This document is a walkthrough of the documents and code in the folder to develop and scale a 3D model using data output from MorphometriX or CollatriX, and also explains the process to identify the optimal models for a given dataset.

1. Start with the document **How to construct a 3D model in Blender**, whichcontains instructions and screenshots of the model building process in Blender.
2. From dorsal images of the study species, use MorphometriX and/or CollatriX to generate a file resembling **example\_data/L0/example-MorphometriX-output.csv** in this folder., which contains total length (TL) and width measurements at 5% TL intervals.
   1. At this stage, only individuals which have all 17width measurements and TL should be included.
3. From dorsal and lateral images of the study species, use outputs from MorphometriX and/or CollatriX (subsequent heights and widths measurements) to calculate mean height-width (HW) ratios. Convert these ratios to a csv file matching the format of **example\_data/L1/example-HW-ratios.csv**, which contains mean HW ratios from the Australian dataset described in the manuscript.
4. Open **instructions\_scale-models\_output-SA-V.blend**, whichis a blender file that scales a 3D model using width measurements and height-width ratios.
5. Follow the instructions in [this video](https://www.youtube.com/watch?v=gyRoY9QUNg0), which explains how to install the pandas module for python in blender.
6. Within the Blender file, open the script **calc\_vols\_and\_SA** and follow the script, which will output surface area and volume estimates by 5% segment for each individual in your dataset.
   1. Make sure the associated volume and surface area files were written correctly.
7. Open **instructions\_generate-all-width-combos\_adults-and-juveniles.R**, which will average all your TL and width data for adults and juveniles, respectively. It will also generate all 131,072 combinations of these average measurements for the next step.
8. Return to the Blender file and transition to the script titled **all\_adult\_combos** (or **all\_juvenile\_combos).** 
   1. Ensure that the input file is specified as **example\_data\L3\\mean\_adult-morph\_combos.csv** and the output file is specified as **example\_data\L4\\mean\_adult\_combos.csv**
   2. Exchange ‘adult’ for ‘juvenile’ as appropriate in terms of script use and file selection. The remainder of this file will refer only to the adult version as the juvenile version follows the same workflow.
   3. Test the line of code **test\_run=list(scale\_whales(range(10)))**.
   4. If it works properly, change the number 10 to **len(humpback\_morphs)** and run the code.This will tell the code to generate one model for every row in the input file. It will take ~12 hours to run, probably varying based on processing power.
   5. When it is done, run the remainder of the script to save the calculated volumes.
      1. We have included example datafiles to guide the interested user, but the above step and remaining steps do not have associated datafiles because of the length of time the code takes to run.
9. Open **instructions\_select-candidate-models.R** and run the code, which will identify the candidate models which are sufficient to move on to the next step.
   1. The specific number of widths required and error threshold is up to the user to decide. These values can be changed in the code file. The code as written selects models with 2-5 widths and <5% error as sufficient.
10. Return to the Blender file and exchange the input file on the adult script to **example\_data\L5\\adult\_candidate\_models.csv** and the output file to **example\_data\L6\\adult\_candidate\_model\_volumes.csv.**
    1. Test the line of code **test\_run=list(scale\_whales(range(10)))**.
    2. If it works properly, change the number 10 to **len(humpback\_morphs)** and run the code.This will tell the code to generate one model for every row in the input file. The amount of time this code will take is directly proportional to the number of rows in the input file.
    3. When it is done, run the remainder of the script to save the calculated volumes.
11. **Open instructions\_evaluate-candidate-models.R**, which will identify the optimal models that were sufficient as per the user’s choice.
    1. Again, the specific number of widths required and error threshold is up to the user to decide. These values can be changed in the code file. The code as written selects models with 2-5 widths and <5% error as sufficient.
    2. The optimal models (i.e., the specific combinations of widths for each reproductive class) will be output as a csv file.
12. Future measurement efforts can be cross-referenced with these optimal models to determine if the measurements taken for an individual are sufficient to estimate volume.