	3AK	57	Hazard-rate	Cosine	COVARIATE12	35
Bi	3AK	58	Hazard-rate	Simple polynomial	COVARIATE12	35
Bi	3AK	59	Half-normal	Cosine	COVARIATE13	38
Bi	3AK	60	Half-normal	Hermite polynomial	COVARIATE13	38
Bi	3AK	61	Hazard-rate	Cosine	COVARIATE13	38
Bi	3AK	62	Hazard-rate	Simple polynomial	COVARIATE13	38
Bi	3AK	63	Half-normal	Cosine	COVARIATE14	39
Bi	3AK	64	Half-normal	Hermite polynomial	COVARIATE14	39
Bi	3AK	65	Hazard-rate	Cosine	COVARIATE14	39
Bi	3AK	66	Hazard-rate	Simple polynomial	COVARIATE14	39
Bi	3AK	67	Half-normal	Cosine	COVARIATE19	43
Bi	3AK	68	Half-normal	Hermite polynomial	COVARIATE19	43
Bi	3AK	69	Hazard-rate	Cosine	COVARIATE19	43
Bi	3AK	70	Hazard-rate	Simple polynomial	COVARIATE19	43
Bi	3AK	71	Half-normal	Cosine	SQUIRREL	45
Bi	3AK	72	Half-normal	Hermite polynomial	SQUIRREL	45
Bi	3AK	73	Hazard-rate	Cosine	SQUIRREL	45
Bi	3AK	74	Hazard-rate	Simple polynomial	SQUIRREL	45
Bi	4Ru	1	Half-normal	Cosine	none	none
Bi	4Ru	2	Half-normal	Hermite polynomial	none	none
Bi	4Ru	3	Uniform	Cosine	none	none
Bi	4Ru	4	Uniform	Simple polynomial	none	none
Bi	4Ru	5	Hazard-rate	Cosine	none	none
Bi	4Ru	6	Hazard-rate	Simple polynomial	none	none
Bi	4Ru	7	Half-normal	Cosine	VISIT	1
Bi	4Ru	8	Half-normal	Hermite polynomial	VISIT	1
Bi	4Ru	9	Hazard-rate	Cosine	VISIT	1

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
Bi	4Ru	10	Hazard-rate	Simple polynomial	VISIT	1
Bi	4Ru	11	Half-normal	Cosine	CLUSTER_SIZE	2
Bi	4Ru	12	Half-normal	Hermite polynomial	CLUSTER_SIZE	2
Bi	4Ru	13	Hazard-rate	Cosine	CLUSTER_SIZE	2
Bi	4Ru	14	Hazard-rate	Simple polynomial	CLUSTER_SIZE	2
Bi	4Ru	15	Half-normal	Cosine	MINSINCEDAWN	4
Bi	4Ru	16	Half-normal	Hermite polynomial	MINSINCEDAWN	4
Bi	4Ru	17	Hazard-rate	Cosine	MINSINCEDAWN	4
Bi	4Ru	18	Hazard-rate	Simple polynomial	MINSINCEDAWN	4
Bi	4Ru	19	Half-normal	Cosine	HABITAT	5
Bi	4Ru	20	Half-normal	Hermite polynomial	HABITAT	5
Bi	4Ru	21	Hazard-rate	Cosine	HABITAT	5
Bi	4Ru	22	Hazard-rate	Simple polynomial	HABITAT	5
Bi	4Ru	23	Half-normal	Cosine	DUFFCOVERPERC	9
Bi	4Ru	24	Half-normal	Hermite polynomial	DUFFCOVERPERC	9
Bi	4Ru	25	Hazard-rate	Cosine	DUFFCOVERPERC	9
Bi	4Ru	26	Hazard-rate	Simple polynomial	DUFFCOVERPERC	9
Bi	4Ru	27	Half-normal	Cosine	SHRUBSPERC135CM	10
Bi	4Ru	28	Half-normal	Hermite polynomial	SHRUBSPERC135CM	10
Bi	4Ru	29	Hazard-rate	Cosine	SHRUBSPERC135CM	10
Bi	4Ru	30	Hazard-rate	Simple polynomial	SHRUBSPERC135CM	10
Bi	4Ru	31	Half-normal	Cosine	CANOPYPERC	11
Bi	4Ru	32	Half-normal	Hermite polynomial	CANOPYPERC	11
Bi	4Ru	33	Hazard-rate	Cosine	CANOPYPERC	11
Bi	4Ru	34	Hazard-rate	Simple polynomial	CANOPYPERC	11
Bi	4Ru	35	Half-normal	Cosine	UNDERSTORYCOVERPE	12
Bi	4Ru	36	Half-normal	Hermite polynomial	UNDERSTORYCOVERPE	12
Bi	4Ru	37	Hazard-rate	Cosine	UNDERSTORYCOVERPE	12
Bi	4Ru	38	Hazard-rate	Simple polynomial	UNDERSTORYCOVERPE	12
Bi	4Ru	39	Half-normal	Cosine	LEAFBROWSINGPERC	13
Bi	4Ru	40	Half-normal	Hermite polynomial	LEAFBROWSINGPERC	13
Bi	4Ru	41	Hazard-rate	Cosine	LEAFBROWSINGPERC	13
Bi	4Ru	42	Hazard-rate	Simple polynomial	LEAFBROWSINGPERC	13
Bi	4Ru	43	Half-normal	Cosine	FLOWERSNO	14
Bi	4Ru	44	Half-normal	Hermite polynomial	FLOWERSNO	14
Bi	4Ru	45	Hazard-rate	Cosine	FLOWERSNO	14
Bi	4Ru	46	Hazard-rate	Simple polynomial	FLOWERSNO	14
Bi	4Ru	47	Half-normal	Cosine	CANOPYTREESNO	15
Bi	4Ru	48	Half-normal	Hermite polynomial	CANOPYTREESNO	15

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
Bi	4Ru	49	Hazard-rate	Cosine	CANOPYTREESNO	15
Bi	4Ru	50	Hazard-rate	Simple polynomial	CANOPYTREESNO	15
Bi	4Ru	51	Half-normal	Cosine	HIGHESTTREEM	16
Bi	4Ru	52	Half-normal	Hermite polynomial	HIGHESTTREEM	16
Bi	4Ru	53	Hazard-rate	Cosine	HIGHESTTREEM	16
Bi	4Ru	54	Hazard-rate	Simple polynomial	HIGHESTTREEM	16
Bi	4Ru	55	Half-normal	Cosine	HIGHESTDBHCM	17
Bi	4Ru	56	Half-normal	Hermite polynomial	HIGHESTDBHCM	17
Bi	4Ru	57	Hazard-rate	Cosine	HIGHESTDBHCM	17
Bi	4Ru	58	Hazard-rate	Simple polynomial	HIGHESTDBHCM	17
Bi	4Ru	59	Half-normal	Cosine	PLOT_TYPE	18
Bi	4Ru	60	Half-normal	Hermite polynomial	PLOT_TYPE	18
Bi	4Ru	61	Hazard-rate	Cosine	PLOT_TYPE	18
Bi	4Ru	62	Hazard-rate	Simple polynomial	PLOT_TYPE	18
Bi	4Ru	63	Half-normal	Cosine	MOSSPERC	19
Bi	4Ru	64	Half-normal	Hermite polynomial	MOSSPERC	19
Bi	4Ru	65	Hazard-rate	Cosine	MOSSPERC	19
Bi	4Ru	66	Hazard-rate	Simple polynomial	MOSSPERC	19
Bi	4Ru	67	Half-normal	Cosine	LICHENPERC	20
Bi	4Ru	68	Half-normal	Hermite polynomial	LICHENPERC	20
Bi	4Ru	69	Hazard-rate	Cosine	LICHENPERC	20
Bi	4Ru	70	Hazard-rate	Simple polynomial	LICHENPERC	20
Bi	4Ru	71	Half-normal	Cosine	COVARIATE01	25
Bi	4Ru	72	Half-normal	Hermite polynomial	COVARIATE01	25
Bi	4Ru	73	Hazard-rate	Cosine	COVARIATE01	25
Bi	4Ru	74	Hazard-rate	Simple polynomial	COVARIATE01	25
Bi	4Ru	75	Half-normal	Cosine	COVARIATE04	28
Bi	4Ru	76	Half-normal	Hermite polynomial	COVARIATE04	28
Bi	4Ru	77	Hazard-rate	Cosine	COVARIATE04	28
Bi	4Ru	78	Hazard-rate	Simple polynomial	COVARIATE04	28
Bi	4Ru	79	Half-normal	Cosine	COVARIATE05	29
Bi	4Ru	80	Half-normal	Hermite polynomial	COVARIATE05	29
Bi	4Ru	81	Hazard-rate	Cosine	COVARIATE05	29
Bi	4Ru	82	Hazard-rate	Simple polynomial	COVARIATE05	29
Bi	4Ru	83	Half-normal	Cosine	COVARIATE08	32
Bi	4Ru	84	Half-normal	Hermite polynomial	COVARIATE08	32
Bi	4Ru	85	Hazard-rate	Cosine	COVARIATE08	32
Bi	4Ru	86	Hazard-rate	Simple polynomial	COVARIATE08	32
Bi	4Ru	87	Half-normal	Cosine	COVARIATE12	35
Bi	4Ru	88	Half-normal	Hermite polynomial	COVARIATE12	35
Bi	4Ru	89	Hazard-rate	Cosine	COVARIATE12	35
Bi	4Ru	90	Hazard-rate	Simple polynomial	COVARIATE12	35
Bi	4Ru	91	Half-normal	Cosine	COVARIATE15	40
Bi	4Ru	92	Half-normal	Hermite	COVARIATE15	40

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
				polynomial		
Bi	4Ru	93	Hazard-rate	Cosine	COVARIATE15	40
Bi	4Ru	94	Hazard-rate	Simple polynomial	COVARIATE15	40
Bi	4Ru	95	Half-normal	Cosine	COVARIATE16	41
Bi	4Ru	96	Half-normal	Hermite polynomial	COVARIATE16	41
Bi	4Ru	97	Hazard-rate	Cosine	COVARIATE16	41
Bi	4Ru	98	Hazard-rate	Simple polynomial	COVARIATE16	41
Bi	4Ru	99	Half-normal	Cosine	COVARIATE18	42
Bi	4Ru	100	Half-normal	Hermite polynomial	COVARIATE18	42
Bi	4Ru	101	Hazard-rate	Cosine	COVARIATE18	42
Bi	4Ru	102	Hazard-rate	Simple polynomial	COVARIATE18	42
Bi	4Ru	103	Half-normal	Cosine	COVARIATE20	44
Bi	4Ru	104	Half-normal	Hermite polynomial	COVARIATE20	44
Bi	4Ru	105	Hazard-rate	Cosine	COVARIATE20	44
Bi	4Ru	106	Hazard-rate	Simple polynomial	COVARIATE20	44
Bi	4Ru	107	Half-normal	Cosine	COVARIATE21	46
Bi	4Ru	108	Half-normal	Hermite polynomial	COVARIATE21	46
Bi	4Ru	109	Hazard-rate	Cosine	COVARIATE21	46
Bi	4Ru	110	Hazard-rate	Simple polynomial	COVARIATE21	46
Bi	4Ru	111	Half-normal	Cosine	COVARIATE23	47
Bi	4Ru	112	Half-normal	Hermite polynomial	COVARIATE23	47
Bi	4Ru	113	Hazard-rate	Cosine	COVARIATE23	47
Bi	4Ru	114	Hazard-rate	Simple polynomial	COVARIATE23	47
Bi	4Ru	115	Half-normal	Cosine	COVARIATE28	48
Bi	4Ru	116	Half-normal	Hermite polynomial	COVARIATE28	48
Bi	4Ru	117	Hazard-rate	Cosine	COVARIATE28	48
Bi	4Ru	118	Hazard-rate	Simple polynomial	COVARIATE28	48
Bi	4Ru	119	Half-normal	Cosine	COVARIATE30	49
Bi	4Ru	120	Half-normal	Hermite polynomial	COVARIATE30	49
Bi	4Ru	121	Hazard-rate	Cosine	COVARIATE30	49
Bi	4Ru	122	Hazard-rate	Simple polynomial	COVARIATE30	49
Bi	4Ru	123	Half-normal	Cosine	COVARIATE31	50
Bi	4Ru	124	Half-normal	Hermite polynomial	COVARIATE31	50
Bi	4Ru	125	Hazard-rate	Cosine	COVARIATE31	50
Bi	4Ru	126	Hazard-rate	Simple polynomial	COVARIATE31	50
Bi	4Ru	127	Half-normal	Cosine	WIZE	51
Bi	4Ru	128	Half-normal	Hermite polynomial	WIZE	51
Bi	4Ru	129	Hazard-rate	Cosine	WIZE	51
Bi	4Ru	130	Hazard-rate	Simple polynomial	WIZE	51
Bi	5PG	1	Half-normal	Cosine	none	none
Bi	5PG	2	Half-normal	Hermite polynomial	none	none
Bi	5PG	3	Uniform	Cosine	none	none
Bi	5PG	4	Uniform	Simple polynomial	none	none
Bi	5PG	5	Hazard-rate	Cosine	none	none

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
Bi	5PG	6	Hazard-rate	Simple polynomial	none	none
Bi	5PG	7	Half-normal	Cosine	VISIT	1
Bi	5PG	8	Half-normal	Hermite polynomial	VISIT	1
Bi	5PG	9	Hazard-rate	Cosine	VISIT	1
Bi	5PG	10	Hazard-rate	Simple polynomial	VISIT	1
Bi	5PG	11	Half-normal	Cosine	CLUSTER_SIZE	2
Bi	5PG	12	Half-normal	Hermite polynomial	CLUSTER_SIZE	2
Bi	5PG	13	Hazard-rate	Cosine	CLUSTER_SIZE	2
Bi	5PG	14	Hazard-rate	Simple polynomial	CLUSTER_SIZE	2
Bi	5PG	15	Half-normal	Cosine	IDENT	3
Bi	5PG	16	Half-normal	Hermite polynomial	IDENT	3
Bi	5PG	17	Hazard-rate	Cosine	IDENT	3
Bi	5PG	18	Hazard-rate	Simple polynomial	IDENT	3
Bi	5PG	19	Half-normal	Cosine	MINSINCEDAWN	4
Bi	5PG	20	Half-normal	Hermite polynomial	MINSINCEDAWN	4
Bi	5PG	21	Hazard-rate	Cosine	MINSINCEDAWN	4
Bi	5PG	22	Hazard-rate	Simple polynomial	MINSINCEDAWN	4
Bi	5PG	23	Half-normal	Cosine	HABITAT	5
Bi	5PG	24	Half-normal	Hermite polynomial	HABITAT	5
Bi	5PG	25	Hazard-rate	Cosine	HABITAT	5
Bi	5PG	26	Hazard-rate	Simple polynomial	HABITAT	5
Bi	5PG	27	Half-normal	Cosine	EPIPHYTESCAT	6
Bi	5PG	28	Half-normal	Hermite polynomial	EPIPHYTESCAT	6
Bi	5PG	29	Hazard-rate	Cosine	EPIPHYTESCAT	6
Bi	5PG	30	Hazard-rate	Simple polynomial	EPIPHYTESCAT	6
Bi	5PG	31	Half-normal	Cosine	BARESOILPERC	8
Bi	5PG	32	Half-normal	Hermite polynomial	BARESOILPERC	8
Bi	5PG	33	Hazard-rate	Cosine	BARESOILPERC	8
Bi	5PG	34	Hazard-rate	Simple polynomial	BARESOILPERC	8
Bi	5PG	35	Half-normal	Cosine	DUFFCOVERPERC	9
Bi	5PG	36	Half-normal	Hermite polynomial	DUFFCOVERPERC	9
Bi	5PG	37	Hazard-rate	Cosine	DUFFCOVERPERC	9
Bi	5PG	38	Hazard-rate	Simple polynomial	DUFFCOVERPERC	9
Bi	5PG	39	Half-normal	Cosine	CANOPYPERC	11
Bi	5PG	40	Half-normal	Hermite polynomial	CANOPYPERC	11
Bi	5PG	41	Hazard-rate	Cosine	CANOPYPERC	11
Bi	5PG	42	Hazard-rate	Simple polynomial	CANOPYPERC	11
Bi	5PG	43	Half-normal	Cosine	HIGHESTTREEM	16
Bi	5PG	44	Half-normal	Hermite polynomial	HIGHESTTREEM	16
Bi	5PG	45	Hazard-rate	Cosine	HIGHESTTREEM	16
Bi	5PG	46	Hazard-rate	Simple polynomial	HIGHESTTREEM	16
Bi	5PG	47	Half-normal	Cosine	HIGHESTDBHCM	17
Bi	5PG	48	Half-normal	Hermite polynomial	HIGHESTDBHCM	17

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
Bi	5PG	49	Hazard-rate	Cosine	HIGHESTDBHCM	17
Bi	5PG	50	Hazard-rate	Simple polynomial	HIGHESTDBHCM	17
Bi	5PG	51	Half-normal	Cosine	COVARIATE01	25
Bi	5PG	52	Half-normal	Hermite polynomial	COVARIATE01	25
Bi	5PG	53	Hazard-rate	Cosine	COVARIATE01	25
Bi	5PG	54	Hazard-rate	Simple polynomial	COVARIATE01	25
Bi	5PG	55	Half-normal	Cosine	COVARIATE06	30
Bi	5PG	56	Half-normal	Hermite polynomial	COVARIATE06	30
Bi	5PG	57	Hazard-rate	Cosine	COVARIATE06	30
Bi	5PG	58	Hazard-rate	Simple polynomial	COVARIATE06	30
Bi	5PG	59	Half-normal	Cosine	COVARIATE11	34
Bi	5PG	60	Half-normal	Hermite polynomial	COVARIATE11	34
Bi	5PG	61	Hazard-rate	Cosine	COVARIATE11	34
Bi	5PG	62	Hazard-rate	Simple polynomial	COVARIATE11	34
Bi	5PG	63	Half-normal	Cosine	COVARIATE12	35
Bi	5PG	64	Half-normal	Hermite polynomial	COVARIATE12	35
Bi	5PG	65	Hazard-rate	Cosine	COVARIATE12	35
Bi	5PG	66	Hazard-rate	Simple polynomial	COVARIATE12	35
Bi	6Ba	1	Half-normal	Cosine	none	none
Bi	6Ba	2	Half-normal	Hermite polynomial	none	none
Bi	6Ba	3	Uniform	Cosine	none	none
Bi	6Ba	4	Uniform	Simple polynomial	none	none
Bi	6Ba	5	Hazard-rate	Cosine	none	none
Bi	6Ba	6	Hazard-rate	Simple polynomial	none	none
Bi	6Ba	7	Half-normal	Cosine	VISIT	1
Bi	6Ba	8	Half-normal	Hermite polynomial	VISIT	1
Bi	6Ba	9	Hazard-rate	Cosine	VISIT	1
Bi	6Ba	10	Hazard-rate	Simple polynomial	VISIT	1
Bi	6Ba	11	Half-normal	Cosine	CLUSTER_SIZE	2
Bi	6Ba	12	Half-normal	Hermite polynomial	CLUSTER_SIZE	2
Bi	6Ba	13	Hazard-rate	Cosine	CLUSTER_SIZE	2
Bi	6Ba	14	Hazard-rate	Simple polynomial	CLUSTER_SIZE	2
Bi	6Ba	15	Half-normal	Cosine	FLOWERSNO	14
Bi	6Ba	16	Half-normal	Hermite polynomial	FLOWERSNO	14
Bi	6Ba	17	Hazard-rate	Cosine	FLOWERSNO	14
Bi	6Ba	18	Hazard-rate	Simple polynomial	FLOWERSNO	14
Bi	6Ba	19	Half-normal	Cosine	PLOT_TYPE	18
Bi	6Ba	20	Half-normal	Hermite polynomial	PLOT_TYPE	18
Bi	6Ba	21	Hazard-rate	Cosine	PLOT_TYPE	18
Bi	6Ba	22	Hazard-rate	Simple polynomial	PLOT_TYPE	18
Bi	6Ba	23	Half-normal	Cosine	MOSSPERC	19
Bi	6Ba	24	Half-normal	Hermite polynomial	MOSSPERC	19
Bi	6Ba	25	Hazard-rate	Cosine	MOSSPERC	19
Bi	6Ba	26	Hazard-rate	Simple polynomial	MOSSPERC	19

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
Bi	6Ba	27	Half-normal	Cosine	LICHENPERC	20
Bi	6Ba	28	Half-normal	Hermite polynomial	LICHENPERC	20
Bi	6Ba	29	Hazard-rate	Cosine	LICHENPERC	20
Bi	6Ba	30	Hazard-rate	Simple polynomial	LICHENPERC	20
Bi	6Ba	31	Half-normal	Cosine	LEAFS	21
Bi	6Ba	32	Half-normal	Hermite polynomial	LEAFS	21
Bi	6Ba	33	Hazard-rate	Cosine	LEAFS	21
Bi	6Ba	34	Hazard-rate	Simple polynomial	LEAFS	21
Bi	6Ba	35	Half-normal	Cosine	DIAMNEXTLAKE	22
Bi	6Ba	36	Half-normal	Hermite polynomial	DIAMNEXTLAKE	22
Bi	6Ba	37	Hazard-rate	Cosine	DIAMNEXTLAKE	22
Bi	6Ba	38	Hazard-rate	Simple polynomial	DIAMNEXTLAKE	22
Bi	6Ba	39	Half-normal	Cosine	DISTNEXTLAKE	23
Bi	6Ba	40	Half-normal	Hermite polynomial	DISTNEXTLAKE	23
Bi	6Ba	41	Hazard-rate	Cosine	DISTNEXTLAKE	23
Bi	6Ba	42	Hazard-rate	Simple polynomial	DISTNEXTLAKE	23
Bi	6Ba	43	Half-normal	Cosine	GRASSPERC	24
Bi	6Ba	44	Half-normal	Hermite polynomial	GRASSPERC	24
Bi	6Ba	45	Hazard-rate	Cosine	GRASSPERC	24
Bi	6Ba	46	Hazard-rate	Simple polynomial	GRASSPERC	24
Bi	6Ba	47	Half-normal	Cosine	COVARIATE01	25
Bi	6Ba	48	Half-normal	Hermite polynomial	COVARIATE01	25
Bi	6Ba	49	Hazard-rate	Cosine	COVARIATE01	25
Bi	6Ba	50	Hazard-rate	Simple polynomial	COVARIATE01	25
Bi	6Ba	51	Half-normal	Cosine	COVARIATE02	26
Bi	6Ba	52	Half-normal	Hermite polynomial	COVARIATE02	26
Bi	6Ba	53	Hazard-rate	Cosine	COVARIATE02	26
Bi	6Ba	54	Hazard-rate	Simple polynomial	COVARIATE02	26
Bi	6Ba	55	Half-normal	Cosine	COVARIATE03	27
Bi	6Ba	56	Half-normal	Hermite polynomial	COVARIATE03	27
Bi	6Ba	57	Hazard-rate	Cosine	COVARIATE03	27
Bi	6Ba	58	Hazard-rate	Simple polynomial	COVARIATE03	27
Bi	6Ba	59	Half-normal	Cosine	COVARIATE05	29
Bi	6Ba	60	Half-normal	Hermite polynomial	COVARIATE05	29
Bi	6Ba	61	Hazard-rate	Cosine	COVARIATE05	29
Bi	6Ba	62	Hazard-rate	Simple polynomial	COVARIATE05	29
Bi	6Ba	63	Half-normal	Cosine	COVARIATE06	30
Bi	6Ba	64	Half-normal	Hermite polynomial	COVARIATE06	30
Bi	6Ba	65	Hazard-rate	Cosine	COVARIATE06	30
Bi	6Ba	66	Hazard-rate	Simple polynomial	COVARIATE06	30
Bi	6Ba	67	Half-normal	Cosine	COVARIATE07	31
Bi	6Ba	68	Half-normal	Hermite polynomial	COVARIATE07	31
Bi	6Ba	69	Hazard-rate	Cosine	COVARIATE07	31

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
Bi	6Ba	70	Hazard-rate	Simple polynomial	COVARIATE07	31
Bi	6Ba	71	Half-normal	Cosine	COVARIATE08	32
Bi	6Ba	72	Half-normal	Hermite polynomial	COVARIATE08	32
Bi	6Ba	73	Hazard-rate	Cosine	COVARIATE08	32
Bi	6Ba	74	Hazard-rate	Simple polynomial	COVARIATE08	32
Bi	6Ba	75	Half-normal	Cosine	COVARIATE10	33
Bi	6Ba	76	Half-normal	Hermite polynomial	COVARIATE10	33
Bi	6Ba	77	Hazard-rate	Cosine	COVARIATE10	33
Bi	6Ba	78	Hazard-rate	Simple polynomial	COVARIATE10	33
Bi	6Ba	79	Half-normal	Cosine	POMARINE_JAEGER	52
Bi	6Ba	80	Half-normal	Hermite polynomial	POMARINE_JAEGER	52
Bi	6Ba	81	Hazard-rate	Cosine	POMARINE_JAEGER	52
Bi	6Ba	82	Hazard-rate	Simple polynomial	POMARINE_JAEGER	52
TW	1CR	1	Half-normal	Cosine	none	none
TW	1CR	2	Half-normal	Hermite polynomial	none	none
TW	1CR	3	Uniform	Cosine	none	none
TW	1CR	4	Uniform	Simple polynomial	none	none
TW	1CR	5	Hazard-rate	Cosine	none	none
TW	1CR	6	Hazard-rate	Simple polynomial	none	none
TW	1CR	7	Half-normal	Cosine	VISIT	1
TW	1CR	8	Half-normal	Hermite polynomial	VISIT	1
TW	1CR	9	Hazard-rate	Cosine	VISIT	1
TW	1CR	10	Hazard-rate	Simple polynomial	VISIT	1
TW	1CR	11	Half-normal	Cosine	STATUS	4
TW	1CR	12	Half-normal	Hermite polynomial	STATUS	4
TW	1CR	13	Hazard-rate	Cosine	STATUS	4
TW	1CR	14	Hazard-rate	Simple polynomial	STATUS	4
TW	1CR	15	Half-normal	Cosine	HABITAT	5
TW	1CR	16	Half-normal	Hermite polynomial	HABITAT	5
TW	1CR	17	Hazard-rate	Cosine	HABITAT	5
TW	1CR	18	Hazard-rate	Simple polynomial	HABITAT	5
TW	1CR	19	Half-normal	Cosine	EPIPHYTESCAT	6
TW	1CR	20	Half-normal	Hermite polynomial	EPIPHYTESCAT	6
TW	1CR	21	Hazard-rate	Cosine	EPIPHYTESCAT	6
TW	1CR	22	Hazard-rate	Simple polynomial	EPIPHYTESCAT	6
TW	1CR	23	Half-normal	Cosine	MOSSLICHENCAT	7
TW	1CR	24	Half-normal	Hermite polynomial	MOSSLICHENCAT	7
TW	1CR	25	Hazard-rate	Cosine	MOSSLICHENCAT	7
TW	1CR	26	Hazard-rate	Simple polynomial	MOSSLICHENCAT	7
TW	1CR	27	Half-normal	Cosine	BARESOILPERC	8
TW	1CR	28	Half-normal	Hermite polynomial	BARESOILPERC	8
TW	1CR	29	Hazard-rate	Cosine	BARESOILPERC	8
TW	1CR	30	Hazard-rate	Simple polynomial	BARESOILPERC	8
TW	1CR	31	Half-normal	Cosine	SHRUBSPERC135CM	9

