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ABSTRACT

For several reasons including population dynamics, urbanisation, agricultural intensification and climate change, bird populations all over the world fluctuate in their distributions and abundances. To access these changes, conservationists are interested in modelling abundance by either using relative or true abundance. Raw survey data origin from a state process describing abundance and an observational process depending on this state process. Therefore, imperfect detection needs to be accounted for in order to display abundance correctly. One way to do this is by using repeated point counts at several locations in order to access detectability while incorporating spatiotemporal variability to the analysis. Thus, in this study, I used consecutively repeated point counts (4 x 5 minutes) at several sites during the breeding season in West Brabant (Netherlands). Standardly, visits per site were conducted once in the first half (P1) and once in the second half (P2) of the breeding season, although some sites were visited only once. I aimed to examine, if additional five-minute counts yielded additional observations, or if all species and pairs are observable in the first five minutes. Additionally, I was interested, if longer counting durations also yield less biased values on estimated abundance per species. Therefore, I investigated the added value of an increase in counting duration by comparing the number of observed species in 5, 10, 15 and 20 minutes. Furthermore, I compared variation within five-minute counts and the frequencies of observations per species. I also compared the mean number of passerines and nonpasserines between periods and assessed the relative amount of display behaviour observed per species. Finally, I estimated abundance using N-mixture models and thus, accounted for imperfect detection. I implied time of day, time of year and the number of other observations per five-minute count to the detection model and the relative share of open, forest and urban area to the abundance model. My results found that most species were detected in the first five minutes, while added values disproportionately increased with additional five-minute counts. The mean number of observations for passerines and nonpasserines differed significantly both between and among groups. Passerines showed significantly more display behaviour than nonpasserines. Most species were only detected once or twice per visit. On average, one five-minute count yielded half the observations obtained from four five-minute counts. The used state and detection variables explained significant amounts of the variance in the observed data. An increase in point count duration resulted in less overestimated species. Although the additional value of raw count data is widely researched, the effect on estimations is researched to a lesser extent. My results indicate a counting duration of 10 minutes to be most effective on the number of observations. However, the effect of counting duration on estimations suggests three-five-minute counts to achieve most accurate estimations. I suggest, for large-scale surveys like the breeding bird atlas of the Netherlands, two five minutes and two visits are sufficient to estimate abundance correctly.

1. INTRODUCTION

Birds from all over the world suffer from population declines due to agricultural intensification (Newton 2004), climate change (Crick 2004, Thomas et al. 2004), habitat fragmentation (Fischer & Lindenmayer 2007) and urbanisation (McKinney 2002, Sol et al. 2014), while only few species benefit from human dispersal and its consequences (Møller 2009). Subsequently, the population size and distribution of many species do not only decrease, but may shift latitudinally and/or altitudinally and thus, underlie constant change (Barbet-Massin et al. 2012). As birds are important indicators for changes in species richness, bird research yields great advantages in the investigation of biodiversity (Bryce et al. 2002, Bult & Poelmans 2007, Larsen et al. 2012). These advantages include assessable species richness and relatively simple identification, great knowledge of habitat claims and distribution, data availability and their comparatively rapid response to environmental changes (Bibby 1999, Bibby et al. 2000, Bult & Poelmans 2007, Larsen et al. 2012, Schmeller et al. 2012). Thus, modelling birds can be successfully used to infer on the integrity of ecosystems and help satisfying increasing demands on up-to-date bird data in many different countries (Bryce et al. 2002, Sierdsema & van Loon 2008). Unfortunately, concern alone does not allow to recognise fluctuations in populations and their dynamics and thus, quantitative research is very important. The two single most basic state variables for the research in birds are distribution (or occupancy) and abundance (population size) (Balmford et al. 2003, Bart 2005, Kéry and Royle 2015). Both distribution and abundance can only be defined by discretely specifying the space they refer to and may require further discretisation of a surveyed region into "sites" (Kéry & Royle 2015). A species' distribution refers to its spatial arrangement and therefore describes the portion of occupied space within a study area (Kéry & Royle 2015, MacKenzie et al. 2006). By contrast, a species' abundance represents its' frequency within a study area and thus, population size (Gregory et al. 2004, McGill et al. 2007). It may often be of advantage to aim for the examination of abundance rather than occupancy as, despite their indisputable linkage, occupancy merely summarises abundance (Gaston et al. 2000, Kéry & Royle 2015). However, complete knowledge about abundance allows perfect inference on occupancy but inference is not so simple the other way around (Kéry & Royle 2015).

Thus, even though occupancy data can be elaborated statistically to compute abundance posteriorly, it is reasonable to directly address abundance whenever feasible (He & Gaston 2000, Kéry & Royle 2015, MacKenzie & Nichols 2004). The state of knowledge of avian abundance from regional to transnational areas is often illustrated in breeding bird atlases such as the Breeding Atlas of Britain and Ireland (Balmer et al. 2013), the Breeding Bird Atlas of the Netherlands 2012 – 2015 (Schekkerman et al. 2012, Sovon, unpublished) or the EBCC Atlas of European Breeding Birds (Hagemeijer & Blair 1997). Often, these atlases impart recent scientific findings to a wide range of people and simultaneously illustrate the current state and historical changes in abundance (Gibbons et al. 2007, Risley et al. 2012). Although quantities and current states are apparent from the summarised illustrations in breeding bird atlases, the underlying factors influencing specific abundance are much more difficult to interpret. Understanding abundance is indeed complicated, as birds from all over the world differ in their social and territorial behaviours, which in return shape their density and breeding habits (Thiollay & Jullien 1998). Besides, a species' abundance is usually influenced by a number of factors including food supply, habitat structure, species composition and its proximity and influence due to human settlements (Gregory et al. 2004, Lichstein et al. 2002, Mancke & Gavin 2000). Therefore, abundance is hardly uniform throughout a study area and varies among sites both within and between species (Kéry et al. 2005, Thompson 2002). Birds of the temperate region, however, breed within a relatively short time frame of a few weeks, referred to as the breeding season. Within this breeding season, birds occupy territories in a suitable habitat and can therefore be found in relatively confined spaces (Gregory et al. 2004). Thus, the breeding season is a suitable timeframe to evaluate breeding pairs or territories at a given area without having to worry too much about fluctuations during this time.

One possible approach to collect abundance-data is by applying closed capture-mark-recapture methods (e.g. Gregory et al. 2004, Lindberg 2012). Reconfirmation of sightings or captures of previously marked birds in a closed population allow conclusions about capture probability and therefore, estimating population size (Lindberg 2012). These methods are capable of accessing unique information such as post-fledging survival (Wernham et al. 2002) and yield certain advantages relevant to understanding population dynamics (Gregory et al. 2004, Lindberg 2012). However, species with small populations and low capture rates are difficult to approach with capture-mark-recapture methods (MacKenzie & Kendall 2002, Royle 2004a). Instead, counting unidentified specimen regardless of their identity often is a lot more practicable and thus, more commonly used in temperate regions to evaluate species abundance (Gregory et al. 2004, Fiske & Chandler 2011). The most logical approach to gather abundance-data using such surveys is a full census of all breeding birds within a specific area. Problematically, a full census may, depending on the size of the area of interest, require immense effort from numerous observers, and might thus often exceed practical limits (Bibby 2000, Butler et al. 2015). Therefore, a more convenient approach is to survey fractions of an area of interest (Emlen 1971, Gregory et al. 2004). The currently most used methods to survey population size are mapping, line transects and point transects (or point counts) (Buckland 2006, Gregory et al. 2004, Rosenstock et al. 2002). Mapping is a widespread technique to gather data on breeding bird abundances by counting territories over a predefined area (Gregory et al. 2004). Transects are powerful surveying methods capable of gaining qualitative data with remote survey effort and are assumed to be very difficult to substitute (Gregory et al. 2004, Järvinen 1976). While line transects are used for continuous sampling of occurring species from a predefined route, observers remain at predefined locations for a certain duration when conducting point counts (Buckland 2006, Gregory et al. 2004). Point counts are a popular tool among ornithologists, which is why they are used in various small and large-scale studies, including this one (Alldredge et al. 2007a, Gregory et al. 2004, Rosenstock et al. 2002).

Typically, point count data are characterised by a large amount of “zeros” and relatively few observations per site and species (e.g. Kéry & Royle 2015, Royle 2004b, Royle & Dorazio 2008). However, while raw counts only allow to confirm the presence of a certain species on a given location, its absence is far more difficult to prove. Thus, detection probability needs to be accounted for (Alldredge et al. 2007b, MacKenzie 2005, Royle et al. 2005). Furthermore, while abundance is a state variable that is assumed to stay constant throughout the breeding season, this assumption cannot be made for detection probability (Gu & Swihart 2004, He & Gaston 2003). Non-detection may be the result of a species truly not being present at a site, or the consequence of not being noticed by the observer (MacKenzie 2005, Tyre et al. 2003). Therefore, different counts may result from site-specific factors, but simultaneously are influenced by the observational process itself (Iknayan et al. 2014). Factors known to influence the observation of birds are site-specific, such as vegetation structure (Pacifici et a. 2008) or species-specific such as time of day (Conway et al. 2004, Verner & Ritter 1986), day of year (Selmi & Boulinier 2003), individual heterogeneity (Iknayan et al. 2014) or distance to the observer (Gregory et al. 2004, Simons et al. 2007). Detection also varies between species and locations. Additionally, detection may differ substantially between observers (Alldredge et al. 2006, Conway et al. 2004). Assuming perfect detection from raw count data may therefore lead to severely biased abundance estimates (MacKenzie 2005, Rosenstock et al. 2002, Royle et al. 2005). For that reason, detection probability needs to be accounted for (Alldredge et al. 2007b, Royle et al. 2005). These problems can be targeted by aggregating information from surveyed sites on the basis of a repeated-measures structure with observations from “M” sites and “J” visits (Johnson 2008, Kéry & Royle 2015). This aggregation is often referred to as a “meta-population design” and allows accounting for site-specific abundance, while maintaining the information from site-specific covariates (Kéry & Royle 2015, Royle & Dorazio 2008). Sampling methods such as double-observer sampling (Nichols et al. 2000), removal sampling (Farnsworth et al. 2002), site-occupancy sampling (Fiske & Chandler 2011), distance sampling (Buckland et al. 1993, Reidy et al. 2011) and repeated point counts (Royle 2004a) are all capable of implying these repeated-measures designs (Fiske & Chandler 2011). While processing data from these designs, spatial replication allows to understand site-specific abundance. Additionally, repeated visits to the same sites help understanding temporal variation regarding detectability

(Iknayan et al. 2014, Lele et al. 2012). Applied to large scale monitoring, such implications allow precise estimates regarding population size and are thus very effective for a better understanding of the underlying factors influencing local abundance and detectability (Sauer & Link 2011).

In this study, I used the repeated-measures structure of consecutively executed, repeated point counts to understand the effect of point count duration on species richness and observed pairs in West Brabant (Netherlands). As this study was conducted as part of the new breeding bird atlas of the Netherlands, I thus adopted the for the project precasted methodology, except for the elongated duration of point counts per visit (see Schekkerman et al. 2012). For this reason, I used four five-minute counts compared to the single or double (if observers volunteer for it) five-minute counts standardly used for the breeding bird atlas of the Netherlands 2012 – 2015 (Schekkerman et al. 2012, Sovon 2012). Even though the effect of point count duration on the observed individuals and species has been investigated for decades (e.g. Lynch 1995), the influence of point count duration and the number of repeated point counts on the estimation of abundance is less clear to many scientists. Also, the specific information gained by using several counts consecutively compared to one elongated count is poorly investigated to my knowledge.
For that reason, (1) I examined, if the number of species increased in direct correlation to counting effort or if longer counting durations are a waste of time. The effect of point count duration on the observable species richness plays a significant role for scientists and ornithologists interested in modelling these species. This is because only species detected on some of the surveyed sites allow further investigation of their underlying range and density. Importantly, species composition, densities per species, the observer's detection capabilities and different habitats are factors known to affect detections not only of individuals but species (Boulinier et al. 1998, Kéry & Schmid 2006). Similarly, (2) I examined this correlation on the number of observed pairs. The specific structure of consecutive point counts allows to address several questions that cannot be answered from data of a single elongated count. Two visits to each site executing such consecutive point counts allow further understanding of the differences in the number of observations over the breeding season for each species. I therefore examined (a) the distribution of observations over the number of five-minute counts for each species. I assume that species with most of their observations in only one or two five-minute counts are much more likely to be missed in any random five-minute count and are therefore best surveyed with longer point counts. Alternatively, one or two five-minute counts should be sufficient for species regularly detected in all four five-minute counts. Furthermore, (b) I investigated, if more five-minute counts correspondingly yield more observations or if one or two five-minute counts already produce all the observations per site and species. Finally, (c) I compared the number of observations per species and five-minute count to see, if all five-minute counts roughly yield the same number of observations. Further, (3) I investigated the differences in display behaviour of passerines and nonpasserines. Species mainly detected because of their song need to be surveyed when song activity peaks, while those mostly detected visually can be surveyed outside of their singing activity as well. Finally, (4) I used hierarchical models to distinguish between the state process determining abundance and the detection process approaching detectability conditional to this abundance (Fiske & Chandler 2011, Kéry & Royle 2015, Royle & Dorazio 2008). I used so called N-mixture models, a specific type of hierarchical models, to treat site specific-abundances as random variables and to assume a binomial distribution for the observational process, while a Poisson- or negative binomial distribution is assumed to model species abundance (Royle 2004b). I accounted for spatial differences in abundance by using the habitat composition in a diameter of 200 m around each point count location. Observational differences were accounted for by implying time after sunrise and day of year to my detection model. Additionally, I was interested in the effect of the number of observed individuals per site on the detection. As noise level influences detection probability, I presumed some effect of the number of birds present on detecting one specific, possibly very distant or quiet individual (e.g. Parris & Schneider 2008, Simons et al. 2007). Therefore, I used the number of present birds in each five-minute count as a third variable for modelling the detection process.

2. MATERIAL AND METHODS

2.1 Study Area

West Brabant (Figure 1) forms the western part of the Dutch province of North Brabant and can be geologically separated from the rest of the province by the Roer Valley Graben (Sierdsema 2007). The western border is formed by the Brabant Wall and the river Scheldt while the northern border is formed by the rivers New Merwede and Hollands Diep, both part of the Rhine-Meuse-Scheldt-Delta. It is thus bounded by the provinces of Zeeland in the west, South Holland and Gelderland in the north and directly abuts to Belgium in the south. West Brabant's total area aggregates to an expanse of 1695 km² (Sierdsema 2007). Despite its relatively small size, West Brabant proves to be of both scenic and geologic complexity which directly reflects in botanic and faunal biodiversity (Sierdsema 2007). Historically, the tertiary formations of Boom, Breda and Oosterhout are impermeable to water. However, Pleistocene fluvial deposits of sandy soil enable seepage of large quantities of water in the southern part of West-Brabant (Sierdsema 2007). Conversely, Holocene deposits of water-resistant marine clay, caused by the sea level rise after the last ice age, lead to seeping spring water in the northern and north-western part of West-Brabant. This abrupt transition of Pleistocene sandy soils and Holocene clay soil is unique to the western Part of the Brabant Wall and houses exceptional biocenoses (Sierdsema 2007). Additionally, the regions were drastically shaped by anthropomorphic landscapes and only very few areas, such as De Biesbosch, remain unaffected (Sierdsema 2007).

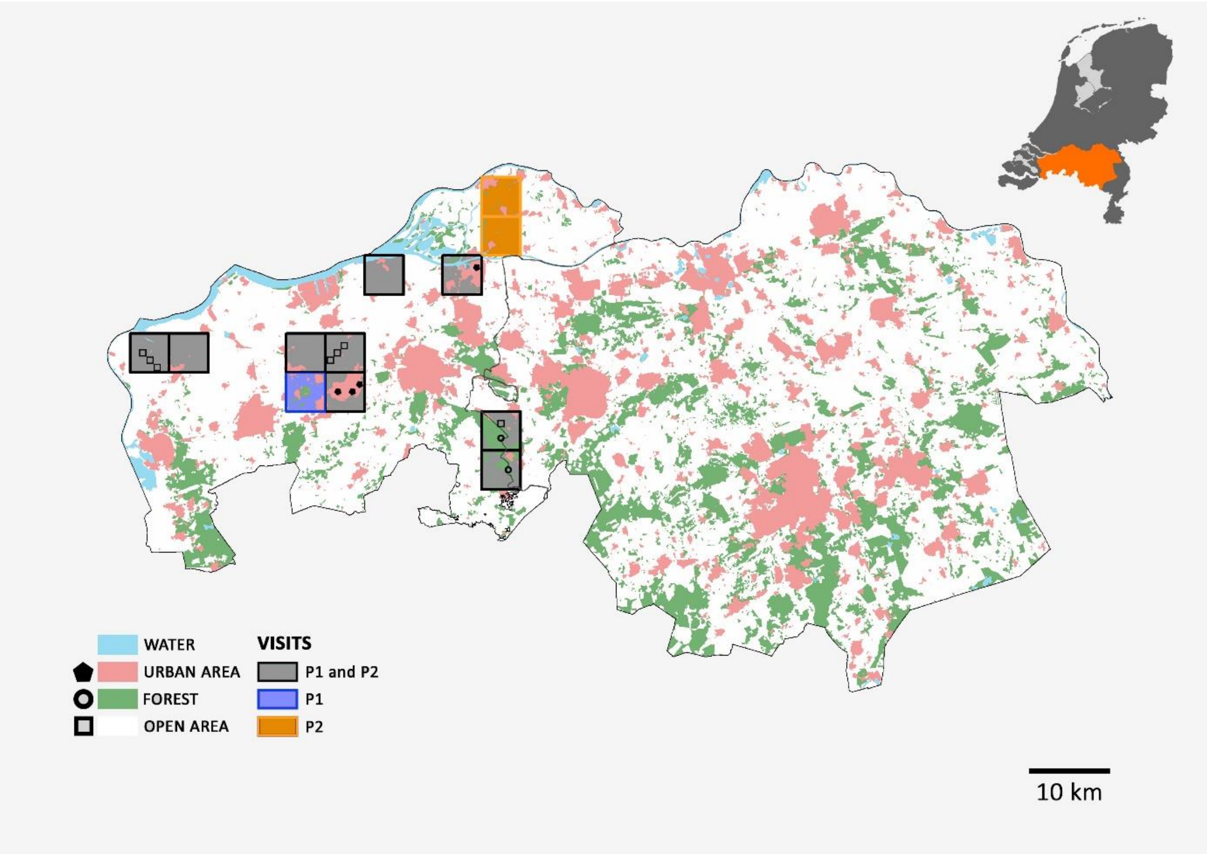

Figure 1 **Map of North Brabant.** This graph shows the atlasblocks in West Brabant surveyed in this study. Black atlasblocks were visited both in period one (April 1st – May 15th 2015) and period two (May 16th – June 30th 2015). Blue atlasblocks were only surveyed in the first period (P1), orange ones only in the second period (P2). Urban area, forests and water are shown separately, remaining habitats are not outlined specifically. Top-right illustration gives the Netherlands with North Brabant highlighted in bright orange. West Brabant is separated from Middle- and East Brabant by a solid black line. Symbols left of the legend and in atlasblocks give specific sites with more than 90 % urban area (pentagon), more than 90 % forest area (circle) and more than 95 % open area.

2.2 Study Objects
Although West Brabant only covers 4.8 % of the Netherlands (Sierdsema 2007), nearly all regular, national breeding birds breed in West Brabant. Several species even occur with an overproportional share of the Dutch population (Sierdsema 2007). According to Bult et al. (2007), 170 species of birds were ascertained to breed during the fieldwork in 1989 – 1996 and 2000 – 2002 in West Brabant. 86 species (5 introduced) bred in relatively large quantities whereas 20 were occasional breeders (2 introduced) and 11 only were formerly breeding in the past (Bult et al. 2007). An additional 23 species are categorised as (rare) potential breeders, including five allochthonous species. All 12 introduced species were either directly introduced to the Netherlands or originate from populations introduced to other European countries. The recent total number of West Brabant's breeding birds, however, may underlie marginal divergence to this number. The breeding bird survey of 1998 - 2000 revealed a total of 236 bird species breeding in the Netherlands with at least 29 of these being allochthonous species (Hustings et al. 2002).

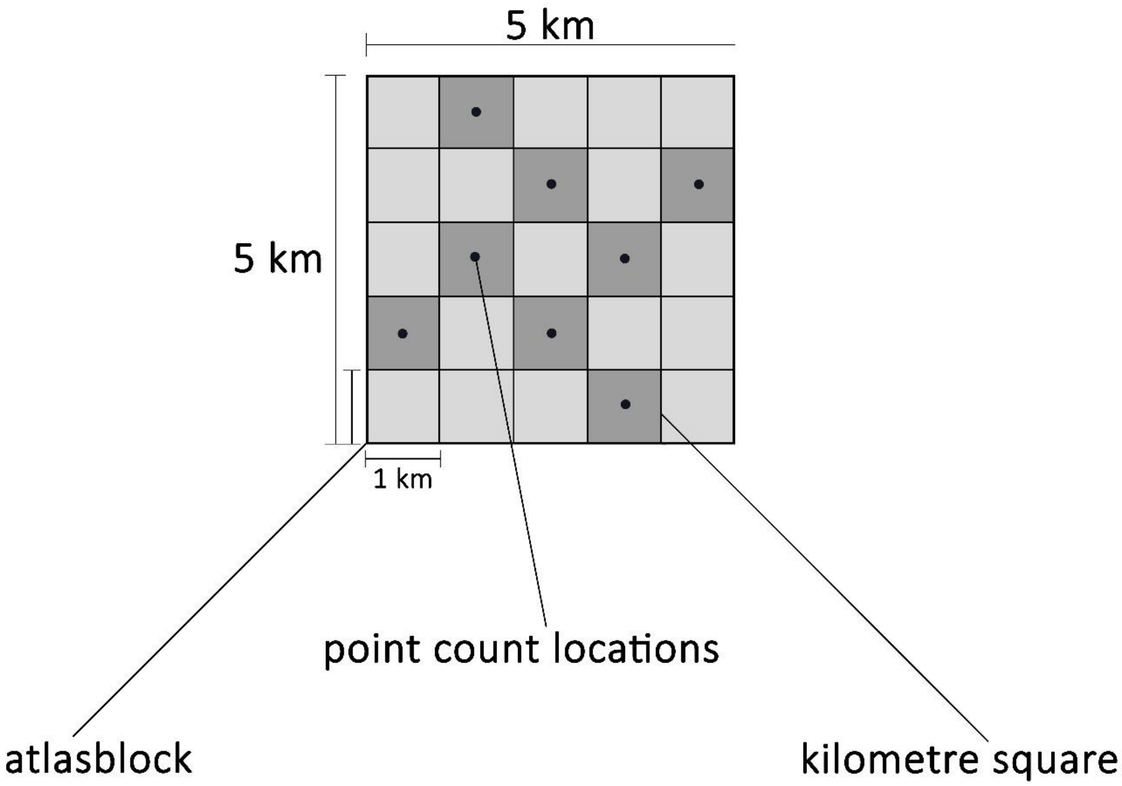

Figure 2 Scheme of atlasblocks and kilometre squares following the standardised fieldwork for the new Breeding Bird Atlas for the Netherlands 2012 – 2015 (Schekkerman et al. 2012). The dark areas comprise the "golden grid" kilometre squares with point count locations in the centre.

2.3 Data Recording
The land coverage of the Netherlands can be divided into 1.685 uniquely identifiable atlasblocks (Figure 2, Table 1) (Sovon 2012). Each atlasblock typically measures 5 x 5 km and can be further separated into 25 kilometre squares, measuring 1 x 1 km respectively (Sovon 2002). Eight specific kilometre squares, referred to as "golden grid", are surveyed under nationally standardised conditions using both grid and point count surveys (Schekkerman et al. 2012). The centre of this golden grid, shifted to the closest accessible piece of land if necessary, generated the location for the point counts for this study, following a regular sampling approach (Gregory et al. 2004). The fieldwork for this study was carried out in a single breeding season, defined as the timespan between April 1st 2015 and June 30th 2015 and was conducted by a single observer. Due to the restrictions for the Breeding Bird Atlas of the Netherlands 2012 - 2015, sites were to be visited twice during one breeding season (Sovon

2012). Therefore, the breeding season was separated into two periods, the first one (P1) lasting from April 1st to May 15th and the second one (P2) lasting from May 16th to June 30th. Furthermore, all five-minute counts were to be executed between sunrise and six hours after sunrise (Sovon 2012).

Table 1 **Glossary.** Glossary listing important terms used in this study (left), followed by a definition to distinguish them from similar words (right).

TERM	DEFINITION
atlasblock	The entire country of the Netherlands is subdivided into "atlasblocks". Although they may be deformed towards borders or coast lines, a typical atlasblock measures 5 x 5 kilometres. Each atlasblock can be uniquely identified by a 3- or 4-digit number.
five-minute count	A "five-minute count" defines the execution of counting all birds on a given location for a timespan of five minutes.
golden grid	The "golden grid" specifically defines eight kilometre square in which all standardised point counts were conducted during the fieldwork of this study.
kilometre square	A "kilometre square" is a subdivision of an atlasblock and measures 1 x 1 kilometre. Thus, an atlasblock comprises of 25 kilometre squares, each recognisable by a 2-digit number only given once per atlasblock.
obsCovs	Covariates used for modelling detection probability describing observation circumstances. "DayNr" describes the date of a visit as a whole number (according to Gregorian calendar). "StartTime" describes the time past sunrise in minutes for the beginning of each five-minute count. "SiteObsNr" describes the number of observations of other birds during the current five-minute count.
observation	The visual or acoustic detection of an individual or pair, presumed belonging to the same territory. Thus, both male Common Chaffinch and a presumable pair of Dunnocks counted as one observation.
period 1 (P1)	"P1" is defined as the first half of the season in which five-minute-counts were conducted, namely from April 1st 2015 to May 15th 2015.
period 2 (P2)	"P2" is defined as the second half of the season in which five-minute-counts were conducted, namely from May 16th 2015 to June 30th 2015.
point count	A "point count" defines the method used to survey all breeding birds at all sites visited for the purpose of this study.
season	The (breeding) "season" defines the timespan in which five-minute counts were conducted, lasting from April 1st 2015 to June 30th 2015.
site	The "site" is the location a five-minute count is conducted at.
siteCovs	Covariates used for modelling abundance describing site characteristics. "Open_Area" is defined as all areas including meadows and agricultural land (and included water surface only for the Mallard, *Anas platyrhynchos*). "Forest_Area" is defined as areas including trees. "Urban_Area" is defined as anthropologically used areas.
visit	A "visit" comprises all five-minute counts at a site for a single day. For this study, all visits entailed four five-minute counts consecutively following each other.
yObs	Observation matrix with one column per five-minute count including binomial detection/non-detection data and one row per visited site.

For the purpose of this study, 12 of the 96 atlasblocks in West Brabant (Figure 2) layed the foundation for 136 visits conducted at 81 sites, although some statistics were processed only for the 55 sites visited in both periods (Appendix Table 1). Each visit included four five-minute counts consecutively following each other. The first five-minute count was started immediately upon arrival and thus, each visit summed up to exactly 20 minutes per site. All observations were expressly noted on an open radius point-centred map regarding to the specific five-minute count and the exact location of their first detection, undiscriminating between visual and acoustic detection. Maps with auxiliary radius lines at 50, 100 and 150 m were used in predominantly closed habitats (forest, urban area), while maps with lines at 100, 200 and 300 m were used in predominantly open habitats (agricultural land etc.) to simplify distance estimation. Prior to counting, I recorded date, time of day and the counting conditions. The number of observations per five-minute count was extracted posteriorly once the counts were finished. While the date remained constant for the entire visit, the time of day and the number of observations varied for each of the five-minute counts. Therefore, all observations within a specific five-minute count obtained the same starting time and number of observations. Birds were surveyed in pairs, meaning that a single Common Chaffinch or a presumable pair of Dunnocks were each recorded as one observation, therefore counting the numbers of breeding pairs, not the individuals. Additionally, each detected “pair” was suffixed with the highest observed breeding code for the entire visit to ease the interpretation on breeding probability. For categorising the breeding behaviour, breeding codes were used following the national scheme for the breeding bird atlas of the Netherlands 2012 - 2015 (see Appendix). Birds clearly intending of flying over a survey area without any strive of landing, such as high-flying migrating individuals, were not included in this survey. Detection and non-detection were denoted separately for each of the four five-minute counts for each observation and later combined to a binomial four-digit code of information (Appendix Figure 1). While “1” indicated detection, “0” indicated non-detection. Correspondingly, a singing chaffinch with the code “1111” was seen in all four counts, while a pair of blackbirds with “0101” was only detected in the second and fourth five-minute count. All observations were mapped in such a way that they were assignable to each specific point count, thus reducing chance for double-counts to a minimum. Therefore, individuals detected immediately after an already observed bird either stopped its vocal activity or hid behind an obstacle, were presumed to be the same individual. Between counts, only major movements of the same individual or pair were annotated. Species well known for breeding clustered in dense aggregations (such as herons or Rooks) were treated with exceptional caution. While binoculars (10 x magnification) helped to simplify visual detection, no tools were used to ease acoustic detection. All sites were visited independently regarding day and weather conditions to the point where circumstances such as heavy rain or wind above 3 Beaufort obviously influenced the birds’ activity and thus, detection probability.

2.4 R-Script and Statistical Analysis

All confidence intervals were set to 95 % and significance is referred to as $p \leq 0.05$ %.

2.4.1 R Script

All data were arranged and processed using the statistical computing software R (version 3.2.2, R Core Team 2015) and the text editor Tinn-R (version 4.00.03.05, Faria 2012). The original digitalised dataframe imported from the Sovon-database needed further adjustment due to an hh-mm-ss format for the starting time of each five-minute count and a yyyy-mm-dd format for the date of each visit. Thus, data were processed using R’s base-package (R Core Team 2015) and the lubridate-package (Grolemund & Wickham 2011) in order to convert the starting time to integers of minutes after sunrise. The date was converted to the corresponding day of year using the same two packages. All graphs were built using R’s graphics-package (R Core Team 2015) and saved using the grDevices-package (R Core Team 2015). All tables were first designed in R, saved using the utils-package (R Core Team 2015) and further processed in Windows Excel and Windows Word (Microsoft Office 2010). Goodness of fit-tests for selected N-mixture models were performed using the Nmix.gof.test- function of R’s AICcmodavg- package (Mazerolle 2016).

All observational data were gathered in a single dataframe called “AllData” (Appendix Table 2). It included a column for the species’ ID (“EuringID”) and the site it was located at (“SiteID”). The binomial detection code was listed both in a single column for the entire visit (“Detection_Code”) and in four separate columns for each five-minute count (“ObsCount1” – “Obscount4”). The day (“DayNr”) and starting time (“StartTime1” – “StartTime4”) were later used as observational covariates while the habitat composition (“Open_Area”, “Forest_Area”, and “Urban_Area”) was used for the estimation of abundance. The DayNr-column refers to the date of the visit and is assignable to the day of year. The time covariate refers to the beginning of each specific five-minute count and expresses the minutes after sunrise. The site-covariables represent the relative share of the three habitat types within 200 meters around the point count location. The column “Amount” was later used for counting purposes (Appendix Table 2).

2.4.2 Statistics

"Species Overview"

For further examination and to enable comparison between P1 and P2, the "AllData"- dataframe was split into separate dataframes per period, "AllDataP1" and "AllDataP2". The number of observed species was compared between the two periods P1 and P2, but also over the counting duration for 5, 10, 15 and 20 minutes. For comparability, only data from the 55 sites visited in both periods were compared between periods using the mean number of species detected per duration. A paired t-test was used to compare mean number of observed species between periods.

Additionally, I calculated the mean number of observations for all passerines and nonpasserines in P1 and P2 both for all sites visited (n = 81) and the subset of 55 sites visited in both periods (see 3.1.2). I compared the mean number of passerines between P1 and P2 and did so for nonpasserines and all observations too. To compare the mean numbers of observations, paired t-tests were used for the comparison within passerines, nonpasserines and all observations, while Welch two sample t-tests were used to compare passerines and nonpasserines with each other in P1 and P2.

"Single Species Analysis"

All species exceeding 20 observations for sites visited in both periods (n = 55) were examined in more detail. This was the case for 38 species. To maintain lucidity throughout this thesis, six main species were picked to represent patterns and general structure of detection and estimations throughout the 38 species. All results for the other species can be found in the appendix. These species were picked for several practical reasons including a decent number of observation per five-minute count and period, as well as for pointing out patterns in species of different habitats. The six species are Northern Lapwing (*Vanellus vanellus*), Common Wood Pigeon (*Columba palumbus*), European Robin (*Erithacus rubecula*), Common Blackbird (*Turdus merula*), Eurasian Blackcap (*Sylvia atricapilla*) and Common Chaffinch (*Fringilla coelebs*). While Northern Lapwings are typical farm- and grassland species, the other species need a certain amount of canopy cover to build their nests. European Robins are bound to an adequate cover of scrubs and trees and are most active in the beginning of the breeding season. Common Blackbirds and Common Chaffinches both appear frequently in forested and urban habitats. Eurasian Blackcaps are the only short-distance migrants treated in this selection (Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007).

Data on relative territorial behaviour were obtained by dividing the number of observations with breeding code 2 per period (singing or displaying individual in suitable breeding habitat) by the total number of observations at all sites (n = 81) for P1 and P2 (Appendix Table 4 and 5).

To assess the relative frequency a species was observed with, I compared the number of observations in four categories. The combined observations of both periods were categorised into "seen in one five-minute count" (1x5), "seen in two five-minute counts" (2x5), "seen in three five-minute counts" (3x5) and "seen in four five-minute counts" (4x5), therefore indicating if an observation was made in (any) one, two, three or all four five-minute counts. All observations were treated as mutually exclusive and thus only appear once per category. The observed and expected frequency distributions were compared using a Pearson's chi-squared test goodness of fit statistic. Following the very simplified assumption (excluding all biological effects) that detection and non-detection are equally likely ($p = 0.5$), detection per category can be modelled using a binomial distribution. Thus, observed detection is compared to the following statements (only 1-4 of which are implemented to the analysis):

(0) Detection in <u>zero</u> five-minute counts: $(1-p)^4$
(1) Detection in <u>one</u> five-minute-count: $4p(1-p)^3$
(2) Detection in <u>two</u> five-minute-counts: $6p^2(1-p)^2$
(3) Detection in <u>three</u> five-minute-counts: $4p(1-p)$
(4) Detection in <u>four</u> five-minute-counts: p^4

The standardised fieldwork for the Dutch breeding bird atlas uses a single five-minute count. To comprehend the added value of additional five-minute counts, the observations of the first, the first two, the first three and all four counts were compared descriptively.

To compare variability within five-minute counts within and between periods, observations per species were also analysed for first, second, third and fourth five-minute count specifically. As the same potential pair might have been seen in two different five-minute counts per period, categories cannot be seen as mutually exclusive. Therefore, the sum of all four categories combined displays the number of observations rather than number of observed pairs. Pearson's Chi-squared tests were performed to compare the distributions between counts in P1 and P2.

