Multiplexed sequencing files and bioinformatic pipeline for “**Advanced airborne eDNA sampling allows robust spatiotemporal characterisation of vertebrate communities”**

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Running title: Optimised air eDNA sampling for vertebrate surveys

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**Summary**

This folder includes the r scripts and datafiles use to analyse vertebrate communities detected with airborne eDNA at three different experiments and three nature areas in Denmark. At each nature area vertebrate communities were sequenced using two primer sets:16Smam (a primer pair targeting mitochondrial 16S region of mammals with an appx. 90 bp amplicon size) and BirT (a primer pair targeting the mitochondrial 12S region of birds with an appx. 260 bp amplicon length). Data from each primer set was analysed separately.

**Files and descriptions**

* Each folder contains r scripts and data belonging to the three main experiments of the project: Experiment 1 (KalvebodeFællede), Experiment 2 (Æbelø) and Experiment 3 (Lille Vildmose).
* Within each Experiment folder there are two folders dedicated for each of the metabarcoding primers used in the study (16S mam and BirT).
* In these folders there are r scripts and data files used for analyses.