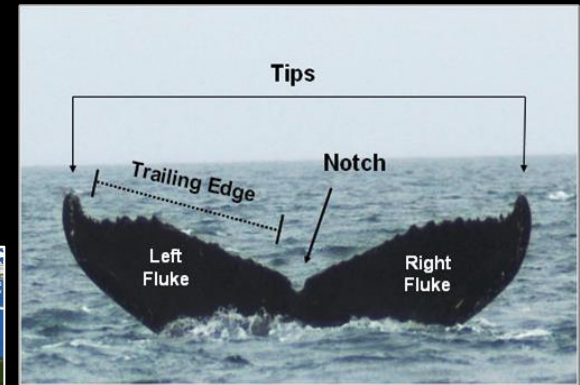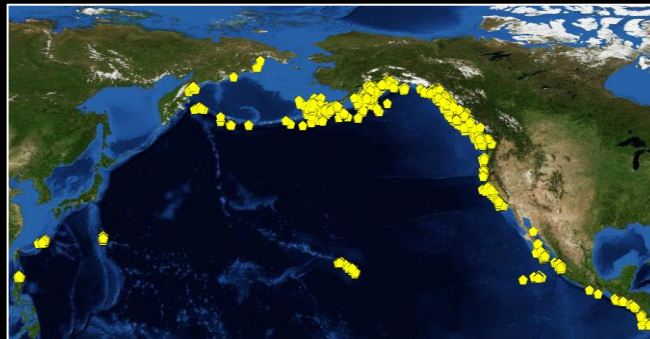# *geneGIS:*

Geoanalytical Tools for Individual-Based Genetic Records

Dori Dick, Shaun Walbridge, Dawn Wright, John Calambokidis,
Erin Falcone, Debbie Steel, Tomas Follett,
Jason Holmberg, C. Scott Baker

http://www.nationalgeographicstock.com/ngsimages/explore/explorecomp.jsf?xsys=SE&id=1231238

http://www.afsc.noaa.gov/ABL/Humpback/WhyPhoto.htm

2014 Esri User Conference

Driving Factors

- Marine ecosystem declining

- Loss of biodiversity, loss of ecosystem goods and services

- Marine ecosystem based management (EBM)

- Marine spatial planning

©Dori Dick

http://www.americanreef.org/marinedebris.html

http://halogentv.com/articles/did-bp-do-anything-right/

© Nicole Mackey

http://www.seaturtlefoundation.org/stf-current-projects/campaigns/marine-debris/

Landscape/ Seascape Genetics

- Study spatial ecological processes by combining population genetics, landscape ecology and spatial analysis to understand how the seascape influences population structure

- Critical to detecting, predicting and mitigating the effects of changes to seascape and climate

- Aid in conservation actions and provide alternative scenarios

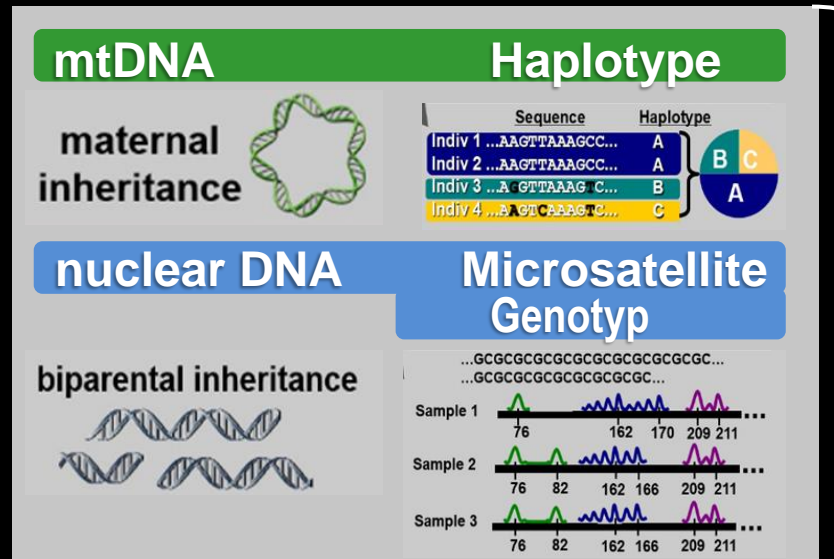↑ **Spatially-Explicit Genetic Data** ➕ **Seascape Genetics** ➖ **Novel Analysis Opportunities**

Case Study: Whales and Dolphins

- Large-scale, long-term

- Individual-based, repeated sightings of individuals

Photo-identification   *Genetic Analysis*

1000s records

100s records

- Habitat use, distribution & movement patterns, pop^n structure, social organization

The Problem…

Whale & Dolphin Research:

- Individual-based studies using photo-identification and genetics are becoming more common
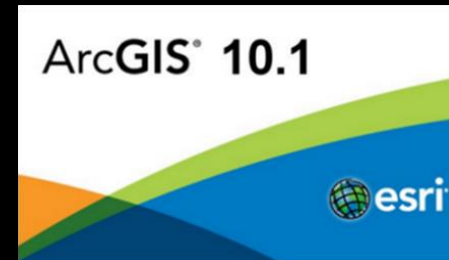

- Integration of these databases is rare

- Few tools exist to handle, explore or visualize the spatial patterns of such data

The Solution…

Our Approach:

- Provide suite of ArcGIS tools for use with integrated individual-based data

- Must be easily accessible for non-GIS users

- Tools and geoprocessing scripts open source

geneGIS Framework
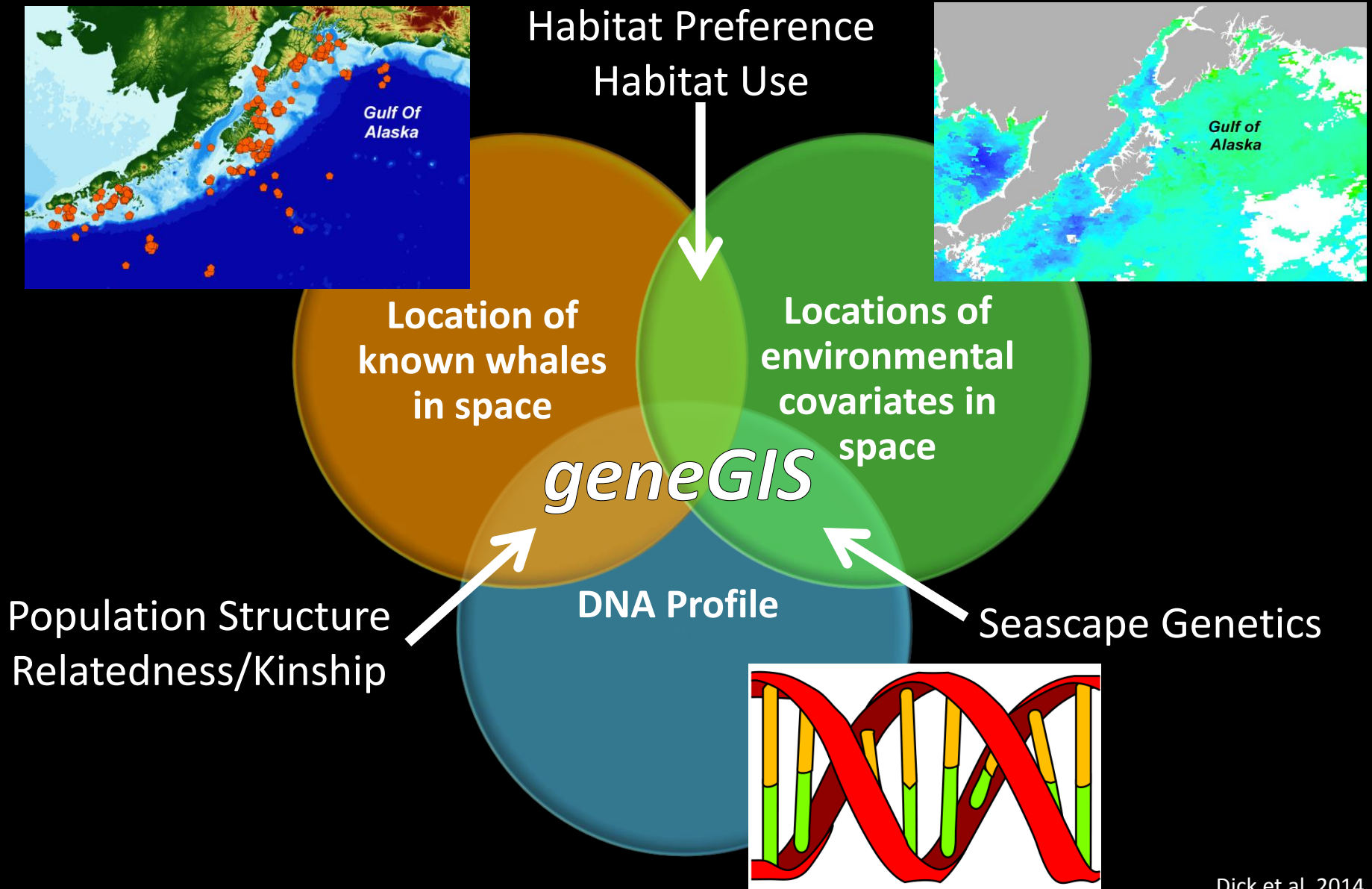
Tool Architecture

- Python 2.7 - geoprocessing scripts

- ArcGIS 10.1
  - ➤ Python toolbox (.pyt)

  - ➤ Python Add-In (.esriaddin)

- Toolbar

Dick et al. 2014
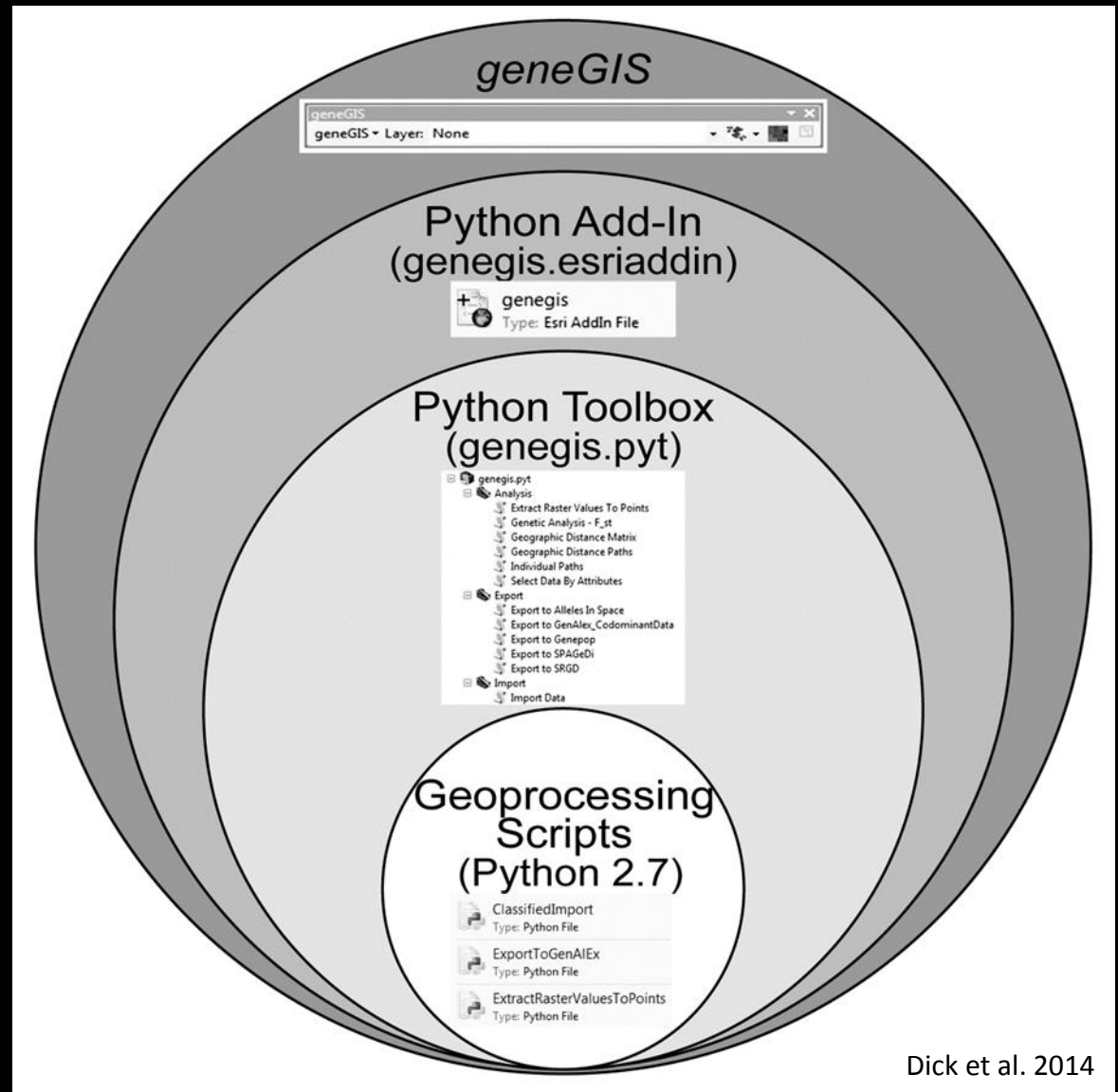
Our database

- *geneGIS* developed and implemented using SPLASH*, an integrated & extended database of N. Pacific humpback whale records

