iBats Jersey -Review

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1.0 Introduction

1.1 Scope of the report

This report contains analyses of ultrasonic recordings of bat echolocation calls collected by States of Jersey Natural Environment Officers during July and August between 2011-2015.

1.2 Background

Ultrasonic recordings were made along 11 transect routes repeated in July and August of each year from 2011-2015, to monitor bat populations. These recordings pick up bat echolocation calls which can be used to identify bats to species level. By geo-referencing these calls, a map of species locations can be generated, and trend analyses can be used to assess changes to bat populations over time. Obtaining reliable trend estimates usually requires monitoring over a longer period than 5 years, hence trend estimates within this report are regarded as preliminary. This report also updates a previous power analyses based on the results of surveys over the last 5 years to assess the suitability of the current monitoring program to detect changes in bat populations over a longer period.

2.0 Methods

2.1 Data collection

Recordings were made according to the iBats protocol for car-based acoustic surveying (Jones *et al.*, 2013). Transects were driven at 15 mph starting 30-45 minutes after sunset, using a Tranquillity Transect time-expansion bat detector to detect echolocation calls. The bat detector was set to time-expansion x10 with a recording period of 320ms. This means the detector records sound internally for 320 ms then plays it back into the recorder 10 times slower for 3200ms. Sound was recorded to an SD card as a WAV file using either an Edirol R-09HR or Roland R-05 recording device. A GPS track of the transect route was recorded using a Samsung GT-S7710 phone with OruxMaps or other GPS options. The sound recorder and GPS track were set to start recording at the same time so that the position of the car when each bat is recorded could be determined. Each recorded bat call was subsequently georeferenced using this GPS track.

Eleven transect routes were driven twice a year in July and August from 2011-2015 (Figure 1). Surveys were only carried out during 'fine' weather; i.e. when the air temperature was greater than 7°C, and no more than very light rain or wind. Occasionally, transects were repeated a third time due to adverse weather conditions during a transect, or batteries running out during a recording. Where possible, all 3 repeats have been included in the analyses here, so for some years there may be 3 repeats of particular transects (see Table 1). The following metadata were also recorded at the start and end of each transect: temperature (°C); cloud cover (%); rain (dry, drizzle, light); and wind speed (calm, light, or breezy). Humidity data for the start and end of each transect was obtained from the States of Jersey Department for Environment - Meteorological Section.



Figure 1. A map of the eleven transect routes in Jersey.

2.1.1 Faulty recordings

Occasionally, soundfiles may not record properly due to detector faults. In these instances, sections of the soundfile and corresponding GPX file have been removed. Rarely, a transect could not be included in the analyses at all due to a faulty recording (see Table 1). Where a diversion was in place during the transect, the corresponding section of soundfile and GPX file were removed.

Year	Transect	Fault Description	Action taken
2011	T04 -0721	Recording cuts out at 19m55.8s and	Soundfile length adjusted.
		restarts at 20m17.2s	
2011	T09- 0726	Detector malfunction	Transect excluded from analyses. Route was repeated again to compensate.
2013	T01-0804	Faulty recording from 31m11s - end	Soundfile and GPX length cut from the start of the fault.
2013	T02-0725	Batteries ran out midway through transect.	Transect repeated again. Both included in analyses.
2013	T05-0701	Faulty recording throughout – looks like bat detector sensitivity was not set to full.	Transect excluded from analyses.
2013	T05-0811	Blank recording	Transect excluded from analyses.
2014	T02	Repeated 3 times due to bad weather on first.	All included in analyses
2014	T02-0701	Faulty connection between 6m -9m38s.	Section removed from soundfile.
2015	T02-0701	Recording blank from 72m13s -end	Soundfile and GPX file cut.

Table 1. Summary of faulty recordings occurring during iBats monitoring surveys and howthese were used in the analysis.

2.2 Analyses

2.2.1 Extracting, identifying, and georeferencing bat calls

Bat calls were extracted and identified from ultrasonic recordings using a semi–automated method (see Appendix 1 for full instructions on the methods used). Each transect recording was separated into a series of one minute recordings using Slice–audio file-splitter software. This aids analyses by decreasing file sizes. BatSound software was used to visualise each minute of ultrasonic recordings and it was determined whether or not bat calls were present in each file. Sonobat v.3.1.7p (Szewczak, 2014) was then used to extract call parameters from each bat call in the recordings. Sonobat uses amplitude threshold filters and recognition of smooth frequency changes over time to find calls and to fit a frequency-time trend line to the shape of the call, from which a number of measurements are extracted. Automatic feature extraction removes operator measurement bias from call parameters. All call feature extractions were visually inspected and calls where the measurement line did not fit the call accurately (i.e. the fitted line included background noise or echo) were rejected.

iBatsID (Walters *et al.*, 2012) was used to identify the calls extracted by Sonobat to species level. iBatsID reads in a Sonobat text file with the extracted call parameters, and using ensembles of artificial neural networks and a large European database of recordings, classifies recordings to species level, providing a probability of correct classification for each call, see Walters *et al.* (2012). Given the inherent uncertainty in classification of some species, it is recommended that species-level classification is not accepted for *Myotis* species using this classifier, and these should be classified to genus level only.

The 'full network' option in iBatsID was selected (equating to species-level classification), and calls with a correct species-level classification probability of <60% were reclassified to species group level, as either 'Unknown *Pipistrellus*', 'Unknown Serotine/Leisler's/Noctule' or 'Unknown Long-eared'. All species classified as *Myotis* were reclassified as 'Unknown *Myotis*'. As the iBatsID classification tool includes all European species, calls classified as species which are known not to occur on Jersey were also reclassified as unknowns at the group level. For example, calls identified as *Miniopterus schreibersii* were reclassified as 'Unknown *Pipistrellus*' as *M. schreibersii* falls within the Pipistrelle grouping in the ID tool, see Walters *et al.* (2012).

Calls were georeferenced using the GPS track recorded alongside each ultrasonic recording. The 'start time in file' extracted by Sonobat was used to provide the time of each bat call, which was subsequently matched with the closest time location recording from the GPS file, using a custom–written script in R (R Development Core Team, 2011) (see Appendix 1 for R scripts).

2.2.2 Diversity and relative abundance

Many calls recorded will belong to a sequence of calls from an individual bat, and therefore to avoid overestimating the number of individual bats recorded, some further processing is required to determine the number of bat passes and to give an ID to an entire sequence of calls rather than individual calls.

Calls are assigned to sequences by visual assessment of the call files to determine which calls belong within the same sequence. Sequences may span more than one 320ms 'snapshot' within the recording, but if there are no calls in the subsequent snapshot, calls thereafter are always considered to be a new sequence. Each individual sequence of calls represents a single bat pass.

