

New species of bonneted bat, genus *Eumops* (Chiroptera: Molossidae) from the lowlands of western Ecuador and Peru

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We describe and formally name a species of bonneted bat (genus *Eumops*), which is a member of the *E. glaucinus* complex. Closely related species are *E. glaucinus*, *E. ferox*, and *E. floridanus*. The conceptual basis for the description of this species is the Genetic Species Concept with speciation by the Bateson-Dobzhansky-Muller model. The new species is distinguished from all other species of bats by its unique karyotype (2N = 38, FN = 54), sequence of the mitochondrial cytochrome-*b* gene, and genetic markers revealed through analysis of Amplified Fragment Length Polymorphisms. The series from the type locality (Ecuador, Guayas) is comprised of seven specimens. Morphologically, the new species is smaller than *E. floridanus* and *E. glaucinus*, but is indistinguishable from *E. ferox*. The new species is significantly smaller in size than *E. glaucinus* in six out of eight measurements and is distinguishable from *E. glaucinus* based on length of maxillary toothrow and zygomatic breadth. The geographic range of *E. wilsoni*, as currently documented, is the dry forests of southwestern Ecuador and adjacent northwestern Peru. We propose the common name for this species be Wilson's bonneted bat.

Key words: Genetic Species Concept, AFLPs, cytochrome-*b*, karyotypes, bonneted bats, *Eumops*, operational species criteria

A relaxed molecular clock places an evolutionary timescale on the origins of North American big-eared bats (Vespertilionidae: *Corynorhinus*)

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The notoriously fragmented nature of the chiropteran fossil record has made it extremely difficult to resolve issues of evolutionary history based solely on morphological data. Placing estimates on dates of divergence for taxa, as well as developing a reliable calibration for a molecular clock, has been problematic due to a deficiency in reliable fossil calibration points, and a lack of statistical power in the analyses available, as well as the mistreatment of the available data. We obtained sequence data from the hypervariable D-loop of the mitochondrial DNA control region of *Corynorhinus rafinesquii*, *C. mexicanus*, and the five recognized subspecies of *C. townsendii* and employed a relaxed molecular clock model to test competing hypotheses of evolution for big-eared bats in North America. Our analyses indicate interspecific divergences occurred during the Pliocene, with *C. rafinesquii* diverging from the other *Corynorhinus* relatively early, during periods of increased warmth and significantly higher sea levels, and *C. townsendii* and *C. mexicanus* diverging relatively late, possibly during the cooler periods leading up to the Pleistocene. Intraspecific divergences within *C. townsendii* appear to have occurred as a result of repeated glacial advances during the Pleistocene, with the *C. t. ingens* and *C. t. virginianus* lineages arising at relatively the same time as *C. t. pallescens* and *C. t. australis*, and recent rapid population decline producing the disjunct distribution of *C. t. ingens* and *C. t. virginianus*. Dating and demographic analyses indicate all species of *Corynorhinus* are likely undergoing population decline.

Key words: *Corynorhinus*, big-eared bats, mtDNA, molecular clock, Pliocene, Pleistocene

**Geographic and phylogeographic variation in *Chaerephon leucogaster*
(Chiroptera: Molossidae) of Madagascar and the western Indian Ocean islands
of Mayotte and Pemba**

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We examine patterns of morphological and genetic variation in *Chaerephon leucogaster* (family Molossidae) on Madagascar, Mayotte in the Comoros Archipelago, and the offshore Tanzanian island of Pemba. Five external, 10 cranial, and eight dental measurements of animals from different Malagasy populations (grouped according to bioclimatic regions) show differences in the degree of sexual dimorphism and size variation. Further, the population on Mayotte is largely identical in size to those from western Madagascar, and animals from Pemba are notably larger than those from Madagascar and Mayotte. Cytochrome *b* genetic distances across samples from these islands were low (maximum 0.0035) and animals from Pemba and Mayotte shared cytochrome *b* haplotypes with Malagasy bats. D-loop data showed some concordance between haplotype distribution, geographical position (latitude and island), and the bioclimatic zones. Animals from Pemba and Mayotte formed a unique D-loop haplotype, which was a minimum of six mutational steps different from Malagasy haplotypes. Within Madagascar, certain haplotypes were exclusive to the north (13°S latitude band) and arid southwest (22° and 23°S latitudes) regions. In general, there was no clear concordance between variation in haplotype distribution, latitude, altitude or gender. Where concordance occurred, the genetic distances involved were not sufficiently high to warrant the definition of new taxonomic units. Hence, based on current genetic information, patterns of morphological variation of the Madagascar populations and differences between Pemba and Mayotte/Madagascar are best explained as inter-population variation and may be adaptive, associated with different climatic regimes and associated ecological variables.

