# USE OF HARVEST DERIVATION TECHNIQUES IN GOOSE MANAGEMENT

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**Abstract:** Three genera of North American geese (*Anser, Branta, Chen*) are divided into 7 species, 19 subspecies, and 34 populations for management purposes. Harvest is often an important source of adult mortality in geese, and population-specific management allows for greater flexibility and control of hunting regulations across a species' geographic range. Population designations are often based on relatively discrete nesting and/or wintering distributions of a group of geese within a subspecies. However, populations that are not easily distinguishable often overlap geographically during some portions of the annual cycle. This can greatly complicate harvest management, particularly when management objectives differ among closely related populations. Population-specific harvest monitoring requires that harvested birds from these populations can be differentiated from one another. Several techniques have been developed to accomplish this, each having their own limitations, and mainly have been used to estimate harvest composition in areas with multiple sympatric populations. In addition, harvest derivation techniques have been used in assessing relative vulnerability of different populations to harvest, in evaluations of the effectiveness of regulation changes, and in identification of molt migrants during banding operations on northern nesting areas. Future changes in size and distribution of goose populations will likely increase the need for accurate harvest derivation techniques.

**WHAT INFORMATION CAN WATERFOWL PARTS COLLECTION SURVEYS PROVIDE FOR GOOSE RESEARCH AND MANAGEMENT?**

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**Abstract:** For several decades, U. S. and Canadian hunters participating in waterfowl parts collection surveys have provided managers with tail fans from the geese they harvested. These surveys were initially designed to provide species and age composition data derived directly from the tail fans, as well as temporal and geographic distribution data reported by the hunters who submitted the tail fans. Combining these data with estimates of total goose harvest derived from annual questionnaire surveys yields species-specific harvest estimates at the flyway, state and county levels, and/or estimates for early, regular and late seasons. In the U. S., we recently began collecting goose primary feather tips in addition to tail fans, to improve our ability to age geese accurately. The Canadian Wildlife Service and the Mississippi, Central and Pacific Flyways in the U. S. also measure Canada goose (*Branta canadensis*) tail feathers to classify the birds according to size. Along with harvest location data, the tail measurement can be used to identify the subspecies/population of the bird, thereby providing subspecific/population harvest estimates. This enables managers to refine their harvest management regimes for key Canada goose populations. Waterfowl parts collection surveys can also provide researchers with large biological samples of goose feathers, along with reliable harvest location and date data, to help determine harvest derivation.

# CREATING AND APPLYING STANDARDIZED GENETIC DATA SETS FOR NATURAL RESOURCE MANAGEMENT: INSIGHTS AND LESSONS FROM THE PACIFIC SALMON EXPERIENCE

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**Abstract**: Population genetic approaches can provide high resolution, cost effective data for discriminating different breeding populations and accurately estimating their contributions to mixed commercial and sport harvests. However, large-scale regional harvest management and conservation programs require the integrated contributions of multiple agencies and laboratories because harvests/impacts: often impact stocks of diverse geographic origins, often span political/national jurisdictions, and are often co-managed by multiple agencies. An informal consortium of genetics labs has worked to develop regional, coast-wide, and Pacific Rim fishery management and conservation approaches for Pacific salmon and other salmonids since 1986. Initial efforts involving up to six laboratories resulted in large, standardized allozyme data sets and mixed-fishery analyses for Chinook (254 populations, 45 loci), chum (273 populations, 20 loci), pink (175 populations, 10 loci), and sockeye salmon (165 populations, 14 loci) and for steelhead (103 populations, 42 loci). Current initiatives are focused on developing microsatellite DNA approaches for Chinook salmon (105 – 250 populations, 15 loci) as well as other species such as sockeye, coho, chum, and bull trout. Because the information content of shared databases is determined by the weakest contributions, inter-lab differences in procedures, instrumentation, infrastructure, and philosophy can limit both power and resolution. Building a large, multi-lab, standardized database is time consuming, expensive, and challenging. Keys to successful genetic approaches include: clearly defined goals and objectives, buy-in by all relevant agencies and laboratories, adequate and representative sampling of baseline populations and mixtures, an agreed-to suite of core loci to be screened, consistent and objective methods of genotyping/allele binning, QA/QC procedures to evaluate and promote data comparability across labs and over time, standardized statistical methods for baseline creation and mixture analysis, and open sharing of methods and data among labs. Flexibility and compromise in the interest of adopting the best approaches and building consensus are essential to success.

# MORPHOLOGY AND PLUMAGE AS A BASIS FOR SUBSPECIFIC AND POPULATION DISCRIMINATION

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**Abstract:** Phenotypic characteristics have been widely used to discern the breeding origins of harvested geese in admixed migration or winter groups. We review measurement and analysis of geographic variation in anserine morphology and plumage, and discuss how phenotypic characteristics have been used to assess harvest composition. Critical assumptions of such programs are that phenotypic measurements on nesting areas are representative of local populations, and that measurements on harvest areas are adequate to discern breeding origin. Potential sources of error include the presence of molt migrants on nesting areas, undetected clinal variation, hybridization, environmental plasticity in growth, and observer variability in measurements. We discuss in detail geographic variation in morphology and plumage of Pacific Flyway Canada geese and the use of phenotypic characteristics to assess composition of harvest in western Oregon and southwest Washington.

