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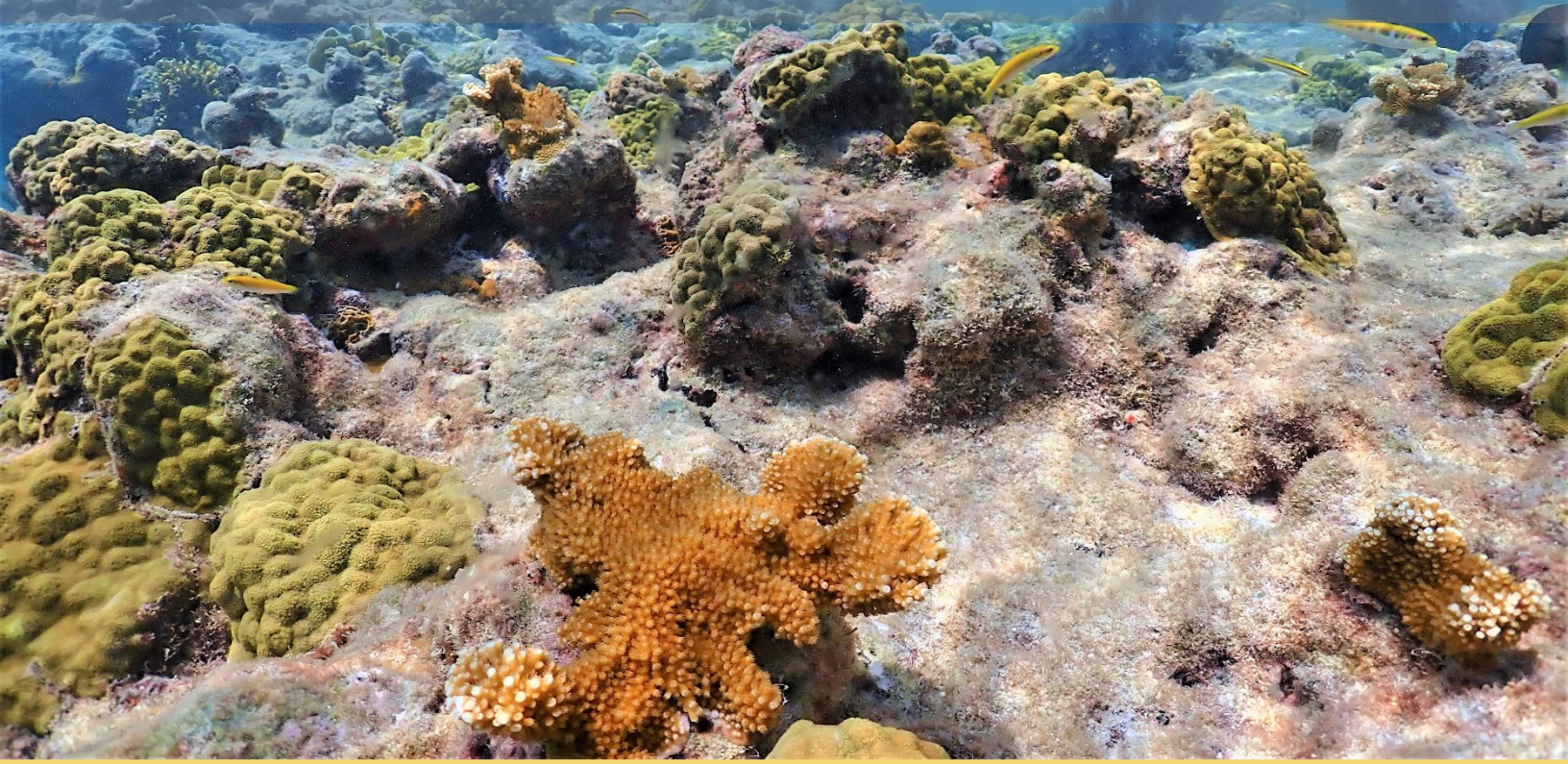
Standard operating procedures for the use of large-area imaging in tropical shallow water coral reef monitoring, research, and restoration:

Applications for Mission: Iconic Reefs restoration in the Florida Keys National Marine Sanctuary



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NOAA NOS National Centers for Coastal Ocean Science

Standard operating procedures for the use of large-area imaging in tropical shallow water coral reef monitoring, research, and restoration:

Applications for Mission: Iconic Reefs restoration in the Florida Keys National Marine Sanctuary

Prepared By

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Executive Summary

This is a standard operating procedure (SOP) for the implementation of large-area imaging (LAI) to support coral reef science. LAI refers to an approach that leverages structure-from-motion (SfM) photogrammetry to generate a variety of composite digital representations of sessile benthic communities. These digital reconstructions can be visualized as 3-dimensional (3D) models, 2-dimensional (2D) map views (e.g., orthoprojections) and a variety of other image-based products from which a variety of key ecological metrics can be extracted. The first section of this document covers the generation of 3D models and associated products using imagery collected in the field and processed with the photogrammetric software Agisoft Metashape (Agisoft LLC, St. Petersburg, Russia). Next, instructions are provided for the use of the custom software platform Viscore for the extraction of benthic percent cover data, coregistration of time series imagery, generation of 2D map views, and project management. The final section provides guidance on the extraction of coral demographic data using the artificial intelligence (AI)–based data extraction software TagLab.

The approach described herein was developed with guidance from the software developers of Viscore and TagLab, along with the Sandin Lab at the Scripps Institution of Oceanography, University of California (UC) San Diego. This SOP has been tailored to support the evaluation of coral reefs as part of active projects by the National Oceanic and Atmospheric Administration (NOAA) National Ocean Service (NOS) National Centers for Coastal Ocean Science (NCCOS), and it was specifically developed to evaluate NOAA's *Mission: Iconic Reefs* (M:IR) coral restoration in the Florida Keys National Marine Sanctuary. This document provides foundational guidance on the use of these software packages for a broad audience interested in the application of LAI for coral reef monitoring, research, and restoration. The workflows that are described do not represent a comprehensive summary of the functionality and capabilities of Metashape, Viscore, or TagLab. A general overview regarding the use of LAI for coral reef science can be found in Edwards et al. (2023), as well as in the detailed SOPs provided by the various contributing authors therein.

Introduction to the Imagery Analysis Workflow

The large-area imaging (LAI) approach is divided into four steps of the "LAI Pipeline": 1- *image collection*, 2- *model construction*, 3- *ecological analysis*, and 4- *data curation*. This SOP provides detailed instructions for the implementation of steps 2 and 3 of the pipeline as used by NCCOS to evaluate benthic communities on shallow-water coral reefs. As data curation occurs throughout the LAI pipeline, it is partially addressed herein, and specifics of the image collection approach used by NCCOS can be found in Sandin et al. (2023).

The first step in the analysis workflow provided in this SOP describes the application of Agisoft Metashape Professional Version 1.8.4, commercially available photogrammetry software (https://www.agisoft.com), to create 3D reconstructions from overlapping 2D images collected in the field (Sandin et al., 2023). 3D model generation begins after image collection in the field (Figure 1) and, in this workflow, Metashape is primarily used to create a 3D dense point cloud (DPC) and a 2D orthomosaic (*Section I. Agisoft Metashape*). Next, the 3D DPC is imported into the custom software Viscore to extract data on benthic cover, generate 2D orthoprojections and coregister 3D models that are collected through time at the same location (*Section II. Viscore*). The use of Viscore for project management and data curation is also a key step of this workflow, and details of this functionality are also described. Finally, orthoprojected 2D map views generated in Viscore are imported into the publicly available software TagLab (Pavoni et al., 2022), where individual coral colonies are segmented to generate coral size structure data and, when time series imagery is available, tracked through time to generate demographic data (*Section III. TagLab*). Ecological data analyses are conducted using R, although the R scripts used by NCCOS are not provided at this time.

Throughout this SOP, words formatted in the `Courier New` font denote an item requiring an action by the user (e.g., In the Windows search bar, type `Command Prompt` to open a Command Prompt window and type `–input` then hit Enter).

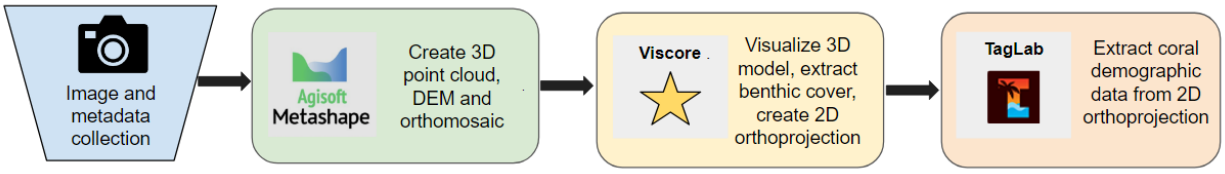


Figure 1. Diagram of image analyses workflow and software.

SECTION I. AGISOFT METASHAPE

Agisoft Metashape is photogrammetric software that uses a variety of techniques, including SfM, to generate detailed 3D models from 2D imagery of natural scenes. Model reconstruction is conducted with minimal user input and requires only highly overlapping (60%–80%) monocular imagery to generate 3D models, though more detailed imagery results in higher model quality. In practice, information regarding scale, depth, and location (e.g., latitude/longitude) is collected in the field. Four weighted scale bars (45 cm) are placed throughout the plot, along with six weighted tiles (markers) at which depth measurements are collected with a handheld depth gauge. All scale bars and markers are constructed using coded targets provided by Metashape, and GPS coordinates are collected from the surface above each of the 6 markers. This depth and scale information can be used by Metashape during model construction and, in some instances, can improve model accuracy and precision. In addition to the 3D model that is generated, a variety of additional derived products, such as orthomosaics and digital elevation models, are also created.

The process of generating 3D models is a computationally intense process that relies heavily on both graphics processing unit (GPU) and central processing unit (CPU) resources. For more information regarding needed computational resources, please refer to Edwards et al. (2023). Additionally, the general approach taken in this section has been adapted in part from methods established in Over et al. (2021), with changes made to accommodate conducting this work in the underwater environment, as well as the requirements of M:IR.

This section provides an overview of five general steps to generate a 3D model and other derived products in Metashape (Figure 2).

1. **Sparse Point Cloud (SPC) Generation.** Features in overlapping images are identified and matched to estimate the position and orientation of each image collected in the field, resulting in the creation of an SPC.
2. **Marker Detection and Verification.** Markers and scale bars configured with coded targets are placed in plots during imaging and are automatically identified by Metashape. Scale bar length and depth, which are collected in the field during imaging at each marker, are then provided to Metashape and added to the SPC.
3. **SPC Error Reduction and Optimization.** Error reduction and optimization of SPC geometry is conducted to improve SPC geometric accuracy.
4. **Dense Point Cloud (DPC) Generation.** A higher resolution and visually detailed 3D model, known as a DPC, is generated.
5. **Digital Elevation Model (DEM) and Orthomosaic Generation.** The DPC is used to create a textured mesh, which is then used to create a DEM and 2D orthomosaic.