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
TW	1CR	32	Half-normal	Hermite polynomial	SHRUBSPERC135CM	9
TW	1CR	33	Hazard-rate	Cosine	SHRUBSPERC135CM	9
TW	1CR	34	Hazard-rate	Simple polynomial	SHRUBSPERC135CM	9
TW	1CR	35	Half-normal	Cosine	UNDERSTORYCOVERPE	11
TW	1CR	36	Half-normal	Hermite polynomial	UNDERSTORYCOVERPE	11
TW	1CR	37	Hazard-rate	Cosine	UNDERSTORYCOVERPE	11
TW	1CR	38	Hazard-rate	Simple polynomial	UNDERSTORYCOVERPE	11
TW	1CR	39	Half-normal	Cosine	HIGHESTDBHCM	12
TW	1CR	40	Half-normal	Hermite polynomial	HIGHESTDBHCM	12
TW	1CR	41	Hazard-rate	Cosine	HIGHESTDBHCM	12
TW	1CR	42	Hazard-rate	Simple polynomial	HIGHESTDBHCM	12
TW	1CR	43	Half-normal	Cosine	MINSINCEDAWN	15
TW	1CR	44	Half-normal	Hermite polynomial	MINSINCEDAWN	15
TW	1CR	45	Hazard-rate	Cosine	MINSINCEDAWN	15
TW	1CR	46	Hazard-rate	Simple polynomial	MINSINCEDAWN	15
TW	2Ni	1	Half-normal	Cosine	none	none
TW	2Ni	2	Half-normal	Hermite polynomial	none	none
TW	2Ni	3	Uniform	Cosine	none	none
TW	2Ni	4	Uniform	Simple polynomial	none	none
TW	2Ni	5	Hazard-rate	Cosine	none	none
TW	2Ni	6	Hazard-rate	Simple polynomial	none	none
TW	2Ni	7	Half-normal	Cosine	VISIT	1
TW	2Ni	8	Half-normal	Hermite polynomial	VISIT	1
TW	2Ni	9	Hazard-rate	Cosine	VISIT	1
TW	2Ni	10	Hazard-rate	Simple polynomial	VISIT	1
TW	2Ni	11	Half-normal	Cosine	CLUSTER_SIZE	2
TW	2Ni	12	Half-normal	Hermite polynomial	CLUSTER_SIZE	2
TW	2Ni	13	Hazard-rate	Cosine	CLUSTER_SIZE	2
TW	2Ni	14	Hazard-rate	Simple polynomial	CLUSTER_SIZE	2
TW	2Ni	15	Half-normal	Cosine	CUPLABEL	3
TW	2Ni	16	Half-normal	Hermite polynomial	CUPLABEL	3
TW	2Ni	17	Hazard-rate	Cosine	CUPLABEL	3
TW	2Ni	18	Hazard-rate	Simple polynomial	CUPLABEL	3
TW	2Ni	19	Half-normal	Cosine	STATUS	4
TW	2Ni	20	Half-normal	Hermite polynomial	STATUS	4
TW	2Ni	21	Hazard-rate	Cosine	STATUS	4
TW	2Ni	22	Hazard-rate	Simple polynomial	STATUS	4
TW	2Ni	23	Half-normal	Cosine	HABITAT	5
TW	2Ni	24	Half-normal	Hermite polynomial	HABITAT	5
TW	2Ni	25	Hazard-rate	Cosine	HABITAT	5
TW	2Ni	26	Hazard-rate	Simple polynomial	HABITAT	5

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
TW	2Ni	27	Half-normal	Cosine	EPIPHYTESCAT	6
TW	2Ni	28	Half-normal	Hermite polynomial	EPIPHYTESCAT	6
TW	2Ni	29	Hazard-rate	Cosine	EPIPHYTESCAT	6
TW	2Ni	30	Hazard-rate	Simple polynomial	EPIPHYTESCAT	6
TW	2Ni	31	Half-normal	Cosine	SHRUBSPERC135CM	9
TW	2Ni	32	Half-normal	Hermite polynomial	SHRUBSPERC135CM	9
TW	2Ni	33	Hazard-rate	Cosine	SHRUBSPERC135CM	9
TW	2Ni	34	Hazard-rate	Simple polynomial	SHRUBSPERC135CM	9
TW	2Ni	35	Half-normal	Cosine	CANOPYPERC	10
TW	2Ni	36	Half-normal	Hermite polynomial	CANOPYPERC	10
TW	2Ni	37	Hazard-rate	Cosine	CANOPYPERC	10
TW	2Ni	38	Hazard-rate	Simple polynomial	CANOPYPERC	10
TW	2Ni	39	Half-normal	Cosine	UNDERSTORYCOVERPE	11
TW	2Ni	40	Half-normal	Hermite polynomial	UNDERSTORYCOVERPE	11
TW	2Ni	41	Hazard-rate	Cosine	UNDERSTORYCOVERPE	11
TW	2Ni	42	Hazard-rate	Simple polynomial	UNDERSTORYCOVERPE	11
TW	2Ni	43	Half-normal	Cosine	HIGHESTDBHCM	12
TW	2Ni	44	Half-normal	Hermite polynomial	HIGHESTDBHCM	12
TW	2Ni	45	Hazard-rate	Cosine	HIGHESTDBHCM	12
TW	2Ni	46	Hazard-rate	Simple polynomial	HIGHESTDBHCM	12
TW	2Ni	47	Half-normal	Cosine	HIGHESTTREEM	13
TW	2Ni	48	Half-normal	Hermite polynomial	HIGHESTTREEM	13
TW	2Ni	49	Hazard-rate	Cosine	HIGHESTTREEM	13
TW	2Ni	50	Hazard-rate	Simple polynomial	HIGHESTTREEM	13
TW	2Ni	51	Half-normal	Cosine	CANOPYTREESNO	14
TW	2Ni	52	Half-normal	Hermite polynomial	CANOPYTREESNO	14
TW	2Ni	53	Hazard-rate	Cosine	CANOPYTREESNO	14
TW	2Ni	54	Hazard-rate	Simple polynomial	CANOPYTREESNO	14
TW	2Ni	55	Half-normal	Cosine	MINSINCEDAWN	15
TW	2Ni	56	Half-normal	Hermite polynomial	MINSINCEDAWN	15
TW	2Ni	57	Hazard-rate	Cosine	MINSINCEDAWN	15
TW	2Ni	58	Hazard-rate	Simple polynomial	MINSINCEDAWN	15
TW	2Ni	59	Half-normal	Cosine	VISIT_EFFORT	16
TW	2Ni	60	Half-normal	Hermite polynomial	VISIT_EFFORT	16
TW	2Ni	61	Hazard-rate	Cosine	VISIT_EFFORT	16
TW	2Ni	62	Hazard-rate	Simple polynomial	VISIT_EFFORT	16
TW	2Ni	63	Half-normal	Cosine	BUG__870	38
TW	2Ni	64	Half-normal	Hermite polynomial	BUG__870	38
TW	2Ni	65	Hazard-rate	Cosine	BUG__870	38
TW	2Ni	66	Hazard-rate	Simple polynomial	BUG__870	38
TW	2Ni	67	Half-normal	Cosine	BUG__OTHER_RED	39

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
TW	2Ni	68	Half-normal	Hermite polynomial	BUG__OTHER_RED	39
TW	2Ni	69	Hazard-rate	Cosine	BUG__OTHER_RED	39
TW	2Ni	70	Hazard-rate	Simple polynomial	BUG__OTHER_RED	39
TW	2Ni	71	Half-normal	Cosine	INSECT__869	40
TW	2Ni	72	Half-normal	Hermite polynomial	INSECT__869	40
TW	2Ni	73	Hazard-rate	Cosine	INSECT__869	40
TW	2Ni	74	Hazard-rate	Simple polynomial	INSECT__869	40
TW	2Ni	75	Half-normal	Cosine	SPIDER__SMALL_RED	41
TW	2Ni	76	Half-normal	Hermite polynomial	SPIDER__SMALL_RED	41
TW	2Ni	77	Hazard-rate	Cosine	SPIDER__SMALL_RED	41
TW	2Ni	78	Hazard-rate	Simple polynomial	SPIDER__SMALL_RED	41
TW	2Ni	79	Half-normal	Cosine	TOAD	42
TW	2Ni	80	Half-normal	Hermite polynomial	TOAD	42
TW	2Ni	81	Hazard-rate	Cosine	TOAD	42
TW	2Ni	82	Hazard-rate	Simple polynomial	TOAD	42
TW	3AK	1	Half-normal	Cosine	none	none
TW	3AK	2	Half-normal	Hermite polynomial	none	none
TW	3AK	3	Uniform	Cosine	none	none
TW	3AK	4	Uniform	Simple polynomial	none	none
TW	3AK	5	Hazard-rate	Cosine	none	none
TW	3AK	6	Hazard-rate	Simple polynomial	none	none
TW	3AK	7	Half-normal	Cosine	VISIT	1
TW	3AK	8	Half-normal	Hermite polynomial	VISIT	1
TW	3AK	9	Hazard-rate	Cosine	VISIT	1
TW	3AK	10	Hazard-rate	Simple polynomial	VISIT	1
TW	3AK	11	Half-normal	Cosine	CLUSTER_SIZE	2
TW	3AK	12	Half-normal	Hermite polynomial	CLUSTER_SIZE	2
TW	3AK	13	Hazard-rate	Cosine	CLUSTER_SIZE	2
TW	3AK	14	Hazard-rate	Simple polynomial	CLUSTER_SIZE	2
TW	3AK	15	Half-normal	Cosine	CUPLABEL	3
TW	3AK	16	Half-normal	Hermite polynomial	CUPLABEL	3
TW	3AK	17	Hazard-rate	Cosine	CUPLABEL	3
TW	3AK	18	Hazard-rate	Simple polynomial	CUPLABEL	3
TW	3AK	19	Half-normal	Cosine	HABITAT	5
TW	3AK	20	Half-normal	Hermite polynomial	HABITAT	5
TW	3AK	21	Hazard-rate	Cosine	HABITAT	5
TW	3AK	22	Hazard-rate	Simple polynomial	HABITAT	5
TW	3AK	23	Half-normal	Cosine	MOSSLICHENCAT	7
TW	3AK	24	Half-normal	Hermite polynomial	MOSSLICHENCAT	7
TW	3AK	25	Hazard-rate	Cosine	MOSSLICHENCAT	7
TW	3AK	26	Hazard-rate	Simple polynomial	MOSSLICHENCAT	7
TW	3AK	27	Half-normal	Cosine	VISIT_EFFORT	16
TW	3AK	28	Half-normal	Hermite polynomial	VISIT_EFFORT	16

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
TW	3AK	29	Hazard-rate	Cosine	VISIT_EFFORT	16
TW	3AK	30	Hazard-rate	Simple polynomial	VISIT_EFFORT	16
TW	3AK	31	Half-normal	Cosine	COVARIATE04	20
TW	3AK	32	Half-normal	Hermite polynomial	COVARIATE04	20
TW	3AK	33	Hazard-rate	Cosine	COVARIATE04	20
TW	3AK	34	Hazard-rate	Simple polynomial	COVARIATE04	20
TW	3AK	35	Half-normal	Cosine	COVARIATE07	21
TW	3AK	36	Half-normal	Hermite polynomial	COVARIATE07	21
TW	3AK	37	Hazard-rate	Cosine	COVARIATE07	21
TW	3AK	38	Hazard-rate	Simple polynomial	COVARIATE07	21
TW	3AK	39	Half-normal	Cosine	COVARIATE08	22
TW	3AK	40	Half-normal	Hermite polynomial	COVARIATE08	22
TW	3AK	41	Hazard-rate	Cosine	COVARIATE08	22
TW	3AK	42	Hazard-rate	Simple polynomial	COVARIATE08	22
TW	3AK	43	Half-normal	Cosine	COVARIATE09	23
TW	3AK	44	Half-normal	Hermite polynomial	COVARIATE09	23
TW	3AK	45	Hazard-rate	Cosine	COVARIATE09	23
TW	3AK	46	Hazard-rate	Simple polynomial	COVARIATE09	23
TW	3AK	47	Half-normal	Cosine	COVARIATE10	24
TW	3AK	48	Half-normal	Hermite polynomial	COVARIATE10	24
TW	3AK	49	Hazard-rate	Cosine	COVARIATE10	24
TW	3AK	50	Hazard-rate	Simple polynomial	COVARIATE10	24
TW	3AK	51	Half-normal	Cosine	COVARIATE11	25
TW	3AK	52	Half-normal	Hermite polynomial	COVARIATE11	25
TW	3AK	53	Hazard-rate	Cosine	COVARIATE11	25
TW	3AK	54	Hazard-rate	Simple polynomial	COVARIATE11	25
TW	3AK	55	Half-normal	Cosine	COVARIATE12	26
TW	3AK	56	Half-normal	Hermite polynomial	COVARIATE12	26
TW	3AK	57	Hazard-rate	Cosine	COVARIATE12	26
TW	3AK	58	Hazard-rate	Simple polynomial	COVARIATE12	26
TW	3AK	59	Half-normal	Cosine	COVARIATE13	27
TW	3AK	60	Half-normal	Hermite polynomial	COVARIATE13	27
TW	3AK	61	Hazard-rate	Cosine	COVARIATE13	27
TW	3AK	62	Hazard-rate	Simple polynomial	COVARIATE13	27
TW	3AK	63	Half-normal	Cosine	COVARIATE14	28
TW	3AK	64	Half-normal	Hermite polynomial	COVARIATE14	28
TW	3AK	65	Hazard-rate	Cosine	COVARIATE14	28
TW	3AK	66	Hazard-rate	Simple polynomial	COVARIATE14	28
TW	3AK	67	Half-normal	Cosine	COVARIATE15	29
TW	3AK	68	Half-normal	Hermite polynomial	COVARIATE15	29
TW	3AK	69	Hazard-rate	Cosine	COVARIATE15	29
TW	3AK	70	Hazard-rate	Simple polynomial	COVARIATE15	29
TW	3AK	71	Half-normal	Cosine	COVARIATE18	30
TW	3AK	72	Half-normal	Hermite	COVARIATE18	30

Typ e	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
				polynomial		
TW	3AK	73	Hazard-rate	Cosine	COVARIATE18	30
TW	3AK	74	Hazard-rate	Simple polynomial	COVARIATE18	30
TW	3AK	75	Half-normal	Cosine	ANT__SMALL	43
TW	3AK	76	Half-normal	Hermite polynomial	ANT__SMALL	43
TW	3AK	77	Hazard-rate	Cosine	ANT__SMALL	43
TW	3AK	78	Hazard-rate	Simple polynomial	ANT__SMALL	43
TW	3AK	79	Half-normal	Cosine	BOREAL_CHICKADEE	44
TW	3AK	80	Half-normal	Hermite polynomial	BOREAL_CHICKADEE	44
TW	3AK	81	Hazard-rate	Cosine	BOREAL_CHICKADEE	44
TW	3AK	82	Hazard-rate	Simple polynomial	BOREAL_CHICKADEE	44
TW	4Ru	1	Half-normal	Cosine	none	none
TW	4Ru	2	Half-normal	Hermite polynomial	none	none
TW	4Ru	3	Uniform	Cosine	none	none
TW	4Ru	4	Uniform	Simple polynomial	none	none
TW	4Ru	5	Hazard-rate	Cosine	none	none
TW	4Ru	6	Hazard-rate	Simple polynomial	none	none
TW	4Ru	7	Half-normal	Cosine	VISIT	1
TW	4Ru	8	Half-normal	Hermite polynomial	VISIT	1
TW	4Ru	9	Hazard-rate	Cosine	VISIT	1
TW	4Ru	10	Hazard-rate	Simple polynomial	VISIT	1
TW	4Ru	11	Half-normal	Cosine	CLUSTER_SIZE	2
TW	4Ru	12	Half-normal	Hermite polynomial	CLUSTER_SIZE	2
TW	4Ru	13	Hazard-rate	Cosine	CLUSTER_SIZE	2
TW	4Ru	14	Hazard-rate	Simple polynomial	CLUSTER_SIZE	2
TW	4Ru	15	Half-normal	Cosine	CUPLABEL	3
TW	4Ru	16	Half-normal	Hermite polynomial	CUPLABEL	3
TW	4Ru	17	Hazard-rate	Cosine	CUPLABEL	3
TW	4Ru	18	Hazard-rate	Simple polynomial	CUPLABEL	3
TW	4Ru	19	Half-normal	Cosine	HABITAT	5
TW	4Ru	20	Half-normal	Hermite polynomial	HABITAT	5
TW	4Ru	21	Hazard-rate	Cosine	HABITAT	5
TW	4Ru	22	Hazard-rate	Simple polynomial	HABITAT	5
TW	4Ru	23	Half-normal	Cosine	HIGHESTTREEM	13
TW	4Ru	24	Half-normal	Hermite polynomial	HIGHESTTREEM	13
TW	4Ru	25	Hazard-rate	Cosine	HIGHESTTREEM	13
TW	4Ru	26	Hazard-rate	Simple polynomial	HIGHESTTREEM	13
TW	4Ru	27	Half-normal	Cosine	MINSINCEDAWN	15
TW	4Ru	28	Half-normal	Hermite polynomial	MINSINCEDAWN	15
TW	4Ru	29	Hazard-rate	Cosine	MINSINCEDAWN	15
TW	4Ru	30	Hazard-rate	Simple polynomial	MINSINCEDAWN	15
TW	4Ru	31	Half-normal	Cosine	LICHENPERC	18
TW	4Ru	32	Half-normal	Hermite polynomial	LICHENPERC	18
TW	4Ru	33	Hazard-rate	Cosine	LICHENPERC	18

Typ e	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
TW	4Ru	34	Hazard-rate	Simple polynomial	LICHENPERC	18
TW	4Ru	35	Half-normal	Cosine	MOSSPERC	19
TW	4Ru	36	Half-normal	Hermite polynomial	MOSSPERC	19
TW	4Ru	37	Hazard-rate	Cosine	MOSSPERC	19
TW	4Ru	38	Hazard-rate	Simple polynomial	MOSSPERC	19
TW	4Ru	39	Half-normal	Cosine	COVARIATE01	31
TW	4Ru	40	Half-normal	Hermite polynomial	COVARIATE01	31
TW	4Ru	41	Hazard-rate	Cosine	COVARIATE01	31
TW	4Ru	42	Hazard-rate	Simple polynomial	COVARIATE01	31
TW	4Ru	43	Half-normal	Cosine	COVARIATE03	32
TW	4Ru	44	Half-normal	Hermite polynomial	COVARIATE03	32
TW	4Ru	45	Hazard-rate	Cosine	COVARIATE03	32
TW	4Ru	46	Hazard-rate	Simple polynomial	COVARIATE03	32
TW	4Ru	47	Half-normal	Cosine	COVARIATE05	33
TW	4Ru	48	Half-normal	Hermite polynomial	COVARIATE05	33
TW	4Ru	49	Hazard-rate	Cosine	COVARIATE05	33
TW	4Ru	50	Hazard-rate	Simple polynomial	COVARIATE05	33
TW	4Ru	51	Half-normal	Cosine	COVARIATE11	25
TW	4Ru	52	Half-normal	Hermite polynomial	COVARIATE11	25
TW	4Ru	53	Hazard-rate	Cosine	COVARIATE11	25
TW	4Ru	54	Hazard-rate	Simple polynomial	COVARIATE11	25
TW	4Ru	55	Half-normal	Cosine	COVARIATE19	34
TW	4Ru	56	Half-normal	Hermite polynomial	COVARIATE19	34
TW	4Ru	57	Hazard-rate	Cosine	COVARIATE19	34
TW	4Ru	58	Hazard-rate	Simple polynomial	COVARIATE19	34
TW	4Ru	59	Half-normal	Cosine	COVARIATE21	35
TW	4Ru	60	Half-normal	Hermite polynomial	COVARIATE21	35
TW	4Ru	61	Hazard-rate	Cosine	COVARIATE21	35
TW	4Ru	62	Hazard-rate	Simple polynomial	COVARIATE21	35
TW	5PG	1	Half-normal	Cosine	none	none
TW	5PG	2	Half-normal	Hermite polynomial	none	none
TW	5PG	3	Uniform	Cosine	none	none
TW	5PG	4	Uniform	Simple polynomial	none	none
TW	5PG	5	Hazard-rate	Cosine	none	none
TW	5PG	6	Hazard-rate	Simple polynomial	none	none
TW	5PG	7	Half-normal	Cosine	VISIT	1
TW	5PG	8	Half-normal	Hermite polynomial	VISIT	1
TW	5PG	9	Hazard-rate	Cosine	VISIT	1
TW	5PG	10	Hazard-rate	Simple polynomial	VISIT	1
TW	5PG	11	Half-normal	Cosine	CUPLABEL	3
TW	5PG	12	Half-normal	Hermite polynomial	CUPLABEL	3
TW	5PG	13	Hazard-rate	Cosine	CUPLABEL	3
TW	5PG	14	Hazard-rate	Simple polynomial	CUPLABEL	3
TW	5PG	15	Half-normal	Cosine	HABITAT	5

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
TW	5PG	16	Half-normal	Hermite polynomial	HABITAT	5
TW	5PG	17	Hazard-rate	Cosine	HABITAT	5
TW	5PG	18	Hazard-rate	Simple polynomial	HABITAT	5
TW	5PG	19	Half-normal	Cosine	EPIPHYTESCAT	6
TW	5PG	20	Half-normal	Hermite polynomial	EPIPHYTESCAT	6
TW	5PG	21	Hazard-rate	Cosine	EPIPHYTESCAT	6
TW	5PG	22	Hazard-rate	Simple polynomial	EPIPHYTESCAT	6
TW	5PG	23	Half-normal	Cosine	COVARIATE01	31
TW	5PG	24	Half-normal	Hermite polynomial	COVARIATE01	31
TW	5PG	25	Hazard-rate	Cosine	COVARIATE01	31
TW	5PG	26	Hazard-rate	Simple polynomial	COVARIATE01	31
TW	5PG	27	Half-normal	Cosine	COVARIATE05	33
TW	5PG	28	Half-normal	Hermite polynomial	COVARIATE05	33
TW	5PG	29	Hazard-rate	Cosine	COVARIATE05	33
TW	5PG	30	Hazard-rate	Simple polynomial	COVARIATE05	33
TW	5PG	31	Half-normal	Cosine	COVARIATE06	37
TW	5PG	32	Half-normal	Hermite polynomial	COVARIATE06	37
TW	5PG	33	Hazard-rate	Cosine	COVARIATE06	37
TW	5PG	34	Hazard-rate	Simple polynomial	COVARIATE06	37
TW	5PG	35	Half-normal	Cosine	COVARIATE08	22
TW	5PG	36	Half-normal	Hermite polynomial	COVARIATE08	22
TW	5PG	37	Hazard-rate	Cosine	COVARIATE08	22
TW	5PG	38	Hazard-rate	Simple polynomial	COVARIATE08	22
TW	5PG	39	Half-normal	Cosine	COVARIATE11	25
TW	5PG	40	Half-normal	Hermite polynomial	COVARIATE11	25
TW	5PG	41	Hazard-rate	Cosine	COVARIATE11	25
TW	5PG	42	Hazard-rate	Simple polynomial	COVARIATE11	25
TW	5PG	43	Half-normal	Cosine	COVARIATE12	26
TW	5PG	44	Half-normal	Hermite polynomial	COVARIATE12	26
TW	5PG	45	Hazard-rate	Cosine	COVARIATE12	26
TW	5PG	46	Hazard-rate	Simple polynomial	COVARIATE12	26
TW	6Ba	1	Half-normal	Cosine	none	none
TW	6Ba	2	Half-normal	Hermite polynomial	none	none
TW	6Ba	3	Uniform	Cosine	none	none
TW	6Ba	4	Uniform	Simple polynomial	none	none
TW	6Ba	5	Hazard-rate	Cosine	none	none
TW	6Ba	6	Hazard-rate	Simple polynomial	none	none
TW	6Ba	7	Half-normal	Cosine	VISIT	1
TW	6Ba	8	Half-normal	Hermite polynomial	VISIT	1
TW	6Ba	9	Hazard-rate	Cosine	VISIT	1
TW	6Ba	10	Hazard-rate	Simple polynomial	VISIT	1
TW	6Ba	11	Half-normal	Cosine	CLUSTER_SIZE	2
TW	6Ba	12	Half-normal	Hermite polynomial	CLUSTER_SIZE	2

Type	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
TW	6Ba	13	Hazard-rate	Cosine	CLUSTER_SIZE	2
TW	6Ba	14	Hazard-rate	Simple polynomial	CLUSTER_SIZE	2
TW	6Ba	15	Half-normal	Cosine	CUPLABEL	3
TW	6Ba	16	Half-normal	Hermite polynomial	CUPLABEL	3
TW	6Ba	17	Hazard-rate	Cosine	CUPLABEL	3
TW	6Ba	18	Hazard-rate	Simple polynomial	CUPLABEL	3
TW	6Ba	19	Half-normal	Cosine	STATUS	4
TW	6Ba	20	Half-normal	Hermite polynomial	STATUS	4
TW	6Ba	21	Hazard-rate	Cosine	STATUS	4
TW	6Ba	22	Hazard-rate	Simple polynomial	STATUS	4
TW	6Ba	23	Half-normal	Cosine	BARESOILPERC	8
TW	6Ba	24	Half-normal	Hermite polynomial	BARESOILPERC	8
TW	6Ba	25	Hazard-rate	Cosine	BARESOILPERC	8
TW	6Ba	26	Hazard-rate	Simple polynomial	BARESOILPERC	8
TW	6Ba	27	Half-normal	Cosine	VISIT_EFFORT	16
TW	6Ba	28	Half-normal	Hermite polynomial	VISIT_EFFORT	16
TW	6Ba	29	Hazard-rate	Cosine	VISIT_EFFORT	16
TW	6Ba	30	Hazard-rate	Simple polynomial	VISIT_EFFORT	16
TW	6Ba	31	Half-normal	Cosine	GRASSPERC	17
TW	6Ba	32	Half-normal	Hermite polynomial	GRASSPERC	17
TW	6Ba	33	Hazard-rate	Cosine	GRASSPERC	17
TW	6Ba	34	Hazard-rate	Simple polynomial	GRASSPERC	17
TW	6Ba	35	Half-normal	Cosine	LICHENPERC	18
TW	6Ba	36	Half-normal	Hermite polynomial	LICHENPERC	18
TW	6Ba	37	Hazard-rate	Cosine	LICHENPERC	18
TW	6Ba	38	Hazard-rate	Simple polynomial	LICHENPERC	18
TW	6Ba	39	Half-normal	Cosine	MOSSPERC	19
TW	6Ba	40	Half-normal	Hermite polynomial	MOSSPERC	19
TW	6Ba	41	Hazard-rate	Cosine	MOSSPERC	19
TW	6Ba	42	Hazard-rate	Simple polynomial	MOSSPERC	19
TW	6Ba	43	Half-normal	Cosine	COVARIATE01	31
TW	6Ba	44	Half-normal	Hermite polynomial	COVARIATE01	31
TW	6Ba	45	Hazard-rate	Cosine	COVARIATE01	31
TW	6Ba	46	Hazard-rate	Simple polynomial	COVARIATE01	31
TW	6Ba	47	Half-normal	Cosine	COVARIATE02	36
TW	6Ba	48	Half-normal	Hermite polynomial	COVARIATE02	36
TW	6Ba	49	Hazard-rate	Cosine	COVARIATE02	36
TW	6Ba	50	Hazard-rate	Simple polynomial	COVARIATE02	36
TW	6Ba	51	Half-normal	Cosine	COVARIATE08	22
TW	6Ba	52	Half-normal	Hermite polynomial	COVARIATE08	22
TW	6Ba	53	Hazard-rate	Cosine	COVARIATE08	22
TW	6Ba	54	Hazard-rate	Simple polynomial	COVARIATE08	22
TW	6Ba	55	Half-normal	Cosine	COVARIATE10	24
TW	6Ba	56	Half-normal	Hermite	COVARIATE10	24