The species identity for each sequence is assigned based on the following rules:

- Calls with a classification probability of <60% are ignored.
- Any call identified to a species known not to occur in Jersey is re-classified to the species-group stage as either 'Unknown Pipistrelle', or 'Unknown Serotine/Leisler's/Noctule'. The main example of this is calls classified as *Miniopterus schreibersii* a southern European species which can be confused with *Pipistrellus pipistrellus* or *Pipistrellus pygmaeus*. Calls classified as *M. schreibersii* are therefore reclassified as Unknown *Pipistrellus*.
- If there are calls identified as different species within the sequence, the sequence is identified based on the species representing the majority of calls within the sequence.
- If there is not a majority species ID to which the sequence can be assigned (i.e. the same number of calls within the sequence are assigned to each species), the sequence is assigned to the species-group stage as either 'Unknown Pipistrelle', 'Unknown Serotine/Leisler's/Noctule' or 'Unknown Long-eared'. Sequences which cannot be assigned to a species-group stage unknown are simply classified as 'Unknown'.

Species diversity is then calculated as the number of different species recorded in each year. Relative abundance is calculated as the number of passes of each bat species per minute of recording, for each year.

Diversity and abundance were calculated for three different thresholds of call classification probability, at 60, 70 and 80%. In simple terms this equates to certainty of classification. Calls not meeting these thresholds for probability of correct classification were reclassified to the group stage as either Unknown *Pipistrellus*', 'Unknown Serotine/Leisler's/Noctule' or 'Unknown Long-eared', and diversity and abundance re-calculated. A sequence will remain classified to species level as long as it still contains a single call meeting the classification threshold after reclassification. Increasing the threshold reduces the possibility for misclassification of calls, but also increases the number of calls which are not classified to species level.

2.2.2.1 Pipistrellus kuhlii

A number of bat passes each year in the Jersey surveys were identified as *Pipistrellus kuhlii*. Records of juvenile *P. kuhlii* have been recently identified on Jersey making this likely to be a resident species (pers comm. David Tipping 2015), rather than a misclassification of other resident pipistrelle species. Therefore in the main results section below the results are calculated with the *P. kuhlii* sequences included rather than classified as 'Unknown *Pipistrellus*'.

2.2.2.2 Nyctalus noctula

In addition a small number of *Nyctalus noctula* calls were detected in 3 of the 5 years of the iBats surveys. Although this species has not been definitively recorded in Jersey, itspresence has been suspected.

2.2.3 Trend analyses

Population trends were calculated for all bats as well as with individual species with enough data (*Pipistrellus pipistrellus* and *Pipistrellus pygmaeus*). A generalised additive model (GAM) was implemented using the framework of the mgcv 1.8-4 package (Wood, 2011). GAMs were used as they offer more flexibility than a linear trend model, producing a

smoothed curve of annual abundance index values. The method followed was that used by Fewster *et al.* (2000). This is also the method implemented by the Bat Conservation Trust in calculating bat population trends for the UK (Barlow *et al.*, 2015). As the GAM fit is less reliable at the first year, the baseline year (index = 1.0) was set as the second year in the time series (2012). The index of abundance, l(t), was calculated as:

$$I(t) = \frac{\text{total predicted count for year t}}{\text{total predicted count for base year}}$$

It was assumed that the data followed a Poisson distribution. Degrees of smoothing in each model was usually set to 0.4 times the number of years of survey data. A lower degree of smoothing decreases the size of the confidence intervals, which were obtained by using bootstrap techniques, directly from the index curve. 399 bootstrap replicates were obtained for each GAM and the confidence intervals were set to 95%. The significance of the trend, at p<0.05, was determined by whether the confidence intervals in the final year of surveys (2015) overlapped with the population abundance index of the baseline year (2012).

GAM models can include covariates for factors that could influence the means. Possible covariates here include environmental conditions of the iBats monitoring transect such as: start and end temperature (°C); start and end cloud cover (%); rain (dry, drizzle, light); wind speed (calm, light, breezy) and humidity. The covariates used in the GAMS were decided by carrying out General Linear Mixed Models (GLMMs) to investigate factors that may influence results. Percentage cloud cover at the start of the iBats monitoring transect was found to have a statistically significant impact on the means for all bats and *P. pygmaeus*. Therefore cloud cover was included as a covariate in the GAM trend analyses for these groups. For *P. pipistrellus* the start temperature and start cloud cover were found to be significant in the GLMMs and were included as covariates in the trend analysis. It is important to include covariates in trend analyses as although the covariates used may not have a strong effect on the overall trend, they can affect the width of the confidence intervals. For both species, trends were also calculated for four different classification thresholds (no threshold, 60%, 70% and 80%) to investigate the impact of different classification thresholds on calculated population trends.

2.2.4 Power analyses

Power analyses were carried out for *Pipistrellus pipistrellus* and *P. pygmaeus* using estimates of bat count variabilities based on the results of the 2011-2015 Jersey surveys updating previous analyses carried out in Jersey by Langton (2011). Variabilities were estimated for transects, years, transects within years, and replicate surveys using REML (Zuur *et al.*, 2009), using the lme4 package in R (Bates *et al.*, 2014). Models were fitted based on log-transformed counts of bat encounters per transect event, with year also fitted as a fixed effect to account for variability between years due to changes in bat populations. The power to detect a linear trend of given magnitude was then calculated as a function of the variance estimates.

2.3 Limitations of analyses

Using car based acoustic survey methods allows large areas to be surveyed in relatively short periods of time. However, there are some limitations to this method and these fall into 3 categories: 1) Not all bat species are equally likely to be recorded; 2) Not all calls/call sequences can be reliably identified; 3) Not all calls recorded can be extracted and analysed.

1) Not all bat species are equally likely to be recorded. Some species are underrepresented in acoustic surveys, either due to the type of echolocation call they use, or to a behavioural preference for non-edge type habitat, meaning they are not found as often along roads. For example *Plecotus* and *Rhinolophus* species are under-represented in acoustic survey, with two plausible explanations. These species have low intensity calls and therefore their calls cannot be detected over long distances, reducing the number of possible recordings compared to species with higher intensity calls. Also, previous research has shown that these species show preference for more densely vegetated areas and so they may not be found beside roads as often as species which prefer open or edge type habitats. Similarly, most *Myotis* species prefer woodland or riparian habitats so are less likely to be recorded along roadsides. In Jersey, this means that the following species are unlikely to be recorded in sufficient numbers to allow monitoring through car based acoustic transects: Grey long-eared bat, Brown long-eared bat, Greater horseshoe bat, *Myotis* species.