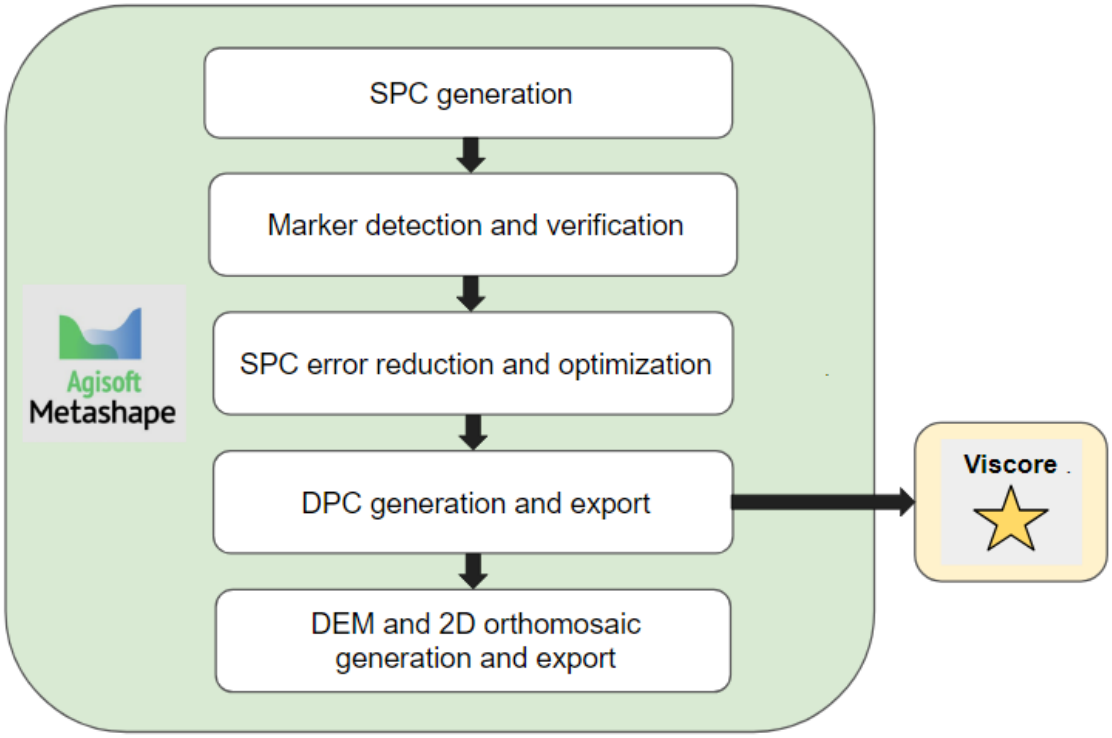


Figure 2. Diagram of steps for generating a 3D model and other derived products in Agisoft Metashape prior to exporting 3D model data for use in Viscore.

1. Preparation

A. Summary of Person Effort

Although generating models in Metashape requires significant computing power (*Appendix 1.A.*), the process requires relatively little human intervention. The Metashape workflow described here uses customized Python scripts for efficiency (Table 1), reproducibility, and minimal user implementation. Alternatively, fully manual (non-scripting based) model generation is outlined as a secondary option.

Table 1. Summary of workflow steps and time required in terms of effort in the Metashape workflow. Effort is represented as approximate time required (in minutes) for manual steps or scripted steps, where applicable.

Workflow Stage	Workflow Action	Person Effort (minutes)	
		Manual	Scripted
Preparation for the Metashape workflow	Transcribe field data	5	
	Rotating raw images	5	
SPC generation	-	5	
Marker detection and verification	Marker detection	5	< 1
	Verification of depth markers	< 60	
	Resize region	5	
Optimization and error reduction of the SPC	-	< 60	5
Building the DPC	-	5	< 1
Building DEM and orthomosaic	Preparation	< 10	
	Building	< 10	5
Export 3D model data for Viscore	-	< 10	
Total processing time		≤ 185	≤ 110

B. Requirements

Agisoft Metashape Professional Version 1.8.4. Program and license available at https://www.agisoft.com/downloads/installer

Python 3.9 (64-bit). Available at https://www.python.org/downloads

Customized Python Scripts. https://github.com/MSE-NCCOS-NOAA/MIR-Metashape-Scripts, which contains the following scripts:

1. image_rotator.py
2. MIR_Metashape_Processing_Part_I.py
3. MIR_Metashape_Processing_Part_II.py
4. MIR_Metashape_Processing_Part_III.py
5. extract_meta.py

For NCCOS and M:IR staff, all software and dependencies will need prior approval and support from IT to install.

C. Project Organization

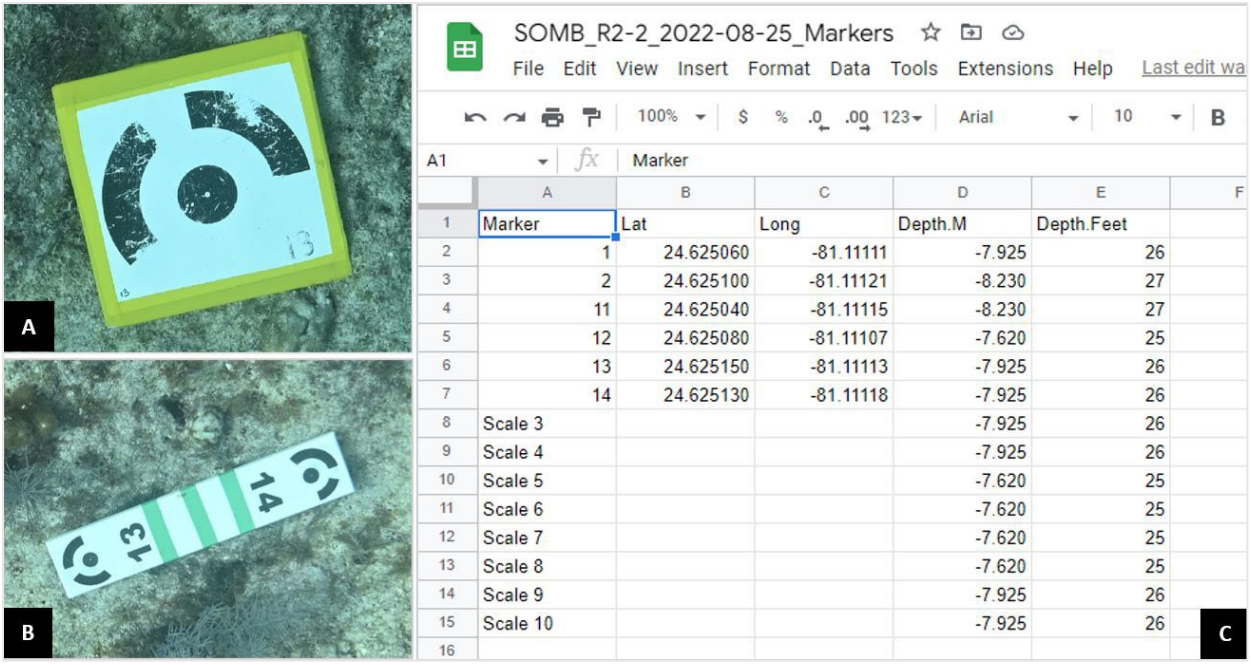
Create a project folder (e.g., MIR_NCCOS) on the designated processing drive (e.g., E:/). Within this project folder, create the following three folders:

1. **Raw_Imagery**. This folder contains subfolders for each individual plot, each of which contains the imagery used to generate the respective 3D model. Folder structure for individual plots should use the following standardized naming convention: Location_Plot-Subplot_YYYY-MM-DD (e.g., the folder associated with an imagery collection at Sombrero plot R2-2 on August 25, 2022, is labeled as SOMB-R2-2_2022-08-25_JPEG).
2. **Agisoft_Project_Data_Exports**. This folder holds all of the project files created from the model generation process in Metashape. This folder should also contain the downloaded customized Python scripts used in the Metashape workflow. Folder structure for individual plots should be named using the same standardized naming convention as the plot imagery folder (e.g., SOMB-R2-2_2022-08-25).
3. **Metadata.** This folder holds a copy of the field data sheet and the site metadata file transcribed from the field data sheet. The copy of the field data sheet should be named using the standardized naming convention (e.g., SOMB-R2-2_2022-08-25_Datasheet).

D. Metadata: Transcribe Field Data

Depth and location metadata are collected at temporary markers (Figure 3A–B) deployed in the field during imaging and are used in several steps of the Metashape workflow. Metadata collected on data sheets in the field are transcribed into a .csv file using Microsoft Excel and stored in the plot-specific Metadata folder (e.g., SOMB_R2-2_2022-08-25) along with a copy of the field data sheet.

1. From the field data sheet, transcribe the depths and coordinates onto the site metadata file (Figure 3C). Name the site metadata using the project's naming convention (e.g., SOMB_R2-2_2022-08-25_Markers). Depths should be in meters and have negative values.



	A	B	C	D	E	F
1	Marker	Lat	Long	Depth.M	Depth.Feet	
2	1	24.625060	-81.11111	-7.925	26	
3	2	24.625100	-81.11121	-8.230	27	
4	11	24.625040	-81.11115	-8.230	27	
5	12	24.625080	-81.11107	-7.620	25	
6	13	24.625150	-81.11113	-7.925	26	
7	14	24.625130	-81.11118	-7.925	26	
8	Scale 3			-7.925	26	
9	Scale 4			-7.925	26	
10	Scale 5			-7.620	25	
11	Scale 6			-7.620	25	
12	Scale 7			-7.620	25	
13	Scale 8			-7.620	25	
14	Scale 9			-7.925	26	
15	Scale 10			-7.925	26	
16						

Figure 3. Depth markers (A) and scale bars (B) are deployed in the plot during imaging. Depth measurements and GPS information are collected at each of the 6 depth markers, and depths are also collected at the scale bars (C).

E. Rotation of Raw Images

Depending on the camera model used, images will be displayed in either landscape or portrait mode with varying degrees of rotation from the orientation in which they were collected (i.e., 90 degrees, 180 degrees, 270 degrees; Figure 4). To prevent complication with display of raw images in various Viscore workflows, it is preferrable to lock images in the landscape orientation in which they were collected before use in Metashape. Python version 3.7 or more recent (64-bit) must be installed in order to rotate images.

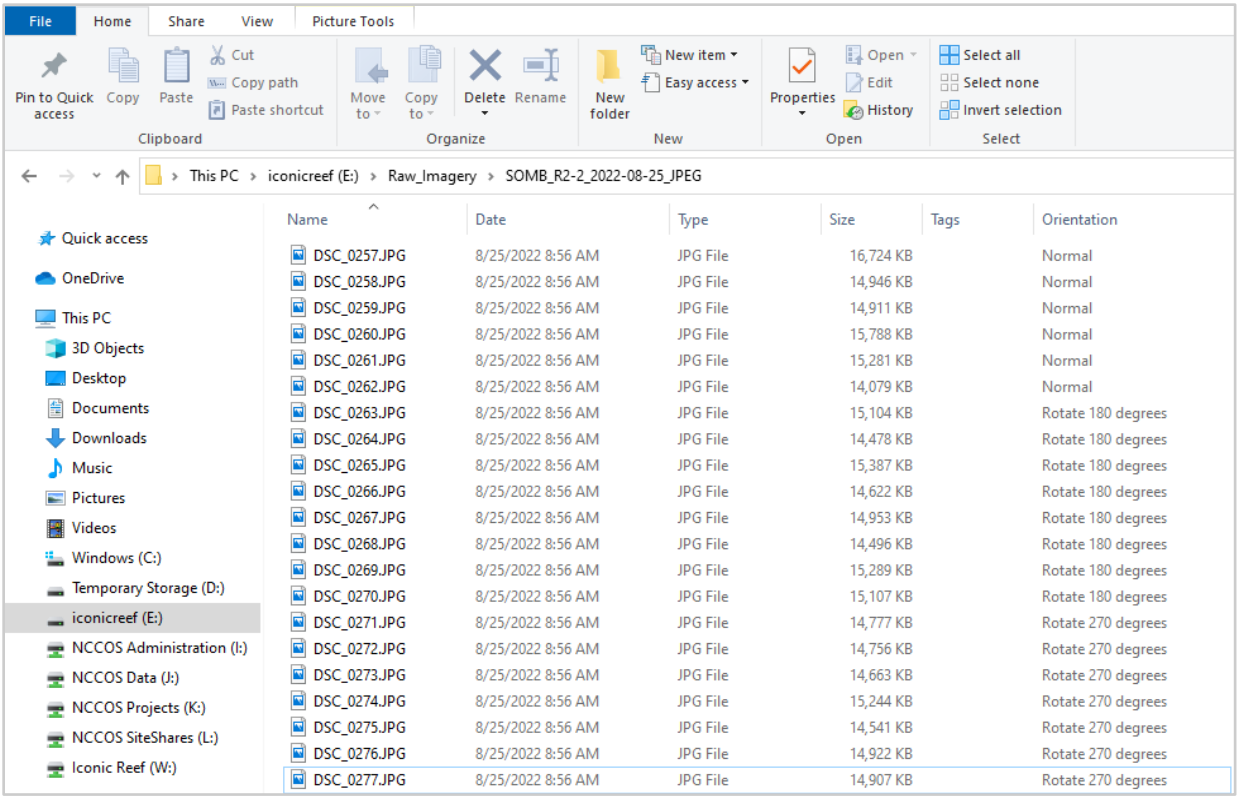


Figure 4. File Explorer window showing different image orientations (i.e., normal, 180 degrees, and 270 degrees) in the `Orientation` column (far right).

