

INTEGRATING GENETICS INTO THE IMPORTANT MARINE MAMMAL AREAS (IMMA) IDENTIFICATION PROCESS

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1. CONTEXT AND RELEVANCE

Genetic tools provide unique information for marine protection, management, and spatial planning. The genetic toolbox can be used to address questions at multiple scales, including the individual (e.g., parent analysis), population (e.g., demographic population units, genetic connectivity, effective population size, genetic diversity), and species (e.g., taxonomic units, cryptic species, natural selection). However, while the importance of accounting for evolutionary process in ecosystem management has been recognized by a number of policy mechanisms, the integration of genetic information into marine protected area and spatial planning efforts has been generally lacking.

In 2008, the Convention on Biological Diversity (CBD) agreed on a set of seven scientific criteria to guide the identification and prioritization of ecologically or biologically significant marine areas (EBSAs). These criteria have subsequently been formally adopted by a number of other initiatives, including the IUCN Joint WCPA/SSC Marine Mammal Protected Area Task Force for the identification of Important Marine Mammal Areas (IMMAs). Genetic information has the potential to be highly informative in the application of these criteria in a manner that complements and enhances existing approaches based on biodiversity metrics, habitat maps, satellite tracking studies, and expert opinion.

The reasoning behind this implementation gap is not because the integration of genetic information into marine protection and spatial planning is not possible. Indeed, genetic information has been successfully used in a number of marine protected area planning efforts and there are a number of new techniques that enable the spatial representation of genetic information. Rather, it is a knowledge and communication gap between geneticists and the marine policy and management community that appears to be the primary driver. Spanning this knowledge gap is now of particular importance as the identification of important marine areas is being driven at a global scale by international policy mechanisms.

Over the past few years, there has been significant progress made towards the integration of genetics into marine protection and spatial planning processes, and a number of valuable case studies on a suite of marine taxa have emerged. Geneticists are increasingly active in applying their findings and formulating recommendations relevant to marine protected area planning, and marine planners are beginning to seek new ways to evolve existing spatial planning tools to account for genetic information. Notwithstanding this progress, there has not yet been a unified and coordinated effort to develop a standardized approach to integrate genetics that could support a variety of marine protection and spatial planning processes, including the application of the EBSA and IMMA criteria.

Developing a standardized approach to integrating genetics into marine protection and spatial planning efforts is one of our key research priorities and our work on this issue has

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evolved over a series of meetings, discussions and papers during the past four years. In 2012, we hosted a symposium at the 2nd International Marine Conservation Congress (IMCC2) with the view to develop a framework for interpreting genetic data alongside oceanographic information in a way that can support marine protection efforts (Mendez et al. 2010; 2011). The primary output of this symposium was a short communication, *Marine Spatial Planning 2.0: Genes and satellites to conserve seascape dynamics* (Mendez et al. *in press*). We have also highlighted the progress made on integrating genetics and oceanographic information in a letter published in *Trends in Ecology and Evolution* (Kershaw & Rosenbaum, 2014). We then broadened our efforts at the 2013 3rd International Marine Protected Area Congress (IMPAC3) in Marseille where we presented on the general utility of the genetic 'toolbox' in marine protection. It was during subsequent discussions with geneticists and marine planners, including members of the IUCN Joint WCPA/SSC Marine Mammal Protected Area Task Force, that the need for a standardized approach to integrating genetics into marine protection and spatial planning was articulated.

In August 2014, at the 3rd International Marine Conservation Congress (IMCC3), we convened an international team of geneticists and spatial planners at a Focus Group entitled *Developing an approach for integrating genetics into MPA design and spatial planning processes*. Based on our previous discussions and presentations, it was clear that such an approach would require the ability to visualize genetic information alongside other data types commonly used for spatial planning (e.g., habitat models, satellite tracking) in a way that is ecologically meaningful and useful for planners. Clear guidance to the policy and management community on the importance of this information and how to interpret it would also be essential.

This document represents the culmination of the key findings and conclusions from our work to date on developing a standardized approach to integrating genetics into marine protection and spatial planning processes. This effort is still at an early stage of development, which means that it can be used to both inform and also be informed by the testing of the draft criteria used in the identification of Important Marine Mammal Areas (IMMAs). It is our hope that both of these processes can occur simultaneously and an applied case study can be developed, which will illustrate how this approach can be applied and tailored to the protection of marine mammals.