  ➢ 8,000+ naturally marked individuals

  ➢ 2,700 associated DNA profiles (10 microsatellite loci, mtDNA, sex)
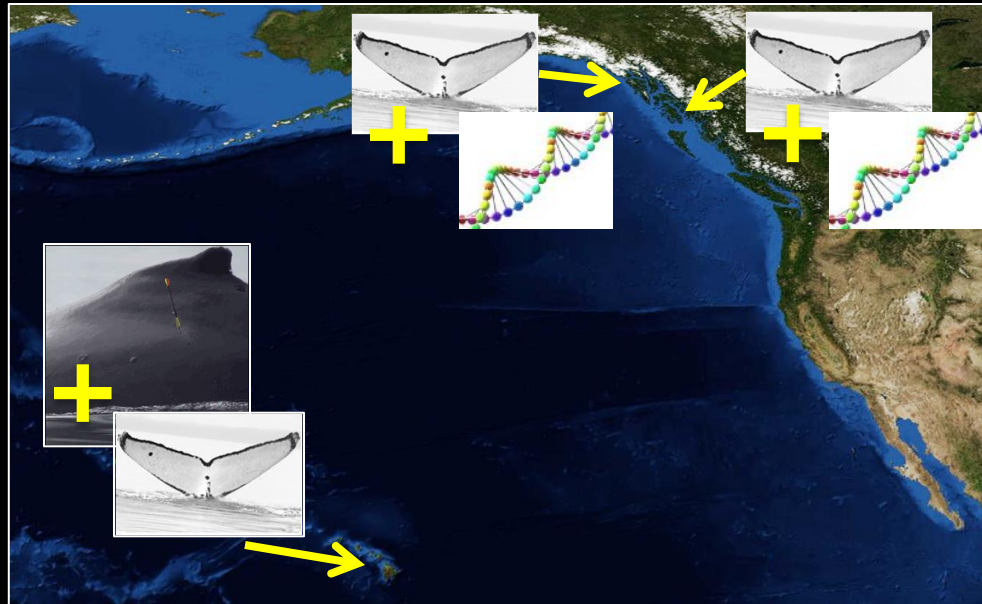
*Structure of Populations, Levels of Abundance and Status of Humpback Whales in the North Pacific
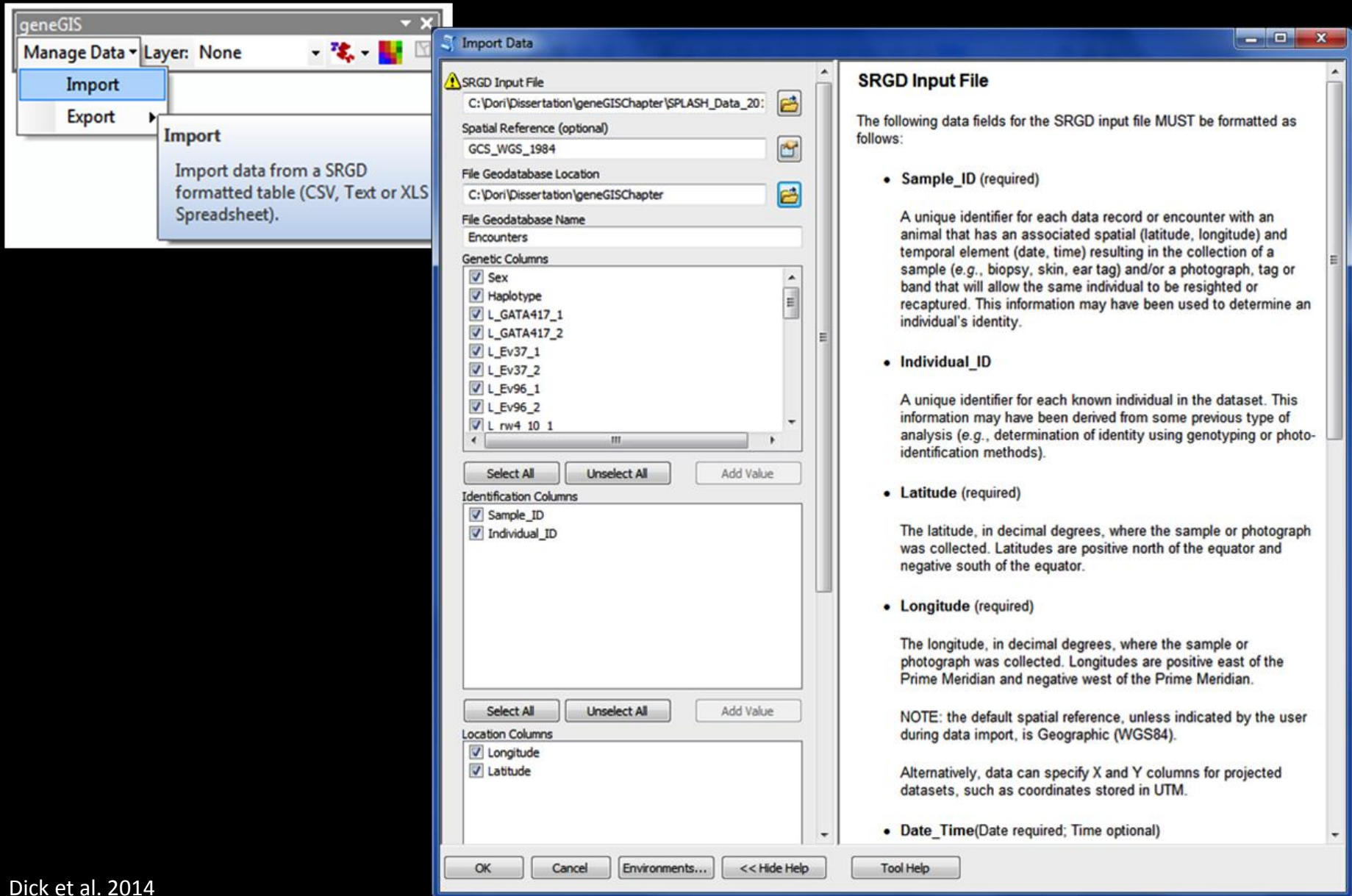
Working within *geneGIS*

- To provide a suite of ArcGIS tools to researchers who want to:

    1. Visualize genetic data on a map

    2. Spatially explore, display, and select data

    3. Export data to formats required by other genetic analyses software

    4. Extract data from environmental layers

    5. Conduct basic spatial analyses

Working within *geneGIS*

To provide *quantitative* approach to *conservation priorities* by mapping spatial data and attributes of individuals to improve ability to *study influence of seascape on population structure*

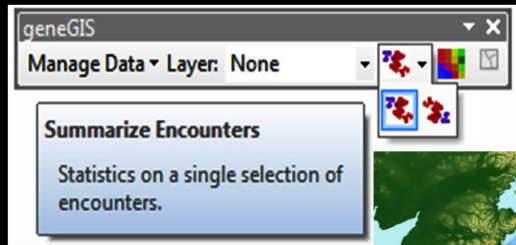# 1. Data Visualization

1. Data Visualization

All encounters of known individuals from the SPLASH Program
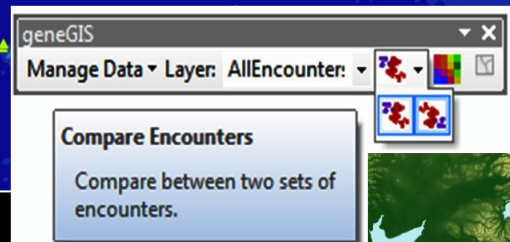
Dick et al. 2014

2. Spatially Explore, Display and Select

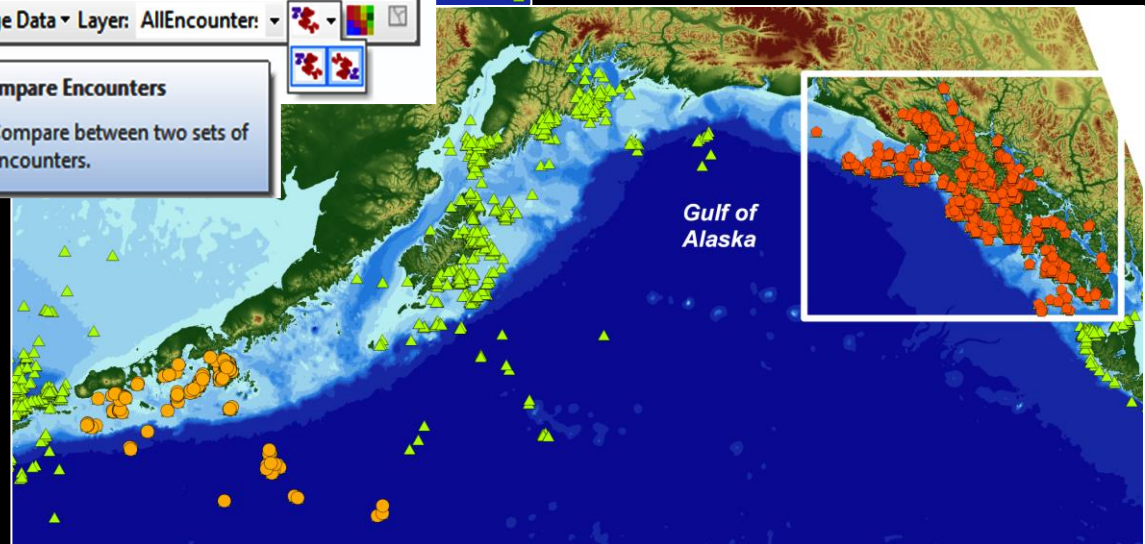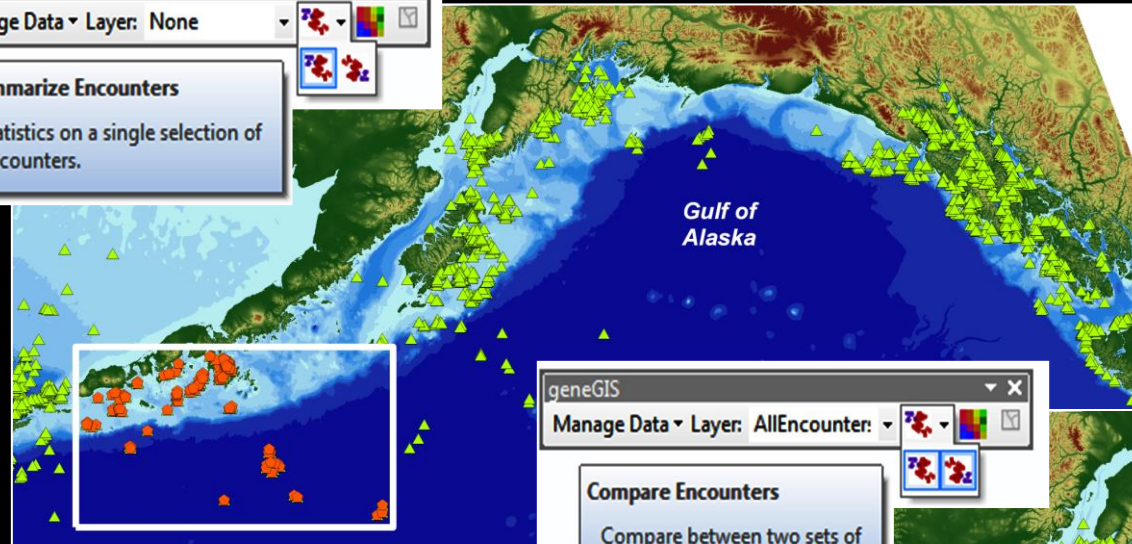Are humpback whale populations in the Western Gulf of Alaska and Southeast Alaska genetically differentiated?

