FILAMO Mobility Report

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Grant: PhD student Mobility

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Introduction

I am currently in the second year of my PhD project investigating the demography and sociality of killer whales (*Orcinus orca*) at Marion Island in the Southern Ocean. Additionally, I am investigating the effect of various environmental and climatic variables on various aspects of demography and social structure. I am making use of 12 years of photographic records collected opportunistically and during dedicated observations at Marion Island as part of the Marion Island Marine Mammal Programme's ongoing research at Marion Island. I applied for the FILAMO Mobility grant in order to gain experience in social structure and demographic analyses and interpretation from my PhD co-supervisor, Dr. Ryan Reisinger.

Detailed breakdown of learning and work

Prior to my arrival, the work I had completed for my PhD was predominantly preparatory. I became acquainted with the literature and sorted and error checked all sightings, photos and IDs of individuals within these sightings. I received a brief introduction to programme MARK and was working through its specific literature but was far from being efficient in it. The following bullet points summarise what was achieved during each week of my 9 week visit to the CEBC:

- [Week 1 and 2] During the first two weeks, I built on my previous knowledge of MARK and worked my way through various examples. By the end of this week, I was accustomed to running numerous models and varying parameters. I ended the second week by analysing the data specific to my PhD. I determined the most parsimonious POPAN and Pradel Lambda capture-recapture models and obtained survival, population size and growth rate estimates. During this period, I also developed a life table of the study population. This table included details on each animal such as when they were first seen, when they were last seen, their estimated period of birth, estimated age and when calves they produced. This was achieved by extracting data from the observation histories and by analysing temporally distant photographs. From this table I could determine the calving rate of the population.
- [Week 3 and 4] Through discussions with Dr. Ryan Reisinger following interpretation of my progress during weeks 1 and 2, it was decided that in order to build on my

results, I would need to run Multi-State models. I attempted to do this in MARK but was advised by various researchers in the CEBC that RMARK would be a more practical approach. I therefore 'converted' what I had learned in MARK and determined how the same was done in RMARK. This conversion took time to implement but I was eventually able to re-analyse my data and run Multi-State, POPAN and Pradel Lambda capture-recapture models. I was now able to obtain sex and class specific survival, population growth rates and movement probabilities. More importantly though, I developed an R-Script for these analyses which sped up the process and made it easier to repeat analyses. This was a highly beneficial learning period and I obtained input and help from various researchers and students on this. These results will form the base of my first chapter pertaining to the demography of killer whales at Marion Island.

- [Week 5] Now that various aspects of the demography had been determined, I now needed to determine the effect of environmental and climatic variables on various aspects of demography. Firstly, I obtained environmental and climatic variables using various sources including the use of 'Xtractomatic' in R which Dr. Reisinger helped me with extensively. Due to the time spent developing an R-Script in weeks 2 and 3, I was able to quickly adjust the script in order to factor in the environmental and climatic variables as co-variates. I was able to determine the effect of various co-variates on survival and graph co-variate predictions based on these results. These results will be used in my second chapter.
- [Week 6 and 7] Now that I had covered the majority of the analyses pertaining to demography, I moved on to the sociality aspect of my PhD. To determine the relationships between individuals, I made use of SOCPROG. The use of SOCPROG was demonstrated to me by Dr. Reisinger and once I was comfortable with the basics I determined the half-weight-index's (HWI) for each animal in the population, the various clusters, obtained network statistics and graphed network plots. This week provided me with a great introduction into social structure analyses and a basis that I could develop various questions that I wished to answer such as the temporal and seasonal variation of associations. As was the case with the demographic analyses, it was suggested that I shifted analyses into the R environment. This was suggested due to the recent advances of the packages 'asnipe' and 'igraph' meaning that I could obtain the same outputs as I could with SOCPROG but with easier repeatability. I therefore spent a fair amount of time developing an R-Script to run social network analyses. This proved (again) to be highly advantageous as I was able to re-run analyses with little stress and effort following minor adjustments to the original data set. Additionally, the network analyses were exported and network plots were drawn using the GePhi programme which Dr. Reisinger helped me understand and taught me the basics. These social network results and plots form the basis of my third chapter.
- [Week 8] With the aid of this R-Script, I was able to extract measures of social structure (HWI, strength of associations, number of associations etc.) and use these as co-variates and their effect on survival. To do this, I made use of the script I

- developed in weeks 3 and 4. The results obtained from these analyses will be used in my fourth chapter.
- [Week 9] During my final week, I began investigating Generalised Estimating Equations (GEE's). These would be used to determine the correlation between environmental and climatic variables and measures of social structure. Before I was due to leave the CEBC I managed to compose an R-Script to do these analyses and briefly tested it. I however ran out of time and was unable to obtain a full set of results but this will not be difficult to achieve as I have a working R-Script. The development of this R-Script was a bonus as I had not budgeted to get this far when I initially set out a work plan.

Conclusion

In conclusion, I believe that the time I spent at the CEBC was a success. I was able to develop R-Scripts, run full analyses and obtain results for 4 of my proposed chapters. This is what I set out to achieve and I am happy that it work out. As an extra bonus, I was able to provisionally set up an R-Script for analyses for a fifth chapter and it should not take too much time to obtain results from this when I am back at my home institute.

I believe that the successfulness of my visit to the CEBC was due to my close proximity to my co-supervisor, Dr. Reisinger and the standard work ethic of the laboratory. The presence of numerous, top-of-their-field, researchers in this laboratory also provided me with a greater opportunity to obtain feedback and insight into my analyses and interpretation. This would not have been possible without being in close proximity to these individuals as the insight I gained is generally difficult to convey over email communication. This research visit has propelled my PhD and put me in a great position to be able to potentially finish within the next 14 months. Thank you FILAMO for providing me with this opportunity, I will forever be grateful for it!