

***geneGIS*: Computational Tools for Spatial Analyses of DNA Profiles with Associated Photo-Identification and Telemetry Records of Marine Mammals**

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LONG-TERM GOALS

We are developing computational tools for improved visual exploration and spatial analysis of DNA profiles, with accompanying photo-identification records or telemetry tracks of marine mammals. Referred to as *geneGIS*, the computational tools provide the ability to display, browse, select, filter and summarize spatio-temporal relationships of these individual-based records and associated data from molecular markers and ecomarkers (e.g., stable isotopes). A toolbox of software applications allows basic summaries of spatially selected data and export of data in standard tabular and database formats (e.g., XLS, CSV, MDB, KML), as well as specialized formats required for programs commonly used in molecular ecology and capture-mark-recapture. The data format complies with OBIS standards and the database architecture is compatible with the Arc Marine data model, providing a link with other datasets and tools needed for an integrated description of the genetic and environmental ‘seascape’ of cetaceans. We have implemented *geneGIS* as toolboxes in the desktop version of ArcGIS 10.1 and through programmatic enhancements of the web-based *Shepherd Project* using DNA profiles and photo-identification records derived from an ocean-wide survey of humpback whales in the North Pacific (*SPLASH* and *geneSPLASH*). We have recently been granted access to a subset of photo-identification sighting records and associated DNA profiles from the North Atlantic Right Whale Consortium for implementation in *geneGIS*. Spatio-temporal analyses of databases from long-lived, migratory whales will be suitable for informing conceptual models of cetacean populations, including

the Population Consequences of Acoustic Disturbance (PCAD) and the Testing of Spatial Structure Methods (TOSSM).

OBJECTIVES

The overall objectives can be ordered into five tasks (with related subtasks):

- Task 1: Develop database architecture following Arc Marine data model for integration and display of DNA profiles with photo-identification and telemetry records in a stand-alone ArcGIS framework, and enhanced features of a web-based application (*Shepherd Project*) currently designed for display and visual exploration of photo-identification catalogues.
- Task 2: Develop ArcGIS tools for data query, visual exploration and basic statistical summaries for spatial and temporal partitions of individual-based records (DNA profiles, photo-identification records and telemetry tracks).
- Task 3: Enhance user-directed spatial/temporal selection and export of individual-based records for advanced statistical analyses. This will include tools to export data compatible with existing software used for genetic analyses and capture-mark-recapture.
- Task 4: Demonstrate functionality of *geneGIS* and web-based application through importation and integration of existing large-scale datasets of photo-identification records from the Structure of Populations, Levels of Abundance and Status of Humpbacks program in the North Pacific (*SPLASH*) and associated DNA profiles from biopsy samples (*geneSPLASH*).
- Task 5: Prepare a comprehensive user guide for all software functions and analyses implemented in the system.

APPROACH

The computational developments of *geneGIS* follow two approaches: 1) tools within a web-based program for displaying individual identification photographs and information from linked DNA profiles, including a graphical user interface (GUI) through a Google Map interface; and 2) tools within ArcGIS, the most widely available software for GIS and advanced spatial analysis. The intent is to benefit from the strengths of each approach while assuring compatibility and interoperability through a common database architecture and simplified import/export functions.

The web-based approach is being developed under subcontract to Jason Holmberg of the *Shepherd Project*, with support of John Calambokidis and Erin Falcone of Cascadia Research Collective. This approach takes advantage of an existing open-source software framework supporting capture-mark-recapture (CMR) studies of marine megafauna by the *Shepherd Project* (Holmberg *et al.* 2008). This software framework provides a scalable, web-based platform for CMR data management and was selected by Cascadia Research Collective to develop and host the SPLASH photo-identification catalog (available in beta version as <http://www.splashcatalog.org>). With support from the *geneGIS* initiative, the software framework of the *Shepherd Project* has been modified to include DNA profiles, providing a computational environment suitable for integrated studies of molecular ecology and CMR (<http://www.splashcatalog.org/latestgenegis/>).

The ArcGIS approach is being directed by the PI through Oregon State University(OSU), with support from Professor Dawn Wright (on leave from OSU as Esri Chief Scientist), her PhD student at OSU, Dori Dick, her research assistant at Esri, Shaun Walbridge, and members of the Marine Mammal Institute (MMI), including Tomas Follet and Debbie Steel. This approach takes advantage of previous experience with management of a whale telemetry database under the Arc Marine data model (Lord-Castillo *et al.* 2009; Wright *et al.* 2007). With support from the *geneGIS* initiative, we are developing tools to import and visualize spatial distributions and selection of individual identification records, as well as raster-based data extraction from environmental layers available in the ArcGIS environment.

WORK COMPLETED

- 1) Integrated database of photo-identification records and DNA profiles representing the *SPLASH* and *geneSPLASH* project;
- 2) Import/Export functions for individual-based records into ArcGIS (SRGD.csv and Arc Marine) and *Shepherd Project*;
- 3) *geneGIS* tool for spatial selection and comparison in ArcGIS;
- 4) *geneGIS* tools for data extraction from environmental data layers in ArcGIS;
- 5) Implementation of integrated *SPLASH/geneSPLASH* in Java-based, web-accessible database through the *Shepherd Project*; and
- 6) *geneGIS* tools for custom analysis of molecular ecology and Capture-Mark-Recapture (CMR) in the *Shepherd Project*.