Typ e	Study area	Model no	Model key function	Model series expansion	MCDS covariates	Name extention
				polynomial		
TW	6Ba	57	Hazard-rate	Cosine	COVARIATE10	24
TW	6Ba	58	Hazard-rate	Simple polynomial	COVARIATE10	24

7.4 PRESENCE Model Definitions

Study area	Type	Model
1CR	Bi	1 group, Constant P
1CR	Bi	1 group, Survey-specific P
1CR	Bi	BareSoil
1CR	Bi	CanopyPerc
1CR	Bi	CanopyTrees
1CR	Bi	Cov04
1CR	Bi	Cov05
1CR	Bi	Cov12
1CR	Bi	DuffCover
1CR	Bi	Epiphytes
1CR	Bi	Flowers
1CR	Bi	Habitat
1CR	Bi	HighestDBH
1CR	Bi	HighestTree
1CR	Bi	LeafBrowsing
1CR	Bi	Manakin
1CR	Bi	Min
1CR	Bi	MossLichen
1CR	Bi	Shrubs
1CR	Bi	TurkeyVulture
1CR	Bi	Understory
2Ni	Bi	1 group, Constant P
2Ni	Bi	1 group, Survey-specific P
2Ni	Bi	BareSoil
2Ni	Bi	CanopyPerc
2Ni	Bi	DuffCover
2Ni	Bi	Epiphytes
2Ni	Bi	Habitat
2Ni	Bi	HighestDBH
2Ni	Bi	HighestTree
2Ni	Bi	Min
2Ni	Bi	MossLichen
2Ni	Bi	Shrubs
2Ni	Bi	TurkeyVulture
2Ni	Bi	Understory
3AK	Bi	1 group, Constant P
3AK	Bi	1 group, Survey-specific P
3AK	Bi	CanopyPerc
3AK	Bi	CanopyTrees
3AK	Bi	Cov07
3AK	Bi	Cov1
3AK	Bi	Cov11
3AK	Bi	Cov12
3AK	Bi	Cov13
3AK	Bi	Cov14
3AK	Bi	Cov19
3AK	Bi	DuffCover
3AK	Bi	Habitat
3AK	Bi	HighestDBH

Study area	Type	Model
3AK	Bi	HighestTree
3AK	Bi	Min
3AK	Bi	Model
3AK	Bi	MossLichen
3AK	Bi	Squirrel
4Ru	Bi	1 group, Constant P
4Ru	Bi	1 group, Survey-specific P
4Ru	Bi	CanopyPerc
4Ru	Bi	CanopyTrees
4Ru	Bi	Cov01
4Ru	Bi	Cov04
4Ru	Bi	Cov05
4Ru	Bi	Cov08
4Ru	Bi	Cov12
4Ru	Bi	Cov15
4Ru	Bi	Cov16
4Ru	Bi	Cov18
4Ru	Bi	Cov19
4Ru	Bi	Cov20
4Ru	Bi	Cov21
4Ru	Bi	Cov23
4Ru	Bi	Cov28
4Ru	Bi	Cov30
4Ru	Bi	Cov31
4Ru	Bi	DuffCover
4Ru	Bi	Flowers
4Ru	Bi	Habitat
4Ru	Bi	HighDBH
4Ru	Bi	HighTree
4Ru	Bi	LichenPerc
4Ru	Bi	Min
4Ru	Bi	MossPerc
4Ru	Bi	Shrubs
4Ru	Bi	Understory
4Ru	Bi	Wize
5PG	Bi	1 group, Constant P
5PG	Bi	1 group, Survey-specific P
5PG	Bi	BareSoil
5PG	Bi	CanopyPerc
5PG	Bi	Cov01
5PG	Bi	Cov06
5PG	Bi	Cov11
5PG	Bi	Cov12
5PG	Bi	DuffCover
5PG	Bi	Epiphytes
5PG	Bi	Habitat
5PG	Bi	HighestDBH
5PG	Bi	HighestTree
5PG	Bi	Min
6Ba	Bi	1 group, Constant P
6Ba	Bi	1 group, Survey-specific P
6Ba	Bi	BareSoil
6Ba	Bi	Cov01

Study area	Type	Model
6Ba	Bi	Cov02
6Ba	Bi	Cov03
6Ba	Bi	Cov05
6Ba	Bi	Cov06
6Ba	Bi	Cov07
6Ba	Bi	Cov08
6Ba	Bi	Cov10
6Ba	Bi	DiamLake
6Ba	Bi	DistLake
6Ba	Bi	Flowers
6Ba	Bi	GrassPerc
6Ba	Bi	Leafs
6Ba	Bi	LichenPerc
6Ba	Bi	MossPerc
6Ba	Bi	PomarineJaeger
6Ba	Bi	SurveyEffort
1CR	TW	1 group, Constant P
1CR	TW	1 group, Survey-specific P
1CR	TW	BareSoil
1CR	TW	Epiphytes
1CR	TW	Habitat
1CR	TW	HighestDBH
1CR	TW	Min
1CR	TW	MossLichen
1CR	TW	Shrubs
1CR	TW	Understory
2Ni	TW	1 group, Constant P
2Ni	TW	1 group, Survey-specific P
2Ni	TW	Bug870
2Ni	TW	BugOtherRed
2Ni	TW	CanopyPerc
2Ni	TW	CanopyTrees
2Ni	TW	Epipytes
2Ni	TW	Habitat
2Ni	TW	HighestDBH
2Ni	TW	HighestTree
2Ni	TW	Insect869
2Ni	TW	Min
2Ni	TW	Shrubs
2Ni	TW	SpiderSmallRed
2Ni	TW	Toad
2Ni	TW	Understory
2Ni	TW	VisitEffort
3AK	TW	1 group, Constant P
3AK	TW	1 group, Survey-specific P
3AK	TW	AntSmall
3AK	TW	BorealChickadee
3AK	TW	Cov04
3AK	TW	Cov07
3AK	TW	Cov08
3AK	TW	Cov09
3AK	TW	Cov10
3AK	TW	Cov11

Study area	Type	Model
3AK	TW	Cov12
3AK	TW	Cov13
3AK	TW	Cov14
3AK	TW	Cov15
3AK	TW	Cov18
3AK	TW	Habitat
3AK	TW	Min
3AK	TW	MossLichen
3AK	TW	SurveyEffort
4Ru	TW	1 group, Constant P
4Ru	TW	1 group, Survey-specific P
4Ru	TW	Cov01
4Ru	TW	Cov03
4Ru	TW	Cov05
4Ru	TW	Cov11
4Ru	TW	Cov19
4Ru	TW	Cov21
4Ru	TW	Habitat
4Ru	TW	HighestTree
4Ru	TW	LichenPerc
4Ru	TW	Min
4Ru	TW	MossPerc
5PG	TW	1 group, Constant P
5PG	TW	1 group, Survey-specific P
5PG	TW	Cov01
5PG	TW	Cov05
5PG	TW	Cov06
5PG	TW	Cov08
5PG	TW	Cov11
5PG	TW	Cov12
5PG	TW	Epiphytes
5PG	TW	Habitat
5PG	TW	Min
6Ba	TW	1 group, Constant P
6Ba	TW	1 group, Survey-specific P
6Ba	TW	BareSoil
6Ba	TW	Cov01
6Ba	TW	Cov02
6Ba	TW	Cov08
6Ba	TW	Cov10
6Ba	TW	GrassPerc
6Ba	TW	LichenPerc
6Ba	TW	MossPerc
6Ba	TW	SurveyEffort