2) Not all calls/call sequences can be reliably identified. The species for which data can be reliably collected by acoustic transects are restricted to those which are easily identifiable from echolocation calls. At present this excludes *Myotis* species, which can only be reliably identified to genus level with our classifier. Other classifiers have shown some success with classifying the European *Myotis* to species but these are yet to be fully documented or published. Further, some other species can be difficult to reliably separate to species level leading to 'Unknowns' in the dataset. The percentage of call sequences per year in this dataset which were identified to species-level ranged from 94.4 – 96.2% (Table 2), suggesting that identification issues only have a minor impact on this dataset.

Survey Year	2011	2012	2013	2014	2015
Number of sequences					
recorded	580	530	462	697	705
Number of sequences					
identified to species	558	502	438	658	678
Percentage of					
sequences identified					
to species	96.21	94.72	94.81	94.40	96.17

Table 2. Number of bat call sequences recorded per year in Jersey and the percentage classified to species level.

3) Not all calls recorded can be extracted and analysed. Calls which are particularly quiet, or where there is noise or echo surrounding the call (a high noise-to-signal ratio) may impede the software used (Sonobat v.3.1.7p) from being able to extract call parameters, and therefore calls may be missed in the analysis. This means the number of call sequences recorded may be underestimated. Using the August 2015 data collected here, it was estimated that 26% of sequences may be missed by Sonobat (397 sequences were extracted by Sonobat out of 536 counted visually in Batsound). However this is unlikely to lead to bias in generating trend estimates as the proportion of sequences which are not able to be extracted in Sonobat is unlikely to change year on year, so long as the same version of Sonobat or other different software or an improved classifier would therefore require reanalysis of all the recordings made over the survey and monitoring period.

Although we are only able to produce individual trend analyses for *Pipistrellus pipistrellus* (common pipistrelle) and *Pipistrellus pygmaeus* (soprano pipistrelle), we include

recommendations for monitoring of other species which are not picked up often enough during acoustic car-based surveys in section 4.0 below.

3.0 Results

3.1 Summary of recordings

The number of call sequences recorded per year ranges between 462-705, from 21-23 transects (Table 3), with between 94.4-96.2% of sequences classified to species level when no call classification threshold is used (Table 3).

Transects cover most of the island, with bats recorded throughout the island (Figure 2 a-f). *Pipistrellus pipistrellus, P. pygmaeus* and *P. nathusii* appear to be distributed throughout the island, whereas records for *E. serotinus* appear to be concentrated in the North West of the island (Appendix 2), although this may just reflect the overall lower number of records for this species.

Survey Year	2011	2012	2013	2014	2015
Number of					
sequences recorded	580	530	462	697	705
Number of transects	22	22	21	23	22
Total recording time					
(S)	95160	94518	87833	100367	97829
Percentage of					
sequences identified					
to species level (no					
threshold)	96.21	94.72	94.81	94.40	96.17

Table 3. Summary of the numbers of bat call sequences recorded each year in Jersey and the percentage classified to species level at different call classification thresholds.

Figure 2. Locations of bat passes (using a classification threshold of zero) for all species recorded in Jersey during iBats monitoring surveys for a) all years; b) 2011; c) 2012; d) 2013; e) 2014; and f) 2015.





Nyctalus noctula

• Unknown Serotine/ Noctule/ Leisler's

3.2 Species diversity and relative abundance

Nine species were recorded between 2011-2015, with the number of species recorded in a single year ranging from 6 to 8 (Table 4). The species recorded are: *Eptesicus serotinus, Nyctalus leisleri, Nyctalus noctula, Pipistrellus kuhlii, Pipistrellus nathusii ,Pipistrellus pipistrellus pygmaeus, Plecotus auritus,* and *Plecotus austriacus.* The most commonly recorded species across every year was *P. pipistrellus* (77.5-83.5% of passes) followed by *P. pygmaeus* (8.3-13.8% of passes), and *P. kuhlii* (1.55-3.21%) (Table 4). *Plecotus auritus* was only recorded once in a single year (2013) and *Plecotus austriacus* was only recorded once in a single year (2013) and *Plecotus austriacus* was only recorded once in a single year (2013) and *Plecotus austriacus* was only recorded once in a single year (2013) and *Plecotus austriacus* was only recorded once in a single year (2013) and *Plecotus austriacus* was only recorded once in a single year (2013) and *Plecotus austriacus* was only recorded once in a single year (2013) and *Plecotus austriacus* was only recorded once across 2 years (2014-2015). *Myotis* bats (classified as Unknown *Myotis*) were recorded only once (2013) over the 5 year period.

Survey Year	2011	2012	2013	2014	2015
Total number of species recorded	6	7	8	7	7
	Numbe	r of passes	(% of total	annual bat	passes)
Eptesicus serotinus	4	4	2	3	6
	(0.69)	(0.75)	(0.43)	(0.43)	(0.85)
Nyctalus leisleri	0	1	1	1	0
	(0)	(0.19)	(0.22)	(0.14)	(0)
Nyctalus noctula	1	1	0	0	1
	(0.17)	(0.19)	(0)	(0)	(0.14)
Pipistrellus kuhlii	9	17	10	13	11
	(1.55)	(3.21)	(2.16)	(1.87)	(1.56)
Pipistrellus nathusii	3	9	5	4	7
	(0.52)	(1.70)	(1.08)	(0.57)	(0.99)
Pipistrellus pipistrellus	484	426	376	540	582
	(83.45)	(80.38)	(81.39)	(77.47)	(82.55)
Pipistrellus pygmaeus	57	44	43	96	70
	(9.83)	(8.30)	(9.31)	(13.77)	(9.93)
Plecotus auritus	0	0	1	0	0
	(0)	(0)	(0.22)	(0)	(0)
Plecotus austriacus	0	0	0	1	1
	(0)	(0)	(0)	(0.14)	(0.14)
Unknown Pipistrellus	21	27	23(4.98)	38	26(3.69)
	(3.62)	(5.09)		(5.45)	
Unknown Noctule/Serotine/Leisler's	1	1	0	1	1
	(0.17)	(0.19)	(0)	(0.14)	(0.14)
Unknown Plecotus	0	0	0	0	0
	(0)	(0)	(0)	(0)	(0)
Unknown <i>Myotis</i>	0	0	1	0	0
	(0)	(0)	(0.22)	(0)	(0)
TOTAL Passes	580	530	462	697	705

Table 4. Number of passes of each bat species recorded per year in Jersey, with the percentage of total annual bat passes in parenthesis.