To perform image rotation, first locate the plot image folder within the raw imagery folder (e.g., E:\Raw_Imagery\SOMB_R2-2_2022-08-25_JPEG), and the image rotator script (image_rotator.py).

1. In the Windows search bar, type `Command Prompt` to open a Command Prompt window.
    A. Navigate to the folder containing the script. If necessary, first change the working drive by typing the drive letter into the Command Prompt (e.g., C drive to the E drive; Figure 5). The Command Prompt will reflect the change to the designated working drive (e.g., E:\>).

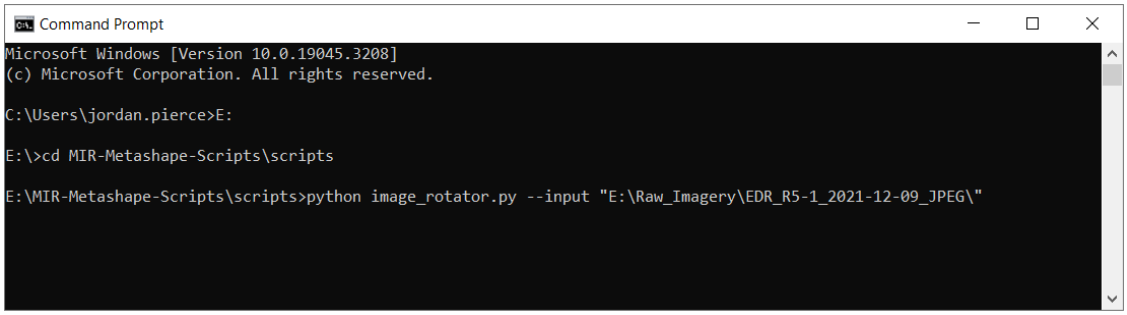


Figure 5. Command Prompt window showing correct inputs described in steps A–C.

    B. Within the working drive, use the change directory command (i.e., cd) to change the directory to the folder containing the script. To run the script, type `python`, the name

of the script (i.e., image_rotator.py), followed by the file path for the image folder (e.g., E:\Raw_Imagery\SOMB_R2-2_2022-08-25_JPEG) as an input argument. Press Enter to execute the script (Figure 5). For convenience, copy the file path for the image folder by using Shift + right-click over the image folder to open the context menu and select `Copy as path` (Figure 6).

- To rotate images for a plot:
  Use script: image_rotator.py
  Type the following: `--input`, followed by the file path to the image folder.

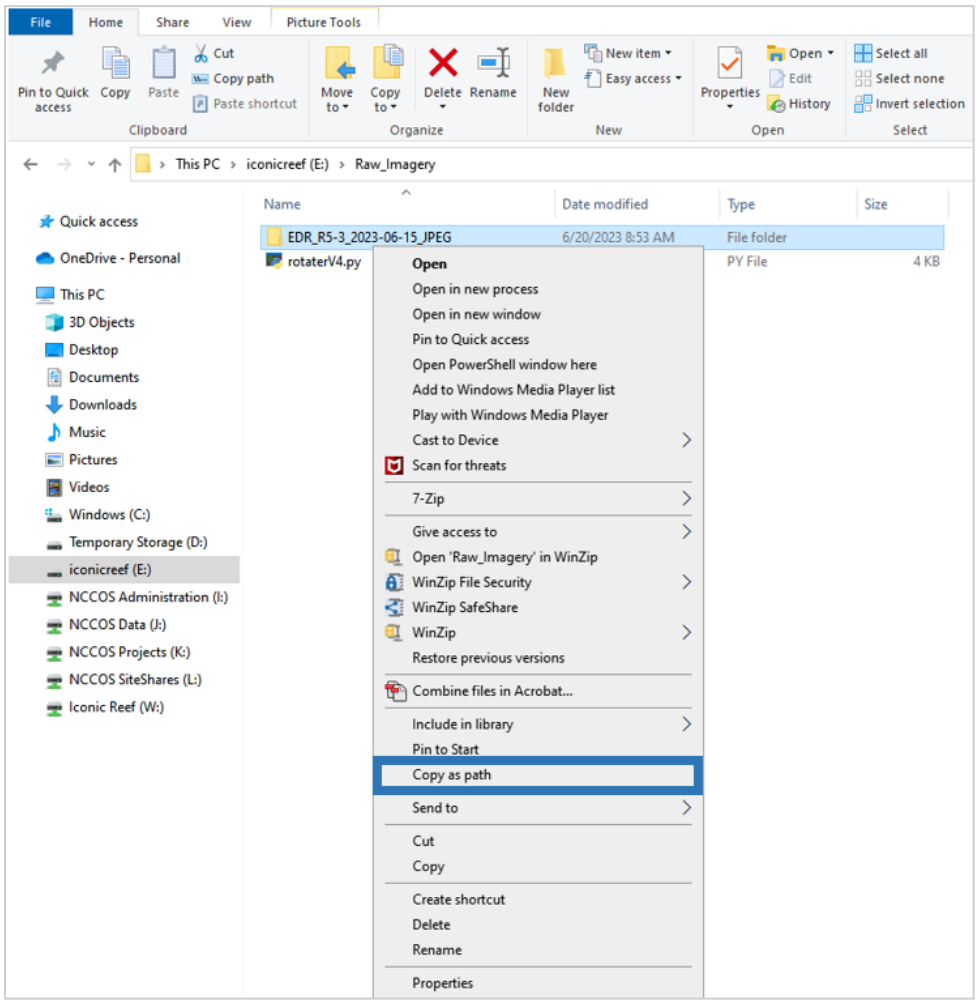


Figure 6. File Explorer window showing context menu containing `Copy as path`.

C. The image_rotator.py script requires multiple dependencies, including: dill, exif, and exifread. If these or any other needed dependencies were not previously installed, use the package installer for python (pip) to do so. Running the script without these dependencies installed will result in an error (e.g., `No module named exif`). If the error message appears, install package(s) as detailed below.

- In Command Prompt, type `pip install` and each of the named packages separated by a space and press Enter. This will download and install each of the packages. After the packages are installed, image_rotator.py can be run to rotate the images.

2. The script will begin rotating the images in the folder where they are located. The Command Prompt will display a message when the process is complete.
3. To confirm the rotation was successful, navigate to the plot image folder and right-click on the toolbar that indicates the name, data, type, etc. of the images in the folder. From the context menu, select `More` and then `Orientation` in the new Choose Details window. If the rotation was successful, all of the images should read `Normal` under the `Orientation` column.

2. Agisoft Metashape Workflow

A. Building the SPC

Photo alignment matches detected features across a collection of photos to estimate the position and orientation of each image. This results in the creation of an SPC, a type of model that serves as the foundation for the Metashape workflow. SPC generation can be done manually or via scripts.

A1. Check the Metashape Global Preferences

This workflow only requires the minimum default global preferences and can be further optimized using some selections in the Preferences menu. However, for the purposes of this SOP, keep the defaults. For further explanation on the settings and their meanings refer to Over et al. (2021).

1. Open the Metashape software.
2. Navigate to `Tools > Preferences` (Figure 7).
3. On the General tab set the `Theme` to Light.
4. On the GPU tab, verify the GPUs installed on the computer are checked, and `Use CPU when performing GPU accelerated processing` is unchecked.

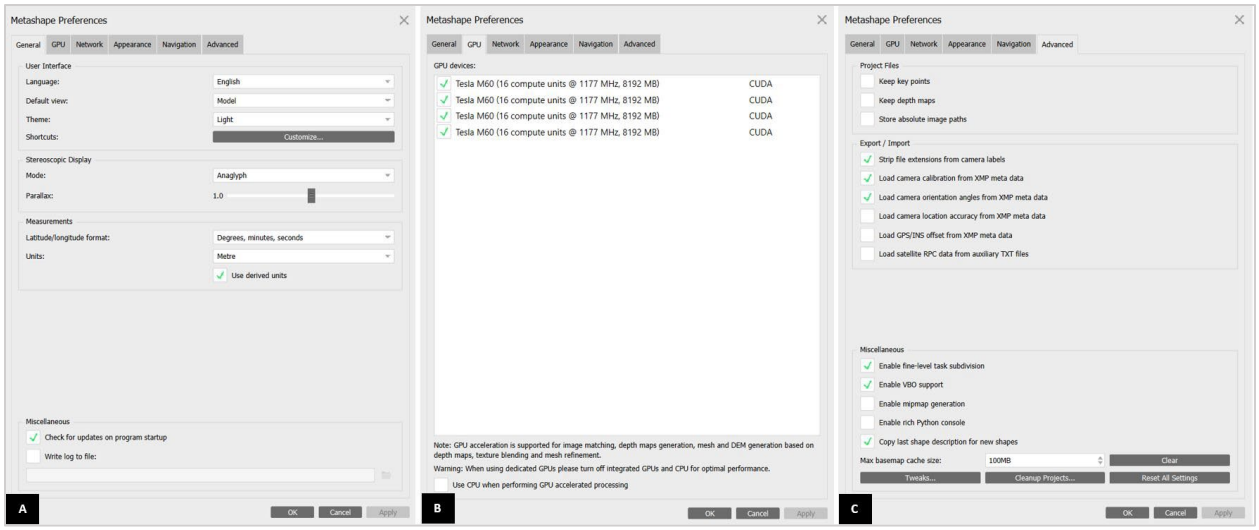


Figure 7. Global preferences are found under the Tools menu and include (A) `General` preferences, (B) `GPU` devices available and (C) `Advanced` settings. (A) General preferences that may be set include `Language` and `Theme`. In order to accelerate processing, available GPUs (B) must be selected. Other preferences (C) may be changed, although defaults settings are acceptable.

A2. SPC Generation (Manual)

1. Open File Explorer, navigate to the `Agisoft_Project_Data_Exports` folder, and create a new folder using the naming convention associated with the plot (e.g., SOMB_R2-2_2022-08-25).
2. In Metashape, save the project file (`File > Save As`) in the plot folder created in step 1. Be sure to name the project file using the naming convention associated with the plot.
3. Navigate to the Workspace pane on the left side of the window. Right-click on `Chunk 1` to open the context menu, select `Add` and then `Add Folder`.
4. A new window will open. Navigate to the `Raw_Imagery` folder, and then select the plot image folder (e.g., SOMB_R2-2_2022-08-25_JPEG).
5. Metashape will begin loading the photos, and a new window will open called `Add Photos`. Select `Single Cameras` and click `OK`. The photos will load in the Photos pane within the main Metashape window.
6. Right-click on `Chunk 1`, select `Process` from the context menu and then `Align Photos`.
7. A new window Align Photos will appear. Change the settings according to Figure 8, and click `OK` to begin SPC generation. Key settings are briefly described below:
    A. `Accuracy`: when set to high, images are processed at their native resolution. Choosing medium or low accuracy can reduce processing times, but results in downsampling of images and can reduce the number of available matches between images.
    B. `Generic preselection`: allows for preliminary matching of sequential image pairs, in some cases dramatically reducing processing time.

C. `Key point limit`: refers to the total number of features that are identified in each image. Higher values can increase processing time, but allow for more precise matching between images. The value shown here has been chosen to balance model precision with processing time.

D. `Tie point limit`: the number of features used to match images. When set to 0, all available key points can be used for image matching. Generally, a greater number of tie points improves image matching.

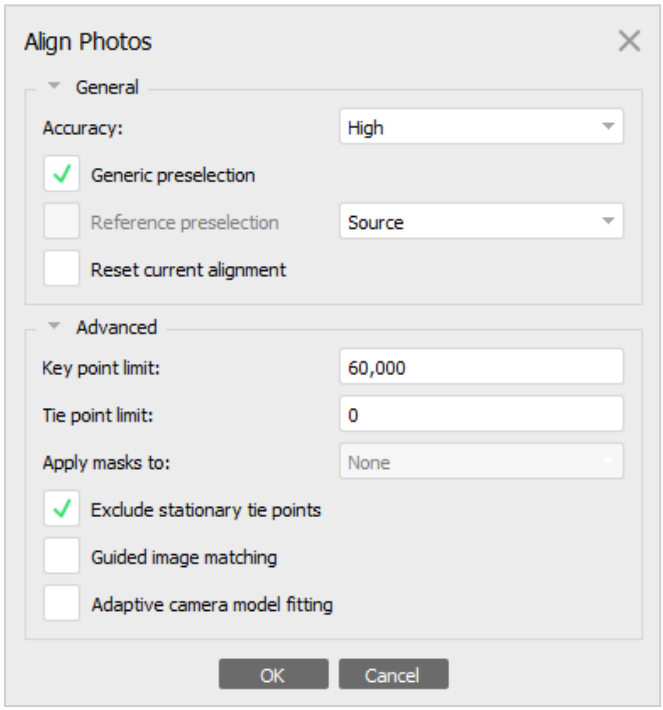


Figure 8. Align Photos window with settings for photo alignment as described in step 7.