<u>Full Model</u>

Both abundance and detection probability were modelled for all species with no less than 20 observations at sites visited in both periods (n = 33) and were computed using the unmarked package (Fiske & Chandler 2011). Unmarked offers a wide range of so called hierarchical models. By presuming an observation as a combination of the partly latent abundance and a detection process conditional on this abundance, these models conditionally relate abundance and detection to each other (Kéry & Royle 2015). Wherever the overdispersion-parameter c-hat indicated overdispersion, negative binomial mixtures were used instead of the otherwise used Poisson distribution to model the latent abundance distribution. Specifically, binomial-Poisson mixture models were used to model abundance by assuming a Poisson-distribution while detection was modelled assuming a binomial distribution conditional on the abundance (Royle 2004b). Under these assumptions, the abundance per site is treated as a random effect. The integration of the binomial likelihood for observed counts over plausible values of abundance allows computation of the marginal likelihood of the counts at each site (Royle 2004b). To fit mixture models for repeated point count data as described by Royle (2004b), data was first prepared and then fitted using the fitting-function pcount() in unmarked. Each model required an observation-matrix called "yObs" representing the binomial observational code for each five-minute count. This matrix was amplified by a "siteCovs" dataframe including parameters for modelling the abundance and an "obsCovs" list, including the parameters for modelling the detection probability (Table 1).

The dataframe for the abundance parameters includes one column for each parameter and one row per visited site. The relative frequencies of the three habitat variables "Open_Area", "Forest_Area" and "Urban_Area" within 200 m around each site were pooled to a list (siteCovs) containing the proportional share for terrestrial open habitat, forests and urban habitat correspondingly. Importantly, these three habitat variables do not contain 100 % of the entire surface area. To avoid collinearity during analysis, habitat types not perfectly fitting any of these three criteria (e.g. "water" or "paths") were omitted from analysis so that their sum did not reach 100 % when there was more than one habitat type per site (Table 1). For further calculations of the estimated mean number of pairs per site, it is important to exclude surfaces like "water" or "reed" for all birds that do not regularly appear or nest in these habitats. Of the 33 species further investigated with binomial-Poisson Mixture Models, the Mallard, *Anas platyrhynchos*, was the only species regularly observed on water. Thus, water is only included to "Open_Area" for the Mallard, while the siteCovs for all other species remain identical (open terrestrial habitat, forests and urban habitat). All abundance-covariates were scaled by dividing them by 100 to ensure comparability among them. The list for the detection parameters included one dataframe for each parameter with one column per visit and one row per visited site. While "DayNr" was the same for all visits per site in each period (but might have differed from other sites), "StartTime" and "SiteObsNr" differed between five-minute counts. ObsCovs were scaled using the default of the scale-function in R's base package. Therefore, each element is subtracted by the mean and divided by the standard deviation of the entire column.

All models were fitted to data from sites only visited in both periods (n = 55) for each species. In total, 494 models were tested using all combinations of 26 formulas for the detection process and 19 formulas for the state process (Table 2). Model selection was based on ranking the models by AIC, (Akaike Information Criterion) (Akaike 1973). All Models with a delta-AIC ≤ 2 compared to the model with the lowest AIC score were believed as equivalently fitting models and listed in a data frame called "BestModelList" for each species. First, model selection was based on reducing insignificant terms for the detection model as long as only one model was left (backward elimination) or all terms showed significant p-values in which case no further reduction was conducted. In a second step, the remaining models in "BestModelList" were processed using the same methods for the abundance model until only one model was left. If two models included the same number of significant terms and further reduction was impossible, I picked the model with the lower AIC. All selected, best models per species were tested for goodness of fit with a Pearson's chi square statistic using the Nmix.gof.test- function of R's AICcmodavg-package. Per species, 1000 simulations were computed to assess the Pearson's chi square statistic comparing the observed and expected counts. Based on these fitted models, abundance estimations were computed for (1) observations from the first five-minute count of both periods, (2) the first and second five-minute counts of both periods, (3) the first, second and third five-minute counts of both periods as well as (4) period 1 and (5) period 2 and (6) all five-minute counts. Estimation was based on the extracted best unbiased predictors of the posterior distributions of the latent abundance by using empirical Bayes methods (Fiske & Chandler 2011).

Table 2 List of Formulas for all species with more than 20 observations (n = 33) at sites visited in both periods. Each of these formulas were fitted for each species showing more than 20 observations at sites visited in both periods. Formulas with the prefix "Det_" are fitted for testing their influence on detection probability following the first tilde in the pcount-function, those with the prefix "Abu" are fitted for testing the parameters on influencing abundance and followed the second tilde. Each detection formula was combined with each abundance formula and fitted in a model for model selection by AIC. The number following the underscore indicates the number of terms within the formula. Small letters indicate a = StartTime, b = DayNr and c = SiteObsNr for the detection formula and a = Open_Area, b = Forest_Area and c = Urban_Area for the abundance formula. A number following a small letter indicates an additional quadratic term to the otherwise linear terms. Accordingly, the detection model "Det_3ab2" uses three terms, a linear term for StartTime (a) and a linear and a quadratic term for DayNr (b).

DETECTION MODEL	FORMULA
Det _1a	StartTime
Det_1b	DayNr
Det_1c	SiteObsNr
Det_2a2	StartTime + I(StartTime^2)
Det_2b2	DayNr + I(DayNr^2)
Det_2c2	SiteObsNr + I(SiteObsNr^2)
Det_2ab	StartTime + DayNr
Det_2ac	StartTime + DayNr
Det_2bc	DayNr + SiteObsNr
Det_3a2b	StartTime + DayNr + I(StartTime^2)
Det_3ab2	StartTime + DayNr + I(DayNr^2)
Det_3a2c	StartTime + SiteObsNr + I(StartTime^2)
Det_3ac2	StartTime + SiteObsNr + I(SiteObsNr^2)
Det_3b2c	DayNr + SiteObsNr + I(DayNr^2)
Det_3bc2	DayNr + SiteObsNr + I(SiteObsNr^2)
Det_3abc	StartTime + DayNr + SiteObsNr
Det_4a2b2	StartTime + DayNr + I(StartTime^2) + I(DayNr^2)
Det_4a2c2	StartTime + SiteObsNr + I(StartTime^2) + I(SiteObsNr^2)
Det_4b2c2	DayNr + SiteObsNr + I(DayNr^2) + I(ObsNr^2)
Det_4a2bc	StartTime + DayNr + SiteObsNr + I(StartTime^2)

DETECTION MODEL	FORMULA
Det_4ab2c	StartTime + DayNr + SiteObsNr + I(DayNr^2)
Det_4abc2	StartTime + DayNr + SiteObsNr + I(SiteObsNr^2)
Det_5a2b2c	StartTime + DayNr + SiteObsNr + I(StartTime^2) + I(DayNr^2)
Det_5a2bc2	StartTime + DayNr + SiteObsNr + I(StartTime^2) + I(SiteObsNr^2)
Det_5ab2c2	StartTime + DayNr + SiteObsNr + I(DayNr^2) + I(SiteObsNr^2)
Det_6a2b2c2	StartTime + DayNr + SiteObsNr + I(StartTime^2) + I(DayNr^2) + I(SiteObsNr^2)
ABUNDANCE MODEL	**FORMULA**
Abu_1a	Open_Area
Abu_1b	Forest_Area
Abu_1c	Urban_Area
Abu_2a2	Open_Area + I(Open_Area^2)
Abu_2b2	Forest_Area + I(Forest_Area^2)
Abu_2c2	Urban_Area + I(Urban_Area^2)
Abu_2ab	Open_Area + Forest_Area
Abu_2ac	Open_Area + Urban_Area
Abu_2bc	Forest_Area + Urban_Area
Abu_3a2b	Open_Area + Forest_Area + I(Open_Area^2)
Abu_3ab2	Open_Area + Forest_Area + I(Forest_Area^2)
Abu_3a2c	Open_Area + Urban_Area + I(Open_Area^2)
Abu_3ac2	Open_Area + Urban_Area + I(Urban_Area^2)
Abu_3b2c	Forest_Area + Urban_Area + I(Forest_Area^2)
Abu_3bc2	Forest_Area + Urban_Area + I(Urban_Area^2)
Abu_3abc	Open_Area + Forest_Area + Urban_Area
Abu_4a2b2	Open_Area + Forest_Area + I(Open_Area^2) + I(Forest_Area^2)
Abu_4a2c2	Open_Area + Urban_Area + I(Open_Area^2) + I(Urban_Area^2)
Abu_4b2c2	Forest_Area + Urban_Area + I(Forest_Area^2) +I(Urban_Area^2)

3. RESULTS

3.1 Species Overview

3.1.1 Number of Observed Species

I visited 81 sites between April 1st 2015 and June 30th 2015, 55 of which were visited both in P1 and in P2. At all sites, 96 species were observed. The majority (54.74 %) of these species were passerines (52), fewer nonpasserines (43 species) were detected (45.26 %). The number of observed species was higher in P1 (76) than in P2 (86).

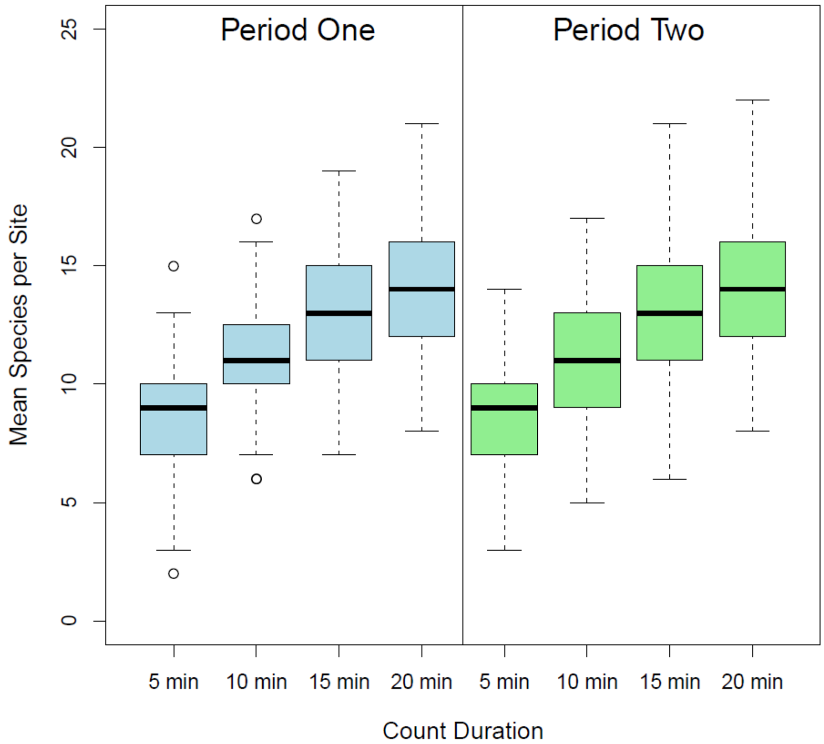

Figure 3 **Mean Number of Species per Site.** The graph shows the mean number of observed species per site at all sites visited in both periods (n = 55) between April 1st 2015 and June 30th 2015. Boxplots in blue (left) show means in P1 while boxplots in green (right) show means in P2 for a counting duration of 5, 10, 15 and 20 minutes. Top and bottom of boxes indicate upper and lower quartile with the median highlighted in between. Whiskers indicate upper and lower quartiles + 1.5 interquartile range (IQR). Circles indicate outliers outside of the upper or lower quartile + 1.5 IQR.

85 of the recorded species were observed in the subset of 55 sites visited in both periods. Again, passerines were more numerous (49 species) than nonpasserines (36 species). The first five-minute count yielded 72 species with an additional six species observed in the second, and another four species in the third five-minute count. On average, the first five minutes on average yielded 8 species per site (P1: 8.64 SD 2.42, P2: 8.62 SD 2.20) while 11 were detected in the first ten minutes (P1: 11.22 SD 2.45, P2: 11.05 SD 2.77), 13 within the first fifteen minutes (P1: 12.82 SD 2.89, P2: 12.87 SD 2.97) and 14 species within twenty minutes (P1: 14.18 SD 3.04, P2: 13.98 SD 2.99) (Figure 3). There was no significant difference between the mean number of detected species per site compared between P1 and P2 ($p = 0.625$, paired t-test, $n = 55$).

3.1.2 Mean Number of Observations per Site

The number of total observations for all sites summed up to 1447 in P1 and 1444 in P2 and thus totally accounted for 2891 observations during the entire season (21.26 per site and visit).

The mean number of observations per site at the entire dataset was 22.97 (SD 6.30) in P1 (63 sites) and 19.78 (SD 4.65) in P2 (73 sites). The 55 sites visited in both periods yielded very similar results, where 2335 observations (21.23 per site and visit) were made during the entire season. Passerines were the more frequent group per site in both periods (P1: 16.53 SD 5.51, P2: 14.76 SD 3.41), while observations of nonpasserines were less frequent (P1: 6.24 SD 4.62, P2: 4.93 SD 3.09). The true differences in the mean number of observations per site varied between visits in P1 and P2 for passerines ($p = 0.003$, paired t-test, $n = 55$), nonpasserines ($p = 0.023$, paired t-test, $n = 55$) and all observations ($p < 0.001$, Welch two sampled t-test, $n = 55$). This is also true for the differences in the mean number of observations of passerines and nonpasserines in P1 ($p < 0.001$, Welch two sampled t-test, $n = 55$) and P2 ($p < 0.001$, Welch two sampled t-test, $n = 55$).

In total, 38 species were detected more than 20 times at all sites. These 38 species formed the basis of the single species analysis in section 3.2, but N-mixture models were computed using data only of the 33 species seen more than 20 times in the subset of 55 sites.

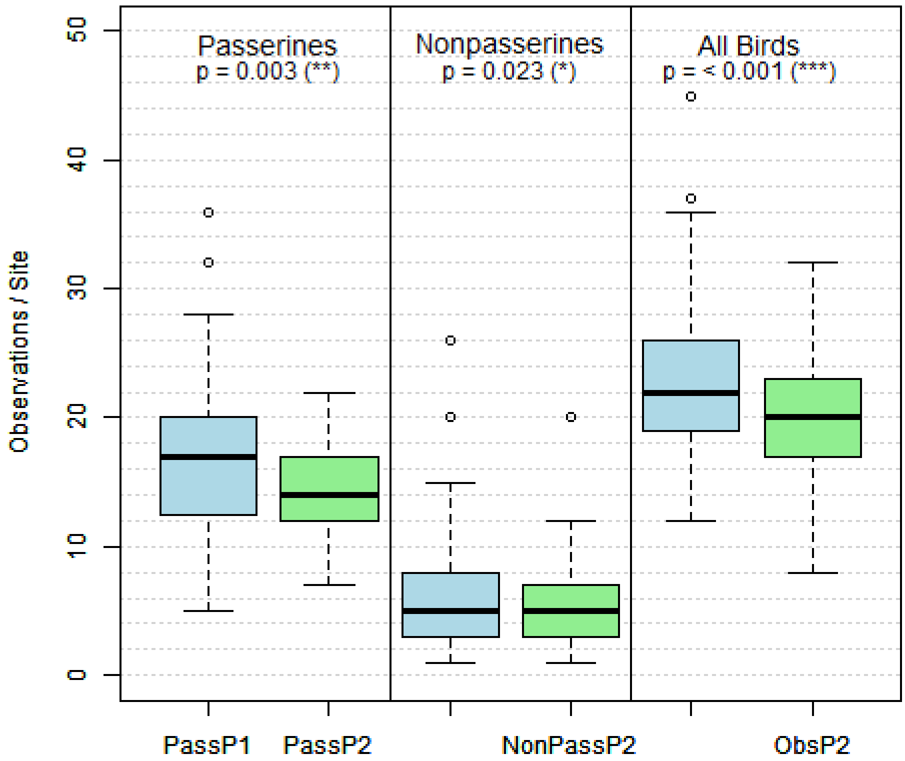

Figure 4 **Mean Number of Observations at Sites Visited in Both Periods.** Boxplots showing mean number of observations for of passerines (Pass) and nonpasserines (NonPass) as well as their combined observations (Obs) in P1 (blue) and P2 (green) at a subset of 55 sites always visited in both periods. Top and bottom of boxes indicate upper and lower quartile with the median highlighted in between. Whiskers indicate upper and lower quartiles + 1.5 interquartile range (IQR). Circles indicate outliers outside of the upper or lower quartile + 1.5 IQR. Abbreviations stand for: (n) number of sites, (P1) Period One, (P2) Period Two.

3.2 Single Species Analysis

3.2.1 Relative Display Behaviour per Species

Out of the 38 species detected with at least 20 observations at all sites in both periods, passerines were detected more often showing display behaviour (breeding code 2) as the highest detected form of territorial behaviour compared to nonpasserines (Table 3, Appendix Table 4). As only the highest breeding code per five-minute count was notated, these percentages needed to be interpreted conservatively. Nonpasserines showed drastically lower detections categorised with breeding code 2 both in P1 (mean: 9.67 %, range: 0.00 – 34.48 %) and P2 (mean: 7.82 %, range: 0.00 – 36.73 %). In comparison, passerines were more commonly observed showing display behaviour in P1 (mean: 54.78 %, range: 0 – 100 %) and P2 (mean: 52.08 %, range: 0 – 100 %). Except for corvid species, display behaviour for all passerines was only observed in the form of singing. Eurasian Coots, Eurasian Oystercatchers, Common Swift, Western Jackdaws and Carrion Crows were never observed displaying. On the other hand, all observations of Eurasian Wrens and Willow Warblers were exclusively categorised using breeding code 2.

Both the Northern Lapwing and the Common Wood Pigeon displayed in less than 30 % of the occasions in P1 and P2 (see Table 3). The emphasised passerine species all were detected displaying over 30 % of the observations, three of these species even over 80 %. Only the Common Blackbird was singing in 31.37 % of the cases in P1, but more often, in 45.78 % of the cases, in P2. Whereas Common Wood Pigeons Eurasian Blackcaps and Common Chaffinches were detected about equally often with display behaviour in P1 and P2, such behaviour decreased drastically for Eurasian Robins and was not even observed anymore in P2 for the Northern Lapwing.

Table 3 Number of Relative Display Behaviour and Number of Observations per Period. Numbers of observations (Obs), and relative display (DispBeh) for the Northern Lapwing, the Wood Pigeon, the European Robin, the Common Blackbird, the Eurasian Blackcap and the Common Chaffinch for period one (P1) and period two (P2). The Obs-columns include all observations during four five-minute point counts within each period. Display behaviour is defined as breeding code 2 as used by the New Breeding Bird Atlas of the Netherlands 2012 – 2015 (see Appendix).

Species Name	EuringID	DispBehP1 [%]	ObsP1	DispBehP2 [%]	ObsP2
Northern Lapwing	4930	4.35	46	0	31
Common Wood Pigeon	6700	27.27	99	31.17	77
European Robin	10990	91.67	36	73.68	19
Common Blackbird	11870	31.37	102	45.78	83
Eurasian Blackcap	12770	93.33	30	95.83	48
Common Chaffinch	16360	82.11	95	88.35	103

3.2.2 Observations per Number of Five-Minute Counts

The majority of species were most frequently observed in 1x5 or 2x5 minutes rather than 3x5 or 4x5 minutes (Figure 5, Appendix Figure 2). The expected values for a binomially distributed detection probability of 50 % distribute suggested most observations in 2x5 minutes, while fewest birds were assumed to appear in 4x5 minutes. 18 of 38 species (47.37 %) showed a distribution similar to this expected distribution. However, the majority of species (52.63 %) significantly differed from this distribution (Figure 5, Appendix Figure 2). The detection pattern for 11 species indicated detections below 50 %, but exceeded 50 % in 6 species. An additional 3 species did not show obvious peaks within any of the categories and are thus difficult to interpret.

Common Wood Pigeons, Common Blackbirds and Eurasian Blackcaps all shared the most commonly observed distribution with most observations in a single five-minute count and a decreasing trend to fewest observations in the fourth count (Figure 5). Although similar to the previous distribution, European Robins were obviously detected most frequently in one five-minute count, observations in the other categories were less frequent but equally likely. The Common Chaffinch was the most abundant species counted and could be found 198 times during the entire season. Most individuals were detected in two five-minute counts (31.31 %), fewest in three five-minute counts but lacking obvious peaks. Northern Lapwings were among the only seven species with most observations in all four five-minute counts and thus differed significantly from the expected detection probability of 50 %. In the most extreme cases, up to 69 % of the observations occurred in only a single five-minute count.

3.2.3 Added Value of Additional Five-minute Counts

To understand if longer counting durations (or additional five-minute counts) correspondingly make further observations possible, the number of observations per species was assessed for the first, the first two, the first three and all four five-minute counts (Figure 6). Again, I wanted to use data from all species exceeding 20 observations at all sites. However, data for the Common Swift were discarded for calculating the following means as there were no observations within the first two counts of P1. On average, the first five minutes obtained about half of the observations per species in P1 (mean: 51.09 SD 17.7 %) and P2 (mean: 55.77 SD 12.72 %). The first ten minutes accounted for about three thirds of the observations per species, 73.82 SD 13.76 % in P1 and 76.73 SD 12.31 % in P2. Within the first fifteen minutes, 87.98 SD 9.66 % of the observations were detected in P1 while 92.59 SD 6.04 % of the observations were made in the first 15 minutes of P2 (Appendix Figure 3). Differences in the relative added value between both periods were only analysed descriptively, but seemingly did not differ much between P1 and P2 within species.

For all species, observations increased compared to the first five-minute count. For 23 species including the Common Wood Pigeon, this increase was unstructured in one of the periods as observations between categories did not perfectly corresponded with the increase of added five-minute counts (Figure 6). The observations for four species increased in an unstructured fashion in both periods, including Common Wood Pigeon and Eurasian Blackcap. For ten species including European Robin, Common Blackbird and Common Chaffinch, observations decreased and accumulation curves flattened out in both periods. Only for the Blue Tit, observations increased constantly with the additional five-minute counts for both periods.

3.2.4 Variation in Observations per Five-minute Count Between Periods

To assess comprehend variability within counts, I compared observations in 1st, 2nd, 3rd and 4th five-minute count for both P1 and P2 for each species at all sites visited in both periods. None of the 38 species detected with more than 20 observations in the entire data set showed significant differences in the distribution between five-minute counts in P1 and P2 (Appendix Table 2). Nonetheless, patterns between periods differed widely across species. For 10 species including Northern Lapwings and Eurasian Robins, observations in all five-minute counts were more frequent in P1 (Figure 7). On the other hand, for 13 species including Eurasian Blackcaps and Common Chaffinches, observations were more common in P2. The remaining 15 species showed mixed frequencies not following any specific pattern. Wood Pigeons and Common Blackbirds were amongst the six species showing identical counts for P1 and P2 in at least one five-minute count. All but three species followed no specific pattern and were unpredictably observed within the four five-minute counts per period. Three species, however, showed the same pattern in both periods over all five-minute counts. Eurasian Oystercatchers and Great Spotted Woodpeckers both showed fewest observations in the first five-minute count and then increased continuously up to the fourth count in both periods. Inversely, the Common Whitethroat was detected the most in the first five-minute count of P1 and P2 and then decreased over all following five-minute counts.

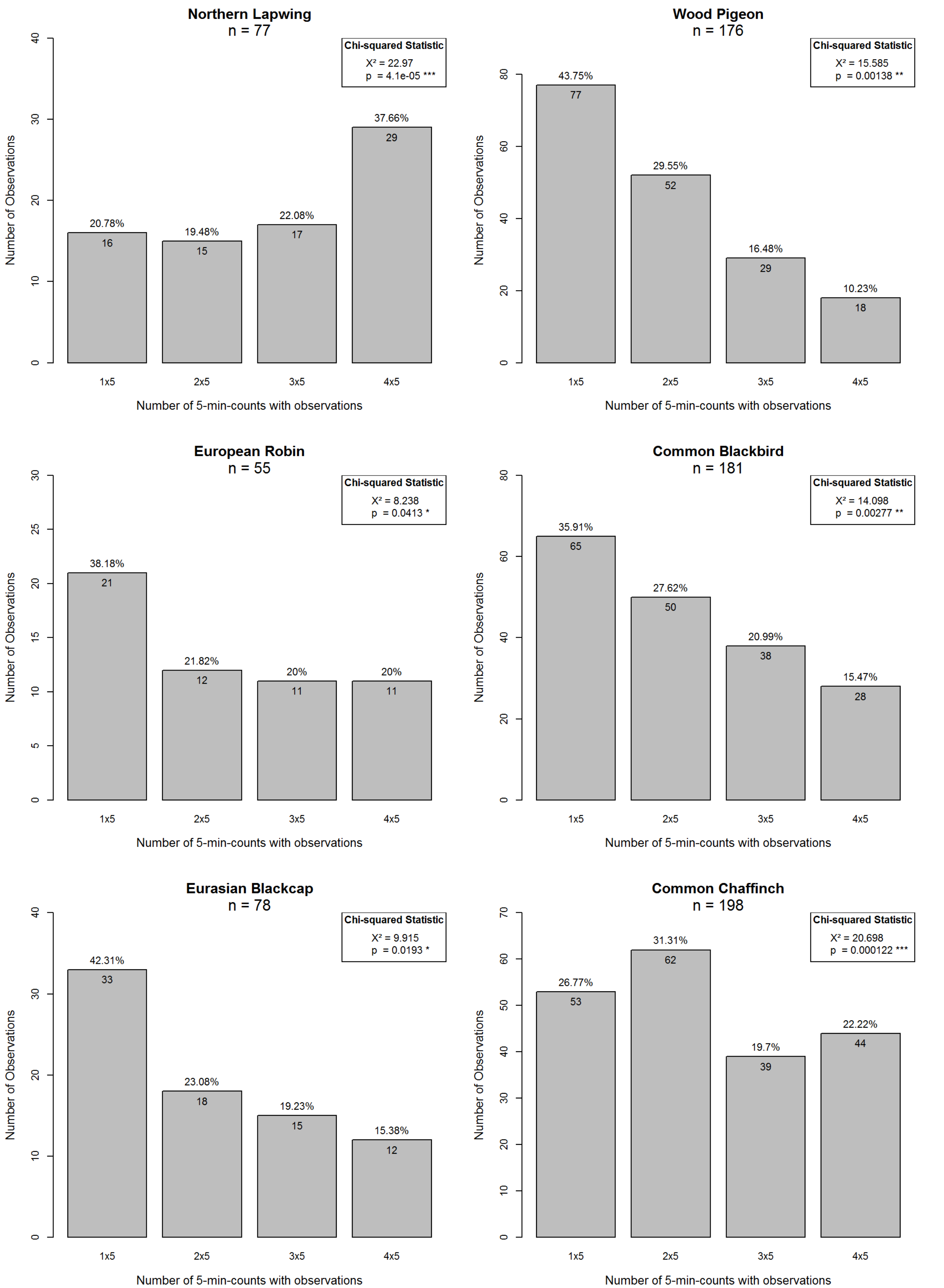

Figure 5 **Numbers of Observations for Any One, Two, Three and All Five-Minute Counts.** Combined frequencies of all observations for six species counted in one, two, three and all four five-minute counts during the entire season between April 1st and June 30th 2015 for all sites visited (n = 81 sites). Numbers above bar plots give relative percentage of observations to total observations per species and season.

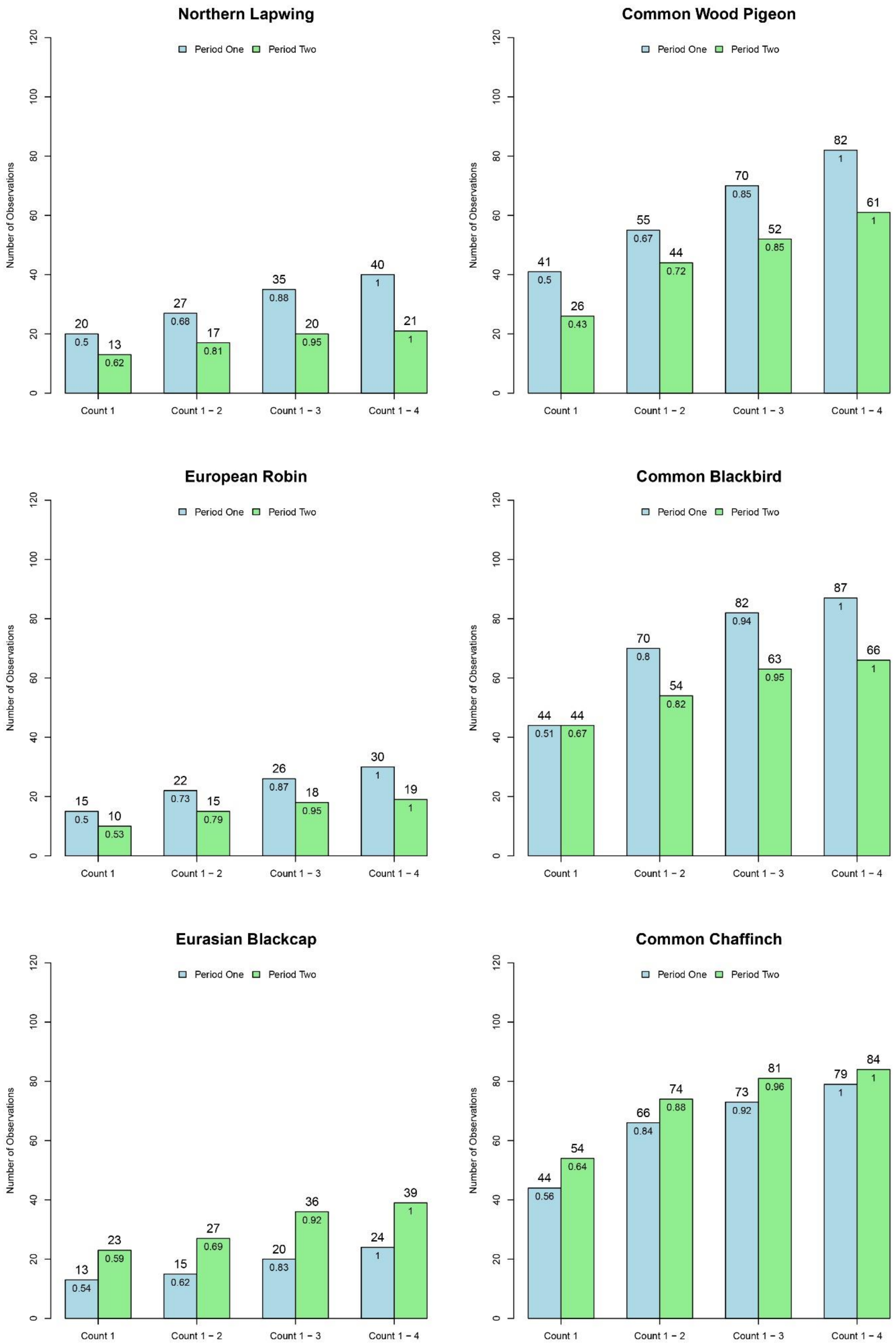

Figure 6 Number of Observations and Added Value of Repeated Five-minute Counts. Frequencies of six species counted in the first, the first two, the first three and all four five-minute counts during P1 (blue) and P2 (green). Numbers above bars give counted numbers per bar, numbers below give the fraction of observed in all five-minute counts.

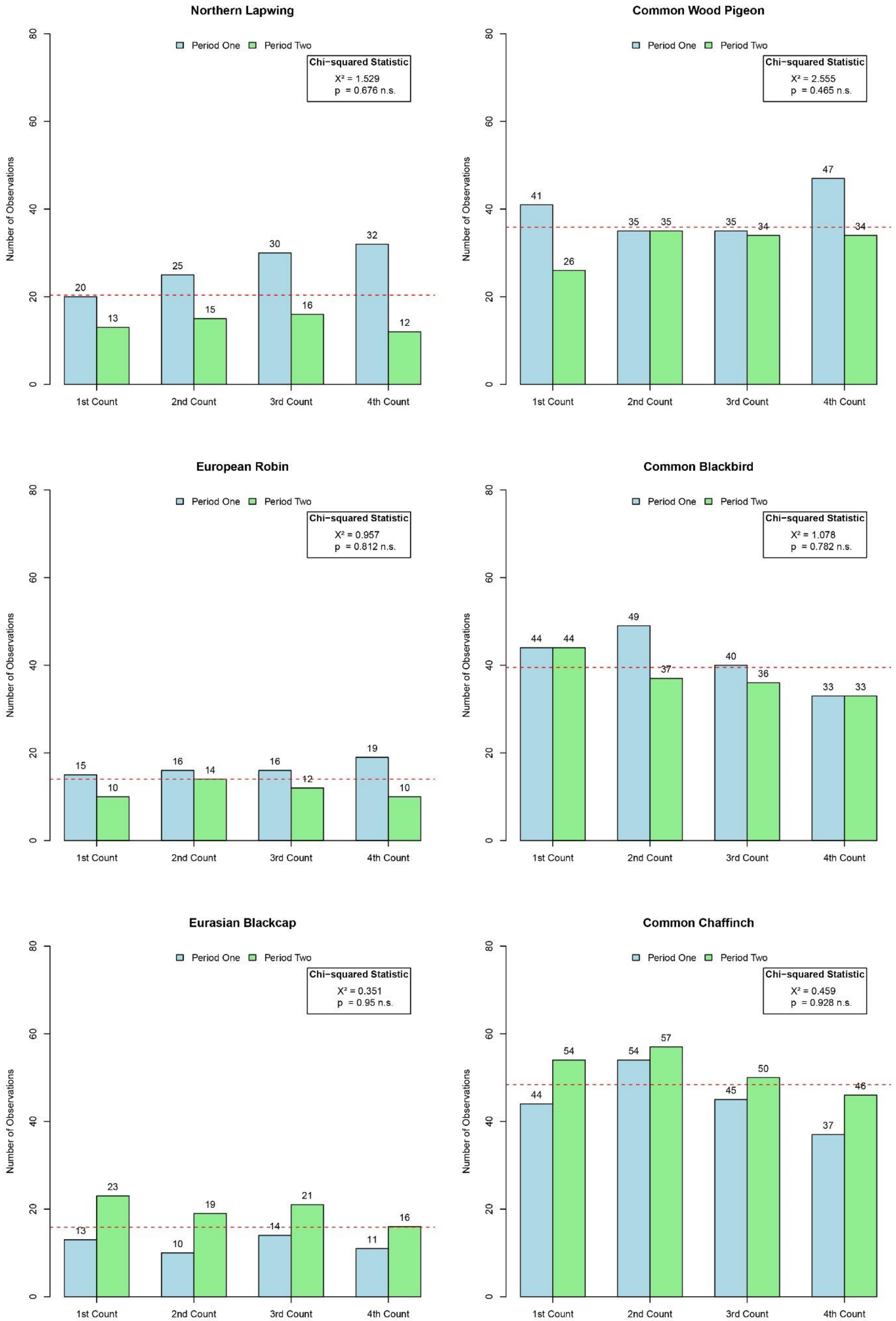

Figure 7 Number of Observations and Added Value of Repeated Five-minute Counts. Frequencies of six species counted in the first, the first two, the first three and all four five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per bar, numbers below give the fraction of observed in all five-minute counts.

3.2.5 N-Mixture Models: Detection and Abundance Estimations

N-mixture models were computed for all 33 species with more than 20 observations at sites visited in both periods, at first using a Poisson distribution to describe the latent abundance distribution. For 8 species, a negative binomial distribution was used to model the latent abundance as c-hat values and AIC indicated a more adequate fit for the best models of these species (Appendix Table 6). Goodness of fit-tests for the final model of all species indicated lack of fit for four species (Eurasian Wren, Common Chiffchaff, Blue Tit, Great Tit). For three species (Stock Dove, Common Swift and Common Starling), the c-hat near zero for the best final model indicated lack of fit.