7.5 Detailed Species Lists (Valid ITIS Taxonomy)

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
Bi	1CR	9	Ani	Cuculiformes	Cuculidae	Crotophaga	not identified
Bi	1CR	8	Bird	not identified	not identified	not identified	not identified
Bi	1CR	1	Bird of Prey	not identified	not identified	not identified	not identified
Bi	1CR	1	Bird, big	not identified	not identified	not identified	not identified
Bi	1CR	3	Crake	Gruiformes	Rallidae	not identified	not identified
Bi	1CR	15	Dove	Columbiformes	Columbidae	not identified	not identified
Bi	1CR	2	Falcon	Ciconiiformes	Falconidae	Falco	not identified
Bi	1CR	61	Flycatcher	Passeriformes	Tyrannidae	not identified	not identified
Bi	1CR	1	Golden-bellied Flycatcher	Passeriformes	Tyrannidae	Myiodynastes	hemichrysus
Bi	1CR	3	Golden-hooded Tanager	Passeriformes	Thraupidae	Tangara	larvata
Bi	1CR	2	Gray-necked Woodpecker	Piciformes	Picidae	not identified	not identified
Bi	1CR	28	Great Kiskadee	Passeriformes	Tyrannidae	Pitangus	sulphuratus
Bi	1CR	2	Groove-billed Ani	Cuculiformes	Cuculidae	Crotophaga	sulcirostris
Bi	1CR	128	Hummingbird	Apodiformes	Trochilidae	not identified	not identified
Bi	1CR	10	Kiskadee	Passeriformes	Tyrannidae	Pitangus	not identified
Bi	1CR	1	Lattice-tailed Trogon	Trogoniformes	Trogonidae	Trogon	clathratus
Bi	1CR	1	Laughing Falcon	Ciconiiformes	Falconidae	Herpetotheres	cachinnans
Bi	1CR	1	Lesser Kiskadee	Passeriformes	Tyrannidae	Pitangus	lictor
Bi	1CR	1	Little	not identified	not identified	not identified	not identified
Bi	1CR	16	Manakin	Passeriformes	Pipridae	not identified	not identified
Bi	1CR	5	Mealy Parrot	Psittaciformes	Psittacidae	Amazona	farinosa
Bi	1CR	2	Motmot	Coraciiformes	Momotidae	not identified	not identified
Bi	1CR	125	Oropendula	Passeriformes	Icteridae	Psarocolius	not identified
Bi	1CR	2	Pale-vented Thrush	Passeriformes	Turdidae	Turdus	obsoletus
Bi	1CR	20	Parrot	Psittaciformes	Psittacidae	not identified	not identified
Bi	1CR	14	Parrot, large	Psittaciformes	Psittacidae	not identified	not identified
Bi	1CR	1	Parrot, little	Psittaciformes	Psittacidae	not identified	not identified
Bi	1CR	1	Rainbird	not identified	not identified	not identified	not identified
Bi	1CR	1	Raptor, small	not identified	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
Bi	1CR	3	Saltatron	not identified	not identified	not identified	not identified
Bi	1CR	12	Scarlet-rumped Tanager	Passeriformes	Thraupidae	Ramphocelus	passerinii
Bi	1CR	30	Seedeater	Passeriformes	Thraupidae	not identified	not identified
Bi	1CR	3	Smooth-billed Ani	Cuculiformes	Cuculidae	Crotophaga	ani
Bi	1CR	47	Songbird	Passeriformes	not identified	not identified	not identified
Bi	1CR	1	Songbird, brown	Passeriformes	not identified	not identified	not identified
Bi	1CR	1	Songbird, little	Passeriformes	not identified	not identified	not identified
Bi	1CR	1	Squirrel Cuckoo	Cuculiformes	Cuculidae	Piaya	cayana
Bi	1CR	1	Steep-forehead Flycatcher	Passeriformes	Tyrannidae	not identified	not identified
Bi	1CR	2	Swallow	Passeriformes	Hirundinidae	not identified	not identified
Bi	1CR	1	Swift	Apodiformes	Apodidae	not identified	not identified
Bi	1CR	10	Tanager	Passeriformes	Thraupidae	not identified	not identified
Bi	1CR	1	Thrush	Passeriformes	not identified	not identified	not identified
Bi	1CR	1	Tick Bird	not identified	not identified	not identified	not identified
Bi	1CR	7	Toucan	Piciformes	Ramphastidae	not identified	not identified
Bi	1CR	3	Treecreper	Passeriformes	Certhiidae	not identified	not identified
Bi	1CR	12	Turkey Vulture	Ciconiiformes	Ciconiidae	Cathartes	aura
Bi	1CR	3	Vulture	Ciconiiformes	Ciconiidae	not identified	not identified
Bi	1CR	38	Woodpecker	Piciformes	Picidae	not identified	not identified
Bi	1CR	4	Yellow-bellied Flycatcher	Passeriformes	Tyrannidae	Empidonax	flaviventris
DT	1CR	1	Butterfly, blue-black	Lepidoptera	not identified	not identified	not identified
DT	1CR	3	Butterfly, small yellow	Lepidoptera	not identified	not identified	not identified
DT	1CR	3	Butterfly, white	Lepidoptera	not identified	not identified	not identified
DT	1CR	8	Butterfly, yellow	Lepidoptera	not identified	not identified	not identified
DT	1CR	3	Frog, red Dendrobatus	Anura	Dendrobatidae	Dendrobates	pumilio
TW	1CR	116	ant	Hymenoptera	Formicidae	not identified	not identified
TW	1CR	7	ant, small	Hymenoptera	Formicidae	not identified	not identified
TW	1CR	1	ant, winged	Hymenoptera	Formicidae	not identified	not identified
TW	1CR	1	beetle, ground	Coleoptera	not identified	not identified	not identified
TW	1CR	2	beetle, long & slim	Coleoptera	not identified	not identified	not identified
TW	1CR	1	bug	Hemiptera	not identified	not identified	not identified
TW	1CR	16	cricket	Orthoptera	not identified	not identified	not identified
TW	1CR	1	moth	Lepidoptera	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
TW	1CR	1	salamander	Caudata	not identified	not identified	not identified
TW	1CR	47	spider	Araneae	not identified	not identified	not identified
TW	1CR	2	wasp	Hymenoptera	not identified	not identified	not identified
Bi	2Ni	5	Ani	Cuculiformes	Cuculidae	Crotophaga	not identified
Bi	2Ni	65	Banded Wren	Passeriformes	Troglodytidae	Thryothorus	pleurostictus
Bi	2Ni	1	Black-headed Trogon	Trogoniformes	Trogonidae	Trogon	melanocephalus
Bi	2Ni	4	Brown-crested Flycatcher	Passeriformes	Tyrannidae	Myiarchus	tyrannulus
Bi	2Ni	4	Cattle Egret	Ciconiiformes	Ardeidae	Bubulcus	ibis
Bi	2Ni	11	Dove	Columbiformes	Columbidae	not identified	not identified
Bi	2Ni	11	Flycatcher	Passeriformes	Tyrannidae	not identified	not identified
Bi	2Ni	17	Gray Hawk	Ciconiiformes	Accipitridae	Buteo	nitidus
Bi	2Ni	3	Great Kiskadee	Passeriformes	Tyrannidae	Pitangus	sulphuratus
Bi	2Ni	2	Groove-billed Ani	Cuculiformes	Cuculidae	Crotophaga	sulcirostris
Bi	2Ni	7	Hawk	Ciconiiformes	Accipitridae	not identified	not identified
Bi	2Ni	3	Hoffmann's Woodpecker	Piciformes	Picidae	Melanerpes	hoffmannii
Bi	2Ni	4	Hummingbird	Apodiformes	Trochilidae	not identified	not identified
Bi	2Ni	2	Jay	Passeriformes	Corvidae	not identified	not identified
Bi	2Ni	1	Magnificent Frigatebird	Ciconiiformes	Fregatidae	Fregata	magnificens
Bi	2Ni	1	Masked Tityra	Passeriformes	Cotingidae	Tityra	semifasciata
Bi	2Ni	5	Parakeet	Psittaciformes	Psittacidae	Aratinga	not identified
Bi	2Ni	14	Parrot	Psittaciformes	Psittacidae	not identified	not identified
Bi	2Ni	9	Parrot, large	Psittaciformes	Psittacidae	not identified	not identified
Bi	2Ni	1	Pauraque	Strigiformes	Caprimulgidae	Nyctidromus	albicollis
Bi	2Ni	3	Red-billed Pigeon	Columbiformes	Columbidae	Patagioenas	flavirostris
Bi	2Ni	1	Seedeater	Passeriformes	Thraupidae	not identified	not identified
Bi	2Ni	13	Songbird	Passeriformes	not identified	not identified	not identified
Bi	2Ni	6	Swallow	Passeriformes	Hirundinidae	not identified	not identified
Bi	2Ni	1	Swift	Apodiformes	Apodidae	not identified	not identified
Bi	2Ni	1	Tanager	Passeriformes	Thraupidae	not identified	not identified
Bi	2Ni	41	Turkey Vulture	Ciconiiformes	Ciconiidae	Cathartes	aura
Bi	2Ni	5	unknown	not identified	not identified	not identified	not identified
Bi	2Ni	3	Vaux's Swift	Apodiformes	Apodidae	Chaetura	vauxi
Bi	2Ni	1	Vulture	Ciconiiformes	Ciconiidae	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
Bi	2Ni	99	White-throated Magpie Jay	Passeriformes	Corvidae	Calocitta	formosa
Bi	2Ni	16	Woodpecker	Piciformes	Picidae	not identified	not identified
Bi	2Ni	1	Yellow-naped Parrot	Psittaciformes	Psittacidae	Amazona	auropalliata
DT	2Ni	2	Butterfly, black-red	Lepidoptera	not identified	not identified	not identified
DT	2Ni	3	Butterfly, black-yellow	Lepidoptera	not identified	not identified	not identified
DT	2Ni	3	Butterfly, grey	Lepidoptera	not identified	not identified	not identified
DT	2Ni	1	Butterfly, large yellow	Lepidoptera	not identified	not identified	not identified
DT	2Ni	2	Butterfly, orange	Lepidoptera	not identified	not identified	not identified
DT	2Ni	2	Butterfly, orange-white	Lepidoptera	not identified	not identified	not identified
DT	2Ni	1	Butterfly, small black	Lepidoptera	not identified	not identified	not identified
DT	2Ni	1	Butterfly, small white	Lepidoptera	not identified	not identified	not identified
DT	2Ni	1	butterfly, swallowtail	Lepidoptera	Papilionidae	Papilio	not identified
DT	2Ni	36	Butterfly, white	Lepidoptera	not identified	not identified	not identified
DT	2Ni	9	Butterfly, yellow	Lepidoptera	not identified	not identified	not identified
TW	2Ni	58	ant	Hymenoptera	Formicidae	not identified	not identified
TW	2Ni	4	ant, red	Hymenoptera	Formicidae	not identified	not identified
TW	2Ni	9	ant, small	Hymenoptera	Formicidae	not identified	not identified
TW	2Ni	1	ant, small black	Hymenoptera	Formicidae	not identified	not identified
TW	2Ni	24	ant, small red	Hymenoptera	Formicidae	not identified	not identified
TW	2Ni	1	beetle, 1002-1004	Coleoptera	not identified	not identified	not identified
TW	2Ni	6	beetle, 866	Coleoptera	not identified	not identified	not identified
TW	2Ni	39	beetle, 868	Coleoptera	not identified	not identified	not identified
TW	2Ni	1	beetle, 872	Coleoptera	not identified	not identified	not identified
TW	2Ni	2	beetle, 873	Coleoptera	not identified	not identified	not identified
TW	2Ni	14	beetle, 874	Coleoptera	not identified	not identified	not identified
TW	2Ni	1	beetle, 884	Coleoptera	not identified	not identified	not identified
TW	2Ni	4	beetle, 891	Coleoptera	not identified	not identified	not identified
TW	2Ni	4	beetle, 893	Coleoptera	not identified	not identified	not identified
TW	2Ni	5	beetle, 929	Coleoptera	not identified	not identified	not identified
TW	2Ni	1	beetle, 933	Coleoptera	not identified	not identified	not identified
TW	2Ni	1	beetle, 934	Coleoptera	not identified	not identified	not identified
TW	2Ni	1	beetle, 937	Coleoptera	not identified	not identified	not identified
TW	2Ni	1	beetle, 939-941	Coleoptera	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
TW	2Ni	1	beetle, 957	Coleoptera	not identified	not identified	not identified
TW	2Ni	1	beetle, 999	Coleoptera	not identified	not identified	not identified
TW	2Ni	7	beetle, ground	Coleoptera	not identified	not identified	not identified
TW	2Ni	14	beetle, other	Coleoptera	not identified	not identified	not identified
TW	2Ni	1	beetle, small	Coleoptera	not identified	not identified	not identified
TW	2Ni	6	bristletail	not identified	not identified	not identified	not identified
TW	2Ni	1	bug, 1001	Hemiptera	not identified	not identified	not identified
TW	2Ni	1	bug, 870	Hemiptera	not identified	not identified	not identified
TW	2Ni	1	bug, 926	Hemiptera	not identified	not identified	not identified
TW	2Ni	1	bug, 928	Hemiptera	not identified	not identified	not identified
TW	2Ni	1	bug, 946	Hemiptera	not identified	not identified	not identified
TW	2Ni	1	bug, 961	Hemiptera	not identified	not identified	not identified
TW	2Ni	3	bug, other	Hemiptera	not identified	not identified	not identified
TW	2Ni	1	bug, other red	Hemiptera	not identified	not identified	not identified
TW	2Ni	6	caterpillar, 875	Lepidoptera	not identified	not identified	not identified
TW	2Ni	5	caterpillar, 877	Lepidoptera	not identified	not identified	not identified
TW	2Ni	2	caterpillar, 942-943	Lepidoptera	not identified	not identified	not identified
TW	2Ni	58	centipede, 881	not identified	not identified	not identified	not identified
TW	2Ni	4	centipede, 882	not identified	not identified	not identified	not identified
TW	2Ni	3	centipede, 944	not identified	not identified	not identified	not identified
TW	2Ni	7	cricket	Orthoptera	not identified	not identified	not identified
TW	2Ni	1	earth worm	Haplotaxida	not identified	not identified	not identified
TW	2Ni	2	insect, 869	not identified	not identified	not identified	not identified
TW	2Ni	7	insect, other	not identified	not identified	not identified	not identified
TW	2Ni	36	mite, red	Acariformes	Acariformes	not identified	not identified
TW	2Ni	1	mite, red 925	Acariformes	not identified	not identified	not identified
TW	2Ni	1	moth	Lepidoptera	not identified	not identified	not identified
TW	2Ni	1	scorpion, 938	Scorpiones	not identified	not identified	not identified
TW	2Ni	1	snail, 1006	not identified	not identified	not identified	not identified
TW	2Ni	3	spider	Araneae	not identified	not identified	not identified
TW	2Ni	1	spider, black 892	Araneae	not identified	not identified	not identified
TW	2Ni	1	spider, red	Araneae	not identified	not identified	not identified
TW	2Ni	21	spider, small	Araneae	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
TW	2Ni	2	spider, small red	Araneae	not identified	not identified	not identified
TW	2Ni	85	springtail	Collembola	not identified	not identified	not identified
TW	2Ni	1	toad	Anura	Bufonidae	Bufo	not identified
TW	2Ni	12	woodlouse	Isopoda	not identified	not identified	not identified
TW	2Ni	1	woodlouse, 954-955	Isopoda	not identified	not identified	not identified
TW	2Ni	1	worm	not identified	not identified	not identified	not identified
Bi	3AK	3	American Robin	Passeriformes	Turdidae	Turdus	migratorius
Bi	3AK	3	Boreal Chickadee	Passeriformes	Paridae	Poecile	hudsonica
Bi	3AK	7	Chickadee	Passeriformes	Paridae	not identified	not identified
Bi	3AK	7	Corvidae	Passeriformes	Corvidae	not identified	not identified
Bi	3AK	2	Dark-eyed Junco	Passeriformes	Emberizidae	Junco	hyemalis
Bi	3AK	14	Gray Jay	Passeriformes	Corvidae	Perisoreus	canadensis
Bi	3AK	39	Gull	Ciconiiformes	Laridae	not identified	not identified
Bi	3AK	3	Junco	Passeriformes	Emberizidae	Junco	not identified
Bi	3AK	1	Northern Flicker	Piciformes	Picidae	Colaptes	auratus
Bi	3AK	4	Sandhill Crane	Gruiformes	Gruidae	Grus	canadensis
Bi	3AK	302	Songbird	Passeriformes	not identified	not identified	not identified
Bi	3AK	99	Sparrow	Passeriformes	Emberizidae	not identified	not identified
Bi	3AK	200	squirrel	Rodentia	Sciuridae	Sciurus	not identified
Bi	3AK	1	Tit	not identified	not identified	not identified	not identified
Bi	3AK	1	White-crowned Sparrow	Passeriformes	Emberizidae	Zonotrichia	leucophrys
Bi	3AK	3	Woodpecker	Piciformes	Picidae	not identified	not identified
Bi	3AK	3	Yellow-rumped Warbler	Passeriformes	Parulidae	Dendroica	coronata
TW	3AK	12	ant	Hymenoptera	Formicidae	not identified	not identified
TW	3AK	2	ant, small	Hymenoptera	Formicidae	not identified	not identified
TW	3AK	1	bee	Hymenoptera	not identified	not identified	not identified
TW	3AK	8	beetle	Coleoptera	not identified	not identified	not identified
TW	3AK	17	beetle, underground-hiding	Coleoptera	not identified	not identified	not identified
TW	3AK	1	bug	Hemiptera	not identified	not identified	not identified
TW	3AK	1	caterpillar, black-hairy	Lepidoptera	not identified	not identified	not identified
TW	3AK	2	fly	Diptera	not identified	not identified	not identified
TW	3AK	1	grasshopper	Orthoptera	Acrididae	not identified	not identified
TW	3AK	4	green insect	not identified	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
TW	3AK	2	mite, red	Acariformes	not identified	not identified	not identified
TW	3AK	3	mouse	Rodentia	Muridae	not identified	not identified
TW	3AK	7	other insect	not identified	not identified	not identified	not identified
TW	3AK	91	spider	Araneae	not identified	not identified	not identified
TW	3AK	1	spider, small	Araneae	not identified	not identified	not identified
TW	3AK	3	spider, small black	Araneae	not identified	not identified	not identified
TW	3AK	14	spider, small red	Araneae	not identified	not identified	not identified
TW	3AK	7	spider, tiny	Araneae	not identified	not identified	not identified
TW	3AK	56	springtail	Collembola	not identified	not identified	not identified
TW	3AK	4	woodlouse	Isopoda	not identified	not identified	not identified
Bi	4Ru	4	Bird	not identified	not identified	not identified	not identified
Bi	4Ru	1	Blue Flank juv	not identified	not identified	not identified	not identified
Bi	4Ru	2	bluetail	Passeriformes	Muscicapidae	Tarsiger	not identified
Bi	4Ru	105	Chickadee	Passeriformes	Paridae	not identified	not identified
Bi	4Ru	2	Crow	Passeriformes	Corvidae	not identified	not identified
Bi	4Ru	2	Dove	Columbiformes	Columbidae	not identified	not identified
Bi	4Ru	3	Emberiza	Passeriformes	Emberizidae	Emberiza	not identified
Bi	4Ru	1	Falcon	Ciconiiformes	Falconidae	Falco	not identified
Bi	4Ru	1	Finch	Passeriformes	Fringillidae	not identified	not identified
Bi	4Ru	2	Flycatcher	Passeriformes	Muscicapidae	not identified	not identified
Bi	4Ru	3	Grasshopper Warbler	Passeriformes	Sylviidae	Locustella	naevia
Bi	4Ru	1	Gull	Ciconiiformes	Laridae	not identified	not identified
Bi	4Ru	4	Hazelgrouse	Galliformes	Phasianidae	Tetrastes	bonasia
Bi	4Ru	32	Jungle Crow	Passeriformes	Corvidae	Corvus	levaillantii
Bi	4Ru	1	Juv passerine	Passeriformes	not identified	not identified	not identified
Bi	4Ru	94	Kinglet	Passeriformes	Regulidae	Regulus	not identified
Bi	4Ru	1	Kohlmeise	Passeriformes	Paridae	Parus	major
Bi	4Ru	1	longtailed tit	Passeriformes	Paridae	not identified	not identified
Bi	4Ru	3	Merganser	Anseriformes	Anatidae	Mergus	merganser
Bi	4Ru	42	Nutcracker	Passeriformes	Corvidae	Nucifraga	not identified
Bi	4Ru	3	nuthatch	Passeriformes	Sittidae	Sitta	not identified
Bi	4Ru	6	Oriental Dove	Columbiformes	Columbidae	Streptopelia	orientalis
Bi	4Ru	8	Oriental Finch	Passeriformes	Fringillidae	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
Bi	4Ru	10	Oriental Greenfinch	Passeriformes	Fringillidae	Carduelis	sinica
Bi	4Ru	2	Oriental Pigeon	Columbiformes	Columbidae	not identified	not identified
Bi	4Ru	18	Pacific Swift	Apodiformes	Apodidae	Apus	pacificus
Bi	4Ru	4	passerine	Passeriformes	not identified	not identified	not identified
Bi	4Ru	2	Rain Call Bird	not identified	not identified	not identified	not identified
Bi	4Ru	5	Raptor	not identified	not identified	not identified	not identified
Bi	4Ru	1	Raven	Passeriformes	Corvidae	Corvus	not identified
Bi	4Ru	1	stellers sea eagle juv	Ciconiiformes	Accipitridae	Haliaeetus	pelagicus
Bi	4Ru	2	Tannenmeise	Passeriformes	Paridae	Periparus	ater
Bi	4Ru	2	Teseewee	not identified	not identified	not identified	not identified
Bi	4Ru	1	Thriller	not identified	not identified	not identified	not identified
Bi	4Ru	1	Thrush	Passeriformes	Turdidae	not identified	not identified
Bi	4Ru	1	Tistiwee	not identified	not identified	not identified	not identified
Bi	4Ru	1	Titi tititit	not identified	not identified	not identified	not identified
Bi	4Ru	11	Tsilp	not identified	not identified	not identified	not identified
Bi	4Ru	2	Wagtail	Passeriformes	Motacillidae	Motacilla	not identified
Bi	4Ru	38	Warbler	Passeriformes	not identified	not identified	not identified
Bi	4Ru	2	Weidenmeise	Passeriformes	Paridae	Poecile	montana
Bi	4Ru	37	Winter Wren	Passeriformes	Troglodytidae	Troglodytes	troglodytes
Bi	4Ru	30	wize	not identified	not identified	not identified	not identified
Bi	4Ru	6	wize wize	not identified	not identified	not identified	not identified
Bi	4Ru	10	Woodpecker	Piciformes	Picidae	not identified	not identified
TW	4Ru	1	aimbia	not identified	not identified	not identified	not identified
TW	4Ru	1	aimbia, little	not identified	not identified	not identified	not identified
TW	4Ru	5	Beetle	Coleoptera	not identified	not identified	not identified
TW	4Ru	3	bibienka	not identified	not identified	not identified	not identified
TW	4Ru	6	Carabidae	Coleoptera	Carabidae	not identified	not identified
TW	4Ru	1	caterpillar	Lepidoptera	not identified	not identified	not identified
TW	4Ru	6	Cenocosiets	Opiliones	not identified	not identified	not identified
TW	4Ru	3	Cestianka	Lithobiomorpha	Lithobiidae	Lithobius	not identified
TW	4Ru	1	changa	not identified	not identified	not identified	not identified
TW	4Ru	1	changa (2)	not identified	not identified	not identified	not identified
TW	4Ru	1	cinacost	not identified	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
TW	4Ru	54	Collembola	Collembola	not identified	not identified	not identified
TW	4Ru	1	collisea	not identified	not identified	not identified	not identified
TW	4Ru	4	costianka	Lithobiomorpha	Lithobiidae	Lithobius	not identified
TW	4Ru	26	cycsegusa	not identified	not identified	not identified	not identified
TW	4Ru	1	expoxata	not identified	not identified	not identified	not identified
TW	4Ru	3	fly little	Diptera	not identified	not identified	not identified
TW	4Ru	1	fly, small special	Diptera	not identified	not identified	not identified
TW	4Ru	1	insects	not identified	not identified	not identified	not identified
TW	4Ru	7	mouse	Rodentia	Muridae	not identified	not identified
TW	4Ru	1	nayesdink	not identified	not identified	not identified	not identified
TW	4Ru	1	nayesdink, little	not identified	not identified	not identified	not identified
TW	4Ru	20	Protura	Protura	not identified	not identified	not identified
TW	4Ru	1	Sinocoset	Opiliones	not identified	not identified	not identified
TW	4Ru	11	Spider	Araneae	not identified	not identified	not identified
TW	4Ru	6	spider with slim long legs	Araneae	not identified	not identified	not identified
TW	4Ru	11	spider, big	Araneae	not identified	not identified	not identified
TW	4Ru	25	spider, little	Araneae	not identified	not identified	not identified
TW	4Ru	2	spider, midsize	Araneae	not identified	not identified	not identified
TW	4Ru	1	spider, palekolane	Araneae	not identified	not identified	not identified
TW	4Ru	6	Staphilin	Staphylinidae	not identified	not identified	not identified
TW	4Ru	1	tick	Ixodida	not identified	not identified	not identified
TW	4Ru	1	ucene	not identified	not identified	not identified	not identified
TW	4Ru	17	worm	not identified	not identified	not identified	not identified
Bi	5PG	6	Balu	not identified	not identified	not identified	not identified
Bi	5PG	60	bird	not identified	not identified	not identified	not identified
Bi	5PG	1	Bird Chreak	not identified	not identified	not identified	not identified
Bi	5PG	1	bird fly over	not identified	not identified	not identified	not identified
Bi	5PG	1	bird, medium	not identified	not identified	not identified	not identified
Bi	5PG	1	Birds of Prey	not identified	not identified	not identified	not identified
Bi	5PG	3	Black Hawk	Ciconiiformes	Accipitridae	not identified	not identified
Bi	5PG	1	Broken Flute	not identified	not identified	not identified	not identified
Bi	5PG	6	call	not identified	not identified	not identified	not identified
Bi	5PG	1	Canopy Bird	not identified	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
Bi	5PG	1	Check bird	not identified	not identified	not identified	not identified
Bi	5PG	2	Chickchickchickachick	not identified	not identified	not identified	not identified
Bi	5PG	1	Chilk Twitz	not identified	not identified	not identified	not identified
Bi	5PG	1	Chilp	not identified	not identified	not identified	not identified
Bi	5PG	1	Ching	not identified	not identified	not identified	not identified
Bi	5PG	3	Chirp	not identified	not identified	not identified	not identified
Bi	5PG	1	chirp loud	not identified	not identified	not identified	not identified
Bi	5PG	2	Chitter	not identified	not identified	not identified	not identified
Bi	5PG	1	Clink	not identified	not identified	not identified	not identified
Bi	5PG	1	Cockatoo	Psittaciformes	Psittacidae	Cacatua	not identified
Bi	5PG	5	Craw, Bird of Paradise	Passeriformes	Paradisaeidae	not identified	not identified
Bi	5PG	26	dove	Columbiformes	Columbidae	not identified	not identified
Bi	5PG	1	dove, psurr deep	Columbiformes	Columbidae	not identified	not identified
Bi	5PG	1	falcon	Ciconiiformes	Falconidae	Falco	not identified
Bi	5PG	1	feep	not identified	not identified	not identified	not identified
Bi	5PG	1	Fiep	not identified	not identified	not identified	not identified
Bi	5PG	1	Fitz	not identified	not identified	not identified	not identified
Bi	5PG	1	flowerpiercer	not identified	not identified	not identified	not identified
Bi	5PG	23	Flute	not identified	not identified	not identified	not identified
Bi	5PG	1	Flute melodious	not identified	not identified	not identified	not identified
Bi	5PG	2	Flute song	not identified	not identified	not identified	not identified
Bi	5PG	1	Flycatcher	Passeriformes	Monarchidae	not identified	not identified
Bi	5PG	1	Flycatcher tschirrp	Passeriformes	Monarchidae	not identified	not identified
Bi	5PG	1	Flycatcher, similar willie	Passeriformes	Monarchidae	not identified	not identified
Bi	5PG	10	Fowl	Galliformes	not identified	not identified	not identified
Bi	5PG	2	fruit pecker	not identified	not identified	not identified	not identified
Bi	5PG	1	fruit pecker white cheek	not identified	not identified	not identified	not identified
Bi	5PG	5	gleaner	not identified	not identified	not identified	not identified
Bi	5PG	1	gleaner, white cheek	not identified	not identified	not identified	not identified
Bi	5PG	7	Hawk	Ciconiiformes	Accipitridae	not identified	not identified
Bi	5PG	9	Hornbill	Bucerotiformes	Bucerotidae	not identified	not identified
Bi	5PG	1	Jackah call	not identified	not identified	not identified	not identified
Bi	5PG	1	Jackljakl	not identified	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
Bi	5PG	2	Kau Kau, Bird of Paradise	Passeriformes	Paradisaeidae	not identified	not identified
Bi	5PG	1	loud call	not identified	not identified	not identified	not identified
Bi	5PG	8	melodious song	not identified	not identified	not identified	not identified
Bi	5PG	1	Melodious Song, like sylvia warbler	not identified	not identified	not identified	not identified
Bi	5PG	2	Palm Cockatoo	Psittaciformes	Psittacidae	Probosciger	aterrimus
Bi	5PG	9	Parakeet	Psittaciformes	Psittacidae	Aratinga	not identified
Bi	5PG	6	Parrot	Psittaciformes	Psittacidae	not identified	not identified
Bi	5PG	2	Parrot, little	Psittaciformes	Psittacidae	not identified	not identified
Bi	5PG	2	pewee like North American Pewee	not identified	not identified	not identified	not identified
Bi	5PG	1	Piwi	not identified	not identified	not identified	not identified
Bi	5PG	2	pschorr	not identified	not identified	not identified	not identified
Bi	5PG	1	Psitt	not identified	not identified	not identified	not identified
Bi	5PG	1	Queek	not identified	not identified	not identified	not identified
Bi	5PG	1	Quit	not identified	not identified	not identified	not identified
Bi	5PG	30	Rezina, rezina	Passeriformes	Paradisaeidae	not identified	not identified
Bi	5PG	1	schrill	not identified	not identified	not identified	not identified
Bi	5PG	3	song	not identified	not identified	not identified	not identified
Bi	5PG	34	Songbird	Passeriformes	not identified	not identified	not identified
Bi	5PG	1	Songbird little	Passeriformes	not identified	not identified	not identified
Bi	5PG	4	songbird tshirp	Passeriformes	not identified	not identified	not identified
Bi	5PG	1	Songbird tsilp	Passeriformes	not identified	not identified	not identified
Bi	5PG	6	Swallow	Passeriformes	Hirundinidae	not identified	not identified
Bi	5PG	7	swirrl	not identified	not identified	not identified	not identified
Bi	5PG	1	sylvia song	not identified	not identified	not identified	not identified
Bi	5PG	1	Thrush	Passeriformes	Turdidae	not identified	not identified
Bi	5PG	1	Trach trach	not identified	not identified	not identified	not identified
Bi	5PG	2	tschick	not identified	not identified	not identified	not identified
Bi	5PG	2	tschirp	not identified	not identified	not identified	not identified
Bi	5PG	2	tsi tsi	not identified	not identified	not identified	not identified
Bi	5PG	50	tsilp	not identified	not identified	not identified	not identified
Bi	5PG	1	Tsilp tsilp	not identified	not identified	not identified	not identified
Bi	5PG	2	Tsirp	not identified	not identified	not identified	not identified
Bi	5PG	1	wae wae wae	not identified	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
Bi	5PG	1	wake wake	not identified	not identified	not identified	not identified
Bi	5PG	1	warning call	not identified	not identified	not identified	not identified
Bi	5PG	28	White Cockatoo	Psittaciformes	Psittacidae	Cacatua	alba
Bi	5PG	1	Wieeh	not identified	not identified	not identified	not identified
Bi	5PG	3	Willie	not identified	not identified	not identified	not identified
Bi	5PG	2	witz	not identified	not identified	not identified	not identified
Bi	5PG	5	wiz wiz	not identified	not identified	not identified	not identified
Bi	5PG	6	Wize wize	not identified	not identified	not identified	not identified
Bi	5PG	5	woodpecker	Piciformes	Picidae	not identified	not identified
Bi	5PG	1	wren	Passeriformes	Troglodytidae	not identified	not identified
TW	5PG	1	ant, big	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	3	ant, big black	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	8	ant, big yellow	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	19	ant, black	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	1	ant, little	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	6	ant, little black	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	2	ant, little red	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	1	ant, medium black	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	2	ant, red	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	3	ant, tiny	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	22	ant, tiny black	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	12	ant, tiny red	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	1	ant, tiny yellow	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	5	ant, yellow	Hymenoptera	Formicidae	not identified	not identified
TW	5PG	1	bug	Hemiptera	not identified	not identified	not identified
TW	5PG	1	bug, coackroach type	Dictyoptera	not identified	not identified	not identified
TW	5PG	1	bug, little	Hemiptera	not identified	not identified	not identified
TW	5PG	1	bug, medium	Hemiptera	not identified	not identified	not identified
TW	5PG	1	bug, tiny	Hemiptera	not identified	not identified	not identified
TW	5PG	1	caterpillar	Lepidoptera	not identified	not identified	not identified
TW	5PG	45	Collembola	Collembola	not identified	not identified	not identified
TW	5PG	2	collembola long antennae	Collembola	not identified	not identified	not identified
TW	5PG	3	collembola, big yellow	Collembola	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
TW	5PG	1	collembola, black-yellow	Collembola	not identified	not identified	not identified
TW	5PG	2	collembola, yellow	Collembola	not identified	not identified	not identified
TW	5PG	3	earth grille, mid size long antennae	Orthoptera	not identified	not identified	not identified
TW	5PG	1	eintagsfliege, 4 wing	Ephemeroptera	not identified	not identified	not identified
TW	5PG	1	floh	Siphonaptera	not identified	not identified	not identified
TW	5PG	6	fly	Diptera	not identified	not identified	not identified
TW	5PG	1	fly with legs and antennae	Diptera	not identified	not identified	not identified
TW	5PG	1	fly, tiny	Diptera	not identified	not identified	not identified
TW	5PG	7	fruitfly	Diptera	not identified	not identified	not identified
TW	5PG	1	fruitfly black	Diptera	not identified	not identified	not identified
TW	5PG	1	fruitfly grey	Diptera	not identified	not identified	not identified
TW	5PG	2	fruitfly, blue	Diptera	not identified	not identified	not identified
TW	5PG	1	fruitfly, pink	Diptera	not identified	not identified	not identified
TW	5PG	9	fruitfly, white	Diptera	not identified	not identified	not identified
TW	5PG	1	Grille small	Orthoptera	not identified	not identified	not identified
TW	5PG	1	grille, mid size long antennae	Orthoptera	not identified	not identified	not identified
TW	5PG	1	insect	not identified	not identified	not identified	not identified
TW	5PG	1	kaefer middle	Coleoptera	not identified	not identified	not identified
TW	5PG	1	laufkaefer	Coleoptera	Carabidae	not identified	not identified
TW	5PG	3	marienkaeferlarve	Coleoptera	Coccinellidae	not identified	not identified
TW	5PG	3	milbe, red	Acariformes	not identified	not identified	not identified
TW	5PG	2	milbe, spring	Acariformes	not identified	not identified	not identified
TW	5PG	2	millipede, big	not identified	not identified	not identified	not identified
TW	5PG	1	millipede, small	not identified	not identified	not identified	not identified
TW	5PG	1	miskaefer medium	Coleoptera	Geotrupidae	not identified	not identified
TW	5PG	1	mosquito	Diptera	Culicidae	not identified	not identified
TW	5PG	1	mosquito, jumping	Diptera	Culicidae	not identified	not identified
TW	5PG	1	rainworm	Haplotaxida	Lumbricidae	not identified	not identified
TW	5PG	2	rainworm little	Haplotaxida	Lumbricidae	not identified	not identified
TW	5PG	1	schnellkaefer	Coleoptera	Elateridae	not identified	not identified
TW	5PG	4	spider, little	Araneae	not identified	not identified	not identified
TW	5PG	3	spider, little black	Araneae	not identified	not identified	not identified
TW	5PG	3	spider, little long legs	Araneae	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
TW	5PG	1	spider, medium	Araneae	not identified	not identified	not identified
TW	5PG	1	spider, tiny black	Araneae	not identified	not identified	not identified
TW	5PG	2	spring floh, blue	not identified	not identified	not identified	not identified
TW	5PG	8	springfloh	not identified	not identified	not identified	not identified
TW	5PG	5	springfloh mit antennae	not identified	not identified	not identified	not identified
TW	5PG	1	Springfloh yellow	not identified	not identified	not identified	not identified
TW	5PG	5	springfloh, long antennae	not identified	not identified	not identified	not identified
TW	5PG	1	tausenfuesser medium	not identified	not identified	not identified	not identified
TW	5PG	1	weevil medium	Coleoptera	Curculionidae	not identified	not identified
TW	5PG	1	wurm	not identified	not identified	not identified	not identified
Bi	6Ba	1	Brant	Anseriformes	Anatidae	Branta	bernicla
Bi	6Ba	1	Dowitcher	Ciconiiformes	Scolopacidae	Limnodromus	not identified
Bi	6Ba	18	Dunlin	Ciconiiformes	Scolopacidae	Calidris	alpina
Bi	6Ba	2	Eider Duck	Anseriformes	Anatidae	Somateria	mollissima
Bi	6Ba	1	Glaucous Gull	Ciconiiformes	Laridae	Larus	hyperboreus
Bi	6Ba	112	Lapland Bunting	Passeriformes	Emberizidae	Calcarius	lapponicus
Bi	6Ba	1	Lemming	Rodentia	Muridae	Lemmus	not identified
Bi	6Ba	48	Longbilled Dowitcher	Ciconiiformes	Scolopacidae	Limnodromus	scolopaceus
Bi	6Ba	1	Longtailed Duck	Anseriformes	Anatidae	Clangula	hyemalis
Bi	6Ba	1	Loon	Ciconiiformes	Gaviidae	Gavia	immer
Bi	6Ba	1	Pacific Loon	Ciconiiformes	Gaviidae	Gavia	pacifica
Bi	6Ba	1	Parasitic Jaeger	Ciconiiformes	Stercorariidae	Stercorarius	parasiticus
Bi	6Ba	37	Pectoral Sandpiper	Ciconiiformes	Scolopacidae	Calidris	melanotos
Bi	6Ba	1	Phalarope	Ciconiiformes	Scolopacidae	Phalaropus	not identified
Bi	6Ba	49	Pomarine Jaeger	Ciconiiformes	Stercorariidae	Stercorarius	pomarinus
Bi	6Ba	59	Red Phalarope	Ciconiiformes	Scolopacidae	Phalaropus	fulicarius
Bi	6Ba	13	Red-necked Phalarope	Ciconiiformes	Scolopacidae	Phalaropus	lobatus
Bi	6Ba	65	Semipalmated Sandpiper	Ciconiiformes	Scolopacidae	Calidris	pusilla
Bi	6Ba	1	Snow Bunting	Passeriformes	Emberizidae	Plectrophenax	nivalis
Bi	6Ba	2	Spectacled Eider	Anseriformes	Anatidae	Somateria	fischeri
Bi	6Ba	1	Swans	Anseriformes	Anatidae	Cygnus	not identified
Bi	6Ba	3	Western Sandpiper	Ciconiiformes	Scolopacidae	Calidris	mauri
TW	6Ba	4	beetle	Coleoptera	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
TW	6Ba	83	beetle, flat	Coleoptera	not identified	not identified	not identified
TW	6Ba	1	beetle, gold-green	Coleoptera	not identified	not identified	not identified
TW	6Ba	1	beetle, green	Coleoptera	not identified	not identified	not identified
TW	6Ba	1	beetle, little	Coleoptera	not identified	not identified	not identified
TW	6Ba	1	beetle, little green	Coleoptera	not identified	not identified	not identified
TW	6Ba	6	beetle, slim	Coleoptera	not identified	not identified	not identified
TW	6Ba	1	caterpillar worm	Lepidoptera	not identified	not identified	not identified
TW	6Ba	1	caterpillar, big	Lepidoptera	not identified	not identified	not identified
TW	6Ba	1	caterpillar, hairy	Lepidoptera	not identified	not identified	not identified
TW	6Ba	1	caterpillar, small	Lepidoptera	not identified	not identified	not identified
TW	6Ba	37	fly	Diptera	not identified	not identified	not identified
TW	6Ba	2	fly, little	Diptera	not identified	not identified	not identified
TW	6Ba	32	Fruitfly	Diptera	not identified	not identified	not identified
TW	6Ba	3	fruitfly, little	Diptera	not identified	not identified	not identified
TW	6Ba	8	fruitfly, tiny	Diptera	not identified	not identified	not identified
TW	6Ba	3	larvae	not identified	not identified	not identified	not identified
TW	6Ba	1	larvae big	not identified	not identified	not identified	not identified
TW	6Ba	1	larvae with legs	not identified	not identified	not identified	not identified
TW	6Ba	1	larvae, long	not identified	not identified	not identified	not identified
TW	6Ba	1	Marienkaeferlarve	Coleoptera	Coccinellidae	not identified	not identified
TW	6Ba	1	Microworm	not identified	not identified	not identified	not identified
TW	6Ba	20	Milbe	Acariformes	not identified	not identified	not identified
TW	6Ba	2	Milbe, micro	Acariformes	not identified	not identified	not identified
TW	6Ba	1	Milbe, tiny	Acariformes	not identified	not identified	not identified
TW	6Ba	22	mosquito	Diptera	Culicidae	not identified	not identified
TW	6Ba	1	Rueckenschwimmkaefer	Hemiptera	Notonectidae	not identified	not identified
TW	6Ba	22	Schuster	Diptera	Tipulidae	not identified	not identified
TW	6Ba	2	schuster, big	Diptera	Tipulidae	not identified	not identified
TW	6Ba	1	Schuster, large	Diptera	Tipulidae	not identified	not identified
TW	6Ba	1	Schuster, no wings	Diptera	Tipulidae	not identified	not identified
TW	6Ba	61	spider	Araneae	not identified	not identified	not identified
TW	6Ba	1	spider (underwater)	Araneae	not identified	not identified	not identified
TW	6Ba	3	spider, big	Araneae	not identified	not identified	not identified

Type	Study area	No of Obs.	Narrative	Order	Family	Genus	Species
TW	6Ba	15	spider, little	Araneae	not identified	not identified	not identified
TW	6Ba	125	spider, tiny	Araneae	not identified	not identified	not identified
TW	6Ba	8	Springmilbe	Acariformes	not identified	not identified	not identified
TW	6Ba	1	Springmilbe, tiny	Acariformes	not identified	not identified	not identified
TW	6Ba	3	springschwanz	Collembola	not identified	not identified	not identified

7.6 Random Forests Models with Hightest ROC Values

Study area	Type	Data	Model	Target narrative	ROC value
1CR	Bi	all	*Covariates*	Ani	0.856
1CR	Bi	aur	*Covariates*	Ani	n/a
1CR	Bi	ran	*Covariates*	Ani	0.927
1CR	Bi	sys	*Covariates*	Ani	0.751
1CR	Bi	vis	*Covariates*	Ani	0.714
1CR	Bi	all	*Interspecies*	Ani	0.858
1CR	Bi	aur	*Interspecies*	Ani	n/a
1CR	Bi	ran	*Interspecies*	Ani	0.927
1CR	Bi	sys	*Interspecies*	Ani	0.728
1CR	Bi	vis	*Interspecies*	Ani	0.714
1CR	Bi	all	*Covariates*	Dove	0.344
1CR	Bi	aur	*Covariates*	Dove	0.65
1CR	Bi	ran	*Covariates*	Dove	0.032
1CR	Bi	sys	*Covariates*	Dove	0.496
1CR	Bi	vis	*Covariates*	Dove	0.042
1CR	Bi	all	*Interspecies*	Dove	0.374
1CR	Bi	aur	*Interspecies*	Dove	0.672
1CR	Bi	ran	*Interspecies*	Dove	0.032
1CR	Bi	sys	*Interspecies*	Dove	0.496
1CR	Bi	vis	*Interspecies*	Dove	0.042
1CR	Bi	all	*Covariates*	Flycatcher	0.623
1CR	Bi	aur	*Covariates*	Flycatcher	0.626
1CR	Bi	ran	*Covariates*	Flycatcher	0.414
1CR	Bi	sys	*Covariates*	Flycatcher	0.620
1CR	Bi	vis	*Covariates*	Flycatcher	0.654
1CR	Bi	all	*Interspecies*	Flycatcher	0.578
1CR	Bi	aur	*Interspecies*	Flycatcher	0.581
1CR	Bi	ran	*Interspecies*	Flycatcher	0.327
1CR	Bi	sys	*Interspecies*	Flycatcher	0.58
1CR	Bi	vis	*Interspecies*	Flycatcher	0.649
1CR	Bi	all	*Covariates*	Great Kiskadee	0.698
1CR	Bi	aur	*Covariates*	Great Kiskadee	0.697
1CR	Bi	ran	*Covariates*	Great Kiskadee	0.753
1CR	Bi	sys	*Covariates*	Great Kiskadee	0.668
1CR	Bi	vis	*Covariates*	Great Kiskadee	0.643
1CR	Bi	all	*Interspecies*	Great Kiskadee	0.698
1CR	Bi	aur	*Interspecies*	Great Kiskadee	0.732
1CR	Bi	ran	*Interspecies*	Great Kiskadee	0.724
1CR	Bi	sys	*Interspecies*	Great Kiskadee	0.662
1CR	Bi	vis	*Interspecies*	Great Kiskadee	0.659
1CR	Bi	all	*Covariates*	Hummingbird	0.756
1CR	Bi	aur	*Covariates*	Hummingbird	0.608
1CR	Bi	ran	*Covariates*	Hummingbird	0.704
1CR	Bi	sys	*Covariates*	Hummingbird	0.752
1CR	Bi	vis	*Covariates*	Hummingbird	0.813
1CR	Bi	all	*Interspecies*	Hummingbird	0.738
1CR	Bi	aur	*Interspecies*	Hummingbird	0.584
1CR	Bi	ran	*Interspecies*	Hummingbird	0.692
1CR	Bi	sys	*Interspecies*	Hummingbird	0.734