3.2.1 Encounter rates

The numbers of bats recorded ranged from 0.32 - 0.43 per minute (Table 5). Overall encounter rates were lowest in 2013 and highest in 2015, which reflects the situation for the most commonly encountered species (*P. pipistrellus*). Encounter rate estimates are likely to underestimate the true encounter rate for bats in Jersey, as not all calls recorded are able to be extracted and analysed from recordings (see section 2.3 above).

	Encounter rate (bats/minute of recording)							
Species	2011	2012	2013	2014	2015			
Eptesicus serotinus	0.0025	0.0025	0.0014	0.0018	0.0037			
Nyctalus leisleri	0.0000	0.0006	0.0007	0.0006	0.0000			
Nyctalus noctula	0.0006	0.0006	0.0000	0.0000	0.0006			
Pipistrellus kuhlii	0.0057	0.0108	0.0068	0.0078	0.0067			
Pipistrellus nathusii	0.0019	0.0057	0.0034	0.0024	0.0043			
Pipistrellus pipistrellus	0.3052	0.2704	0.2569	0.3228	0.3569			
Pipistrellus pygmaeus	0.0359	0.0279	0.0294	0.0574	0.0429			
Plecotus auritus	0.0000	0.0000	0.0007	0.0000	0.0000			
Plecotus austriacus	0.0000	0.0000	0.0000	0.0006	0.0006			
Unknown Pipistrellus	0.0132	0.0171	0.0157	0.0227	0.0159			
Unknown Serotine/Noctule/Leisler's	0.0006	0.0006	0.0000	0.0006	0.0006			
Unknown <i>Plecotus</i>	0.0000	0.0000	0.0000	0.0000	0.0000			
Unknown <i>Myotis</i>	0.0000	0.0000	0.0007	0.0000	0.0000			
TOTAL Encounter Rate	0.3657	0.3364	0.3156	0.4167	0.4324			

Table 5. Numbers of each species encountered per minute of recording, for each year.

3.2.2 Classification thresholds

The percentage of bat passes classified to species level reduces as the classification threshold is increased, to a minimum classification rate of between 91.3-93.3% of passes when an 80% classification threshold is applied (Table 6).

	Percentage of passes identified to species level								
Threshold Level	2011	2012	2013	2014	2015				
None	96.21	94.72	94.81	94.40	96.17				
60%	95.34	93.96	93.72	93.68	95.18				
70%	94.31	93.02	92.86	92.54	94.61				
80%	92.41	92.26	91.56	91.25	93.30				

Table 6. Percentage of bat passes identified to species level at different call classification thresholds.

Applying thresholds appears to impact individual species similarly, i.e., the percentage of total bat passes classified as each species reduces as the threshold is increased and the percentage of Unknowns increases (Table 7).

	Perce	ntage of to	otal bat pa	isses
Threshold level	None	60%	70%	80%
Eptesicus serotinus	0.64	0.54	0.44	0.40
Nyctalus leisleri	0.10	0.07	0.07	0.03
Nyctalus noctula	0.10	0.07	0.07	0.03
Pipistrellus kuhlii	2.02	1.88	1.85	1.71
Pipistrellus nathusii	0.94	0.87	0.77	0.64
Pipistrellus pipistrellus	80.97	80.56	80.13	79.52
Pipistrellus pygmaeus	10.42	10.32	10.12	9.92
Plecotus auritus	0.03	0.03	0.03	0.03
Plecotus austriacus	0.07	0.07	0.03	0.03
Unknown Pipistrellus	4.54	5.25	6.02	7.09
Unknown				
Noctule/Serotine/Leisler's	0.13	0.30	0.40	0.50
Unknown Plecotus	0.00	0.00	0.03	0.03
Unknown <i>Myotis</i>	0.03	0.03	0.03	0.03

Table 7. Percentage of total bat passes classified as each species, across all years, for each threshold level.

3.3 Trends in abundance

Trend analyses shows that overall there appears to be an increasing trend in bat numbers, with an increase of approximately 19% between 2012-2015 (Figure 3a). Both *P. pipistrellus* and *P. pygmaeus* also show significant increasing trends, with respective increases of 34% and 51% between 2012-2015 (Figure 3b & c). These results should however, be taken with a certain level of caution due to the short time period of monitoring so far (see section 3.4 – Power Analysis).

3.3.1 Impact of call classification threshold level on trends

Changing the call classification threshold has very little impact on abundance trends for *P. pipistrellus* and *P. pygmaeus*; the overall trends are the same at all threshold levels, with minor changes to the confidence limits around the trends (Figures 4 aand b).

3.3.2 Comparison to UK species trends

The species trends for *P. pipistrellus* and *P. pygmaeus* in Jersey are consistent with those in the UK – with both species also showing a significant increasing trend in the UK in 2014. 2015 trends for the UK are not yet available.







Figure 3: The index curves of (*a*) all species; (*b*) Pipistrellus pipistrellus; and (*c*) Pipistrellus pygmaeus. The solid line gives the index curve and the dashed lines are the upper and lower 95% bootstrapped confidence intervals. The horizontal solid line represents the baseline abundance index (1.0), which was set at 2012.



Figure 4: The index curves of (*a*) *Pipistrellus pipistrellus; and* (*b*) *Pipistrellus pygmaeus at different call classification thresholds (none, 60%, 70% and 80%). The solid line gives the*

index curve and the dashed lines are the upper and lower 95% bootstrapped confidence intervals. The horizontal solid line represents the baseline abundance index (1.0), which was set at 2012.

3.4 Power analyses

Our power analysis using estimates of bat count variabilities based on the results of the 2011-2015 Jersey surveys (Table 8) shows that surveying 11 routes twice per year is sufficient over a ten year monitoring programme to detect declines of 6% or greater per year for P. pipistrellus, and declines of 8% or greater per year for P. pygmaeus. Power is lower for P. pygmaeus due to their lower abundance in Jersey compared to P. pipistrellus. These power analysis figures for both species are lower compared to Langton's (Langton, 2011) power analysis of the Jersey iBats survey. This is likely to be due to the lower encounter rate we found for bats in Jersey, compared to Ireland, for which data was used to estimate power in Langton (2011). Encounter rates in Ireland are around 2 bats/Km (or 0.8 per minute based on driving at 24kmph/15 mph) whereas encounter rates in Jersey are between 0.32 - 0.43 per minute. The difference in encounter rate is more than likely due to methodological differences between the two surveys, as calls were extracted manually from the Irish data thus maximising the number of calls detected. Improvements to methods for automatically extracting bat calls from recordings will increase the number of calls detected in Jersey and therefore the encounter rate, which in turn should improve power to detect smaller population changes.