The best model for 21 species included “StartTime” as a variable and its impact on the detection process yielded significant effects for all but two of them (White Wagtail, Common Blackbird) (Appendix Table 6). For four of the remaining 19 species, detection probability increased gradually over the breeding season (Common Swift, Barn Swallow, Common Chiffchaff, Western Jackdaw). Five species showed decreasing detection probabilities over the season (Common Pheasant, Stock Dove, Common Wood Pigeon, Dunnock, Common Goldfinch). Five species had higher detection probabilities in the beginning and the end of the breeding season but dropped in the middle (Eurasian Oystercatcher, Eurasian Skylark, European Robin, Eurasian Blackcap, European Greenfinch). Detection probability obviously peaked in the middle of the breeding season for five species (Northern Lapwing, Common Whitethroat, Blue Tit, Short-toed Treecreeper, House Sparrow).

For 15 species, the detection model included “DayNr”, which significantly influenced detection probability for 14 of these species (except for Tree Pipit). Four species were increasingly detected throughout the season (Mallard, Common Swift, European Robin, Common Chaffinch). For four species (Northern Lapwing, Common Blackbird, Great Tit, Western Jackdaw), detection constantly decreased throughout the season. Whereas detection probability peaked in mid-season for three species (Eurasian Wren, Eurasian Blackcap, European Greenfinch), it had its minimum mid-season for another three species (Common Whitethroat, Willow Warbler, Common Starling).

The best final model included “SiteObsNr” for 23 species as a variable on the detection probability and was significant for all but one species (House Sparrow). Detection increased with increasing number of total detections per site for 19 species (Mallard, Common Pheasant, Northern Lapwing, Common Wood Pigeon, Collared Dove, Common Swift, Great Spotted Woodpecker, Dunnock, European Robin, Song Thrush, Common Whitethroat, Eurasian Blackcap, Great Tit, Eurasian Magpie, Western Jackdaw, Carrion Crow, Common Starling, House Sparrow, European Greenfinch). Detection probability for four species first increased with an increasing number of observations, but then again dropped once the number of observations increased even more (Eurasian Oystercatcher, Stock Dove, Common Blackbird, Common Chiffchaff).

The best abundance model of 17 species included the relative amount of open area within a 200m diameter around the observer and for all but the Barn Swallow, the open area significantly influenced the abundance of these species. Abundance increased linearly with increasing open area for two species (Northern Lapwing, Tree Pipit). Conversely, abundance was decreased with open area for five species (Common Swift, Great Spotted Woodpecker, Eurasian Blackcap, Willow Warbler, Western Jackdaw). The abundance of the Common Whitethroat first decreased with more open area, but again increased with increasing open area. For eight species, abundance first increased with more open spaces, but then decreased again (Common Pheasant, Common Wood Pigeon, Collared Dove, Dunnock, Common Blackbird, Common Chiffchaff, Eurasian Magpie, House Sparrow).

For 16 species the abundance was significantly influenced by the forest area and for two additional species (Great Tit, European Goldfinch), forest area was included in the final model. For three species, abundance significantly increased with increasing forest area (Tree Pipit, Common Starling, Common Chaffinch). For four species, increasing forest area reduced abundance significantly (Mallard, Eurasian Oystercatcher, Eurasian Skylark, Carrion Crow). The abundance of three species first decreased with increasing forest area but then decreased drastically (European Robin, Common Whitethroat, Short-toed Treecreeper). Stock Doves, White Wagtails and Western Jackdaws first decreased with increasing forest area, but then again increased in density.

For 18 species, the amount of urban area was included as a variable affecting abundance, although only 16 of these species were significantly influenced by the amount of urban area (except for Eurasian Wren and Song Thrush). The abundance of four species increased with increasing urban area (Collared Dove, Dunnock, House Sparrow, European Greenfinch). Conversely, seven species decreased in more urbanised areas (Mallard, Great Spotted Woodpecker, Eurasian Skylark, Eurasian Blackcap, Willow Warbler, Eurasian Magpie, Carrion Crow). The Eurasian Oystercatcher first decreased with increasing urban area, but again increased after a drop. Four species showed an obvious peak in their abundance in areas of about half urban area, but then again decreased in more densely urbanised areas (Stock Dove, Blue Tit, Great Tit, Common Starling).
Abundance estimations based on only the first five-minute count of each period yielded extremely high estimations of over 300 pairs for all sites for 17 species (Appendix Table 8). Estimations based on two five-minute counts per period only estimated over 300 pairs for three species. Estimations of over 300 pairs occurred for two species with estimations from the first three five-minute counts per period. For two species (Mallard, Common Swift), estimations exceeded 450 pairs for all five-minute counts.
For eight species, estimations were drastically higher from data solely based on counts in P1, all other species presented similar estimations of breeding pairs.

At the 55 sites visited in both periods, a total of 40 observations of Northern Lapwings were made in P1 while 21 were detected in P2. Based on the estimations from the first period (est. 70.9 pairs), observations reached 56.42 % of the estimated numbers. For the second period, both the estimated and the counted number of pairs were lower. In total, 92.24 pairs of Northern Lapwings were estimated to appear over all 55 sites meaning a mean of 1.68 (SD 3.22) pairs per site (Table 5). While 82 observations of Wood Pigeons were made in P1, 61 were detected in P2. Based on the estimations, 75.52 % of the pairs in P1 and 62.53 % of the pairs in P2 were detected. For all counts, 120.3 pairs were estimated for all 55 sites meaning a mean number of 2.19 (SD 1.23) per site. European Robins were detected 30 times in P1 and 19 times in P2, while 42.37 pairs were estimated in P1 and 20.7 were estimated for P2. In total, observations in P1 reached 63.04 % of the estimation over the entire season (47.59) while those of P2 only reached 39.92 %. On average, 0.87 (SD 1.00) pairs of European Robins per site were estimated from all data. Common Blackbirds were detected more often in P1 than in P2 and estimations for P1 were at 131.03 while for P2 94.29 pairs were estimated for the 55 sites. The combined counts from P1 and P2 lead to an estimation of 171.45 pairs of Common Blackbirds. Therefore, an average of 3.12 (SD 1.92) pairs of Common Blackbirds was estimated per site. Detections were higher for European Blackcaps in P2 (39) than in P1 (24). Based on the estimation over the entire season on all 55 sites, 75.22 % of Blackcaps were detected in P2 while only 46.29 % were observed in P2. On average, this means a mean abundance of 0.95 (SD 0.97) pairs per site. Common Chaffinches showed an estimated mean abundance of 2.06 (SD 1.26) per site, summing up to 113.42 estimated pairs for all sites visited in both periods. However, only 79 pairs were detected in P1 while 84 observations were made in P2 (Table 5).

Table 4 Number of Counted and Estimated Abundances for the Six Selected Species. CtdP1 includes all counted "pairs" at 55 sites in P1. CtdP2 lists all observations at 55 sites in P2. EstP1 and EstP2 show the estimated numbers using the best AIC-selected Model (given by Det and Abu, see Table 2) in the corresponding period (as for counted = CtdP1 and CtdP2). Estimated Season states the estimated abundance calculated by data from the entire season between April 1st and June 30th 2015.

SpeciesID	SpeciesName	DET	ABU	Est 1x5	Est 2x5	Est 3x5	Ctd P1	Est P1	Ctd P2	Est P2	Est S
4930	Northern Lapwing	4a2bc	1a	52.59	51.08	79.38	40	70.89	21	24.42	92.24
6700	Common Wood Pigeon	2ac	2a2	104.90	117.54	105.53	82	108.58	61	97.55	120.32
10990	European Robin	4a2b2	2b2	932.30	48.24	45.29	30	42.37	19	20.71	47.59
11870	Common Blackbird	4abc2	4abc2	131.16	148.42	170.98	87	131.03	66	94.29	171.45
12770	Eurasian Blackcap	5a2b2c	2ac	59.38	43.08	49.53	24	34.12	39	42.64	51.85
16360	Common Chaffinch	1b	1b	288.14	113.92	114.00	79	75.59	84	82.66	113.42

4. DISCUSSION

4.1 Species Overview

4.1.1 The Effect of Count Duration on the Observable Species Richness

My data on the effect of point count duration on the observable species richness suggest a slight increase in observed species with an increasing number of five-minute counts. The vast majority of species detected at all sites visited in both periods were observed in the first five-minute count (84.71 %). On average, the number of observed species increased from 8 species (57.14%) in the first five-minutes to 14 in all four counts at each site and visit. Such a fast decrease in the added number of species suggests that most of the species can be detected in a very short time. My findings widely coincide with previous studies on this topic. For bird counts during the non-breeding season, Lynch (1995) detected comparably lower rates of 55 % of the totally observed species within the first five and 82 % within the first ten minutes of approximately 1200 winter counts in forested habitats in Mexico. Similarly, the gain of species richness in Britain and Ireland declined with increasing numbers of visited sites and repeated visits for surveyed tetrads in winter (Gillings 2008). Gillings (2008) specified that additional effort of two hours compared to one showed drastic effects on species richness, while gains from an additional third hour only showed minor increase of species richness. The striking variation in the mean numbers of observations per site derive from the great variation in habitat structure among these sites. Approvingly, Shiu & Lee (2003) found that differences in the effect of counting duration on the number of observed species varied between different habitats. Also, Gillings (2008) found species accumulation curves to be much steeper in areas with considerable habitat variation such as coastal areas or upland habitats than in arable land and urban areas. However, detection also depends on the conspicuousness or reservation of species to sing or move from a shelter and therefore also depends on species-specific alert distance and time spent latent (Blumstein et al. 2005). This suggests, that non-detection is not only possible on the individual, but also on the species level. Therefore, my findings only summarise detected species, but make no point about all species truly being present. However, raw counts need to be treated with exceptional care, as unadjusted counts rarely resemble true species richness correctly (Kéry & Schmid 2006). Shiu & Lee (2003) stated that five-minute counts sufficiently reached 80 % of the calculated asymptote of bird species during the breeding season based on the Clench model by Soberòn & Llorete (1993). These findings suggest that the number of present species was higher than those observed. The true number of species, however, was not the primary subject of this study as no estimations can be made for undetected species anyway and are thus not directly relevant for the purpose of this study.

4.1.2 The Mean Number of Observations per Site

The mean number of observations per site varied significantly between both periods, but also showed drastic differences between passerines and nonpasserines. Lower (observed) densities of nonpasserines may be explained by the known relationship between body size and home range (e.g. Haskell et al. 2002, Woodward et al. 2005). Mean body size is remarkably higher in most observed nonpasserines compared to passerine birds and thus, nonpasserines should generally have bigger home ranges. Adult Wood Pigeons for instance, may disperse among an area of around 254 ha (Haynes et al. 2003). Furthermore, the majority of areas surveyed for this study included vast amounts of open farmland. Many farmland species suffer from population declines in recent decades due to agricultural intensification (reviewed in Benton et. al. 2003). One reason for these declines is insufficient food supply (Chamberlain et al. 2000, Newton 2004) and naturally, nonpasserines have a higher food intake thus explaining lower densities and wider home ranges. Naturally, higher home ranges and lower population densities affect the number of observable individuals at a specific site and thus explain fewer detections of nonpasserines than passerines. Differences in the number of observations in P1 and P2 are possibly due to a variation in detectability over time of year (Selmi & Boulinier 2003, see below).

4.2 Single Species Analysis

4.2.1 Relative Display behaviour per Species

The majority of species were detected showing display behaviour as the highest detected breeding code. Crucially, the notation of the highest breeding code per observation per visit (not five-minute count) means no higher breeding code was observed for this observation. Still, a bird could have been detected perching constantly throughout the first fifteen minutes and only started singing in the last five minutes. Furthermore, notations of singing birds were upgraded to a higher breeding code when showing behaviour more securely indicating a territory, such as copula (breeding code 5) or transporting nesting material (breeding code 9). For these reasons, a bird listed with 0 % display behaviour did not automatically never display. For most observations of species, however, especially song birds, other forms of territorial behaviour were observed relatively rarely. In addition to the effects caused by the methodology used for notating display behaviour, a variety of reasons may influence whether or not birds display. Birds only sing to protect their territories against other competitors of the same species and to attract females of the opposite sex (Nowicki & Searcy 2004). Song activity correlates with breeding cycle, but normally stops for the duration of raising offspring (Slagsvold 1977, Wilson and Bart 1985). I observed three patterns in display behaviour between P1 and P2, namely (1) equal display in both periods, (2) more display in P1 and (3) more display in P2. Equal frequencies in display behaviour imply singing males in both periods. Such patterns occur for species with several broods per season, including residents like the Common Wood Pigeon or Common Blackbirds, and short distance migrants like Common Chiffchaffs, or Eurasian Blackcaps (Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007, Slagsvold 1977). However, this does not necessarily mean that peaks are clearly visible to the observer. This is due to the intraspecific overlap between laying and hatching time and thus, causes fluctuation over the entire season rather than showing obvious peaks. Moreover, some species either breed once or twice, such as Common Chaffinches and Great Tits (Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007). Verboven et al. (2001) found that Great Tits facultatively double-breed more commonly in early breeding pairs, while pairs only breeding once tend to breed close to the maximum peak of their main food sources. Accordingly, Visser et al. (2003) stated that the effects of climate change on food availability vary even between small scale populations and that some populations might switch from double-breeding to single broods. Peaks in song activity are thus even more latent for such species. More or less constant singing activity throughout the season is aggravated by the fact that some males may not find mating partners. In this case for example, unmated male Nightingales, *Luscinia megarhynchos*, and other species increase their singing activity until the end of the breeding season (Amrhein et al. 2002, Staicer et al. 2006). Also, Gibbs & Wenny (1993) could show a strong positive effect of the pairing status of male birds on the song output per minute and assessed all unpaired males for two species, but missed between 35 – 50 % of the paired males.

Migrants complicate interpretation when arriving over a longer time span or close to the bound between P1 and P2. Many long distant migrants, like the Garden Warbler, *Sylvia borin*, or the Common Swift, *Apus apus*, arrive as late as the end of April or even in May (Wernham et al. 2002). Early visits in the first breeding period may thus miss such species and explain relatively more observed display behaviour in P2. Furthermore, Blair (2004) found a positive correlation between the number of broods and the level of urbanisation, resulting in species with higher numbers of broods per season in more urbanised habitats. Thus, multiple breeding might appear specifically often in bird species associated with urban proximity. Patterns (1-3) can therefore be justified using these explanations. This is not the case for species showing display in the first, but not in the second period at all, like I observed for the Mallard, the Common Pheasant, the Eurasian Jay and the Eurasian Magpie. Indeed, these species only breed once in a single season in the Netherlands (Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007). For species solely detected on display behaviour, an additional scenario would imply that I only observed displaying individuals and thus produced a bias by not detecting calling or perched birds. However, this chance was minimised by constantly training vocal detections for both songs and calls.

4.2.2 Observations per Number of Five-Minute Counts

I compared the observations per number of five-minute count for each species in order to roughly assess, if detection is more likely in any one or two five-minute counts or, if counting duration needs to be longer for most detections. Indeed, most observations per species most commonly took place in either one or two five-minute counts, while few were detected mostly in all or nearly all five-minute counts. While most detections in one and two five-minute counts suggest detection probability around or below 50%, observations in all or nearly all five-minute counts suggest detection probability higher than 50 %. However, this assumption does not allow to interpret heterogeneity among sites and other parameters affecting detection probability and thus only gives a rough summary on the mean detection probability at all sites over the entire season. The differences among the observations per number of five-minute counts clearly indicate variability between species detection and therefore illustrate the necessity to imply species specific behaviour to the survey design (Buckland 2006). These differences may have several different reasons.

Firstly, duration, frequency and general structure of bird song is known to vary drastically between species, populations and even individuals, not only as a matter of heritability, but because of environmental influence and social learning (e.g. Gil & Gahr 2002, Gil & Slater 2000, Handford & Lougheed 1991). Species showing long intervals between one or few sets of verses are less likely to being detected by song within a single five-minute count than those constantly singing within observable distance. Thus, such species can only be detected by song in few consecutive five-minute counts, even though detection might be easy once they sing. Secondly, birds interspecifically and intraspecifically vary in their locomotion behaviour and whether they leave cover or stay hidden (Aje et al. 2006, Granholm 1983). Some species might thus move into or out of the observable area on a more or less regular basis. Thus, depending on the frequency of these movements, such species may not only cause detections in few, but many consecutive point counts (and potential double counts) (Granholm 1983). On the other hand, species with more observations in 3x5 or 4x5 minutes showed average detection probabilities above 50 %. Next to the previously mentioned reasons, habitat and body size might influence detections in the majority of five-minute counts. Bigger birds generally tend to be detected easier in open rather than closed habitats, although body size obviously is not the only parameter influencing detection probability (Fletcher & Hutto 2006). Both scenarios in which big birds move very little once being detected (e.g. foraging on the ground), and moving regularly (e.g. display behaviour) explain more detections over consecutive five-minute counts. This is also true for species breeding on exposed locations and for those perching in close proximity to the nest, like House Sparrows do on roofs (Kopij 2013).

4.2.3 Added Value on the Number of Observations

The average sum of observations from the first five-minutes per species increased to about double the observations for all four five-minute counts. Thus, additional counts still accrued new pairs constantly. According to the findings of Fuller & Langslow (1984), my results indicate a slower saturation for the accumulation curve of pairs compared to the saturation of accumulation curves for species richness. However, most observed species showed unstructured increase over the additional five-minute counts and are thus difficult to interpret. Thus, increase was not observed to be clearly linear but abruptly increased or decreased between five-minute counts. This is aggravated by the small number of detections for several species as spatiotemporal variability causes stochastic variation in point count data (e.g. Kéry & Royle 2015). Thus, to make a point on whether or not accumulation curves for pairs flatten out for specific species, data sets should be compared for single sites rather than aggregated over point count sites. Unfortunately, however, typical bird point counts yield few observations per site and are thus difficult to interpreted regarding if accumulation curves flatten out or not (Fiske & Chandler 2011, Kéry & Royle 2015). That being said, I observed flattening trends in the added observations for ten passerine species. Among these species I observed Eurasian Wrens and Willow Warblers, both of which were detected singing in 100 %. Five other species were observed singing in more than two thirds of the encounters. Trends for these species may imply that no new individuals enter the survey area, but due to high song rate, nearly all pairs are detected relatively fast. White

Wagtails and Eurasian Magpies are both easily detected due to their regular encounters in open habitats and their striking plumage (Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007). The only species with a positive trend in both periods is the Blue Tit, but stochastic variation may again be the main cause of these trends.

4.2.4 Variation in Observations per Five-minute Count Between Periods

To assess variability within five-minute counts, counts were compared within and between periods. In the majority of the observed species, no specific patterns were observed between or within periods, but varied slightly between five-minute counts for all species. This variation is caused by spatiotemporal variation of detection probability as well as abundance for most of the species (Fiske & Chandler 2011, Kéry & Royle 2015). A higher number of observations for all five-minute counts of one period at least partially indicates higher detectability. Firstly, some species were obviously detected in higher numbers in the first than in the second period. For Mallards, Eurasian Oystercatchers and Northern Lapwings, three nonpasserine species inhabitating open area, higher detections in the first part of the breeding season are well known. All three species nest once a year, display early in the season and are more difficult to detect while hatching offspring (Khil 2015, Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007). In one occasion, I observed a female Mallard with offspring only after about 12 minutes of counting, they were hiding in a vegetated ditch not even three metres from me. Interestingly, Mallards were observed mainly in the first two visits in P1 and the second visit in P2 thus suggesting to avoid being observed (Lima 2009). Four passerine species, European Robin, Common Chiffchaff, Willow Warbler and Western Jackdaw showed prominently more observations in P1 than in P2. The first two, migrants of the Phylloscopus genus, were detected more frequently in the first period possibly due to their arrival date. Some migrating Common Chiffchaffs sing and thus violate the assumption of constant abundance throughout the breeding season (Lindström et al. 2007).

On the other hand, Common Swifts, Barn Swallows, Common House Martins, Eurasian Blackcaps and Common Whitethroats were detected more often in P2. All five are migrants, some of which arrive late in P1 or even at the beginning of P2. Thus, increasing observations in P2 might be influenced by arrival date in which case the assumption on constant abundance throughout the breeding season is, again, violated (Fiske & Chandler 2011, Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007, Wernham et al. 2002). This would suggest to adjust the timeframe in which observations are certainly justified as territorial observations for some of these migrating species.

4.2.5 N-Mixture Models

Several simulation studies showed 55 sites to be a sufficient number of visited locations to estimate abundance properly for species with a detection probability between 20 and 100 % (e.g. Kéry & Royle 2015). N-Mixture models were fitted for 33 species observed with more than 20 observations at the 55 sites visited in both periods. For four species, the chi-square statistic`s p-value for the goodness of fit test exceeded the 95 % confidence interval defined to distinguish between fit and lack of fit. Kéry & Royle (2015) suggest to either discard models with lack of fit as unanalysable, choose a different model for them or to continue with the unfitted model nonetheless. However, clear instructions on the definition of fit or lack of fit are still an under-investigated topic in hierarchical models (Kéry and Royle 2015). Therefore, abundance estimates were calculated even for species failing the goodness of fit test. However, lack of fit means that the variance in the data cannot adequately be described by the model.

Further, for eight species, the default Poisson mixture model was superseded for a negative binomial mixture as overestimation was indicated by relatively high c-hat values. Overdispersion, defined by the variance exceeding the mean, is a common problem with point counts, but can be dealt with in various ways (Mazerolle 2004, Ver Hoef & Boveng 2007). As Mazerolle (2004) and Kéry & Royle (2015) suggested, assumption of lack of fit is reasonable for c-hat values << 1 and >> 4 and thus, c-hat values estimated from my data should still suggest reasonable fit. Similarly, very low values for c-hat might indicate underdispersion or lack of fit (Mazerolle 2004). As the applied negative binomial models

decreased c-hat values and AIC and thus following procedure of Kéry and Royle (2015), the negative binomial abundance distribution was preferred over the Poisson distribution. However, Ver Hoef & Boveng (2007) suggest adequate justification for models commonly used against overdispersion. Linden & Mäntyniemi (2011) advise to best choose a distribution model by formerly understanding the biological reasons for overdispersion and accordingly applying a model either based on linear or quadratic relationships between variance and mean. Negative binomial mixture models allow to account for overdispersion by assuming quadratic relationships between the variance and the mean as commonly resulting from environmental stochasticity or flocking behaviour (Engen et al. 1998, Linden & Mäntyniemi 2011, Ver Hoef & Boveng 2007). All eight species applied with negative binomial distribution models are known to flock, but, from personal observation, might be very easy to observe in some situations (e.g. display flight), while are difficult to detect in other situations (camouflage, hiding etc.) (Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007). This effect might even be amplified by low frequencies of observed display behaviour, but has to be analysed more precisely for secure relationships.
Unfortunately, however, with consecutively counted five-minute counts, there is a problem in creating the yObs data-frame in unmarked. As an example, presume to observe two specific pairs of Northern Lapwings over the first three five-minute counts while one of them does not show in the fourth count. If, however, a completely different pair (let's presume it to appear seconds after losing the pair seen before, but appearing 300 m away from their location so double counting can be ruled out) appears in the fourth five-minute count, the total number of observations for this five-minute count remains two. Thus, each of the four five-minute counts within a single visit provided two observations, but, from counting data consecutively, I can be sure that, in reality, three pairs were present, while the model will only assume two to be the maximum number observed. This problem, to my knowledge, has not been confronted yet and, in my opinion, needs to be corrected, as it may imply bias, especially for data with few observations clustered at few of the sites visited.

For several reasons, N-mixture models can be assumed to adequately compute total abundance estimations from repeated point count data. The N-mixture estimator centres sampling distributions well and performs properly regarding root-mean-square errors (Royle 2004b). This is especially true compared to prior estimators like the one generated by Carroll & Lombard (1985), which requires fixed beta prior parameters of detection probability and show substantial bias, if parameters are chosen insufficiently (Royle 2004b). However, one of the most powerful advantages of N-mixture models remains in their capability to estimate site specific abundance (Kéry 2008, Royle 2004b). Small sample sizes were difficult to approach with previous methods and pooling data often induced loss of valuable site-specific data concerning the detection probability and the abundance of birds (Kéry 2008, Royle 2004b). Accounting for site-specific abundance allows estimation of true, absolute abundance and thus allows illustrations more meaningful than relative abundance estimates.

4.2.6 Abundance Estimations

Estimations for abundance were computed for all 33 species with more than 20 observations at sites visited in both periods (Abundance Table 8). The three variables "StartTime", "DayNr" and "SiteObsNr" were all successfully implied to the models and significantly explained some of the variance in detection probability for several species. This was also true for the abundance variables "Open_Area", "Forest_Area" and "Urban Area". Estimations for abundance were calculated for the first, the first two, the first three and all four five-minute counts for both seasons as well as separately for all four five-minute counts of P1 and P2. Overestimation decreased with the number of implied five-minute counts. Thus, the undoubtedly overestimated "freak estimations" computed for the abundance reduced drastically in many species and thus strongly support to use two or even three five-minute counts to estimate abundance. The best model for Mallards completely overestimated abundance only based on the data of P1 and Common Swifts were overestimated both for data solely based on counts from P1 and P2. Both species are characterised by a wide activity range and often travel significant distances between nest and foraging grounds. As female Mallards begin to nest, paired males, and even more so unpaired males, increase their activity range and gather up with other males (Brasher et al. 2002). Overestimation can thus be explained by larger groups of male Mallards incorrectly identified as residents to the location of observation (Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007). On the other hand, drastically lower estimations for fewer observations of Mallards in P2 may also be explained by unpaired males leaving the breeding habitats (Brasher et al. 2002). Overestimation in Common Swifts can be explained by their huge activity range and the difficulty to detect breeding areas during the day as most Common Swifts only return to their nesting locations in the evening (Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007).

The validity of the estimates of total abundance per km² is difficult to prove. Both parts of the province of North Brabant, West Brabant and Middle and East Brabant, often yield overproportional shares of certain species, while simultaneously, data might be relatively outdated in vulnerable species such as farmland birds (Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007). I therefore think that extrapolation of my data to the area of North Brabant compared with the most recent breeding bird atlas of West Brabant and Middle and East Brabant is both not of practical use and might induce serious bias. Alternatively, I used the average estimates of sites with more than 90 % forest area and urban area and more than 95 % open area to see, if my estimations are adequate (Appendix Table 9). These mean abundances per species were then extrapolated to an area of 1 km² per habitat type as such data do not require giant extrapolation-factors and thus minimise bias. The majority of mean densities per habitat provide almost identical estimates compared to the same locations from the most recent breeding bird Atlas of West Brabant, hereby referred to as "the AWB", atlas of West Brabant (Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007). Estimates for open area sites matched those from the AWB in all but seven of 33 species (four over-estimated, three under-estimated). Common Pheasants, Eurasian Skylarks and House Sparrows, along with other farmland birds, recently registered drastic declines in populations throughout the Netherlands and Europe due to the consequences of agricultural intensification (Chamberlain et al. 2000, Donald et al. 2001, Hole et al. 2002, Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007). These local and regional declines would logically explain lower abundance estimates compared to the previous atlas of 2007. While abundance estimates at open sites for Tree Pipits differed from the AWB data rather slightly, I overestimated Mallards, Carrion Crows and European Goldfinches considerably in these habitats.

Additionally, Common Starlings were overestimated at forested sites and European Goldfinches, again, were overestimated at urban sites compared to estimations of the AWB (Samenwerkingsverband Westbrabantse Vogelwerkgroepen 2007). Overestimation is a known problem with several causes in abundance estimation, but while intuitively, needs to be avoided, prevention often proves to be difficult (Buckland et al. 2008). Overestimation may occur with species frequently entering or leaving the study area and thus increasing the likelihood of double-counting birds (Buckland et al. 2008, Granholm 1983, Cimprich 2009). Overestimation is more likely with an increasing counting duration per site as commonly moving birds may be difficult to distinguish from each other (Fuller & Langslow 1984, Granholm 1983). On the other hand, underestimation was a much more common problem from the estimations based on sites with > 90 % forest or urban area and occurred with roughly a third of the species in question. Commonly, birds appearing in clusters are observed without error at closer range, but tend to be underestimated in greater distances (Buckland et al. 2008). Similarly, species that temporarily change their behaviour in order to escape detection may be detectable by sudden movement at close range while initial detection at a higher distance becomes very difficult (Buckland et al. 2008). Such species tendentially may be underestimated according to their true abundance. Underestimation for specific sites may also be caused by unfavourable conditions at the forest and urban sites picked to assess estimation, as both visits tendentially were late in P1 and P2 in forests. Possibly, the peak of highest detections were missed and could thus explain underestimation for these species.

4.2.7 Estimations of Detection Probability

Even though N-mixture models and unmarked's pcount-function allow the calculation of site and count-specific detection probability, many researchers are not as much interested in the exact number of detection probabilities at a certain site, but in the parameters affecting detection probability within a breeding season. Very often, assessing all these parameters is difficult (Witmer 2005). My data provided evidence for significant influence on detection probability by the time of year, the time of day relative to sunrise and the number of observations at a site. Time of season and time of day have been often proven to influence detection probability significantly (e.g. Lynch 1995, Selmi & Boulinier 2003). Species detection probabilities do not only differ between species of different habitats, but also between species living in the same habitats (Buskirk & McDonald 1995, Ralph et al. 1995). However, my data agree with various findings on the tendency that wetland-dependent species (Nadeau et al. 2008) and forest species (Blake 1992) and birds in general (Gregory et al. 2004) are observed more often in the early morning. Species like birds of prey and Swifts however, are more commonly observed at later hours during the day. While detection trends decreasing after sunrise are clearly understood, detection probabilities positively affected by the number of observations per site may appear counterintuitive at first. One could argue that the chance of detection decreases with an increasing number of observations as chance of missing a bird, especially a visually detected one, rises with the number of birds that have to be noted. I think that a higher number of birds per site indicate high quality habitats for several birds. The chance to detect a specific species, thus increases with the suitability of the habitat rather than the number of observations.

4.2.8 Considerations: travelling time, number of visited sites, number of visits, point count duration

Higher quantities of five-minute counts with correspondingly long travelling times necessarily need to be weighed up against fewer counts with less travelling time (Buskirk & McDonald 1995, Lynch 1995). To maximise counting time and minimise traveling time, Ralph et al. (1995) suggest a counting time of five minutes, if travelling time is below fifteen minutes and a counting time of ten minutes, if travelling time exceeds fifteen minutes. The reduction of travelling time may be of specific value in cases where the number of available survey days are limited or sites are difficult to approach due to geographical barriers (rivers, mountains, islands). For the breeding bird survey of the Netherlands, observers need to travel a distance of more than 1.5 kilometres between sites (Schekkerman et al. 2012). This distance is manageable in 18 minutes by foot and 9 minutes by bike for the average person neglecting the fact that some areas might only be accessible by foot (Jensen et al. 2010, Wirtz & Ries 1992). However, national breeding bird atlases generally contain point count data of thousands of points, which is why stochastic effects induced by site variability is of less magnitude. Thus, whereas adequate numbers of surveyed sites are undoubtedly needed for confident estimations of species richness (and other essential state variables in ecology), most national surveys should include sufficient numbers of surveyed sites. Nonetheless, this might not be the case for all regional or local studies with fewer sites visited. Selmi & Boulinier (2003) found that detectability in resident breeding bird species differs between visits undertaken in the beginning of the breeding season and two months later. They further stress the necessity to consider temporal variation within breeding seasons when estimating species richness, especially when resident species and migratory species occur simultaneously and thus might show differences in nesting phylogeny (Selmi & Boulinier 2003). Siegel et al. (2001) suggest two visits per season to assess species richness for estimating indices on species richness for prioritising conservational purposes as adequate.

These advanced point counts over longer counting durations may entail certain advantages. Counting time may be confined to the early hours after sunrise due to nationally standardised survey protocols, as activity and detection probability decrease over the day for many avian species (Lynch 1995, Ralph et al. 1995). In such cases, longer counting durations may be of advantage, as such counts are less affected by reduced activity levels of birds active only in the early morning (Buskirk & McDonald 1995). It is thus possible to simultaneously detect birds showing retrograde activity and those just starting to get active a few hours after sunrise with only little trade-off for both activity patterns (Lynch 1995).

Conversely, there are additional disadvantages to the already stated overdispersion in previous chapters of this thesis. The observer's preference of certain species or decreasing concentration over long periods of time might affect the effectiveness and comparability of counts (Fuller & Langslow 1984). Unfortunately, I could not correct for observer-bias. This study was only performed by a single observer and thus, interactive effects between observers were non-existent. Nonetheless, all effects produced by this single observer lack direct comparability to other observers and thus, observer-specific biases are extremely difficult to objectify. Effects caused by multiple observers, however, might be easier to account for in the analysis when observers undertake more counts.

4.3 **Conclusions**

The raw count data gathered for this study showed that all first five-minute counts yielded more than 84 % of the species observed compared to the total counting duration of 20 minutes (four five-minute counts). On the other hand, this means an additional 18 % of observed species with four compared to a single five-minute count. I also showed that the number of observed passerine pairs was higher than the number of observations of nonpasserines. However, the mean number of observations per period for both groups decreased in P2. Further, I found that detections of passerines in large part derive from display behaviour for passerines and display behaviour was observed less frequently in nonpasserines. Display also differed between periods for both groups. Many species were detected in only one or two five-minute counts, but observations in all five-minute counts were rare. On a species-specific level, the first five-minute count yielded about half the observations compared to the total of four five-minute counts for an average over all species. Comparison between five-minute counts (within and between periods) showed no specific structure for most species, but indicated higher detection probabilities in one of the two periods for a few species. Abundance estimations were carried out for all 33 species, although four species did not pass goodness of fit tests. Eight species were modelled using a negative binomial distribution for explaining the latent abundance while for the other species, Poisson distributions were used. All six variables were successfully used to model detection and abundance in the tested species. My data indicate that increased counting duration has a positive influence on the accuracy of estimations for most species and reduced bias and "freak estimates" drastically. Similar estimations for one and four five-minute counts were rare.

The magnitude of this study's research complicates finding a simple answer to the question "is it useful to count for more than five or ten minutes?". Both for reaching the maximum number of species and observations per species, single five-minute counts already provide most of the observations and added counts decrease in their added value (Lynch 1995, Buskirk & McDonald 1995). However, my results show more species with "freak estimations" when only a single five-minute count was used for estimating abundance than for estimations based on more five-minute counts. I thus suggest two five-minute counts for large-scale surveys such as the AWB and other regional or national surveys using point counts. Nonetheless, travelling time, the number of available observers and the number of available sites are important factors that need to be considered when designing point count surveys. My data found two five-minute counts to more likely minimise "freak estimates". Compared to four five-minute counts, these shorter counts allow to increase statistical power by surveying more sites instead (Buskirk & McDonald 1995, Shiu & Lee 2003). Simultaneously, they may reduce overestimation by double counting which more often occurs for limited radius point counts (Gates 1995, Granholm 1983). Dettmers et al. (1999) stated that models with two visits performed noticeably better than those with one visit, while three visits seemed unnecessary for studying the relationships between forest songbird densities and habitat variables.

I thus suggest two visits of two five-minute counts for species not being at risk to be double-counted maintaining statistical power with regard to the number of sites visited and the detection probability of the species targeted.