RESULTS

Integrated SPLASH/geneSPLASH databases

The *SPLASH* program provided a comprehensive dataset for implementation within ArcGIS and the *Shepherd Project*. At the inception of this project, *SPLASH* existed as relational database in Microsoft Access with eight primary data tables containing effort, photo-identification, and tissue sampling records for humpback whales collected during five seasons of dedicated research effort in the North Pacific. This database and the associated photographic catalogue are maintained by Cascadia Research Collective. The photo-identification dataset was reconciled prior to this grant, to include over 18,400 encounters with 7,941 unique individuals and repeated encounters with individuals could be tracked throughout the database using an identifier known as the *SPLASHID* number (Calambokidis *et al.* 2008).

A total of 5,675 tissue samples (mostly by biopsy darting) were also collected during *SPLASH*, of which about half were associated with a photo-identification encounter. From this total, 2,720 samples were selected for DNA profiling, including a sex marker, mitochondrial (mt) DNA haplotype sequencing and genotyping at 10 microsatellite loci. As expected, the 10 microsatellites were sufficiently variable to provide a second source of individual identification (Constantine *et al.* 2012; Madon *et al.* 2011). From the 2,720 samples, comparison of genotypes resolved 2,161 individuals. Referred to as *geneSPLASH*, the database of DNA profiles (i.e., a ‘DNA register’ DeSalle and Amato 2004) is maintained by the Cetacean Conservation and Genomics Laboratory, MMI, OSU.

As part of the *geneGIS* initiative, these SPLASH photo-identification records and the *geneSPLASH* DNA profiles were integrated into a master *SPLASH/geneSPLASH* database (e.g., Figures 1 and 4). By review and reconciliation of disagreements in the two sources of identification, we were able to correct a small number of errors in both the photographic and genetic datasets (Falcone and Steel, personal communication). The most common sources of discrepancies were errors in sample assignment that occurred in the field, with internal matches in the photographic catalog. In many cases, a detailed review of data linked to the sample (photos, field notes) allowed correct reassignment to another whale in the same group. Where a sample could not be confidently reassigned to another whale, the link between the sample and the whale was removed and the sample was attributed to an unknown individual. Ultimately, all but two known inconsistencies were resolved through this review process.

After the reconciliation, 1,452 of the individuals identified by DNA profiling were also identified by an associated photo-. These identification records were tracked using the original SPLASHID number allowing information from the DNA profiles to be ‘extended’ across multiple photo-identification encounters. For example, the DNA profile associated with a biopsy sample and a photo-identification encounter collected in Hawaii could be extended to the photo-identification records of that individual in southeastern Alaska (e.g., see Figure 4). The remaining 709 individuals identified only by a DNA profile were assigned a new SPLASHID, increasing the total catalog size from 7,941 to 8,651 unique individuals. The fully integrated database of photo-identification records and DNA profiles is one of the largest yet assembled for living whales.

Database architecture and tabular input files

A database architecture has been agreed to accommodate relational data typical of those used in the collection of individual-based records from photo-identification and telemetry, with the associated collection of tissue samples for genetic analyses and ecomarkers. The architecture and nomenclature conform to Arc Marine and [Darwin Core](#) standards (Wieczorek *et al.* 2012; Lord-Castillo *et al.* 2009; Wright *et al.* 2007), where possible, and can accommodate the current databases developed for telemetry data and DNA profiles at MMI and SPLASH records at Cascadia Research Collective.

We have also developed import options for a simplified tabular structure (e.g., SRGD.csv or Excel) similar to that more commonly used in molecular ecology and Capture-Mark-Recapture. The Spatially Referenced Genetic Data format (or SRGD) is a comma-separated file providing for spatio-temporal records of encounters with individuals and associated DNA profiles (Table 1). Additional data fields relating to the encounter or the individual, such as group size, behavioral roles or ecomarkers, can be placed after the primary fields. The intent is to allow an easy entry into ArcGIS and *Shepherd Project* for access to the *geneGIS* tools by import of files that closely matches the existing data formats used in genotyping and photo-identification.

geneGIS in ArcGIS

Data Visualization, Selection and Export Tools

Tool development in ArcGIS has focused on data import (see Figure 1), followed by spatial selection and export to other genetic analyses applications (e.g. GenAlEx and Genepop) (Step 3) via an ArcGIS 10.1 toolbox and a Python Addin GUI. Figure 2 illustrates a *Use Case* for the spatial selection of the reconciled *SPLASH/geneSPLASH* database, to compare differences in mtDNA frequencies for humpback whales sighted in the western Gulf of Alaska and in southeast Alaska, via export to GenAlEx (Peakall and Smouse 2006).

Environmental Data Extraction Tool

Once data are loaded into ArcGIS, the user may want to also add environmental layers (e.g., bathymetry, sea surface temperature) and extract values for each location where an individual was sighted. This information can be used to conduct more advanced spatial analyses and provide an improved understanding on the influence of the environment on the distribution of a species (environmental seascape of cetaceans). Figure 3 illustrates a workflow example of bathymetric data extraction for all *SPLASH* humpback whale encounters during 2004-2006.