		Power (%) for 11 route	es - 2 surveys per year
% pop redu	ulation ction	P. pipistrellus	P. pygmaeus
Per year	10 years		
1	9.6%	10	9
2	18.3%	20	15
3	26.3%	36	24
4	33.5%	55	37
5	40.1%	73	52
6	46.1%	86	67
7	51.6%	93	79
8	56.6%	97	88
9	61.1%	99	93
10	65.1%	99	96

Table 8. Power of 11 survey routes with 2 surveys per year at detecting various levels of population decline. Cells highlighted in green achieve 80% power for a one-sided test of the significance of a linear decline at P=0.05 after 10 years of surveys.

4.0 Conclusions and recommendations for future monitoring

The current iBats monitoring program provides excellent coverage of bat distributions across Jersey and is effective for determining bat species diversity and relative abundance (given the constraints of identifying calls of all types of bats – see 2.3. Limitations of Analyses). The iBats monitoring programme is sufficient to detect declines in populations of common and soprano pipistrelles (*P. pipistrellus* and *P. pygmaeus*) of between 6-8% per year based on a ten year monitoring program. Methodological improvements to the extraction of bat calls from recordings, which are currently under development, should enable a greater proportion of calls to be analysed, which in turn should increase the power to detect population change. However, this would require the data to be reanalysed using these new software programmes.

Trends in abundance of the two most commonly encountered species (P. pipistrellus and P. pygmaeus) demonstrate significantly increasing trends in Jersey over the period of the monitoring programme (2012-2015), which is in line with bat population trends in the UK (Barlow et al., 2015) and Europe (Haysom et al., 2014). However, further monitoring data is needed to verify the Jersey population trends lines (based on our power analysis). Trends for rarer species in Jersey may not show the same pattern, and alternative monitoring methods may be necessary to determine the state of populations of these other species. For example, static monitoring whereby passive acoustic monitors are set up to record all night in various locations, may be better able to detect those species not well covered by car-based acoustic monitoring, such as Myotis spp, Nyctalus spp, Rhinolophus spp. and Plecotus spp. A study by Newson et al. (2015) in Norfolk had success in surveying a number of these species via passive acoustic detectors although this has not been developed into a monitoring survey at present. The disadvantage of the static detector methodology is largely the cost involved in purchasing passive detectors, and, similarly to car-based acoustic monitoring, the time taken to analyse the recordings. However progress in automated analyses and species identification software are reducing the time taken for analyses is being made rapidly. We recommend that the findings in the report are written up as a scientific publication as they are of significant national and international scientific interest.

5.0 Acknowledgements

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7.0 Appendices

7.1 Appendix 1 - Instructions for automated analysis of iBats recordings

There are 4 steps in the automated analysis of iBats recordings:

- 1) Extracting call parameters from call files
- 2) Identifying calls using IbatsID
- 3) Extracting the GPS location for each call
- 4) Downstream analysis to calculate number of bat passes from the number of calls.

1. Extracting call parameters

Software needed

- Slice Audio File Splitter <u>http://www.nch.com.au/splitter/index.html</u>
- Sonobat version 3.1.7p is best as it has been updated and is better at finding calls in noisy recordings (which often applies to iBats recordings).
- Batsound or similar sonogram viewer.

Instructions

- Use 'Slice' software to split the .wav file recording into 1 minute chunks. This makes it easier for Sonobat to deal with. Open 'Slice', go to 'Add File' and navigate to the .wav file you want to slice. Select 'Slice Into Files Of Duration' and set the duration to 1 minute (00:01:00). In the 'Output Sliced Folder' box, choose where you want the one minute chunks to be saved. Click 'Slice' to begin. This will then add the one minute files to the output file you selected.
- 2) Open Sonobat. The sound file and analyses settings will need to be defined the first time the program is used. Click on the set preferences (set prefs) tab (bottom right of screen) and input the following settings* in the 'default settings for non-Sonobat files' section. See Figure 1.
 - default R/L channel to process: L
 - Sampling frequency: other: 441 kHz
 - Default time expansion: 10
 - Max # of calls to consider per file: 100
 - Acceptable call quality: 0.30
 - Skip calls below this quality: 0.20

Once completed, click on the green Save <Rtn> tab. This will return you to the main screen for analysis.

*Note – these settings are for the standard iBats recording setup using a tranquillity transect and may need to be adjusted if using a different detector depending on the sampling frequency and time-expansion factor used

- 3) Open the first one minute chunk in Batsound and scan through to determine whether there are any bat calls in the file.
- 4) If there are bat calls present, load the file into Sonobat by dragging the file to the box at the top which says 'file or directory drop' or 'drag and drop file here to open'.



Figure 1: Sound file and analysis settings (set prefs tab).

5) Set the filter to manual – 20kHz (unless calls which are below 20kHz have been seen in Batsound). Set the view to 'real time' (using the button switch at the top of the screen next to the file drop box). See Figure 2.



Figure 2. A one-minute soundfile opened in Sonobat.

Find the calls that you have seen in Batsound. Use the cursor to highlight the first call. This zooms in on the call. Zoom until the call fills most of the screen. See Figure 3.

SonoE	Bat 3.1.7p.vi																
	record	open file	up	L del	44	.10 kHz/	16 bit/stereo	fs: 441 kH:	: TE: 10)	< ci	ing co	mpressed 🧯	2	res	olution		2
	[F1]	[F2]	down			T01-07	14_214058 P	art 02 of 73				eallime 🤇		ow		high	
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40 -																	1- T
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2	20 kHz	▼	hold freq	zoom 🔻	10	15	etdario		undo za	om	save	zoomed	tO	0	f	6000	
manual	none	-	10 msec st	d view 🔻	20	30	310 110		unuo 20		sel	ection		8.00)0 sec		
									^				-		- 754		open print panel
Sonol	satch										2)	So	10	Sa	t		set prefs
do la	to Dutes		2000 B						-	/		Softwa	e for Bo	it Call	Analys	is	-
4))	0									L							quit

Figure 3. A call zoomed in on Sonobat.

7) Click on 'std view'. Sonobat should then attempt to fit a measurement line to the call. See Figure 4.



Figure 4. A call with measurement line fit.

8) If the line fits the call perfectly, click 'write data to file'. This creates a text file in the directory above where the .wav file being analysed is stored, containing all the sound parameter measurements for the call. Each new call analysed will be added to this file.