Key words: *Chaerephon leucogaster*, geographic variation, genetic variation, Madagascar, Mayotte, Pemba

Phylogeography of the greater horseshoe bat, *Rhinolophus ferrumequinum* (Chiroptera: Rhinolophidae), in southeastern Europe and Anatolia, with a specific focus on whether the Sea of Marmara is a barrier to gene flow

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Population differentiation during the ice ages, followed by range expansions has significantly contributed to the geographic distribution patterns of the genetic diversity in Europe. In this regard, the Iberian, Italian, Balkan peninsulas and Anatolia comprise important glacial refugia. In different parts of Anatolia, suture zones, where lineages that diverged in the different glacial refugia met again, were observed for several species. In this study, we investigated the mitochondrial genetic differentiation of the greater horseshoe bat, *Rhinolophus ferrumequinum* in southeastern Europe and Anatolia. The mitochondrial DNA analyses indicated a suture zone in central Anatolia, similar to those recorded in other animal species, showing the presence of more than one refugium within the region. The time of the split of these lineages that diverged in allopatry was dated to the Pleistocene. However, the location of this suture zone did not coincide with the Sea of Marmara, not supporting a recent hypothesis, based on microsatellite data, which states that this water body might be an impediment to post glacial gene flow in this species.

Key words: Anatolia, Chiroptera, D-loop, ice age, mitochondrial DNA, phylogeography, *Rhinolophus*

Alcathoe bat (*Myotis alcathoe*) in the Czech Republic: distributional status, roosting and feeding ecology

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Between 2001 and 2008, we recorded *Myotis alcathoe* at nine sites within three distant areas in the Czech Republic. The species identification was confirmed with *cyt b* sequences and four distinct haplotypes were identified. All the localities exhibit surprisingly uniform habitat characteristics: (1) old full-grown oak-hornbeam forests, with (2) numerous large trees in advanced stages of decay are present, and (3) a very small to large water bodies and/or patches of riparian vegetation surrounded by the forest. Using radiotracking techniques, we discovered 27 day roosts of *M. alcathoe*, located mostly in big oak, birch and lime trees inside extensive forest stands. All roosts were fissures or small cavities in a tree trunk and in branches in the canopies, some 16 m above the ground. Bats preferred trees that were higher, had higher canopy and canopy basement and had larger diameter at breast height than other available trees. Roost trees were surrounded by lower trees with lower canopy basements than available trees. Roost trees were in a poorer condition than other available trees. Roosts were occupied by up to 83 individuals in July but usually single individuals were found in the roosts in September. In contrast to syntopic *M. mystacinus* and *M. brandtii*, *M. alcathoe* has never been found in an anthropogenic roost (except for a fissure in concrete electricity pole). Preliminary analysis of the diet showed that nematoceran flies were the most important prey item along with spiders, caddis flies, small moths and neuropterans. In the observed ecological characteristics, *M. alcathoe* markedly differs from other European species of the genus *Myotis*. Its restricted habitat requirements are perhaps responsible for an islet-like pattern of its distribution and suggest an essential conservation value of the habitats of its occurrence.

Key words: radio tracking, diet analysis, tree roosts, forest bats, *Myotis alcathoe*

Recent surveys of bats (Mammalia: Chiroptera) from China. I. Rhinolophidae and Hipposideridae

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We conducted surveys of bats in China between 1999 and 2007, resulting in the identification of at least 62 species. In this paper we present data on 19 species, comprising 12 species from the family Rhinolophidae and seven from the Hipposideridae. Rhinolophids captured were *Rhinolophus affinis*, *R. ferrumequinum*, *R. lepidus*, *R. luctus*, *R. macrotis*, *R. siamensis*, *R. marshalli*, *R. rex*, *R. pearsonii*, *R. pusillus*, *R. sinicus* and *R. stheno*. Because of extensive morphological similarities we question the species distinctiveness of *R. osgoodi* (may be conspecific with *R. lepidus*), *R. paradoxolophus* (which may best be treated as a subspecies of *R. rex*), *R. huananus* (probably synonymous with *R. siamensis*), and we are skeptical as to whether *R. sinicus* is distinct from *R. thomasi*. Hipposiderids captured were *Hipposideros armiger*, *H. cineraceus*, *H. larvatus*, *H. pomona*, *H. pratti*, *Aselliscus stoliczkanus* and *Coelops frithii*. Of these species, two rhinolophids (*Rhinolophus marshalli* and *R. stheno*) and one hipposiderid (*Hipposideros cineraceus*) represent new species records for China. We present data on species' ranges, morphology and echolocation call frequencies, as well as some notes on ecology and conservation status. China hosts a considerable diversity of rhinolophid and hipposiderid bats, yet threats to their habitats and populations are substantial.