# METHODS FOR ESTIMATING DERIVATION OF HARVEST BASED ON MARKED INDIVIDUALS

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**Abstract**: Derivation of the harvest refers to the proportional composition of a specific harvest (e.g., from some specified area of interest) with respect to different source areas (e.g., breeding ground areas). The estimation problem is thus one of trying to estimate the multinomial probabilities of a bird in the harvest of area *a* originating from source areas *b*, *c*, etc. Estimators for these probabilities can be obtained using band recovery data from multiple breeding ground areas. These estimators can be obtained using either traditional capture-recapture thinking or a Bayesian approach. Derivation can also be estimated using a reverse-time capture-recapture approach. We consider recently-developed combination methods that permit estimation using marked animals combined with data on isotopic or genetic signatures that provide additional information about breeding ground origin. Initial models have been based on the assumption of unambiguous signature data, but we show how to develop models permitting misclassification as well. Finally, we emphasize the importance to derivation analyses of abundance information on the breeding ground or source areas.

# USING STABLE ISOTOPE MEASUREMENTS OF FEATHERS TO DETERMINE ORIGIN OF MOLT IN NORTH AMERICAN GEESE: A REVIEW AND IMPLICATIONS FOR MANAGEMENT

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**Abstract:** The measurement of naturally occurring isotopes of several elements in bird feathers can yield information on the origin and foodweb associated with feather growth. For example, the measurement of carbon and nitrogen stable isotopes ($\delta^{13}C$ and $\delta^{15}N$) can readily distinguish between terrestrial and marine or boreal vs. grassland biomes and deuterium ($\delta D$) measurements can reveal approximate latitude of origin across most of the North American continent. In combination, stable isotope measurements of feathers and other tissues can potentially be used to evaluate structure in goose populations and so provide an important new tool in goose harvest management. In this paper I will review the basic principles of isotopic tracking of wildlife and evaluate specific applications to North American goose management issues. Examples from other species groups will include recent analyses of Sandhill Cranes from the Central Flyway and Lesser Scaup from all major flyways. Emphasis will be placed on consideration of both advantages and disadvantages of the stable isotope approach as a fingerprinting tool.

# ESTIMATING POPULATION COMPOSITION OF MIXED HARVESTS AND INDIVIDUALS' SOURCES FROM THEIR TRAITS

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**Abstracts:** Many species of animals, including waterfowl, are comprised of populations that are separated geographically at breeding and have limited genetic exchange. However, their members migrate from the breeding grounds to places where the populations mix. Estimation of the population composition of such mixtures and of the source identities of mixture individuals may be invaluable for scientific studies. In particular, if the species is harvested when occurring in the mixtures, the estimation is vital for management to sustain the separate populations. Traits of the mixture individuals, such as dimensions of their body parts, chemical composition of hard structures and growth patterns on them, or better, their genotypes at multiple loci, can be used for the estimation when the character distributions vary among the populations. The main area of application has been in Pacific salmon fisheries where development of the technique has matured. A review is provided of statistical models and estimation methods, and these are illustrated by applications to genetic microsatellite samples of breeding populations of Richardson's (*B. h. hutchinsii*, *n* = 1), interior (*B. c. interior, n* = 4), and giant (*B. c. maxima, n* = 8) Canada geese (total *n* = 964 individuals).

# MACHINE LEARNING METHODS OF INDIVIDUAL CLASSIFICATION BASED ON CONTINUOUS AND DISCRETE DATA

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**Abstract**: Classification is a fundamental activity in systematic biology and has many applications in management of wildlife populations. Classification is performed by measuring traits that occur in different states for different individuals. Classification methods used in machine learning (e.g., artificial neural networks, decision trees, and k-nearest neighbor clustering) are rarely used in avian studies. Using simulated and empirical data representing a wide range of inter-group variance in discrete genetic and continuous morphological characters, we compared different nonparametric machine learning techniques with parametric likelihood and multivariate Gaussian models for purposes of assigning individuals to their population of origin. For genetics data, classification error rates associated with likelihood and neural network classifiers were consistently lower that k-nearest neighbor and decision tree classifiers. The relative performance of each machine learning classifier improved relative to likelihood estimations, suggesting an ability to "learn" and utilize properties of empirical genetic arrays intrinsic to each group. Using morphological data from mid-continent Canada geese (*Branta canadensis interior and B. c. maxima*) k-nearest neighbor, decision trees, and multivariate Gaussian classifiers consistently outperformed univariate and standard multivariate methods. The utility of machine learning methods are discussed in light of known variance across North American goose species, subspecies, and geographic populations.