To this end, we present some pertinent considerations and opportunities when integrating genetics into marine protection and spatial planning efforts, followed by some key conclusions. A number of examples of how genetic information can be visualized are provided in Appendix 1; we have selected these examples from our IMCC3 Focus Group report that are most relevant to marine mammals, or that illustrate a variety of genetic data types. A broader number of examples are included in the Focus Group report and this document is available upon request. Appendix 2 provides more detailed information on the discussions from the Focus Group on the different types of genetic data that are relevant to marine protection and planning, as well as some of the analyses that can be used to display this information in a spatially explicit manner. Finally, Appendix 3 provides the list of attendees of the IMCC3 Focus Group.

2. CONSIDERATIONS AND WAYS FORWARD

We have identified a number of general considerations and opportunities related to integrating genetic information into the IMMA identification process. Each consideration is described briefly below and will need to be explored in depth during the process.

A. Spatial and temporal sampling

The results generated and conclusions drawn from any genetic analyses are highly sensitive to the sampling scheme adopted. How individuals were sampled spatially and temporally directly influences the determination of population/management units, inferences regarding the dynamism of those units through time, and estimates of genetic diversity. These issues are particularly pertinent to studies of highly mobile and migratory species, where a genetic study may only capture a snapshot of the patterns existing at that particular stage of their migration or life cycle. In light of the fact that comprehensive spatial and temporal sampling is not possible, it is very important that details of the sampling scheme and associated levels of uncertainty be made available to the IMMA planner in a way that is very clear to understand. If not, there is a very high risk that IMMA identification will be made based on highly uncertain or inappropriate data that could be of serious detriment to the management units under consideration. If the assumption is that most IMMA planners are not geneticists, significant effort is needed to explore how this issue can be addressed so that decisions are biologically and ecologically meaningful.

B. Extent and resolution

Related to the issue of sampling, is that of extent and resolution of the data used. Inferences regarding the delineation of management units and the connectivity between may be very different when a study region is 10 km² compared to 100 km², for example. A robust methodology to scale our understanding of management units both up and down has not yet been developed and should be a focus of significant future research. In the interim, explaining this issue clearly to the IMMA planner and/or incorporating this into a measure or metric of uncertainty should be undertaken.

C. Thresholds of “difference”

Prioritization decisions often require information regarding thresholds of “difference”, for example, are management units different or not, are they adequately connected or not, are they genetically diverse or not? As genetic data and information is generally continuous, there is a need to incorporate the ability to explore different thresholds into the IMMA planning tool, so that users can make inferences based on thresholds defined by the IMMA criteria, or to enable the exploration of how genetic inferences change across a range of thresholds. The simplest way to incorporate this into an IMMA planning tool would be to develop a “sliding scale” tool for each relevant genetic metric, which would allow the user to define threshold values *a priori*, or explore how genetic patterns vary with varying thresholds. It was concluded during the IMCC3 Focus Group that these thresholds should be defined as part of the criteria testing process, as they are specific to species and management goals.

D. Uncertainty

Every aspect of genetic analyses carries some component of uncertainty and it is essential that IMMA planners have this uncertainty clearly presented to them so that it can be considered in parallel with the results of the genetic analyses. It was concluded during the IMCC3 Focus Group that uncertainty information could be supplied as metadata/attribute information. However, the challenge lies in communicating this information adequately and clearly to IMMA planners, so that they can include it in any management decisions that are made. A specific consultation process with managers is recommended to develop an approach to addressing this.

E. Predictive framework

Current genetic analyses provide important information for management on species and population patterns, however methods provide a current or historic snapshot rather than enabling predictions of how these patterns may change in the future. Given the need to adaptively manage in the face of environmental change, the ability to make such predictions would be highly useful for IMMA planners. There is therefore a significant need to advance scientific understanding of the mechanisms (i.e., biological, ecological, and evolutionary processes that are driving the genetic patterns observed. Understanding these mechanisms represents an important initial step to developing a predictive evolutionary framework.

3. CONCLUSIONS

Genetic data can inform the IMMA identification process in a variety of ways at the species, population and individual level that are not captured by other types of data and information. There is therefore a significant need to ensure this data is considered in a systematic way during the IMMA identification process in a way that is both accessible and relevant.

There are a wide variety of ways that genetic information can be visualized and integrated successfully into an IMMA identification process at multiple scales. This document highlights a number of considerations in the interpretation of the genetic information once it is visualized and opportunities for further research, both of which need to be explored as part of the development of this approach. Educating IMMA planners on the uncertainty of the data, whilst also providing useful information upon which to base decisions will be important and we recommend be specifically addressed through consultation with IMMA planners. Finally, an important conclusion from the discussions was that not all types of genetic information can be spatially visualized, however they are still extremely valuable and should be integrated into IMMA identification decisions.

