

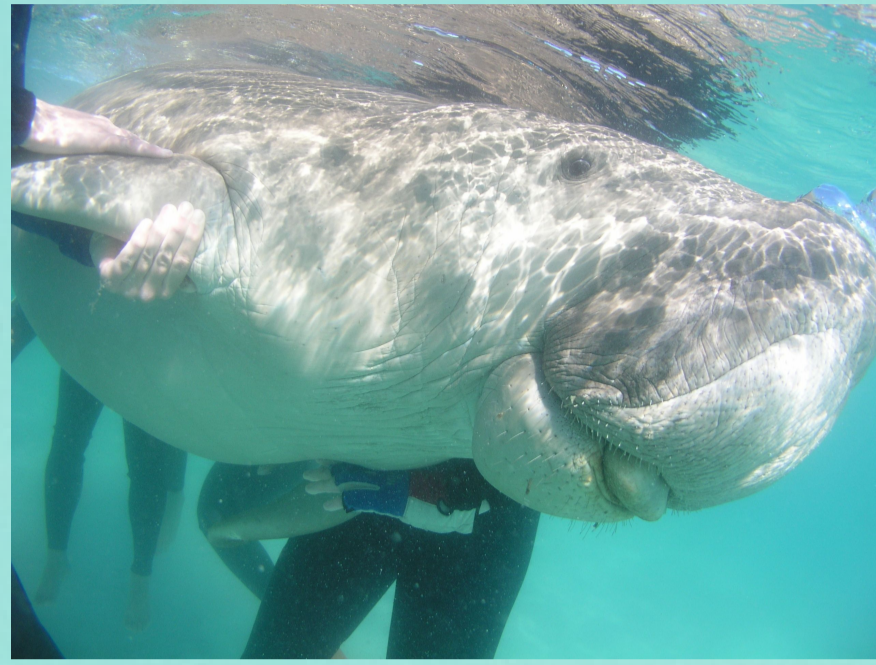
Reconstructing family trees for free-ranging dugongs in southern Queensland, Australia.

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Abstract

The dugong (*Dugong dugon*) is a marine mammal that inhabits tropical and subtropical regions of the western Pacific and Indian Oceans. The cryptic nature and fully marine lifestyle of dugongs present a unique challenge in understanding reproductive behaviour and mating patterns because these cannot be directly observed. For over ten years, the UQ Dugong Research Team has been collecting biological and ecological data on free-ranging dugongs in three locations within southern Queensland, Australia. In this study we used genetic data for individual dugongs sampled by biopsy and then genotyped against a panel of 26 microsatellite loci to identify and discriminate individuals unambiguously. Identity data and genetic relatedness along with biological information including sex, body size and maturity status were used to construct most likely genealogies.



We constructed family trees for >800 individual dugongs sampled in Moreton Bay, >500 from the Great Sandy Straits and >100 from Hervey Bay; this sample includes 170 known cow-calf pairs. Family trees were constructed via Maximum Likelihood Estimation using the Cross-Entropy method informed by biological data using software developed specifically for this project. This software was designed to address challenges inherent in sampling populations of live dugongs, and included strategies to deal with missing data including un-sampled individuals. The software was tested on large simulated populations (with known familial relationships) designed to mimic the genetic and life history characteristics observed in real dugong populations. This work provides the first analysis of family trees for dugongs, and we will discuss the techniques used, the structure of the resulting family trees and the insights these provide. Knowledge of these family trees enhances our understanding of demographics, movement between habitats, and mating strategies; all information that will assist conservation agencies to identify appropriate population management units and thus assist in strategic protection of this vulnerable species.

Methods: Data Collection

- ▶ The UQ Dugong Research Team has been collecting biological and ecological data on free-ranging dugongs within southern Queensland, Australia for more than ten years.
- ▶ Live dugongs have been sampled in Moreton Bay (MB), the Great Sandy Straits (GSS) and Hervey Bay (HB); we also have several samples from necropsied dugongs, including from unknown locations.
- ▶ We have collected a total of 1766 samples of 1176 unique dugongs with up to 6 recaptures of an individual.
- ▶ Dugongs were sampled primarily by either in-water capture or by skin scrape without capture.
- ▶ A panel of 26 microsatellite loci allowed for unambiguous identification of individual dugongs and their heritable genetic identity.
- ▶ Biological data collected includes sex (observed and molecular), body size and maturity status (through hormone analysis).
- ▶ 170 Cow-calf pairs were included in the dataset.