Key words: Chiroptera, distribution, ecology, echolocation, morphology, China, new records

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The reproductive biology of the cave myotis (*Myotis velifer*)

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This study examines the anatomical structure, function and seasonal cyclicality of the male and female reproductive organs of the cave myotis (*Myotis velifer*) in Texas and southern Arizona. The data indicated that this is a monestrous, seasonally breeding species that stores spermatozoa in both sexes during extended winter torpor or hibernation. The male reproductive cycle was characterized by asynchronous function of the testes (spermatogenesis) and accessory sex organs. Structural factors in both sexes and fructose levels in male accessory organs were evaluated for their significance in prolonged spermatozoa storage. The reproductive anatomy and chronology were similar to other temperate-dwelling vespertilionid bats. Dextral dominance was a feature of the female reproductive tract.

Key words: *Myotis velifer*, testes, accessory sex glands, ovary, corpus luteum, spermatozoa storage, epididymis, fructose

Postnatal growth and age estimation in big-footed myotis, *Myotis macrodactylus*

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We quantified the length of the forearm, the body mass and the length of the total gap of the fourth metacarpal-phalangeal joint of marked individuals of big-footed myotis bats (*Myotis macrodactylus*) from birth to flight in Dalazi Cave in Ji'an, Jilin Province, China. By using these data, we develop empirical growth curves, derive growth rates, establish age-predictive equations, and compare growth parameters based on three nonlinear growth models. Neonates of *M. macrodactylus* were born within a half-month period, with length of forearm averaging ca. 38.4% of the size of adult females and body mass averaging ca. 39.6% of their mother's body mass. Length of forearm increased linearly until 14 days after birth (growth rate = 1.20 mm/day), as did body mass until 11 days after birth (growth rate = 0.32 g/day). The length of the total gap of the fourth metacarpal-phalangeal joint decreased linearly from 13 days to 45 days of birth. Two most appropriate linear regression equations predicting the age of young bats were derived from forearm length ($\bar{x} \pm \text{SE}$) from 15.35 ± 0.96 mm to 33.24 ± 1.87 mm and the length of the epiphyseal gap from 13 to 45 days. These two equations make it possible to estimate the age of pups from 1 to 45 days of age in *M. macrodactylus*. Of the three nonlinear growth models (logistic, Gompertz, and von Bertalanffy), the logistic equation provides the best fit to the empirical curves for length of forearm and body mass.

Key words: *Myotis macrodactylus*, postnatal growth, age equations, nonlinear growth models

Skull morphology of two cryptic bat species: *Pipistrellus pipistrellus* and *P. pygmaeus* — a 3D geometric morphometrics approach with landmark reconstruction

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Differences in skull morphology between two cryptic species of bat, *Pipistrellus pipistrellus* ($n = 14$) and *P. pygmaeus* ($n = 15$), originating from Great Britain, were investigated. Four different data sets were analysed: (1) 23 landmarks and (2) 26 landmarks on the dorsal and ventral sides of the cranium, respectively, (3) 49 landmarks on the upper jaw, and (4) 34 landmarks on the labial side of the mandible. For almost all data sets, when compared within sex groups, *P. pipistrellus* were significantly larger than *P. pygmaeus*; the biggest difference being observed in the mandible size. Interspecific differences in shape, analysed by Principal Component Analysis and Discriminant Function Analysis (DFA) of the Procrustes superimposed landmarks, were also mostly visible in the mandible, and were related to dietary differences between the species. For example, the longer and more upright canines of *P. pipistrellus* allow them to pierce harder prey, the bigger molars ease its processing, and the shortened body of the mandible and the more developed coronoid process presumably generate a stronger bite. The shape and size of the mandible proved to be a good characteristic for distinguishing both cryptic taxa. A procedure for estimating missing landmarks for 3D geometric morphometric purposes was created. Our procedure of finding the missing landmarks had no effect on the within-group loss of variation. DFA of data sets with reconstructed versus original (but reduced) landmarks yielded similar results (three versus two misclassified specimens in leave-one-out cross-validation).