We view the integration of genetic information into the IMMA identification process as an exciting opportunity for an intersection between our two efforts. It is our hope that the ideas put forth in this document form the basis of further discussion, testing, and refinement of these methods, which will result in a standardized approach that will serve to enhance marine mammal protection efforts. We ask the participants of the expert workshop to view this contribution as a first step in a longer-term collaboration, and suggest that the development of applied regional or species-specific case studies represent a useful next step towards developing the ideas summarized in this document.

4. REFERENCES (INC. APPENDICES)

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Mendez M, Rosenbaum HC, Wells RS, et al. (2010). Isolation by environmental distance in mobile marine species: molecular ecology of franciscana dolphins at their southern range. *Molecular Ecology*, **19**:2212-2228.

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APPENDIX 1: EXAMPLES OF DATA VISUALIZATION

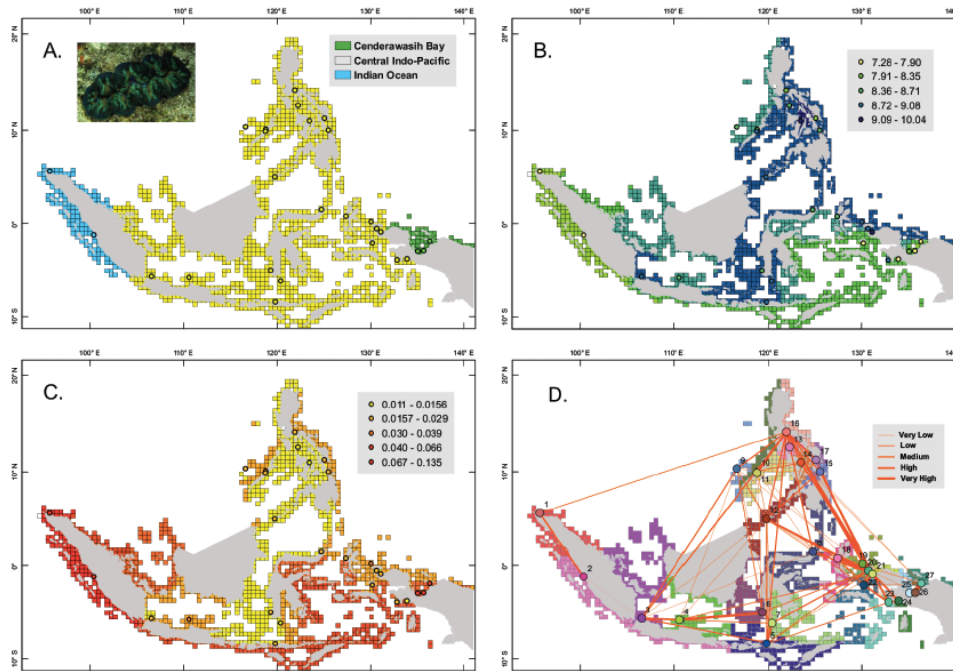


Fig. 1: Spatial representation of four genetic attributes: A) Genetic sub-regions (STRUCTURE cluster analysis); B) Genetic diversity (allelic richness); C) Genetic distinctness (local F_{ST}); and D) Rates and directionality of gene flow (Beger et al. 2014).



Fig. 2: Map showing the distribution of humpback whale mtDNA haplotypes across the northern and central Pacific using the planning tool, geneGIS (Dick et al. 2014). Five distinct population segments are identified (1-5) © C. Scott Baker

