**NatureCounts Dataset Metadata Survey**

**\*Dataset Name**: Canadian Seabird Colony Monitoring Program

**\*Year Started**: Variable, depending on species and colony. Generally 1970 or later.

**\*Year Ended**: Ongoing.

**\*Season and Frequency:** Annually during the breeding season.

**\*Dataset Summary**: Dataset includes model-based indices of regional abundance for colonial seabirds in each of three regions of Canada (Atlantic, Pacific, Arctic).

**\*Goals:** Estimate the status and trend of Canadian colonial seabird populations.

**\*Geographic area covered:** Atlantic, Pacific, and Arctic Canada.

**\*Primary species covered:**

Atlantic Species: Atlantic Puffin, Black-legged Kittiwake, Common Murre, Double-crested Cormorant, Great Black-backed Gull, Great Cormorant, Herring Gull, Leach’s Storm-Petrel, Northern Gannet, Razorbill, Ring-billed Gull

Pacific species: Ancient Murrelet, Cassin’s Auklet, Rhinocerous Auklet, Tufted Puffin

Arctic species: Black-legged Kittiwake, Northern Fulmar, Thick-billed Murre

**\*Field Methods:**

Islands that support large colonies of breeding seabirds are surveyed periodically to provide trend information, though the revisit schedule and field methodologies applied on individual islands vary.

For surface-nesting species (e.g., gannets, cormorants, gulls, kittiwakes, murres) counts of the entire colony were often made directly from the ground, aerial surveys, or photographs.

On large islands where a direct count is not possible, and for burrow-nesting species, a sample of permanent monitoring plots were established on a grid across the extent of the colony. For burrow-nesting species, burrow entrances were counted within monitoring plots and a sample of those were inspected to determine occupancy. Nest densities were then calculated as the product of burrows x occupancy. Total abundance was calculated as the product of nest density and total colony area (estimated by field crews on the island).

**Analytical methods:**

The analysis estimates colony- and regional-level population trajectories using Bayesian hierarchical state-space models. These models decompose spatio-temporal variation in seabird counts into contributions from biological processes of interest (i.e., temporal changes in colony-level population indices) and observation processes (i.e., variation due to imprecision in survey counts). The model includes a GAM structure for the biological process, allowing for smooth and non-linear colony trajectories over time. The model also weights colonies in proportion to their relative abundance in regional summaries; larger colonies have a larger influence on regional trajectories than smaller colonies.

We analyzed data separately for each of three regions in Canada (Atlantic, Pacific, and Arctic Canada).

Analysis was conducted in R, and stored at <https://github.com/davidiles/Status_of_Birds_seabird_analysis_2023>