5. ZUSAMMENFASSUNG

Urbanisierung, Populationsdynamik, landwirtschaftliche Intensivierung und der Klimawandel bedingen die stetige Veränderung örtlicher, regionaler und globaler Vogelpopulationen. Folglich müssen Natur- und Vogelschützer in der Lage sein, diese Veränderungen zu verstehen und quantitativ zu begreifen. Dabei spielt das Verständnis der beiden wichtigsten ökologischen Zustandsgrößen, die Verbreitung und Populationsdichte einer Art, eine besonders wichtige Rolle. Während Indizes nur in der Lage sind, Veränderungen in Form von relativen Populationstrends zu vermitteln, geben quantitative, tatsächliche Populationsgrößen präziseren Aufschluss über die mögliche Veränderung der Individuen oder Paare innerhalb einer Population. Zur korrekten Darstellung von absoluten Populationsgrößen müssen zusätzlich zu den in Felderhebungen beobachteten Vögeln auch solche berücksichtig werden, die zwar anwesend sind, aber nicht durch die Beobachter entdeckt wurden. Die Wahrscheinlichkeit anwesende Individuen auch tatsächlich zu beobachten verändert sich mit einer Vielzahl an Faktoren, beispielsweise mit der Tageszeit, der Jahreszeit und der Beobachtungsdistanz der Zielart, aber variiert auch zwischen Jungen und Erwachsenen, bzw. den Männchen und Weibchen innerhalb derselben Art. Eine von vielen Möglichkeiten, die raumzeitliche Variation der Beobachtungswahrscheinlichkeit in der Analyse der Daten zu berücksichtigen, ist die Felderhebung mit wiederholten Punktzählungen. In dieser Studie wurden mehrerer Zählpunkte in West Brabant (Niederlande) zweimal innerhalb der Brutperiode mit aufeinanderfolgenden Punktzählungen (4 x 5 Minuten) besucht. Die so erhobenen Daten legten den Grundstein für die Berechnung von tatsächlichen Populationsgrößen von 33 Brutvogelarten mithilfe der im R-Paket „unmarked“ und dessen Funktion „pcount“ beinhalteten N-Mixture Modelle. Ziel war die Untersuchung des Mehrwerts von verlängerten Punktzählungen im Vergleich zu den für den niederländischen Brutvogelatlas 2012-2015 standardmäßig verwendeten 5 oder 10 Minuten-Zählungen auf die Artenzahl und die Zahl der beobachteten Paare pro Art. Darum wurden Artenzahl, durchschnittliche Zahl an Beobachtungen und beobachteten Paaren und die relative Häufigkeit von beobachtetem Balzverhalten erhoben, letzteres auch im Vergleich zwischen Singvögeln und Nicht-Singvögeln. Die Berechnungen zur tatsächlichen Populationsdichte dieser Arten wurden mit den Datensets der ersten 5, 10, 15 und 20 Minuten, sowie der jeweiligen Datensets aus beiden Besuchen berechnet. Die Beobachtungswahrscheinlichkeit wurde für alle Arten mit der Kombination der standardisierten Tageszeit nach Sonnenaufgang, des Tages im Jahresverlauf und der Anzahl der anwesenden Vögel pro fünf-Minuten Zählung modelliert. Die Abundanz hingegen wurde mithilfe des relativen Anteils von Offenland, urbanem Raum und Waldfläche innerhalb der ersten 200 m um den Zählpunkt modelliert. Die Wahl des besten Modells wurde mithilfe des Akaike Informationskriteriums (AIC) und einer schrittweise durchgeführten Rückwärtselimination getroffen und mithilfe von Anpassungstests überprüft. Die Ergebnisse dieser Studie zeigen, dass der Großteil der beobachteten Arten bereits innerhalb der ersten 5 oder 10 Minuten beobachtet wird während weitere Beobachtungen nur wenige neue Arten lieferten. Dies trifft auch für die Anzahl der beobachteten Paare innerhalb einer Art zu, obwohl diese Zahlen innerartlich, zwischenartlich und zwischen den Besuchen schwankten. Auch die Beobachtungswahrscheinlichkeiten und Abundanzen, die mithilfe der Modelle errechnet wurden, zeigten unterschiedliche Gewichtungen einzelner Parameter für die verschiedenen Arten. Im Vergleich zu früheren Untersuchungen in West Brabant unterstützt diese Studie die Eignung von N-Mixture Modellen für kleinformatige Felduntersuchungen wie diese, empfiehlt aber Hochrechnung auf größere Flächen nur unter besonderen Umständen, nicht jedoch für Modelle die ausschließlich auf den in dieser Studie verwendeten Parametern basieren. Für die Hochrechnungen der Abundanzen zeigte sich ein Anstieg in der Genauigkeit mit zunehmenden Zählungen, weshalb ich die Verwendung von 10 Minuten-Zählungen für angebracht halte sofern leicht zu überschätzende Arten besonders berücksichtigt werden.

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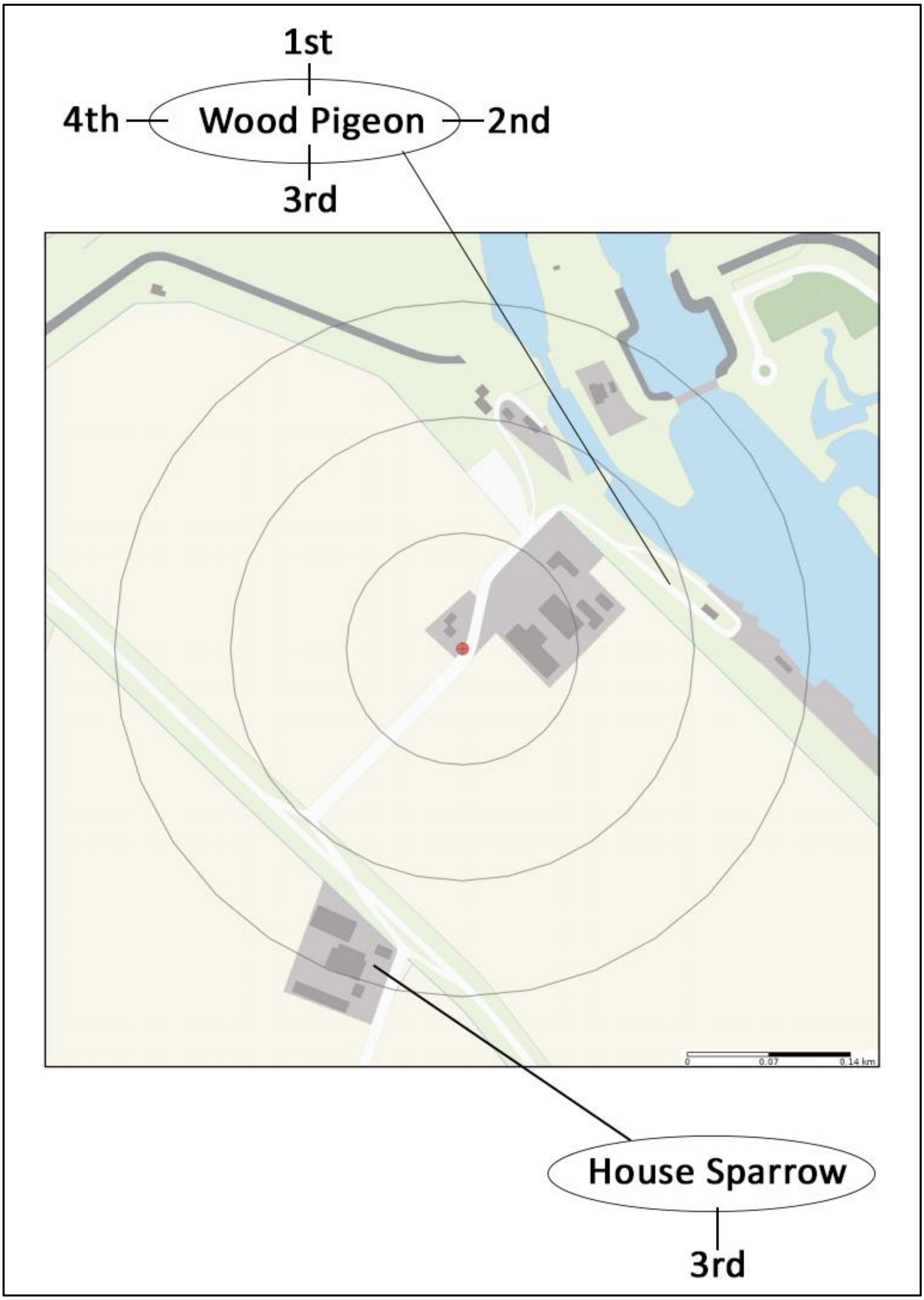
7. APPENDIX

Appendix Table 1 **Visited Sites.** Table listing all kilometre squares visited for performing point counts. Kilometre squares belonging to the same atlasblock were framed for easier perception. Sites marked with "x" were visited in the corresponding period, P1 and / or P2.

SiteID	P1	P2
435412		x
435423		x
435432	x	x
435434	x	x
435443	x	x
435454	x	x
435523		x
435541		x
435812	x	x
435823	x	x
435825	x	x
435832	x	x
435834	x	x
435841	x	x
435843	x	x
435854	x	x
441512		x
441523		x
441525		x
441532		x
441541		x
441543		x
441554		x
442523		x
442525		x
442532		x
442534		x
442541		x
442543		x
442554		x
443212	x	x
443223	x	x
443232	x	
443234	x	x
443243	x	x
443254	x	x
443425	x	x
443432	x	x
443434	x	x
443441	x	x
443443	x	X
443454	x	x

SiteID	P1	P2
445112	x	x
445123	x	x
445125	x	x
445132	x	x
445134	x	x
445141	x	x
445143	x	x
445154	x	x
491823	x	
491825	x	
491832	x	
491834	x	
491841	x	
491843	x	
491854	x	
501112	x	x
501123	x	x
501125	x	x
501132	x	x
501134	x	x
501141	x	x
501143	x	x
501154	x	x
502512	x	x
502523	x	x
502525	x	x
502532	x	x
502534	x	x
502541	x	x
502543	x	x
502554	x	x
503512	x	x
503523	x	x
503525	x	x
503532	x	x
503534	x	x
503541	x	x
503543	x	x
503554	x	x



Appendix Figure 1 **Point Map Example.** This figure shows an example map (kilometre square 4354-12) including two hypothetically detected species. The Common Wood Pigeon was seen in all four counts (1111) as indicated by the 4 short lines and the according numeric indicator for the corresponding five-minute count. The House Sparrow was only detected in the 3rd count (0010). Lines projecting into the map indicate the location of the detection on the map. Auxiliary lines are drawn at 100, 200 and 300 m.

Appendix Table 2 "AllData" Data Frame Overview. Table shows head (first six rows) of the "AllData"-file including all observational data and the including covariates per site. "SiteID" defines the specific kilometre square as indicated by the scheme for fieldwork for the Breeding Bird Atlas of the Netherlands 2012 – 2015. "EuringID" and "Breeding_Code" follow the Euring exchange code (Speek et. al. 2001). "Amount" is a placeholder for organising numbers of observations. "Detection_Code" is a four-digit binomial code indicating detection (1) or non-detection (0) for each five-minute count. "ObsCount1" – "ObsCount4" are substrings for the observational status per five-minute count. The site covariables (Open_Area, Forest_Area, Urban_Area) list the percentage of land-area within a diameter of 200 m around the point count location. "DayNr" indicates the day of the year by number. "StartTimeC1" – "StartTimeC4" list the five-minute count's starting time according to the minutes past sunrise.

> head(AllData)

	SiteID	**EuringID**	**Amount**	**Breeding_Code**	**Detection_Code**	**ObsCount1**
1	435412	6700	1	1	0111	0
2	435412	15600	1	3	0001	0
3	435412	15910	1	6	1111	1
4	435412	15910	1	6	1111	1
5	435412	4500	1	1	0001	0
6	435412	11870	1	2	1111	1

	ObsCount2	**ObsCount3**	**ObsCount4**	**Open_Area**	**Forest_Area**	**Urban_Area**
1	1	1	1	87,373	0	8,5838
2	0	0	1	87,373	0	8,5838
3	1	1	1	87,373	0	8,5838
4	1	1	1	87,373	0	8,5838
5	0	0	1	87,373	0	8,5838
6	1	1	1	87,373	0	8,5838

	DayNr	**StartTimeC1**	**StartTimeC2**	**StartTimeC3**	**StartTimeC4**
1	153	231	236	241	246
2	153	231	236	241	246
3	153	231	236	241	246
4	153	231	236	241	246
5	153	231	236	241	246
6	153	231	236	241	246

Appendix Table 3 Observed Species. "EuringID" shows Euring exchange code (Speek et al. 2001). English and scientific names follow Svensson et al. (2011). The number of observations refers to all observations from all sites (n = 81 sites).

EURINGID	**SPECIES (ENGLISH)**	**SPECIES (SCIENTIFIC)**	**NR OF OBS. (ALL SITES)**
70	Little Grebe	*Tachybaptus ruficollis*	1
90	Great Crested Grebe	*Podiceps cristatus*	2
120	Black-necked Grebe	*Podiceps nigricollis*	1
720	Great Cormorant	*Phalacrocorax carbo*	3
1220	Grey Heron	*Ardea cinerea*	1
1240	Purple Heron	*Ardea purpurea*	1
1440	Eurasian Spoonbill	*Platalea leucorodia*	1
1520	Mute Swan	*Cygnus olor*	1

1610	Greylag Goose	*Anser anser*	7
1661	Canada Goose	*Branta canadensis*	16
1700	Egyptian Goose	*Alopochen aegyptiacus*	12
1730	Common Shelduck	*Tadorna tadorna*	1
1820	Gadwall	*Anas strepera*	12
1860	Mallard	*Anas platyrhynchos*	68
1869	Mallard (f. domesticus)	*Anas platyrhynchos f. domesticus*	2
2030	Tufted Duck	*Aythya fuligula*	10
2600	Western Marsh Harrier	*Circus aeruginosus*	5
2670	Northern Goshawk	*Accipiter gentilis*	1
2690	Eurasian Sparrowhawk	*Accipiter nisus*	3
2870	Common Buzzard	*Buteo buteo*	12
3040	Common Kestrel	*Falco tinnunculus*	7
3100	Eurasian Hobby	*Falco subbuteo*	1
3670	Grey Partridge	*Perdix perdix*	2
3940	Common Pheasant	*Phasianus colchicus*	33
4240	Common Moorhen	*Gallinula chloropus*	6
4290	Eurasian Coot	*Fulica atra*	24
4500	Eurasian Oystercatcher	*Haematopus ostralegus*	53
4930	Northern Lapwing	*Vanellus vanellus*	77
5320	Black-tailed Godwit	*Limosa limosa*	3
5820	Black-headed Gull	*Chroicocephalus ridibundus*	1
5910	Lesser Black-backed Gull	*Larus fuscus*	4
6658	Feral Pigeon	*Columba livia domestica*	5
6680	Stock Dove	*Columba oenas*	47
6700	Common Wood Pigeon	*Columba palumbus*	176
6840	Eurasian Collared Dove	*Streptopelia decaocto*	78
6870	European Turtle Dove	*Streptopelia turtur*	1
7240	Common Cuckoo	*Cuculus canorus*	8
7950	Common Swift	*Apus apus*	52
8310	Common Kingfisher	*Alcedo atthis*	1
8560	European Green Woodpecker	*Picus viridis*	12
8630	Black Woodpecker	*Dryocopus martius*	1
8760	Great Spotted Woodpecker	*Dendrocopos major*	34
8870	Lesser Spotted Woodpecker	*Dryobates minor*	1
9760	Eurasian Skylark	*Alauda arvensis*	30
9810	Sand Martin	*Riparia riparia*	2
9920	Barn Swallow	*Hirundo rustica*	72
10010	Common House Martin	*Delichon urbicum*	27
10090	Tree Pipit	*Anthus trivialis*	22
10110	Meadow Pipit	*Anthus pratensis*	19
10171	Western Yellow Wagtail	*Motacilla flava*	28
10201	White Wagtail	*Motacilla alba*	46
10660	Eurasian Wren	*Troglodytes troglodytes*	115
10840	Dunnock	*Prunella modularis*	45
10990	European Robin	*Erithacus rubecula*	55
11210	Black Redstart	*Phoenicurus ochruros*	4

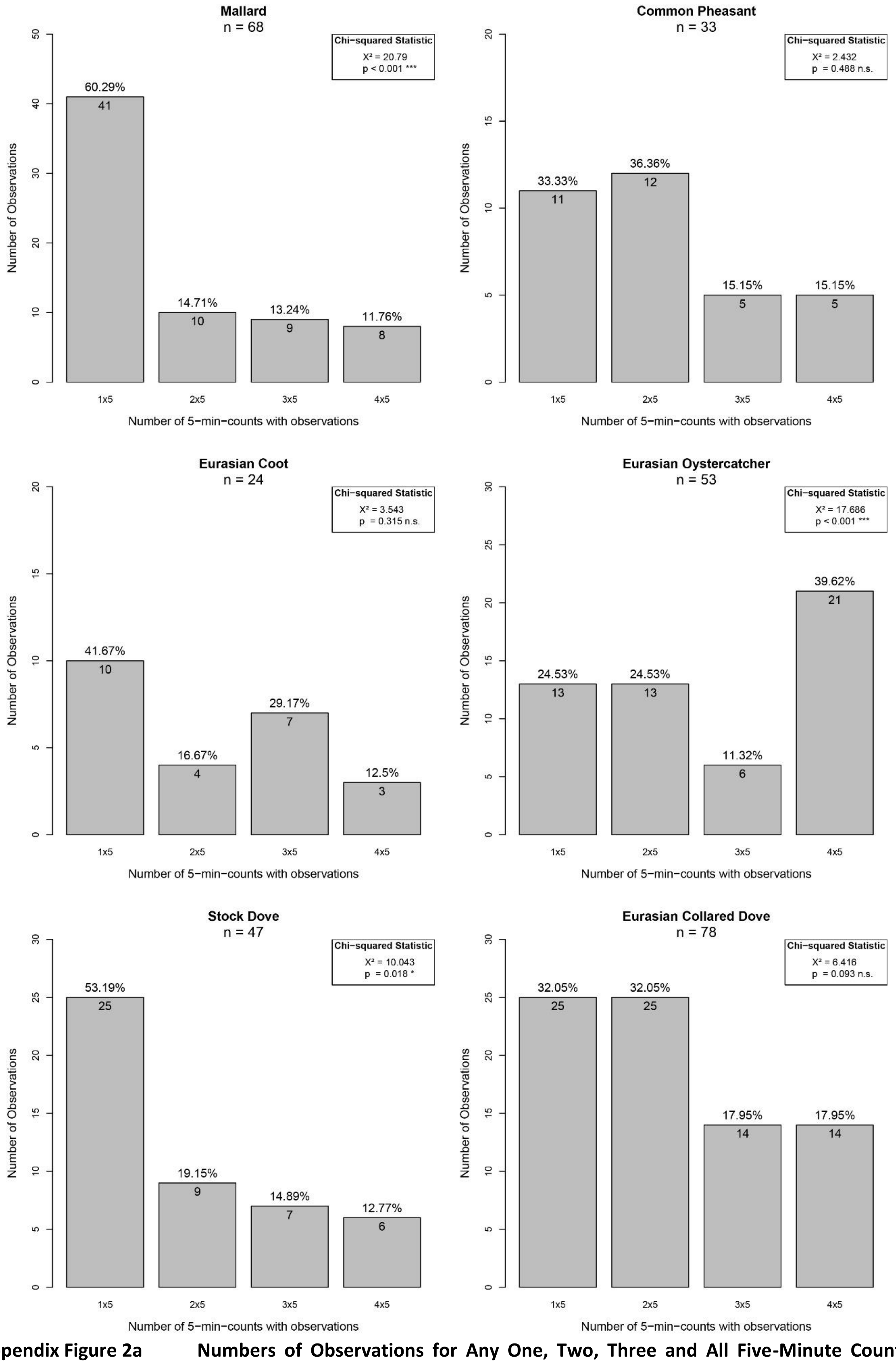
11220	Common Redstart	*Phoenicurus phoenicurus*	4
11390	European Stonechat	*Saxicola rubicola*	13
11870	Common Blackbird	*Turdus merula*	185
12000	Song Thrush	*Turdus philomelos*	27
12020	Mistle Thrush	*Turdus viscivorus*	1
12360	Common Grasshopper Warbler	*Locustella naevia*	1
12500	Marsh Warbler	*Acrocephalus palustris*	7
12510	European Reed Warbler	*Acrocephalus scirpaceus*	17
12590	Icterine Warbler	*Hippolais icterina*	1
12740	Lesser Whitethroat	*Sylvia curruca*	2
12750	Common Whitethroat	*Sylvia communis*	36
12760	Garden Warbler	*Sylvia borin*	23
12770	Eurasian Blackcap	*Sylvia atricapilla*	78
13110	Common Chiffchaff	*Phylloscopus collybita*	148
13120	Willow Warbler	*Phylloscopus trochilus*	43
13140	Goldcrest	*Regulus regulus*	7
14370	Long-tailed Tit	*Aegithalos caudatus*	3
14420	Willow Tit	*Poecile montanus*	1
14540	Crested Tit	*Lophophanes cristatus*	4
14610	Coal Tit	*Periparus ater*	2
14620	Blue Tit	*Cyanistes caeruleus*	62
14640	Great Tit	*Parus major*	107
14790	Eurasian Nuthatch	*Sitta europaea*	2
14870	Short-toed Treecreeper	*Certhia brachydactyla*	31
15080	Golden Oriole	*Oriolus oriolus*	1
15390	Eurasian Jay	*Garrulus glandarius*	22
15490	Eurasian Magpie	*Pica pica*	74
15600	Western Jackdaw	*Corvus monedula*	147
15630	Rook	*Corvus frugilegus*	4
15671	Carrion Crow	*Corvus corone*	110
15820	Common Starling	*Sturnus vulgaris*	77
15910	House Sparrow	*Passer domesticus*	82
15980	Tree Sparrow	*Passer montanus*	4
16360	Common Chaffinch	*Fringilla coelebs*	198
16490	European Greenfinch	*Chloris chloris*	48
16530	European Goldfinch	*Carduelis carduelis*	35
16600	Common Linnet	*Linaria cannabina*	17
17170	Hawfinch	*Coccothraustes coccothraustes*	3
18570	Yellowhammer	*Emberiza citrinella*	4
18770	Common Reed Bunting	*Emberiza schoeniclus*	8

Appendix Table 4 **Breeding Codes.** Breeding codes and according definition as defined for the new breeding bird atlas of the Netherlands (Sovon 2012). Codes were translated from Dutch to English. Square brackets indicate personal expansion.

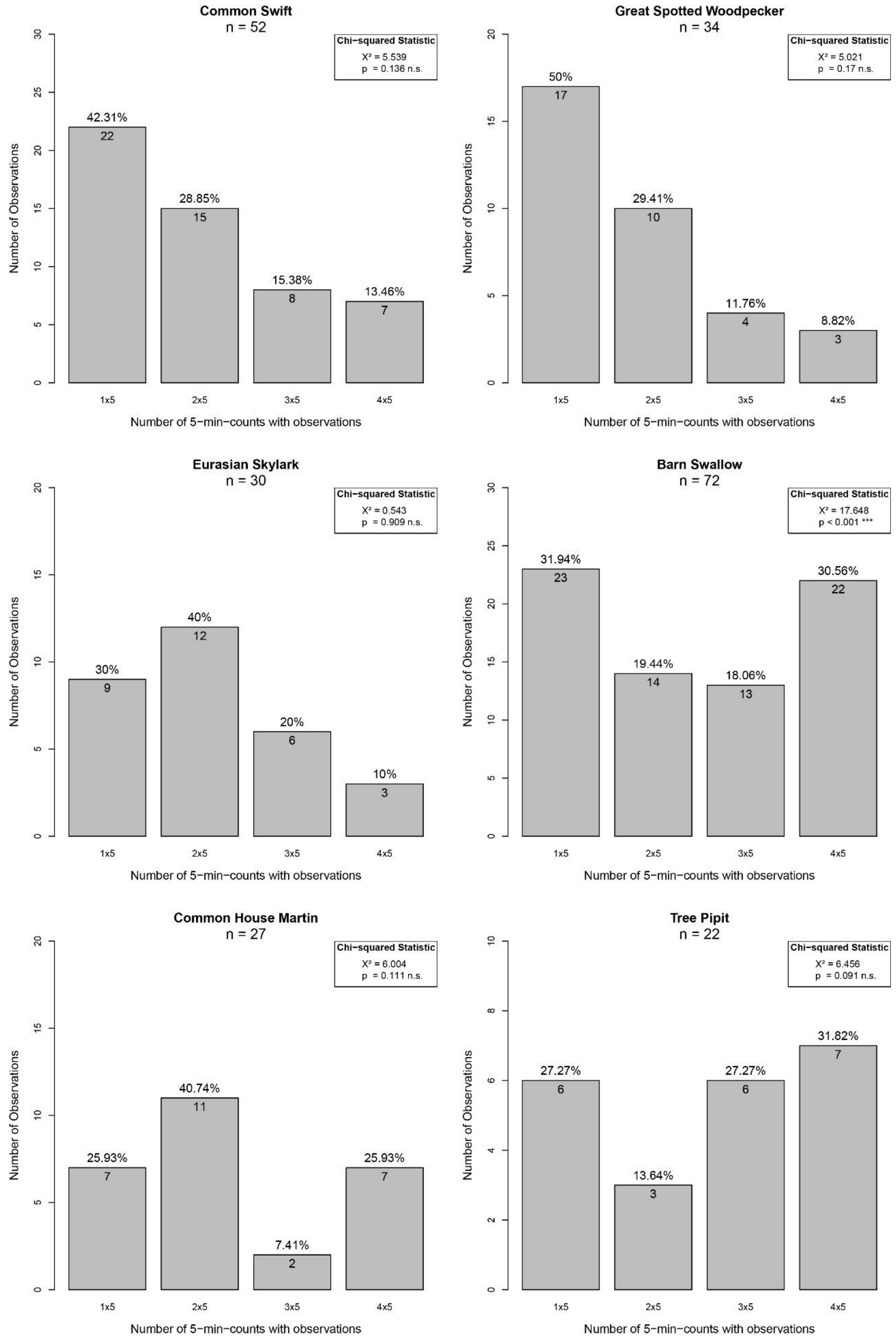
Breeding Code	Definition
1	Detection of an adult individual in a possible breeding habitat with no signs of breeding.
2	Single detection of a singing or displaying individual in a suitable breeding habitat.
3	Detection of a pair within the [by Sovon officially prescribed] breeding dates.
4	Territorial behaviour (singing, display, etc.) detected at the same site for at least two days set apart by at least ten days. [Mostly not useful in field].
5	Displaying pair (and copula) in a suitable breeding habitat. A male feeding a female is also to be noted with this breeding code.
6	Visit of a possible nest site, for example when House Sparrows disappear behind a roof gutter.
7	Any sort of alarming behaviour (cry of fear etc.) that suggests presence of a nest or youngs. As many people use this behaviour without breeding as well, special attention and caution is obligatory.
8	Bird [female] with brood patch (but not always a trustworthy sign for certain breeding).
9	Transport of nesting material, building a nest or digging of a nesting hole.
10	Distraction behaviour. The bird fakes an injury and tries to distance the observer off a nest. This behaviour is typical for birds in open landscapes, e.g. ducks, stilts and songbirds such as Common Reed Buntings.
11	Freshly used nest or eggshells.
12	Freshly fledged youngs of altricial birds or freshly walking precocial birds. This code needs to be treated with exceptional care. Species like terns, gulls, swallows, Rooks, European Starling, Common Crossbills, Siskins and Common Redpolls can travel large distances in their juvenile plumage. For this reason, this code needs to be used only on birds that can barely fly.
13	Nest in use with unknown content, for example when parents visit but insight into nest is not possible or when parents actively breed. This code is mostly used for bird colonies.
14	Transport of food or excretion. Transport of excrements is a behaviour mostly useful for songbirds. However, gulls, birds of prey and some other species care for their youngs for a long period of time (see breeding code 12) and terns and kingfishers fly great distances with food and thus can be detected outside of the breeding habitat.
15	Nest with eggs.
16	Nest with visually or acoustically detected youngs in it.

Appendix Table 5 **Observed Display Behaviour.** Table lists display behaviour for species (given by Euring exchange code according to Speek et al. 2001 and English name according to Svensson et al. 2011). “DispBheP1”, “DispBehP2” and “DispBehS” list relative amount of display behaviour compared to the total number of observations per period P1 or P2 and the entire season S (“ObsP1”, “ObsP2”, “ObsS”) for all sites (n = 81) visited during the entire season.

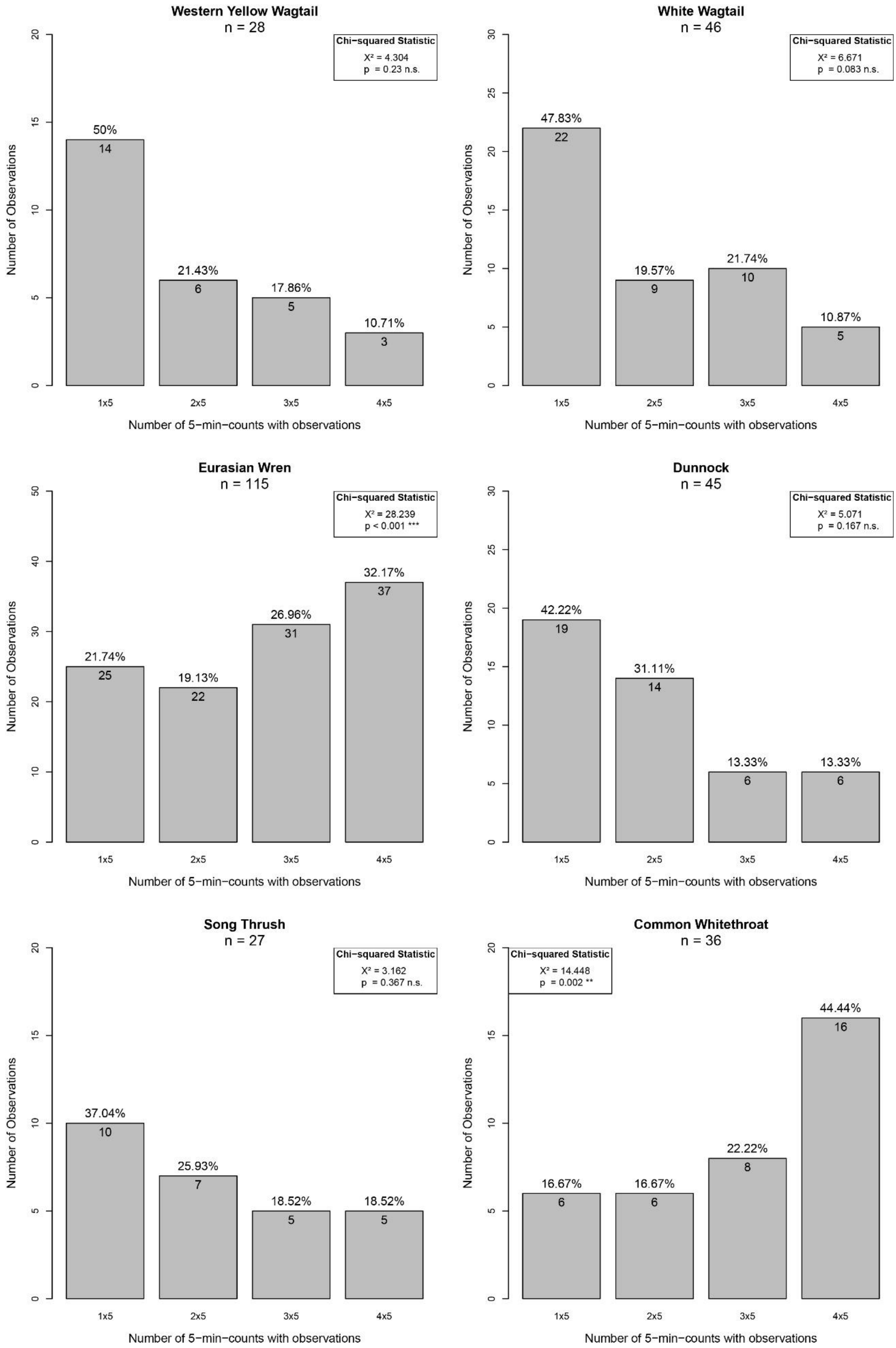
EuringID	Species	DispBehP1	ObsP1	DispBehP2	ObsP2	DispBehS	ObsS
1860	Mallard	2,04	49	0	19	1,47	68
3940	Common Pheasant	8,33	12	0	21	3,03	33
4290	Eurasian Coot	0	9	0	15	0	24
4500	Eurasian Oystercatcher	0	25	0	28	0	53
4930	Northern Lapwing	4,35	46	0	31	2,6	77
6680	Stock Dove	7,69	26	4,76	21	6,38	47
6700	Common Wood Pigeon	27,27	99	31,17	77	28,98	176
6840	Eurasian Collared Dove	34,48	29	36,73	49	35,9	78
7950	Common Swift	0	3	0	49	0	52
8760	Great Spotted Woodpecker	12,5	16	5,56	18	8,82	34
9760	Eurasian Skylark	90	10	90	20	90	30
9920	Barn Swallow	16	25	17,02	47	16,67	72
10010	Common House Martin	0	1	0	26	0	27
10090	Tree Pipit	91,67	12	80	10	86,36	22
10171	Western Yellow Wagtail	10	10	11,11	18	10,71	28
10201	White Wagtail	9,09	22	8,33	24	8,7	46
10660	Eurasian Wren	100	52	100	63	100	115
10840	Dunnock	96,15	26	84,21	19	91,11	45
10990	European Robin	91,67	36	73,68	19	85,45	55
11870	Common Blackbird	31,37	102	45,78	83	37,84	185
12000	Song Thrush	66,67	9	83,33	18	77,78	27
12750	Common Whitethroat	91,67	12	87,5	24	88,89	36
12760	Garden Warbler	100	4	94,74	19	95,65	23
12770	Eurasian Blackcap	93,33	30	95,83	48	94,87	78
13110	Common Chiffchaff	94,51	91	94,74	57	94,59	148
13120	Willow Warbler	100	30	100	13	100	43
14620	Blue Tit	71,43	42	45	20	62,9	62
14640	Great Tit	75	64	53,49	43	66,36	107
14870	Short-toed Treecreeper	87,5	16	73,33	15	80,65	31
15390	Eurasian Jay	9,09	11	0	11	4,55	22
15490	Eurasian Magpie	7,32	41	0	33	4,05	74
15600	Western Jackdaw	0	86	0	61	0	147
15671	Carrion Crow	0	56	0	54	0	110
15820	Common Starling	9,76	41	5,56	36	7,79	77
15910	House Sparrow	33,33	33	40,82	49	37,8	82
16360	Common Chaffinch	82,11	95	88,35	103	85,35	198
16490	European Greenfinch	53,85	26	50	22	52,08	48
16530	European Goldfinch	22,22	18	35,29	17	28,57	35



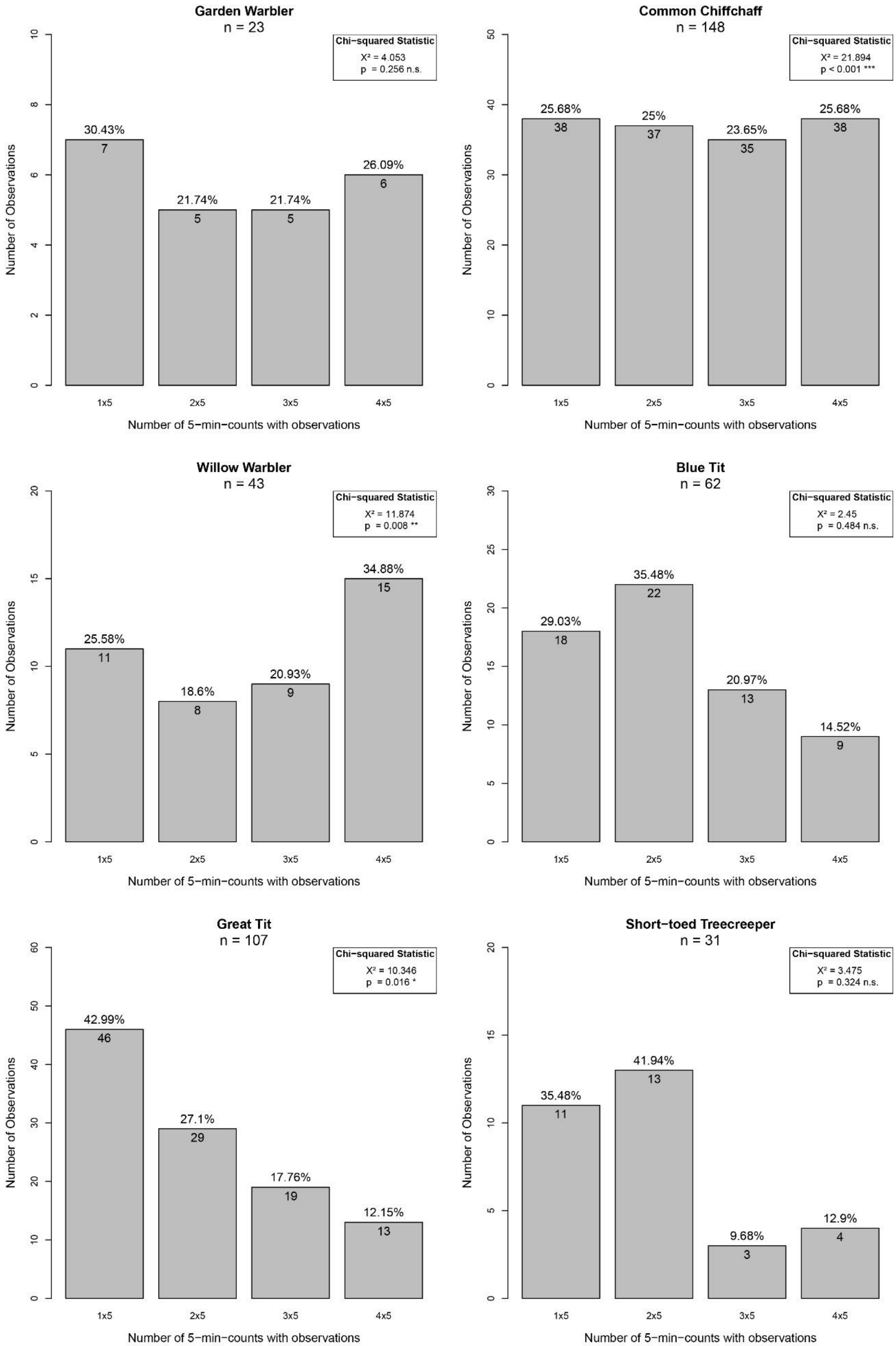
Appendix Figure 2a Numbers of Observations for Any One, Two, Three and All Five-Minute Counts. Combined frequencies of all observations for six species counted in one, two, three and all four five-minute counts during the entire season between April 1st and June 30th 2015 for all sites visited (n = 81 sites). Numbers above bar plots give relative percentage of observations to total observations per species and season. X^2 gives chi-square value, p gives p-value of chi-square statistic.