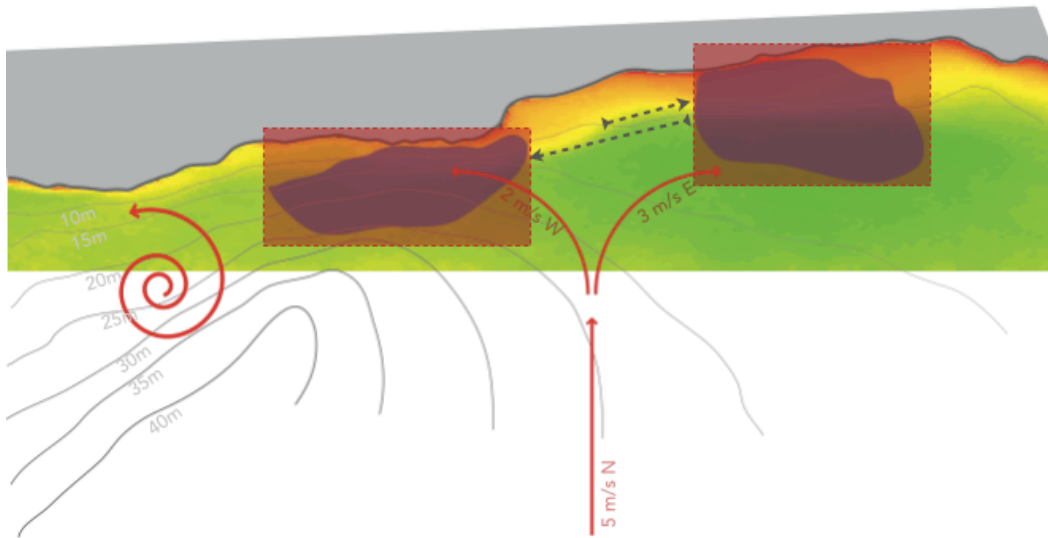


Fig. 3: Two putative genetically differentiated populations (blue polygons) overlaid with proposed marine protected area boundaries (red rectangles) and oceanographic data including sea surface temperature, bathymetric contours and major currents and eddies. © Martin Mendez

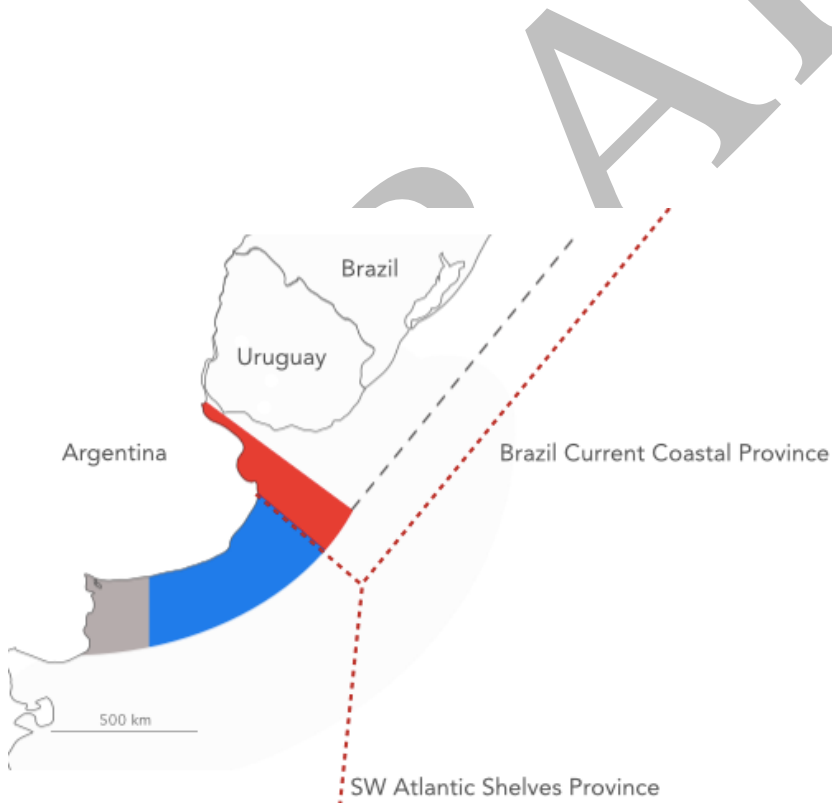


Fig. 4: The location of three genetically differentiated populations of franciscana dolphin (*P. blainvillei*) overlaid with the location of oceanographic provinces within Argentina's exclusive economic zone (EEZ). © Martin Mendez

APPENDIX 2. HOW CAN GENETIC DATA/INFORMATION BE INTEGRATED INTO THE IMMA PROCESS?

Genetic data/information can inform the identification of IMMAs in three primary ways: A) Defining units; B) Assessing connectivity; and C) Measuring status and trends:

A. Units

Genetic tools can provide a means of quantifying similarity and differentiation between units at multiple scales, i.e. individuals and kin-relationships, demographic populations, species, and communities/ecosystems. When determining how to visualize units to inform the identification of IMMAs, two types may need to be considered: i) *a priori* units (including individuals); and ii) Non *a priori* units.

i) a priori units

Species/Community level: At the species level, there the number of species in a defined area is often a key criterion of a marine management measure. The representation of species level genetic diversity is therefore an important measure to include in the identification of IMMAs. For example:

- ⇒ Levels of genetic diversity within a species (Appendix 1, Fig. 1B)
- ⇒ Levels of species diversity within a defined area
- ⇒ Diversity hot-spots or cold-spots

Population level: At the population level, the most common way to identify whether pre-defined units are demographically distinct or not is to employ a suite of differentiation indices, such as population-specific F_{ST} , pairwise F_{ST} , ϕ_{ST} , Jost's D , etc.

