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.

If you only need to scale models (most cases):

1. 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.
2. 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.
3. Open **generic-humpback-model-scaling.blend.** Make sure both the 3D viewport window and the coding window are open. Change the file paths for the morphometric data you are using (described in step 1) and the height:width ratios (described in step 2) and make sure that Blender can open them.
4. Define your variables. The objects **model\_names**, **first\_width\_column**, **last\_width\_column**, **tl\_column**, and **whale\_id\_column** must be defined as strings (with quotation marks). These variables tell python which columns to use to scale the model, and later to append metadata to the csv that will be exported.
5. Copy and paste the code one function at a time up through the function **scale\_whales** into the console, hit Enter, and evaluate the output. It is recommended to print the files that you loaded in to make sure python is reading them correctly (e.g., type **humpback\_morphs** into the console and hit Enter).
   1. If you copy and paste all the code in one huge chunk, python may throw an error; in this case, just carefully run code one function at a time and try again.
6. Run the line of code that begins with “test\_run”. Blender will be unresponsive for a short period of time (proportional to the number of rows in your morphometric dataframe). When it is complete, python will print the runtime of the code.
7. Run the subsequent lines of code and test that the dataframe **test\_vols** prints as expected. If so, run the final lines of code after changing the output file to a descriptive name.
8. Make sure the csv was output correctly. There should be one column each for Animal ID, total length, and reproductive class. There will also be 17 columns which contain the segment-specific lengths for the 3D model, in m3. Each of these columns correspond to the volume of a specific 5% lengthwise segment of the whale; for example, the first column contains the segment of the whale from the rostrum to 5% of the total length. However, the last column contains the volume of the 3D model from 85% total length to the fluke notch, as 85% is the last measured location that can be used for this 3D model. If you are only interested in the total volume of the whale, just sum these columns together for each whale.

If you want to quantify volume error as a function of the number of width measurements used to scale the models:

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.