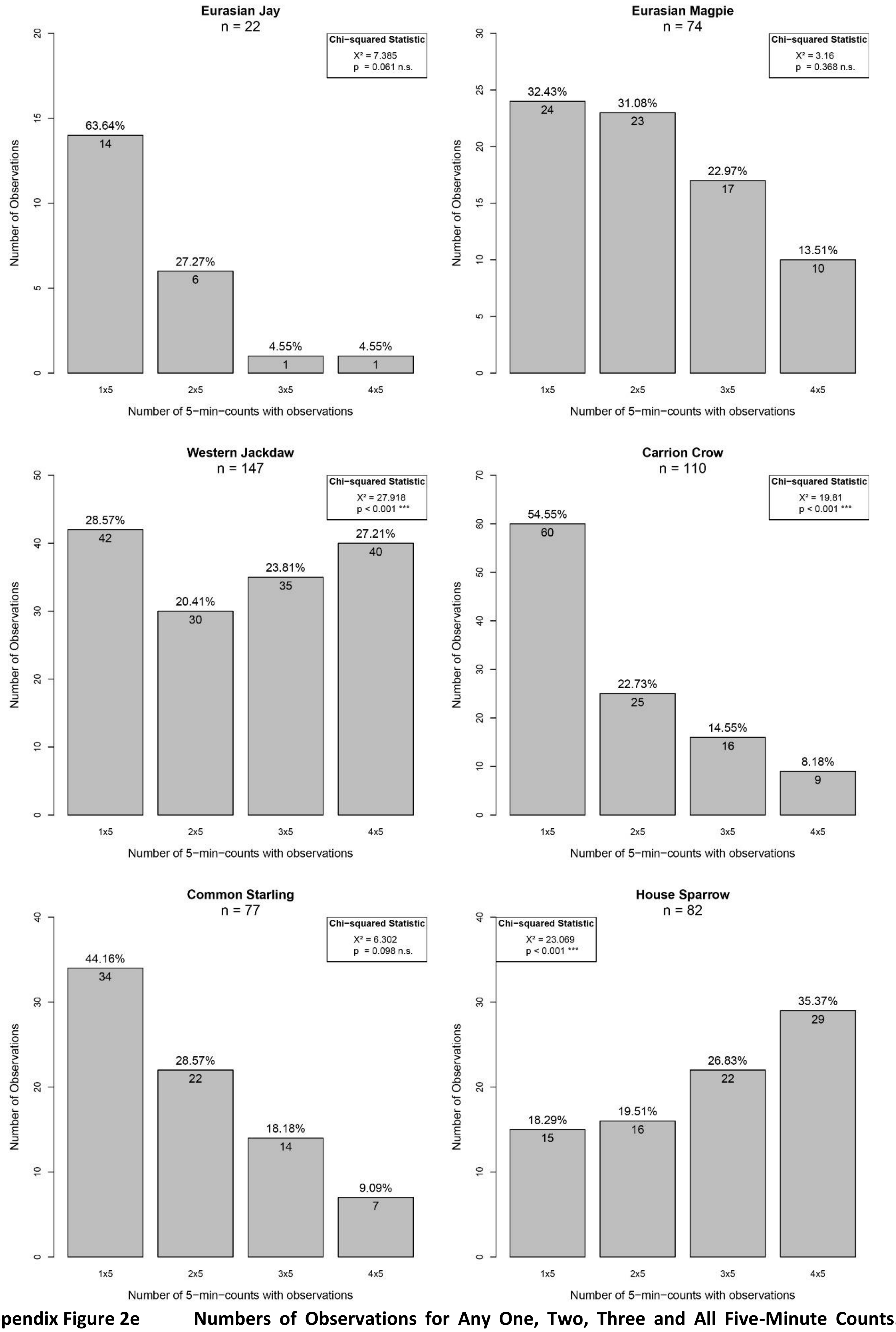
Appendix Figure 2b Numbers of Observations for Any One, Two, Three and All Five-Minute Counts. Combined frequencies of all observations for six species counted in one, two, three and all four five-minute counts during the entire season between April 1st and June 30th 2015 for all sites visited (n = 81 sites). Numbers above bar plots give relative percentage of observations to total observations per species and season. X^2 gives chi-square value, p gives p-value of chi-square statistic.



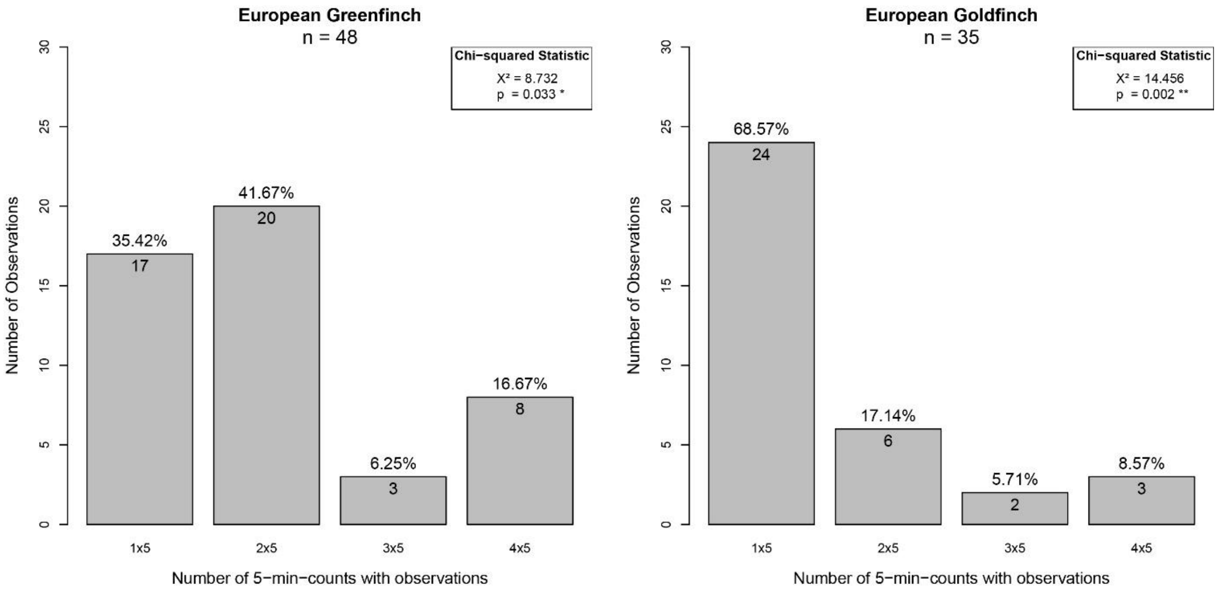
Appendix Figure 2c Numbers of Observations for Any One, Two, Three and All Five-Minute Counts. Combined frequencies of all observations for six species counted in one, two, three and all four five-minute counts during the entire season between April 1st and June 30th 2015 for all sites visited (n = 81 sites). Numbers above bar plots give relative percentage of observations to total observations per species and season. X^2 gives chi-square value, p gives p-value of chi-square statistic.



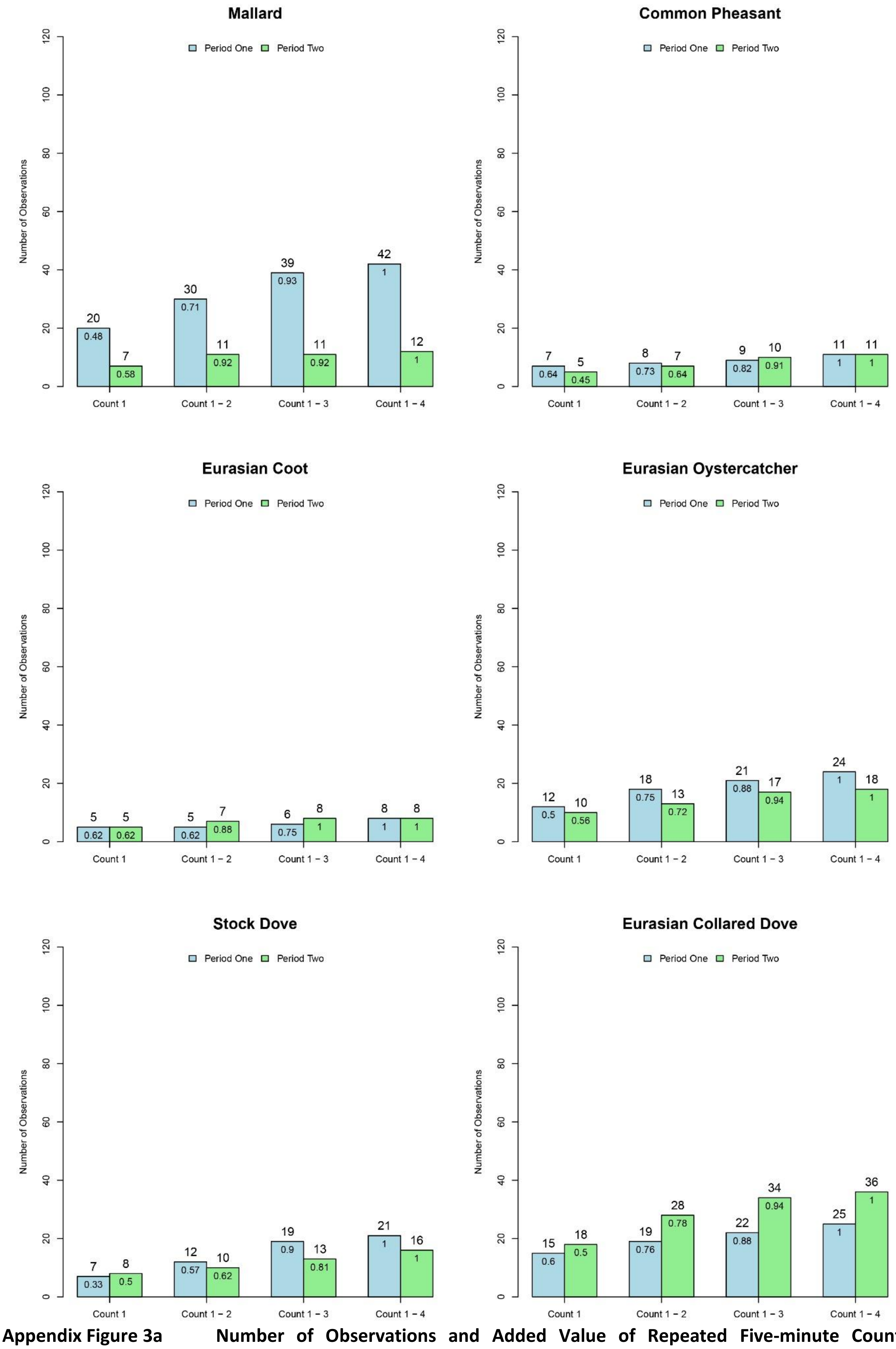
Appendix Figure 2d Numbers of Observations for Any One, Two, Three and All Five-Minute Counts. Combined frequencies of all observations for six species counted in one, two, three and all four five-minute counts during the entire season between April 1st and June 30th 2015 for all sites visited (n = 81 sites). Numbers above bar plots give relative percentage of observations to total observations per species and season. X^2 gives chi-square value, p gives p-value of chi-square statistic.



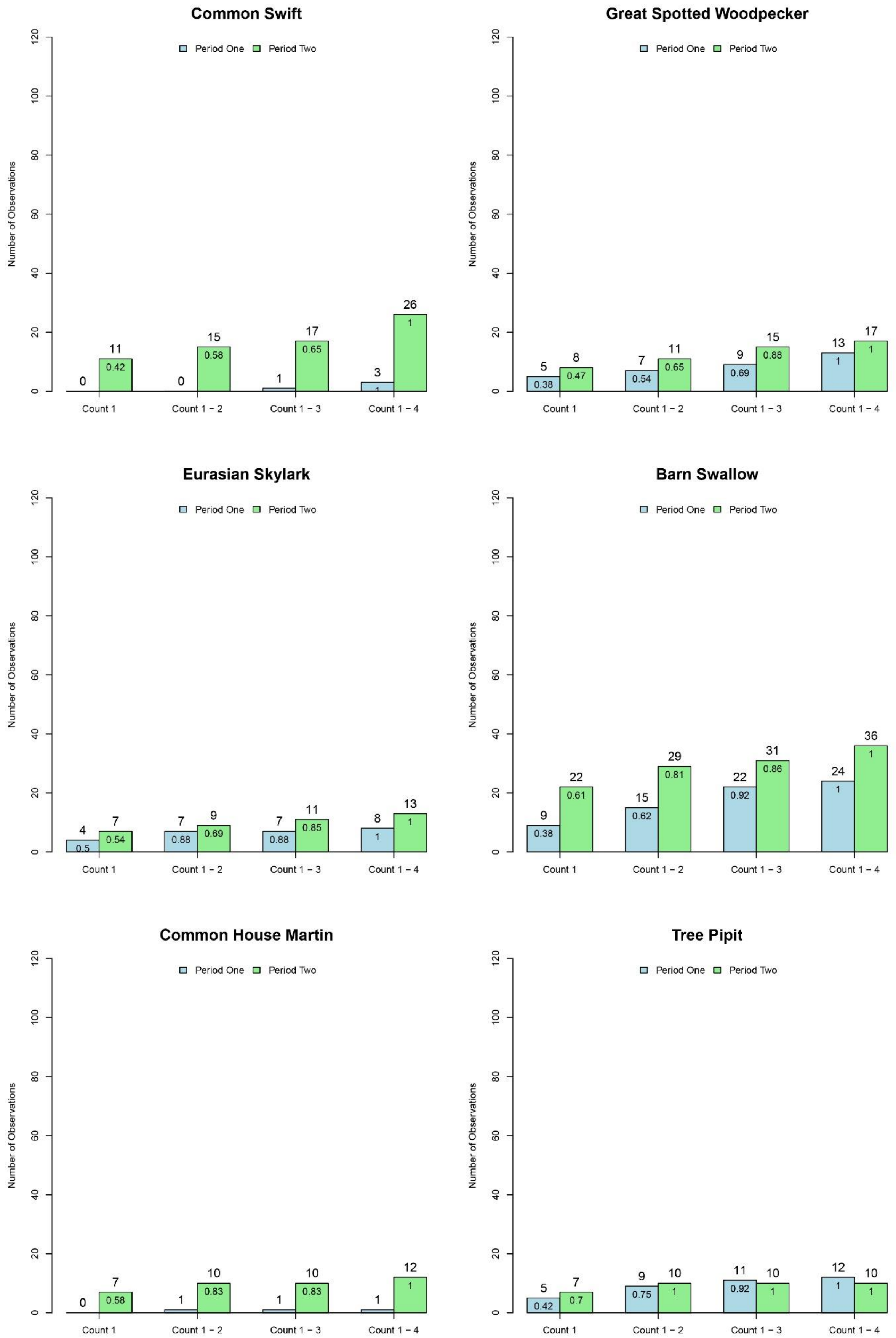
Appendix Figure 2e **Numbers of Observations for Any One, Two, Three and All Five-Minute Counts.** Combined frequencies of all observations for six species counted in one, two, three and all four five-minute counts during the entire season between April 1st and June 30th 2015 for all sites visited (n = 81 sites). Numbers above bar plots give relative percentage of observations to total observations per species and season. X^2 gives chi-square value, p gives p-value of chi-square statistic.



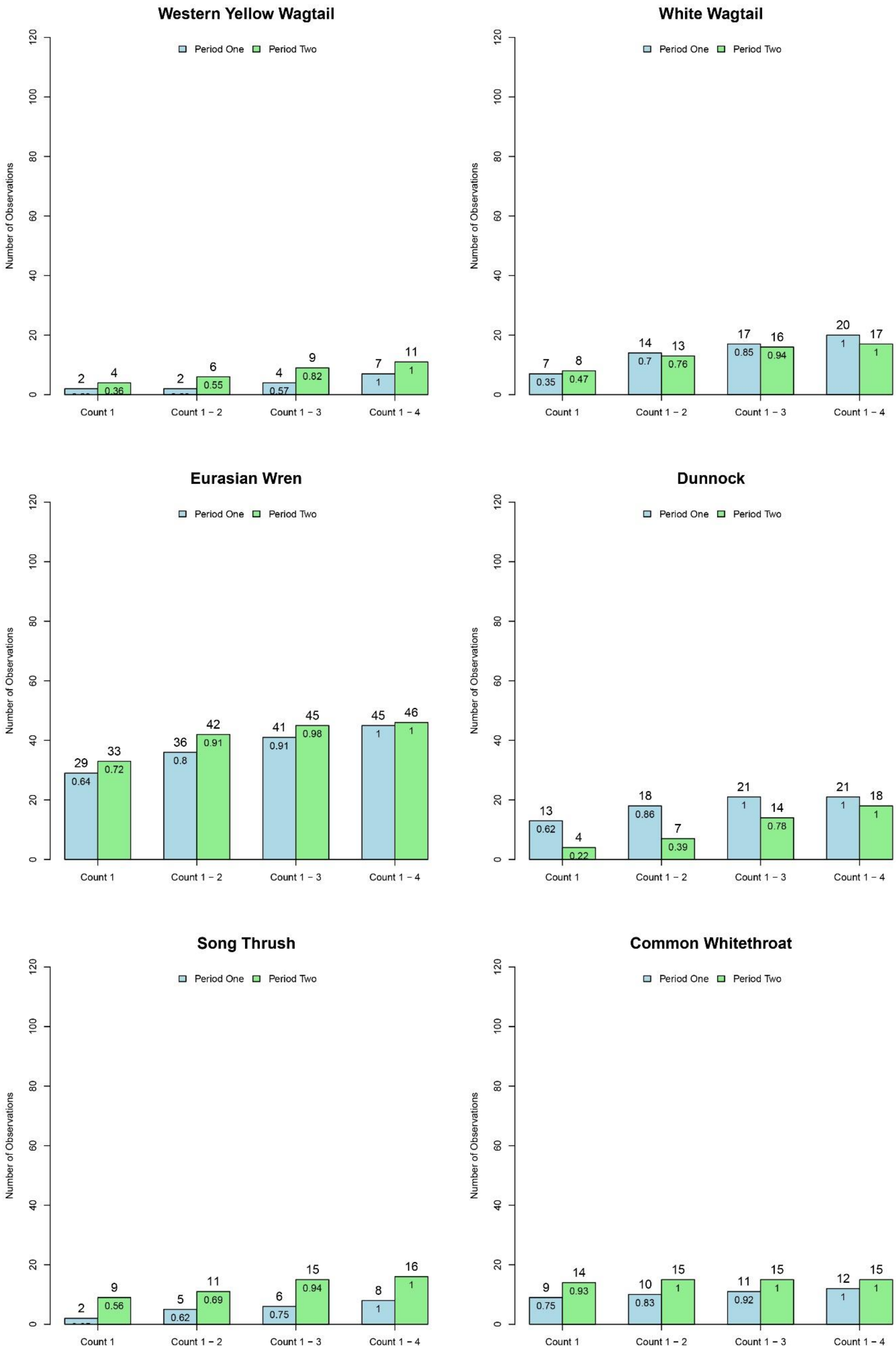
Appendix Figure 2e Numbers of Observations for Any One, Two, Three and All Five-Minute Counts. Combined frequencies of all observations for six species counted in one, two, three and all four five-minute counts during the entire season between April 1st and June 30th 2015 for all sites visited (n = 81 sites). Numbers above bar plots give relative percentage of observations to total observations per species and season. X^2 gives chi-square value, p gives p-value of chi-square statistic.



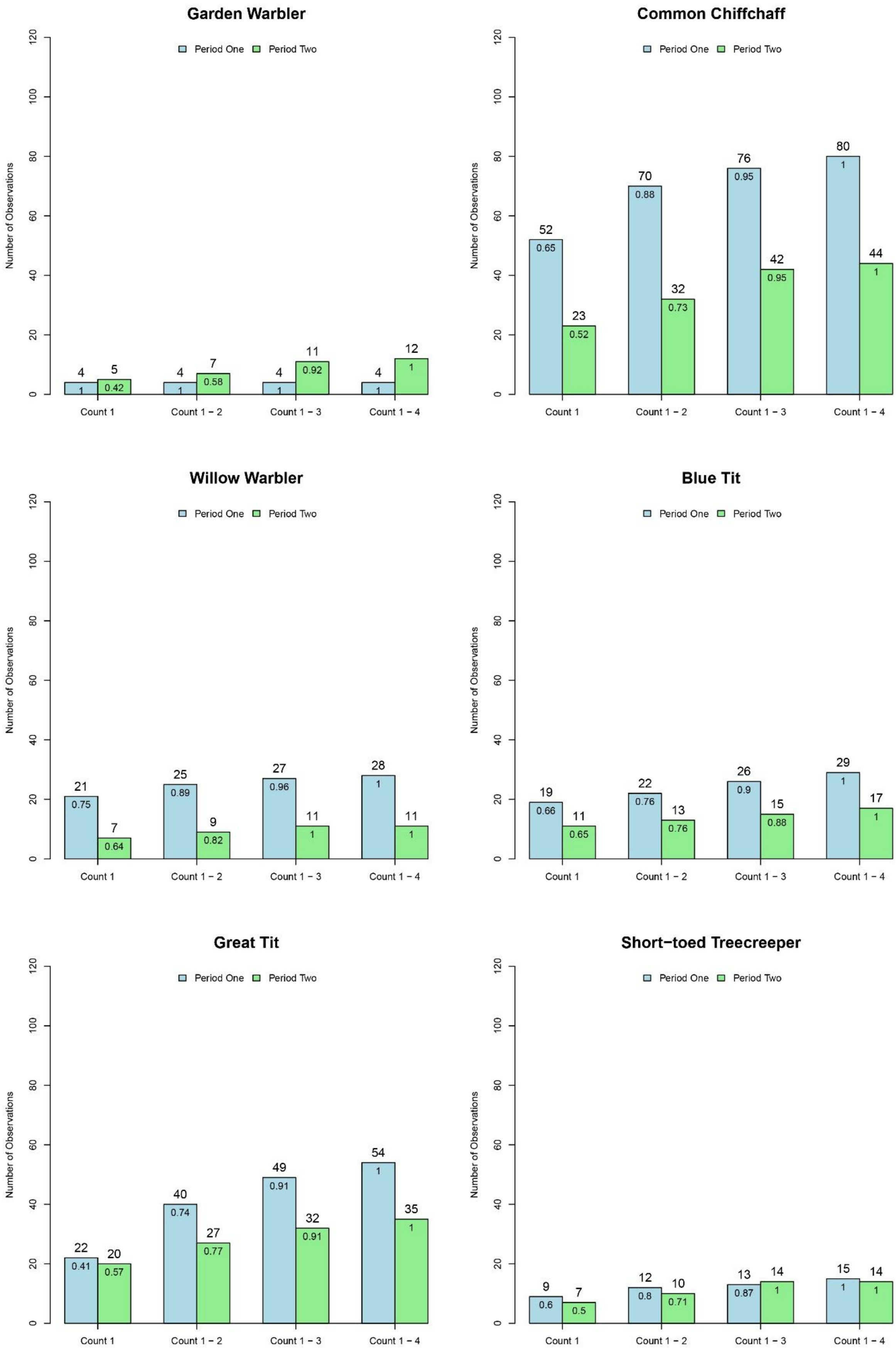
Appendix Figure 3a Number of Observations and Added Value of Repeated Five-minute Counts. Frequencies of six species counted in the first, the first two, the first three and all four five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per bar, numbers below give the fraction of observed in all five-minute counts.



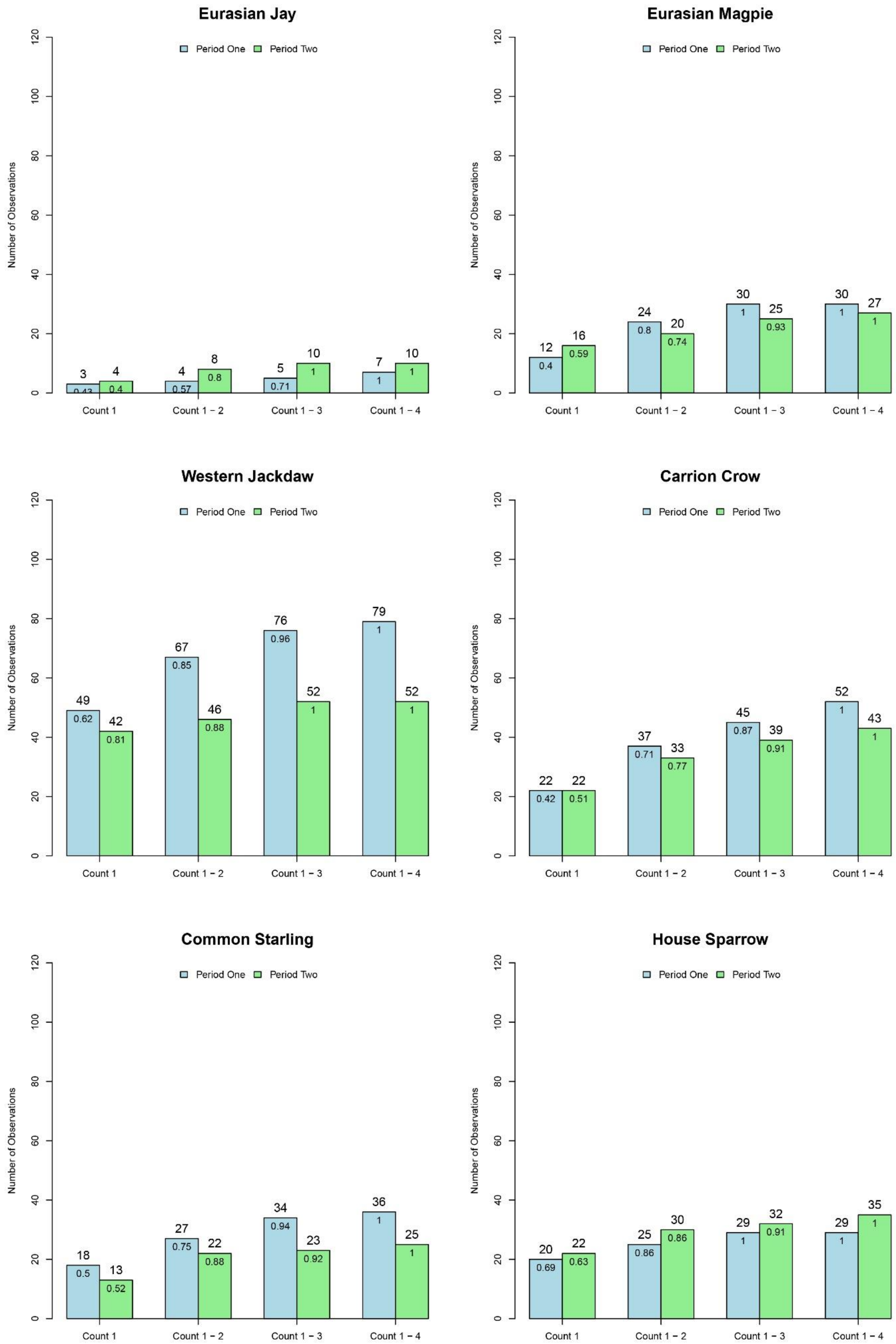
Appendix Figure 3b Number of Observations and Added Value of Repeated Five-minute Counts. Frequencies of six species counted in the first, the first two, the first three and all four five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per bar, numbers below give the fraction of observed in all five-minute counts.



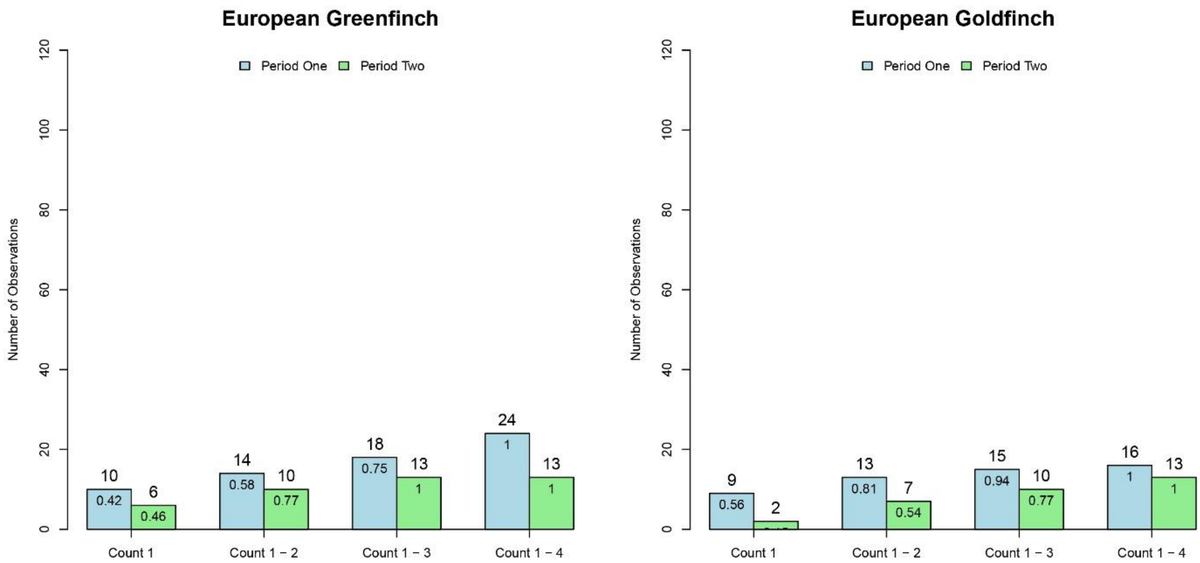
Appendix Figure 3c Number of Observations and Added Value of Repeated Five-minute Counts. Frequencies of six species counted in the first, the first two, the first three and all four five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per bar, numbers below give the fraction of observed in all five-minute counts.



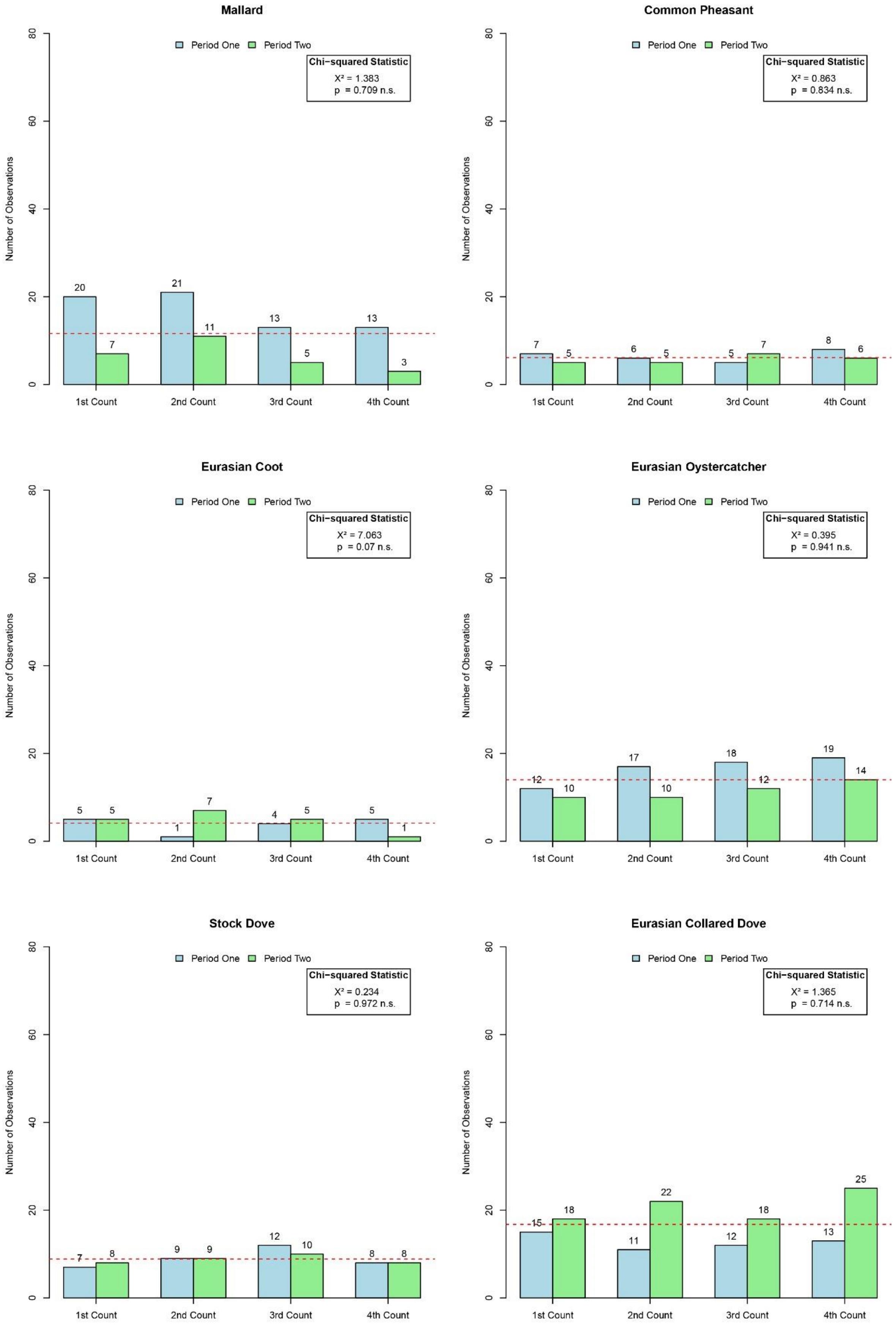
Appendix Figure 3d Number of Observations and Added Value of Repeated Five-minute Counts. Frequencies of six species counted in the first, the first two, the first three and all four five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per bar, numbers below give the fraction of observed in all five-minute counts.