Study area	Type	Data	Model	Target narrative	ROC value
1CR	Bi	vis	*Interspecies*	Hummingbird	0.797
1CR	Bi	all	*Covariates*	Kiskadee	0.655
1CR	Bi	aur	*Covariates*	Kiskadee	0.648
1CR	Bi	ran	*Covariates*	Kiskadee	n/a
1CR	Bi	sys	*Covariates*	Kiskadee	0.666
1CR	Bi	vis	*Covariates*	Kiskadee	0.046
1CR	Bi	all	*Interspecies*	Kiskadee	0.679
1CR	Bi	aur	*Interspecies*	Kiskadee	0.645
1CR	Bi	ran	*Interspecies*	Kiskadee	n/a
1CR	Bi	sys	*Interspecies*	Kiskadee	0.655
1CR	Bi	vis	*Interspecies*	Kiskadee	0.046
1CR	Bi	all	*Covariates*	Manakin	0.851
1CR	Bi	aur	*Covariates*	Manakin	0.741
1CR	Bi	ran	*Covariates*	Manakin	0.753
1CR	Bi	sys	*Covariates*	Manakin	0.815
1CR	Bi	vis	*Covariates*	Manakin	n/a
1CR	Bi	all	*Interspecies*	Manakin	0.857
1CR	Bi	aur	*Interspecies*	Manakin	0.741
1CR	Bi	ran	*Interspecies*	Manakin	0.709
1CR	Bi	sys	*Interspecies*	Manakin	0.825
1CR	Bi	vis	*Interspecies*	Manakin	n/a
1CR	Bi	all	*Plot*	Manakin	0.646
1CR	Bi	all	*Covariates*	Mealy Parrot	0.930
1CR	Bi	aur	*Covariates*	Mealy Parrot	n/a
1CR	Bi	ran	*Covariates*	Mealy Parrot	n/a
1CR	Bi	sys	*Covariates*	Mealy Parrot	0.883
1CR	Bi	vis	*Covariates*	Mealy Parrot	0.87
1CR	Bi	all	*Interspecies*	Mealy Parrot	0.908
1CR	Bi	aur	*Interspecies*	Mealy Parrot	n/a
1CR	Bi	ran	*Interspecies*	Mealy Parrot	n/a
1CR	Bi	sys	*Interspecies*	Mealy Parrot	0.883
1CR	Bi	vis	*Interspecies*	Mealy Parrot	0.892
1CR	Bi	all	*Plot*	Mealy Parrot	0.063
1CR	Bi	all	*Covariates*	Oropendula	0.631
1CR	Bi	aur	*Covariates*	Oropendula	0.535
1CR	Bi	ran	*Covariates*	Oropendula	0.524
1CR	Bi	sys	*Covariates*	Oropendula	0.641
1CR	Bi	vis	*Covariates*	Oropendula	0.6
1CR	Bi	all	*Interspecies*	Oropendula	0.635
1CR	Bi	aur	*Interspecies*	Oropendula	0.524
1CR	Bi	ran	*Interspecies*	Oropendula	0.505
1CR	Bi	sys	*Interspecies*	Oropendula	0.642
1CR	Bi	vis	*Interspecies*	Oropendula	0.576
1CR	Bi	all	*Plot*	Oropendula	0.018
1CR	Bi	all	*Covariates*	Parrot	0.820
1CR	Bi	aur	*Covariates*	Parrot	0.897
1CR	Bi	ran	*Covariates*	Parrot	0.037
1CR	Bi	sys	*Covariates*	Parrot	0.951
1CR	Bi	vis	*Covariates*	Parrot	0.753
1CR	Bi	all	*Interspecies*	Parrot	0.818
1CR	Bi	aur	*Interspecies*	Parrot	0.897
1CR	Bi	ran	*Interspecies*	Parrot	0.032
1CR	Bi	sys	*Interspecies*	Parrot	0.906

Study area	**Type**	**Data**	**Model**	**Target narrative**	**ROC value**
1CR	Bi	vis	*Interspecies*	Parrot	0.789
1CR	Bi	all	*Plot*	Parrot	0.438
1CR	Bi	all	*Covariates*	Parrot, large	0.870
1CR	Bi	aur	*Covariates*	Parrot, large	0.804
1CR	Bi	ran	*Covariates*	Parrot, large	n/a
1CR	Bi	sys	*Covariates*	Parrot, large	0.841
1CR	Bi	vis	*Covariates*	Parrot, large	0.916
1CR	Bi	all	*Interspecies*	Parrot, large	0.847
1CR	Bi	aur	*Interspecies*	Parrot, large	0.804
1CR	Bi	ran	*Interspecies*	Parrot, large	n/a
1CR	Bi	sys	*Interspecies*	Parrot, large	0.846
1CR	Bi	vis	*Interspecies*	Parrot, large	0.918
1CR	Bi	all	*Plot*	Parrot, large	0.476
1CR	Bi	all	*Covariates*	Scarlet-rumped Tanager	0.747
1CR	Bi	aur	*Covariates*	Scarlet-rumped Tanager	n/a
1CR	Bi	ran	*Covariates*	Scarlet-rumped Tanager	0.463
1CR	Bi	sys	*Covariates*	Scarlet-rumped Tanager	0.729
1CR	Bi	vis	*Covariates*	Scarlet-rumped Tanager	0.481
1CR	Bi	all	*Interspecies*	Scarlet-rumped Tanager	0.748
1CR	Bi	aur	*Interspecies*	Scarlet-rumped Tanager	n/a
1CR	Bi	ran	*Interspecies*	Scarlet-rumped Tanager	0.276
1CR	Bi	sys	*Interspecies*	Scarlet-rumped Tanager	0.729
1CR	Bi	vis	*Interspecies*	Scarlet-rumped Tanager	0.481
1CR	Bi	all	*Plot*	Scarlet-rumped Tanager	0.938
1CR	Bi	all	*Covariates*	Seedeater	0.798
1CR	Bi	aur	*Covariates*	Seedeater	0.731
1CR	Bi	ran	*Covariates*	Seedeater	0.774
1CR	Bi	sys	*Covariates*	Seedeater	0.851
1CR	Bi	vis	*Covariates*	Seedeater	0.721
1CR	Bi	all	*Interspecies*	Seedeater	0.812
1CR	Bi	aur	*Interspecies*	Seedeater	0.636
1CR	Bi	ran	*Interspecies*	Seedeater	0.752
1CR	Bi	sys	*Interspecies*	Seedeater	0.858
1CR	Bi	vis	*Interspecies*	Seedeater	0.711
1CR	Bi	all	*Plot*	Seedeater	0.962
1CR	Bi	all	*Covariates*	Tanager	0.811
1CR	Bi	aur	*Covariates*	Tanager	n/a
1CR	Bi	ran	*Covariates*	Tanager	0.853
1CR	Bi	sys	*Covariates*	Tanager	0.820
1CR	Bi	vis	*Covariates*	Tanager	0.631
1CR	Bi	all	*Interspecies*	Tanager	0.797
1CR	Bi	aur	*Interspecies*	Tanager	n/a
1CR	Bi	ran	*Interspecies*	Tanager	0.853
1CR	Bi	sys	*Interspecies*	Tanager	0.795
1CR	Bi	vis	*Interspecies*	Tanager	0.599
1CR	Bi	all	*Plot*	Tanager	0.958
1CR	Bi	all	*Covariates*	Toucan	0.706
1CR	Bi	aur	*Covariates*	Toucan	0.045
1CR	Bi	ran	*Covariates*	Toucan	n/a
1CR	Bi	sys	*Covariates*	Toucan	0.649
1CR	Bi	vis	*Covariates*	Toucan	0.801
1CR	Bi	all	*Interspecies*	Toucan	0.652
1CR	Bi	aur	*Interspecies*	Toucan	0.045

Study area	Type	Data	Model	Target narrative	ROC value
1CR	Bi	ran	*Interspecies*	Toucan	n/a
1CR	Bi	sys	*Interspecies*	Toucan	0.595
1CR	Bi	vis	*Interspecies*	Toucan	0.809
1CR	Bi	all	*Plot*	Toucan	0.567
1CR	Bi	all	*Covariates*	Turkey Vulture	0.622
1CR	Bi	aur	*Covariates*	Turkey Vulture	n/a
1CR	Bi	ran	*Covariates*	Turkey Vulture	n/a
1CR	Bi	sys	*Covariates*	Turkey Vulture	0.726
1CR	Bi	vis	*Covariates*	Turkey Vulture	0.32
1CR	Bi	all	*Interspecies*	Turkey Vulture	0.624
1CR	Bi	aur	*Interspecies*	Turkey Vulture	n/a
1CR	Bi	ran	*Interspecies*	Turkey Vulture	n/a
1CR	Bi	sys	*Interspecies*	Turkey Vulture	0.672
1CR	Bi	vis	*Interspecies*	Turkey Vulture	0.182
1CR	Bi	all	*Plot*	Turkey Vulture	0.768
1CR	Bi	all	*Covariates*	Woodpecker	0.585
1CR	Bi	aur	*Covariates*	Woodpecker	0.73
1CR	Bi	ran	*Covariates*	Woodpecker	0.648
1CR	Bi	sys	*Covariates*	Woodpecker	0.553
1CR	Bi	vis	*Covariates*	Woodpecker	0.392
1CR	Bi	all	*Interspecies*	Woodpecker	0.577
1CR	Bi	aur	*Interspecies*	Woodpecker	0.732
1CR	Bi	ran	*Interspecies*	Woodpecker	0.581
1CR	Bi	sys	*Interspecies*	Woodpecker	0.535
1CR	Bi	vis	*Interspecies*	Woodpecker	0.366
1CR	Bi	all	*Plot*	Woodpecker	0.377
2Ni	Bi	all	*Covariates*	Ani	0.591
2Ni	Bi	all	*Interspecies*	Ani	0.321
2Ni	Bi	all	*Plot*	Ani	0.385
2Ni	Bi	aur	*Covariates*	Ani	0.076
2Ni	Bi	aur	*Interspecies*	Ani	0.038
2Ni	Bi	ran	*Covariates*	Ani	0.036
2Ni	Bi	ran	*Interspecies*	Ani	0.036
2Ni	Bi	sys	*Covariates*	Ani	0.695
2Ni	Bi	sys	*Interspecies*	Ani	0.498
2Ni	Bi	vis	*Covariates*	Ani	0.336
2Ni	Bi	vis	*Interspecies*	Ani	0.211
2Ni	Bi	all	*Covariates*	Banded Wren	0.780
2Ni	Bi	all	*Interspecies*	Banded Wren	0.757
2Ni	Bi	all	*Plot*	Banded Wren	0.674
2Ni	Bi	aur	*Covariates*	Banded Wren	0.541
2Ni	Bi	aur	*Interspecies*	Banded Wren	0.54
2Ni	Bi	ran	*Covariates*	Banded Wren	0.67
2Ni	Bi	ran	*Interspecies*	Banded Wren	0.604
2Ni	Bi	sys	*Covariates*	Banded Wren	0.790
2Ni	Bi	sys	*Interspecies*	Banded Wren	0.756
2Ni	Bi	vis	*Covariates*	Banded Wren	0.398
2Ni	Bi	vis	*Interspecies*	Banded Wren	0.272
2Ni	Bi	all	*Covariates*	Dove	0.747
2Ni	Bi	all	*Interspecies*	Dove	0.679
2Ni	Bi	all	*Plot*	Dove	0.693
2Ni	Bi	aur	*Covariates*	Dove	0.508
2Ni	Bi	aur	*Interspecies*	Dove	0.505

Study area	Type	Data	Model	Target narrative	ROC value
2Ni	Bi	ran	*Covariates*	Dove	n/a
2Ni	Bi	ran	*Interspecies*	Dove	n/a
2Ni	Bi	sys	*Covariates*	Dove	0.695
2Ni	Bi	sys	*Interspecies*	Dove	0.623
2Ni	Bi	vis	*Covariates*	Dove	0.833
2Ni	Bi	vis	*Interspecies*	Dove	0.834
2Ni	Bi	all	*Covariates*	Flycatcher	0.717
2Ni	Bi	all	*Interspecies*	Flycatcher	0.637
2Ni	Bi	all	*Plot*	Flycatcher	0.604
2Ni	Bi	aur	*Covariates*	Flycatcher	0.642
2Ni	Bi	aur	*Interspecies*	Flycatcher	0.787
2Ni	Bi	ran	*Covariates*	Flycatcher	0.024
2Ni	Bi	ran	*Interspecies*	Flycatcher	0.152
2Ni	Bi	sys	*Covariates*	Flycatcher	0.928
2Ni	Bi	sys	*Interspecies*	Flycatcher	0.843
2Ni	Bi	vis	*Covariates*	Flycatcher	n/a
2Ni	Bi	vis	*Interspecies*	Flycatcher	n/a
2Ni	Bi	all	*Covariates*	Gray Hawk	0.759
2Ni	Bi	all	*Interspecies*	Gray Hawk	0.738
2Ni	Bi	all	*Plot*	Gray Hawk	0.510
2Ni	Bi	aur	*Covariates*	Gray Hawk	0.805
2Ni	Bi	aur	*Interspecies*	Gray Hawk	0.748
2Ni	Bi	ran	*Covariates*	Gray Hawk	0.232
2Ni	Bi	ran	*Interspecies*	Gray Hawk	0.152
2Ni	Bi	sys	*Covariates*	Gray Hawk	0.767
2Ni	Bi	sys	*Interspecies*	Gray Hawk	0.793
2Ni	Bi	vis	*Covariates*	Gray Hawk	0.682
2Ni	Bi	vis	*Interspecies*	Gray Hawk	0.712
2Ni	Bi	all	*Covariates*	Hawk	0.506
2Ni	Bi	all	*Interspecies*	Hawk	0.546
2Ni	Bi	all	*Plot*	Hawk	0.728
2Ni	Bi	aur	*Covariates*	Hawk	0.63
2Ni	Bi	aur	*Interspecies*	Hawk	0.628
2Ni	Bi	ran	*Covariates*	Hawk	0.048
2Ni	Bi	ran	*Interspecies*	Hawk	0.036
2Ni	Bi	sys	*Covariates*	Hawk	0.580
2Ni	Bi	sys	*Interspecies*	Hawk	0.57
2Ni	Bi	vis	*Covariates*	Hawk	0.044
2Ni	Bi	vis	*Interspecies*	Hawk	0.039
2Ni	Bi	all	*Covariates*	Parakeet	0.480
2Ni	Bi	all	*Interspecies*	Parakeet	0.283
2Ni	Bi	all	*Plot*	Parakeet	0.290
2Ni	Bi	aur	*Covariates*	Parakeet	n/a
2Ni	Bi	aur	*Interspecies*	Parakeet	n/a
2Ni	Bi	ran	*Covariates*	Parakeet	0.119
2Ni	Bi	ran	*Interspecies*	Parakeet	0.036
2Ni	Bi	sys	*Covariates*	Parakeet	0.176
2Ni	Bi	sys	*Interspecies*	Parakeet	0.042
2Ni	Bi	vis	*Covariates*	Parakeet	0.274
2Ni	Bi	vis	*Interspecies*	Parakeet	0.229
2Ni	Bi	all	*Covariates*	Parrot	0.910
2Ni	Bi	all	*Interspecies*	Parrot	0.91
2Ni	Bi	all	*Plot*	Parrot	0.624

Study area	Type	Data	Model	Target narrative	ROC value
2Ni	Bi	aur	*Covariates*	Parrot	0.042
2Ni	Bi	aur	*Interspecies*	Parrot	0.038
2Ni	Bi	ran	*Covariates*	Parrot	0.762
2Ni	Bi	ran	*Interspecies*	Parrot	0.811
2Ni	Bi	sys	*Covariates*	Parrot	0.867
2Ni	Bi	sys	*Interspecies*	Parrot	0.869
2Ni	Bi	vis	*Covariates*	Parrot	0.897
2Ni	Bi	vis	*Interspecies*	Parrot	0.898
2Ni	Bi	all	*Covariates*	Parrot, large	0.592
2Ni	Bi	all	*Interspecies*	Parrot, large	0.562
2Ni	Bi	all	*Plot*	Parrot, large	0.243
2Ni	Bi	aur	*Covariates*	Parrot, large	0.042
2Ni	Bi	aur	*Interspecies*	Parrot, large	0.038
2Ni	Bi	ran	*Covariates*	Parrot, large	0.036
2Ni	Bi	ran	*Interspecies*	Parrot, large	0.036
2Ni	Bi	sys	*Covariates*	Parrot, large	0.624
2Ni	Bi	sys	*Interspecies*	Parrot, large	0.516
2Ni	Bi	vis	*Covariates*	Parrot, large	0.378
2Ni	Bi	vis	*Interspecies*	Parrot, large	0.332
2Ni	Bi	all	*Covariates*	Swallow	0.283
2Ni	Bi	all	*Interspecies*	Swallow	0.201
2Ni	Bi	all	*Plot*	Swallow	0.424
2Ni	Bi	aur	*Covariates*	Swallow	0.038
2Ni	Bi	aur	*Interspecies*	Swallow	0.038
2Ni	Bi	ran	*Covariates*	Swallow	0.036
2Ni	Bi	ran	*Interspecies*	Swallow	0.036
2Ni	Bi	sys	*Covariates*	Swallow	0.475
2Ni	Bi	sys	*Interspecies*	Swallow	0.42
2Ni	Bi	vis	*Covariates*	Swallow	0.357
2Ni	Bi	vis	*Interspecies*	Swallow	0.183
2Ni	Bi	all	*Covariates*	Turkey Vulture	0.750
2Ni	Bi	all	*Interspecies*	Turkey Vulture	0.67
2Ni	Bi	all	*Plot*	Turkey Vulture	0.498
2Ni	Bi	aur	*Covariates*	Turkey Vulture	n/a
2Ni	Bi	aur	*Interspecies*	Turkey Vulture	n/a
2Ni	Bi	ran	*Covariates*	Turkey Vulture	0.679
2Ni	Bi	ran	*Interspecies*	Turkey Vulture	0.679
2Ni	Bi	sys	*Covariates*	Turkey Vulture	0.640
2Ni	Bi	sys	*Interspecies*	Turkey Vulture	0.544
2Ni	Bi	vis	*Covariates*	Turkey Vulture	0.576
2Ni	Bi	vis	*Interspecies*	Turkey Vulture	0.533
2Ni	Bi	all	*Covariates*	White-throated Magpie Jay	0.628
2Ni	Bi	all	*Interspecies*	White-throated Magpie Jay	0.586
2Ni	Bi	all	*Plot*	White-throated Magpie Jay	0.601
2Ni	Bi	aur	*Covariates*	White-throated Magpie Jay	0.734
2Ni	Bi	aur	*Interspecies*	White-throated Magpie Jay	0.705
2Ni	Bi	ran	*Covariates*	White-throated Magpie Jay	0.573
2Ni	Bi	ran	*Interspecies*	White-throated Magpie	0.514

Study area	**Type**	**Data**	**Model**	**Target narrative**	**ROC value**
				Jay	
2Ni	Bi	sys	*Covariates*	White-throated Magpie Jay	0.598
2Ni	Bi	sys	*Interspecies*	White-throated Magpie Jay	0.574
2Ni	Bi	vis	*Covariates*	White-throated Magpie Jay	0.587
2Ni	Bi	vis	*Interspecies*	White-throated Magpie Jay	0.565
2Ni	Bi	all	*Covariates*	Woodpecker	0.651
2Ni	Bi	all	*Interspecies*	Woodpecker	0.61
2Ni	Bi	all	*Plot*	Woodpecker	0.569
2Ni	Bi	aur	*Covariates*	Woodpecker	0.59
2Ni	Bi	aur	*Interspecies*	Woodpecker	0.511
2Ni	Bi	ran	*Covariates*	Woodpecker	0.104
2Ni	Bi	ran	*Interspecies*	Woodpecker	0.146
2Ni	Bi	sys	*Covariates*	Woodpecker	0.667
2Ni	Bi	sys	*Interspecies*	Woodpecker	0.602
2Ni	Bi	vis	*Covariates*	Woodpecker	0.502
2Ni	Bi	vis	*Interspecies*	Woodpecker	0.479
3AK	Bi	all	*Covariates*	Chickadee	0.909
3AK	Bi	all	*Interspecies*	Chickadee	0.912
3AK	Bi	all	*Plot*	Chickadee	0.769
3AK	Bi	aur	*Covariates*	Chickadee	0.933
3AK	Bi	aur	*Interspecies*	Chickadee	0.933
3AK	Bi	ran	*Covariates*	Chickadee	n/a
3AK	Bi	ran	*Interspecies*	Chickadee	n/a
3AK	Bi	sys	*Covariates*	Chickadee	0.911
3AK	Bi	sys	*Interspecies*	Chickadee	0.888
3AK	Bi	vis	*Covariates*	Chickadee	n/a
3AK	Bi	vis	*Interspecies*	Chickadee	n/a
3AK	Bi	all	*Covariates*	Gull	0.570
3AK	Bi	all	*Interspecies*	Gull	0.574
3AK	Bi	all	*Plot*	Gull	0.019
3AK	Bi	aur	*Covariates*	Gull	n/a
3AK	Bi	aur	*Interspecies*	Gull	n/a
3AK	Bi	ran	*Covariates*	Gull	n/a
3AK	Bi	ran	*Interspecies*	Gull	n/a
3AK	Bi	sys	*Covariates*	Gull	0.531
3AK	Bi	sys	*Interspecies*	Gull	0.327
3AK	Bi	vis	*Covariates*	Gull	0.279
3AK	Bi	vis	*Interspecies*	Gull	0.214
3AK	Bi	all	*Covariates*	Sparrow	0.642
3AK	Bi	all	*Interspecies*	Sparrow	0.649
3AK	Bi	all	*Plot*	Sparrow	0.430
3AK	Bi	aur	*Covariates*	Sparrow	0.528
3AK	Bi	aur	*Interspecies*	Sparrow	0.509
3AK	Bi	ran	*Covariates*	Sparrow	0.623
3AK	Bi	ran	*Interspecies*	Sparrow	0.647
3AK	Bi	sys	*Covariates*	Sparrow	0.632
3AK	Bi	sys	*Interspecies*	Sparrow	0.624
3AK	Bi	vis	*Covariates*	Sparrow	0.832
3AK	Bi	vis	*Interspecies*	Sparrow	0.822
3AK	Bi	all	*Covariates*	squirrel	0.555

Study area	**Type**	**Data**	**Model**	**Target narrative**	**ROC value**
3AK	Bi	all	*Interspecies*	squirrel	0.564
3AK	Bi	all	*Plot*	Squirrel	0.855
3AK	Bi	aur	*Covariates*	squirrel	0.467
3AK	Bi	aur	*Interspecies*	squirrel	0.478
3AK	Bi	ran	*Covariates*	squirrel	0.401
3AK	Bi	ran	*Interspecies*	squirrel	0.412
3AK	Bi	sys	*Covariates*	squirrel	0.566
3AK	Bi	sys	*Interspecies*	squirrel	0.563
3AK	Bi	vis	*Covariates*	squirrel	0.917
3AK	Bi	vis	*Interspecies*	squirrel	0.917
4Ru	Bi	all	*Covariates*	Chickadee	0.629
4Ru	Bi	all	*Interspecies*	Chickadee	0.647
4Ru	Bi	all	*Plot*	Chickadee	0.649
4Ru	Bi	aur	*Covariates*	Chickadee	0.623
4Ru	Bi	aur	*Interspecies*	Chickadee	0.64
4Ru	Bi	ran	*Covariates*	Chickadee	0.528
4Ru	Bi	ran	*Interspecies*	Chickadee	0.528
4Ru	Bi	sys	*Covariates*	Chickadee	0.658
4Ru	Bi	sys	*Interspecies*	Chickadee	0.66
4Ru	Bi	vis	*Covariates*	Chickadee	0.587
4Ru	Bi	vis	*Interspecies*	Chickadee	0.601
4Ru	Bi	all	*Covariates*	Jungle Crow	0.665
4Ru	Bi	all	*Interspecies*	Jungle Crow	0.689
4Ru	Bi	all	*Plot*	Jungle Crow	0.402
4Ru	Bi	aur	*Covariates*	Jungle Crow	0.799
4Ru	Bi	aur	*Interspecies*	Jungle Crow	0.765
4Ru	Bi	ran	*Covariates*	Jungle Crow	0.862
4Ru	Bi	ran	*Interspecies*	Jungle Crow	0.862
4Ru	Bi	sys	*Covariates*	Jungle Crow	0.574
4Ru	Bi	sys	*Interspecies*	Jungle Crow	0.634
4Ru	Bi	vis	*Covariates*	Jungle Crow	0.119
4Ru	Bi	vis	*Interspecies*	Jungle Crow	0.034
4Ru	Bi	all	*Covariates*	Kinglet	0.625
4Ru	Bi	all	*Interspecies*	Kinglet	0.613
4Ru	Bi	all	*Plot*	Kinglet	0.034
4Ru	Bi	aur	*Covariates*	Kinglet	0.638
4Ru	Bi	aur	*Interspecies*	Kinglet	0.637
4Ru	Bi	ran	*Covariates*	Kinglet	0.583
4Ru	Bi	ran	*Interspecies*	Kinglet	0.552
4Ru	Bi	sys	*Covariates*	Kinglet	0.576
4Ru	Bi	sys	*Interspecies*	Kinglet	0.588
4Ru	Bi	vis	*Covariates*	Kinglet	0.626
4Ru	Bi	vis	*Interspecies*	Kinglet	0.629
4Ru	Bi	all	*Covariates*	Nutcracker	0.685
4Ru	Bi	all	*Interspecies*	Nutcracker	0.685
4Ru	Bi	all	*Plot*	Nutcracker	0.478
4Ru	Bi	aur	*Covariates*	Nutcracker	0.622
4Ru	Bi	aur	*Interspecies*	Nutcracker	0.643
4Ru	Bi	ran	*Covariates*	Nutcracker	0.862
4Ru	Bi	ran	*Interspecies*	Nutcracker	0.862
4Ru	Bi	sys	*Covariates*	Nutcracker	0.644
4Ru	Bi	sys	*Interspecies*	Nutcracker	0.659
4Ru	Bi	vis	*Covariates*	Nutcracker	0.742