A3. SPC Generation (Scripted)

1. Open File Explorer and navigate to the plot image folder (e.g., SOMB_R2-2_2022-08-25_JPEG). Use Shift + right-click to open the context menu and select `Copy as path` to copy the file path for the image folder.
2. In Metashape, navigate to the topmost toolbar and click on `Tools`, then choose `Run Script` from the drop-down menu.
3. A new window will appear: Run Python Script (Figure 9). When using a script for the first time, it will need to be selected using the `Browse` option. Click on the folder icon (`Browse`), then navigate to the folder containing the appropriate script based on the instructions below.

- To process photo alignment for one plot (Figure 9):
  Use script: MIR_Metashape_Processing_Part_I.py
  Type the following: `--input`, followed by the file path for the image folder (e.g., --input "E:\Raw_Imagery\SOMB_R2-2_2022-08-25_JPEG").
  Click `OK` to start processing the alignment.

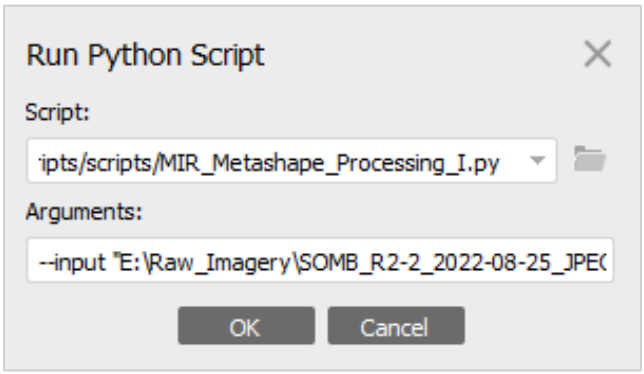


Figure 9. Run Python Script window with script and arguments for SPC generation for one plot.

- There are two ways to generate SPCs for multiple plots using a single batch processing script:
  i. Use script: MIR_Metashape_Processing_Part_I.py
  Type the following: `--input`, followed by the file paths of the folders containing the raw images to be processed (e.g., --input "E:\Raw_Imagery\SOMB_R2-2_2022-08-25_JPEG" "E:\Raw_Imagery\SOMB_R3-2_2022-09-26_JPEG"). When providing multiple paths, separate each path with a space only.
  ii. Use script: MIR_Metashape_Processing_Part_I.py
  Provide arguments as a text file that contains the paths for the image folders (e.g., --input "E:\Agisoft_Project_Data_Exports\ProcessingQueue.txt").
    - To create a .txt file: Navigate to the Agisoft_Project_Data_Exports folder and right-click within the window. From the context menu, select `New > Text Document`. Save the Text Document (.txt) as `ProcessingQueue.txt`.
    - Copy the paths to the raw images for the various plots whose SPCs will be generated in the same batch process.
      - Shift + right-click, `Copy as Path` (e.g., E:\Raw_Imagery\SOMB_R2-2_2022-08-25_JPEG) for the image folders that need alignment, and paste the paths into a text file (Figure 10).
      - Remove quotation marks around the file paths, and be sure there is no extra spacing between paths.
      - Place each path on a separate line.
      - Save text document.

- To avoid long queue times during SPC generation, it is recommended to avoid batch processing more than six plots at a time.

Click `OK` to start processing the alignment

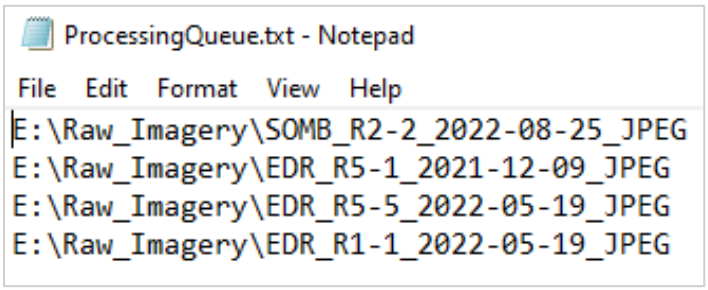


Figure 10. Text file containing raw image paths for SPC generation for two or more plots. Each path must appear on a separate line with no hanging spaces after a given path.

A4. Completion of SPC Generation

Once the photo alignment process is complete (either manually or via script), an SPC will have been generated, and Chunk 1 will indicate the number of photos that were aligned and the number of tie points (Figure 11). Photo alignment using a script will generate a copy of Chunk 1 and therefore show a new chunk called Copy of Chunk 1 in the Workspace pane (Figure 11). Rename Chunk 1 to `SPC Generation` and Copy of Chunk 1 to `Marker Verification`.

The project files will be stored in the project folder (e.g., SOMB_R2-2_2022-08-25) under Agisoft_Project_Data_Exports. The Metashape project file that is used for processing will be saved as a PSX file (e.g., SOMB_R2-2_2022-08-25.psx), and the data themselves will be saved in a .files folder archive (e.g., SOMB_R2-2_2022-08-25.files).

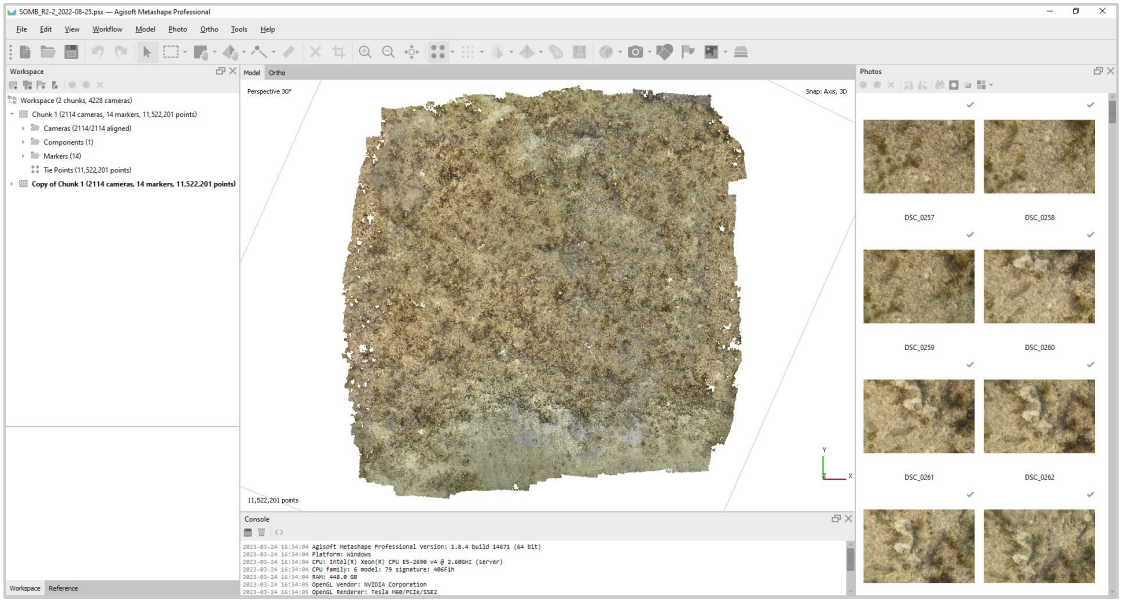


Figure 11. Completed SPC Generation. The number of tie points and aligned photos are indicated in the Workspace pane to the left under `Chunk 1`. A copy of Chunk 1 has been generated for later use.

Check the SPC for holes (e.g., patches with no points) as these can result in reduced model accuracy and in some cases represent missing data that precludes downstream ecological analyses altogether. Holes may be due to moving structures on the benthos (e.g., sea fans) and can also result from insufficient overlap during image collection. While smaller holes are acceptable, and in many cases are filled in during DPC generation, larger holes will propagate to the DPC and orthomosaic and preclude the ability to perform many downstream ecological analyses. Large holes will typically correspond with gaps in the image acquisition pattern. To view the estimated location of the camera as images were captured (shown as black dashes; Figure 12), select the Show Cameras tool on the far right of the toolbar. If the holes correspond to systematic errors during image collection, it is strongly recommended to redo image collection rather than attempt ad hoc model correction.

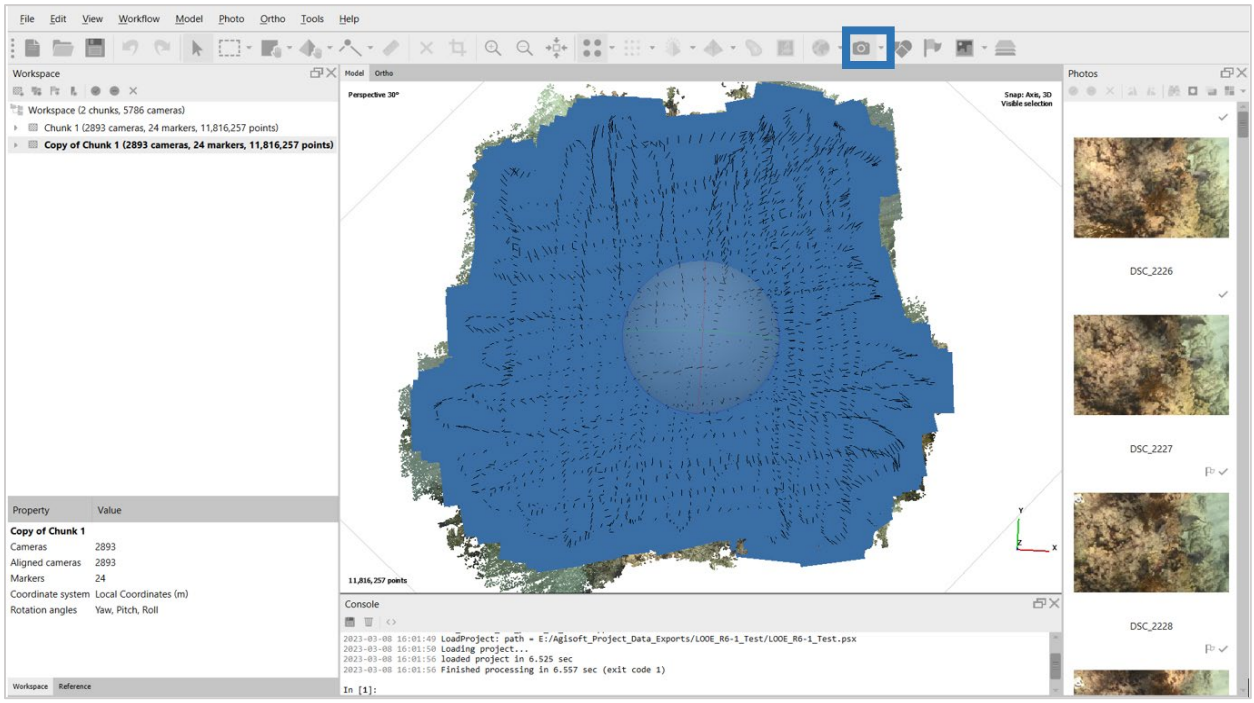


Figure 12. The Show Cameras tool shows the estimated location of the camera (center of each image shown with black dashes) as images were captured.

B. Marker Detection and Verification

The Detect Markers tool in Metashape can be used to automatically identify images with coded targets, preventing the need to visually search through thousands of photos to identify markers. Coded targets provided by Agisoft are printed onto markers that are deployed in the plot during image collection. When GPS information is available for these markers, they can also be used as ground control points to geo-reference the 3D DPC (*2E. Building the DEM and Orthomosaic*).

B1. Marker Detection (Manual)

1. Navigate to the topmost toolbar and click on `Tools`, then from the drop-down menu, hover over `Markers` and select `Detect Markers`.
2. A new window Detect Markers will appear. Change the settings as shown in Figure 13, and click `OK`. Since the coded targets are directly from Agisoft, Metashape will then begin detecting markers and preparing the photos for the next step.