## INTRA-SPECIFIC PHENOTYPIC AND GENETIC VARIATION IN GREATER WHITE-FRONTED GEESE: POPULATION, FLYWAY, AND CONTINENTAL VARIATION

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**Abstract:** Greater white-fronted geese (*Anser albifrons*) in North America breed nearly continuously across tundra and boreal forest habitats from the Yukon-Kuskokwim Delta and Seward Peninsula in western Alaska to the western shore of northern Hudson Bay. They are currently managed according to flyway boundaries with geese breeding south and west of the Alaska Range in Alaska migrating down the Pacific Flyway, and geese breeding elsewhere in Alaska and across Canada constituting the mid-continent population that migrates down the Central and Mississippi Flyways. All white-fronts within each flyway are generally accorded the same management status, despite analyses of leg-band data identifying within-flyway population differences in migration behavior, distribution, and survival rates. Discrimination among white-front populations has proven difficult because of continuously varying phenotypic traits among sympatric-wintering birds. Implementation of population-specific management practices, particularly as they may relate to harvest of admixed wintering populations, necessitates recognition of population-specific identifiers, no matter the nature of the marker. We present information on phenotypic variation of greater white-fronted geese from across their breeding range in North America, and compare our findings with similar data from Palearctic populations. Genetics data is also presented for geese from 6 breeding areas representing populations from two flyways in North America, as well as Asia and Greenland. Genetics data include information (12 - 30 individuals per population) from mitochondrial DNA (400-600 base pairs of control region and the cytochrome B gene), intron 7 of the nucelar beta fibrinogen gene (307 base pairs) and 7 nuclear microsatellite loci. We interpret our findings relative to individual movement data and potential gene flow, surmised from 5 decades of leg band recovery data.

# VARIATION IN SNOW AND ROSS'S GEESE AT SPECIES, SUBSPECIES AND POPULATION LEVELS ACROSS NORTH AMERICA

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**Abstract:** White geese in the genus Chen (*Chen caerulescens and C. rossii*) are among the most numerous species of waterfowl. These species breed across large and discontinuous segments of tundra habitat from Wrangel Island in northeastern Russia to Greenland. Two species and three subspecies are recognized and multiple populations have snow geese have been identified for purposes of management. The abundance and breeding and wintering distributions of Ross's geese and blue and white color phases of lesser snow geese have changed considerably in recent years. Morphological similarity and mixing of Ross's geese with lesser snow geese in western and central North America are impediments to single-species and population-specific management. We highlight background on migration and changes in abundance and distribution in light of known information on phenotypic and genetic differentiation at subspecies and population levels.

**PHENOTYPIC AND GENETIC VARIATION IN NEARCTIC BREEDING BRANT: ASSESSMENT OF MARKERS FOR ADMIXTURE ANALYSIS**

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**Abstract:** Brant (*Branta bernicla*) in North America breed nearly continuously across coastal habitats from the Yukon-Kuskokwim Delta in Alaska to the western shore of northern Ellesmere Island. They are currently managed according to subspecific or stock designations. Brant geese breeding in Alaska, northeastern Russia, northwestern Canada (Black Brant) and western high arctic (WHA brant) migrate south along the Pacific Flyway to winter in lagoons along the North American Pacific coast. Brant geese breeding in northeastern Canada winter either in Ireland (eastern high arctic brant), or along the Atlantic coast of North America (Atlantic Brant). Band returns suggest WHA brant winter in coastal lagoons along northwestern Washington State, admixing with Black Brant from populations in Alaska and northwestern Canada. Discrimination among brant forming admixed wintering populations is difficult because phenotypic traits vary among sympatric-wintering birds. Population-specific management practices, particularly as they may relate to harvest of admixed wintering populations, would benefit from population-specific markers, regardless of the type of marker used. We present information on phenotypic and genetic variation of brant from across several breeding populations in North America. Genetic data include information (16 - 42 individuals per population) from 400 base pairs of the mitochondrial DNA control region, 12 autosomal, and two z-specific nuclear microsatellite loci, and are compared with similar data from populations in Europe (the Netherlands) and Russia (Lena River Delta). We examine the applicability of these markers for determining the source of individuals in admixed populations, and interpret our findings relative to information from mark-resighting data.

# VARIATION IN CANADA GEESE AT SPECIES, SUBSPECIES, AND POPULATION LEVELS ACROSS NORTH AMERICA

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**Abstract:** Two species and eleven subspecies of Canada geese (*Branta canadensis and B. hutchinsii*) breed across the greatest area and greatest diversity of habitats of any goose species in North America. Canada geese are primarily managed on the basis of winter distribution, following Flyway boundaries. Subspecies and breeding populations are recognized within each Flyway and management is pursued at subspecies and breeding population levels. Subspecies and populations co-occur as mixtures at most times during migration and on wintering areas. Recent harvest management efforts have been directed at increasing rates of mortality of abundant resident large-bodied subspecies and populations while ensuring the viability and diversity of other numerically less abundant northern-breeding migratory groups. To accomplish management goals, there exists a tremendous diversity in plumage, morphology, and genetic characters that provide sufficient variation identify breeding location of origin at many spatial and taxonomic levels prescribed by managers. We describe geographic and taxonomic variation in phenotypic and genetic characters across North America. We discuss the mechanisms that have led to observed diversity, and how successfully characters have been used in harvest derivation.