Study area	Type	Data	Model	Target narrative	ROC value
4Ru	Bi	vis	*Interspecies*	Nutcracker	0.663
4Ru	Bi	all	*Covariates*	Oriental Dove	0.494
4Ru	Bi	all	*Interspecies*	Oriental Dove	0.494
4Ru	Bi	all	*Plot*	Oriental Dove	0.370
4Ru	Bi	aur	*Covariates*	Oriental Dove	0.5
4Ru	Bi	aur	*Interspecies*	Oriental Dove	0.262
4Ru	Bi	ran	*Covariates*	Oriental Dove	n/a
4Ru	Bi	ran	*Interspecies*	Oriental Dove	n/a
4Ru	Bi	sys	*Covariates*	Oriental Dove	0.538
4Ru	Bi	sys	*Interspecies*	Oriental Dove	0.538
4Ru	Bi	vis	*Covariates*	Oriental Dove	0.039
4Ru	Bi	vis	*Interspecies*	Oriental Dove	0.051
4Ru	Bi	all	*Covariates*	Oriental Finch	0.701
4Ru	Bi	all	*Interspecies*	Oriental Finch	0.801
4Ru	Bi	all	*Plot*	Oriental Finch	0.226
4Ru	Bi	aur	*Covariates*	Oriental Finch	0.291
4Ru	Bi	aur	*Interspecies*	Oriental Finch	0.191
4Ru	Bi	ran	*Covariates*	Oriental Finch	0.862
4Ru	Bi	ran	*Interspecies*	Oriental Finch	0.862
4Ru	Bi	sys	*Covariates*	Oriental Finch	0.756
4Ru	Bi	sys	*Interspecies*	Oriental Finch	0.572
4Ru	Bi	vis	*Covariates*	Oriental Finch	0.14
4Ru	Bi	vis	*Interspecies*	Oriental Finch	0.201
4Ru	Bi	all	*Covariates*	Oriental Greenfinch	0.487
4Ru	Bi	all	*Interspecies*	Oriental Greenfinch	0.475
4Ru	Bi	all	*Plot*	Oriental Greenfinch	0.087
4Ru	Bi	aur	*Covariates*	Oriental Greenfinch	0.417
4Ru	Bi	aur	*Interspecies*	Oriental Greenfinch	0.427
4Ru	Bi	ran	*Covariates*	Oriental Greenfinch	n/a
4Ru	Bi	ran	*Interspecies*	Oriental Greenfinch	n/a
4Ru	Bi	sys	*Covariates*	Oriental Greenfinch	0.473
4Ru	Bi	sys	*Interspecies*	Oriental Greenfinch	0.493
4Ru	Bi	vis	*Covariates*	Oriental Greenfinch	n/a
4Ru	Bi	vis	*Interspecies*	Oriental Greenfinch	n/a
4Ru	Bi	all	*Covariates*	Pacific Swift	0.734
4Ru	Bi	all	*Interspecies*	Pacific Swift	0.72
4Ru	Bi	all	*Plot*	Pacific Swift	0.194
4Ru	Bi	aur	*Covariates*	Pacific Swift	0.78
4Ru	Bi	aur	*Interspecies*	Pacific Swift	0.756
4Ru	Bi	ran	*Covariates*	Pacific Swift	0.633
4Ru	Bi	ran	*Interspecies*	Pacific Swift	0.607
4Ru	Bi	sys	*Covariates*	Pacific Swift	0.714
4Ru	Bi	sys	*Interspecies*	Pacific Swift	0.696
4Ru	Bi	vis	*Covariates*	Pacific Swift	0.577
4Ru	Bi	vis	*Interspecies*	Pacific Swift	0.58
4Ru	Bi	all	*Covariates*	Raptor	0.802
4Ru	Bi	all	*Interspecies*	Raptor	0.821
4Ru	Bi	all	*Plot*	Raptor	0.500
4Ru	Bi	aur	*Covariates*	Raptor	0.771
4Ru	Bi	aur	*Interspecies*	Raptor	0.771
4Ru	Bi	ran	*Covariates*	Raptor	n/a
4Ru	Bi	ran	*Interspecies*	Raptor	n/a
4Ru	Bi	sys	*Covariates*	Raptor	0.746

Study area	Type	Data	Model	Target narrative	ROC value
4Ru	Bi	sys	*Interspecies*	Raptor	0.768
4Ru	Bi	vis	*Covariates*	Raptor	n/a
4Ru	Bi	vis	*Interspecies*	Raptor	n/a
4Ru	Bi	all	*Covariates*	Tsilp	0.547
4Ru	Bi	all	*Interspecies*	Tsilp	0.583
4Ru	Bi	all	*Plot*	Tsilp	0.431
4Ru	Bi	aur	*Covariates*	Tsilp	0.598
4Ru	Bi	aur	*Interspecies*	Tsilp	0.521
4Ru	Bi	ran	*Covariates*	Tsilp	n/a
4Ru	Bi	ran	*Interspecies*	Tsilp	n/a
4Ru	Bi	sys	*Covariates*	Tsilp	0.490
4Ru	Bi	sys	*Interspecies*	Tsilp	0.501
4Ru	Bi	vis	*Covariates*	Tsilp	n/a
4Ru	Bi	vis	*Interspecies*	Tsilp	n/a
4Ru	Bi	all	*Covariates*	Warbler	0.631
4Ru	Bi	all	*Interspecies*	Warbler	0.634
4Ru	Bi	all	*Plot*	Warbler	0.548
4Ru	Bi	aur	*Covariates*	Warbler	0.658
4Ru	Bi	aur	*Interspecies*	Warbler	0.651
4Ru	Bi	ran	*Covariates*	Warbler	n/a
4Ru	Bi	ran	*Interspecies*	Warbler	n/a
4Ru	Bi	sys	*Covariates*	Warbler	0.576
4Ru	Bi	sys	*Interspecies*	Warbler	0.569
4Ru	Bi	vis	*Covariates*	Warbler	0.238
4Ru	Bi	vis	*Interspecies*	Warbler	0.115
4Ru	Bi	all	*Covariates*	Winter Wren	0.691
4Ru	Bi	all	*Interspecies*	Winter Wren	0.68
4Ru	Bi	all	*Plot*	Winter Wren	0.576
4Ru	Bi	aur	*Covariates*	Winter Wren	0.665
4Ru	Bi	aur	*Interspecies*	Winter Wren	0.667
4Ru	Bi	ran	*Covariates*	Winter Wren	n/a
4Ru	Bi	ran	*Interspecies*	Winter Wren	n/a
4Ru	Bi	sys	*Covariates*	Winter Wren	0.667
4Ru	Bi	sys	*Interspecies*	Winter Wren	0.666
4Ru	Bi	vis	*Covariates*	Winter Wren	n/a
4Ru	Bi	vis	*Interspecies*	Winter Wren	n/a
4Ru	Bi	all	*Covariates*	wize	0.650
4Ru	Bi	all	*Interspecies*	wize	0.633
4Ru	Bi	all	*Plot*	wize	0.438
4Ru	Bi	aur	*Covariates*	wize	0.659
4Ru	Bi	aur	*Interspecies*	wize	0.653
4Ru	Bi	ran	*Covariates*	wize	0.515
4Ru	Bi	ran	*Interspecies*	wize	0.515
4Ru	Bi	sys	*Covariates*	wize	0.622
4Ru	Bi	sys	*Interspecies*	wize	0.614
4Ru	Bi	vis	*Covariates*	wize	0.216
4Ru	Bi	vis	*Interspecies*	wize	0.205
4Ru	Bi	all	*Covariates*	wize wize	0.797
4Ru	Bi	all	*Interspecies*	wize wize	0.797
4Ru	Bi	all	*Plot*	wize wize	0.000
4Ru	Bi	aur	*Covariates*	wize wize	0.803
4Ru	Bi	aur	*Interspecies*	wize wize	0.803
4Ru	Bi	ran	*Covariates*	wize wize	n/a

Study area	**Type**	**Data**	**Model**	**Target narrative**	**ROC value**
4Ru	Bi	ran	*Interspecies*	wize wize	n/a
4Ru	Bi	sys	*Covariates*	wize wize	0.799
4Ru	Bi	sys	*Interspecies*	wize wize	0.781
4Ru	Bi	vis	*Covariates*	wize wize	n/a
4Ru	Bi	vis	*Interspecies*	wize wize	n/a
4Ru	Bi	all	*Covariates*	Woodpecker	0.572
4Ru	Bi	all	*Interspecies*	Woodpecker	0.559
4Ru	Bi	all	*Plot*	Woodpecker	0.566
4Ru	Bi	aur	*Covariates*	Woodpecker	0.531
4Ru	Bi	aur	*Interspecies*	Woodpecker	0.519
4Ru	Bi	ran	*Covariates*	Woodpecker	0.034
4Ru	Bi	ran	*Interspecies*	Woodpecker	0.034
4Ru	Bi	sys	*Covariates*	Woodpecker	0.519
4Ru	Bi	sys	*Interspecies*	Woodpecker	0.52
4Ru	Bi	vis	*Covariates*	Woodpecker	n/a
4Ru	Bi	vis	*Interspecies*	Woodpecker	n/a
5PG	Bi	all	*Covariates*	Balu	0.070
5PG	Bi	all	*Interspecies*	Balu	0.04
5PG	Bi	aur	*Covariates*	Balu	0.073
5PG	Bi	aur	*Interspecies*	Balu	0.042
5PG	Bi	ran	*Covariates*	Balu	n/a
5PG	Bi	ran	*Interspecies*	Balu	n/a
5PG	Bi	sys	*Covariates*	Balu	0.072
5PG	Bi	sys	*Interspecies*	Balu	0.042
5PG	Bi	vis	*Covariates*	Balu	n/a
5PG	Bi	vis	*Interspecies*	Balu	n/a
5PG	Bi	all	*Covariates*	call	0.583
5PG	Bi	all	*Interspecies*	call	0.446
5PG	Bi	aur	*Covariates*	call	0.473
5PG	Bi	aur	*Interspecies*	call	0.393
5PG	Bi	ran	*Covariates*	call	n/a
5PG	Bi	ran	*Interspecies*	call	n/a
5PG	Bi	sys	*Covariates*	call	0.496
5PG	Bi	sys	*Interspecies*	call	0.272
5PG	Bi	vis	*Covariates*	call	n/a
5PG	Bi	vis	*Interspecies*	call	n/a
5PG	Bi	all	*Covariates*	Craw, Bird of Paradise	0.507
5PG	Bi	all	*Interspecies*	Craw, Bird of Paradise	0.318
5PG	Bi	aur	*Covariates*	Craw, Bird of Paradise	0.367
5PG	Bi	aur	*Interspecies*	Craw, Bird of Paradise	0.227
5PG	Bi	ran	*Covariates*	Craw, Bird of Paradise	n/a
5PG	Bi	ran	*Interspecies*	Craw, Bird of Paradise	n/a
5PG	Bi	sys	*Covariates*	Craw, Bird of Paradise	0.621
5PG	Bi	sys	*Interspecies*	Craw, Bird of Paradise	0.465
5PG	Bi	vis	*Covariates*	Craw, Bird of Paradise	n/a
5PG	Bi	vis	*Interspecies*	Craw, Bird of Paradise	n/a
5PG	Bi	all	*Covariates*	Flute	0.578
5PG	Bi	all	*Interspecies*	Flute	0.519
5PG	Bi	aur	*Covariates*	Flute	0.451
5PG	Bi	aur	*Interspecies*	Flute	0.458
5PG	Bi	ran	*Covariates*	Flute	0.383
5PG	Bi	ran	*Interspecies*	Flute	0.288
5PG	Bi	sys	*Covariates*	Flute	0.488

Study area	Type	Data	Model	Target narrative	ROC value
5PG	Bi	sys	*Interspecies*	Flute	0.499
5PG	Bi	vis	*Covariates*	Flute	n/a
5PG	Bi	vis	*Interspecies*	Flute	n/a
5PG	Bi	all	*Covariates*	Fowl	0.654
5PG	Bi	all	*Interspecies*	Fowl	0.6
5PG	Bi	aur	*Covariates*	Fowl	0.607
5PG	Bi	aur	*Interspecies*	Fowl	0.722
5PG	Bi	ran	*Covariates*	Fowl	0.031
5PG	Bi	ran	*Interspecies*	Fowl	0.031
5PG	Bi	sys	*Covariates*	Fowl	0.691
5PG	Bi	sys	*Interspecies*	Fowl	0.691
5PG	Bi	vis	*Covariates*	Fowl	0.038
5PG	Bi	vis	*Interspecies*	Fowl	0.038
5PG	Bi	all	*Covariates*	gleaner	0.750
5PG	Bi	all	*Interspecies*	gleaner	0.683
5PG	Bi	aur	*Covariates*	gleaner	n/a
5PG	Bi	aur	*Interspecies*	gleaner	n/a
5PG	Bi	ran	*Covariates*	gleaner	0.031
5PG	Bi	ran	*Interspecies*	gleaner	0.031
5PG	Bi	sys	*Covariates*	gleaner	0.815
5PG	Bi	sys	*Interspecies*	gleaner	0.731
5PG	Bi	vis	*Covariates*	gleaner	0.174
5PG	Bi	vis	*Interspecies*	gleaner	0.149
5PG	Bi	all	*Covariates*	Hawk	0.322
5PG	Bi	all	*Interspecies*	Hawk	0.268
5PG	Bi	aur	*Covariates*	Hawk	0.571
5PG	Bi	aur	*Interspecies*	Hawk	0.589
5PG	Bi	ran	*Covariates*	Hawk	0.031
5PG	Bi	ran	*Interspecies*	Hawk	0.031
5PG	Bi	sys	*Covariates*	Hawk	0.350
5PG	Bi	sys	*Interspecies*	Hawk	0.275
5PG	Bi	vis	*Covariates*	Hawk	0.301
5PG	Bi	vis	*Interspecies*	Hawk	0.117
5PG	Bi	all	*Covariates*	Hornbill	0.291
5PG	Bi	all	*Interspecies*	Hornbill	0.24
5PG	Bi	aur	*Covariates*	Hornbill	0.109
5PG	Bi	aur	*Interspecies*	Hornbill	0.04
5PG	Bi	ran	*Covariates*	Hornbill	0.041
5PG	Bi	ran	*Interspecies*	Hornbill	0.031
5PG	Bi	sys	*Covariates*	Hornbill	0.390
5PG	Bi	sys	*Interspecies*	Hornbill	0.294
5PG	Bi	vis	*Covariates*	Hornbill	0.746
5PG	Bi	vis	*Interspecies*	Hornbill	0.859
5PG	Bi	all	*Covariates*	melodious song	0.308
5PG	Bi	all	*Interspecies*	melodious song	0.193
5PG	Bi	aur	*Covariates*	melodious song	0.315
5PG	Bi	aur	*Interspecies*	melodious song	0.25
5PG	Bi	ran	*Covariates*	melodious song	0.417
5PG	Bi	ran	*Interspecies*	melodious song	0.156
5PG	Bi	sys	*Covariates*	melodious song	0.250
5PG	Bi	sys	*Interspecies*	melodious song	0.174
5PG	Bi	vis	*Covariates*	melodious song	n/a
5PG	Bi	vis	*Interspecies*	melodious song	n/a

Study area	Type	Data	Model	Target narrative	ROC value
5PG	Bi	all	*Covariates*	Parakeet	0.884
5PG	Bi	all	*Interspecies*	Parakeet	0.842
5PG	Bi	all	*Plot*	Parakeet	0.537
5PG	Bi	aur	*Covariates*	Parakeet	n/a
5PG	Bi	aur	*Interspecies*	Parakeet	n/a
5PG	Bi	ran	*Covariates*	Parakeet	0.457
5PG	Bi	ran	*Interspecies*	Parakeet	0.33
5PG	Bi	sys	*Covariates*	Parakeet	0.932
5PG	Bi	sys	*Interspecies*	Parakeet	0.823
5PG	Bi	vis	*Covariates*	Parakeet	0.512
5PG	Bi	vis	*Interspecies*	Parakeet	0.341
5PG	Bi	all	*Covariates*	Parrot	0.320
5PG	Bi	all	*Interspecies*	Parrot	0.257
5PG	Bi	all	*Plot*	Parrot	0.000
5PG	Bi	aur	*Covariates*	Parrot	0.044
5PG	Bi	aur	*Interspecies*	Parrot	0.044
5PG	Bi	ran	*Covariates*	Parrot	0.021
5PG	Bi	ran	*Interspecies*	Parrot	0.021
5PG	Bi	sys	*Covariates*	Parrot	0.072
5PG	Bi	sys	*Interspecies*	Parrot	0.042
5PG	Bi	vis	*Covariates*	Parrot	0.053
5PG	Bi	vis	*Interspecies*	Parrot	0.024
5PG	Bi	all	*Covariates*	Rezina, rezina	0.733
5PG	Bi	all	*Interspecies*	Rezina, rezina	0.676
5PG	Bi	all	*Plot*	Rezina, rezina	0.208
5PG	Bi	aur	*Covariates*	Rezina, rezina	0.753
5PG	Bi	aur	*Interspecies*	Rezina, rezina	0.754
5PG	Bi	ran	*Covariates*	Rezina, rezina	0.687
5PG	Bi	ran	*Interspecies*	Rezina, rezina	0.7
5PG	Bi	sys	*Covariates*	Rezina, rezina	0.751
5PG	Bi	sys	*Interspecies*	Rezina, rezina	0.701
5PG	Bi	vis	*Covariates*	Rezina, rezina	0.843
5PG	Bi	vis	*Interspecies*	Rezina, rezina	0.8
5PG	Bi	all	*Covariates*	Swallow	0.795
5PG	Bi	all	*Interspecies*	Swallow	0.839
5PG	Bi	all	*Plot*	Swallow	0.031
5PG	Bi	aur	*Covariates*	Swallow	0.045
5PG	Bi	aur	*Interspecies*	Swallow	0.045
5PG	Bi	ran	*Covariates*	Swallow	0.865
5PG	Bi	ran	*Interspecies*	Swallow	0.865
5PG	Bi	sys	*Covariates*	Swallow	0.804
5PG	Bi	sys	*Interspecies*	Swallow	0.841
5PG	Bi	vis	*Covariates*	Swallow	0.496
5PG	Bi	vis	*Interspecies*	Swallow	0.496
5PG	Bi	all	*Covariates*	swirrl	0.554
5PG	Bi	all	*Interspecies*	swirrl	0.535
5PG	Bi	all	*Plot*	swirrl	0.056
5PG	Bi	aur	*Covariates*	swirrl	0.556
5PG	Bi	aur	*Interspecies*	swirrl	0.502
5PG	Bi	ran	*Covariates*	swirrl	n/a
5PG	Bi	ran	*Interspecies*	swirrl	n/a
5PG	Bi	sys	*Covariates*	swirrl	0.613
5PG	Bi	sys	*Interspecies*	swirrl	0.539

Study area	**Type**	**Data**	**Model**	**Target narrative**	**ROC value**
5PG	Bi	vis	*Covariates*	swirrl	n/a
5PG	Bi	vis	*Interspecies*	swirrl	n/a
5PG	Bi	all	*Covariates*	tsilp	0.686
5PG	Bi	all	*Interspecies*	tsilp	0.654
5PG	Bi	all	*Plot*	tsilp	0.196
5PG	Bi	aur	*Covariates*	tsilp	0.627
5PG	Bi	aur	*Interspecies*	tsilp	0.627
5PG	Bi	ran	*Covariates*	tsilp	0.667
5PG	Bi	ran	*Interspecies*	tsilp	0.599
5PG	Bi	sys	*Covariates*	tsilp	0.661
5PG	Bi	sys	*Interspecies*	tsilp	0.624
5PG	Bi	vis	*Covariates*	tsilp	n/a
5PG	Bi	vis	*Interspecies*	tsilp	n/a
5PG	Bi	all	*Covariates*	White Cockatoo	0.825
5PG	Bi	all	*Interspecies*	White Cockatoo	0.777
5PG	Bi	all	*Plot*	White Cockatoo	0.466
5PG	Bi	aur	*Covariates*	White Cockatoo	0.674
5PG	Bi	aur	*Interspecies*	White Cockatoo	0.516
5PG	Bi	ran	*Covariates*	White Cockatoo	n/a
5PG	Bi	ran	*Interspecies*	White Cockatoo	n/a
5PG	Bi	sys	*Covariates*	White Cockatoo	0.830
5PG	Bi	sys	*Interspecies*	White Cockatoo	0.75
5PG	Bi	vis	*Covariates*	White Cockatoo	0.721
5PG	Bi	vis	*Interspecies*	White Cockatoo	0.543
5PG	Bi	all	*Covariates*	wiz wiz	0.591
5PG	Bi	all	*Interspecies*	wiz wiz	0.433
5PG	Bi	all	*Plot*	wiz wiz	0.635
5PG	Bi	aur	*Covariates*	wiz wiz	0.66
5PG	Bi	aur	*Interspecies*	wiz wiz	0.574
5PG	Bi	ran	*Covariates*	wiz wiz	n/a
5PG	Bi	ran	*Interspecies*	wiz wiz	n/a
5PG	Bi	sys	*Covariates*	wiz wiz	0.557
5PG	Bi	sys	*Interspecies*	wiz wiz	0.616
5PG	Bi	vis	*Covariates*	wiz wiz	n/a
5PG	Bi	vis	*Interspecies*	wiz wiz	n/a
5PG	Bi	all	*Covariates*	Wize wize	0.274
5PG	Bi	all	*Interspecies*	Wize wize	0.241
5PG	Bi	all	*Plot*	Wize wize	0.448
5PG	Bi	aur	*Covariates*	Wize wize	0.428
5PG	Bi	aur	*Interspecies*	Wize wize	0.433
5PG	Bi	ran	*Covariates*	Wize wize	n/a
5PG	Bi	ran	*Interspecies*	Wize wize	n/a
5PG	Bi	sys	*Covariates*	Wize wize	0.228
5PG	Bi	sys	*Interspecies*	Wize wize	0.097
5PG	Bi	vis	*Covariates*	Wize wize	0.038
5PG	Bi	vis	*Interspecies*	Wize wize	0.038
5PG	Bi	all	*Covariates*	woodpecker	0.372
5PG	Bi	all	*Interspecies*	woodpecker	0.295
5PG	Bi	all	*Plot*	woodpecker	0.308
5PG	Bi	aur	*Covariates*	woodpecker	0.134
5PG	Bi	aur	*Interspecies*	woodpecker	0.073
5PG	Bi	ran	*Covariates*	woodpecker	0.031
5PG	Bi	ran	*Interspecies*	woodpecker	0.031

Study area	Type	Data	Model	Target narrative	ROC value
5PG	Bi	sys	*Covariates*	woodpecker	0.370
5PG	Bi	sys	*Interspecies*	woodpecker	0.248
5PG	Bi	vis	*Covariates*	woodpecker	0.242
5PG	Bi	vis	*Interspecies*	woodpecker	0.156
6Ba	Bi	all	*Covariates*	Dunlin	0.547
6Ba	Bi	all	*Interspecies*	Dunlin	0.541
6Ba	Bi	all	*Plot*	Dunlin	0.597
6Ba	Bi	ran	*Covariates*	Dunlin	0.256
6Ba	Bi	ran	*Interspecies*	Dunlin	0.139
6Ba	Bi	sys	*Covariates*	Dunlin	0.602
6Ba	Bi	sys	*Interspecies*	Dunlin	0.602
6Ba	Bi	all	*Covariates*	Lapland Bunting	0.523
6Ba	Bi	all	*Interspecies*	Lapland Bunting	0.521
6Ba	Bi	all	*Plot*	Lapland Bunting	0.428
6Ba	Bi	ran	*Covariates*	Lapland Bunting	0.666
6Ba	Bi	ran	*Interspecies*	Lapland Bunting	0.627
6Ba	Bi	sys	*Covariates*	Lapland Bunting	0.468
6Ba	Bi	sys	*Interspecies*	Lapland Bunting	0.46
6Ba	Bi	all	*Covariates*	Longbilled Dowitcher	0.561
6Ba	Bi	all	*Interspecies*	Longbilled Dowitcher	0.56
6Ba	Bi	all	*Plot*	Longbilled Dowitcher	0.394
6Ba	Bi	ran	*Covariates*	Longbilled Dowitcher	0.5
6Ba	Bi	ran	*Interspecies*	Longbilled Dowitcher	0.484
6Ba	Bi	sys	*Covariates*	Longbilled Dowitcher	0.545
6Ba	Bi	sys	*Interspecies*	Longbilled Dowitcher	0.546
6Ba	Bi	all	*Covariates*	Pectoral Sandpiper	0.653
6Ba	Bi	all	*Interspecies*	Pectoral Sandpiper	0.671
6Ba	Bi	all	*Plot*	Pectoral Sandpiper	0.393
6Ba	Bi	ran	*Covariates*	Pectoral Sandpiper	n/a
6Ba	Bi	ran	*Interspecies*	Pectoral Sandpiper	n/a
6Ba	Bi	sys	*Covariates*	Pectoral Sandpiper	0.613
6Ba	Bi	sys	*Interspecies*	Pectoral Sandpiper	0.615
6Ba	Bi	all	*Covariates*	Pomarine Jaeger	0.629
6Ba	Bi	all	*Interspecies*	Pomarine Jaeger	0.626
6Ba	Bi	all	*Plot*	Pomarine Jaeger	0.597
6Ba	Bi	ran	*Covariates*	Pomarine Jaeger	0.331
6Ba	Bi	ran	*Interspecies*	Pomarine Jaeger	0.307
6Ba	Bi	sys	*Covariates*	Pomarine Jaeger	0.709
6Ba	Bi	sys	*Interspecies*	Pomarine Jaeger	0.716
6Ba	Bi	all	*Covariates*	Red Phalarope	0.585
6Ba	Bi	all	*Interspecies*	Red Phalarope	0.577
6Ba	Bi	all	*Plot*	Red Phalarope	0.620
6Ba	Bi	ran	*Covariates*	Red Phalarope	0.387
6Ba	Bi	ran	*Interspecies*	Red Phalarope	0.371
6Ba	Bi	sys	*Covariates*	Red Phalarope	0.589
6Ba	Bi	sys	*Interspecies*	Red Phalarope	0.594
6Ba	Bi	all	*Covariates*	Red-necked Phalarope	0.630
6Ba	Bi	all	*Interspecies*	Red-necked Phalarope	0.682
6Ba	Bi	all	*Plot*	Red-necked Phalarope	0.304
6Ba	Bi	ran	*Covariates*	Red-necked Phalarope	0.66
6Ba	Bi	ran	*Interspecies*	Red-necked Phalarope	0.634
6Ba	Bi	sys	*Covariates*	Red-necked Phalarope	0.576
6Ba	Bi	sys	*Interspecies*	Red-necked Phalarope	0.59