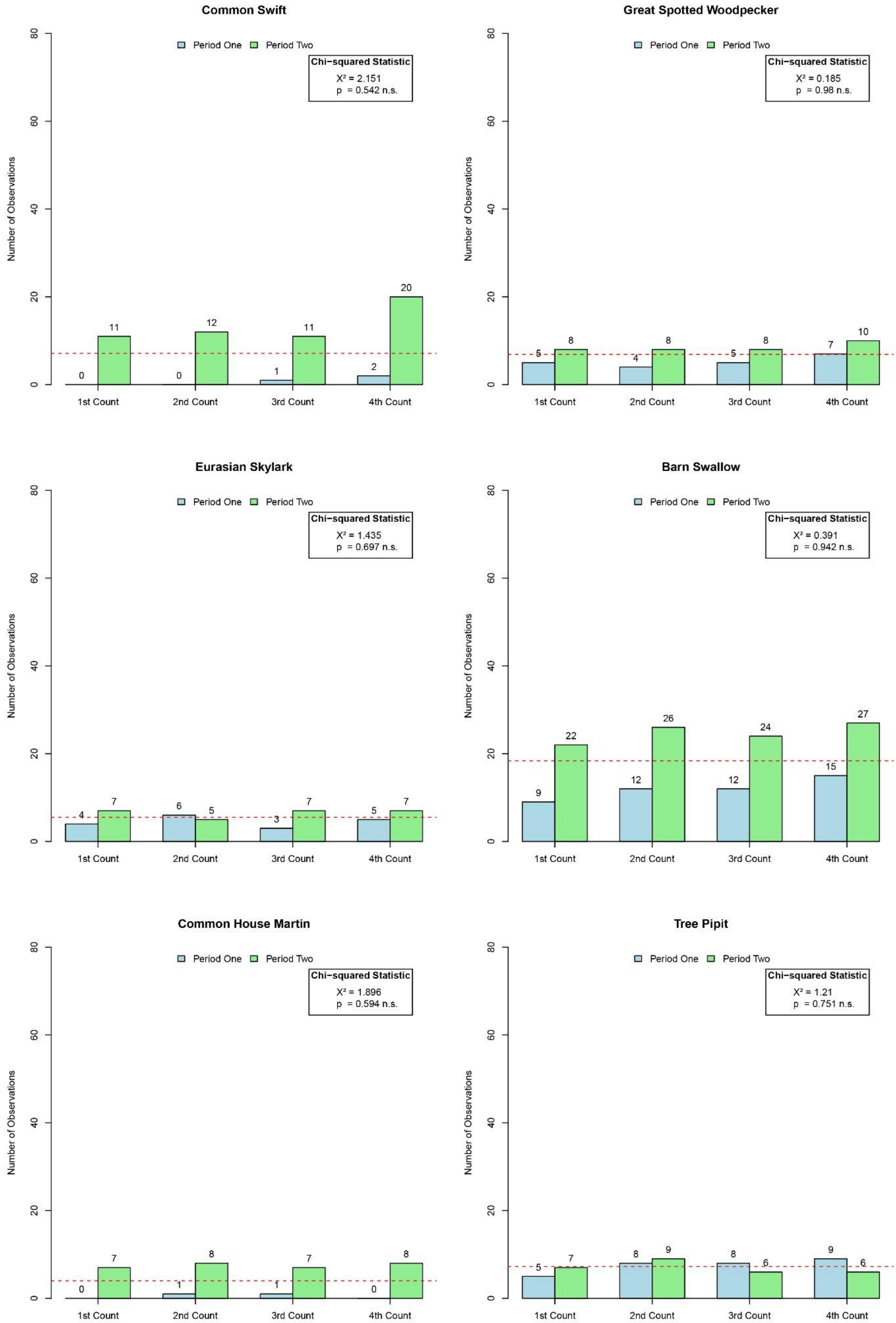
Appendix Figure 3e Number of Observations and Added Value of Repeated Five-minute Counts. Frequencies of six species counted in the first, the first two, the first three and all four five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per bar, numbers below give the fraction of observed in all five-minute counts.



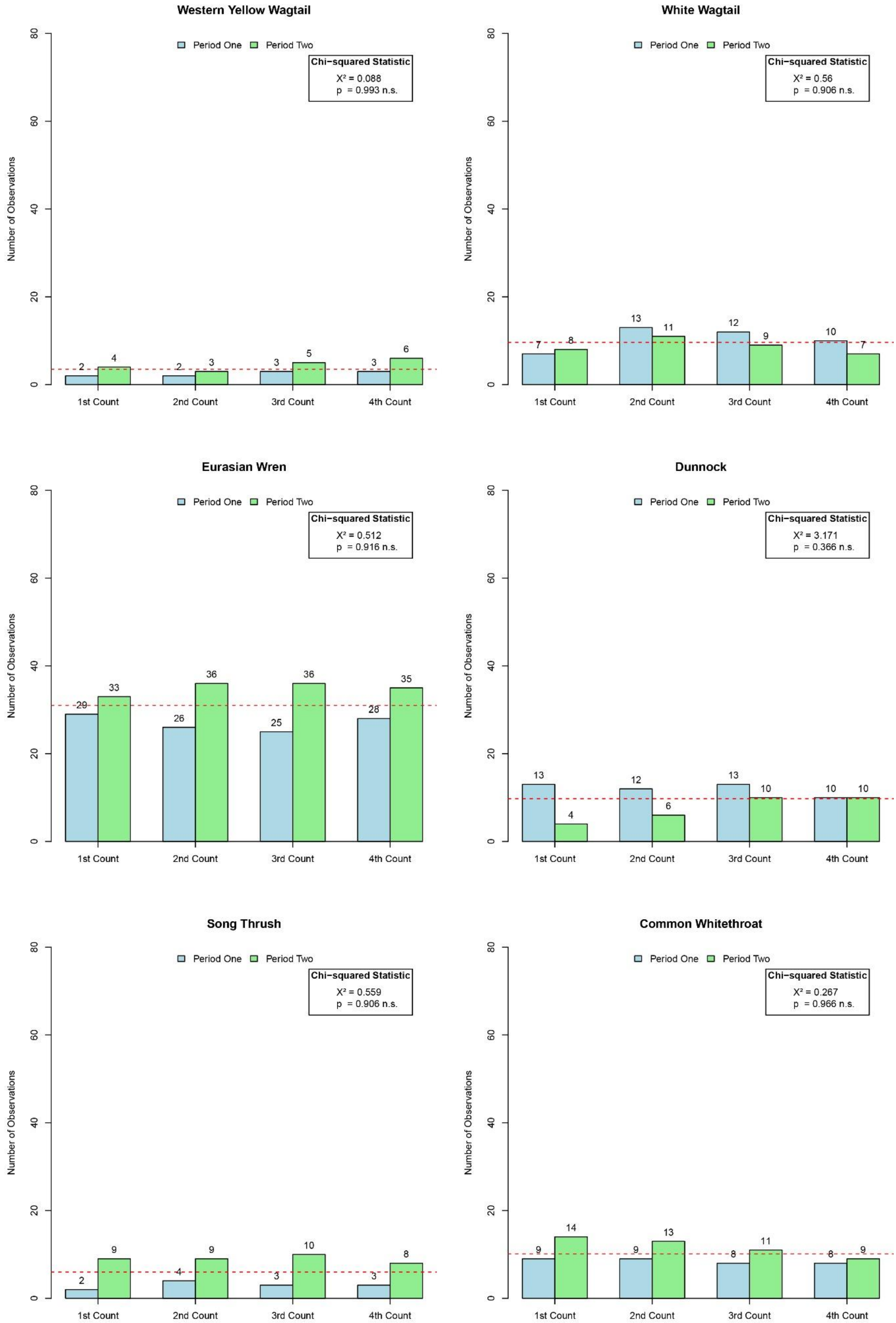
Appendix Figure 3f Number of Observations and Added Value of Repeated Five-minute Counts. Frequencies of six species counted in the first, the first two, the first three and all four five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per bar, numbers below give the fraction of observed in all five-minute counts.



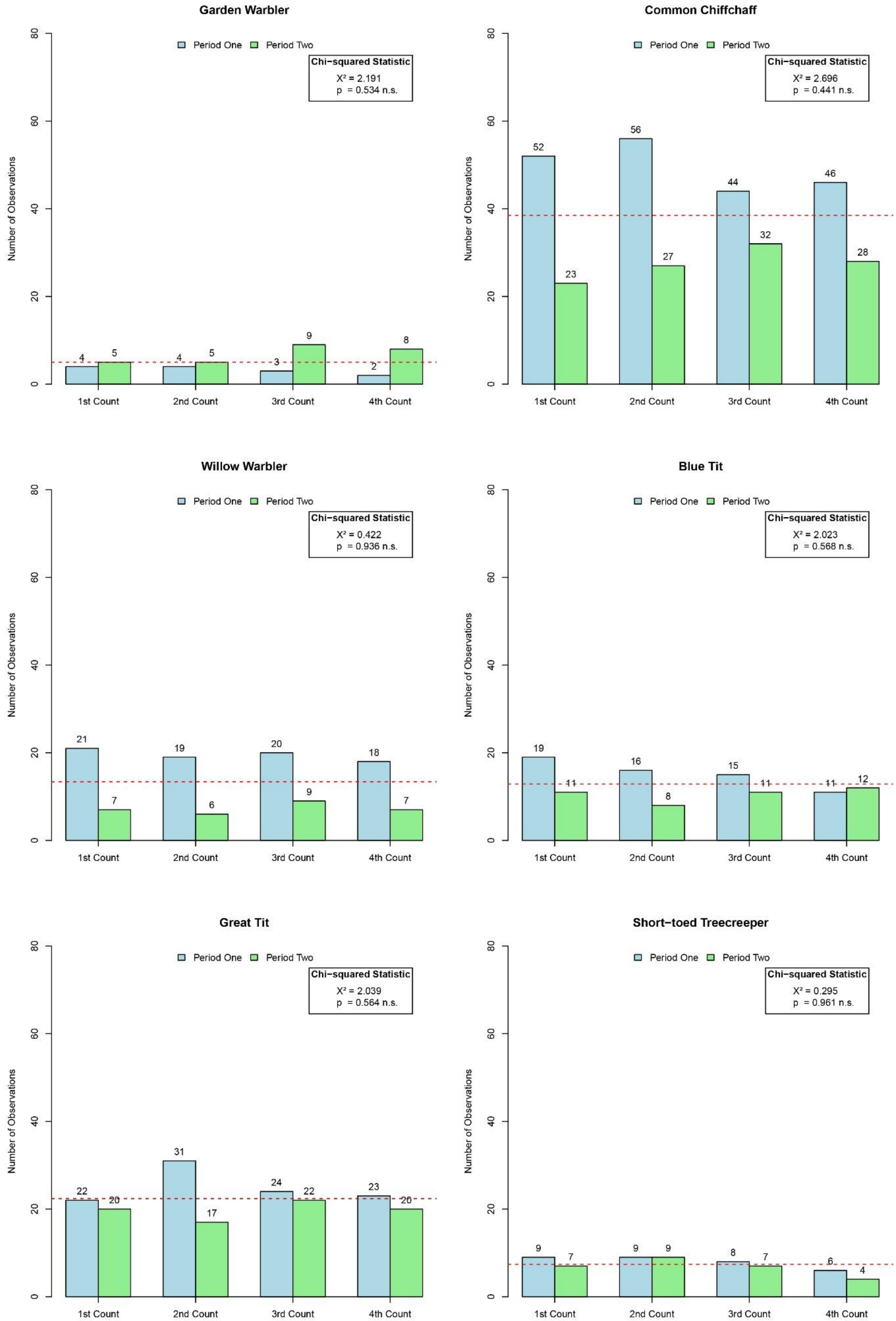
Appendix Figure 4a Number of Observations per Five-minute Count. Numbers of observations for six species counted in the first, second, third and fourth five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per five-minute count. Red dotted line gives mean values.



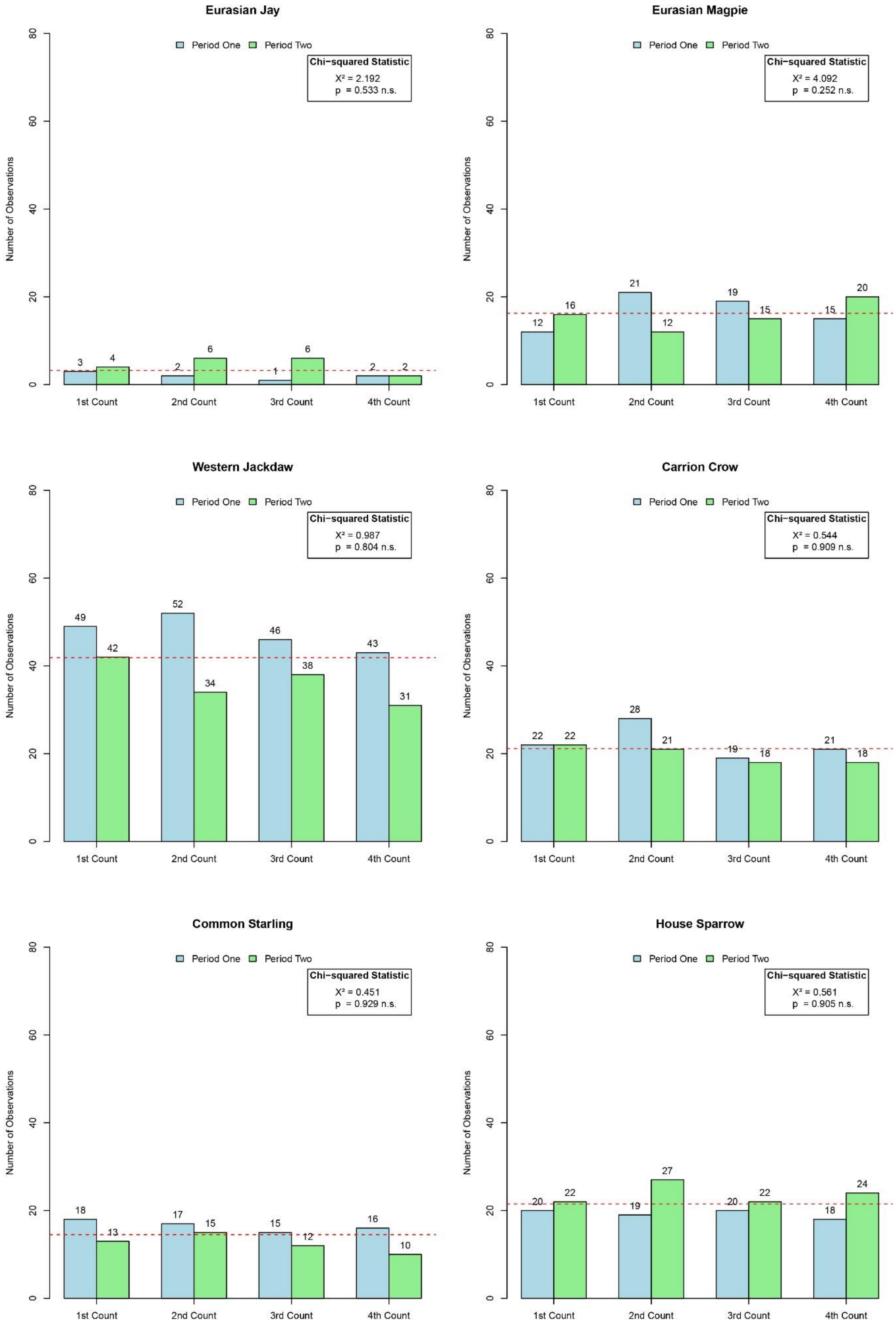
Appendix Figure 4b Number of Observations per Five-minute Count. Numbers of observations for six species counted in the first, second, third and fourth five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per five-minute count. Red dotted line gives mean values.



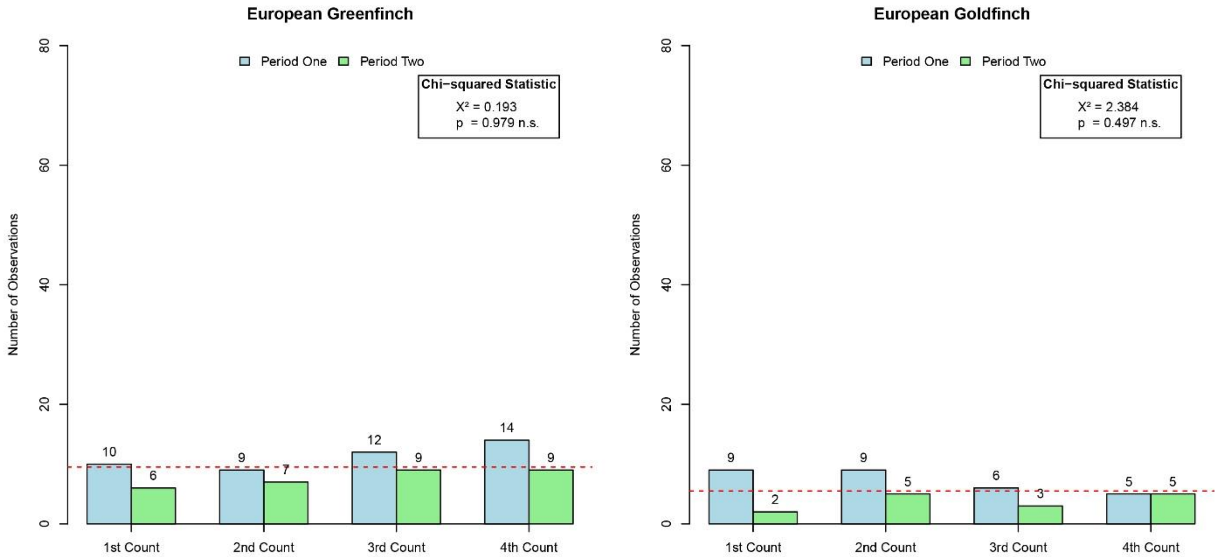
Appendix Figure 4c Number of Observations per Five-minute Count. Numbers of observations for six species counted in the first, second, third and fourth five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per five-minute count. Red dotted line gives mean values.



Appendix Figure 4d Number of Observations per Five-minute Count. Numbers of observations for six species counted in the first, second, third and fourth five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per five-minute count. Red dotted line gives mean values.



Appendix Figure 4e **Number of Observations per Five-minute Count.** Numbers of observations for six species counted in the first, second, third and fourth five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per five-minute count. Red dotted line gives mean values.



Appendix Figure 4f Number of Observations per Five-minute Count. Numbers of observations for six species counted in the first, second, third and fourth five-minute counts during P1 (blue) and P2 (green) at sites visited in both periods (n = 55 sites). Numbers above bars give counted numbers per five-minute count. Red dotted line gives mean values.

Appendix Table 6 **Goodness of Fit for Final Models.** "EuringID" and "Species" define species according to Speek et al. (2001) and Svensson et al. (2011). "Det" and "Abu" list short codes for the detection and abundance models (see Table 2). "Mix." Defines mixture for calculating the latent abundance by either a poisson distribution (P) or a negative binomial distribution (NB). "chi²" gives Pearson's chi-square value for 1.000 bootstrapped samples to assess the N-mixture models fit. "p-value" gives the proportion of simulated test statistics bigger or equal the observed test statistic. "c-hat" is calculated by the division of the observed test statistic by the mean of the simulated test statistic. "RSME" lists the root-mean-square error as defined by the sample standard deviation for the differences between simulated and observed values.

EuringID	Species	Det	Abu	Mix	chi²	p-value	c-hat	RSME
1860	Mallard	Det_2bc	Abu_3bc2	NB	1426.927	0.875	1.453	0.66
3940	Common Pheasant	Det_2ac	Abu_2a2	P	243.463	0.44	0.91	0.338
4500	Eurasian Oystercatcher	Det_4a2c2	Abu_3bc2	P	335.44	0.565	0.997	0.573
4930	Northern Lapwing	Det_4a2bc	Abu_1a	NB	635.235	0.384	0.842	0.931
6680	Stock Dove	Det_3ac2	Abu_4b2c2	NB	696.124	0.859	0	0.411
6700	Wood Pigeon	Det_2ac	Abu_2a2	P	398.543	0.214	0.932	0.718
6840	Collared Dove	Det_1c	Abu_3a2c	P	281.156	0.039	0.719	0.508
7950	Common Swift	Det_3abc	Abu_2ab	NB	1057.184	0.897	0	0.543
8760	Great Spotted Woodpecker	Det_1c	Abu_2ac	P	315.941	0.077	0.8	0.329
9760	Eurasian Skylark	Det_2a2	Abu_2bc	P	186.683	0.231	0.783	0.28
9920	Barn Swallow	Det_1a	Abu_1a	NB	550.029	0.381	0.871	0.577
10090	Tree Pipit	Det_1b	Abu_2ab	P	262.643	0.342	0.855	0.38
10201	White Wagtail	Det_1a	Abu_2b2	P	520.521	0.951	1.297	0.415
10660	Eurasian Wren	Det_2b2	Abu_1c	P	266.841	0	0.619	0.572
10840	Dunnock	Det_2ac	Abu_3a2c	P	327.713	0.208	0.827	0.375
10990	European Robin	Det_4a2bc	Abu_2b2	P	406.776	0.302	0.949	0.45
11870	Common Blackbird	Det_4abc2	Abu_2a2	P	398.726	0.229	0.936	0.779
12000	Song Thrush	Det_1c	Abu_1c	P	398.607	0.248	0.929	0.325
12750	Common Whitethroat	Det_5a2b2c	Abu_4a2b2	P	384.95	0.73	1.076	0.41
12770	Eurasian Blackcap	Det_5a2b2c	Abu_2ac	P	397.077	0.366	0.945	0.49
13110	Common Chiffchaff	Det_3ac2	Abu_2a2	P	340.334	0.002	0.796	0.731
13120	Willow Warbler	Det_2b2	Abu_2ac	P	438.545	0.854	1.157	0.506
14620	Blue Tit	Det_2a2	Abu_2c2	P	361.091	0.011	0.84	0.436
14640	Great Tit	Det_2bc	Abu_3bc2	P	361.011	0.005	0.841	0.584
14870	Short-toed Treecreeper	Det_2a2	Abu_2b2	P	391.056	0.495	0.91	0.324
15490	Eurasian Magpie	Det_1c	Abu_3a2c	P	323.602	0.116	0.833	0.475
15600	Western Jackdaw	Det_3abc	Abu_3ab2	NB	652.738	0.551	0.992	1.015
15671	Carrion Crow	Det_1c	Abu_2bc	P	504.864	0.959	1.175	0.676
15820	Common Starling	Det_3b2c	Abu_3bc2	NB	618.035	0.772	0	0.603
15910	House Sparrow	Det_3a2c	Abu_3a2c	NB	565.88	0.757	1.108	0.797
16360	Common Chaffinch	Det_1b	Abu_1b	P	373.444	0.076	0.861	0.849
16490	European Greenfinch	Det_5a2b2c	Abu_1c	P	398.276	0.246	0.926	0.396
16530	European Goldfinch	Det_1a	Abu_1b	P	406.595	0.741	1.059	0.327

Appendix Table 7 Parameters and Results for N-mixture Models. Each species (n = 33) with at least 20 observations at 55 sites visited in both periods was fitted with N-mixture models. Table shows estimates (EST), standard errors (SE), z-score (Z), p-values (P(>|Z|), significance (SIGN.) and Akaike information criterion (AIC) of best model selected by AIC and stepwise backward elimination. Abundance is modelled through a log-link, detection probability through a logit-link. The latent abundance distribution is either modelled as a poisson distribution (mixture = "P") or a negative-binomial distribution (mixture = "NB"). Asterisk are categorised by n.s. (p > 0.05), * (p < 0.05), ** (p < 0.01) and *** (p < 0.001).

	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Mallard (mixture = „NB")						423.85
Abundance						
(Intercept)	2.92	0.58	5.06	< 0.001	***	
Forest_Area	-6.40	2.41	-2.66	0.008	**	
Urban_Area	-7.18	3.38	-2.12	0.034	*	
I(Urban_Area^2)	7.14	4.01	1.78	0.075	n.s.	
Detection						
(Intercept)	-3.58	0.51	-7.03	< 0.001	***	
DayNr	0.38	0.18	2.17	0.030	*	
SiteObsNr	0.54	0.17	3.22	0.001	**	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Common Pheasant (mixture = „P")						227.74
Abundance						
(Intercept)	-42.60	18.40	-2.31	0.021	*	
Open_Area	99.80	43.80	2.28	0.023	*	
I(Open_Area^2)	-58.00	25.90	-2.24	0.025	*	
Detection						
(Intercept)	-1.52	0.30	-5.04	< 0.001	***	
StartTime	-0.66	0.23	-2.87	0.004	**	
SiteObsNr	0.72	0.22	3.25	0.001	**	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Eurasian Oystercatcher (mixture = „P")						346.05
Abundance						
(Intercept)	1.10	0.25	4.33	< 0.001	***	
Forest_Area	-23.0	7.21	-3.20	0.001	**	
Urban_Area	-11.1	3.11	-3.55	< 0.001	***	
I(Urban _Area^2)	10.3	3.32	3.10	0.002	**	
Detection						
(Intercept)	-1.17	0.31	-3.78	< 0.001	***	
StartTime	0.37	0.19	1.89	0.058	n.s.	
SiteObsNr	0.72	0.16	4.56	< 0.001	***	
I(StartTime^2)	0.62	0.21	2.93	0.003	**	
I(SiteObsNr^2)	-0.17	0.08	-2.14	0.032	*	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Northern Lapwing (mixture = „NB")						404.12
Abundance						
(Intercept)	-3.25	1.05	-3.10	0.002	**	
Open_Area	4.77	1.29	3.70	< 0.001	***	
Detection						
(Intercept)	-0.20	0.35	-0.57	0.568	n.s.	
StartTime	-0.44	0.16	-2.79	0.005	**	
DayNr	-0.42	0.17	-2.46	0.014	*	
SiteObsNr	0.82	0.14	6.07	< 0.001	***	
I(StartTime^2)	-1.16	0.25	-4.74	< 0.001	***	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**

Stock Dove (mixture = „NB“)						345.76
Abundance						
(Intercept)	0.76	0.56	1.36	0.175	n.s.	
Forest_Area	-13.12	5.33	-2.46	0.014	*	
Urban_Area	6.08	2.78	2.19	0.029	*	
I(Forest _Area^2)	12.96	5.60	2.32	0.021	*	
I(Urban _Area^2)	-10.07	3.97	-2.54	0.011	*	
Detection						
(Intercept)	-2.19	0.62	-3.51	< 0.001	***	
StartTime	-0.38	0.18	-2.05	0.041	*	
SiteObsNr	0.22	0.22	1.04	0.299	n.s.	
I(SiteObsNr^2)	-0.33	0.17	-1.97	0.049	*	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Wood Pigeon (mixture = „P“)						807.97
Abundance						
(Intercept)	0.28	0.37	0.77	0.439	n.s.	
Open_Area	3.12	1.46	2.13	0.033	*	
I(Open_Area^2)	-3.00	1.36	-2.21	0.027	*	
Detection						
(Intercept)	-0.97	0.17	-5.77	< 0.001	***	
StartTime	-0.27	0.12	-2.26	0.024	*	
SiteObsNr	0.61	0.11	5.50	< 0.001	***	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Collared Dove (mixture = „P“)						371.61
Abundance						
(Intercept)	-6.28	2.08	-3.02	0.003	**	
Open_Area	12.92	3.62	3.57	< 0.001	***	
Urban_Area	6.60	2.00	3.30	< 0.001	***	
I(Open_Area^2)	-8.64	2.55	-3.38	< 0.001	***	
Detection						
(Intercept)	-0.53	0.21	-2.48	0.013	*	
SiteObsNr	00.51	0.17	2.96	0.003	**	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Common Swift (mixture = „NB“)						250.16
Abundance						
(Intercept)	3.61	0.66	5.50	< 0.001	***	
Open_Area	-2.02	0.90	-2.24	0.025	*	
Forest_Area	-4.87	1.76	-2.77	0.006	**	
Detection						
(Intercept)	-4.76	0.51	-9.41	< 0.001	***	
StartTime	0.70	0.25	2.84	0.004	**	
DayNr	0.59	0.19	3.11	0.002	**	
SiteObsNr	1.06	0.20	5.40	< 0.001	***	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Great Spotted Woodpecker (mixture = „P“)						278.12
Abundance						
(Intercept)	1.99	0.44	4.54	< 0.001	***	
Open_Area	-2.42	0.51	-4.79	< 0.001	***	
Urban_Area	-5.80	1.90	-3.05	0.002	**	
Detection						
(Intercept)	-1.99	0.38	-5.31	< 0.001		
SiteObsNr	0.69	0.21	3.28	0.001		
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Eurasian Skylark (mixture = „P“)						174.18
Abundance						
(Intercept)	0.11	0.34	0.33	0.743	n.s.	
Forest_Area	-33.44	15.29	-2.19	0.029	*	

Urban_Area	-7.35	3.65	-2.01	0.044	*	
<u>Detection</u> (Intercept) StartTime I(StartTime^2)	 -1.25 -0.19 0.77	 0.41 0.23 0.32	 -3.04 -0.82 2.37	 0.002 0.413 0.018	 ** n.s. *	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Barn Swallow (mixture = „NB“)						453.31
<u>Abundance</u> (Intercept) OpenArea	 -0.27 1.32	 0.70 0.75	 -0.38 1.75	 0.703 0.080	 n.s. n.s.	
<u>Detection</u> (Intercept) StartTime	 -1.80 0.19	 0.59 0.18	 -3.05 1.05	 0.002 0.294	 ** n.s.	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Tree Pipit (mixture = „P“)						184.12
<u>Abundance</u> (Intercept) Open_Area Forest_Area	 -12.70 11.70 13.60	 5.36 5.59 5.43	 -2.36 2.09 2.50	 0.018 0.037 0.012	 * * *	
<u>Detection</u> (Intercept) DayNr	 < 0.001 -0.19	 0.27 0.29	 < 0.001 -0.66	 1.000 0.508	 n.s. n.s.	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
White Wagtail (mixture = „P“)						352.57
<u>Abundance</u> (Intercept) Forest_Area I(Forest _Area^2)	 < 0.001 -0.14 0.14	 0.24 5.87 6.13	 < 0.001 -2.32 2.20	 1.000 0.020 0.028	 n.s. * *	
<u>Detection</u> (Intercept) StartTime	 -1.07 -0.31	 0.23 0.19	 -4.66 -1.62	 < 0.001 0.105	 *** n.s.	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Eurasian Wren (mixture = „P“)						691.49
<u>Abundance</u> (Intercept) Urban_Area	 0.30 -0.63	 0.15 0.54	 1.92 -1.18	 0.055 0.240	 n.s. n.s.	
<u>Detection</u> (Intercept) DayNr I(DayNr^2)	 0.41 0.52 -0.63	 0.19 0.15 0.14	 2.18 3.55 -4.50	 0.029 < 0.001 < 0.001	 * *** ***	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Dunnock (mixture = „P“)						321.17
<u>Abundance</u> (Intercept) Open_Area Urban_Area I(Open_Area^2)	 -6.37 12.54 7.66 -6.82	 2.47 3.83 2.42 2.32	 -2.58 3.28 3.17 -2.95	 0.001 0.001 0.002 0.003	 ** ** ** **	
<u>Detection</u> (Intercept) StartTime SiteObsNr	 -2.47 -0.48 0.43	 0.53 0.18 0.21	 -4.69 -2.66 2.06	 < 0.001 0.008 0.039	 *** ** *	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
European Robin (mixture = „P“)						419.24
<u>Abundance</u> (Intercept) Forest_Area	 -0.69 5.20	 0.25 1.71	 -2.76 3.05	 0.006 0.002	 ** **	

I(Forest _Area^2)	-4.11	2.00	-2.06	0.039	*	
Detection (Intercept) StartTime DayNr SiteObsNr I(StartTime^2)	 -1.30 -0.06 0.37 0.37 0.34	 0.29 0.17 0.16 0.18 0.17	 -4.55 -0.38 2.32 2.08 2.02	 < 0.001 0.703 0.020 0.038 0.044	 *** n.s. * * *	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Common Blackbird (mixture = „P“)						832.12
Abundance (Intercept) Open_Area I(Open_Area^2)	 1.31 2.13 -3.21	 0.29 1.20 1.19	 4.52 1.77 -2.69	 < 0.001 0.076 0.007	 *** n.s. **	
Detection (Intercept) StartTime DayNr SiteObsNr I(SiteObsNr^2)	 -1.25 -0.19 -0.35 0.66 -0.17	 0.21 0.10 0.09 0.12 0.07	 -5.94 -1.95 -3.73 5.72 -2.40	 < 0.001 0.051 < 0.001 < 0.001 0.016	 *** n.s. *** *** *	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Song Thrush (mixture = „P“)						270.32
Abundance (Intercept) Urban_Area	 -0.46 -1.27	 0.29 1.00	 -1.58 -1.26	 0.114 0.206	 n.s. n.s.	
Detection (Intercept) SiteObsNr	 -1.40 0.61	 0.27 0.24	 -5.16 2.56	 < 0.001 0.010	 *** *	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Common Whitethroat (mixture = „P“)						275.94
Abundance (Intercept) Open_Area Forest_Area I(Open_Area^2) I(Forest _Area^2)	 -0.71 -8.91 21.56 9.64 -39.63	 0.89 4.54 6.50 4.91 14.34	 -0.79 -1.96 3.32 2.30 -2.76	 0.427 0.050 < 0.001 0.021 0.006	 n.s. n.s. *** * **	
Detection (Intercept) StartTime DayNr SiteObsNr I(StartTime^2) I(DayNr^2)	 -0.87 -1.07 0.35 0.64 -0.78 0.63	 0.47 0.27 0.24 0.19 0.23 0.30	 -1.86 -3.99 1.46 3.34 -3.33 2.11	 0.063 < 0.001 0.145 < 0.001 < 0.001 0.035	 n.s. *** n.s. *** *** *	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Eurasian Blackcap (mixture = „P“)						465.43
Abundance (Intercept) Open_Area Urban_Area	 1.01 -1.12 -3.20	 0.35 0.47 1.08	 2.92 -2.36 -2.97	 0.004 0.018 0.003	 ** * **	
Detection (Intercept) StartTime DayNr SiteObsNr I(StartTime^2) I(DayNr^2)	 -0.65 -0.03 0.55 0.41 0.33 -0.63	 0.29 0.17 0.22 0.18 0.16 0.20	 -2.24 -0.19 2.54 2.34 2.04 -3.13	 0.025 0.850 0.011 0.020 0.041 0.002	 * n.s. * * * **	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Common Chiffchaff (mixture = „P“)						834.47