Key words: geometric morphometrics, skull morphology, diet, cryptic species, *Pipistrellus* spp., landmark reconstruction

Designing effective habitat studies: quantifying multiple sources of variability in bat activity

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Common aims of habitat studies are to differentiate between (i) suitable and unsuitable sites for a given species, and (ii) sites used by different communities of species. To quantify differences between sites, field data of site use must be precise enough that true underlying between-site variability is not masked by within-site measurement error. We designed a pilot study to guide the development of a survey protocol for a habitat study on bats in an agricultural landscape in southeastern Australia. Three woodland sites and two scattered tree sites of 2 ha each were surveyed for nine consecutive nights. At three locations within each site (spaced > 50 m apart) one or two Anabat detectors were mounted 1 m above ground or in a tree (2 m above ground). We used mixed regression models to quantify multiple sources of variability in bat calling activity, and graphical data analysis to visualise how increases in survey effort were likely to affect inference. For the five most active species, we found that typically over 40% of variability in nightly detections occurred at the between-site level; approximately 10% occurred between locations within sites; approximately 20% was explained by night-to-night differences; and approximately 30% of variability was not attributable to systematic variation within experimental units. Differences in community composition between sites were clearly evident when two or more detectors per site were used for four or more nights. We conclude with six general considerations for the design of effective habitat studies. These are to (i) consider key contrasts of interest; (ii) use data from mild, calm, dry nights only; (iii) calibrate detectors; (iv) use multiple detectors where possible, or move a single detector within a site; (v) survey for multiple nights; and (vi) where vertical differentiation in habitat use is likely, mount detectors at different heights. These considerations need to be balanced within the context of financial and logistical constraints.

Key words: Anabat detectors, survey effort, southeastern Australia, scattered trees, paddock trees, woodlands, bats

Insectivorous bat activity at cenotes in the Yucatan Peninsula, Mexico

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The behaviour and habitat associations of aerial insectivorous bats are poorly understood despite constituting up to 65% of bat species in the Neotropics. In 2003, 2004 and 2005 we quantified the activity of insectivorous bats and their insect prey at pastureland and forest sites with and without cenotes (water-filled sinkholes) in the Yucatan Peninsula, Mexico. We used a time-expansion bat detector to survey each habitat for 24 nights and analysed 2,880 one-minute recorded sequences to determine bat activity. We identified 14 species and five phonic types belonging to four families. Bat activity and the average number of bat species acoustically sampled each night were significantly greater in habitats with cenotes than in those without. *Pteronotus personatus* and an unidentified molossid were recorded exclusively at cenotes. *Peropteryx macrotis* showed the highest activity of all bat species. In all habitats insects were more abundant during the rainy season but only in pastureland was bat activity significantly greater during the rainy season. Insect abundance was correlated with bat activity only at cenotes in pastureland. Cenotes are important foraging habitats for insectivorous bats as 16 species, 84% of those revealed by this study, were recorded feeding in these habitats and the number of feeding buzzes was higher in comparison to habitats without cenotes. Protection of cenotes and their surrounding vegetation should be a management priority in order to conserve the high diversity of insectivorous bats associated with these distinctive habitats.

Key words: Chiroptera, echolocation, insects, pastureland, time-expansion, water resources, Mexico

Habitat selection in *Nathusius' pipistrelle (Pipistrellus nathusii)*: the importance of wetlands

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Wetlands are internationally recognized as a crucial habitat type for the conservation of many migratory birds. Despite the fact that many bats are also long-distant migrants, the importance of foraging habitats for sustaining migrant bats has to date received little attention. We analyzed habitat selection patterns in the migrant bat, *Nathusius' pipistrelle* *Pipistrellus nathusii*, in the southernmost part of its range (Iberian Peninsula), an area in which both mating and hibernation occur. We found that natural wetlands and riparian habitats (*Phragmites* reed beds) were positively selected, whereas human-transformed aquatic habitats (rice paddies) were avoided. Although semi-natural human-managed wetlands are perceived as being valuable for many species, our data emphasizes the importance of preserving natural wetlands (including riparian forests) as appropriate habitats for sustaining crucial phases of the life cycle of this bat. Agricultural transformation of the land is likely to be detrimental to this species since it reduces the availability of its preferred foraging habitat.