- 9) If the whole call is not displayed on the screen then increase the std view time (pale blue box) until the whole call is displayed.
- 10) If the line isn't fitting the call because of high level of background noise then use a manual filter and choose a frequency below the minimum frequency of the call. Select the call again and see if the measurement line now fits the call. If it does click 'write data to file'
- 11) Click 'end std view to go back and select the next call.
- 12) DO NOT click write data to file if the line is measuring noise or is not a good fit to the call. Changing the std view time can help achieve a better line fit. Also, making sure the call is zoomed so it fills most of the screen before clicking 'std view' can help ensure that Sonobat measures the call well.
- 13) Measure each of the calls in the file in the same way.

2. Identifying calls using iBatsID (Europe)

iBatsID (Europe) is a species classification tool developed by The Zoological Society of London and Bat Conservation Trust which reads in a Sonobat text file with extracted call parameters, and using ensembles of artificial neural networks and a large European database of recordings, classifies recordings to species (see Walters *et al.* (2012) and https://sites.google.com/site/ibatsresources/iBatsID).

Given the uncertainty in the classifications for some species, it is recommended that specieslevel classification is not accepted for species in the lowest quartile of probability of correct classification (less than 70%). This means *Myotis* species should be classified to genus level only.

How to use iBatsID (Europe)

To open iBatsID click on the link: <u>iBatsID</u> or go to <u>http://ibatsid.cloudapp.net/</u>

Inputting Data

The text file output from Sonobat can either be copy/pasted directly into iBatsID (use Ctrl+A to select all, Ctrl+C to copy and Ctrl+V to paste), or the file can be loaded by clicking **'Load Data From File'** and then navigating to the file on your computer.

NB. Please ensure decimal points are displayed as full stops (.) rather than commas (,). If commas are used rather than full stops, IbatsID will not be able to correctly identify calls. Commas can be changed to full stops in the text file using the 'find and replace' function in a text editor.

Classifying calls

To cut down post-processing time, calls are classified using the whole network. To run the network in this way select **'Use Full Network'** and ensure the **'Download result as file**' box is selected. Click **'Classify calls**' to begin classification. See Figure 5. A pop-up window will enable you to select where you want the results to be saved.

iBats ID (Europe)

Identify European bat echolocation calls using the ensembles of neural networks described in <u>Walters et al. 2012</u>. Enter call data for each species you want to identify. Data should be in the text file format exported by SonoBat (<u>www.sonobat.com</u>). Each row should be data for a single call.

	2014 sliced Calls 2466.64	0416 0.00000	0 10.050503	2.605509 45.270061	52.097170 45.160	014 0.93000	04 45.335229
01-0714_214056 Part 01 01 73.Wav	2014 sliced Calls 2575.40	5166 0.00000	0 10.050503	2.799000 44.074102	51.422799 44.249	513 7.17290	50 44.790050
01-0714_214058 Part 01 of 73.wav	2014 sliced Calls 2637.31	5545 0.00000	010.656583	2.075401 45.011676	50.735134 45.011	5/6 5.7234	08 45.020324
01-0714_214058 Part 01 of 73.wav	2014 sliced Calls 2684.35	4646 0.00000	010.656583	1.701726 45.391406	51.268038 45.382	J94 5.88594	43 45.412796
01-0714_214058 Part 02 of 73.wav	Bat Road Transects 2014	2014 sliced	2748.018939	0.000000 10.656583	4.942565 44.863744	58.535012	44.803014
01-0714_214058 Part 02 of 73.wav	Bat Road Transects 2014	2014 sliced	2828.120755	0.000000 10.656583	4.473728 44.930128	60.072159	43.950087
01-0714_214058 Part 02 of 73.wav	Bat Road Transects 2014	2014 sliced	2917.524153	0.000000 10.656583	4.126822 44.447765	55.547638	44.362199
01-0714_214058 Part 02 of 73.wav	Bat Road Transects 2014	2014 sliced	2995.045429	0.000000 10.656583	3.978374 44.827743	55.017163	44.380070
01-0714_214058 Part 02 of 73.wav	Bat Road Transects 2014	2014 sliced	1731.251631	0.000000 10.656583	4.071833 43.829322	51.450657	43.686997
01-0/14_214058 Part 02 of 73.wav	Bat Road Transects 2014	2014 sliced	1914.913828	0.000000 10.656583	3.923724 42.810661	49.305423	42.602279
01-0714_214058 Part 25 of 73.wav	Bat Road Transects 2014	2014 sliced	5185.321262	0.000000 10.656583	1.980389 49.026173	58.035471	48.368220
01-0714_214058 Part 25 of 73.wav	Bat Road Transects 2014	2014 sliced	5329.507997	0.000000 10.656583	1.951495 48.532521	67.989415	45.747369
01-0714_214058 Part 25 of 73.wav	Bat Road Transects 2014	2014 sliced	5363.639685	0.000000 10.656583	1.706457 50.097255	66.269300	48.455795
01-0714_214058 Part 26 of 73.wav	Bat Road Transects 2014	2014 sliced	250.554790	0.000000 10.656583	7.423712 45.833671	57.537176	45.454866
01-0714_214058 Part 26 of 73.wav	Bat Road Transects 2014	2014 sliced	331.419290	0.000000 10.656583	6.458445 45.858388	60.593611	45.729821
01-0714_214058 Part 26 of 73.wav	Bat Road Transects 2014	2014 sliced	417.454461	0.000000 10.656583	7.427474 45.414480	55.369803	45.275064
01-0714_214058 Part 27 of 73.wav	Bat Road Transects 2014	2014 sliced	2318.721445	0.000000 10.656583	5.647531 45.755666	52.823855	45.488159
01-0714_214058 Part 27 of 73.wav	Bat Road Transects 2014	2014 sliced	2318.737545	0.000000 10.656583	5.604129 45.725307	52.601396	45.504679
01-0714_214058 Part 27 of 73.wav	Bat Road Transects 2014	2014 sliced	2402.501577	0.000000 10.656583	6.073087 45.550016	50.371584	45.350883
01-0714_214058 Part 27 of 73.wav	Bat Road Transects 2014	2014 sliced	2569.341630	0.000000 10.656583	6.561265 45.371523	51.182765	45.005578 (
01-0714_214058 Part 30 of 73.wav	Bat Road Transects 2014	2014 sliced	5688.824384	0.000000 10.656583	1.871787 46.453180	53.043785	45.538076
01-0714_214058 Part 31 of 73.wav	Bat Road Transects 2014	2014 sliced	1240.697930	0.000000 10.656583	2.726266 47.898334	69.864232	45.155520 :
01-0714_214058 Part 31 of 73.wav	Bat Road Transects 2014	2014 sliced	1332.152373	0.000000 10.656583	5.010842 45.754089	64.294275	45.550787
01-0714_214058 Part 31 of 73.wav	Bat Road Transects 2014	2014 sliced	1418.888279	0.000000 10.656583	4.374122 45.480301	70.637156	45.398528
01-0714 214058 Pert 32 of 73 wey	Bat Road Transects 2014	2014 sliced	2311.885026	0.000000 10.656583	4.603073 45.930962	51.810493	45.462729
01-0114_2140301 alt 52 0113.0000	Bet Road Transacts 2014	2014 sliced	2399.357907	0.000000 10.656583	3.896802 46.026744	54.010093	45.828136
01-0714_214058 Part 32 of 73.wav	Dal Nudu Hanseuls 2014						
01-0714_214058 Part 32 of 73.wav 01-0714_214058 Part 36 of 73.wav	Bat Road Transects 2014	2014 sliced	779.536052	0.000000 10.656583	6.203081 44.226773	54.525428	42.628535

