was likely to occur. This map shows areas of coincidence of 9 models of most models (Phillips et al. 2017) as a logistic threshold to extract all areas where each species occurring in any cell. We used the value 0.3 approximating the 10 percentile training presence value data table. Models return values ranging from 0 to 1 representing the likelihood of a species the sum of models for seven species using recent records together with all environmental and projection is best suited for measuring areas and distances at a continent scale. This map shows continent and Arabian Peninsula plus offshore islands at exactly 1km² resolution. We projected all relevant to vultures. In total 97 such datasets were created or refined to span the entire African update environmental datasets and introduce new anthropogenic datasets that would be ecologically used another output of the ARDB to help identify habitat strongholds for African vultures notably in

**METHODS:**

used another output of the ARDB to help identify habitat strongholds for African vultures notably in areas not visited by observers. Distribution models were developed by the ARDB and refined for this project on African vultures using Maxent software (Phillips et al. 2017). Special efforts were made to update environmental datasets and introduce new anthropogenic datasets that would be ecologically relevant to vultures. In total 97 such datasets were created or refined to span the entire African continent and Arabian Peninsula plus offshore islands at exactly 1km² resolution. We projected all data into Lambert Azimuth Equal Area projection using 20 degrees as the central meridian. This map shows the sum of models for seven species using recent records together with all environmental and anthropogenic datasets To overcome sampling bias we developed an observer bias dataset by buffering 10km around all the records in the database and around all the roads driven in the surveys data table. Models return values ranging from 0 to 1 representing the likelihood of a species occurring in any cell. We used the value 0.3 approximating the 10 percentile training presence value of most models (Phillips et al. 2017) as a logistic threshold to extract all areas where each species was likely to occur. This map shows areas of coincidence of 9 models.

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