Key words: *Pipistrellus nathusii*, habitat selection, wetlands, conservation, migrant, mating

Host-parasite interactions of tropical bats in Puerto Rico

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Bats are receiving increasing attention in the parasitological world due to their potential role as reservoir hosts for zoonotic pathogens. However, details of the macroparasitic fauna (helminths and ectoparasites) are currently recorded and studied. Here, we start to address this paucity of data by detailing a study where we have documented the macroparasite fauna of a sample of tropical bats (*Mormoops blainvillei*, *Pteronotus quadridens*, and *Monophyllus redmani*) from Puerto Rico. Additionally, we investigated the possible host characteristics influencing the prevalence and intensity of macroparasite infection. Macroparasites were collected and identified from three species of bat, which were thoroughly washed and dissected. The overall parasite community of all three bat species consisted of a range of ectoparasites as well as the cestode *Vampirolepis christensoni* and the nematode *Capillaria pusilla*, although there was considerable variation in the parasite community of each individual species. We discovered bat flies of a previously undescribed species of the *Nycterophilia* genus as well as new parasite records for all three species of bats. All parasites had an aggregated distribution within the host population. Differences were observed in the intensity of the helminths between bat species, but not for ectoparasite prevalence. As the helminth intensity increased so the ectoparasite intensity decreased. Overall, the helminth intensity was female-biased and increased, for both sexes with increasing body mass; no sex-bias or body mass effects were associated with ectoparasite prevalence.

Key words: *Mormoops blainvillei*, *Pteronotus quadridens*, *Monophyllus redmani*, macroparasites, parasite infection, tropical bats, Puerto Rico, Caribbean

Group-specific signatures in the echolocation calls of female little brown bats (*Myotis lucifugus*) are not an artefact of clutter at the roost entrance

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In species where conspecifics form discrete social groups, the production of signals advertising group membership may promote cohesion among group members. Female little brown bats (*Myotis lucifugus*) show high fidelity to maternity roost sites where they aggregate in large numbers every spring to rear young. While the presence of group-specific signatures has been demonstrated in the echolocation calls of this species, differential clutter at recording sites may account for the observed differences. Bats optimize their ability to maneuver and detect prey within a given environment by tailoring their echolocation calls to physical attributes of that environment. Therefore, if clutter is responsible for the apparent group specificity in the calls of little brown bats, groups of bats experiencing similar levels of clutter at roost entrances should emit similar calls. We examined the effect of differential clutter on the emergence calls of *M. lucifugus* by comparing recorded echolocation calls of bats emerging from three maternity roosts in Georgian Bay, Ontario. The roosts varied in distance from each other and in their proximity to surrounding clutter. The more distant group emerged in an environment with clutter deemed intermediate to the two more proximate roost entrances and yet was the most acoustically distinct. The finding that similarity among emergence calls correlated better with spatial proximity than with the level of clutter around roost entrances is consistent with the development of true group-specific signatures in the emergence calls of *M. lucifugus*.

Key words: *Myotis lucifugus*, echolocation, group signature, clutter, emergence call

Functions of bat social calls: the influence of local abundance, interspecific interactions and season on the production of pipistrelle (*Pipistrellus pipistrellus*) type D social calls

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We studied the social call rate of the common pipistrelle (*Pipistrellus pipistrellus*) in natural habitats in relation to the presence or absence of conspecifics and of other bat species by acoustical and behavioural monitoring and analyses. The relative frequency of type D social calls increased, when more than one individual of *P. pipistrellus* was present, compared to one individual. The data confirm the assumption that one function of social calls is repelling conspecifics (food patch defence hypothesis). In the presence of other species of the genus *Pipistrellus* or of other genera, the mean social call rate did not significantly increase, except when *P. pygmaeus* was present. Hence, social call production as a food patch defence typically is not significantly influenced by interspecific interactions. This directs to niche separation concerning the foraging mode of different species. The closely related species *P. pipistrellus* and *P. pygmaeus* may compete for resources and communicate by type D social calls. Pipistrelles are known to use a series of type D social calls during songflights. For instance, males use this calling behaviour to attract females and repel competing males. During the mating season *P. pipistrellus* produced social calls more frequently when other pipistrelle species were absent. This shows that interspecific recognition may influence the mating behaviour of *P. pipistrellus*. Competing for non-food resources like mating roosts may cause bats to keep calm in the presence of other species.