Descriptor	Total #	Gender			Size Class		
		M	F	?	Adult	Sub-adult	Juvenile
MB	652	257	317	78	402	139	111
GS	301	117	145	39	177	73	51
HB	65	32	33	0	45	8	12
O	42	19	19	4	33	3	6

In this study, we considered 1060 unique dugongs with the strongest available genetic data.

Methods: Pedigree Reconstruction

- ▶ Pedigree reconstruction is a difficult computational problem - there are $O(N^N)$ possible pedigrees, many of which are not biologically reasonable or consistent.
- ▶ We constructed the maximum likelihood pedigree using the Cross Entropy method for combinatorial optimization. This construction was performed using software designed specifically for this project.
- ▶ The likelihood of a pedigree is the sum of the transition probabilities for each relationship within the pedigree, provided that it is consistent.

$$\max_{\mathcal{P} \in \mathcal{F}} LL_{\mathcal{P}}(\mathcal{P}) = \max_{\mathcal{P} \in \mathcal{F}} \sum_{(c, p_1, p_2) \in \mathcal{P}} LOD(c, p_1, p_2),$$

$$LOD(g_A, g_B, g_C) = \log \frac{T(g_A | g_B, g_C)}{Pr(g_A)}$$

- ▶ Pedigree consistency is certain due to mathematical technology presented by Alumdevar (2003). We used biological data to inform construction, restricting parent-pairs by sex and parent-offspring relationships using size class and sample date to infer possible maturity.
- ▶ The system is flexible: it can handle populations with arbitrary numbers of individuals or loci, incomplete sampling, missing biological information (such as unknown sex), and errors in genetic data (missing or incorrect loci).

Methods: Validation

- ▶ Initial testing of the pedigree reconstruction system was on large simulated populations (with known familial relationships) designed to mimic the genetic and life history characteristics observed in real dugong populations.
- ▶ Validation in the real data set was performed by careful analysis of extracted relationships, comparisons of known cow-calf pairs, recapture histories, capture locations and growth curves.

Results: Population-Level Summary

- ▶ The maximum likelihood pedigree on these 1060 dugongs detected 814 parent-offspring relationships.
- ▶ Of the individuals detected as parents, 173 were female (33.7% of all females in the population), 124 were male (29.1% of all males) and 41 were of unknown gender (33.9% of individuals with unknown gender). The difference in proportions is not statistically significant.
- ▶ Parents were detected to have between 1 and 11 offspring. Figure 1 shows the number of offspring per individual grouped by sex: the differences in distribution were not statistically significant. Figure 3 shows the number of offspring per individual grouped by sample location: these distributions were also not significantly different.