Abundance						
(Intercept)	0.07	0.39	0.18	0.856	n.s.	
Open_Area	3.21	1.51	2.13	0.033	*	
I(Open_Area^2)	-2.99	1.38	-2.16	0.031	*	
Detection						
(Intercept)	-0.43	0.18	-2.42	0.016	*	
StartTime	0.45	0.11	3.97	< 0.001	***	
SiteObsNr	0.39	0.11	3.55	< 0.001	***	
I(SiteObsNr^2)	-0.19	0.06	-2.85	0.004	**	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Willow Warbler (mixture = „P“)						345.66
Abundance						
(Intercept)	1.32	0.33	4.00	< 0.001	***	
Open_Area	-2.08	0.51	-4.09	< 0.001	***	
Urban_Area	-6.22	2.36	-2.64	0.008	**	
Detection						
(Intercept)	-1.24	0.28	-4.48	< 0.001	***	
DayNr	-0.83	0.26	-3.22	0.001	**	
I(DayNr^2)	0.95	0.22	4.39	< 0.001	***	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Blue Tit (mixture = „P“)						442.55
Abundance						
(Intercept)	-0.51	0.26	-2.01	0.045	*	
Urban_Area	5.51	1.98	2.79	0.005	**	
I(Urban _Area^2)	-5.87	2.34	-2.50	0.012	*	
Detection						
(Intercept)	-0.52	0.26	-2.02	0.043	*	
StartTime	0.003	0.17	0.02	0.986	n.s.	
I(StartTime^2)	-0.54	0.19	-2.88	0.004	**	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Great Tit (mixture = „P“)						666.38
Abundance						
(Intercept)	0.42	0.27	1.52	0.129	n.s.	
Forest_Area	0.75	0.51	1.48	0.138	n.s.	
Urban_Area	4.00	1.57	2.56	0.011	*	
I(Urban _Area^2)	-4.56	1.80	-2.53	0.011	*	
Detection						
(Intercept)	-1.50	0.26	-5.75	< 0.001	***	
DayNr	-0.25	0.12	-2.02	0.043	*	
SiteObsNr	0.26	0.12	2.12	0.034	*	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Short-toed Treecreeper (mixture = „P“)						250.89
Abundance						
(Intercept)	-1.40	0.40	-3.47	< 0.001	***	
Forest_Area	8.27	2.10	3.94	< 0.001	***	
I(Forest _Area^2)	-5.36	2.33	-2.30	0.022	*	
Detection						
(Intercept)	-1.26	0.53	-2.36	0.018	*	
StartTime	-1.07	0.29	-3.67	< 0.001	***	
I(StartTime^2)	-0.89	0.30	-2.94	0.003	**	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Eurasian Magpie (mixture = „P“)						430.72
Abundance						
(Intercept)	-8.13	2.35	-3.46	< 0.001	***	
Open_Area	14.62	3.94	3.70	< 0.001	***	
Urban_Area	7.43	2.22	3.34	< 0.001	***	
I(Open_Area^2)	-6.81	2.37	-2.87	0.004	**	

Detection (Intercept) SiteObsNr	 -0.72 0.45	 0.20 0.15	 -3.70 3.00	 < 0.001 0.003	 *** **	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Western Jackdaw (mixture = „NB“)						703.93
Abundance (Intercept) Open_Area Forest_Area I(Forest _Area^2)	 1.98 -1.35 -10.03 8.25	 0.45 0.60 3.40 3.79	 4.38 -2.26 -2.95 2.18	 < 0.001 0.024 0.003 0.029	 *** * ** *	
Detection (Intercept) StartTime DayNr SiteObsNr	 -0.77 0.27 -0.34 0.47	 0.19 0.13 0.10 0.11	 -3.95 2.06 -3.49 4.23	 < 0.001 0.039 < 0.001 < 0.001	 *** * *** ***	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Carrion Crow (mixture = „P“)						640.40
Abundance (Intercept) Forest_Area Urban_Area	 1.08 -1.87 -1.79	 0.20 0.70 0.63	 5.53 -2.68 -2.86	 < 0.001 0.007 0.004	 *** ** **	
Detection (Intercept) SiteObsNr	 -1.34 0.46	 0.19 0.11	 -6.98 4.26	 < 0.001 < 0.001	 *** ***	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Common Starling (mixture = „NB“)						454.98
Abundance (Intercept) Forest_Area Urban_Area I(Urban _Area^2)	 0.14 2.69 7.11 -7.55	 0.44 0.85 2.61 2.83	 0.32 3.16 2.72 -2.67	 0.749 0.002 0.007 0.008	 n.s. ** ** **	
Detection (Intercept) DayNr SiteObsNr I(DayNr^2)	 -3.40 -1.43 0.68 0.68	 0.45 0.23 0.15 0.22	 -7.53 -6.34 4.46 3.04	 < 0.001 < 0.001 < 0.001 0.002	 *** *** *** **	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
House Sparrow (mixture = „NB“)						464.63
Abundance (Intercept) Open_Area Urban_Area I(Open_Area^2)	 -7.16 17.48 6.47 -11.41	 2.34 5.34 2.05 3.80	 -3.05 3.27 3.15 -3.00	 0.002 0.001 0.002 0.003	 ** ** ** **	
Detection (Intercept) StartTime SiteObsNr I(StartTime^2)	 -0.27 -0.17 0.28 -0.47	 0.31 0.18 0.16 0.22	 -0.88 -0.97 1.71 -2.18	 0.381 0.331 0.087 0.030	 n.s. n.s. n.s. *	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
Common Chaffinch (mixture = „P“)						915.08
Abundance (Intercept) Forest_Area	 0.59 0.84	 0.13 0.33	 4.40 2.56	 < 0.001 0.011	 *** *	
Detection (Intercept) DayNr	 -0.32 0.19	 0.14 0.09	 -2.31 2.10	 0.021 0.036	 * *	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**

European Greenfinch (mixture = „P“)						333.88
<u>Abundance</u> (Intercept) Urban_Area	 -1.02 2.55	 0.30 0.51	 -3.42 4.99	 < 0.001 < 0.001	 *** ***	
<u>Detection</u> (Intercept) StartTime DayNr SiteObsNr I(StartTime^2) I(DayNr^2)	 -1.45 0.43 -0.02 0.40 0.48 -0.45	 0.37 0.22 0.21 0.16 0.21 0.22	 -3.91 1.98 -0.07 2.57 2.29 -2.06	 < 0.001 0.047 0.941 0.010 0.022 0.039	 *** * n.s. * * *	
	EST	**SE**	**Z**	**P(>|Z|)**	**SIGN.**	**AIC**
European Goldfinch (mixture = „P“)						262.32
<u>Abundance</u> (Intercept) Forest_Area	 0.61 -5.36	 0.41 3.08	 1.50 -1.74	 0.312 0.081	 n.s. n.s.	
<u>Detection</u> (Intercept) StartTime	 -2.86 -0.88	 0.46 0.24	 -6.25 -3.74	 < 0.001 < 0.001	 *** ***	

Appendix Table 8 **Estimations and Observations**. Table lists estimated number of pairs for the first five-minute counts (“Est1x5”), the first two five-minute counts (“Est2x5”) and the first three five-minute counts (“Est3x5”) as well as all five-minute counts of P1 (“EstP1”), P2 (“EstP2”) and the entire season (“EstFull”) at sites visited in both periods (n = 55 sites). The number of observations for P1 and P2 are given in “ObsP1” and “ObsP2” for each species (“SpeciesID” and “SpeciesName” according to Speek et al. 2001 and Svensson et al. 2011).

SpeciesID	SpeciesName	Est1x5	Est2x5	Est3x5	ObsP1	EstP1	ObsP2	EstP2	EstFS
1860	Mallard	395.95	399.81	445.95	42	539.57	12	18.06	464.53
3940	Common Pheasant	305.52	21.45	29.56	11	14.12	11	13.43	29.25
4500	Eurasian Oystercatcher	1113.14	48.65	42.78	24	29.57	18	24.03	46.22
4930	Northern Lapwing	52.59	51.08	79.38	40	70.89	21	24.42	92.24
6680	Stock Dove	740.18	769.13	606.60	21	42.58	16	23.31	98.34
6700	Common Wood Pigeon	104.90	117.54	105.53	82	108.58	61	97.55	120.32
6840	Eurasian Collared Dove	60.03	32.71	40.94	25	29.93	36	34.42	38.98
7950	Common Swift	128.19	328.36	250.43	3	503.14	26	419.62	455.70
8760	Great Spotted Woodpecker	600.59	67.78	60.37	13	30.69	17	24.96	61.57
9760	Eurasian Skylark	13.51	15.28	14.77	8	10.68	13	12.86	15.42
9920	Barn Swallow	47.76	44.57	78.41	24	31.58	36	34.52	105.09
10090	Tree Pipit	12.97	15.24	13.82	12	12.88	10	10.38	15.32
10201	White Wagtail	50.96	28.58	34.77	20	20.40	17	20.50	36.46
10660	Eurasian Wren	75.88	78.39	70.78	45	48.23	46	46.11	66.84
10840	Dunnock	749.96	74.86	122.93	21	22.39	18	27.24	88.16
10990	European Robin	932.30	48.24	45.29	30	42.37	19	20.71	47.59
11870	Common Blackbird	131.16	148.42	170.98	87	131.03	66	94.29	171.45
12000	Song Thrush	2790.41	25.09	27.85	8	19.05	16	18.46	29.27
12750	Common Whitethroat	73.62	31.75	31.61	12	11.08	15	19.72	30.79
12770	Eurasian Blackcap	59.38	43.08	49.53	24	34.12	39	42.64	51.85
13110	Common Chiffchaff	3386.18	160.14	103.68	80	82.23	44	50.15	104.33
13120	Willow Warbler	828.29	35.69	36.99	28	26.96	11	11.78	36.58
14620	Blue Tit	1383.10	42.22	45.99	29	34.26	17	18.32	49.49
14640	Great Tit	1885.65	108.04	148.07	54	81.99	35	37.72	117.50
14870	Short-toed Treecreeper	663.87	50.27	43.95	15	74.25	14	28.64	57.07

15490	Eurasian Magpie	42.39	55.96	45.07	30	34.48	27	29.80	46.47
15600	Western Jackdaw	174.35	106.10	104.97	79	90.80	52	54.97	116.70
15671	Carrion Crow	92.14	104.23	103.72	52	65.03	43	61.42	104.90
15820	Common Starling	732.42	266.61	139.82	36	80.00	25	73.84	184.39
15910	House Sparrow	34.30	52.24	62.60	29	33.38	35	48.38	61.26
16360	Common Chaffinch	288.14	113.92	114.00	79	75.59	84	82.66	113.42
16490	European Greenfinch	62.41	35.65	43.43	24	47.98	13	15.33	46.81
16530	European Goldfinch	2807.35	129.40	98.95	16	33.81	13	56.91	74.28

Appendix Table 9 **Estimations per km².** Table lists species by Euring exchange code and name according to Speek et al. (2001) and Svensson et al. (2011). "ObsDist" gives the observable distance of each species in meters, based on the estimations for the entire season (see Appendix Table 8). Pairs are estimated from data of sites with 95 % (Open) or 90 % (Forest and Urban) cover of the corresponding habitat type. "Conf"-columns give the 95 % confidence interval of the estimations (upper and lower values).

SpeciesID	Species	Dist	Open	ConfOpen	Forest	ConfForest	Urban	ConfUrban
1860	Mallard	400	56	22.17 - 106.01	0	0 - 0.99	17	3.48 - 48.74
3940	Common Pheasant	450	1	0.67 - 2.47	0	0 - 0	0	0 - 0
4500	Eurasian Oystercatcher	550	3	1.65 - 5.11	0	0 - 0	1	0.53 - 1.58
4930	Northern Lapwing	400	8	5.68 - 12.79	0	0 - 0.99	0	0 - 0
6680	Stock Dove	350	4	1.48 - 11.51	3	1.3 - 9.09	1	0.65 - 2.6
6700	Common Wood Pigeon	350	5	3.71 - 9.28	1	0 - 6.5	5	3.9 - 7.8
6840	Eurasian Collared Dove	300	0	0 - 0	0	0 - 0	6	4.42 - 10.61
7950	Common Swift	500	6	0.18 - 25.46	0	0 - 2.55	30	6.37 - 77.99
8760	Great Spotted Woodpecker	400	1	0.57 - 4.55	14	6.96 - 22.88	0	0 - 0
9760	Eurasian Skylark	500	1	1.09 - 2.55	0	0 - 0	0	0 - 0
9920	Barn Swallow	250	6	2.91 - 16.73	0	0 - 5.09	6	2.55 - 15.28
10090	Tree Pipit	300	1	1.01 - 1.01	5	3.54 - 7.07	0	0 - 0
10201	White Wagtail	300	2	1.52 - 5.05	2	1.77 - 5.31	5	3.54 - 9.73
10660	Eurasian Wren	250	6	5.09 - 8	5	5.09 - 7.64	3	2.55 - 7.64
10840	Dunnock	250	1	0 - 8	0	0 - 0	27	14.01 - 43.29
10990	European Robin	200	1	0 - 6.82	16	11.94 - 27.85	5	3.98 - 11.94
11870	Common Blackbird	300	4	2.53 - 9.09	12	3.54 - 24.76	18	13.26 - 25.64
12000	Song Thrush	300	2	1.01 - 5.56	3	1.77 - 7.07	1	0.88 - 3.54
12750	Common Whitethroat	250	3	2.18 - 5.82	0	0 - 0	1	1.27 - 2.55
12770	Eurasian Blackcap	300	3	2.53 - 6.57	8	7.07 - 14.15	0	0 - 2.65
13110	Common Chiffchaff	300	4	2.02 - 8.08	4	3.54 - 7.07	4	2.65 - 7.96
13120	Willow Warbler	250	0	0 - 2.18	9	5.09 - 17.83	0	0 - 0
14620	Blue Tit	250	2	2.18 - 5.09	4	2.55 - 10.19	4	2.55 - 7.64
14640	Great Tit	300	5	2.02 - 10.61	10	3.54 - 19.45	7	5.31 - 10.61
14870	Short-toed Treecreeper	250	1	0.73 - 5.09	26	10.19 - 48.38	2	1.27 - 6.37
15490	Eurasian Magpie	400	1	1.14 - 3.13	0	0 - 0	2	1.49 - 2.49
15600	Western Jackdaw	250	12	7.28 - 20.37	7	5.09 - 12.73	20	15.28 - 28.01
15671	Carrion Crow	300	11	5.56 - 19.2	1	0 - 3.54	3	1.77 - 7.07
15820	Common Starling	250	4	0.73 - 18.19	111	35.65 - 241.92	8	5.09 - 14.01
15910	House Sparrow	200	3	2.27 - 4.55	0	0 - 0	6	3.98 - 9.95
16360	Common Chaffinch	350	4	2.97 - 6.31	9	6.5 - 11.69	5	4.55 - 7.8
16490	European Greenfinch	250	1	0.73 - 5.82	3	2.55 - 5.09	22	11.46 - 38.2
16530	European Goldfinch	200	15	6.82 - 32.97	0	0 - 0	17	9.95 - 33.82