These measures of genetic differentiation between *a priori* units can be visualized in an IMMA planning tool using approaches such as:

- ⇒ Heat map / kriging of population-specific F_{ST}
- ⇒ Haplotype distributions (Appendix 1, Fig. 2)
- ⇒ Kernel distribution of genetic differences (Appendix 1, Fig. 3-4)
- ⇒ Genetic differentiation analytics

Individual: Individuals are, by *de facto*, identified *a priori*. The range size of individuals and their relatedness/kinship within defined areas, for example, may provide useful insights into the delineation of units of management. Approaches to represent this information spatially include:

- ⇒ Individual kernel distributions (interpreting genetic data alongside satellite telemetry)
- ⇒ Relatedness/kinship measures (continuous metric)

ii) Non *a priori* units

Species/Community level: When the boundaries of species are not clear (e.g., when hybridization may be in occurrence or when species are cryptic/not easily identifiable when sampling) phylogenetic analysis can be undertaken to identify species-level units. These units can then be visualized in the same manner as described for *a priori* units:

- ⇒ Similarity/differentiation indices between pre-defined areas (continuous metric) (Appendix 1, Fig. 1A)
- ⇒ Clustering of units sampled in different areas represented by spatial interpolation

Population level: Clustering methods can be used to detect genetically different groups within a sample when populations cannot be identified *a priori* or to act as an independent test of those predefined groups:

- ⇒ Clustering analysis of individuals sampled in different areas represented by spatial interpolation

B, Connectivity

For the identification of IMMAS, multilocus-genotype methods that assign individuals to local populations and provide estimates of migration on an ecological timescale (i.e., demographic connectivity) are considered the most relevant as it provides estimates of recent connectivity between management units and also retention of individuals within a single unit. Movements of individuals identified by genetic capture-recapture analysis (the identification of the same individual in different locations and/or different years using genetic methods) can be used as an indicator of real-time movements and therefore is also of relevance to management.

i) Demographic connectivity

Demographic connectivity can be estimated using methods that assign individuals to local populations using multilocus genotype data and provide estimates of migration. Multilocus-genotype methods are based on complex likelihood models that include several parameters and are implemented by computationally intensive Bayesian methods (e.g., BayesAss; BIMr). Using these methods genetic data can be combined with other sources of information to increase their power or to test hypotheses about the effect of environmental or physical processes. The outputs of these methods can be represented as:

- ⇒ Network diagrams
- ⇒ Connectivity matrices
- ⇒ Genetic capture-recapture (e.g., straight lines, individual range maps, symbols representing number of recaptures)

In either the case of network diagrams or connectivity matrices, it would be useful for the user to be able to easily identify when connectivity estimates fall below a certain threshold value that may be stated in the IMMA criteria/objectives. This can easily be addressed by

incorporating a toggle or slide tool, which would enable users to easily observe how levels of connectivity change with different threshold values.

C) Measuring status and trends

Genetic tools also offer a means of measuring the status of the units identified using the methods above, and to assess how the status of these units changes through time. There are a number of measures that would be useful in this regard, including the ability to measure population reduction including the detection of historic population bottlenecks, effective population size, population diversity, and species diversity. Most measures of genetic diversity and N_e can be described by a simple summary statistic. Therefore, in terms of visualization, the value of the statistic could be used to color-code a polygon that represents the management unit, once its boundaries have been identified. There are, however, a number of different ways to calculate metrics of diversity and effective population size, and so it will be important to adopt a standard approach for all data included in the IMMA identification process (or it will be necessary to incorporate a conversion factor following raw data entry). There are a number of options that could be considered when visualizing this type of information:

- ⇒ Raw variables (e.g., effective number of alleles, number of haplotypes, haplotype diversity, nucleotide diversity, etc.) (Appendix 1, Fig. 1B).
- ⇒ Standardized variables (i.e., each measure of diversity could be converted to a standardized scale prior to being color-coded).
- ⇒ Composite variable (i.e., a single composite measure of “genetic diversity”).

APPENDIX 3: LIST OF ATTENDEES AT THE IMCC3 FOCUS GROUP

Organizers:

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