Study area	Type	Data	Model	Target narrative	ROC value
6Ba	Bi	all	*Covariates*	Semipalmated Sandpiper	0.458
6Ba	Bi	all	*Interspecies*	Semipalmated Sandpiper	0.463
6Ba	Bi	all	*Plot*	Semipalmated Sandpiper	0.403
6Ba	Bi	ran	*Covariates*	Semipalmated Sandpiper	0.536
6Ba	Bi	sys	*Covariates*	Semipalmated Sandpiper	0.461
6Ba	Bi	sys	*Interspecies*	Semipalmated Sandpiper	0.462
1CR	DT	all	*Covariates*	Butterfly, yellow	0.906
1CR	DT	ran	*Covariates*	Butterfly, yellow	0.4
1CR	DT	sys	*Covariates*	Butterfly, yellow	0.969
1CR	DT	all	*Interspecies*	Butterfly, yellow	0.953
1CR	DT	ran	*Interspecies*	Butterfly, yellow	0.6
1CR	DT	sys	*Interspecies*	Butterfly, yellow	0.969
1CR	DT	all	*Plot*	Butterfly, yellow	0.815
2Ni	DT	all	*Covariates*	Butterfly, white	0.629
2Ni	DT	all	*Interspecies*	Butterfly, white	0.609
2Ni	DT	all	*Plot*	Butterfly, white	0.305
2Ni	DT	ran	*Covariates*	Butterfly, white	0.857
2Ni	DT	ran	*Interspecies*	Butterfly, white	0.821
2Ni	DT	sys	*Covariates*	Butterfly, white	0.528
2Ni	DT	sys	*Interspecies*	Butterfly, white	0.487
2Ni	DT	all	*Covariates*	Butterfly, yellow	0.65
2Ni	DT	all	*Interspecies*	Butterfly, yellow	0.665
2Ni	DT	all	*Plot*	Butterfly, yellow	0.456
2Ni	DT	ran	*Covariates*	Butterfly, yellow	n/a
2Ni	DT	ran	*Interspecies*	Butterfly, yellow	n/a
2Ni	DT	sys	*Covariates*	Butterfly, yellow	0.598
2Ni	DT	sys	*Interspecies*	Butterfly, yellow	0.574
1CR	TW	all	*Covariates*	ant	0.847
1CR	TW	all	*Interspecies*	ant	0.831
1CR	TW	all	*Covariates*	ant, small	0.634
1CR	TW	all	*Interspecies*	ant, small	0.667
1CR	TW	all	*Covariates*	cricket	0.838
1CR	TW	all	*Interspecies*	cricket	0.816
1CR	TW	all	*Covariates*	spider	0.44
1CR	TW	all	*Interspecies*	spider	0.446
2Ni	TW	all	*Covariates*	ant	0.696
2Ni	TW	all	*Interspecies*	ant	0.699
2Ni	TW	all	*Covariates*	ant, small	0.661
2Ni	TW	all	*Interspecies*	ant, small	0.612
2Ni	TW	all	*Covariates*	ant, small red	0.581
2Ni	TW	all	*Interspecies*	ant, small red	0.496
2Ni	TW	all	*Covariates*	beetle, 866	0.652
2Ni	TW	all	*Interspecies*	beetle, 866	0.473
2Ni	TW	all	*Covariates*	beetle, 868	0.724
2Ni	TW	all	*Interspecies*	beetle, 868	0.72
2Ni	TW	all	*Covariates*	beetle, 874	0.736
2Ni	TW	all	*Interspecies*	beetle, 874	0.722
2Ni	TW	all	*Covariates*	beetle, 929	0.53
2Ni	TW	all	*Interspecies*	beetle, 929	0.142
2Ni	TW	all	*Covariates*	beetle, ground	0.461
2Ni	TW	all	*Interspecies*	beetle, ground	0.181
2Ni	TW	all	*Covariates*	bristletail	0.379
2Ni	TW	all	*Interspecies*	bristletail	0.232

Study area	Type	Data	Model	Target narrative	ROC value
2Ni	TW	all	*Covariates*	caterpillar, 875	0.637
2Ni	TW	all	*Interspecies*	caterpillar, 875	0.487
2Ni	TW	all	*Covariates*	caterpillar, 877	0.324
2Ni	TW	all	*Interspecies*	caterpillar, 877	0.089
2Ni	TW	all	*Covariates*	centipede, 881	0.77
2Ni	TW	all	*Interspecies*	centipede, 881	0.728
2Ni	TW	all	*Covariates*	cricket	0.773
2Ni	TW	all	*Interspecies*	cricket	0.68
2Ni	TW	all	*Covariates*	spider, small	0.604
2Ni	TW	all	*Interspecies*	spider, small	0.519
2Ni	TW	all	*Covariates*	springtail	0.958
2Ni	TW	all	*Interspecies*	springtail	0.925
3AK	TW	all	*Covariates*	ant	0.85
3AK	TW	all	*Interspecies*	ant	0.833
3AK	TW	all	*Covariates*	beetle	0.365
3AK	TW	all	*Interspecies*	beetle	0.349
3AK	TW	all	*Covariates*	beetle, underground-hiding	0.676
3AK	TW	all	*Interspecies*	beetle, underground-hiding	0.696
3AK	TW	all	*Covariates*	spider	0.604
3AK	TW	all	*Interspecies*	spider	0.567
3AK	TW	all	*Covariates*	spider, small red	0.724
3AK	TW	all	*Interspecies*	spider, small red	0.746
3AK	TW	all	*Covariates*	spider, tiny	0.506
3AK	TW	all	*Interspecies*	spider, tiny	0.463
3AK	TW	all	*Covariates*	springtail	0.951
3AK	TW	all	*Interspecies*	springtail	0.939
4Ru	TW	all	*Covariates*	Beetle	0.441
4Ru	TW	all	*Interspecies*	Beetle	0.421
4Ru	TW	all	*Covariates*	Carabidae	0.76
4Ru	TW	all	*Interspecies*	Carabidae	0.763
4Ru	TW	all	*Covariates*	Collembola	0.616
4Ru	TW	all	*Interspecies*	Collembola	0.614
4Ru	TW	all	*Covariates*	cycsegusa	0.74
4Ru	TW	all	*Interspecies*	cycsegusa	0.723
4Ru	TW	all	*Covariates*	mouse	0.83
4Ru	TW	all	*Interspecies*	mouse	0.817
4Ru	TW	all	*Covariates*	Protura	0.709
4Ru	TW	all	*Interspecies*	Protura	0.681
4Ru	TW	all	*Covariates*	Spider	0.223
4Ru	TW	all	*Interspecies*	Spider	0.124
4Ru	TW	all	*Covariates*	spider with slim long legs	0.897
4Ru	TW	all	*Interspecies*	spider with slim long legs	0.897
4Ru	TW	all	*Covariates*	spider, big	0.694
4Ru	TW	all	*Interspecies*	spider, big	0.666
4Ru	TW	all	*Covariates*	spider, little	0.628
4Ru	TW	all	*Interspecies*	spider, little	0.627
4Ru	TW	all	*Covariates*	Staphilin	0.658
4Ru	TW	all	*Interspecies*	Staphilin	0.604
4Ru	TW	all	*Covariates*	worm	0.645
4Ru	TW	all	*Interspecies*	worm	0.613
5PG	TW	all	*Covariates*	ant, big yellow	0.955

Study area	Type	Data	Model	Target narrative	ROC value
5PG	TW	all	*Interspecies*	ant, big yellow	0.927
5PG	TW	all	*Covariates*	ant, black	0.498
5PG	TW	all	*Interspecies*	ant, black	0.525
5PG	TW	all	*Covariates*	ant, little black	0.644
5PG	TW	all	*Interspecies*	ant, little black	0.6
5PG	TW	all	*Covariates*	ant, tiny black	0.39
5PG	TW	all	*Interspecies*	ant, tiny black	0.393
5PG	TW	all	*Covariates*	ant, tiny red	0.915
5PG	TW	all	*Interspecies*	ant, tiny red	0.855
5PG	TW	all	*Covariates*	ant, yellow	0.734
5PG	TW	all	*Interspecies*	ant, yellow	0.658
5PG	TW	all	*Covariates*	fly	0.565
5PG	TW	all	*Interspecies*	fly	0.527
5PG	TW	all	*Covariates*	fruitfly	0.603
5PG	TW	all	*Interspecies*	fruitfly	0.561
5PG	TW	all	*Covariates*	fruitfly, white	0.795
5PG	TW	all	*Interspecies*	fruitfly, white	0.783
5PG	TW	all	*Covariates*	springfloh	0.51
5PG	TW	all	*Interspecies*	springfloh	0.385
5PG	TW	all	*Covariates*	springfloh mit antennae	0.84
5PG	TW	all	*Interspecies*	springfloh mit antennae	0.818
5PG	TW	all	*Covariates*	springfloh, long antennae	0.561
5PG	TW	all	*Interspecies*	springfloh, long antennae	0.475
6Ba	TW	all	*Covariates*	beetle, flat	0.678
6Ba	TW	all	*Interspecies*	beetle, flat	0.639
6Ba	TW	all	*Covariates*	beetle, slim	0.802
6Ba	TW	all	*Interspecies*	beetle, slim	0.661
6Ba	TW	all	*Covariates*	fly	0.696
6Ba	TW	all	*Interspecies*	fly	0.679
6Ba	TW	all	*Covariates*	Fruitfly	0.841
6Ba	TW	all	*Interspecies*	Fruitfly	0.802
6Ba	TW	all	*Covariates*	fruitfly, tiny	0.664
6Ba	TW	all	*Interspecies*	fruitfly, tiny	0.651
6Ba	TW	all	*Covariates*	Milbe	0.821
6Ba	TW	all	*Interspecies*	Milbe	0.797
6Ba	TW	all	*Covariates*	mosquito	0.871
6Ba	TW	all	*Interspecies*	mosquito	0.810
6Ba	TW	all	*Covariates*	Schuster	0.313
6Ba	TW	all	*Interspecies*	Schuster	0.223
6Ba	TW	all	*Covariates*	spider	0.548
6Ba	TW	all	*Interspecies*	spider	0.527
6Ba	TW	all	*Covariates*	spider, little	0.852
6Ba	TW	all	*Interspecies*	spider, little	0.798
6Ba	TW	all	*Covariates*	spider, tiny	0.729
6Ba	TW	all	*Interspecies*	spider, tiny	0.694
6Ba	TW	all	*Covariates*	Springmilbe	0.867
6Ba	TW	all	*Interspecies*	Springmilbe	0.811

7.7 Allocation of Narrative Names to Biological Order/Family

Study area	Level	Target	Pooled narratives
1CR	Order	Passeriformes	Flycatcher
1CR	Order	Passeriformes	Golden-bellied Flycatcher
1CR	Order	Passeriformes	Golden-hooded Tanager
1CR	Order	Passeriformes	Great Kiskadee
1CR	Order	Passeriformes	Kiskadee
1CR	Order	Passeriformes	Lesser Kiskadee
1CR	Order	Passeriformes	Manakin
1CR	Order	Passeriformes	Oropendula
1CR	Order	Passeriformes	Pale-vented Thrush
1CR	Order	Passeriformes	Scarlet-rumped Tanager
1CR	Order	Passeriformes	Seedeater
1CR	Order	Passeriformes	Songbird
1CR	Order	Passeriformes	Songbird, brown
1CR	Order	Passeriformes	Songbird, little
1CR	Order	Passeriformes	Steep-forehead Flycatcher
1CR	Order	Passeriformes	Swallow
1CR	Order	Passeriformes	Tanager
1CR	Order	Passeriformes	Thrush
1CR	Order	Passeriformes	Treecreper
1CR	Order	Passeriformes	Yellow-bellied Flycatcher
1CR	Order	Piciformes	Gray-necked Woodpecker
1CR	Order	Piciformes	Toucan
1CR	Order	Piciformes	Woodpecker
1CR	Order	Psittaciformes	Mealy Parrot
1CR	Order	Psittaciformes	Parrot
1CR	Order	Psittaciformes	Parrot, large
1CR	Order	Psittaciformes	Parrot, little
2Ni	Order	Acariformes	mite, red
2Ni	Order	Acariformes	mite, red 925
2Ni	Order	Araneae	spider
2Ni	Order	Araneae	spider, black 892
2Ni	Order	Araneae	spider, red
2Ni	Order	Araneae	spider, small
2Ni	Order	Araneae	spider, small red
2Ni	Order	Ciconiiformes	Cattle Egret
2Ni	Order	Ciconiiformes	Gray Hawk
2Ni	Order	Ciconiiformes	Hawk
2Ni	Order	Ciconiiformes	Magnificent Frigatebird
2Ni	Order	Ciconiiformes	Turkey Vulture
2Ni	Order	Ciconiiformes	Vulture
2Ni	Order	Lepidoptera	Butterfly, black-red
2Ni	Order	Lepidoptera	Butterfly, black-yellow
2Ni	Order	Lepidoptera	Butterfly, grey
2Ni	Order	Lepidoptera	Butterfly, large yellow
2Ni	Order	Lepidoptera	Butterfly, orange
2Ni	Order	Lepidoptera	Butterfly, orange-white
2Ni	Order	Lepidoptera	Butterfly, small black
2Ni	Order	Lepidoptera	Butterfly, small white
2Ni	Order	Lepidoptera	butterfly, swallowtail
2Ni	Order	Lepidoptera	Butterfly, white

Study area	Level	Target	Pooled narratives
2Ni	Order	Lepidoptera	Butterfly, yellow
2Ni	Order	Lepidoptera	caterpillar, 875
2Ni	Order	Lepidoptera	caterpillar, 877
2Ni	Order	Lepidoptera	caterpillar, 942-943
2Ni	Order	Lepidoptera	moth
2Ni	Order	Passeriformes	Banded Wren
2Ni	Order	Passeriformes	Brown-crested Flycatcher
2Ni	Order	Passeriformes	Flycatcher
2Ni	Order	Passeriformes	Great Kiskadee
2Ni	Order	Passeriformes	Jay
2Ni	Order	Passeriformes	Masked Tityra
2Ni	Order	Passeriformes	Seedeater
2Ni	Order	Passeriformes	Songbird
2Ni	Order	Passeriformes	Swallow
2Ni	Order	Passeriformes	Tanager
2Ni	Order	Passeriformes	White-throated Magpie Jay
3AK	Order	Araneae	spider
3AK	Order	Araneae	spider, small
3AK	Order	Araneae	spider, small black
3AK	Order	Araneae	spider, small red
3AK	Order	Araneae	spider, tiny
3AK	Order	Coleoptera	beetle
3AK	Order	Coleoptera	beetle, underground-hiding
3AK	Order	Passeriformes	American Robin
3AK	Order	Passeriformes	Boreal Chickadee
3AK	Order	Passeriformes	Chickadee
3AK	Order	Passeriformes	Corvidae
3AK	Order	Passeriformes	Dark-eyed Junco
3AK	Order	Passeriformes	Gray Jay
3AK	Order	Passeriformes	Junco
3AK	Order	Passeriformes	Songbird
3AK	Order	Passeriformes	Sparrow
3AK	Order	Passeriformes	White-crowned Sparrow
3AK	Order	Passeriformes	Yellow-rumped Warbler
4Ru	Order	Araneae	Spider
4Ru	Order	Araneae	spider with slim long legs
4Ru	Order	Araneae	spider, big
4Ru	Order	Araneae	spider, little
4Ru	Order	Araneae	spider, midsize
4Ru	Order	Araneae	spider, palekolane
4Ru	Order	Passeriformes	bluetail
4Ru	Order	Passeriformes	Chickadee
4Ru	Order	Passeriformes	Crow
4Ru	Order	Passeriformes	Emberiza
4Ru	Order	Passeriformes	Finch
4Ru	Order	Passeriformes	Flycatcher
4Ru	Order	Passeriformes	Grasshopper Warbler
4Ru	Order	Passeriformes	Jungle Crow
4Ru	Order	Passeriformes	Juv passerine
4Ru	Order	Passeriformes	Kinglet
4Ru	Order	Passeriformes	Kohlmeise
4Ru	Order	Passeriformes	longtailed tit
4Ru	Order	Passeriformes	Nutcracker
4Ru	Order	Passeriformes	nuthatch

Study area	Level	Target	Pooled narratives
4Ru	Order	Passeriformes	Oriental Finch
4Ru	Order	Passeriformes	Oriental Greenfinch
4Ru	Order	Passeriformes	passerine
4Ru	Order	Passeriformes	Raven
4Ru	Order	Passeriformes	Tannenmeise
4Ru	Order	Passeriformes	Thrush
4Ru	Order	Passeriformes	Wagtail
4Ru	Order	Passeriformes	Warbler
4Ru	Order	Passeriformes	Weidenmeise
4Ru	Order	Passeriformes	Winter Wren
5PG	Order	Acariformes	milbe, red
5PG	Order	Acariformes	milbe, spring
5PG	Order	Araneae	spider, little
5PG	Order	Araneae	spider, little black
5PG	Order	Araneae	spider, little long legs
5PG	Order	Araneae	spider, medium
5PG	Order	Araneae	spider, tiny black
5PG	Order	Collembola	Collembola
5PG	Order	Collembola	collembola long antennae
5PG	Order	Collembola	collembola, big yellow
5PG	Order	Collembola	collembola, black-yellow
5PG	Order	Collembola	collembola, yellow
5PG	Order	Diptera	fly
5PG	Order	Diptera	fly with legs and antennae
5PG	Order	Diptera	fly, tiny
5PG	Order	Diptera	fruitfly
5PG	Order	Diptera	fruitfly black
5PG	Order	Diptera	fruitfly grey
5PG	Order	Diptera	fruitfly, blue
5PG	Order	Diptera	fruitfly, pink
5PG	Order	Diptera	fruitfly, white
5PG	Order	Diptera	mosquito
5PG	Order	Diptera	mosquito, jumping
5PG	Order	Passeriformes	Craw, Bird of Paradise
5PG	Order	Passeriformes	Flycatcher
5PG	Order	Passeriformes	Flycatcher tschirrp
5PG	Order	Passeriformes	Flycatcher, similar willie
5PG	Order	Passeriformes	Kau Kau, Bird of Paradise
5PG	Order	Passeriformes	Rezina, rezina
5PG	Order	Passeriformes	Songbird
5PG	Order	Passeriformes	Songbird little
5PG	Order	Passeriformes	songbird tshirp
5PG	Order	Passeriformes	Songbird tsilp
5PG	Order	Passeriformes	Swallow
5PG	Order	Passeriformes	Thrush
5PG	Order	Passeriformes	wren
5PG	Order	Psittaciformes	Cockatoo
5PG	Order	Psittaciformes	Palm Cockatoo
5PG	Order	Psittaciformes	Parakeet
5PG	Order	Psittaciformes	Parrot
5PG	Order	Psittaciformes	Parrot, little
5PG	Order	Psittaciformes	White Cockatoo
6Ba	Order	Ciconiiformes	Dowitcher
6Ba	Order	Ciconiiformes	Dunlin

Study area	Level	Target	Pooled narratives
6Ba	Order	Ciconiiformes	Glaucous Gull
6Ba	Order	Ciconiiformes	Longbilled Dowitcher
6Ba	Order	Ciconiiformes	Loon
6Ba	Order	Ciconiiformes	Pacific Loon
6Ba	Order	Ciconiiformes	Parasitic Jaeger
6Ba	Order	Ciconiiformes	Pectoral Sandpiper
6Ba	Order	Ciconiiformes	Phalarope
6Ba	Order	Ciconiiformes	Pomarine Jaeger
6Ba	Order	Ciconiiformes	Red Phalarope
6Ba	Order	Ciconiiformes	Red-necked Phalarope
6Ba	Order	Ciconiiformes	Semipalmated Sandpiper
6Ba	Order	Ciconiiformes	Western Sandpiper
6Ba	Order	Coleoptera	beetle
6Ba	Order	Coleoptera	beetle, flat
6Ba	Order	Coleoptera	beetle, gold-green
6Ba	Order	Coleoptera	beetle, green
6Ba	Order	Coleoptera	beetle, little
6Ba	Order	Coleoptera	beetle, little green
6Ba	Order	Coleoptera	beetle, slim
6Ba	Order	Coleoptera	Marienkaeferlarve
6Ba	Order	Diptera	fly
6Ba	Order	Diptera	fly, little
6Ba	Order	Diptera	Fruitfly
6Ba	Order	Diptera	fruitfly, little
6Ba	Order	Diptera	fruitfly, tiny
6Ba	Order	Diptera	mosquito
6Ba	Order	Diptera	Schuster
6Ba	Order	Diptera	schuster, big
6Ba	Order	Diptera	Schuster, large
6Ba	Order	Diptera	Schuster, no wings
6Ba	Order	Passeriformes	Lapland Bunting
6Ba	Order	Passeriformes	Snow Bunting
1CR	Family	Thraupidae	Golden-hooded Tanager
1CR	Family	Thraupidae	Scarlet-rumped Tanager
1CR	Family	Thraupidae	Seedeater
1CR	Family	Thraupidae	Tanager
1CR	Family	Tyrannidae	Flycatcher
1CR	Family	Tyrannidae	Golden-bellied Flycatcher
1CR	Family	Tyrannidae	Great Kiskadee
1CR	Family	Tyrannidae	Kiskadee
1CR	Family	Tyrannidae	Lesser Kiskadee
1CR	Family	Tyrannidae	Steep-forehead Flycatcher
1CR	Family	Tyrannidae	Yellow-bellied Flycatcher
2Ni	Family	Formicidae	ant
2Ni	Family	Formicidae	ant, red
2Ni	Family	Formicidae	ant, small
2Ni	Family	Formicidae	ant, small black
2Ni	Family	Formicidae	ant, small red
3AK	Family	Emberizidae	Dark-eyed Junco
3AK	Family	Emberizidae	Junco
3AK	Family	Emberizidae	Sparrow
3AK	Family	Emberizidae	White-crowned Sparrow
4Ru	Family	Corvidae	Crow
4Ru	Family	Corvidae	Jungle Crow

Study area	Level	Target	Pooled narratives
4Ru	Family	Corvidae	Nutcracker
4Ru	Family	Corvidae	Raven
4Ru	Family	Paridae	Chickadee
4Ru	Family	Paridae	Kohlmeise
4Ru	Family	Paridae	longtailed tit
4Ru	Family	Paridae	Tannenmeise
4Ru	Family	Paridae	Weidenmeise
5PG	Family	Formicidae	ant, big
5PG	Family	Formicidae	ant, big black
5PG	Family	Formicidae	ant, big yellow
5PG	Family	Formicidae	ant, black
5PG	Family	Formicidae	ant, little
5PG	Family	Formicidae	ant, little black
5PG	Family	Formicidae	ant, little red
5PG	Family	Formicidae	ant, medium black
5PG	Family	Formicidae	ant, red
5PG	Family	Formicidae	ant, tiny
5PG	Family	Formicidae	ant, tiny black
5PG	Family	Formicidae	ant, tiny red
5PG	Family	Formicidae	ant, tiny yellow
5PG	Family	Formicidae	ant, yellow
5PG	Family	Paradisaeidae	Craw, Bird of Paradise
5PG	Family	Paradisaeidae	Kau Kau, Bird of Paradise
5PG	Family	Paradisaeidae	Rezina, rezina
6Ba	Family	Scolopacidae	Dowitcher
6Ba	Family	Scolopacidae	Dunlin
6Ba	Family	Scolopacidae	Longbilled Dowitcher
6Ba	Family	Scolopacidae	Pectoral Sandpiper
6Ba	Family	Scolopacidae	Phalarope
6Ba	Family	Scolopacidae	Red Phalarope
6Ba	Family	Scolopacidae	Red-necked Phalarope
6Ba	Family	Scolopacidae	Semipalmated Sandpiper
6Ba	Family	Scolopacidae	Western Sandpiper
6Ba	Family	Stercorariidae	Parasitic Jaeger
6Ba	Family	Stercorariidae	Pomarine Jaeger
6Ba	Family	Tipulidae	Schuster
6Ba	Family	Tipulidae	schuster, big
6Ba	Family	Tipulidae	Schuster, large
6Ba	Family	Tipulidae	Schuster, no wings

7.8 *Best Models (DISTANCE Sampling)*

Study area	Target narrative	Type	Data	Model definition	ESW/EDR	D	D LCL	D UCL	D CV	P	P LCL	P UCL
1CR	Flycatcher	Bi	all	26	27.1	117.3	14.8	929.7	1.3	0.4	32.0	0.0
1CR	Flycatcher	Bi	aur	26	30.6	17.4	6.8	44.3	0.5	0.5	18.0	0.2
1CR	Flycatcher	Bi	ran	26								
1CR	Flycatcher	Bi	sys	26	26.9	41.8	24.5	71.2	0.3	0.4	28.0	0.2
1CR	Flycatcher	Bi	vis	26	26.7	17.9	0.8	385.2	2.5	0.4	12.0	0.0
1CR	Hummingbird	Bi	all	16	8.7	2908.0	1992.3	4244.5	0.2	0.2	94.0	0.1
1CR	Hummingbird	Bi	aur	16	12.8	302.3	184.0	496.6	0.3	0.4	61.0	0.3
1CR	Hummingbird	Bi	ran	16	5.5	3257.9	1207.0	8793.8	0.5	0.1	19.0	0.0
1CR	Hummingbird	Bi	sys	16	9.3	780.4	511.5	1190.6	0.2	0.2	73.0	0.2
1CR	Hummingbird	Bi	vis	16	6.1	661.9	409.4	1070.1	0.2	0.1	33.0	0.1
1CR	Oropendula	Bi	all	1	7.7	2296.9	1208.7	4364.7	0.3	0.1	42.0	0.1
1CR	Oropendula	Bi	aur	1	18.4	23.0	7.0	76.3	0.6	0.8	10.0	0.3
1CR	Oropendula	Bi	ran	1	13.4	306.2	61.3	1528.7	0.9	0.4	5.0	0.1
1CR	Oropendula	Bi	sys	1	7.6	768.3	389.0	1517.6	0.4	0.1	36.0	0.1
1CR	Oropendula	Bi	vis	1	6.8	817.9	422.0	1585.3	0.3	0.1	31.0	0.1
1CR	Seedeater	Bi	all	39	7.2	893.8	296.3	2696.3	0.6	0.1	14.0	0.1
1CR	Seedeater	Bi	aur	39		17.7	3.2	97.1	1.0			
1CR	Seedeater	Bi	ran	39		106.1	10.5	1070.6	1.0			
1CR	Seedeater	Bi	sys	39	6.5	410.5	132.2	1275.0	0.6	0.1	13.0	0.1
1CR	Seedeater	Bi	vis	39	7.0	322.7	102.0	1021.3	0.6	0.1	13.0	0.1
1CR	Woodpecker	Bi	all	11	25.1	80.9	0.0	0.0	0.0	0.5	22.0	0.4
1CR	Woodpecker	Bi	aur	11								
1CR	Woodpecker	Bi	ran	11								
1CR	Woodpecker	Bi	sys	11	25.4	22.3	0.0	0.0	0.0	0.5	15.0	0.4
1CR	Woodpecker	Bi	vis	11	23.5	14.6	0.0	0.0	0.0	0.4	9.0	0.3
2Ni	BandedWren	Bi	aur	45	26.8	31.6	18.3	54.7	0.3	0.8	27.0	0.6
2Ni	BandedWren	Bi	ran	45								
2Ni	BandedWren	Bi	sys	45	25.3	36.1	19.3	67.5	0.3	0.7	23.0	0.5
2Ni	BandedWren	Bi	vis	45		47.2	8.4	264.7	0.9			