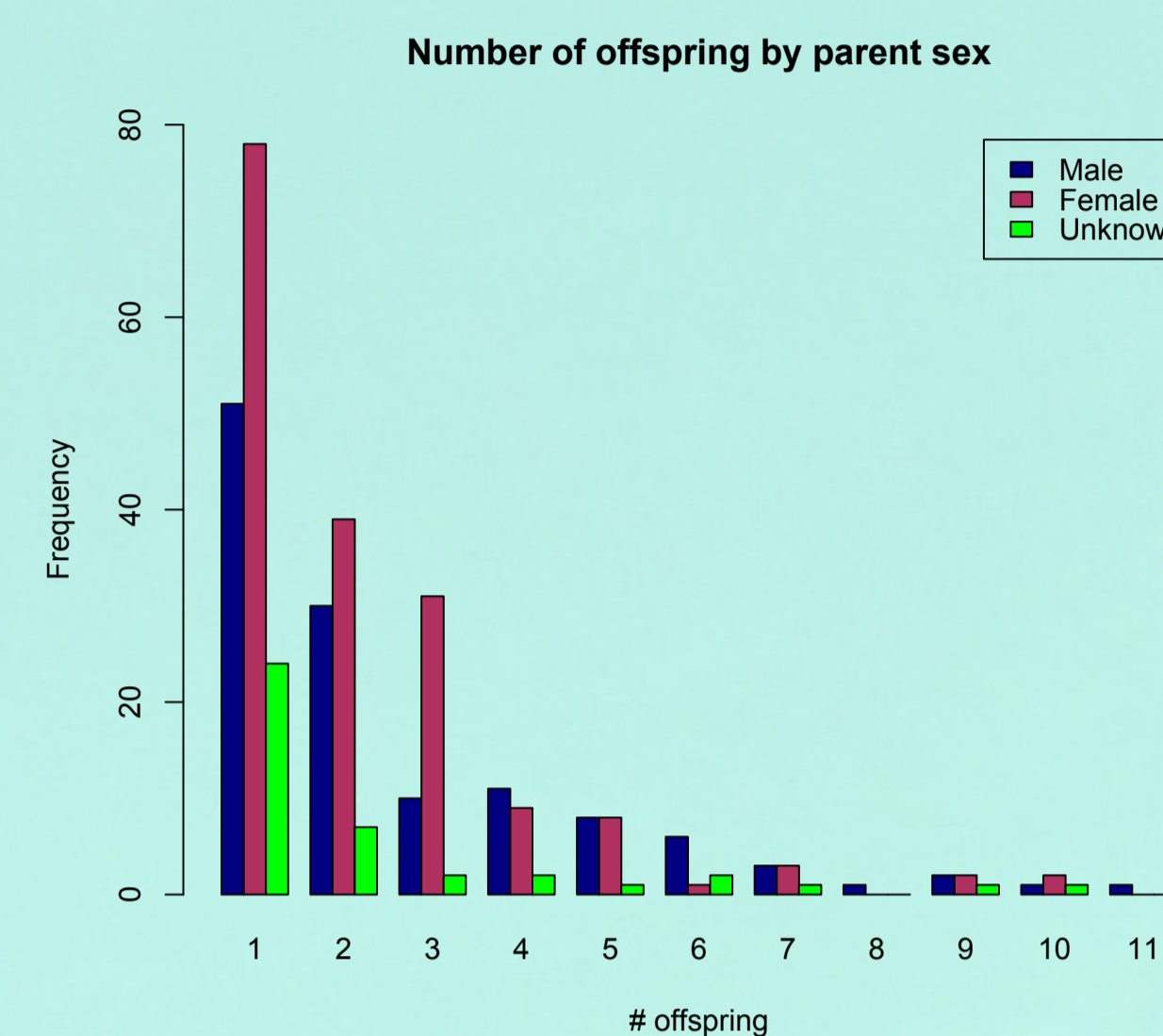


Figure 1: Number of offspring by parent sex

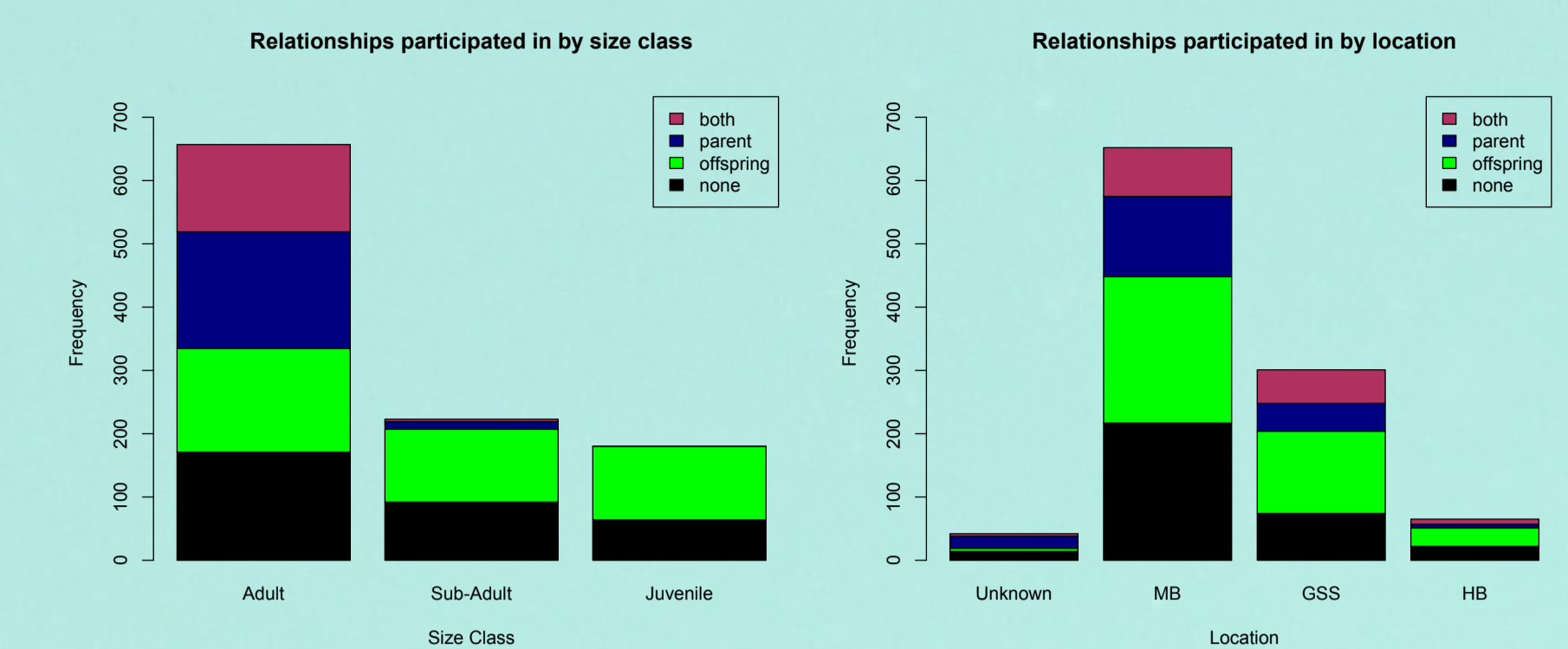


Figure 2: Relationship participation

- ▶ 95% of detected parents were individuals first sampled as adults. No individual sampled as a juvenile has yet been detected as a parent.
- ▶ 142 individuals were detected as being both parents and offspring. Of these, 138 were sampled as adults and 4 were sampled as sub-adults. Relationship participation by size class is shown in Figure 2(a).
- ▶ GSS had a significantly higher proportion of individuals detected as offspring than MB, as well as individuals that were both parents and offspring, but the proportion of parents was lower. Relationship participation by location is shown in Figure 2(b).