Table 1. Required fields, descriptions and data types for the SRGD.csv input file. The fields shown are the minimum recommended data requirements to take advantage of geneGIS tools. Additional fields (e.g., group occurrence, group size, behavior role, ecomarker values) can be included following the required fields.

Field Name	Description	Data Format
Individual_ID	A unique identifier for each individual or sample in your data set	All Integer/All Text
OtherID_1	Optional additional reference number. Provide a brief description in the FieldReference Tab	All Integer/All Text
OtherID_2	Optional. Insert additional columns as needed. Provide a brief description in the FieldReference Tab	All Integer/All Text
Date	Optional. Date of sample, if known.	mm/dd/yyyy
Time	Optional. Time sample taken, if known.	hh:mm:ss
Area	Optional. General region , e.g., Mexico, Oregon	Text
Sub_Area	Optional. Specific area, e.g., Socorro, Newport	Text
Latitude	Latitude of sample in decimal degrees (e.g., 12.8006)	Double/Floating Point
Longitude	Longitude of sample in decimal degrees (e.g., -120.8570)	Double/Floating Point
Sex	Optional. Sex of the individual, if known	Text
Haplotype	Optional. Mitochondrial haplotype of the individual, if known. Provide a brief description in the FieldReference Tab	Text
Locus1_A1	Allele name 1 of Locus 1. Provide a brief description in the FieldReference tab	All Integer/All Text
Locus1_A2	Allele name 2 of Locus 1.	All Integer/All Text
Locus2_A1	Allele name 1 of Locus 2.	All Integer/All Text
Locus2_A2	Allele name 2 of Locus 2. Add as many as you need.	All Integer/All Text

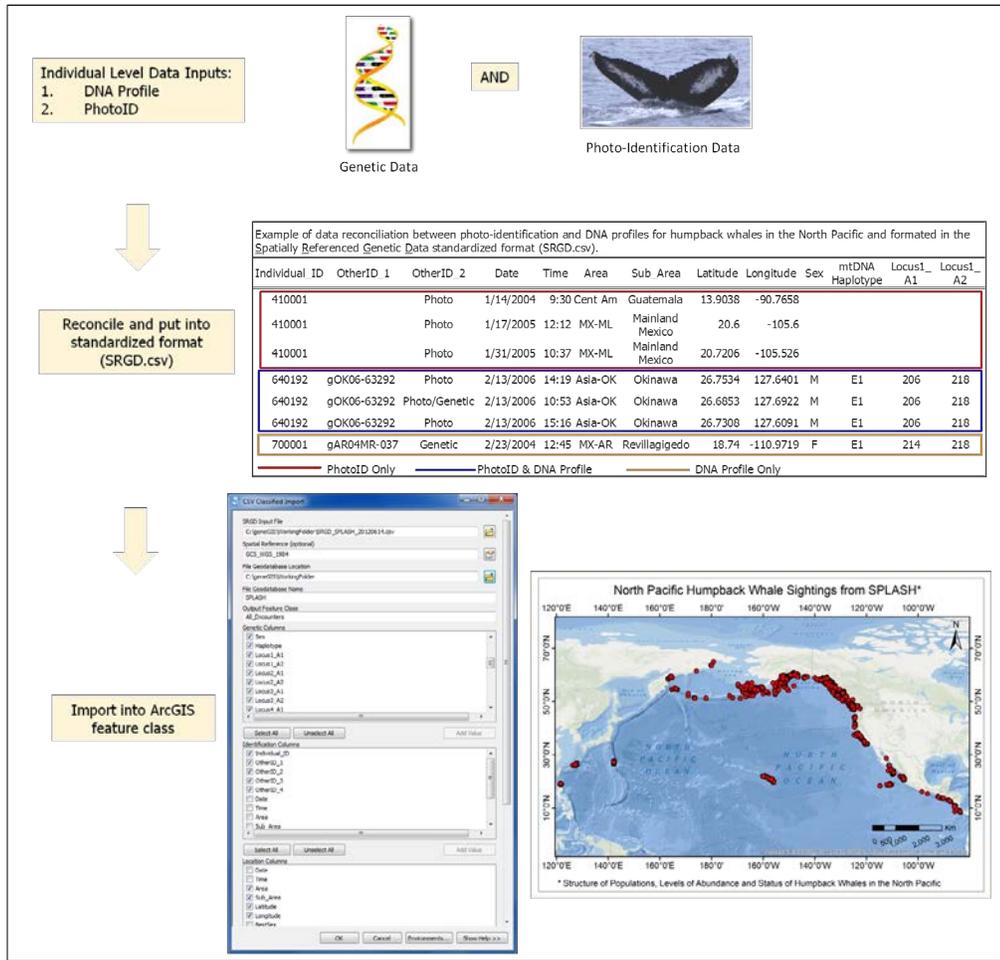
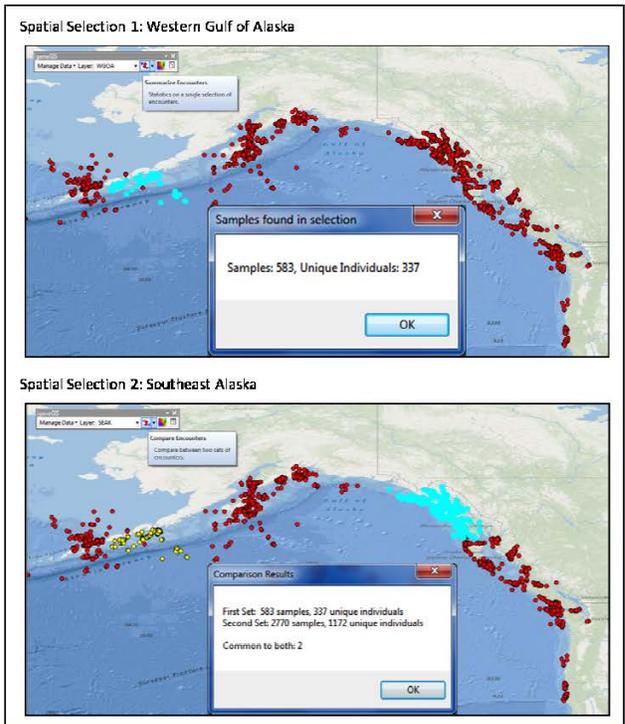