Key words: acoustic communication, competition, interspecific interaction, *Pipistrellus*, social calls

Echolocation calls of bats from Madeira Island: acoustic characterization and implications for surveys

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Acoustic surveys represent a powerful tool to assess bat distribution and habitat preferences and are widely applicable to monitoring and conservation schemes. However, their correct application requires the development of robust and reliable identification procedures. Little information is available on the bats of Madeira Island (Portugal), particularly their ecological requirements, distribution and population trends, and proper guidelines for their monitoring and conservation have yet to be defined. In this study, we present the first analysis of echolocation calls from species occurring on the island to provide a tool for bat identification during acoustic surveys. Seven hundred and ninety one time-expanded recordings of search phase echolocation calls in cluttered and uncluttered habitats of the Macaronesia endemic pipistrelle *Pipistrellus maderensis*, Madeira Leisler's bat *Nyctalus leisleri verrucosus* and grey long-eared bat *Plecotus austriacus* were analysed and an acoustic repertoire with their temporal and spectral features is described. *Pipistrellus maderensis* was easily identified based only on peak frequency while *Plecotus austriacus* and *N. leisleri verrucosus* showed frequency overlap in cluttered backgrounds. Discriminant function analysis was applied to calls of *Plecotus austriacus* and *N. l. verrucosus* resulting in a correct overall classification of 96.7% of calls, with a function based on start frequency, end frequency, duration and interpulse interval. This work provides the first description of *Pipistrellus maderensis* and *N. l. verrucosus* echolocation calls and offers a basis for future bat surveys in order to encourage the development of locally customized conservation strategies.

Key words: bat detector, echolocation, *Pipistrellus maderensis*, *Nyctalus leisleri*, *Plecotus austriacus*, Madeira Archipelago

Detecting bat calls: an analysis of automated methods

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Long-term and large-scale acoustic surveys of bats have become possible with the increased availability of recording hardware and advances in battery and memory storage technologies. The volume of data generated in surveys necessitates automated call detection, either in real time via a triggering function or offline, yet researchers are hesitant to replace traditional hand analysis without a thorough understanding of the accuracy and costs of automated detection. We compared detection accuracy and computational cost of the underlying algorithms used in commercial detectors (a zero-crossing detector, a spectral peak detector, and a high-band energy detector) with a model-based analysis method called the links detector. We predicted that the links detector would be more accurate than the other detectors, producing a larger effective detection range, because the links detector uses more information to make detection decisions. We also predicted that the links detector would be the most computationally expensive algorithm because of the processing needed for the extra information. We quantified the performance of the detectors using a synthetic recording environment, which provided an absolute ground truth for the experiments and allowed us to measure the effective detection range of each algorithm. The zero-crossing and high-band energy detectors, the fastest, were about 40 times faster than the links detector. Most of the computational cost was attributed to the filter used to remove low-frequency noise. The links detector, the most accurate, increased effective detection range by 6–12 m compared to the other detectors depending on species. The results will allow bat researchers to better understand the costs and benefits of automated detection methods.

Key words: Chiroptera, automated detection, synthetic recording environment, links detector

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SHORT NOTES

Selection of timber mortises in a church roof by *Pipistrellus* sp. at 52°N

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Key words: roost selection, hibernation, synanthropy

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SHORT NOTES

**Remaining cryptic during motion — behavioral synchrony in the proboscis bat
(*Rhynchonycteris naso*)**

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Key words: Rhynchonycteris naso, cryptic roosting, behavioral adaptation, synchronous rocking, grooming, urinating

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SHORT NOTES

A strange tale of taillessness in a vespertilionid bat

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Key words: taillessness, Vespertilionidae, individual foraging strategy, fitness, evolution, Phyllostomidae

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SHORT NOTES

Negative consequences of forearm bands that are too small for bats

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Key words: marking methods, ringing, population dynamics, Vespertilionidae, *Nyctalus leisleri*

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SHORT NOTES

Healing rates of wing punch wounds in free-ranging little brown myotis (*Myotis lucifugus*)

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Key words: Chiroptera, energy balance, immune function, *Myotis lucifugus*, wing biopsy, wing damage, wound healing