Figure 5. iBatsID with data loaded and settings selected for call classification.

The results file will show a number of columns, with the first 3 being the call ID, filename and start time in file, and the next 2 being the classification assigned to the call and the associated classification probability. The rest of the columns show the classification probabilities for each of the 34 possible species.

3. Extracting the GPS location for each call

To match calls with the location at which they were recorded you will need the output file from iBatsID containing the filename and time in file of each call, and also the GPX file for the transect.

There are three stages involved in extracting GPS locations for calls:

- 1) Editing the GPX file
- 2) Editing the Call file
- 3) Matching in R
- 1. Editing the GPX file

The GPX file should be opened in MS excel by dragging and dropping the file into Excel. There are a number of error messages which can be okayed and ignored. All columns in the file should be deleted EXCEPT for Latitude, Longitude, Elevation and the date/time stamp. Date and time should be separated into separate columns using the 'text to columns' function under the Data tab. The 'date' column needs reformatting using 'Format cells' to set the category to 'Date' and the type to '14/03/2001'. A column should be added to number each row. The column names should be changed to 'No', 'Lat', 'Long', 'Alt', 'Date', 'Time'. The resultant file should look like the one shown in Figure 6. The file should be saved as a .csv.

	A	В	С	D	E	F	G	Н
1	No	Lat	Long	Alt	Date	Time		
2	1	49.21322	-2.21281	20.80566	06/08/2011	20:16:13		
3	2	49.21341	-2.2129	20.80566	06/08/2011	20:16:19		
4	3	49.21366	-2.21307	20.32495	06/08/2011	20:16:25		
5	4	49.21395	-2.2132	20.32495	06/08/2011	20:16:30		
6	5	49.2142	-2.21324	20.32495	06/08/2011	20:16:35		
7	6	49.21448	-2.21322	20.32495	06/08/2011	20:16:40		
8	7	49.21476	-2.21324	20.80566	06/08/2011	20:16:45		
9	8	49.21503	-2.21343	21.28638	06/08/2011	20:16:50		
10	9	49.2153	-2.21365	22.24756	06/08/2011	20:16:55		
11	10	49.21557	-2.21382	23.20898	06/08/2011	20:17:00		
12	11	49.21586	-2.21399	23.68958	06/08/2011	20:17:05		
13	12	49.21614	-2.21421	23.68958	06/08/2011	20:17:10		
14	13	49.21641	-2.21447	24.17029	06/08/2011	20:17:15		
15	14	49.21666	-2.21476	23.68958	06/08/2011	20:17:20		
16	15	49.21693	-2.21505	22.72827	06/08/2011	20:17:25		
17	16	49.21719	-2.21525	22.24756	06/08/2011	20:17:30		
18	17	49.21745	-2.21543	21.28638	06/08/2011	20:17:35		
19	18	49.21772	-2.21564	20.32495	06/08/2011	20:17:40		

Figure 6. An example of an edited GPX file showing the format required.

2. Editing the call file

The call file output from iBatsID needs some editing to put it in the correct format for matching call locations with the GPX file.

The file should be opened in MS excel. Columns should be added for the transect name – 'Transect', (which can be extracted from the filename), the part number – 'Part'(which can be extracted from the filename), and the time from start of the transect – 'Time_from_start'. The following excel equation should be used to calculate the time from start of the transect in seconds for each call:

=((d2-1)*60)+(e2/100)

where d2 is the column containing the part number, and e2 is the column containing the Start time in file (StartTimeInFile – output from Sonobat). This equation takes the time of the call within the one minute chunk and uses this and the part number to calculate the time from the start of the entire transect.

All other columns should remain unchanged.

The resultant call file should look like the example in Figure 7, with the same headings. This should be saved as a .csv file.

*Please note, each call file should contain calls from one transect recording only. If multiple transects have been analysed together, separate call files should be created for each. R code to split the file and save a different file for each transect recording is included below.

