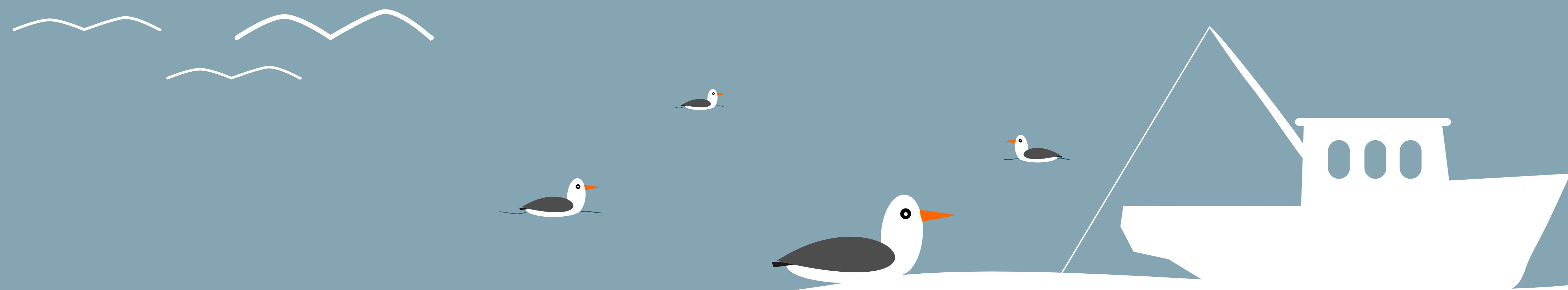


We are developing a simple DNA-based methodology for **species identification of seabird bycatch**.

This will help to **identify species most at risk from bycatch mortality** and **guide conservation management**.



Seabird surveillance: developing a new genetic analysis for bycatch species identification

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INTRODUCTION

- Almost half of seabird species are known or thought to be experiencing population declines (Croxall et al. 2012).
- Mortality due to bycatch in fisheries has been identified as one of the biggest threats to seabirds worldwide.
- Determining the level of risk to each species is difficult due to challenges in identifying caught specimens.
- DNA barcoding is a methodology that uses comparisons of mitochondrial DNA sequence at a standardised locus (COI) for identification of specimens, and would provide a useful tool for bycatch species identification.



OBJECTIVES

- To develop a DNA marker that is simple and universally applicable for identifying seabirds to species level.
- To use known specimens to construct a reference DNA sequence database.
- To develop this methodology for application in fisheries management for identification of species most at risk from bycatch.

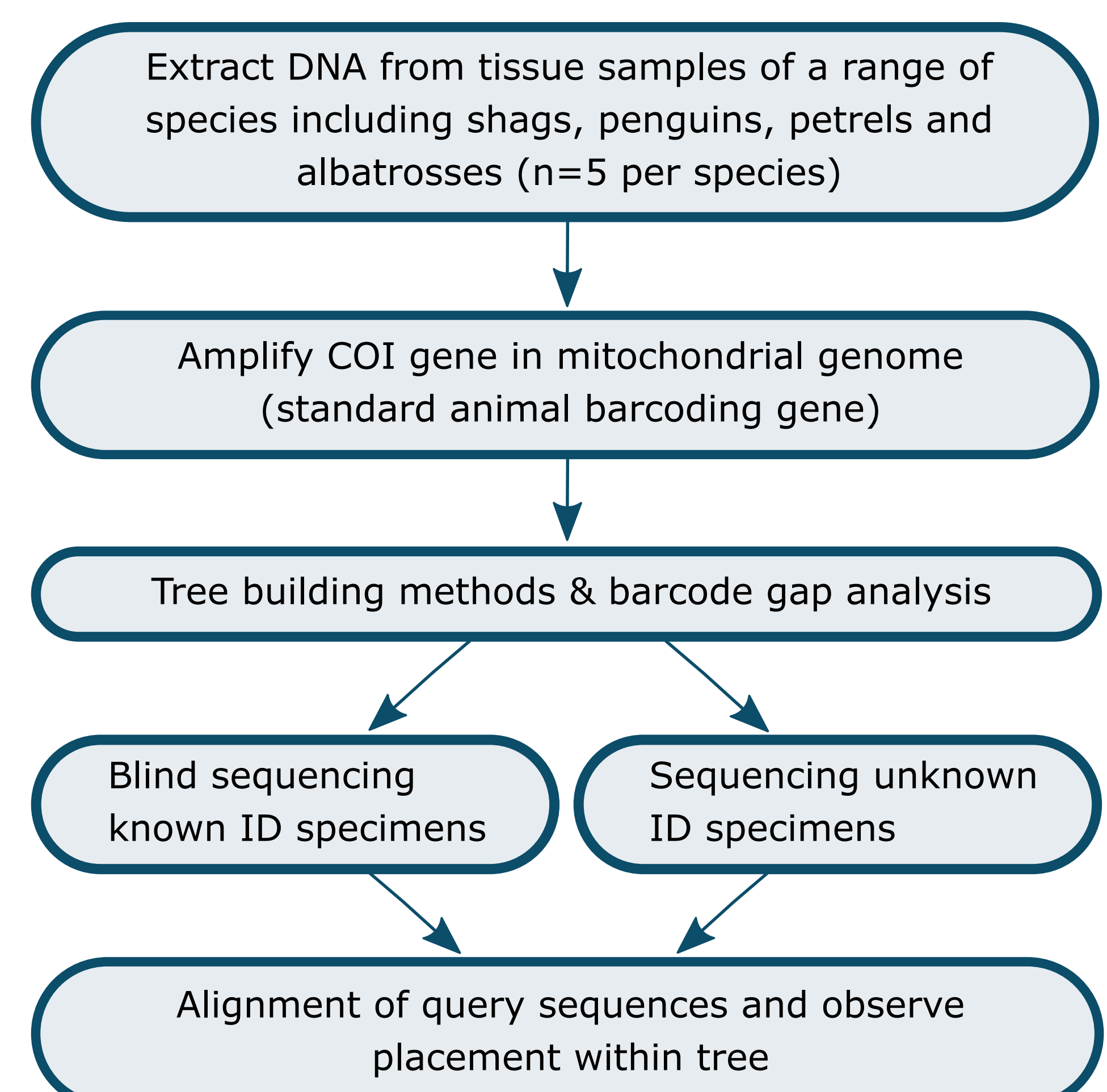
CHALLENGES OF IDENTIFYING SEABIRDS

- Closely related species show morphological similarities.
- Fisheries observers may not be able to accurately identify species.
- Cost and logistical constraints can be a barrier to having whole specimens returned to land for formal identification.
- Identification is further complicated when specimens are degraded or damaged (by fishing gear, sea lice etc).



Bycaught seabird specimens showing damage from fishing operations. Photos: Biz Bell

METHODS



DIVING DEEPER: ALBATROSS GENOMICS

- ✧ This molecular analysis is the beginning of a proposed in-depth whole genome analysis of Antipodean (*Diomedea antipodensis antipodensis*) and Gibson's albatross (*Diomedea a. gibsoni*).
- ✧ High fidelity long-read sequencing technologies will be used for high quality de novo genome assembly of both taxa.
- ✧ Genome-wide SNP markers will provide a high-resolution data set to detect fine-scale population structure.
- ✧ This data will be used to **identify the level of genetic differentiation** between these subspecies and **calculate genetic diversity and effective population sizes (N_e)**.



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