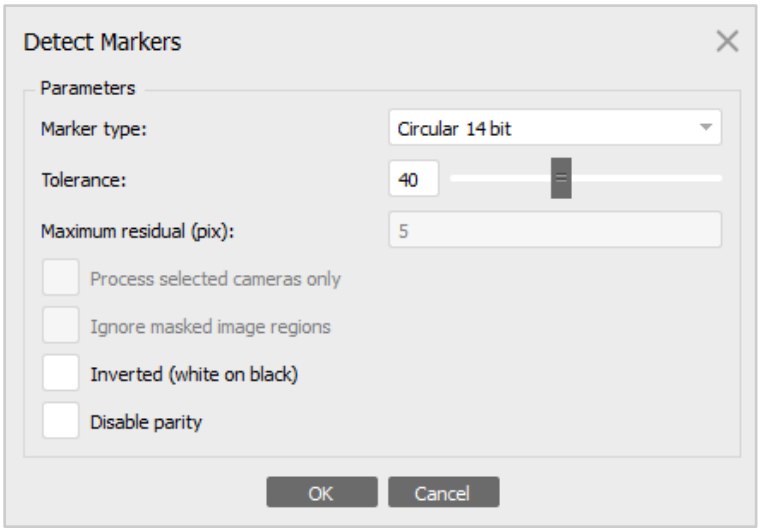


Figure 13. Detect Markers window with settings for marker detection as described in step 2.

B2. Marker Detection (Scripted)

When using the script for model processing, marker detection has already been conducted by the script previously run in section *2A3. SPC Generation (Scripted)*.

B3. Verification of Depth Markers

Marker detection may not identify all of the markers and sometimes incorrectly identifies markers that do not exist. As a result of this, depth markers and scale bars must be verified manually. After markers are verified, they are manually duplicated because automatically detected markers are not provided with X (m), Y (m), and Z (m) coordinates, which are required for later processing steps.

1. Make a copy of the SPC Generation chunk by right-clicking and selecting `Duplicate` from the context menu. Then click `OK`. A new chunk Copy of SPC Generation will appear in the Workspace pane. Rename Copy of SPC Generation to `Marker Verification`. *If the script has been used up to this point, a copy of the chunk will have already been created and renamed manually. See section 2A3. SPC Generation (Scripted).*
2. Be sure the Marker Verification chunk is selected (chunk text will be bold), and navigate to the Reference pane in the bottom-left corner of the window next to Workspace. A list of markers that were detected in section *B1. Marker Detection (Manual)* or *B2. Marker Detection (Scripted)* will now appear in the Reference pane.

3. Right-click on the first detected marker, and select `Filter Photos by Markers` from the context menu (Figure 14). All of the images that have the detected marker will appear in the Photos pane.
4. In the Photos pane, double-click on an image with the perimeter marker or scale bar in the center of the frame (Figure 15). Fully zoom in using the scroll wheel until the pixels are visible and the zoom-in limit is reached.
5. Add a new marker by right-clicking next to the existing marker flag and selecting `Add Marker` from the context menu (Figure 15).

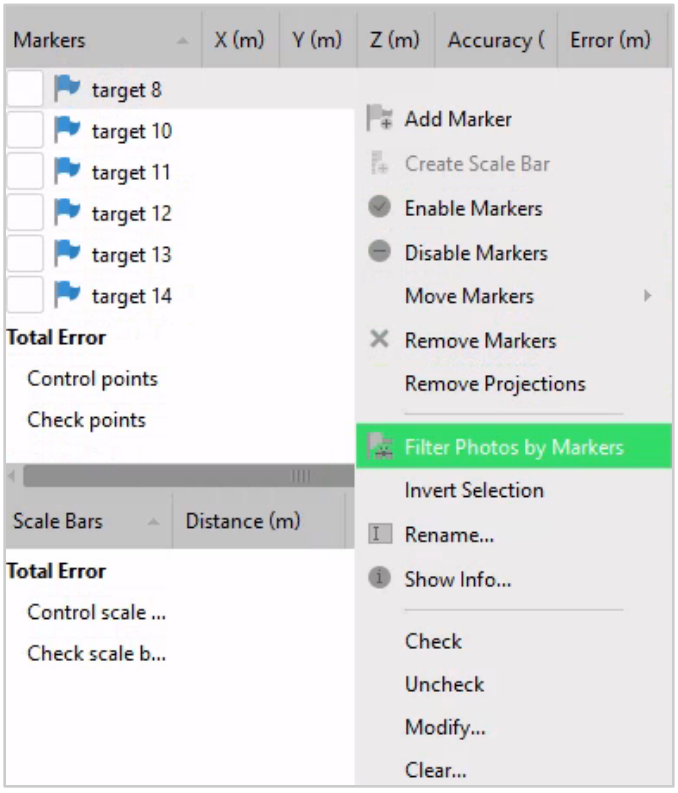


Figure 14. Context menu showing `Filter Photos by Markers` option.

6. In the Reference pane, double-click on the newly added marker (`point 1`) and rename according to the transcribed field data (e.g., 6 for Marker 6 or Scale 8 for Scale bar 8; Figure 16A). Delete the old marker by right-clicking and selecting `Remove Markers` (Figure 16B).
7. Right-click on the renamed marker and choose `Filter Photos by Markers`. This provides the subset of images the marker is associated with.
8. Find high-quality images of the marker, and left-click on the blue flag to move it to the center of the target. Once moved, the flag should turn green. Do this for approximately ¼ of the images (about 10–15). High-quality images (Figure 17A–C) are visually identifiable as those with distinct lines between the pixels. Low-quality images (Figure 17D–F) will have blur between pixels or will not zoom all the way into the center of the marker.

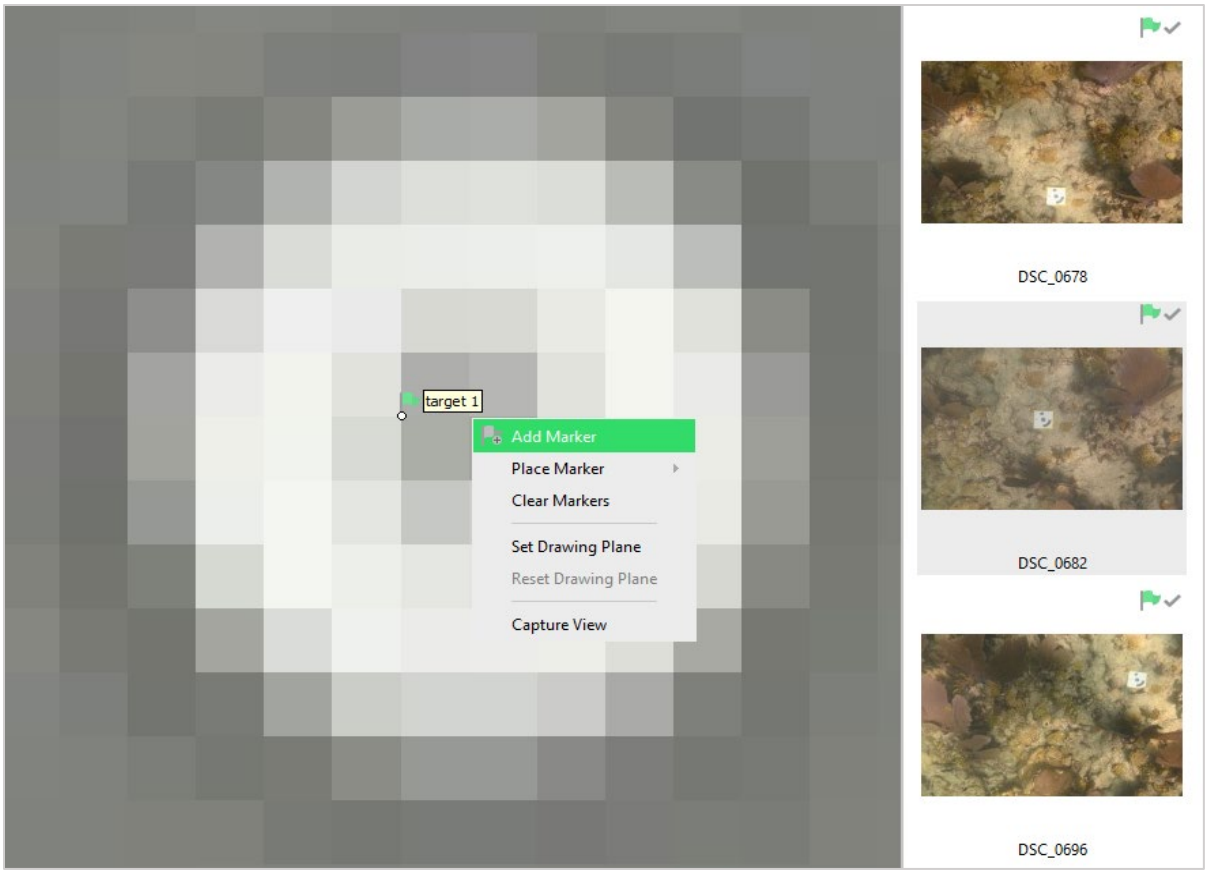


Figure 15. Selection of an image and addition of a new marker.

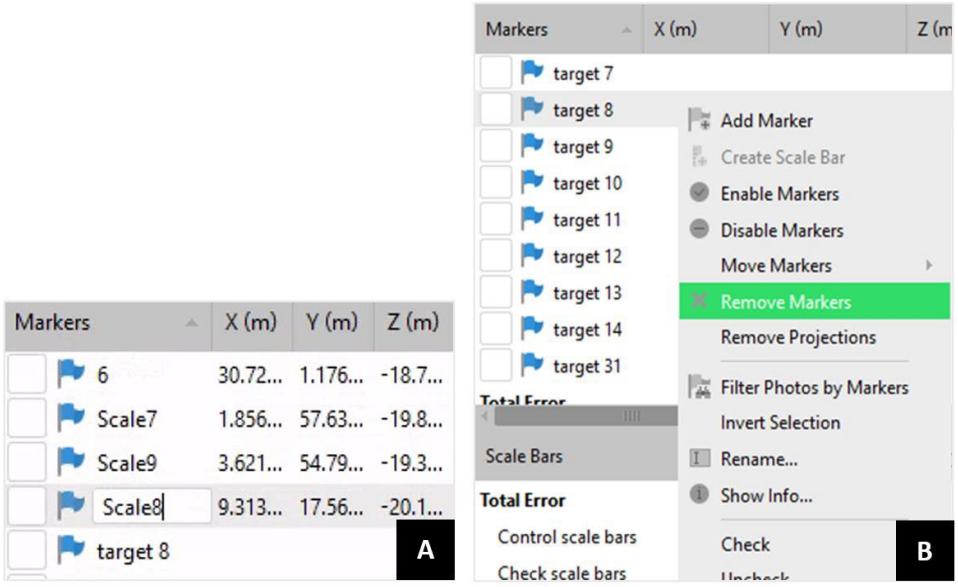


Figure 16. (A) Renaming new marker and (B) removal of old marker.