Dick et al. 2014

3. Data Export & Analysis Outside ArcGIS
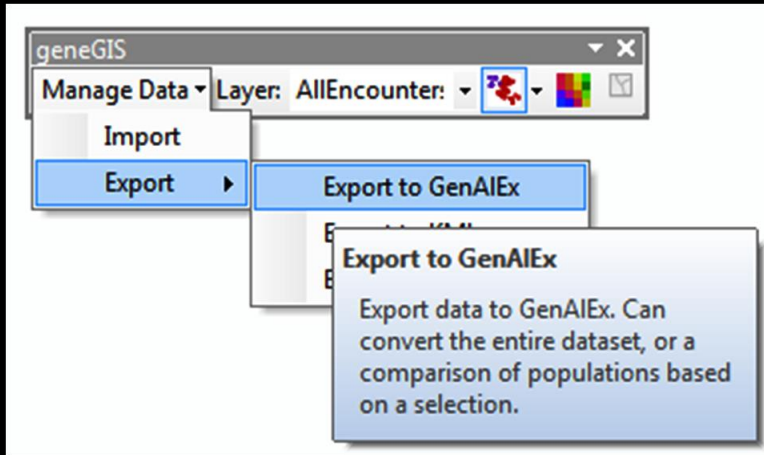
Other Export Options:
Alleles in Space
GenAlEx
Genepop
KML files
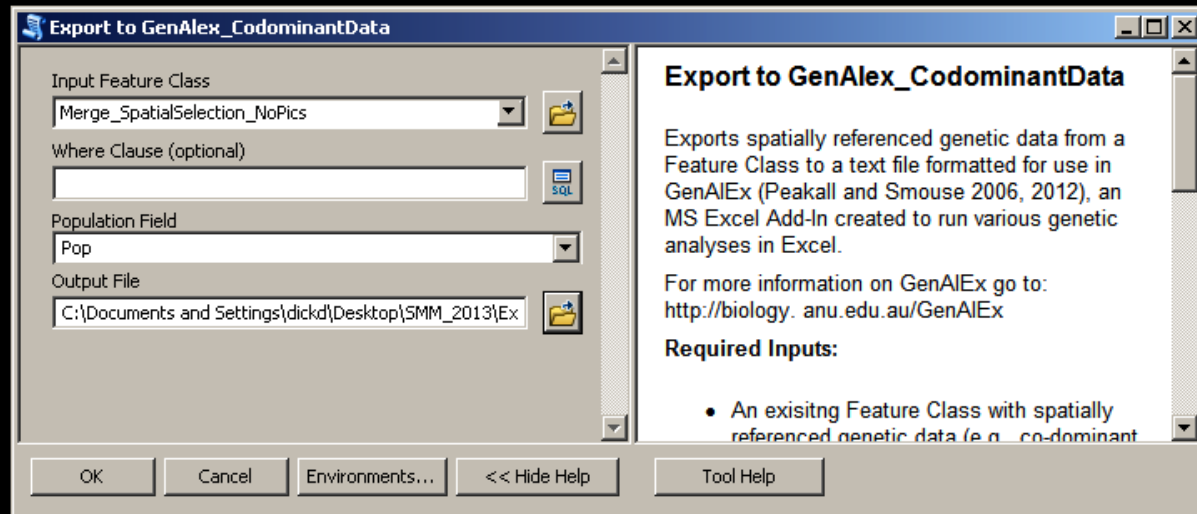
3. Data Export & Analysis Outside ArcGIS

GenAlEx: (F_{ST} = 0.197, p < 0.01)

Populations are significantly genetically differentiated based on mtDNA haplotypes

mt DNA haplotype frequencies for:

A) Western Gulf of Alaska   B) Southeast Alaska

A+ A- A3 A4 A5 E1 E2 E3 E4 E5 E6 E7 E14 F2 F4

Dick et al. 2014
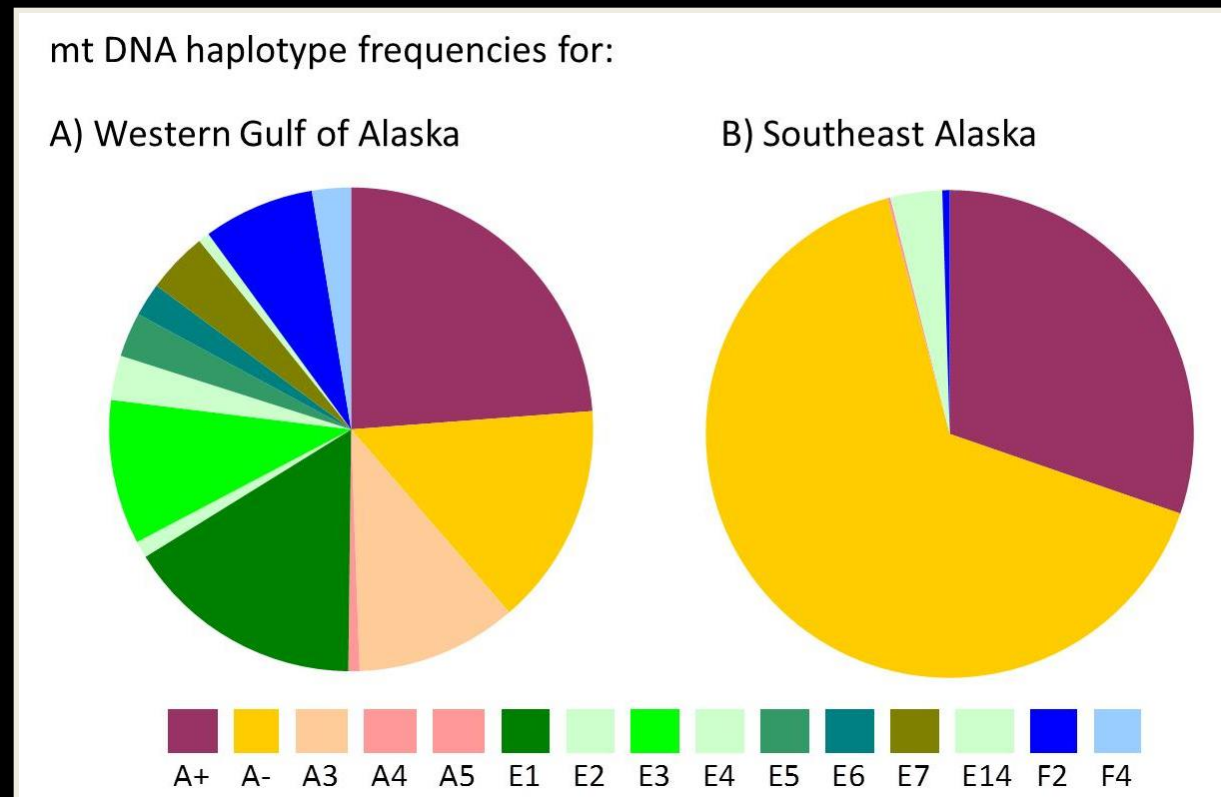
4. Data Extraction

Within a set of whales of known mtDNA haplotype is there any evidence of preference for particular depths?
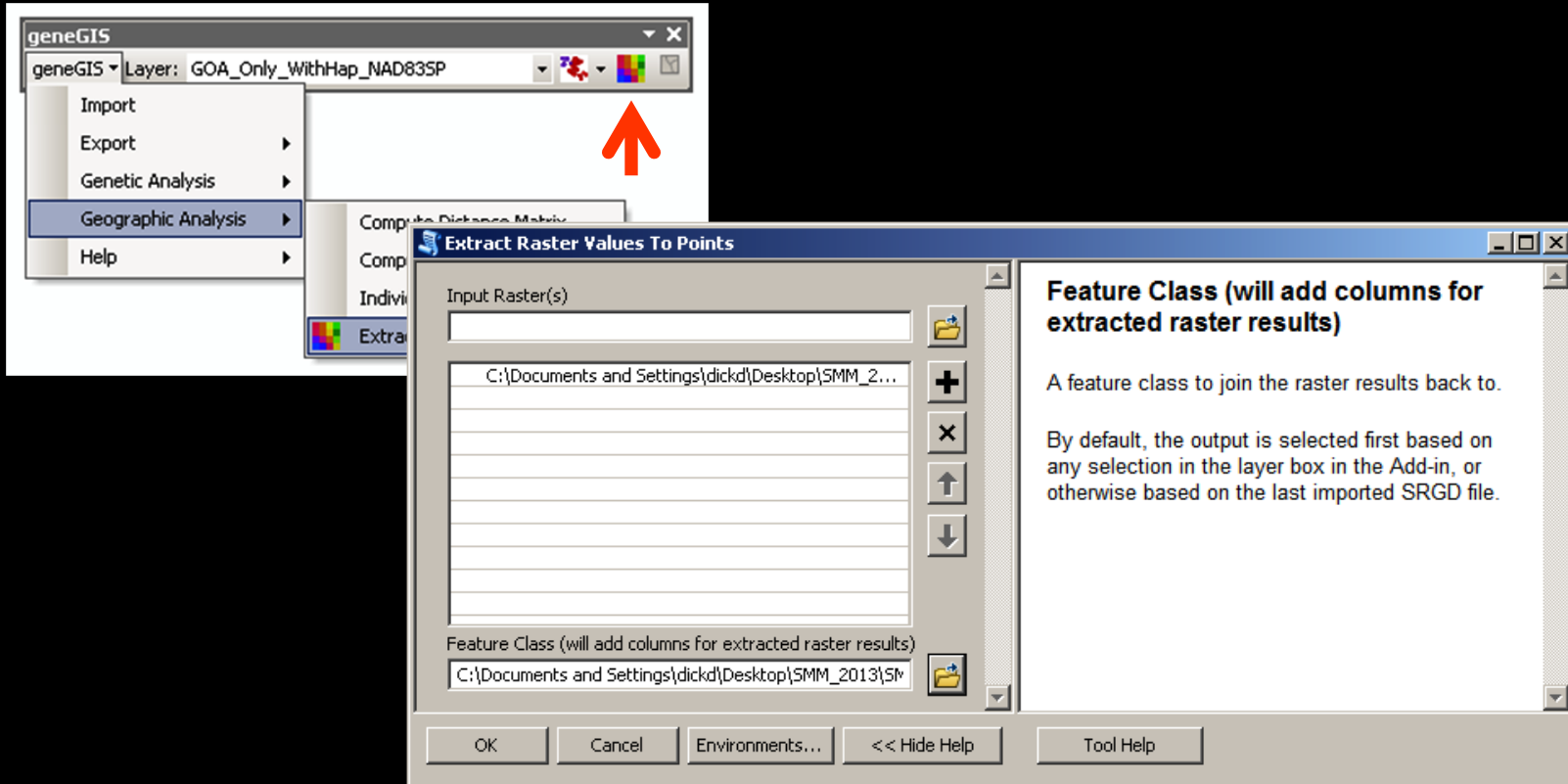
Cell values from a raster surface (bathymetry, SST, Chl a, etc.) are added to the input feature class.