Figure 1. An example of data import to ArcGIS 10.1. Individual-based DNA profiles (geneSPLASH) and photo-identification records (SPLASH) are reconciled and individual encounter records are formatted into a SRGD.csv input file (see Table 1). The CSV Classified Import tool allows the user to dynamically classify data columns into standard fields, such as individual identification codes, spatial/temporal locations and genetic markers (Locus1, Locus2 etc), before creating a new feature class viewable in ArcGIS.

Display location of all encounters with humpback whales in the Gulf of Alaska from SPLASH/geneSPLASH database in ArcGIS.

Spatially select two regional populations, showing number of samples (encounters) and number of unique individuals in each of the two populations.



ArcGIS tool exports the selected records to GenAIEx. The GenAIEx analyses include a measure of genetic differentiation between the two selected populations ($F_{ST} = 0.197$) and a statistical test of the differences, based on a permutation procedure ($p = 0.010$).

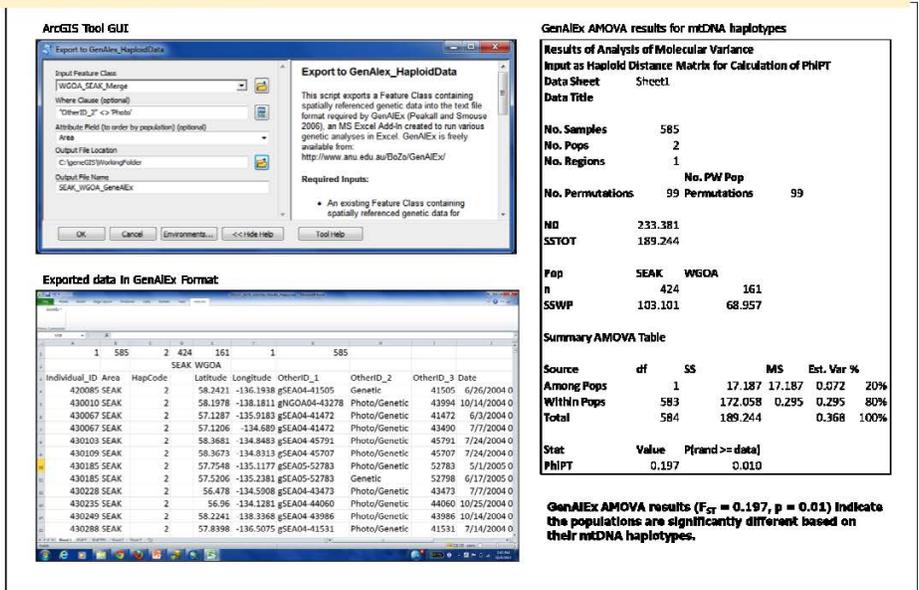


Figure 2. Use case for a spatial selection and population comparison of individually identified humpback whales encountered in the western Gulf of Alaska and southeast Alaska using geneGIS tools in ArcGIS. Spatially selected records are exported for analysis of population differentiation in the Excel Addin GenAIEx (Peakall and Smouse 2006)

Display all encounters with humpback whales from *SPLASH* and add environmental layer (for bathymetry).



Select ArcGIS 10.1 tool for 'Extract Raster Values'



Depth values extracted to attribute table with new field "Depth_m" (highlighted in cyan) and associated encounter record.