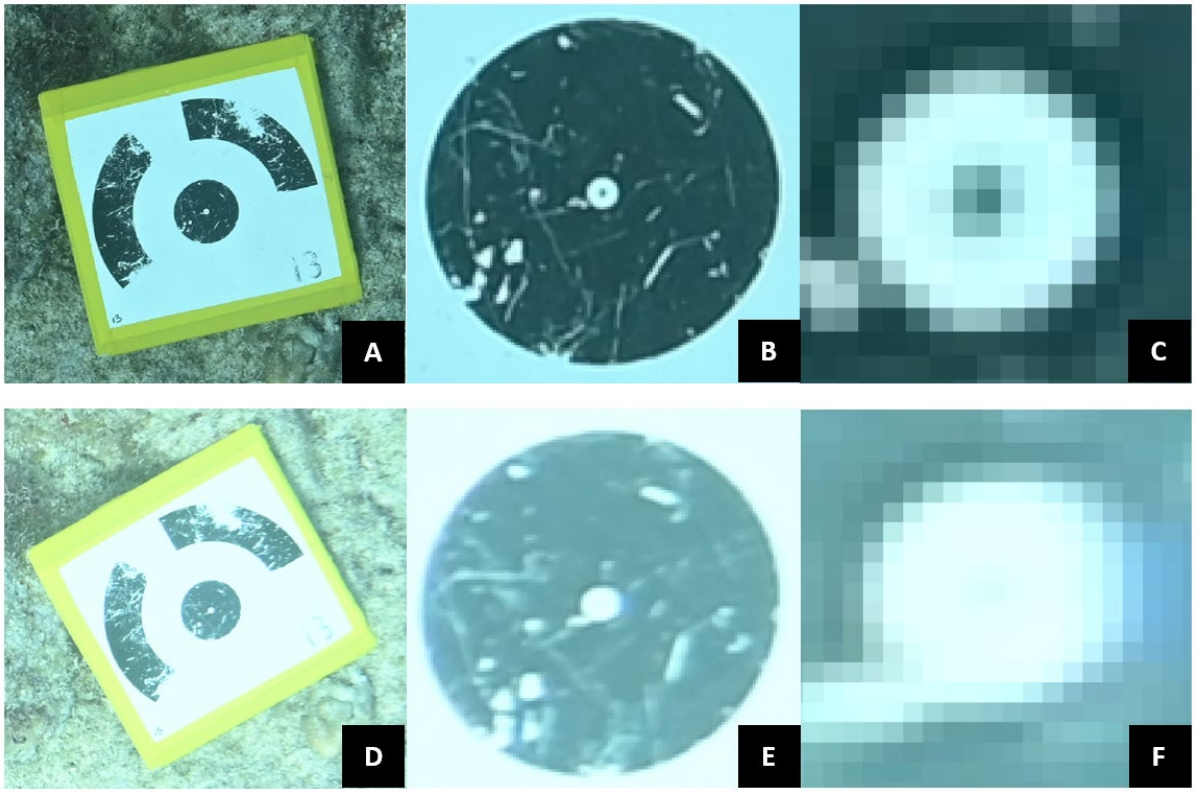


Figure 17. Examples of high-quality image and low-quality images. High-quality images (A) zoomed out, and (B) and (C) zoomed in, and low-quality images (D) zoomed out, and (E) and (F) zoomed in.

9. Repeat steps 3 through 8 for all markers and scale bars. There should be 14 total markers when the process is complete (six single markers and four scale bars with two markers each).
    - When setting the flags for the scale bars, use the Tab key to toggle between the two flags associated with that scale bar that are in the same photo to avoid having to zoom out, find the other marker, and zoom back in.
    - Sometimes, automated marker detection will generate flags for objects that are not markers or scale bars with coded targets. Once step 9 is completed, delete any such erroneously detected markers from the workspace pane.
    - Occasionally markers or scale bars will not be identified by the automated marker detection. If this is the case, the SPC will need to be reviewed to find the missing markers.
        - Using the field data sheet as a guide for where the missing marker or scale bar should be, filter the photos in the area with the Selection tool located next to the arrow icon (Figure 18).

Figure 18. Location of Selection tool in the main toolbar.

    - From the drop-down menu, select `Rectangular Selection`. Draw a square over the area of the SPC where the maker or scale bar should be. The square will turn red. Right-click on the square and select `Filter Photos by Tie Points` from the context menu. This provides the subset of photos that the marker is associated with, similar to step 7.
10. Now that all 14 markers have been placed, confirm that the positions of the markers on the model in Metashape match the position recorded in the field. Depths for each marker will be transcribed from the field data sheet into Metashape. If there is a discrepancy, it can result in erroneous depth information being applied to the model in Metashape, and in some cases, this can impede proper model scaling and orientation. If a discrepancy is observed, reach out to the image collection team for clarification before proceeding with the Metashape workflow. If the issue cannot be rectified, exclude markers and scale bars that are incorrect.
11. Once all of the markers have been verified, the depths (m) associated with each marker from the field data sheet are copied into the Z (m) column in the Reference pane. Double-click on the value in the Z column to edit, and enter the corresponding depth in meters from the transcribed field data sheet. Repeat this process until all depth markers and scale bars have the depth values collected in the field. Note that the depths are recorded as negative values to indicate depths below sea level.
12. Error needs to be accounted for in relation to the X, Y, and Z values. Select all of the markers and scale bars by selecting the first marker and then holding Shift + clicking the last scale bar in the set. Right-click on the selection, and choose `Modify` from the context menu. This will allow editing all of the markers at the same time.
13. A new window named Modify Reference will appear. Under `Column`, select `Accuracy` from the drop-down menu. In the `Value` field, enter `1000/0.3`.
    - At this point, geographic coordinates have not been entered. An inflated error value of 1000 m is provided for the X and Y coordinates in order to prevent Metashape from considering these values during the optimization process, *2C. Optimization and Error Reduction.*
    - 0.3 m is used for the error in the Z-coordinates, reflecting the error in consumer-grade pressure gauges that were used to collect depth measurements.
14. In the Reference pane, check the six depth markers with green check marks (not the scale bar markers; Figure 19), and refresh the Reference pane by clicking the `Update Transform` icon in the toolbar (Figure 20). Click on the model view and press 0 (zero) to view the extent of the model.

- Scale bar markers are left unchecked because 1- *geographic coordinates are not collected for the scale bars during image acquisition*, 2- *the same depth for two scale bar markers (e.g., Scale 3 and Scale 4) may alter the orientation of the model*, and 3- *the more markers that are selected, the higher the likelihood that the model orientation will become warped*. Scale bar markers are created because they may be used to correct resolution during *E1. Building the DEM and Orthomosaic* of the Metashape workflow.

Markers	X (m)	Y (m)	Z (m)	Accuracy (m)
1	36.547657	5.797504	-3.352800	**1000/0.3**
2	-51.169533	-61.046535	-3.352800	**1000/0.3**
11	21.945946	49.468464	-3.657600	**1000/0.3**
12	-67.656059	30.068954	-2.743200	**1000/0.3**
13	37.194599	-42.928120	-3.657600	**1000/0.3**
14	-54.257469	-14.670341	-2.743200	**1000/0.3**
scale 3	-11.675804	-33.916393	-3.048000	**1000/0.3**
scale 4	-10.069078	-35.290562	-3.048000	**1000/0.3**
scale 5	17.396399	-25.423981	-3.657600	**1000/0.3**

Figure 19. Six depth markers checked with green check marks in the Reference pane.

Figure 20. Location of the `Update Transform` icon in the Reference pane toolbar.

B4. Resize Region

After the SPC is generated, a bounding region will appear along with the 3D model. The region will appear as a box that typically bounds the entirety of the model. In some cases, however, the box will be offset from the model and must be resized to ensure that all points associated with the model are used in subsequent steps of the workflow. Region resizing can also be used to exclude stray points at the model margin.

1. Resize the region by navigating to the Region tool located next to the rectangular selection tool (Figure 21).

Figure 21. Location of Region icon in Reference toolbar.

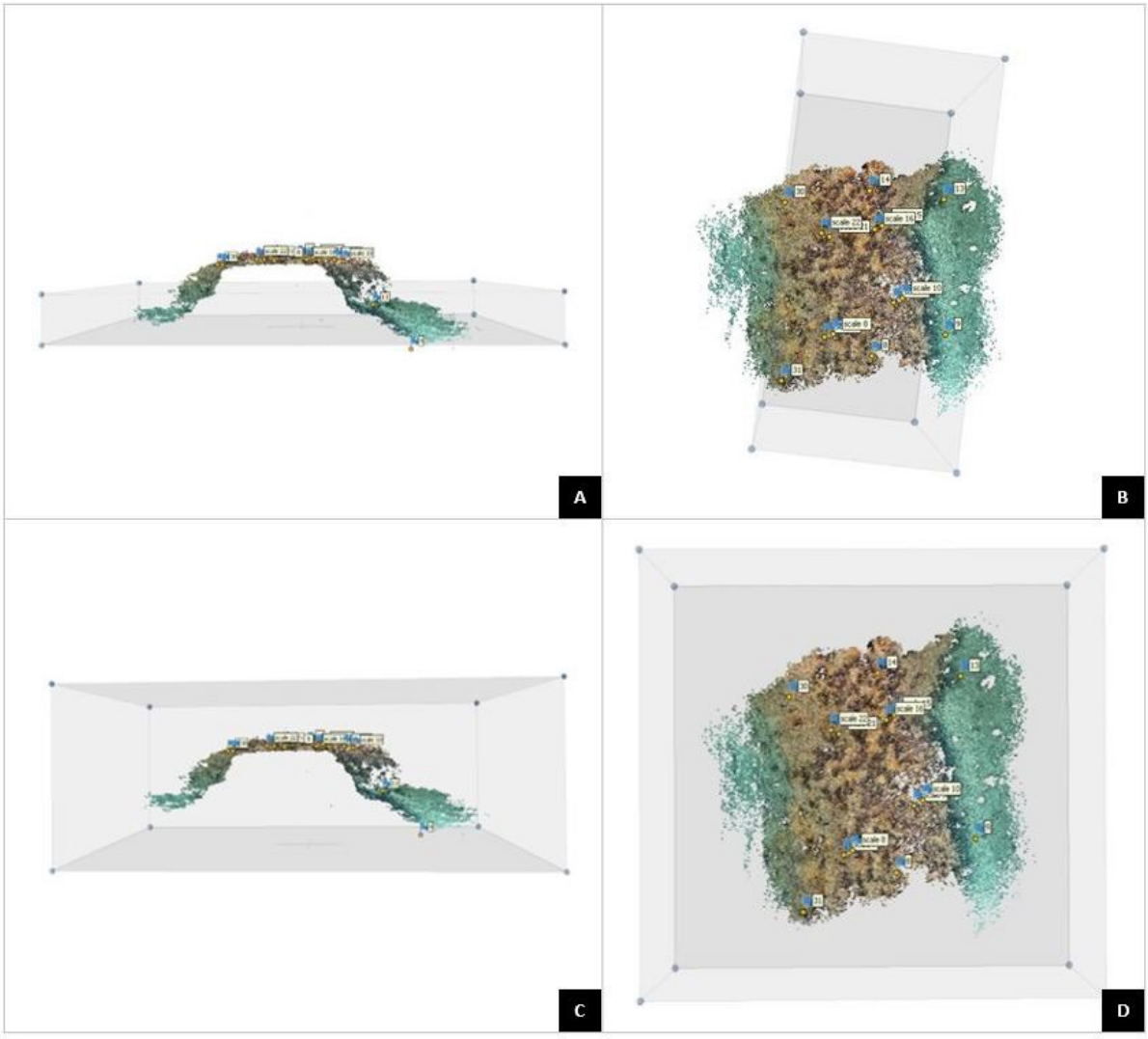


Figure 22. Examples of (A) and (B) incorrect region sizing and (C) and (D) a resized region that encompasses the SPC.

2. From the drop-down menu, select `Resize Region`. Manipulate the size of the region by moving the handles that appear on the corners of the region box. The Rotate Region option from the drop-down menu can be used to manipulate the rotation of the region box. The goal is to avoid cutting out points related to the model during dense cloud generation (Figure 22A–B). A good rule of thumb is to have a reasonable amount of space above, below, and on each side of the model (Figure 22C–D).
    - There are several keyboard shortcuts that are helpful when manipulating the region. To access these shortcuts, navigate to `Model` in the main toolbar and select `Predefined Views` from the context menu.

C. Optimization and Error Reduction

Optimization and error reduction ensure that SPC geometry is as accurate as possible by optimizing the camera calibration and SPC alignment through an error-reduction and recalibration procedure. Points with reconstruction uncertainty, projection accuracy, and reprojection error below a user defined threshold are iteratively removed, and the SPC geometry is optimized at each iteration. This may be accomplished either manually or via script. Ultimately, the objective is to remove the effects of low-quality tie points and improve SPC geometry. For more information on the technical details of the optimization and error reduction procedure and parameter configuration, please refer to Over et al. (2021).

C1. Optimization and Error Reduction of the SPC (Manual)

1. In the Workspace pane, make a copy of the Marker Verification chunk by right-clicking on the chunk and selecting `Duplicate` from the context menu. A new chunk Copy of Marker Verification will appear in the workspace pane. Rename Copy of Marker Verification to `SPC & DPC – Optimized`. This process will alter SPC geometry, and an original copy of the chunk is the easiest way to go back and examine or reprocess the model from its original state, if desired.
2. Right-click on the `SPC & DPC – Optimized` chunk and select `Process` then `Optimize Cameras`. A new window will appear called Optimize Camera Alignment. Change the settings according to Figure 23 and click `OK`.