	АВ	С	D	E	F	G	Н	1	J
1	id Filename	Transect	Part	StartTimeInFile	Time_from_start	Classification	ClassificationProbability	Myotis.na	Myotis.en R
2	1 T01-0714_214235 Part 02	2 T01-0714_214235	2	4754.992186	107.5499219	Pipistrellus pygmaeus	0.89482286	9.22E-10	0.000833
3	2 T01-0714_214235 Part 02	2 T01-0714_214235	2	4828.503167	108.2850317	Miniopterus schreibersii	0.996138932	4.66E-10	0.000119
4	3 T01-0714_214235 Part 02	2 T01-0714_214235	2	4901.574705	109.0157471	Miniopterus schreibersii	0.858644409	3.20E-08	0.023343
5	4 T01-0714_214235 Part 10	T01-0714_214235	10	4590.376802	585.903768	Pipistrellus pipistrellus	0.629214053	2.88E-10	3.07E-09
6	5 T01-0714_214235 Part 10	T01-0714_214235	10	4763.434237	587.6343424	Pipistrellus kuhlii	0.542457082	2.10E-11	6.48E-10
7	6 T01-0714_214235 Part 17	7 T01-0714_214235	17	2645.758115	986.4575812	Pipistrellus pipistrellus	0.999409661	3.49E-11	8.34E-10
8	7 T01-0714_214235 Part 17	7 T01-0714_214235	17	2733.76276	987.3376276	Pipistrellus pipistrellus	0.998360211	8.47E-12	3.71E-10
9	8 T01-0714_214235 Part 17	7 T01-0714_214235	17	2827.617882	988.2761788	Pipistrellus pipistrellus	0.998360377	5.35E-11	1.38E-09
10	9 T01-0714_214235 Part 17	7 T01-0714_214235	17	2920.203699	989.202037	Pipistrellus pipistrellus	0.984146135	6.51E-12	3.84E-10
11	10 T01-0714_214235 Part 20	T01-0714_214235	20	3779.642635	1177.796426	Pipistrellus pipistrellus	0.999243609	3.99E-11	5.30E-09
12	11 T01-0714_214235 Part 20	T01-0714_214235	20	3876.334524	1178.763345	Pipistrellus pipistrellus	0.999365778	6.36E-11	1.65E-07
13	12 T01-0714_214235 Part 24	T01-0714_214235	24	1844.733594	1398.447336	Pipistrellus pipistrellus	0.998887929	2.00E-10	2.33E-06
14	13 T01-0714_214235 Part 24	T01-0714_214235	24	1888.353571	1398.883536	Pipistrellus pipistrellus	0.99935663	1.09E-10	2.21E-06
15	14 T01-0714_214235 Part 24	T01-0714_214235	24	2020.138415	1400.201384	Pipistrellus pipistrellus	0.999611142	1.41E-12	1.45E-09
16	15 T01-0714_214235 Part 24	T01-0714_214235	24	2098.201016	1400.98201	Pipistrellus pipistrellus	0.947084889	5.47E-08	9.48E-05
17	16 T01-0714_214235 Part 26	T01-0714_214235	26	427.657753	1504.276578	Pipistrellus pipistrellus	0.999205831	7.05E-11	2.09E-08
18	17 T01-0714_214235 Part 26	T01-0714_214235	26	501.776613	1505.017766	Pipistrellus pipistrellus	0.999486067	3.48E-11	1.74E-07
19	18 T01-0714_214235 Part 30	T01-0714_214235	30	4433.277945	1784.332779	Pipistrellus pipistrellus	0.998403069	1.69E-11	1.07E-09
20	19 T01-0714_214235 Part 31	T01-0714_214235	31	5795.649299	1857.956493	Pipistrellus pipistrellus	0.999240686	6.10E-11	7.60E-09
21	20 T01-0714_214235 Part 34	T01-0714_214235	34	799.474568	1987.994746	Pipistrellus pipistrellus	0.999190424	3.63E-10	5.52E-06

Figure 7. An example call file showing the format required. Please note, columns *K* – *AP* are not shown and should remain in the format output from iBatsID.

<u>R script to split ibatsID output to different files for each transect recording</u> Filenames highlighted in yellow below will need altering to navigate to the correct file on your computer.

Calls<-read.csv("IbatsID//ibatsid_2015_full.csv", header=T)

N<-unique(Calls\$Transect) for (i in 1:length(N)) {

calls1<-Calls[Calls\$Transect==N[i],]

write.csv(calls1, paste("lbatsID//2015 split//",(N[i]),".csv",sep=""), row.names=F)
}

3. Matching in R

Once the GPX file and call file have been edited as above, an R script can be used to output the GPS location of each bat call. The R code is included below with annotation.

Firstly, open R and set the directory to the folder containing folders with GPX files and Call files (File>Change dir> {navigate to the directory}).

<u>R script</u>

##Read in GPX file and Call file. Filenames highlighted in yellow below will need altering to navigate to the correct file on your computer##

GPS<-read.csv("GPX files//2015 GPX edited//T01-11-07-15.csv", header=T, stringsAsFactors=FALSE)

Calls<-read.csv("lbatsID//2015 split//T01-0711_214330.csv", header=T)

First, convert times in GPS file to time from start - in S

GPS\$Date <- gsub('([0-9]+)/([0-9]+)', '\\3-\\2-\\1', GPS\$Date)

GPS\$Times <- paste(GPS\$Date, GPS\$Time, sep=" ") GPS\$Time_from_start <- with(GPS, as.vector(difftime(Times, Times[1]))) ## Now need to match up call time with closest Time_from_start in GPS for each call file and GPS file.##

eventTimes <- (Calls\$Time_from_start) $\,$ # this gives the times of bat calls from the start of the transect in S

gpsTimes <- (GPS\$Time_from_start) # this gives the times of gps readings from start of transect in S

matching <- abs(outer(eventTimes, gpsTimes, '-')) Calls\$gpsToEvent <- apply(matching, 1, which.min) # this gives the number of the GPS row with the #closest matching time for each event#

Calls\$Latitude<-GPS\$Lat[match(Calls\$gpsToEvent, GPS\$No)] # longitude of closest matching time Calls\$Longitude<-GPS\$Lon[match(Calls\$gpsToEvent, GPS\$No)] # latitude of closest matching time

##Lastly, we need to write the output to a new file. The filename highlighted in yellow #below will need to be altered to where you want the file to be stored on your computer#

write.csv(Calls, "GPS matched/2015/T01-0711_214330.csv", row.names=F)

The output file should be the same as the call file input, but with columns added for latitude and longitude.

4. Downstream analysis

The above instructions provide methodology to obtain an identification and GPS location for each bat call recorded. However, many calls will belong to the same sequence of calls from an individual bat, and therefore some further processing is required to determine the number of bat passes and to give an ID to an entire sequence of calls rather than individual calls. Further, as part of the post-processing of iBatsID output files, it is important to build in rules that reduce the probability of accepting an incorrect species classification.

Calls are assigned to sequences by visual assessment of the call files to determine which calls belong within the same sequence. Sequences may span more than one 320ms 'snapshot' within the recording, but if there are no calls in the subsequent snapshot, calls thereafter are always considered to be a new sequence (see Figure 8).

The species identity for each sequence is assigned based on the following rules:

- Calls with a classification probability of <60% are ignored.
- If there are calls identified as different species within the sequence, the sequence is identified based on the species representing the majority of calls within the sequence.
- If there is not a majority species ID to which the sequence can be assigned (i.e. the same number of calls within the sequence are assigned to each species), the sequence is assigned to the group stage. This is usually either 'Unknown *Pipistrellus'* (where all/majority of calls within the sequence are identified as Group 2 species by IbatsID), or 'Unknown Big Bat' (where all/majority of calls within the sequence are identified as Group 3 species by IbatsID).
- Sequences identified to a species within the *Myotis* genus are classified as 'Unknown <u>Myotis</u> sp.' due to the difficulty of separating *Myotis* species based on their echolocation calls.



Figure 8. *a*) An example of a call sequence spanning 2 snapshots; b) An example of a snapshot containing 2 call sequences.

7.2 Appendix 2 – Maps of species occurrences

Appendix 2 Figure 1. Locations of bat passes (using a classification threshold of zero) for individual species recorded in Jersey during iBats monitoring surveys.