Study area	Target narrative	Type	Data	Model definition	ESW/EDR	D	D LCL	D UCL	D CV	P	P LCL	P UCL
2Ni	White-throated Magpie Jay	Bi	all	43	23.3	152.4	88.0	263.8	0.3	0.6	30.0	0.5
2Ni	White-throated Magpie Jay	Bi	aur	43	23.5	40.9	0.1	20472.3	100.0	0.6	28.0	0.0
2Ni	White-throated Magpie Jay	Bi	ran	43								
2Ni	White-throated Magpie Jay	Bi	sys	43	23.2	42.3	23.2	77.3	0.3	0.6	24.0	0.5
2Ni	White-throated Magpie Jay	Bi	vis	43		47.2	8.4	264.7	0.9			
3AK	Sparrow	Bi	all	12	38.2	16.2	10.3	25.7	0.2	0.6	57.0	0.5
3AK	Sparrow	Bi	aur	12	38.7	11.2	6.9	18.4	0.3	0.6	40.0	0.4
3AK	Sparrow	Bi	ran	12	37.9	11.5	1.7	78.0	1.0	0.6	5.0	0.1
3AK	Sparrow	Bi	sys	12	38.2	17.2	10.6	28.0	0.2	0.6	50.0	0.4
3AK	Sparrow	Bi	vis	12	15.6	85.4	6.1	1202.5	1.9	0.1	15.0	0.0
3AK	Squirrel	Bi	all	15	43.2	17.0	11.0	26.4	0.2	0.7	76.0	0.6
3AK	Squirrel	Bi	aur	15	44.8	15.6	10.4	23.3	0.2	0.8	73.0	0.6
3AK	Squirrel	Bi	ran	15	38.8	20.3	7.0	58.9	0.5	0.6	11.0	0.3
3AK	Squirrel	Bi	sys	15	44.2	16.4	10.4	26.1	0.2	0.8	63.0	0.6
3AK	Squirrel	Bi	vis	15	10.0	35.4	4.0	310.0	1.1	1.0	2.0	0.0
4Ru	Chickadee	Bi	all	1	12.2	572.2	304.0	1077.1	0.3	0.2	66.0	0.1
4Ru	Chickadee	Bi	aur	1	17.1	214.6	125.5	366.9	0.3	0.5	50.0	0.3
4Ru	Chickadee	Bi	ran	1	23.5	132.7	48.3	364.4	0.5	0.9	11.0	0.4
4Ru	Chickadee	Bi	sys	1	11.4	632.8	323.9	1236.1	0.3	0.2	54.0	0.1
4Ru	Chickadee	Bi	vis	1	9.7	237.0	90.4	621.1	0.5	0.2	14.0	0.1
4Ru	Kinglet	Bi	all	43	19.7	193.3	140.2	266.4	0.2	0.2	84.0	0.1
4Ru	Kinglet	Bi	aur	43	19.1	131.7	90.4	191.8	0.2	0.1	61.0	0.1
4Ru	Kinglet	Bi	ran	43								
4Ru	Kinglet	Bi	sys	43	19.8	182.4	128.5	258.9	0.2	0.2	61.0	0.1
4Ru	Kinglet	Bi	vis	43								
4Ru	Nutcracker	Bi	aur	44	31.0	12.5	6.6	23.8	0.3	0.6	15.0	0.4
4Ru	Nutcracker	Bi	ran	44		159.2	16.5	1532.0	1.1			
4Ru	Nutcracker	Bi	sys	44								
4Ru	Nutcracker	Bi	vis	44	14.5	26.2	1.2	550.5	2.0	0.1	6.0	0.0
4Ru	Warbler	Bi	all	20	38.4	26.8	9.0	79.2	0.6	0.6	30.0	0.2
4Ru	Warbler	Bi	aur	20	43.3	11.3	7.0	18.4	0.2	0.8	27.0	0.6
4Ru	Warbler	Bi	ran	20								
4Ru	Warbler	Bi	sys	20	38.4	32.1	10.9	94.3	0.6	0.6	30.0	0.2

Study area	Target narrative	Type	Data	Model definition	ESW/EDR	D	D LCL	D UCL	D CV	P	P LCL	P UCL
4Ru	Warbler	Bi	vis	20	4.9	93.6	0.0	281037.8	1.5	0.0	1.0	0.0
4Ru	Winter Wren	Bi	all	67	30.0	16.5	8.1	33.5	0.4	0.4	19.0	0.2
4Ru	Winter Wren	Bi	aur	67	30.0	16.5	8.1	33.5	0.4	0.4	19.0	0.2
4Ru	Winter Wren	Bi	ran	67								
4Ru	Winter Wren	Bi	sys	67	30.0	19.8	9.9	39.7	0.4	0.4	19.0	0.2
4Ru	Winter Wren	Bi	vis	67								
4Ru	Wize	Bi	all	111	33.2	17.4	5.3	57.7	0.6	0.4	24.0	0.1
4Ru	Wize	Bi	aur	111	32.3	17.1	3.6	81.0	0.9	0.4	22.0	0.1
4Ru	Wize	Bi	ran	111	19.1	35.0	6.4	190.5	0.7	0.9	1.0	0.0
4Ru	Wize	Bi	sys	111								
4Ru	Wize	Bi	vis	111		32.5	7.7	137.2	0.8			
5PG	Flute	Bi	all	3	29.2	16.6	10.2	26.9	0.2	0.3	19.0	0.3
5PG	Flute	Bi	aur	3	29.2	17.1	10.6	27.7	0.2	0.3	19.0	0.3
5PG	Flute	Bi	ran	3	30.0	18.9	5.5	64.9	0.5	1.0	4.0	1.0
5PG	Flute	Bi	sys	3	29.9	15.2	8.6	27.0	0.3	0.4	15.0	0.3
5PG	Flute	Bi	vis	3								
5PG	Tsilp	Bi	all	11	20.8	67.1	0.0	0.0	0.0	0.5	39.0	0.0
5PG	Tsilp	Bi	aur	11	23.0	55.6	0.0	0.0	0.0	0.6	38.0	0.5
5PG	Tsilp	Bi	ran	11	24.5	42.5	0.0	0.0	0.0	0.7	4.0	0.3
5PG	Tsilp	Bi	sys	11	22.6	58.1	0.0	0.0	0.0	0.6	33.0	0.5
5PG	Tsilp	Bi	vis	11								
6Ba	Lapland Bunting	Bi	all	35	26.2	25.0	15.3	40.8	0.2	0.3	52.0	0.2
6Ba	Lapland Bunting	Bi	ran	35		45.3	4.5	457.5	1.0			
6Ba	Lapland Bunting	Bi	sys	35	26.0	29.5	18.1	48.0	0.2	0.3	50.0	0.2
6Ba	Longbilled Dowitcher	Bi	all	36	22.3	17.6	9.2	33.4	0.3	0.3	26.0	0.2
6Ba	Longbilled Dowitcher	Bi	ran	36	30.0	5.9	0.0	#########	100.0	1.0	1.0	0.0
6Ba	Longbilled Dowitcher	Bi	sys	36	22.2	19.0	9.7	37.4	0.3	0.3	23.0	0.2
6Ba	Pectoral Sandpiper	Bi	all	37	30.1	6.3	2.4	16.8	0.5	0.4	16.0	0.2
6Ba	Pectoral Sandpiper	Bi	ran	37								
6Ba	Pectoral Sandpiper	Bi	sys	37	30.1	7.6	2.9	20.0	0.5	0.4	16.0	0.2
6Ba	Pomarine Jaeger	Bi	all	18	13.6	69.9	19.4	251.7	0.7	0.2	19.0	0.1
6Ba	Pomarine Jaeger	Bi	ran	18		117.9	38.6	359.9	0.5			

Study area	Target narrative	Type	Data	Model definition	ESW/EDR	D	D LCL	D UCL	D CV	P	P LCL	P UCL
6Ba	Pomarine Jaeger	Bi	sys	18	12.8	80.0	25.4	252.0	0.6	0.2	16.0	0.1
6Ba	Red Phalarope	Bi	all	52	28.7	20.6	4.6	93.0	0.9	0.4	53.0	0.1
6Ba	Red Phalarope	Bi	ran	52	40.0	6.6	1.7	26.5	0.7	1.0	5.0	0.3
6Ba	Red Phalarope	Bi	sys	52	28.1	22.8	4.8	108.7	0.9	0.3	47.0	0.1
6Ba	Semipalmated Sandpiper	Bi	all	36	19.8	20.8	11.1	38.9	0.3	0.4	24.0	0.3
6Ba	Semipalmated Sandpiper	Bi	ran	36		29.5	2.9	297.4	1.0			
6Ba	Semipalmated Sandpiper	Bi	sys	36	20.0	23.6	12.5	44.4	0.3	0.4	23.0	0.3
2Ni	Butterfly, white	DT	all	4	8.6	98777.7	64350.3	151624.0	0.2	0.6	30.0	0.5
2Ni	Butterfly, white	DT	ran	4	15.0	58333.3	9184.3	370500.8	0.6	1.0	7.0	1.0
2Ni	Butterfly, white	DT	sys	4	8.5	98341.1	58020.3	166682.8	0.3	0.6	23.0	0.4
1CR	Ant	TW	all	32	1.3	2741.2	656.4	11448.0	0.5	0.4	113.0	0.4
1CR	Spider	TW	all	32	1.2	702.5	402.9	1224.7	0.2	0.4	45.0	0.3
2Ni	Ant	TW	all	23	1.0	2090.7	644.1	6786.6	0.5	0.2	55.0	0.2
2Ni	Ant, small red	TW	all	2	1.0	695.1	288.8	1672.8	0.4	0.2	23.0	0.1
2Ni	Beetle, 868	TW	all	2	1.1	1042.8	205.6	5290.1	0.7	0.3	38.0	0.2
2Ni	Centipede, 881	TW	all	1	1.2	1322.9	699.7	2501.3	0.3	0.4	57.0	0.2
2Ni	Spider, small	TW	all	3	1.1	271.0	170.1	431.9	0.2	0.3	20.0	0.2
2Ni	Springtail	TW	all	3	1.2	47207.5	25774.5	86463.1	0.3	0.3	84.0	0.3
3AK	Spider	TW	all	20	1.4	969.6	475.8	1975.9	0.3	0.5	89.0	0.4
3AK	Spider	TW	all	71								
4Ru	Cycsegusa	TW	all	1	1.1	280.9	67.4	1170.5	0.6	0.3	15.0	0.1
4Ru	Protura	TW	all	44	1.5	162.5	41.2	641.6	0.7	0.6	12.0	0.2
4Ru	Spider, little	TW	all	2	1.6	169.2	49.5	578.1	0.6	0.6	16.0	0.2
5PG	Ant, tiny black	TW	all	3	1.4	199.3	67.2	591.6	0.5	0.5	13.0	0.2
6Ba	Beetle, flat	TW	all	2	1.1	1671.5	584.4	4780.6	0.4	0.3	50.0	0.2
6Ba	Fly	TW	all	2	1.3	313.1	132.9	737.5	0.4	0.4	22.0	0.2
6Ba	Fruitfly	TW	all	1	1.4	206.8	77.0	555.6	0.5	0.5	18.0	0.2
6Ba	Milbe	TW	all	1	1.3	120.7	29.3	497.3	0.7	0.4	10.0	0.2
6Ba	Mosquito	TW	all	2	2.0	114.1	19.0	685.7	1.0	1.0	8.0	0.2
6Ba	Schuster	TW	all	2	1.1	220.3	92.9	522.3	0.4	0.3	13.0	0.1
6Ba	Spider	TW	all	1	1.3	542.8	263.2	1119.5	0.3	0.4	43.0	0.2
6Ba	Spider, tiny	TW	all	2	1.1	4131.6	1775.6	9613.9	0.3	0.3	88.0	0.2

7.9 Best Models (PRESENCE)

Study area	Type	Target narrative	Data	Model	AIC	Likelihood	No. Par.	(-2*Log Like)
1CR	Bi	Flycatcher	all	1 group, Survey-specific P	100.45	1	4	92.45
1CR	Bi	Hummingbird	all	Flowers	106.51	1	3	100.51
1CR	Bi	Oropendula	all	TurkeyVulture	124.15	1	3	118.15
1CR	Bi	Seedeater	all	Habitat	58.01	1	7	44.01
1CR	Bi	Woodpecker	all	HighestTree	96.77	1	3	90.77
1CR	Bi	Passeriformes	all	1 group, Survey-specific P	46.26	1	4	38.26
1CR	Bi	Piciformes	all	Min	102.8	1	3	96.80
1CR	Bi	Psittaciformes	all	Min	74.21	1	3	68.21
1CR	Bi	Thraupidae	all	Habitat	54.89	1	7	40.89
1CR	Bi	Tyrannidae	all	1 group, Survey-specific P	116.26	1	4	108.26
1CR	Bi	Flycatcher	aur	1 group, Survey-specific P	94.31	1	4	86.31
1CR	Bi	Hummingbird	aur	DuffCover	113.28	1	3	107.28
1CR	Bi	Oropendula	aur	HighestDBH	104.62	1	3	98.62
1CR	Bi	Passeriformes	aur	LeafBrowsing	114.08	1	3	108.08
1CR	Bi	Piciformes	aur	HighestDBH	61.92	1	3	55.92
1CR	Bi	Psittaciformes	aur	Cov05	37.39	1	3	31.39
1CR	Bi	Seedeater	aur	HighestDBH	26.11	1	3	20.11
1CR	Bi	Thraupidae	aur	HighestDBH	26.11	1	3	20.11
1CR	Bi	Tyrannidae	aur	1 group, Survey-specific P	116.13	1	4	108.13
1CR	Bi	Woodpecker	aur	HighestDBH	58.94	1	3	52.94
1CR	Bi	Flycatcher	ran	Shrubs	18.37	1	3	12.37
1CR	Bi	Hummingbird	ran	Shrubs	18.37	1	3	12.37
1CR	Bi	Oropendula	ran	1 group, Constant P	21.4	1	2	17.40
1CR	Bi	Passeriformes	ran	1 group, Constant P	4	1	2	0.00
1CR	Bi	Piciformes	ran	DuffCover	22.64	1	3	16.64
1CR	Bi	Psittaciformes	ran	Shrubs	15.53	1	3	9.53
1CR	Bi	Seedeater	ran	BareSoil	13.64	1	3	7.64
1CR	Bi	Thraupidae	ran	BareSoil	13.64	1	3	7.64
1CR	Bi	Tyrannidae	ran	DuffCover	22.64	1	3	16.64
1CR	Bi	Woodpecker	ran	Shrubs	18.37	1	3	12.37
1CR	Bi	Flycatcher	sys	1 group, Survey-specific P	85.66	1	4	77.66
1CR	Bi	Hummingbird	sys	Flowers	89.08	1	3	83.08
1CR	Bi	Oropendula	sys	TurkeyVulture	105.71	1	3	99.71
1CR	Bi	Passeriformes	sys	1 group, Survey-specific P	43.92	1	4	35.92
1CR	Bi	Piciformes	sys	Min	84.74	1	3	78.74
1CR	Bi	Psittaciformes	sys	Min	62.72	1	3	56.72
1CR	Bi	Seedeater	sys	Min	48.93	1	3	42.93
1CR	Bi	Thraupidae	sys	Min	46.98	1	3	40.98
1CR	Bi	Tyrannidae	sys	1 group, Survey-specific P	93.93	1	4	85.93
1CR	Bi	Woodpecker	sys	Min	79.47	1	3	73.47
1CR	Bi	Flycatcher	vis	MossLichen	73.85	1	5	63.85
1CR	Bi	Hummingbird	vis	Flowers	114.27	1	3	108.27
1CR	Bi	Oropendula	vis	LeafBrowsing	115.39	1	3	109.39
1CR	Bi	Passeriformes	vis	CanopyTrees	112.32	1	3	106.32
1CR	Bi	Piciformes	vis	Min	88.66	1	3	82.66
1CR	Bi	Psittaciformes	vis	Cov12	58.81	1	3	52.81
1CR	Bi	Seedeater	vis	DuffCover	43.39	1	3	37.39
1CR	Bi	Thraupidae	vis	DuffCover	38.82	1	3	32.82
1CR	Bi	Tyrannidae	vis	MossLichen	84.09	1	5	74.09

Study area	Type	Target narrative	Data	Model	AIC	Likelihood	No. Par.	(-2*Log Like)
1CR	Bi	Woodpecker	vis	HighestDBH	72.66	1	3	66.66
1CR	TW	Ant	all	1 group, Survey-specific P	13.55	1	4	5.55
1CR	TW	Formicidae	all	1 group, Survey-specific P	13.55	1	4	5.55
1CR	TW	Spider	all	1 group, Constant P	4	1	2	0.00
2Ni	Bi	Banded Wren	all	Habitat	104.83	1	7	90.83
2Ni	Bi	Ciconiiformes	all	DuffCover	102.14	0.831	3	96.14
2Ni	Bi	Passeriformes	all	1 group, Survey-specific P	93.1	1	4	85.10
2Ni	Bi	White-throated Magpie Jay	all	1 group, Survey-specific P	125.05	1	4	117.05
2Ni	Bi	Banded Wren	aur	Habitat	104.83	1	7	90.83
2Ni	Bi	Ciconiiformes	aur	1 group, Survey-specific P	57.53	1	4	49.53
2Ni	Bi	Passeriformes	aur	1 group, Survey-specific P	117.99	1	4	109.99
2Ni	Bi	White-throated Magpie Jay	aur	1 group, Survey-specific P	106.75	1	4	98.75
2Ni	Bi	Banded Wren	ran	Shrubs	18.37	1	3	12.37
2Ni	Bi	Ciconiiformes	ran	1 group, Survey-specific P	22	1	4	14.00
2Ni	Bi	Passeriformes	ran	1 group, Constant P	21.4	1	2	17.40
2Ni	Bi	White-throated Magpie Jay	ran	Shrubs	22.3	1	3	16.30
2Ni	Bi	Banded Wren	sys	Habitat	87.77	1	7	73.77
2Ni	Bi	Ciconiiformes	sys	DuffCover	82.28	1	3	76.28
2Ni	Bi	Passeriformes	sys	1 group, Survey-specific P	77.57	1	4	69.57
2Ni	Bi	White-throated Magpie Jay	sys	Min	103.8	1	3	97.80
2Ni	Bi	Banded Wren	vis	Understory	16.81	1	3	10.81
2Ni	Bi	Ciconiiformes	vis	DuffCover	83.05	0.045	3	77.05
2Ni	Bi	Passeriformes	vis	HighestTree	125.38	1	3	119.38
2Ni	Bi	White-throated Magpie Jay	vis	HighestTree	115.4	1	3	109.40
2Ni	TW	Acariformes	all	1 group, Constant P	10.88	1	2	6.88
2Ni	TW	Ant	all	1 group, Constant P	10.88	1	2	6.88
2Ni	TW	Ant, small red	all	1 group, Survey-specific P	19.09	1	4	11.09
2Ni	TW	Araneae	all	1 group, Constant P	14.81	1	2	10.81
2Ni	TW	Beetle, 868	all	1 group, Survey-specific P	13.55	1	4	5.55
2Ni	TW	Centipede, 881	all	1 group, Constant P	4	1	2	0.00
2Ni	TW	Coleoptera	all	1 group, Constant P	10.88	1	2	6.88
2Ni	TW	Formicidae	all	1 group, Constant P	4	1	2	0.00
2Ni	TW	Spider, small	all	1 group, Constant P	17.5	1	2	13.50
2Ni	TW	Springtail	all	1 group, Survey-specific P	8	1	4	0.00
3AK	Bi	Emberizidae	all	1 group, Constant P	128.73	1	2	124.73
3AK	Bi	Passeriformes	all	Squirrel	80.79	1	3	74.79
3AK	Bi	Sparrow	all	Min	126.6	1	3	120.60
3AK	Bi	Squirrel	all	DuffCover	104.87	0.007	3	98.87
3AK	Bi	Emberizidae	ran	Cov13	22.64	1	3	16.64
3AK	Bi	Passeriformes	ran	1 group, Survey-specific P	14.73	1	4	6.73
3AK	Bi	Sparrow	ran	DuffCover	18.37	1	3	12.37
3AK	Bi	Squirrel	ran	1 group, Survey-specific P	17.5	1	4	9.50
3AK	TW	Araneae	all	1 group, Constant P	4	1	2	0.00
3AK	TW	Coleoptera	all	1 group, Constant P	19.28	1	2	15.28
3AK	TW	Spider	all	1 group, Constant P	4	1	2	0.00
3AK	TW	Springtail	all	1 group, Survey-specific P	13.55	1	4	5.55
4Ru	Bi	Chickadee	all	Cov05	117.41	1	3	111.41

Study area	Type	Target narrative	Data	Model	AIC	Likelihood	No. Par.	(-2*Log Like)
4Ru	Bi	Corvidae	all	Cov21	111.38	1	3	105.38
4Ru	Bi	Kinglet	all	HighDBH	116.48	1	3	110.48
4Ru	Bi	Nutcracker	all	Cov21	94.34	1	3	88.34
4Ru	Bi	Paridae	all	Cov05	117.41	1	3	111.41
4Ru	Bi	Passeriformes	all	DuffCover	44.62	1	3	38.62
4Ru	Bi	Warbler	all	1 group, Survey-specific P	110.77	1	4	102.77
4Ru	Bi	Winter Wren	all	Cov01	88.36	1	3	82.36
4Ru	Bi	Wize	all	1 group, Survey-specific P	86.15	1E-04	4	78.15
4Ru	TW	Araneae	all	1 group, Constant P	10.88	1	2	6.88
4Ru	TW	Collembola	all	1 group, Constant P	14.81	1	2	10.81
4Ru	TW	Cycsegusa	all	HighestTree	17.46	1	3	11.46
4Ru	TW	Protura	all	Min	18.37	1	3	12.37
4Ru	TW	Spider, little	all	1 group, Survey-specific P	17	1	4	9.00
5PG	Bi	Flute	all	CanopyPerc	86.98	1	3	80.98
5PG	Bi	Paradisaeidae	all	1 group, Survey-specific P	74.43	1	4	66.43
5PG	Bi	Passeriformes	all	1 group, Survey-specific P	124.3	1	4	116.30
5PG	Bi	Psittaciformes	all	CanopyPerc	96.87	1	3	90.87
5PG	Bi	Tsilp	all	1 group, Survey-specific P	114.31	1	4	106.31
5PG	TW	Ant, tiny black	all	1 group, Constant P	4	1	2	0.00
5PG	TW	Collembola	all	1 group, Constant P	14.81	1	2	10.81
5PG	TW	Diptera	all	1 group, Constant P	17.5	1	2	13.50
5PG	TW	Formicidae	all	1 group, Constant P	4	1	2	0.00
6Ba	Bi	Ciconiiformes	all	1 group, Survey-specific P	42.2	1	4	34.20
6Ba	Bi	Lapland Bunting	all	Cov03	101.1	1	3	95.10
6Ba	Bi	Longbilled Dowitcher	all	Cov03	117.68	1	3	111.68
6Ba	Bi	Passeriformes	all	Cov03	101.1	1	3	95.10
6Ba	Bi	Pectoral Sandpiper	all	DiamLake	99.84	1	3	93.84
6Ba	Bi	Pomarine Jaeger	all	1 group, Survey-specific P	115.45	1	4	107.45
6Ba	Bi	Red Phalarope	all	GrassPerc	122.82	1	3	116.82
6Ba	Bi	schuster	all	1 group, Constant P	14.81	1	2	10.81
6Ba	Bi	Scolopacidae	all	1 group, Constant P	57.99	1	2	53.99
6Ba	Bi	Semipalmated Sandpiper	all	1 group, Constant P	128.05	1	2	124.05
6Ba	Bi	Stercorariidae	all	1 group, Survey-specific P	119.02	1	4	111.02
6Ba	Bi	Ciconiiformes	ran	1 group, Constant P	19.01	1	2	15.01
6Ba	Bi	Lapland Bunting	ran	1 group, Survey-specific P	18.01	1	4	10.01
6Ba	Bi	Longbilled Dowitcher	ran	Cov06	21.28	1	3	15.28
6Ba	Bi	Passeriformes	ran	1 group, Survey-specific P	18.01	1	4	10.01
6Ba	Bi	Pectoral Sandpiper	ran	1 group, Constant P	4	1	2	0.00
6Ba	Bi	Pomarine Jaeger	ran	1 group, Survey-specific P	14.73	1	4	6.73
6Ba	Bi	Red Phalarope	ran	1 group, Survey-specific P	17.5	1	4	9.50
6Ba	Bi	Scolopacidae	ran	1 group, Constant P	19.01	1	2	15.01
6Ba	Bi	Semipalmated Sandpiper	ran	1 group, Constant P	23.1	1	2	19.10
6Ba	Bi	Stercorariidae	ran	1 group, Survey-specific P	14.73	1	4	6.73
6Ba	Bi	Ciconiiformes	sys	1 group, Survey-specific P	21.94	1	4	13.94
6Ba	Bi	Lapland Bunting	sys	Cov03	80.72	1	3	74.72

Study area	Type	Target narrative	Data	Model	AIC	Likelihood	No. Par.	(-2*Log Like)
6Ba	Bi	Longbilled Dowitcher	sys	Flowers	96.19	1	3	90.19
6Ba	Bi	Passeriformes	sys	Cov03	80.72	1	3	74.72
6Ba	Bi	Pectoral Sandpiper	sys	1 group, Constant P	98.16	1	2	94.16
6Ba	Bi	Pomarine Jaeger	sys	Flowers	90.99	0.937	3	84.99
6Ba	Bi	Red Phalarope	sys	GrassPerc	100.56	1	3	94.56
6Ba	Bi	Scolopacidae	sys	1 group, Constant P	40.74	1	2	36.74
6Ba	Bi	Semipalmated Sandpiper	sys	1 group, Constant P	107.85	1	2	103.85
6Ba	Bi	Stercorariidae	sys	Flowers	96	0.705	3	90.00
6Ba	TW	Acariformes	all	1 group, Constant P	17.5	1	2	13.50
6Ba	TW	Araneae	all	1 group, Constant P	4	1	2	0.00
6Ba	TW	beetle, flat	all	1 group, Constant P	10.88	1	2	6.88
6Ba	TW	Coleoptera	all	1 group, Constant P	4	1	2	0.00
6Ba	TW	Diptera	all	1 group, Constant P	4	1	2	0.00
6Ba	TW	fly	all	1 group, Constant P	4	1	2	0.00
6Ba	TW	fruitfly	all	1 group, Constant P	17.5	1	2	13.50
6Ba	TW	Milbe	all	1 group, Survey-specific P	16.32	1	4	8.32
6Ba	TW	mosquito	all	1 group, Survey-specific P	17	1	4	9.00
6Ba	TW	spider	all	1 group, Constant P	10.88	1	2	6.88
6Ba	TW	spider, tiny	all	1 group, Survey-specific P	13.55	1	4	5.55
6Ba	TW	Tipulidae	all	1 group, Constant P	10.88	1	2	6.88

8 Declaration

Hiermit versichere ich gemäß § 9 Abs. 5 der Prüfungsordnung für den integrierten binationalen Master-Studiengang Internationaler Naturschutz (engl.: International Nature Conservation) vom 16.08.2006, dass ich die vorliegende Arbeit selbstständig verfasst und keine anderen als die angegebenen Hilfsmittel verwendet habe. Diese Arbeit wurde nicht in der gleichen oder einer ähnlichen Form bereits einem anderen Prüfungsausschuss vorgelegt und wurde bisher noch nicht veröffentlicht.

Hereby I affirm – according to § 9 section 5 of the examination regulations for the integrated bi-national Master programme International Nature Conservation (deutsch: Internationaler Naturschutz) from 16.08.2006 – that I have penned the present thesis autonomously and that I did not use any other resources than those specified above. This work was not submitted previously in same or similar form to another examination committee and was not yet published.

Dirk

Göttingen, 05 December 2008

Ort/Place, Datum/Date **Name/Name**