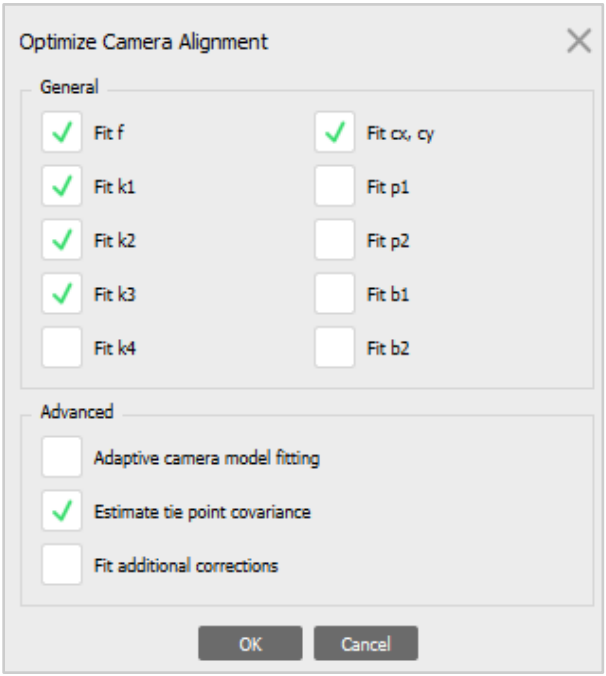


Figure 23. Optimize Camera Alignment window with settings for optimization as described in step 2.

3. In the topmost toolbar, click on `Model` then select `Gradual Selection` from the context menu. A new window will open named Gradual Selection. Under `Criterion`, select `Reconstruction Uncertainty` from the drop-down menu. `Level` is the error threshold, and is adjusted to filter points above or below a particular level of error (all points have some level of error). The total number of points and the number of selected points are displayed in the bottom-left corner of the window (Figure 24). Adjust the slider until 50% of the total points are selected (Figure 24), without exceeding a Level of 12.

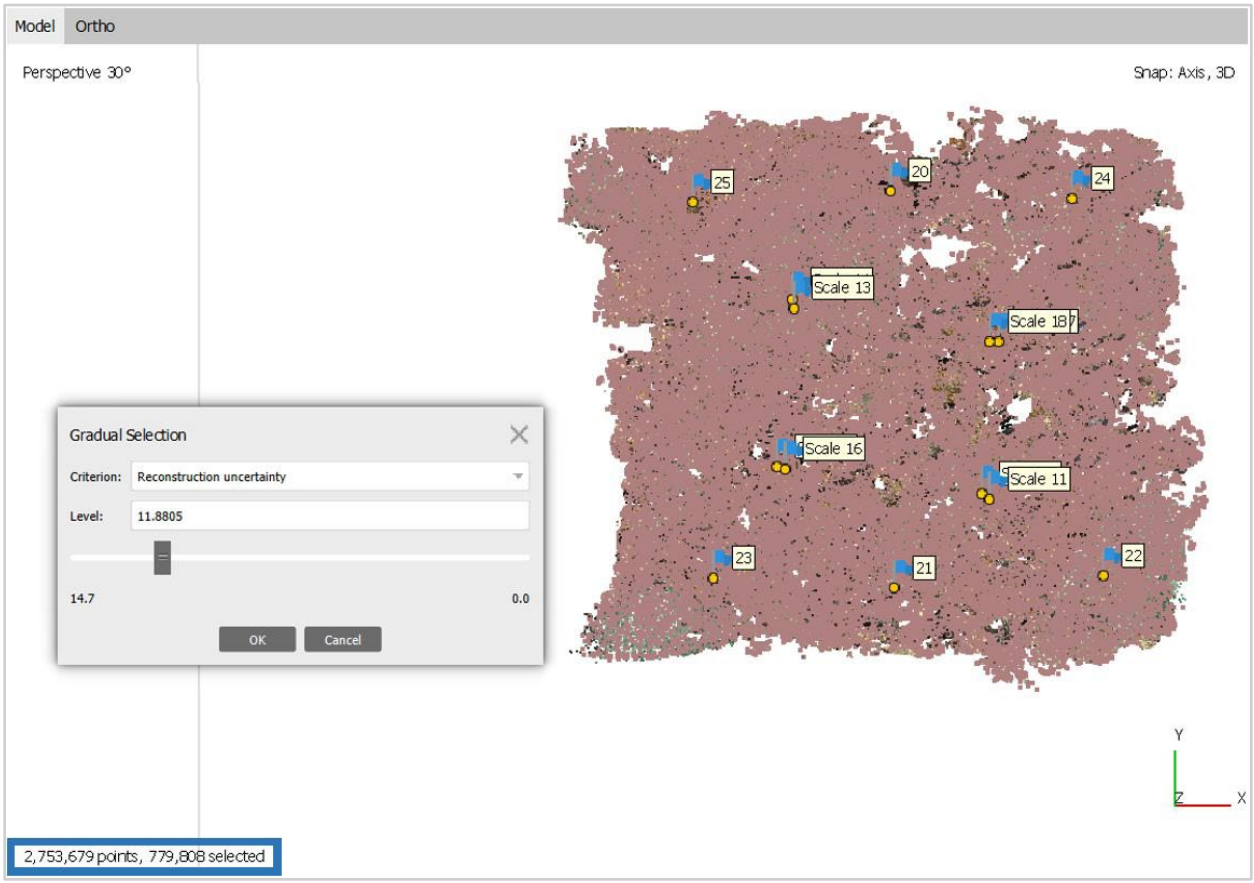


Figure 24. Gradual Selection of Reconstruction Uncertainty indicating 50% of the points are selected. Select up to 50% of points, without exceeding a level of 12.

4. Click `OK`, press the Delete key to remove selected points, and save the file.
5. Repeat step 2, optimize cameras.
6. In the topmost toolbar, click on `Model`, then select `Gradual Selection`. In the Gradual Selection window, under `Criterion`, select `Projection Accuracy` from the drop-down menu. Adjust the slider until 50% of the total points are selected (Figure 24), without exceeding a level of 3.5.
7. Click `OK`, press the Delete key to remove selected points and save the file.
8. Repeat step 2

9. In the topmost toolbar, click on `Model`, then select `Gradual Selection`. In the Gradual Selection window, under `Criterion`, select `Reprojection Error` from the drop-down menu. Adjust the slider until 10% of the points are selected, without exceeding a level of 0.9. During this step, error notifications may arise indicating insufficient number of projections. If these error notifications occur, select `Yes, Unalign Photos` to remove the photos from the calculation.
10. Click `OK`, press the Delete key to remove selected points, and save the file.
11. Optimize cameras again using the same instructions as step 2, but change the settings according to Figure 25 and click `OK`.

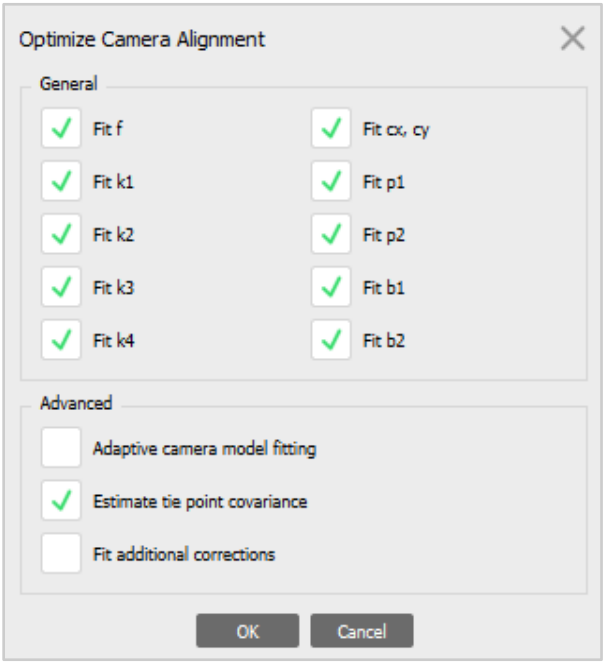


Figure 25. Optimize Camera Alignment window with settings for optimizations described in step 11.

12. In the topmost toolbar, click on `Model`, then select `Gradual Selection`. In the Gradual Selection window, under `Criterion`, select `Reprojection Error` from the drop-down menu. As in step 9, move the slider until 10% of the points have been selected, without exceeding a level of 0.9.
13. Click `OK`, press the Delete key to remove selected points, and save the file.
14. Optimize cameras again using the same instructions and settings as step 11. Click `OK`, and save the file.

C2. Optimization and Error Reduction of the SPC (Scripted)

The next script used in the workflow — MIR_Metashape_Processing_Part_II.py — is used to complete optimization and error reduction of the SPC, and generate the DPC. Before proceeding, be sure that the Marker Verification chunk is selected in the Workspace pane.

1. Navigate to the topmost toolbar, and click on `Tools`, then `Run Script`.

- To process error reduction and build the DPC for one plot:
  Use script: MIR_Metashape_Processing_Part_II.py
  Type the following: `--input`, followed by the file path for the image folder (e.g., --input "E:\Raw_Imagery\SOMB_R2-2_2022-08-25_JPEG").
  Click `OK` to start the error reduction and building of the dense cloud.
- There are two ways to generate DPCs for multiple plots using a single batch processing script:
  i. Use script: MIR_Metashape_Processing_Part_II.py
  Type the following: `--input`, followed by the file paths to the folders containing the raw images to be processed (e.g., --input "E:\Raw_Imagery\SOMB_R2-2_2022-08-25_JPEG" "E:\Raw_Imagery\SOMB_R3-2_2022-09-26_JPEG"). When providing multiple paths, separate each path with a space only.
  ii. Use script: MIR_Metashape_Processing_Part_II.py
  Provide arguments as a text file that contains the paths for the image folders (e.g., --input "E:\Agisoft_Project_Data_Exports\ProcessingQueue.txt").
    - To avoid long queue times during DPC generation, it is recommended to avoid batch processing more than six plots at a time.

  Click `OK` to start the error reduction and building of the dense clouds.

D. Building the DPC

A 3D DPC is created by calculating the depth information for each camera based on estimated camera positions in the SPC. The DPC can then be used for additional steps in the Metashape workflow such as building a DEM (*2E. Building the DEM and Orthomosaic*).

D1. Building the DPC (Manual)

1. Right-click on the `SPC & DPC - Optimized` chunk and select `Process`, then `Build Dense Cloud`. Change the settings as shown in Figure 26, and click `OK`.

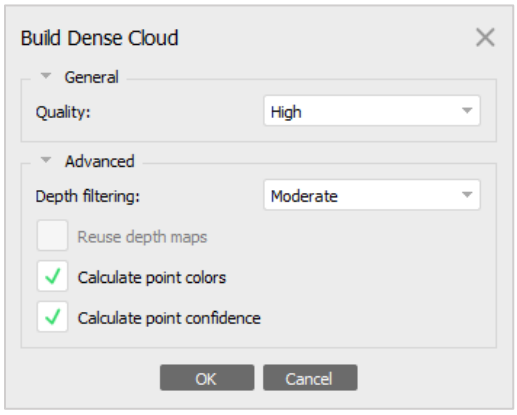


Figure 26. Build Dense Cloud window with settings for building the dense cloud as described in step 1.

D2. Building the DPC (Scripted)

Script-based DPC generation is included in *2C2. Optimization and Error Reduction of the SPC (Scripted)*. Optimization and error reduction of the SPC and the building of dense cloud using a script will generate a copy of the Marker Verification chunk and therefore show a new chunk called `Copy of Marker Verification` in the Workspace pane (Figure 27). Rename this new chunk as `SPC & DPC – Optimized`.