ID	Depth	EncounterID	Observed_1	Observed_2	Observed_3	Observed_4	Date	Time	Area	Sub Area	Latitude	Longitude	Depth_m	Sex
1	43001	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	14:00:00	Cont. Am.	Quadrant 4	43.001	-121.001	1000-1500
2	43002	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	15:00:00	Cont. Am.	Quadrant 4	43.002	-121.002	1000-1500
3	43003	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	16:00:00	Cont. Am.	Quadrant 4	43.003	-121.003	1000-1500
4	43004	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	17:00:00	Cont. Am.	Quadrant 4	43.004	-121.004	1000-1500
5	43005	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	18:00:00	Cont. Am.	Quadrant 4	43.005	-121.005	1000-1500
6	43006	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	19:00:00	Cont. Am.	Quadrant 4	43.006	-121.006	1000-1500
7	43007	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	20:00:00	Cont. Am.	Quadrant 4	43.007	-121.007	1000-1500
8	43008	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	21:00:00	Cont. Am.	Quadrant 4	43.008	-121.008	1000-1500
9	43009	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	22:00:00	Cont. Am.	Quadrant 4	43.009	-121.009	1000-1500
10	43010	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	23:00:00	Cont. Am.	Quadrant 4	43.010	-121.010	1000-1500
11	43011	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	00:00:00	Cont. Am.	Quadrant 4	43.011	-121.011	1000-1500
12	43012	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	01:00:00	Cont. Am.	Quadrant 4	43.012	-121.012	1000-1500
13	43013	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	02:00:00	Cont. Am.	Quadrant 4	43.013	-121.013	1000-1500
14	43014	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	03:00:00	Cont. Am.	Quadrant 4	43.014	-121.014	1000-1500
15	43015	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	04:00:00	Cont. Am.	Quadrant 4	43.015	-121.015	1000-1500
16	43016	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	05:00:00	Cont. Am.	Quadrant 4	43.016	-121.016	1000-1500
17	43017	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	06:00:00	Cont. Am.	Quadrant 4	43.017	-121.017	1000-1500
18	43018	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	07:00:00	Cont. Am.	Quadrant 4	43.018	-121.018	1000-1500
19	43019	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	08:00:00	Cont. Am.	Quadrant 4	43.019	-121.019	1000-1500
20	43020	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	09:00:00	Cont. Am.	Quadrant 4	43.020	-121.020	1000-1500
21	43021	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	10:00:00	Cont. Am.	Quadrant 4	43.021	-121.021	1000-1500
22	43022	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	11:00:00	Cont. Am.	Quadrant 4	43.022	-121.022	1000-1500
23	43023	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	12:00:00	Cont. Am.	Quadrant 4	43.023	-121.023	1000-1500
24	43024	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	13:00:00	Cont. Am.	Quadrant 4	43.024	-121.024	1000-1500
25	43025	Phoca	Phoca	Whale	Whale	Whale	Whale	2004	14:00:00	Cont. Am.	Quadrant 4	43.025	-121.025	1000-1500

Display whale encounters by six depth categories.

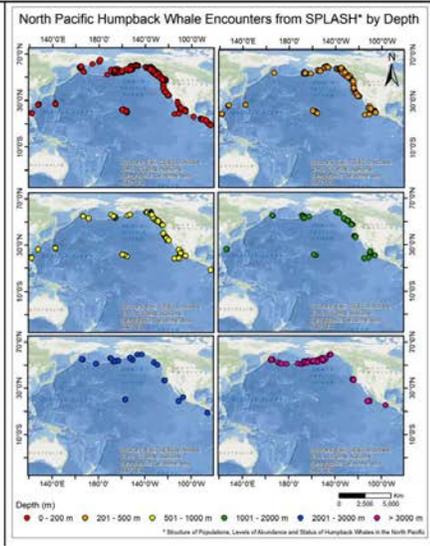


Figure 3. Use case for data extraction from an environmental layer (bathymetry) for encounter locations of humpback whales during the *SPLASH* project. A depth value for every humpback whale encounter during 2004-2006 is extracted from the bathymetric layer and added to each record in the point feature class. The depths for all encounters are then shown for six different depth intervals.

geneGIS in the Shepherd Project

The *Shepherd Project* (<http://www.ecoceanusa.org/shepherd>) is an open-source database framework designed to support studies in capture-mark-recapture (CMR), with recent enhancement to support molecular ecology and social ecology. The *Shepherd Project* is complementary to existing specialized programs for these studies, including Program MARK for estimates of population abundance and trends (White and Burnham 1999), Genepop for estimation of population genetic parameters (Rousset 2008), and SOCPROG for analysis of social affiliations (Whitehead 2009). Features of the *Shepherd Project* include:

- a scalable, collaborative platform for intelligent data storage and management, including advanced, consolidated searching;
- an easy-to-use suite of computation tools that can be extended to meet the needs of studies involving individual identification records and molecular ecology (e.g., photo-identification and DNA profiles);
- the easy export of data to specialized analysis applications (e.g., Genepop, Program Capture) and other software (e.g., Google Map); and
- the export of datasets in biodiversity databases (e.g., GBIF and OBIS);

Documentation for the complete capabilities of the *Shepherd Project* is available at:
<http://www.ecoceanusa.org/shepherd>

Unified Data Search and Display

The *Shepherd Project* was previously selected by Cascadia Research Collective as the ‘on-line’ repository for search and display of the SPLASH photo-identification catalogue. With funding from ONR, the *Shepherd Project* framework has been enhanced to support the integrated database of photo-identification and DNA profiles (Figures 4 and 5).

Spatial Selection and Custom Analysis of Population Differentiation

geneGIS tools have been implemented through six versions (2.x-3.0) to include new capabilities for supporting molecular ecology. These enhancements have resulted in improved data search capabilities and visualization of molecular markers linked to individual identification, as displayed in the following use case (Figure 6).