4. Data Extraction

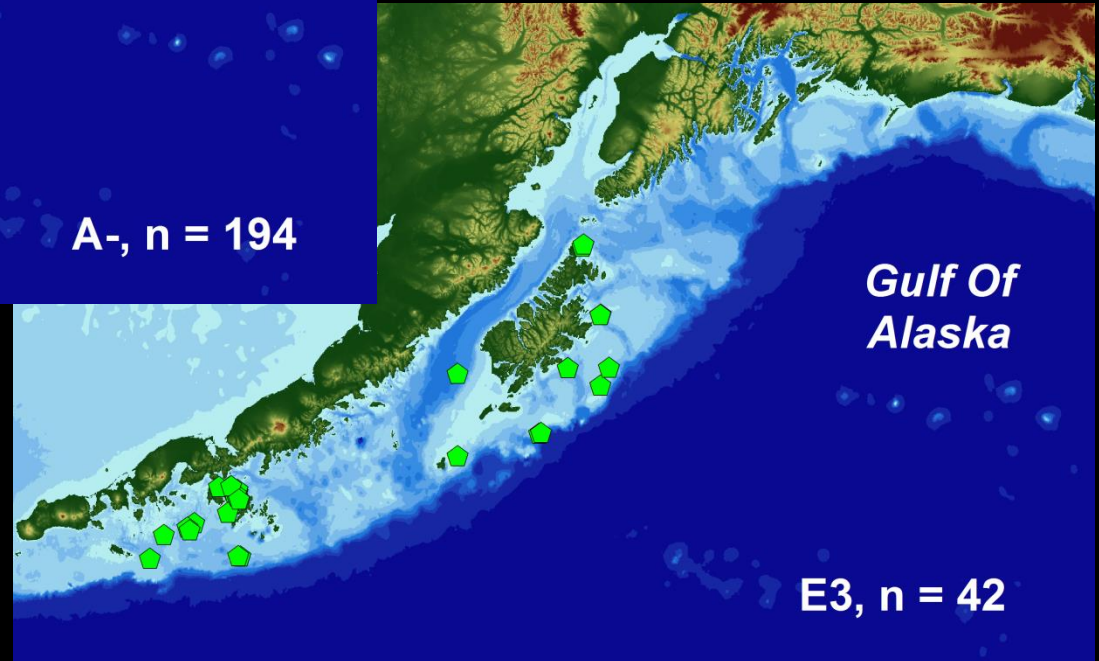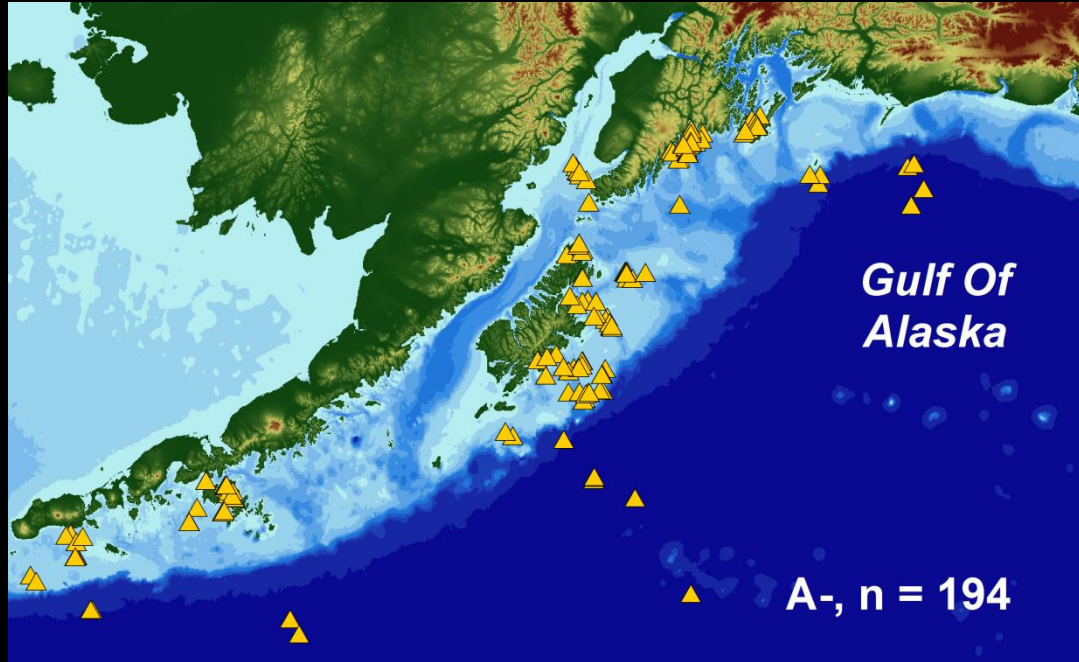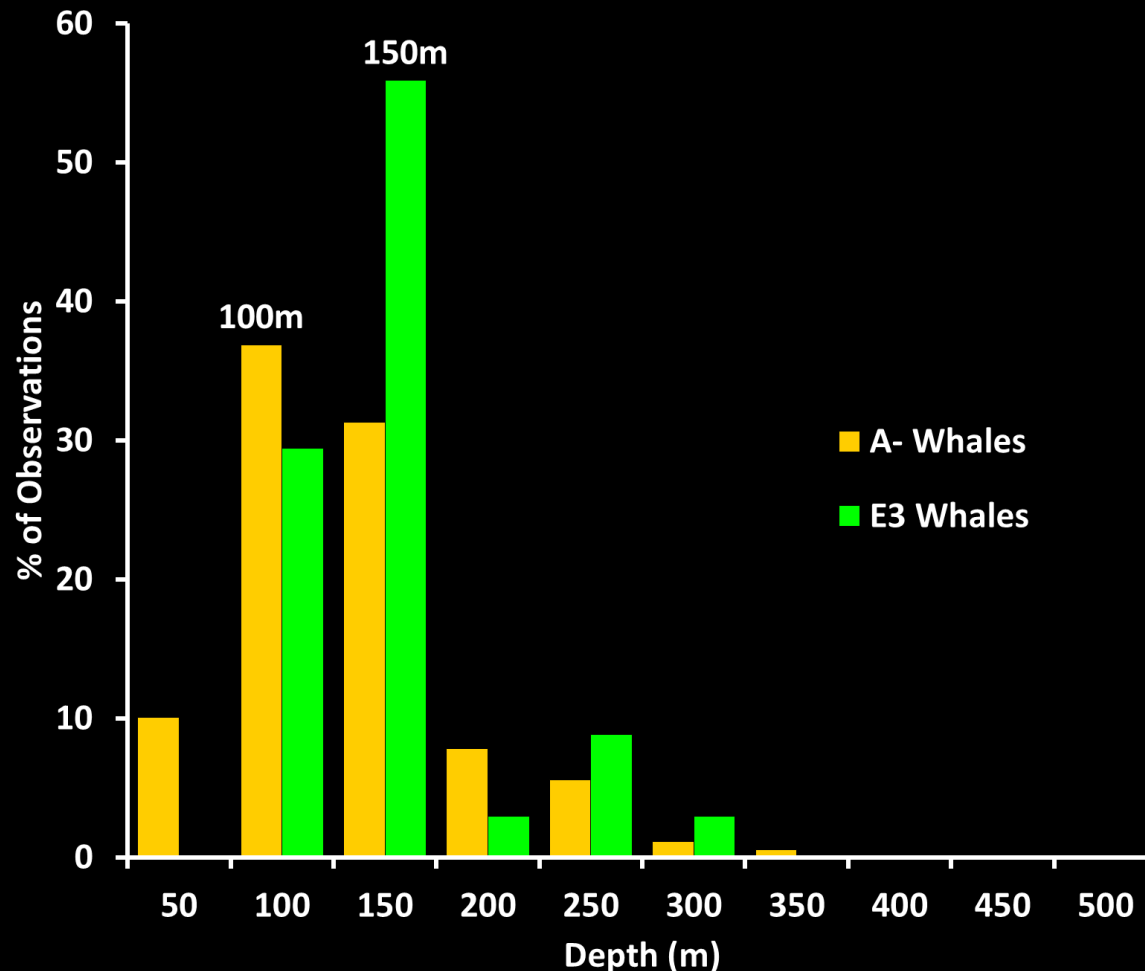Within a set of whales of known mtDNA haplotype is there any evidence of preference for particular depths?