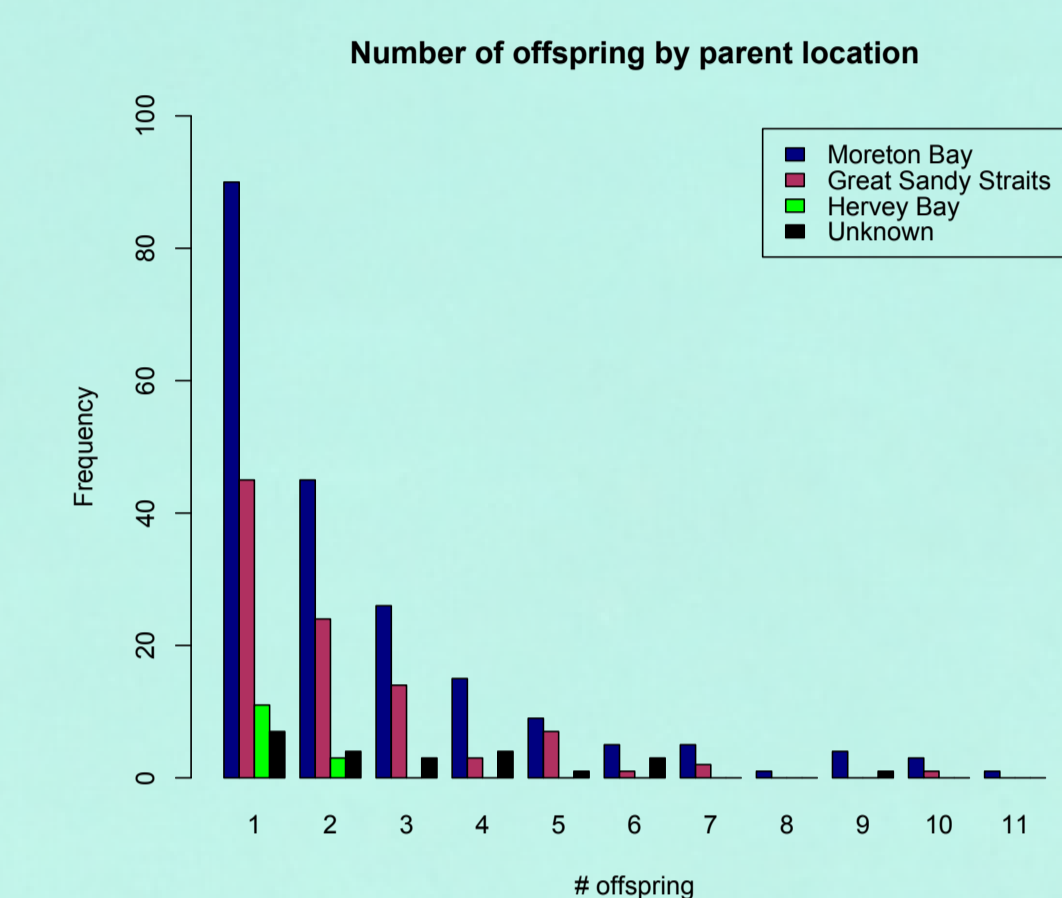


Figure 3: Number of offspring by location

Results: Specific Examples

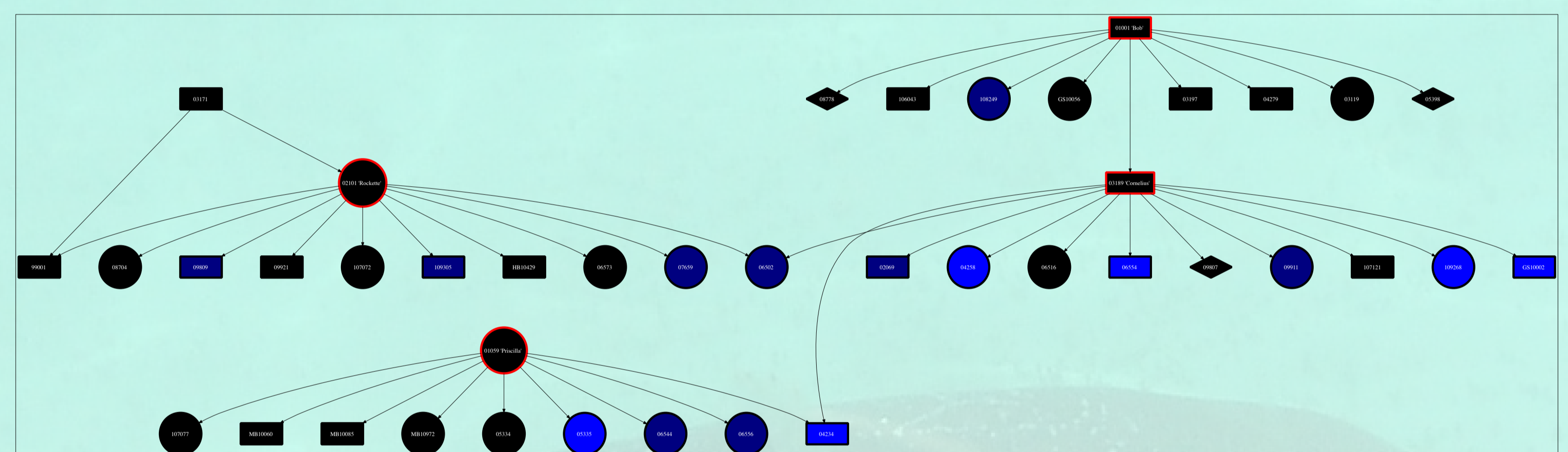


Figure 4: Descendants of individuals 01001, 02101, 01059, 03187

- ▶ Preliminary analysis indicated that a small number of individuals dominate the genealogy in terms of number of offspring and pedigree connectivity. In MB, these include:

- ▶ Bob (01001) an adult male sampled in 2001.
- ▶ Priscilla (01059) an adult female (260cm) sampled in '01.
- ▶ Rockette (02101) an adult female (297cm) sampled in '01, '03 & '05.
- ▶ Cornelius (03189) an adult male (305cm) sampled in '03, '05 & '10.

The detected offspring of these individuals (Figure 4) suggest promiscuous mating of individuals in this population: these individuals share single offspring, but no full-sib pairs.