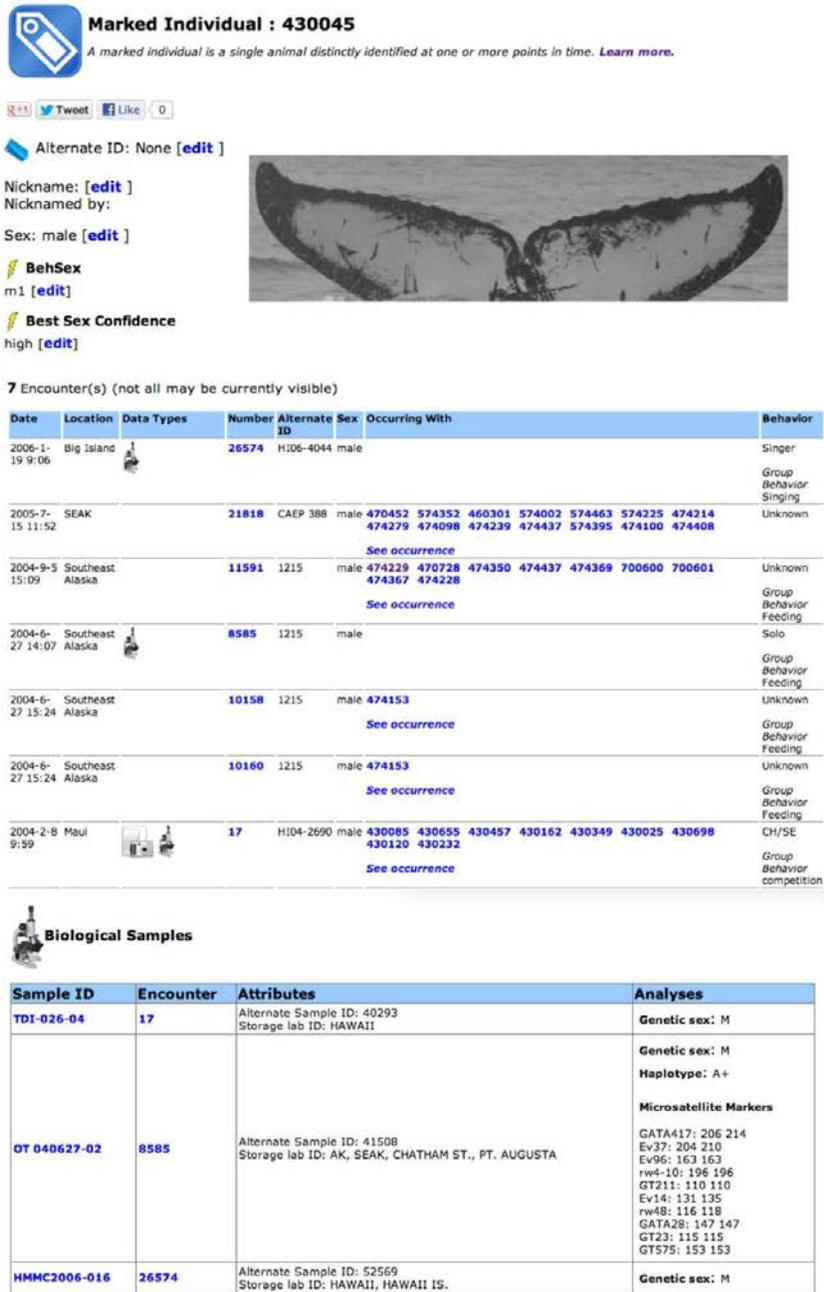


Figure 4. An example display of unified data for encounters with a marked individual using multiple sources of identification in SPLASH/geneSPLASH in the Shepherd Project. The search for individual 430045 shows a summary of 7 encounters from 2004-2006 in either southeastern Alaska or Hawaii. Photo-identification was collected from all 7 encounters. Tissue samples (biopsy or sloughed skin) were collected during encounters 26574 in Hawaii and 8585 in southeastern Alaska. The DNA profile (sex, mtDNA haplotypes and 10 microsatellite genotypes) is available from the sample collected during encounter 8585.

 **Mapping**

If you zoom in too quickly, Google Maps may claim that it does not have the needed maps. Zoom back out, wait a few seconds to allow maps to load in the background, and then zoom in again.

If more than one point is mapped for the marked individual, the map also displays chevrons to guide you from the first sighting (shown as a green icon) to each subsequent sighting over time. The chevrons do NOT represent a path of travel, just a sequential link across time.