Dick et al. 2014

4. Data Extraction

Within a set of whales of known mtDNA haplotype is there any evidence of preference for particular depths?
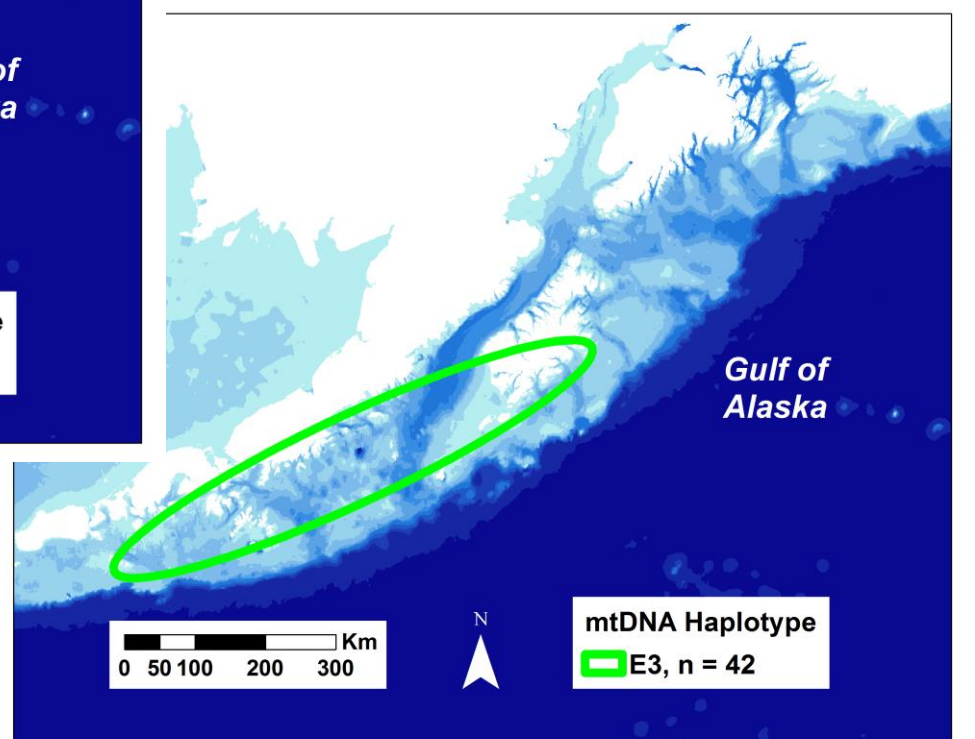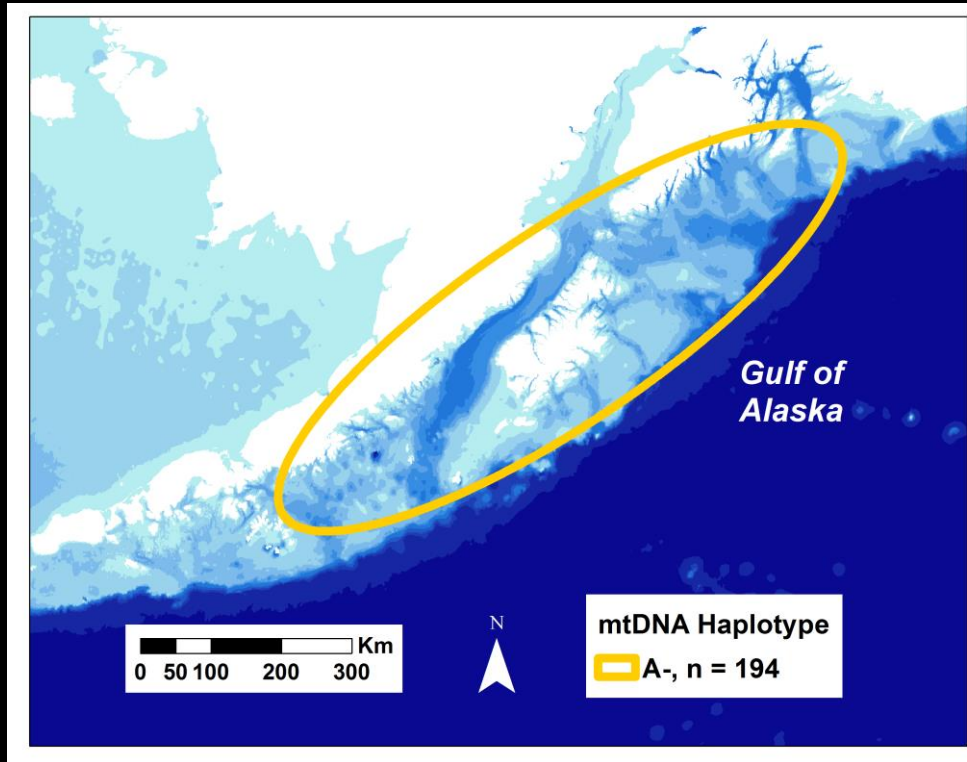
5. Spatial Analyses

How do the spatial distributions of humpback whale haplotypes vary?

- Turn to the Standard ArcGIS ArcToolbox options

- Directional Distribution

- Conduct standard deviation ellipse analysis

- Summarizes central tendency, dispersion and directional trends in X and Y directions
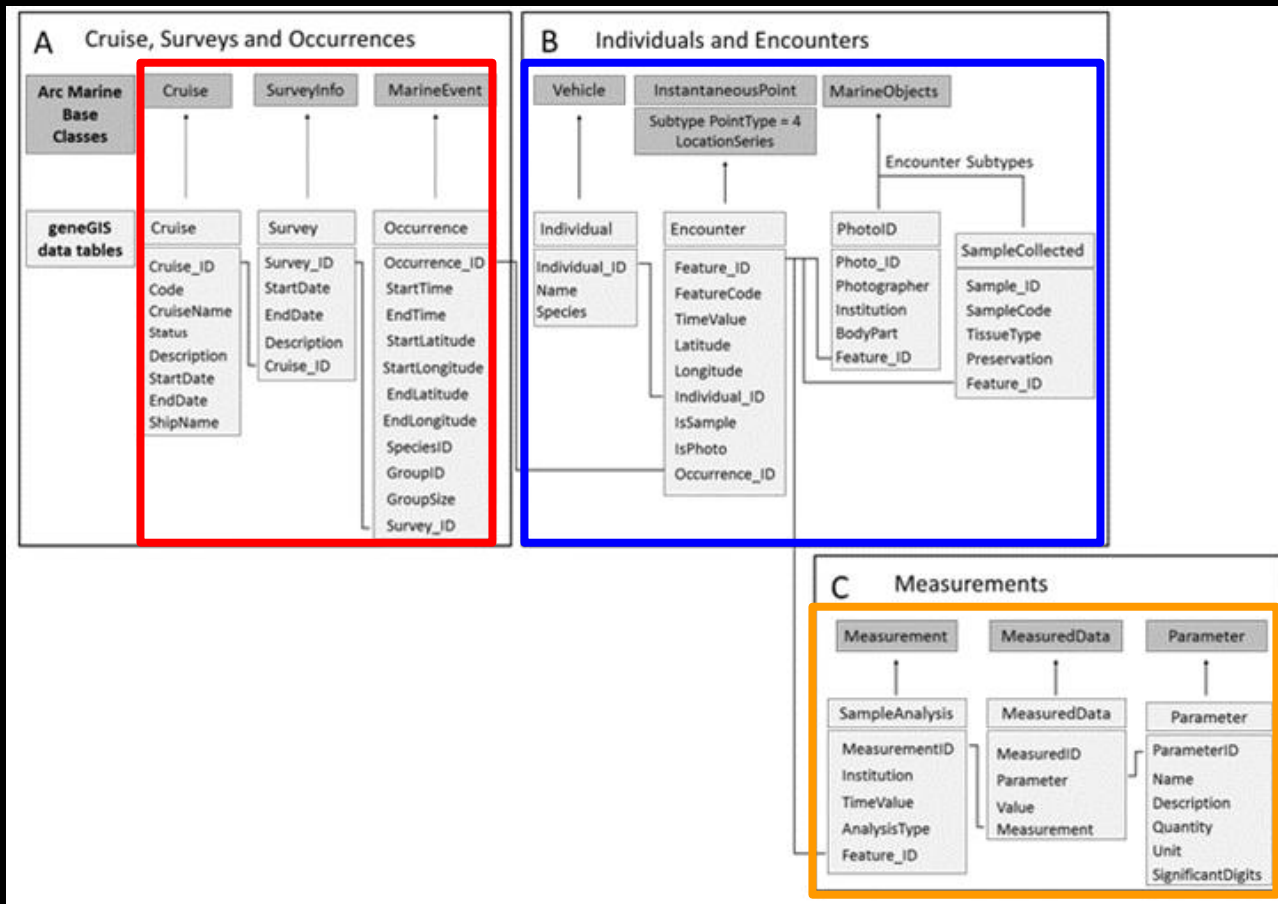
5. Spatial Analyses

How do the spatial distributions of humpback whale haplotypes vary?