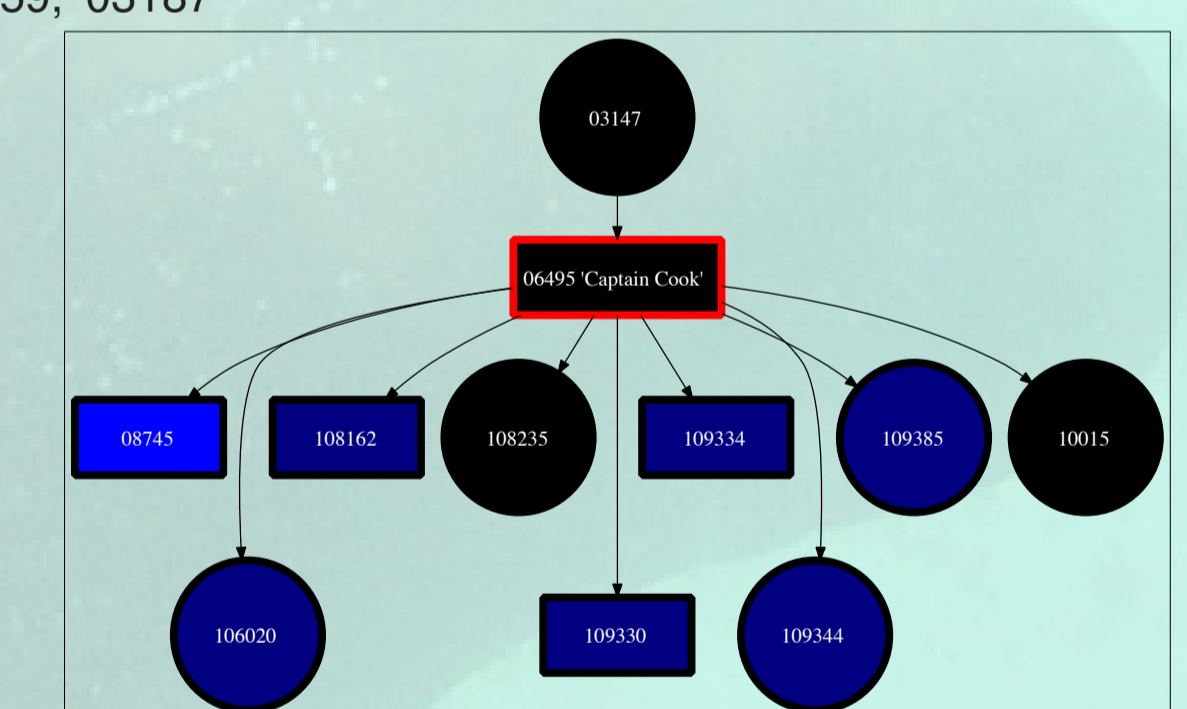


Figure 5: Descendants of 06495

- ▶ The individual 'Captain Cook' (06495), sampled once in Moreton Bay in 2006, has been detected with 9 offspring (Figure 5): 7 of these offspring were sampled in GSS, one in HB and one in MB. Given that the individual was sampled in MB and the offspring in MB was a (large) calf, this implies *movement and breeding* of this individual.

Conclusion

- ▶ Pedigree reconstruction is a very challenging process that has become possible recently due to advances in mathematical technology and readily available computational power.
- ▶ The wealth of biological data collected over the past 10 years for dugongs in southern Queensland, along with the genetic resolution provided by microsatellite analysis, has allowed us to exploit these advances, develop new pedigree reconstruction techniques and construct a pedigree for our sampled dugongs.
- ▶ From this preliminary analysis, we have begun to elucidate mating strategies for dugongs: we have seen indications of promiscuous breeding; we have observed individual adult male dugongs with up to 11 offspring, and adult females with up to 10 offspring; and we have seen some indication of movement between population coupled with breeding events.
- ▶ This preliminary analysis has provided insight into the connectedness of populations and breeding events within them, and further analysis will provide valuable information which will assist conservation agencies with management of the protection of this vulnerable species.

Future Directions

- ▶ Quantify movement and breeding events within and between populations in southern Queensland.
- ▶ Integrate full genealogies for each population with biological attributes.
- ▶ Elucidate further insights into mating strategies and reproductive behaviour for dugongs.
- ▶ Continue to expand and refine pedigree reconstruction and analysis as new data is available.

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