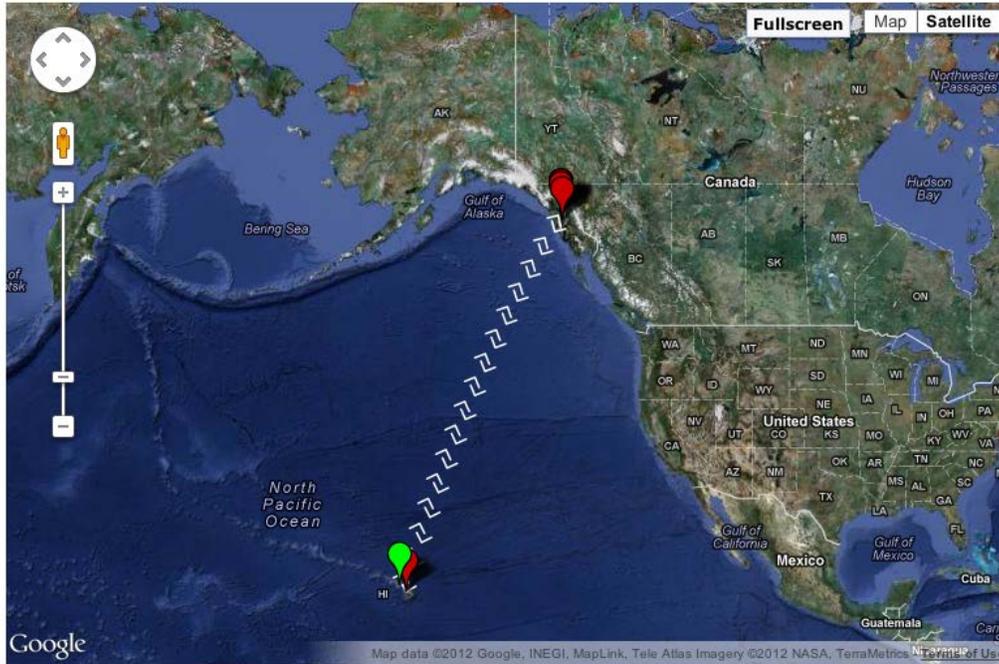


Figure 5.: An example display of unified data for encounters with marked individual using multiple sources of identification in SPLASH/geneSPLASH in Shepherd Project (continued). The Google Map shows the locations of encounters with individual 430045 from 2004-2006. The green icon shows the location of the first encounter and the arrows indicate the sequential links between encounters, showing the documented return migration between Hawaii and southeastern Alaska.

Mapped Search Results



Map aspects: Position only Haplotype Sex

Note: If you zoom in too quickly, Google Maps may claim that it does not have the needed maps. Zoom back out, wait a few seconds to allow maps to load in the background, and then zoom in again.

Display encounters with whales sampled by SPLASH in the Gulf of Alaska, showing mtDNA haplotypes

Spatially select regional populations in Northern Gulf of Alaska (NGOA) and southeast Alaska (SEAK) for comparison of haplotype frequencies



Search comparison displays number of individuals sampled in each of the populations and the number of individuals encountered in both regions.

Search Comparison Results Analysis

Comparison Overview

Shared marked individuals: 7

Haplotypes $F_{ST} = 0.09330658386059466$ (Weir and Cockerham 1984 method)

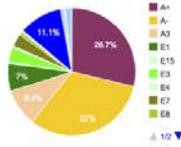
NGOA

No. matching marked individuals: 244

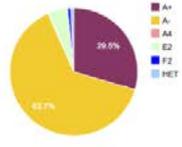
SEAK

No. matching marked individuals: 386

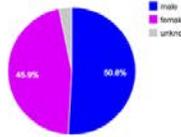
Haplotype Distribution in Marked Individuals



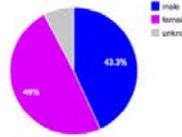
Haplotype Distribution in Marked Individuals



Sex Distribution in Marked Individuals



Sex Distribution in Marked Individuals



Calculates genetic differentiation (F_{ST}) and displays haplotype frequencies and sex ratio for two regional populations.

Figure 6. Use case showing encounters with individually identified humpback whales in the Gulf of Alaska during SPLASH. Each encounter is symbolized with its associated mtDNA from geneSPLASH. Spatial selection of the displayed encounters allows a customized comparison of mtDNA haplotype frequencies and sex ratios, and calculation of a standard index of genetic differentiation (F_{ST}), similar to that implemented through GenAIEx and ArcGIS.