8. R-SCRIPT

```
##################
## Prestructure ##
##################
## Set Working-Directory & Load Packages and Files
  setwd("D:/Studium/AA_Masterarbeit/Fieldwork")
  library(unmarked)
  library(AICcmodavg)
  library(rgl)
  library(AHMbook)
  library(readxl)
  load("MasterThesis_AllData.RData")
  SpeciesNames <- read.csv("MasterThesis_SpeciesNames.csv", sep=";")
  SiteCovsMallard <- read.csv("MasterThesis_SiteCovsPlusWater.csv",
                    row.names = 1, sep = ";")
  ObsDistDF <- read.csv2("SOVON_Observable-Distance.csv", row.names = 1)
  ObsDistDF [,1] <- as.character(ObsDistDF [,1])
  SOVONEstDF <- read.csv2("SOVON_Estimations.csv", row.names = 1)
  SOVONEstDF$SpeciesName <- as.character(SOVONEstDF$SpeciesName)
## Create Working Directories and Lists
  dir.UMFs <- file.path(getwd(), "UMFs")
  dir.Results <- file.path(getwd(), "Results")
  dir.PDFs <- file.path(getwd(), "PDFs")
  dir.GoFs <- file.path(dir.PDFs, "GoodnessOfFit")
  dir.Models <- file.path(getwd(), "Models")
  dir.Covariables <- file.path(getwd(), "Covariables")
  dir.Appendix <- file.path(getwd(), "Appendix")
  dir.create(dir.UMFs)
  dir.create(dir.Models)
  dir.create(dir.Results)
  dir.create(dir.GoFs)
  dir.create(dir.PDFs)
  dir.create(dir.Covariables)
  dir.create(dir.Appendix)
## Prestructure Data
  SepDate <- "135" ## Number of the last day (May 15th) of Period 1
  AllDataP1 <- subset(AllData, DayNr <= SepDate)
  AllDataP2 <- subset(AllData, DayNr > SepDate)
  AllSitesP1 <- data.frame(SiteID = unique(AllDataP1$SiteID))
  AllSitesP2 <- data.frame(SiteID = unique(AllDataP2$SiteID))
  Sites55 <- merge(AllSitesP1, AllSitesP2, by="SiteID")
  AllSpecies <- sort(unique(AllData$EuringID))
  AllSites <- data.frame(SiteID = unique(AllData$SiteID))
  Data55 <- merge(Sites55, AllData, by = "SiteID", all.x = TRUE)
  Data55P1 <- merge(Sites55, AllDataP1, by = "SiteID", all.x = TRUE)
  Data55P2 <- merge(Sites55, AllDataP2, by = "SiteID", all.x = TRUE)

##########################
## 3.1 Species Overview ##
##########################
## 3.1.1) Number of Observed Species
## Species Richness per Site and Period
(NrPassAll <- length(unique(AllData [!(AllData$EuringID < 9000),]$EuringID)))
(PercentPassAll <- NrPassAll / length(unique(AllData$EuringID)))
(NrNonPassAll <- length(unique(AllData [(AllData$EuringID < 9000),]$EuringID)))
(PercentNonPassAll <- NrNonPassAll / length(unique(AllData$EuringID)))
(NrPass55 <- length(unique(Data55 [!(Data55$EuringID < 9000),]$EuringID)))
(PercentPass55 <- NrPass55 / length(unique(Data55$EuringID)))
(NrNonPass55 <- length(unique(Data55 [(Data55$EuringID < 9000),]$EuringID)))
(PercentNonPass55 <- NrNonPass55 / length(unique(Data55$EuringID)))

  SpeciesNr1st <- Data55 [Data55$ObsCount1 == 1,]
  SpeciesNr2nd <- Data55 [Data55$ObsCount1 == 1 | Data55$ObsCount2 == 1,]
  SpeciesNr3rd <- Data55 [Data55$ObsCount1 == 1 | Data55$ObsCount2 == 1 |
          Data55$ObsCount3 == 1,]
  SpeciesNr4th <- Data55 [Data55$ObsCount1 == 1 | Data55$ObsCount2 == 1 |
          Data55$ObsCount3 == 1 | Data55$ObsCount4 == 1,]
  SpeciesNrs <- c(length(unique(SpeciesNr1st$EuringID)),
             length(unique(SpeciesNr2nd$EuringID)),
```

```
            length(unique(SpeciesNr3rd$EuringID)),
            length(unique(SpeciesNr4th$EuringID)))

  for (Interval in c("Data55P1","Data55P2")) {
    ObjectName <- paste("AddedSpecies", substr(Interval, 7, 8), sep = "")
    Interval <- get(Interval)
    AddedSpecies <- data.frame(SiteID = numeric(), FirstOne = numeric(),
                 FirstTwo = numeric(), FirstThree = numeric(),
                 FirstFour = numeric())
    for(currentSiteID in Sites55$SiteID) {
      SiteID <- subset(Interval, SiteID == currentSiteID)
      First <- SiteID [SiteID$ObsCount1 == 1,] $EuringID
      Second <- SiteID [SiteID$ObsCount2 == 1,] $EuringID
      Third <- SiteID [SiteID$ObsCount3 == 1,] $EuringID
      Fourth <- SiteID [SiteID$ObsCount4 == 1,] $EuringID
      AddedSpecies [nrow(AddedSpecies) + 1, 1] <- currentSiteID
      AddedSpecies [nrow(AddedSpecies), 2] <- length(unique(c(First)))
      AddedSpecies [nrow(AddedSpecies), 3] <- length(unique(c(First, Second)))
      AddedSpecies [nrow(AddedSpecies), 4] <- length(unique(c(First, Second,
                  Third)))
      AddedSpecies [nrow(AddedSpecies), 5] <- length(unique(c(First, Second,
                  Third, Fourth)))
    }
    assign(ObjectName, AddedSpecies)
  }
  AddedSpeciesDF <- merge(AddedSpeciesP1, AddedSpeciesP2, by = "SiteID",
                 all = TRUE)
  names(AddedSpeciesDF) <- c("SiteID", "FirstOneP1", "FirstTwoP1",
                   "FirstThreeP1", "FirstFourP1", "FirstOneP2",
                   "FirstTwoP2", "FirstThreeP2", "FirstFourP2")
  MeansSpeciesNr <- colMeans(AddedSpeciesDF [,2:9])
  SDsSpeciesNr <- apply(AddedSpeciesDF [,2:9], 2, sd)
  tTestSpecies <- t.test(AddedSpeciesDF$FirstFourP1, AddedSpeciesDF$FirstFourP2,
              paired = TRUE)

  png(file = file.path(dir.Results, "AddedValueSpecies_Boxplot.png"))
  SiteCoords <- boxplot(AddedSpeciesDF [,2:9], col = c(rep("lightblue", 4),
            rep("lightgreen", 4)), names = c(rep(c("5 min", "10 min",
            "15 min", "20 min"),2)), ylim = c(0,25), xlab = "Count Duration",
            ylab = "Mean Species per Site", cex.lab = 1.2, range = 1.5)
  abline( v = 4.5)
  text(x = 2.5, y = 25, labels = "Period One", cex = 1.5)
  text(x = 6.5, y = 25, labels = "Period Two", cex = 1.5)
  dev.off()

## 3.1.2.) Mean Number of Observations per Site
  for(Interval in c("AllDataP1","AllDataP2")) {
    ObjectName <- paste("ObsPerSite", substr(Interval, 8, 9), sep = "")
    Interval <- get(Interval)
    ObsPerSite <- data.frame(SiteID = numeric(), Pass = numeric(), NonPass =
                 numeric(), Obs = numeric())
    for (currentSiteID in AllSites$SiteID) {
      currentSite <- subset(Interval, SiteID == currentSiteID)
      currentPass <- nrow(currentSite [!(currentSite$EuringID < 9000),])
      currentNonPass <- nrow(currentSite [currentSite$EuringID < 9000,])
      ObsPerSite [nrow(ObsPerSite)+1, 1] <- currentSiteID
      ObsPerSite [nrow(ObsPerSite), 2] <- currentPass
      ObsPerSite [nrow(ObsPerSite), 3] <- currentNonPass
      ObsPerSite [nrow(ObsPerSite), 4] <- nrow(currentSite)
    }
    assign(ObjectName, ObsPerSite)
  }
  ObsPerSite <- merge(ObsPerSiteP1, ObsPerSiteP2, by = "SiteID", all = TRUE)
  names(ObsPerSite) <- c("SiteID", "PassP1", "NonPassP1", "ObsP1", "PassP2",
                 "NonPassP2", "ObsP2")
  ObsPerSite[ObsPerSite == 0] <- NA

  ## Mean and SD for all sites visited in P1 and / or P2
  mean(na.omit(ObsPerSite$ObsP1)) # Mean Nr of Obs for Sites from P1
```

```
  sd(na.omit(ObsPerSite$ObsP1)) # SD for Sites from P1
  mean(na.omit(ObsPerSite$ObsP2)) # Mean Nr of Obs for Sites from P2
  sd(na.omit(ObsPerSite$ObsP2)) # SD for Sites from P2

  ## Mean and SD for sites visited in P1 and P2
  ObsPerSite55 <- ObsPerSite [complete.cases(ObsPerSite),]
  rownames(ObsPerSite55) <- 1:nrow(ObsPerSite55)
  (MeanObsPerSite <- colMeans(ObsPerSite55 [,2:7]))
  (SDObsPerSite <- apply(ObsPerSite55 [,2:7], 2, sd))

  ## t-Tests
  (tTestPass <- t.test(ObsPerSite55$PassP1, ObsPerSite55$PassP2, paired = TRUE))
  (tTestNonPass<- t.test(ObsPerSite55$NonPassP1, ObsPerSite55$NonPassP2,
               paired = TRUE))
  (tTestObs <- t.test(ObsPerSite55$ObsP1, ObsPerSite55$ObsP2, paired = TRUE))
  (tTestP1 <- t.test(ObsPerSite55$PassP1, ObsPerSite55$NonPassP1))
  (tTestP2 <- t.test(ObsPerSite55$PassP2, ObsPerSite55$NonPassP2))


png(file = file.path(dir.Results, "MeanObsBoxPlot.png"))
  SiteCoords <- boxplot(ObsPerSite [,c(2,5,3,6,4,7)], col = c("lightblue",
             "lightgreen", "lightblue", "lightgreen", "lightblue",
             "lightgreen"), ylim = c(0,50), ylab = "Observations / Site",
             range = 1.5)
   grid(0,27)
   text(x = 1.5, y = 49, labels = "Passerines", cex = 1.2)
   text(x = 3.5, y = 49, labels = "Nonpasserines", cex = 1.2)
   text(x = 5.5, y = 49, labels = "All Birds", cex = 1.2)
   text(x = 1.5, y = 47, labels = paste("p =", round(tTestPass$p.value, 3),
         "(**)", sep = " "))
   text(x = 3.5, y = 47, labels = paste("p =", round(tTestNonPass$p.value, 3),
         "(*)", sep = " "))
   text(x = 5.5, y = 47, labels = paste("p =", "< 0.001",
         "(***)", sep = " "))
   abline(v = 2.5)
   abline(v = 4.5)
   boxplot(ObsPerSite [,c(2,5,3,6,4,7)], col = c("lightblue", "lightgreen",
             "lightblue", "lightgreen", "lightblue", "lightgreen"), range = 1.5,
             ylim = c(0,50), ylab = "Observations / Site", add = TRUE)
dev.off()

#############################
## Single Species Analysis ##
#############################
## 3.2.1) Relative Display Behaviour per Species
  DispBehDF <- data.frame()
  for (SpeciesID in AllSpecies) { # Loop over all species seen
    Amount <- nrow(subset(AllData, EuringID == SpeciesID))
    if (Amount < 20) next
    SpeciesName <- SpeciesNames$Species[SpeciesNames$EuringID == SpeciesID]
    currentDispBeh <- c(SpeciesID)
    for (Interval in c("AllDataP1", "AllDataP2", "AllData")) {
      Interval <- get(Interval)
      currentSpecies <- subset(Interval, EuringID == SpeciesID)
      currentObsNr <- nrow(currentSpecies)
      Display <- sum(currentSpecies$Breeding_Code == 2)
      Percent <- round((Display / nrow(currentSpecies)) * 100, 2)
      currentDispBeh <- c(currentDispBeh, Percent, currentObsNr)
    }
    DispBehDF <- rbind(DispBehDF, currentDispBeh)
  } # End of loop over species and relative display

  colnames(DispBehDF) <- c("EuringID", "DispBehP1", "ObsNrP1", "DispBehP2",
                          "ObsNrP2", "DispBehS", "ObsNrS")
  DispBehDF <- merge(DispBehDF, SpeciesNames, by = "EuringID", all.x = TRUE)
  DispBehDF <- DispBehDF [,c(1,8,2:7)]
  Pass <- DispBehDF [!(DispBehDF$EuringID < 9000),] # subset of passerines
  mean(Pass$DispBehP1)
  range(Pass$DispBehP1)
```

```
  mean(Pass$DispBehP2)
  range(Pass$DispBehP2)
  NonPass <- DispBehDF [DispBehDF$EuringID < 9000,] # subset of nonpasserines
  mean(NonPass$DispBehP1)
  range(NonPass$DispBehP1)
  mean(NonPass$DispBehP2)
  range(NonPass$DispBehP2)
  write.csv2(DispBehDF, file = file.path(dir.Appendix, "DispBehDF.csv"))
  DispBehDF_Top6 <- DispBehDF[c(5, 7, 19, 20, 24, 36), ]
  write.csv2(DispBehDF_Top6, file = file.path(dir.Results,
                              "DispBehDF_Top6.csv"))

## 3.2.2) Observations per Number of Five-Minute Counts
  pdf(file = file.path(dir.Appendix, "Barplots_One-Two-Three-Four.pdf"),
           width = 10.5, height = 15.75)
  par(mfrow  = c(3,2))
  for (SpeciesID in AllSpecies) { # Loop over SpeciesID
    if (nrow(subset(AllData, EuringID == SpeciesID)) < 20) next
    currentSpecies <- subset(AllData, EuringID ==
                        SpeciesID) # subsets to "SpeciesID"
    SpeciesName <- SpeciesNames$Species[SpeciesNames$EuringID == SpeciesID]
    FreqDF <- data.frame( table(currentSpecies$Detection_Code))
    colnames(FreqDF) <- c("Detection_Code", "Frequency")
    DetCodeDF <- data.frame(Detection_Code = c("1111", "0111", "1011",
                     "1101", "1110", "0011", "1001", "1100", "1010", "0101",
                     "0110", "1000", "0100", "0010", "0001"), Frequency = 0)
    FreqDF <- rbind(FreqDF, DetCodeDF)
    FreqDF <- aggregate(Frequency ~ Detection_Code, data = FreqDF, FUN = max)
    FreqDF <- merge(DetCodeDF, FreqDF, by = "Detection_Code")
    FreqDF <- subset(FreqDF, select = -Frequency.x)
    names(FreqDF)[names(FreqDF) == "Frequency.y"] <- "Frequency"
    Order <-  c(1,2,4,8,3,5,6,9,10,12,7,11,13,14,15)
    FreqDF <- FreqDF[Order,]
    FreqDF$Count <- c(rep("1x5",4), rep("2x5",6), rep("3x5",4), "4x5")
    FreqDF <-aggregate(Frequency ~ Count, FreqDF, FUN = sum)
    FreqDF <- as.vector(FreqDF$Frequency)

    p = 0.5 # detection probability
    pZero <- (1-p)^4 # chance of detection in 0 of 4 five-minute counts
    pOne <- 4*p*(1-p)^3 # chance of detection in 1 of 4 five-minute counts
    pTwo <- 6*p^2*(1-p)^2 # chance of detection in 2 of 4 five-minute counts
    pThree <- 4*p^3*(1-p) # chance of detection in 3 of 4 five-minute counts
    pFour <- p^4 # chance of detection in 4 of 4 five-minute counts

    EstTotal <- sum(FreqDF) + (pZero * sum(FreqDF))
    expected <- c( pOne * EstTotal, pTwo * EstTotal, pThree * EstTotal,
             pFour * EstTotal)
    ChiSq <- chisq.test(matrix(c(FreqDF, expected), ncol = 2))
    if (ChiSq$p.value <= 0.05) { Significance <- "*" }
    if (ChiSq$p.value <= 0.01) { Significance <- "**"}
    if (ChiSq$p.value <= 0.001){ Significance <- "***"}
    if (ChiSq$p.value >= 0.05) { Significance <- "n.s."}
    Percent <- as.numeric(round(FreqDF / (sum(FreqDF)) * 100, digits = 2))
    ChiValue <- paste("X² = ", round(ChiSq$statistic, 3), sep = "")
    pValue <- paste("p  =", signif(ChiSq$p.value, 3), Significance, sep = " ")
    SiteCoords <- barplot(FreqDF, ylab = "Number of Observations",
              xlab = "Number of 5-min-counts with observations", cex.lab = 1.2,
              main = SpeciesName, names = c("1x5", "2x5", "3x5", "4x5"),
              cex.main = 1.4, ylim = c(0,ceiling(max(FreqDF) / 9) * 10))
    title(sub =  , line = 2.5)
    mtext(paste("n = ", sum(FreqDF), sep =""))
    text(x = SiteCoords, y = FreqDF, label =
           paste(Percent, "%", sep = ""), pos = 3)
    text(x = SiteCoords, y = FreqDF, label = FreqDF, pos = 1)
    pos <- "topright"
    if ( SpeciesID == 12750| SpeciesID == 15910) {
       pos <- "topleft" }
    Legend <- legend(pos, legend = c(ChiValue, pValue),
           title = expression(bold("Chi-squared Statistic")))
```

```
    } # End of loop over detection code / chi-square graphs
  dev.off()

## 3.2.3) Added Value of Additional Five-Minute Counts
  ObsNrsDF <- data.frame(SpeciesName = numeric(), Obs1stOneP1 = numeric(),
       Obs1stTwoP1 = numeric(), Obs1stThreeP1 = numeric(),
       Obs1stFourP1 = numeric(), Obs1stOneP2 = numeric(),
       Obs1stTwoP2 = numeric(), Obs1stThreeP2 = numeric(),
       Obs1stFourP2 = numeric())

  pdf(file = file.path(dir.Appendix, "ObsNrsPerSpecies_TOP6.pdf"),
           width = 10.5, height = 15.75)
  par(mfrow  = c(3,2))
  for( SpeciesID in AllSpecies) {
    if (nrow(subset(AllData, EuringID == SpeciesID)) < 20) next
    SpeciesName <- SpeciesNames$Species[SpeciesNames$EuringID == SpeciesID]
    for( Interval in c("Data55P1", "Data55P2")) {
      currentInterval <- get(Interval)
      currentInterval <- subset(currentInterval, EuringID == SpeciesID, select =
                  c(ObsCount1, ObsCount2, ObsCount3, ObsCount4))
      FirstOne <- currentInterval [currentInterval$ObsCount1 == 1,]
      FirstTwo <- currentInterval [currentInterval$ObsCount1 == 1 |
                     currentInterval$ObsCount2 == 1,]
      FirstThree <- currentInterval [currentInterval$ObsCount1 == 1 |
                     currentInterval$ObsCount2 == 1 |
                     currentInterval$ObsCount3 == 1,]
      FirstFour <- currentInterval [currentInterval$ObsCount1 == 1 |
                     currentInterval$ObsCount2 == 1 |
                     currentInterval$ObsCount3 == 1 |
                     currentInterval$ObsCount4 == 1,]
      ObsNrs <- c(nrow(FirstOne), nrow(FirstTwo), nrow(FirstThree),
                 nrow(FirstFour))
      ObjectName <- paste("ObsNrs", substr(Interval, 7,8), sep = "")
      assign(ObjectName, ObsNrs)
    }
    ObsNrsDF [nrow(ObsNrsDF)+1,1] <- as.character(SpeciesName)
    ObsNrsDF [nrow(ObsNrsDF), 2:9]<- c(ObsNrsP1, ObsNrsP2)
    PercentP1 <- round(ObsNrsP1 / ObsNrsP1 [4] ,2)
    PercentP2 <- round(ObsNrsP2 / ObsNrsP2 [4] , 2)
    SiteCoords <- barplot(rbind(ObsNrsP1, ObsNrsP2), beside = TRUE,
               main = SpeciesName, col = c("lightblue", "lightgreen"),
               ylim = c(0,120), ylab = "Number of Observations", cex.main = 1.6)
    axis(1,  (SiteCoords [1,] + SiteCoords [2,]) / 2, c("Count 1",
            "Count 1 - 2", "Count 1 - 3", "Count 1 - 4"))
    text(x = SiteCoords [1,], y = ObsNrsP1, label =
             PercentP1, pos = 1, cex = 1)
    text(x = SiteCoords [2,], y = ObsNrsP2, label =
             PercentP2, pos = 1, cex = 1)
    text(x = SiteCoords, y = rbind(ObsNrsP1, ObsNrsP2), label =
             rbind(ObsNrsP1, ObsNrsP2), pos = 3, cex = 1.2)
    legend("top", y = 115, c("Period One","Period Two"), fill = c("lightblue",
    "lightgreen"), bty = "n", horiz = TRUE)
  }
  dev.off()
  write.csv2(ObsNrsDF, file = file.path(dir.Results,"ObsNrsDF.csv"))

  colMeans(ObsNrsDF [c(1:8,10:37),2:5] / ObsNrsDF [c(1:8,10:37),5])
  apply(ObsNrsDF [c(1:8,10:37),2:5] / ObsNrsDF [c(1:8,10:37),5], 2,sd)
  colMeans(ObsNrsDF [c(1:8,10:37),6:9] / ObsNrsDF [c(1:8,10:37),9])
  apply(ObsNrsDF [c(1:8,10:37),6:9] / ObsNrsDF [c(1:8,10:37),9],2,sd)

## 3.2.4) Variation in Observations per Five-minute Count Between Periods

  pdf(file = file.path(dir.Appendix, "ObsPerCount55_TOP6.pdf"),
           width = 10.5, height = 15.75)
  par(mfrow  = c(3,2))
  for( SpeciesID in AllSpecies) {
    if (nrow(subset(AllData, EuringID == SpeciesID)) < 20) next
    SpeciesName <- SpeciesNames$Species[SpeciesNames$EuringID == SpeciesID]
```

```
    for( Interval in c("Data55P1", "Data55P2")) {
      currentInterval <- get(Interval)
      currentInterval <- colSums(subset(currentInterval, EuringID == SpeciesID,
                         select = c(ObsCount1, ObsCount2, ObsCount3, ObsCount4)))
      ObjectName <- paste("ObsPerCount", substr(Interval, 7, 8), sep = "")
      assign(ObjectName, currentInterval)
    }
    currentObsPerCount<- as.table(rbind(ObsPerCountP1, ObsPerCountP2))
    ChiSq <- chisq.test(currentObsPerCount)
    if (ChiSq$p.value <= 0.05) { Significance <- "*" }
    if (ChiSq$p.value <= 0.01) { Significance <- "**"}
    if (ChiSq$p.value <= 0.001){ Significance <- "***"}
    if (ChiSq$p.value >= 0.05) { Significance <- "n.s."}
    ChiValue <- paste("X² = ", round(ChiSq$statistic, 3), sep = "")
    pValue <- paste("p  =", signif(ChiSq$p.value, 3), Significance, sep = " ")
    SiteCoords <- barplot(currentObsPerCount, beside = TRUE, ylim = c(0,80),
               col = c("lightblue", "lightgreen"), main = SpeciesName,
               ylab = "Number of Observations", xaxt = "n")
    abline(h = mean(currentObsPerCount), lty = 2, col = "red")
    axis(1, (SiteCoords [1,] + SiteCoords [2,]) / 2,
            c("1st Count", "2nd Count", "3rd Count", "4th Count"))

    text(x = SiteCoords [1,], y = currentObsPerCount [1,], label =
              currentObsPerCount [1,], pos = 3, cex = 1)
    text(x = SiteCoords [2,], y = currentObsPerCount [2,], label =
              currentObsPerCount [2,], pos = 3, cex = 1)
    legend(x = 8.5, y = 75, legend = c(ChiValue, pValue),
           title = expression(bold("Chi-squared Statistic")))
    legend("top", y = 75, c("Period One","Period Two"), fill = c("lightblue",
    "lightgreen"), bty = "n", horiz = TRUE)
  }
  dev.off()
###################
## Covariables ####
###################
## siteCovs
  ## siteCovs for all sites (n = 81)
  AllSiteCovs <- subset(AllData, select = c("SiteID", "Open_Area",
                 "Forest_Area","Urban_Area"))
  AllSiteCovs <- AllSiteCovs[!duplicated(AllSiteCovs),]
  rownames(AllSiteCovs) <- AllSiteCovs$SiteID
  ## unscaled siteCovs (n = 81)
  AllSiteCovs <- subset(AllSiteCovs, select = -c(SiteID))
  write.csv2(AllSiteCovs, file = file.path(dir.Covariables,
                         "SiteCovs_unscaled.csv"))
  save(AllSiteCovs, file = file.path(dir.Covariables,
                   "SiteCovs_unscaled.RData"))
  ## scaled siteCovs (n = 81)
  AllSiteCovs <- AllSiteCovs/100
  write.csv2(AllSiteCovs, file = file.path(dir.Covariables,
                         "SiteCovs_scaled.csv"))
  save(AllSiteCovs, file = file.path(dir.Covariables,
                   "SiteCovs_scaled.RData"))

  ## siteCovs for sites visited in BOTH periods (n = 55)
  SiteCovs55 <- subset(AllData, select = c("SiteID", "Open_Area",
                 "Forest_Area","Urban_Area"))
  SiteCovs55 <- SiteCovs55[!duplicated(SiteCovs55),]
  SiteCovs55 <- merge(Sites55,SiteCovs55, by = "SiteID", all.x = TRUE)
  rownames(SiteCovs55) <- SiteCovs55$SiteID
  ## unscaled siteCovs (n = 55)
  SiteCovs55 <- subset(SiteCovs55, select = -c(SiteID))
  write.csv2(SiteCovs55, file = file.path(dir.Covariables,
                         "SiteCovs55_unscaled.csv"))
  save(SiteCovs55, file = file.path(dir.Covariables,
                   "SiteCovs55_unscaled.RData"))
  ## scaled siteCovs (n = 55)
  SiteCovs55 <- SiteCovs55 / 100
  write.csv2(SiteCovs55, file = file.path(dir.Covariables,
```

```
                           "SiteCovs55_scaled.csv"))
  save(SiteCovs55, file = file.path(dir.Covariables,
                         "SiteCovs55_scaled.RData"))

  ## siteCovs for Mallard (only species with regular observations on water)
  rownames(SiteCovsMallard) <- SiteCovsMallard$SiteID
  SiteCovs55Mallard <- merge(Sites55, SiteCovsMallard,
                    by = "SiteID", all.x = TRUE)
  rownames(SiteCovs55Mallard) <- SiteCovs55Mallard$SiteID
  SiteCovsMallard <- subset(SiteCovsMallard, select = -c(SiteID))
  SiteCovsMallard<- SiteCovsMallard / 100
  SiteCovs55Mallard <- subset(SiteCovs55Mallard, select = -c(SiteID))
  SiteCovs55Mallard <- SiteCovs55Mallard/ 100

## obsCovs
  for (Interval in c("P1", "P2")) {
    DataName <- paste("AllData", Interval, sep = "")
    currentObsCovs <- get(DataName)
    currentObsCovs <- currentObsCovs [,c(1, 13:17)]
    currentObsCovs <- currentObsCovs[!duplicated(currentObsCovs),]
    currentObsCovs <- currentObsCovs[ order(currentObsCovs$SiteID), ]
    currentObsNrDF <- data.frame(SiteID = numeric(), IndNr1 = numeric(),
                   IndNr2 = numeric(), IndNr3 = numeric(),
                   IndNr4 = numeric())
    for (Site in unique(currentObsCovs$SiteID)){
      currentSite <- subset(get(DataName), SiteID == Site)
      currentObsNrDF [nrow(currentObsNrDF)+1,1] <- Site
      currentObsNrDF [nrow(currentObsNrDF),2] <- (sum(currentSite$ObsCount1)-1)
      currentObsNrDF [nrow(currentObsNrDF),3] <- (sum(currentSite$ObsCount2)-1)
      currentObsNrDF [nrow(currentObsNrDF),4] <- (sum(currentSite$ObsCount3)-1)
      currentObsNrDF [nrow(currentObsNrDF),5] <- (sum(currentSite$ObsCount4)-1)
    } # End of loop for CovsObsNrAllP1
    currentObsNrDF <- merge(currentObsCovs, currentObsNrDF, by = "SiteID")
    currentObsNrDF <- merge(AllSites, currentObsNrDF, by = "SiteID",
                    all.x = TRUE)
    Name <- paste("Covs",Interval, sep = "")
    assign(Name, currentObsNrDF)
  } # End of loop over Periods

  AllObsCovs <- merge(CovsP1, CovsP2, by = "SiteID")
  AllObsCovs <- AllObsCovs [, c(1, rep(2,4), rep(11,4), 3:6,
                12:15, 7:10, 16:19)]
  rownames(AllObsCovs) <- AllObsCovs$SiteID
  AllObsCovs <- subset(AllObsCovs, select = -(SiteID))
  colnames(AllObsCovs) <- c("DayNr1", "DayNr2", "DayNr3", "DayNr4", "DayNr5",
                     "DayNr6", "DayNr7", "DayNr8", "TimeC1", "TimeC2",
                     "TimeC3", "TimeC4", "TimeC5", "TimeC6", "TimeC7",
                     "TimeC8", "IndNr1", "IndNr2", "IndNr3", "IndNr4",
                     "IndNr5", "IndNr6", "IndNr7", "IndNr8")
  ObsCovs55 <- AllObsCovs [complete.cases(AllObsCovs),]
  for (Covs in c("AllObsCovs", "ObsCovs55")) {
    ObsCovs <- get(Covs)
    write.csv2(ObsCovs, file = file.path(dir.Covariables,
                    paste(Covs, "_unscaled.csv", sep = "")))
    save(ObsCovs, file = file.path(dir.Covariables,
                 paste(Covs, "_unscaled.RData", sep = "")))
    ObsCovs <- scale(ObsCovs)
    write.csv2(ObsCovs, file = file.path(dir.Covariables,
                       paste(Covs, "_scaled.csv", sep = "")))
    save(ObsCovs, file = file.path(dir.Covariables,
                    paste(Covs, "_scaled.RData", sep = "")))
    ObsCovs <- list("StartTime" = ObsCovs [,9:16], "DayNr" =
               ObsCovs [,1:8], "ObsNr" = ObsCovs [,17:24])
    assign(Covs, ObsCovs)
    if ("AllObsCovs" %in% Covs) next
    ObsCovs1x5 <- list("StartTime" = ObsCovs55$StartTime [,c(1,5)],
                  "DayNr" = ObsCovs55$DayNr [,c(1,5)],
                  "ObsNr" = ObsCovs55$ObsNr [,c(1,5)])
    ObsCovs2x5 <- list("StartTime" = ObsCovs55$StartTime [,c(1:2,5:6)],
```

```
                     "DayNr" = ObsCovs55$DayNr [,c(1:2,5:6)],
                     "ObsNr" = ObsCovs55$ObsNr [,c(1:2,5:6)])
    ObsCovs3x5 <- list("StartTime" = ObsCovs55$StartTime [,c(1:3,5:7)],
                     "DayNr" = ObsCovs55$DayNr [,c(1:3,5:7)],
                     "ObsNr" = ObsCovs55$ObsNr [,c(1:3,5:7)])
    ObsCovsP1 <- list("StartTime" = ObsCovs55$StartTime [,c(1:4)],
                     "DayNr" = ObsCovs55$DayNr [,c(1:4)],
                     "ObsNr" = ObsCovs55$ObsNr [,c(1:4)])
    ObsCovsP2 <- list("StartTime" = ObsCovs55$StartTime [,c(5:8)],
                     "DayNr" = ObsCovs55$DayNr [,c(5:8)],
                     "ObsNr" = ObsCovs55$ObsNr [,c(5:8)])
  } # End of loop over ObsCovs-objects

################
## Best Model ##
################
## Preparation ##
    ## Detection Model
    Det_1a <- formula(~ StartTime)
    Det_1b <- formula(~ DayNr)
    Det_1c <- formula(~ ObsNr)

    Det_2a2 <- formula(~ StartTime + I(StartTime^2))
    Det_2b2 <- formula(~ DayNr + I(DayNr^2))
    Det_2c2 <- formula(~ ObsNr + I(ObsNr^2))

    Det_2ab <- formula(~ StartTime + DayNr)
    Det_2ac <- formula(~ StartTime + ObsNr)
    Det_2bc <- formula(~ DayNr + ObsNr)

    Det_3a2b <- formula(~ StartTime + DayNr + I(StartTime^2))
    Det_3ab2 <- formula(~ StartTime + DayNr + I(DayNr^2))
    Det_3a2c <- formula(~ StartTime + ObsNr + I(StartTime^2))
    Det_3ac2 <- formula(~ StartTime + ObsNr + I(ObsNr^2))
    Det_3b2c <- formula(~ DayNr + ObsNr + I(DayNr^2))
    Det_3bc2 <- formula(~ DayNr + ObsNr + I(ObsNr^2))
    Det_3abc <- formula(~ StartTime + DayNr + ObsNr)

    Det_4a2b2 <- formula(~ StartTime + DayNr + I(StartTime^2) + I(DayNr^2))
    Det_4a2c2 <- formula(~ StartTime + ObsNr + I(StartTime^2) + I(ObsNr^2))
    Det_4b2c2 <- formula(~ DayNr + ObsNr + I(DayNr^2) + I(ObsNr^2))
    Det_4a2bc <- formula(~ StartTime + DayNr + ObsNr + I(StartTime^2))
    Det_4ab2c <- formula(~ StartTime + DayNr + ObsNr + I(DayNr^2))
    Det_4abc2 <- formula(~ StartTime + DayNr + ObsNr + I(ObsNr^2))

    Det_5a2b2c <- formula(~ StartTime + DayNr + ObsNr + I(StartTime^2) +
                  I(DayNr^2))
    Det_5a2bc2 <- formula(~ StartTime + DayNr + ObsNr + I(StartTime^2) +
                  I(ObsNr^2))
    Det_5ab2c2 <- formula(~ StartTime + DayNr + ObsNr + I(DayNr^2) +
                  I(ObsNr^2))
    Det_6a2b2c2 <- formula(~ StartTime + DayNr + ObsNr + I(StartTime^2) +
                   I(DayNr^2) + I(ObsNr^2))

    DetModelsVector <- c("Det_1a", "Det_1b", "Det_1c",   # 1 linear variable
                      "Det_2a2", "Det_2b2", "Det_2c2",    # 1 quadratic v.
                      "Det_2ab", "Det_2ac", "Det_2bc",    # 2 lin. v.
                      "Det_3a2b", "Det_3ab2", "Det_3a2c", # 1 lin. / 1 quad. v.
                      "Det_3ac2", "Det_3b2c", "Det_3bc2", # 1 lin. / 1 quad. v.
                      "Det_3abc",                         # 3 lin. v.
                      "Det_4a2b2", "Det_4a2c2", "Det_4b2c2", # 2 quad. v.
                      "Det_4a2bc", "Det_4ab2c", "Det_4abc2", # 2 lin. / 1 quad. v.
                      "Det_5a2b2c", "Det_5a2bc2", "Det_5ab2c2", # 1 lin. / 2 quad.
                      "Det_6a2b2c2")                            # 3 quadr. v.

    ## Abundance Model
    Abu_1a <- formula(~ Open_Area)
    Abu_1b <- formula(~ Forest_Area)
    Abu_1c <- formula(~ Urban_Area)
```

```
    Abu_2a2 <- formula(~ Open_Area + I(Open_Area^2))
    Abu_2b2 <- formula(~ Forest_Area + I(Forest_Area^2))
    Abu_2c2 <- formula(~ Urban_Area + I(Urban_Area^2))

    Abu_2ab <- formula(~ Open_Area + Forest_Area)
    Abu_2ac <- formula(~ Open_Area + Urban_Area)
    Abu_2bc <- formula(~ Forest_Area + Urban_Area)

    Abu_3a2b <- formula(~ Open_Area + Forest_Area + I(Open_Area^2))
    Abu_3ab2 <- formula(~ Open_Area + Forest_Area + I(Forest_Area^2))
    Abu_3a2c <- formula(~ Open_Area + Urban_Area + I(Open_Area^2))
    Abu_3ac2 <- formula(~ Open_Area + Urban_Area + I(Urban_Area^2))
    Abu_3b2c <- formula(~ Forest_Area + Urban_Area + I(Forest_Area^2))
    Abu_3bc2 <- formula(~ Forest_Area + Urban_Area + I(Urban_Area^2))
    Abu_3abc <- formula(~ Open_Area + Forest_Area + Urban_Area)

    Abu_4a2b2 <- formula(~ Open_Area + Forest_Area + I(Open_Area^2) +
              I(Forest_Area^2))
    Abu_4a2c2 <- formula(~ Open_Area + Urban_Area + I(Open_Area^2) +
              I(Urban_Area^2))
    Abu_4b2c2 <- formula(~ Forest_Area + Urban_Area + I(Forest_Area^2) +
              I(Urban_Area^2))

    AbuModelsVector <- c("Abu_1a", "Abu_1b", "Abu_1c",   # 1 linear variable
                "Abu_2a2", "Abu_2b2", "Abu_2c2",     # 1 quadratic v.
                "Abu_2ab", "Abu_2ac", "Abu_2bc",     # 2 lin. v.
                "Abu_3a2b", "Abu_3ab2", "Abu_3a2c", # 1 lin. / 1 quad. v.
                "Abu_3ac2", "Abu_3b2c", "Abu_3bc2", # 1 lin. / 1 quad. v.
                "Abu_3abc",                          # 3 lin. v.
                "Abu_4a2b2", "Abu_4a2c2", "Abu_4b2c2") # 2 quad. v.

##Model Selection ##
  SpeciesNB <- c(1860, 4930, 6680, 7950, 9920, 15600, 15820,
          15910) # species an NB-mixture is used in pcount()
  for (SpeciesID in AllSpecies){ # "Best Model Loop"
    if (nrow(subset(Data55, EuringID==SpeciesID)) < 20 ) next
    SpeciesName <- as.character(SpeciesNames$Species[SpeciesNames$EuringID ==
                   SpeciesID])
    # yObs
    for (Interval in c("AllDataP1", "AllDataP2")) {
      currentData <- get(Interval)
      currentSpecies <- subset(currentData, EuringID == SpeciesID)
      currentSpecies <- subset(currentSpecies, select=c(SiteID, ObsCount1,
                    ObsCount2, ObsCount3, ObsCount4))
      names(currentSpecies) <- c("SiteID", "ObsC1", "ObsC2", "ObsC3", "ObsC4")
      yObs <- data.frame(SiteID= numeric(), ObsC1= numeric(),
                   ObsC2= numeric(), ObsC3= numeric(), ObsC4= numeric())
      for (Site in unique(currentData$SiteID)) {
        currentSite <- subset(currentSpecies, SiteID == Site)
        currentyObs <- colSums(currentSite [,2:5])
        yObs [nrow(yObs)+1,1] <- Site
        yObs [nrow(yObs),2:5] <- currentyObs
      } # End of loop over sites
      Name <- paste("yObs", substr(Interval, 8, 9), sep = "")
      assign(Name, yObs)
    } # End of loop over interval
    AllyObs <- merge(yObsP1, yObsP2, by = "SiteID", all = TRUE)
    rownames(AllyObs) <- paste(AllyObs$SiteID)
    colnames(AllyObs) <- c("SiteID", "ObsC1", "ObsC2", "ObsC3", "ObsC4",
                    "ObsC5", "ObsC6", "ObsC7", "ObsC8")
    AllyObs <- subset(AllyObs, select=-c(SiteID))
    yObs55 <- AllyObs [complete.cases(AllyObs),]

    ## UMFs
    AllUMF <- unmarkedFramePCount(y = AllyObs, obsCovs = AllObsCovs,
              siteCovs = AllSiteCovs)
    UMF55 <- unmarkedFramePCount(y = yObs55, obsCovs = ObsCovs55,
             siteCovs = SiteCovs55)
```

```
    if (SpeciesID == 1860) {
       UMF55 <- unmarkedFramePCount(yObs55, obsCovs = ObsCovs55,
             siteCovs = SiteCovs55Mallard)}
    save(AllUMF, file = file.path(dir.UMFs, paste("All_UMF_", SpeciesID,
                        ".RData", sep = "")))
    save(UMF55, file = file.path(dir.UMFs, paste("UMF55_", SpeciesID,
                        ".RData", sep = "")))

    ModelList <- data.frame(SpeciesName = numeric(), DetModel = numeric(),
             AbuModel = numeric(), AIC = numeric())
    for (i in 1:length(DetModelsVector)) {
        DetFormula <- strsplit(as.character(get(DetModelsVector [i])), "~") [[2]]
        for (j in 1:length(AbuModelsVector)) {
            AbuFormula <- strsplit(as.character(get(AbuModelsVector [j])), "~")
[[2]]
            currentFormula <- paste("~", DetFormula, "~", AbuFormula, sep = " ")
            if (any(SpeciesNB == SpeciesID)) {
               currentBestModel <- pcount(formula(currentFormula),
                                    UMF55, mixture = "NB")}
            if (!(any(SpeciesNB == SpeciesID))) {
               currentBestModel <- pcount(formula(currentFormula), UMF55)}
            ModelList [nrow(ModelList) + 1, 1] <- SpeciesName
            ModelList [nrow(ModelList), 2] <- DetModelsVector [i]
            ModelList [nrow(ModelList), 3] <- AbuModelsVector [j]
            ModelList [nrow(ModelList), 4] <- currentBestModel@AIC
        } # End of Loop over AbuModelsvector
    } # End of Loop over DetModelsvector
    ModelList <- ModelList [order(ModelList$AIC),]
    write.csv2(ModelList, file = file.path(dir.Models,
                          paste("ModelList_", SpeciesID, ".csv", sep = "")))
    save(ModelList, file = file.path(dir.Models,
       paste("ModelList_55Sites_", SpeciesID, ".RData", sep = "")))
    BestModelList <- ModelList [ModelList$AIC <= (ModelList$AIC [1] +2 ), ]
    write.csv2(BestModelList, file = file.path(dir.Models,
                          paste("BestModelList_55Sites_", SpeciesID, ".csv",
                          sep = "")))
    cat(paste(SpeciesName, " was successful", sep = ""),sep="\n")
  } ## End of loop

#################################
## Model: Goodness of Fit Loop ##
#################################
BestModelsDF <- read.csv("BestModels_55Sites.csv")
BestModelsDF$Det <- as.character(BestModelsDF$Det)
BestModelsDF$Abu <- as.character(BestModelsDF$Abu)

    for (Model in 1:nrow(BestModelsDF)) {
      SpeciesName <- as.character(BestModelsDF$SpeciesName [Model])
      SpeciesID <- SpeciesNames$EuringID [SpeciesNames$Species == SpeciesName]
      FileName <- paste("GofF_55Sites_", SpeciesID, ".pdf", sep ="")
      pdf(file = file.path(dir.GoFs, FileName))
      DetFormula <- strsplit(as.character( get(
                 BestModelsDF$Det [Model])), "~") [[2]]
      AbuFormula <- strsplit(as.character( get(
                 BestModelsDF$Abu [Model])), "~") [[2]]
      currentFormula <- paste("~", DetFormula, "~", AbuFormula, sep = " ")
      UMF55 <- get(load(file = file.path(dir.UMFs, paste("UMF55_", SpeciesID,
             ".RData", sep = ""))))
      if (any(SpeciesNB == SpeciesID)) {
         currentBestModel <- pcount(formula(currentFormula),
         UMF55, mixture = "NB")}
      if (!(any(SpeciesNB == SpeciesID))) {
         currentBestModel <- pcount(as.formula(currentFormula), UMF55)}

        library(parallel)
        cl <- makeCluster(getOption("cl.cores", 4))
        clusterExport(cl, c("currentBestModel", "currentFormula"))
        clusterSetRNGStream(cl, NULL)
        PB_GOF <- clusterEvalQ(cl, {
```

```
            library(AICcmodavg)
            Nmix.gof.test(currentBestModel, nsim = 250)
         })
         stopCluster(cl)
         Samples <- rbind(PB_GOF [[1]] $ t.star, PB_GOF [[2]] $ t.star,
            PB_GOF [[3]] $ t.star, PB_GOF [[4]] $ t.star)
         ChiSquare <- PB_GOF [[1]] $chi.square
         pValue <- length(Samples[Samples <= ChiSquare])/ length(Samples)
         c.hat <- ChiSquare / mean(Samples)
         RSME <- sqrt(mean((currentBestModel@data@y -
                     fitted(currentBestModel))^2, na.rm = TRUE))
         XLab <- paste(BestModelsDF [Model, 3], " // ",
              BestModelsDF [Model, 4], sep = "")
         Title <- expression(paste("Bootstrapped ", chi,
                    "² fit statistic (1.000 Samples)", sep = ""))
         hist(Samples, xlab = XLab, ylab = "Frequency", main = Title)
         abline(v = ChiSquare, col = "red", lty = "dotted")
         abline(v = quantile(Samples, c(0.25, 0.5, 0.75)) [1], col = "grey")
         abline(v = quantile(Samples, c(0.25, 0.5, 0.75)) [2], col = "black")
         abline(v = quantile(Samples, c(0.25, 0.5, 0.75)) [3], col = "grey")
         mtext(line = 0.5, SpeciesName)
         mtext(line = -0.5, paste("p = ", round(pValue, 3), " // chi = ",
                    round(ChiSquare, 3), " // c-hat = ", round(c.hat, 3),
                    " // RSME = ", round(RSME, 3), sep = ""))
     dev.off()
     cat(paste(SpeciesName, " was successful", sep = ""),sep="\n")
     } # End of Loop over BestModelList

######################
## Estimations Loop ##
######################
## For species seen more than 20 times at sites visited in BOTH periods (n = 55)
  AbuPerSiteDF <- data.frame(SpeciesID = numeric(), SpeciesName = numeric(),
                    LowerOpenAbu = numeric(), MeanOpenAbu = numeric(),
                    UpperOpenAbu = numeric(), LowerForestAbu = numeric(),
                    MeanForestAbu = numeric(), UpperForestAbu = numeric(),
                    LowerUrbanAbu = numeric(), MeanUrbanAbu = numeric(),
                    UpperUrbanAbu = numeric())
  MeanDetProb <- data.frame(SpeciesID = numeric(), SpeciesName = numeric(),
            MeanOpen = numeric(), MeanForest = numeric(), MeanUrban = numeric())
  EstNumbers <- data.frame(SpeciesID = numeric(), SpeciesName = numeric(),
              EstN1x5 = numeric(), EstN2x5 = numeric(), EstN3x5 = numeric(),
              EstNP1 = numeric(), EstNP2 = numeric(), EstNFull = numeric(),
              LowConfInt = numeric(), HighConfInt = numeric())
  ObsNumbers <- data.frame(SpeciesID = numeric(), SpeciesName = numeric(),
           ObsNrP1 = numeric(), ObsNrP2 = numeric())

SiteNumbers <- SiteCovs55
rownames(SiteNumbers) <- 1:55
MajorityOpen <- as.numeric(rownames(SiteNumbers[!(SiteNumbers[,1] < 0.95),]))
MajorityForest <- as.numeric(rownames(SiteNumbers[!(SiteNumbers[,2] < 0.9),]))
MajorityUrban <- as.numeric(rownames(SiteNumbers[!(SiteNumbers[,3] < 0.9),]))

BestModelsList <- list()

pdf(file = file.path(dir.PDFs, "Detection-Probability_Habitat_Boxplots.pdf"),
           width = 10.5, height = 15.75)
par(mfrow = c(3,2))
for (Model in 1:nrow(BestModelsDF)) {
    ## Estimated Numbers
    SpeciesName <- as.character(BestModelsDF$SpeciesName [Model])
    SpeciesID <- SpeciesNames$EuringID [SpeciesNames$Species == SpeciesName]
    DetFormula <- as.character( get( BestModelsDF$Det [Model]), "~") [2]
    AbuFormula <- as.character( get( BestModelsDF$Abu [Model]), "~") [2]
    currentFormula <- paste("~", DetFormula, "~", AbuFormula, sep = " ")
    UMF55 <- get(load(file = file.path(dir.UMFs, paste("UMF55_", SpeciesID,
           ".RData", sep = ""))))
    UMF1x5 <- UMF55 [,c(1,5)] #  1st 5-min-count in both periods
    UMF2x5 <- UMF55 [,c(1:2,5:6)] # 1st and 2nd 5-min-counts in both periods
```

```
UMF3x5 <- UMF55 [,c(1:3,5:7)] # 1st, 2nd ad 3rd 5-min-counts in both periods
UMFP1 <-  UMF55 [,c(1:4)] # all 5-min-counts in P1
UMFP2 <-  UMF55 [,c(5:8)] # all 5-min-counts in P2
UMFFull <- UMF55 # all 5-min-counts in both periods

UMFs <- c("UMF1x5", "UMF2x5", "UMF3x5", "UMFP1", "UMFP2", "UMFFull")
for(UMF in UMFs){
  currentUMF <- get(UMF)
  if (any(SpeciesNB == SpeciesID)) {
     currentBestModel <- pcount(formula(currentFormula),
     currentUMF, mixture = "NB")}
  if (!(any(SpeciesNB == SpeciesID))) {
     currentBestModel <- pcount(formula(currentFormula), currentUMF)}
  RandomEffects <- ranef(currentBestModel)
  BUPs <- bup(RandomEffects)
  Name <- paste("BUPs", substring(UMF, 4, nchar(UMF)), sep = "")
  assign(Name, BUPs)
  EstN <- sum(BUPs)
  Name <- paste("EstN", substr(UMF, 4, nchar(UMF)), sep = "")
  assign(Name, EstN)
} # End of loop over UMFs
BestModelFull <- currentBestModel
BestModelsList [[SpeciesName]] <- BestModelFull
ConfIntFull<- colSums(confint(ranef(BestModelFull))) # Full: last in Loop
EstNumbers [nrow(EstNumbers) + 1, 2] <- SpeciesName
EstNumbers [nrow(EstNumbers), c(1,3:10)] <- c(SpeciesID, round(EstN1x5,3),
           round(EstN2x5,3), round(EstN3x5,3), round(EstNP1,3),
           round(EstNP2,3), round(EstNFull,3), ConfIntFull [1],
           ConfIntFull [2])
MeanOpen <- mean(bup(ranef(BestModelFull)) [MajorityOpen])
LowerOpen <- mean(confint(ranef(BestModelFull)) [MajorityOpen, 1])
UpperOpen <- mean(confint(ranef(BestModelFull)) [MajorityOpen, 2])
MeanForest <- mean(bup(ranef(BestModelFull)) [MajorityForest])
LowerForest <- mean(confint(ranef(BestModelFull)) [MajorityForest, 1])
UpperForest <- mean(confint(ranef(BestModelFull)) [MajorityForest, 2])
MeanUrban <- mean(bup(ranef(BestModelFull)) [MajorityUrban])
LowerUrban <- mean(confint(ranef(BestModelFull)) [MajorityUrban, 1])
UpperUrban <- mean(confint(ranef(BestModelFull)) [MajorityUrban, 2])

AbuPerSiteDF [nrow(AbuPerSiteDF) +1 ,] <- c(SpeciesID, 0,
             LowerOpen, MeanOpen, UpperOpen, LowerForest, MeanForest,
             UpperForest, LowerUrban, MeanUrban, UpperUrban)
AbuPerSiteDF [nrow(AbuPerSiteDF), 2] <- SpeciesName

DetProbPerHab <- c()
for (habitat in c("MajorityOpen", "MajorityForest", "MajorityUrban")) {
    habitat <- get(habitat)
  for (count in 1:8) {
    DetProbPerHab <- c(DetProbPerHab,mean(getP(
                   BestModelFull) [habitat, count]))}
}

MeanDetProb [nrow(MeanDetProb) + 1, 1] <- SpeciesID
MeanDetProb [nrow(MeanDetProb), 2] <- SpeciesName
MeanDetProb [nrow(MeanDetProb), 3] <- mean(getP(BestModelFull) [MajorityOpen,])
MeanDetProb [nrow(MeanDetProb), 4] <- mean(getP(BestModelFull)
[MajorityForest,])
MeanDetProb [nrow(MeanDetProb), 5] <- mean(getP(BestModelFull)
[MajorityUrban,])

SiteCoords <- boxplot(DetProbPerHab [1:8], DetProbPerHab [9:16],
           DetProbPerHab [17:24], col = c("white", "green", "coral"),
           ylab = "detection probability (p)", names = c("Open", "Forest",
           "Urban"), main = SpeciesName, range = 1.5)

currentSpecies <- c()
for(Interval in c("Data55P1", "Data55P2")) {
  currentData <- get(Interval)
  currentObsNr <- nrow(subset(currentData, EuringID == SpeciesID))
```

```r
        currentSpecies <- c(currentSpecies, currentObsNr)
      }
      ObsNumbers [nrow(ObsNumbers) + 1, 1] <- SpeciesID
      ObsNumbers [nrow(ObsNumbers), 2] <- as.character(SpeciesName)
      ObsNumbers [nrow(ObsNumbers), 3:4] <- currentSpecies
      cat(paste(SpeciesName, " was successful", sep = ""),sep="\n")
}
dev.off()

save(BestModelsList, file = file.path(dir.Results, "BestModelsList.RData"))
write.csv2(EstNumbers, file = file.path(dir.Appendix,
                       "Estimations_55Sites.csv"))
write.csv2(ObsNumbers, file = file.path(dir.Appendix,
                       "Observations_55Sites.csv"))
write.csv2(AbuPerSiteDF, file = file.path(dir.Results,
                         "EstimationsPerHabitat_55Sites.csv"))

## Abundance per Site
  AbuPerSiteDF <- read.csv2(file = file.path(dir.Results,
              "EstimationsPerHabitat_55Sites.csv"), row.names = 1)
  AbuPerSiteDF <- merge(AbuPerSiteDF, ObsDistDF, by = "SpeciesName", all = TRUE)

## Abundance per km2 per Habitat
  AbuPerkm2 <- AbuPerSiteDF [,c(2,1,3:12)]
  AbuPerkm2 <- AbuPerkm2 [order(AbuPerkm2$SpeciesID),]
  AbuPerkm2 [,c(3:11)] <- AbuPerkm2 [,c(3:11)] * (1 /
              (pi * (AbuPerkm2$Distance)^2 * 10^-6))
  AbuPerkm2 [,3:12] <- round(AbuPerkm2 [,3:12], 2)
  AbuPerkm2$Open <- AbuPerkm2$MeanOpenAbu
  AbuPerkm2$OpenConfInt <- paste(AbuPerkm2$LowerOpenAbu, " - ",
                     AbuPerkm2$UpperOpenAbu, sep = "")
  AbuPerkm2$Forest <- AbuPerkm2$MeanForestAbu
  AbuPerkm2$ForestConfInt <- paste(AbuPerkm2$LowerForestAbu, " - ",
                     AbuPerkm2$UpperForestAbu, sep = "")
  AbuPerkm2$Urban <- AbuPerkm2$MeanUrbanAbu
  AbuPerkm2$UrbanConfInt <- paste(AbuPerkm2$LowerUrbanAbu, " - ",
                     AbuPerkm2$UpperUrbanAbu, sep = "")
  write.csv2(AbuPerkm2, file = file.path(dir.Appendix,
                     "AbundanceEstimationkm2.csv"))
```