mtDNA Haplotype
A-, n = 194

mtDNA Haplotype
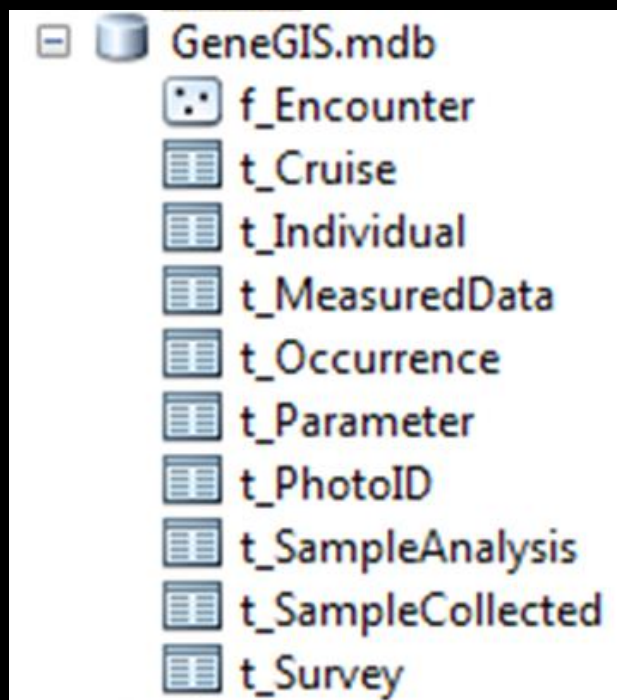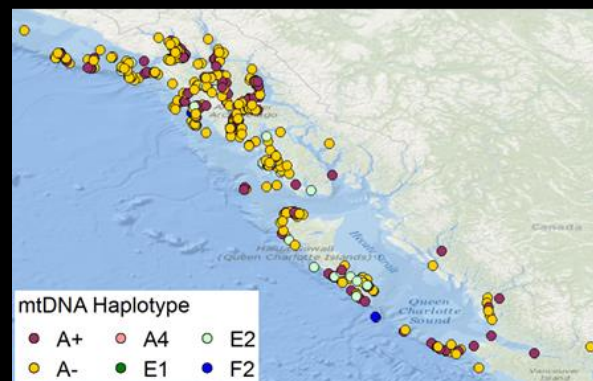E3, n = 42

Gulf of Alaska

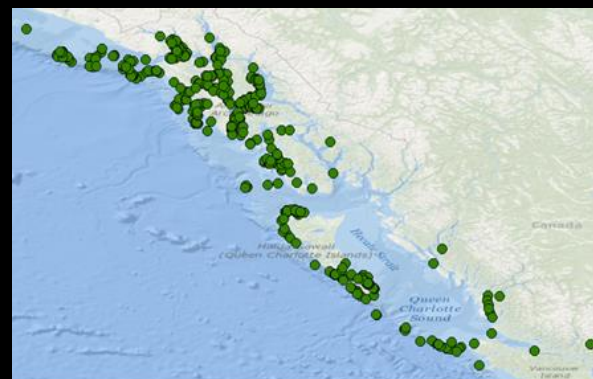Dick et al. 2014

Arc Marine Customization

- Lord-Castillo et al (2009) customization as starting point

- Retain 9 key Arc Marine classes

Dick et al. 2014
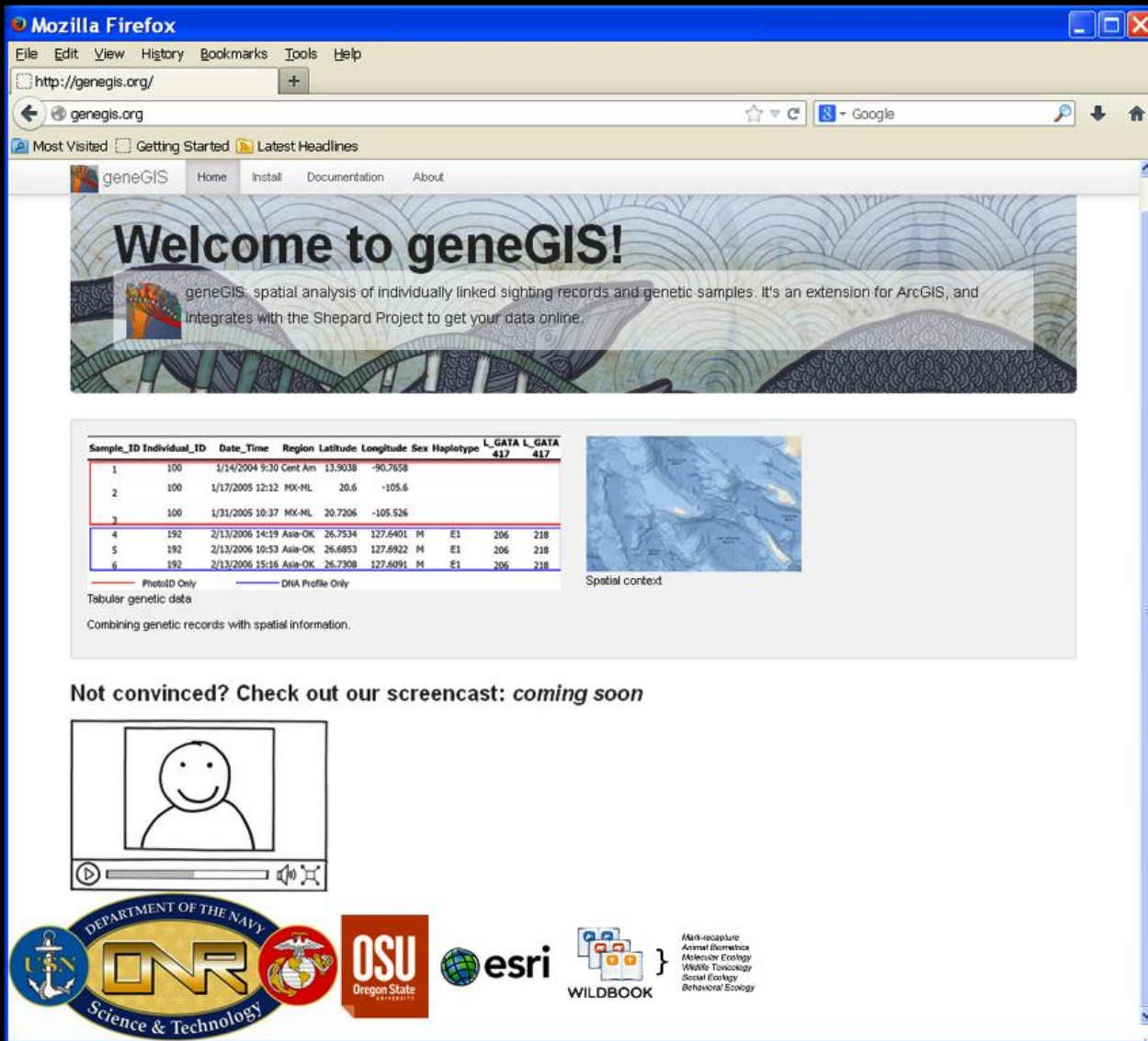
SPLASH Implementation

- 1 feature class of individual encounters

- 9 tables

Sex
- Female
- Male

mtDNA Haplotype
- A+   - A4   - E2
- A-   - E1   - F2

Dick et al. 2014

geneGIS.org

- Installation File with instructions

- Example dataset and tutorial

- Basic background information & documentation including tool help

- Link to GitHub repository

Conclusions

- *geneGIS* provides 2 new advances to molecular ecology
  1. Novel tools for data visualization, spatial selection, environmental data extraction, and spatial analyses for individual-based genetic data
  2. Arc Marine customization for integrated genetic and photo-identification data while providing opportunity to link with others in the broader marine GIS community

- Can now pose and answer questions using environmental information relevant to the study species in *geographic space,* not researcher-defined boundaries

- Envision *geneGIS* will be important tool to enhance understanding of pop structure, ecosystems relationships and human impact across species and ecosystems

Want to learn more?

Mapping Tools: Where the Wild Whales Are

Thursday 11:30 am – 12:00 pm

Demo Theater – Esri Labs Exhibit Hall B

Presented by: Dawn Wright

Shaun Walbridge

Nicole MacKay

Thanks to:

All the researchers involved with SPLASH
Cascadia Research Collective for database maintenance
OSU Cetacean Conservation Genetics Lab for genetic analyses

Full paper available in *Transactions in GIS* (Special Issue): "GIScience Research at the 2014 Esri International User Conference", 18(3):324-350

NOAA Stock Pictures

Contact: dickd@geo.oregonstate.edu