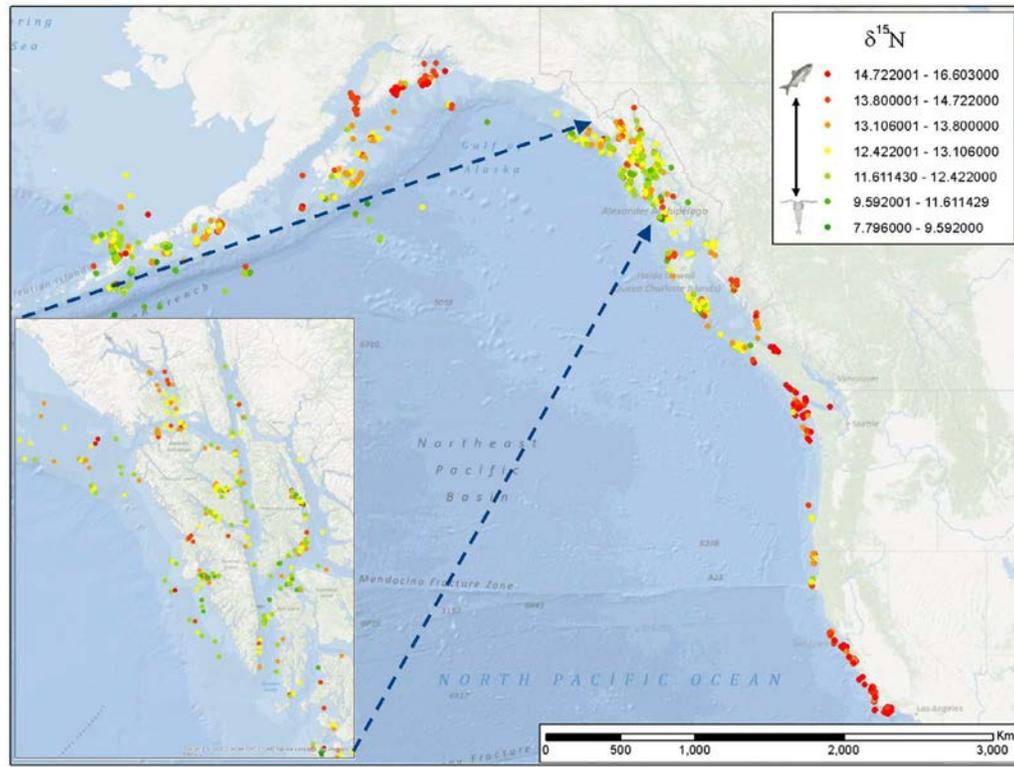


Figure 7. Geographic differences in a representative ecomarker, the stable isotope ^{15}N , from biopsy samples of humpback whales collected during the SPLASH program (Witteveen et al. 2009) and integrated into the Arc Marine data model. The scaling of values suggests differences in the primary trophic level of prey, with consumption of fish (red) dominating off Central California, the Olympic Peninsula, Washington, and inside waters of the northern Gulf of Alaska, and krill (green) dominating in southeastern Alaska. Whales in southeastern Alaska (inset) show apparent individual preferences or local area differences in consumption of fish and krill.

IMPACT/APPLICATIONS

With the development of *geneGIS* tools in ArcGIS we expect to improve access to individual-based records and associated DNA profiles to the community of spatial modelers, and to contribute to the developing fields of landscape and seascape genetics (Etherington 2011; Vandergast et al. 2012). With the *geneGIS* enhancements of the *Shepherd Project* we are developing a unified computational environment for Capture-Mark-Recapture and molecular ecology, including:

- distributed access to consolidated data and *geneGIS* analytic functions through a web browser, supporting distributed collaboration and the consolidation of multiple data sets;
- usable by a non-specialist, allowing non-GIS professionals to spatially explore and filter the data; and
- broader impact by contributing functionality to a open-source software framework also used by researchers for other species of marine megafauna (e.g., whale sharks and manta rays).

Now that *SPLASH/geneSPLASH* have been reconciled and implemented in both the Arc Marine model and the *Shepherd Project* framework, we are seeking additional datasets as exemplars for *geneGIS*. For this, we were recently granted access to a subset of photo-identification sighting records and DNA profiles from the North Atlantic Right Whale (NARW) database through application to the NARW Consortium. As with *SPLASH/geneSPLASH*, individual identification of NARWs has included both photo-identification and DNA profiling (Frasier *et al.* 2009), with photo-identification records maintained through the Digital Image Gathering and Information Tracking System (DIGITS) at the New England Aquarium. Communication is now ongoing with curator of the photo-identification records, Phillip Hamilton, and curator of the DNA profiles, Tim Frasier, on the details of the data loan. It is expected that this will involve several thousand sighting records and associated profiles of a few hundred individuals (Frasier *et al.* 2007).

RELATED PROJECTS

Title: ‘*Examination of health effects and long-term impacts of deployments of multiple tag types on blue, humpback, and gray whales in the eastern North Pacific*’ with funding to Cascadia Research Collective, from the National Oceanographic Partnership Program (NOPP) and Interagency Committee on Ocean Science and Resource Management Integration (ICOSRMI). In collaboration with Cascadia Research Collective, the Marine Mammal Institute (MMI), Oregon State University (OSU) is assisting with the integration of photo-identification records and associated genetic samples, to improve understanding of long-term impact of satellite tagging. The resulting database should be suitable for implementation in *geneGIS*.

Title: ‘*The Shepherd Project*’. This project started as a collaborative software platform for globally coordinated whale shark research, as described in the <http://www.ecoceanusa.org/>. The success of this platform in managing and supporting the growth of the whale shark catalog led to its selection for the web-based implementation of the SPLASH Photo-ID Catalog (<http://www.splashcatalog.org>). Through ongoing development of this open-source platform, the *Shepherd Project* provided for the cross application of new functionality to other long-term studies of individually identified marine mammals or marine megafauna.

Title: ‘*ecoSPLASH*’. This project has provided stable isotope profiles (Carbon and Nitrogen) derived from more than 1,000 skin biopsy samples collected during the SPLASH program. These ecological markers profiles are the linked to individual photo-identification and DNA profiles in the *SPLASH/geneSPLASH* database and have proven informative in descriptions of population structure and the trophic ecology of humpback whales in the North Pacific (Witteveen *et al.* 2009; Witteveen *et al.* 2011a; Witteveen *et al.* 2011b). An initial importation of ¹⁵N values shows dramatic regional and individual differences, reflecting difference in the dietary proportions of fish and krill (Figure 7). Inclusion of isotope profiles in the *geneGIS* computational environment provides the potential for more sophisticated analyses of prey specialization and genetic differentiation among feeding regions.

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Dick, D., D. Wright, J. Calambokidis, J. Holmberg, E. Falcone, T. Follett, D. Steel, B. Slikas, and C. S. Baker. 2012. *geneGIS*: computational tools for spatial analyses of DNA profiles associated and photo-identification records of whales and dolphins. Poster Presentation, The Wildlife Society 19th Annual Conference, Portland, OR, 13-18 October 2012.

Holmberg, J. 2012. *The Shepherd Project*: A software framework for mark-recapture and molecular ecology. Oral Presentation, The Wildlife Society 19th Annual Conference, Portland, OR, 13-18 October 2012.