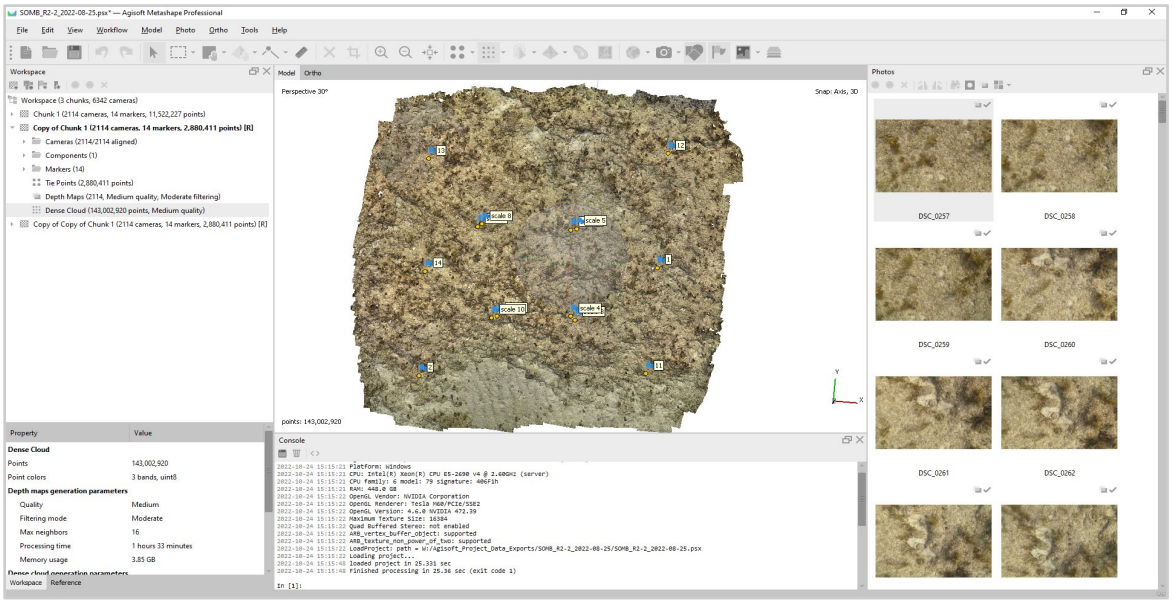


Figure 27. Example of a completed DPC in Metashape with markers and scale bars shown.

E. Building the DEM and Orthomosaic

DEM's are 2D image-based representations of 3D surfaces, where depth (or elevation) values are stored in each pixel as a grid of height values and are typically converted to RGB values for display. Orthomosaics are another 2D product derived from 3D models, and are generated by first orthoprojecting and then blending together the raw images used to generate the 3D model. DPCs generated in *2D. Building the DPC* are first georeferenced with GPS coordinates collected in the field before DEMs and orthomosaics are created. For more additional information on the technical details of DEMs and orthomosaics please see Edwards et al., 2023.

E1. Preparing to Build a DEM and an Orthomosaic

1. Right-click on the `SPC & DPC – Optimized` chunk. Select `Duplicate`, and choose to duplicate with `Depth Map` and `Dense Cloud` checked. A new chunk Copy of SPC & DPC – Optimized will appear in the Workspace pane. Rename Copy of SPC & DPC – Optimized to `DEM & Orthomosaic`.
2. Select the `DEM & Orthomosaic` chunk, and navigate to the Reference pane, and click the `Settings` icon (Figure 28).

Figure 28. Location of the Settings icon in the Reference toolbar.

3. A new window will appear named Reference Settings. Under Coordinate System, change the setting from Local Coordinates (m) to WGS 84 (EPSG:: 4326) using the drop-down menu. This is the setting associated with the GPS used in the field during image acquisition. Change settings according to Figure 29, and click OK.

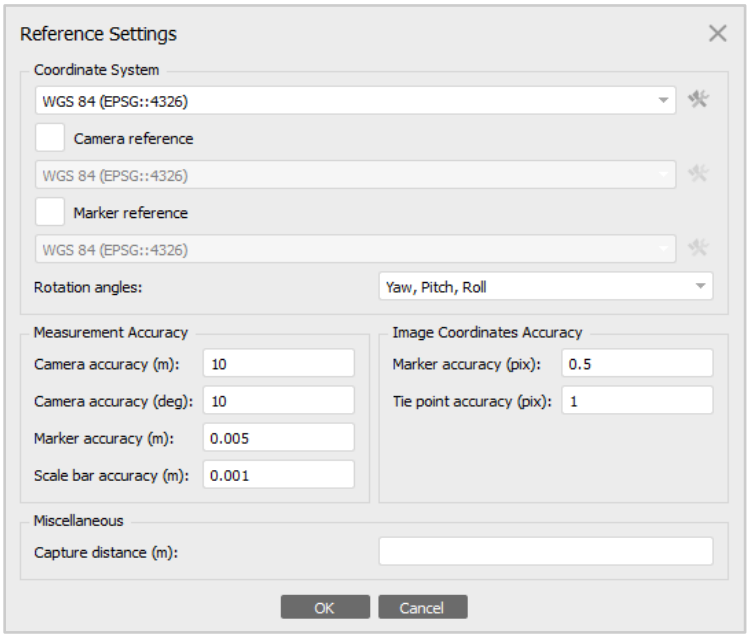


Figure 29. Reference Settings window with WGS 84 (EPSG:: 4326) coordinate system described in step 3.

4. After changing the coordinate system, the marker column headers in the Reference pane will change. X (m) will change to Longitude, Y (m) will change to Latitude, and Z (m) will change to Altitude (m).
5. Replace the local coordinates with the longitude and latitude recorded for each of the six depth markers from the transcribed field data.
6. After the latitudes and longitudes have been added, in the Reference pane, check the six depth markers with green check marks (not the scale bar markers), and refresh the Reference pane by clicking the Update Transform icon in the toolbar. Click on the model view, and press 0 (zero) to view the extent of the model. The model is now georeferenced.
    - When updating the transform, select only those markers with GPS positions recorded. Markers without geographic coordinates will show error values in the millions after georeferencing, and if selected during update transform, can prevent

the model from being placed in the correct location in the updated coordinate system.

7. Check the `Resolution (m)` value to be sure it is a positive number within the appropriate size range (i.e., in the range of positive millimeters). Negative values result in erroneously small DEMs and orthomosaics. Right-click on the `DEM & Orthomosaic` chunk, select `Process`, and then `Build DEM`. A new window called Build DEM will appear (Figure 30). If `Resolution (m)` is positive and within the appropriate size range (Figure 30), close the Build DEM window by clicking `Cancel`, and move on to build the DEM using script or non-script. If the `Resolution (m)` value is negative or larger than the appropriate size range, there is an issue with scale, or a step was missed prior to SPC optimization and error reduction. Scale bars must be manually added to resolve this issue. Manually adding scale bars using the existing scale bar markers provides the correct scale to the model and is detailed below.

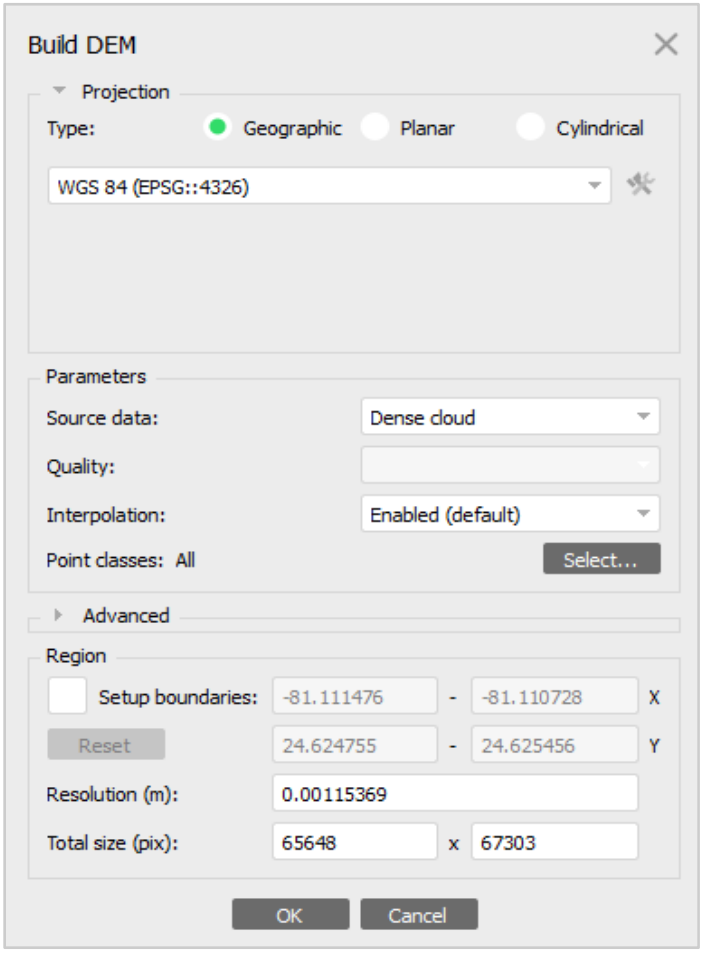


Figure 30. Build DEM window indicating that `Resolution (m)` is positive and in the correct range.

A. Navigate to the markers in the Reference pane, select the two scale bar markers associated with a scale bar (e.g., Scale 3 and Scale 4), right-click on the selection, and

select `Create Scale Bar` from the context menu (Figure 31). Be sure not to check the marker checkboxes.

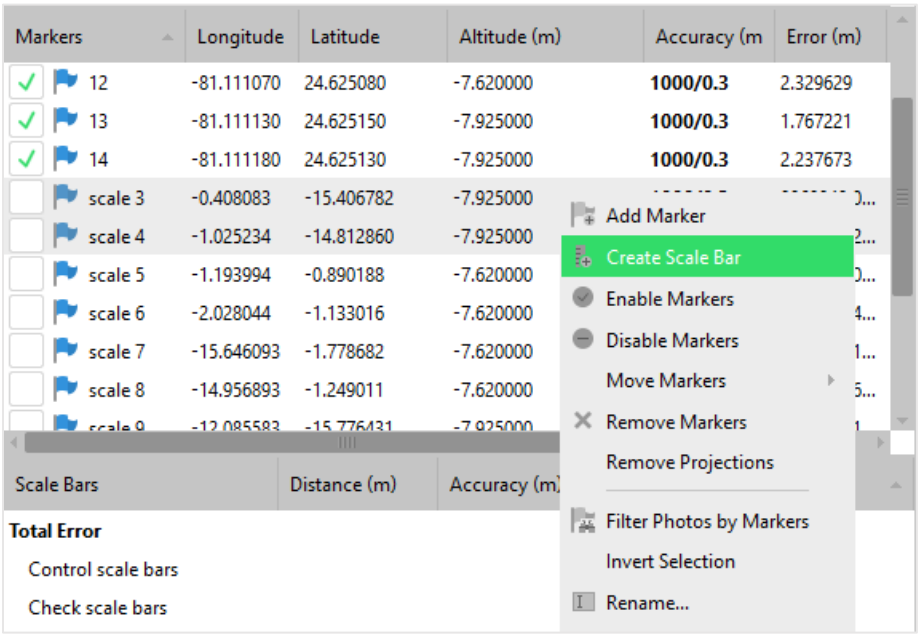


Figure 31. Selection of scale bar markers to create a scale bar.

B. A new scale bar (e.g., Scale3_Scale4) will appear in the window named Scale Bars below the markers window (Figure 32). Set parameters for the scale bar by right-clicking on the scale bar and selecting `Modify` from the context menu.
   - Under `Column`, select `Accuracy` from the drop-down menu, and enter `0.001` m (1 cm) under `Value`.
   - Under `Column`, select `Distance` from the drop-down menu. This is the scale bar length. Enter the appropriate length based on the scale bars used in the field (e.g., 25 cm scale bar will be input as 0.25 m).
   - The scale bar will now show the set distance, accuracy, and calculated error (Figure 32).

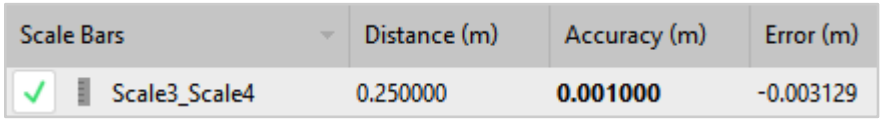


Figure 32. New scale bar with set distance and accuracy.

C. Repeat steps A and B for the remainder of the scale bars.

D. Make sure all of the newly created scale bars are checked, then refresh the Reference pane by clicking the `Update Transform` icon in the toolbar. Click on the `Model` tab, and press 0 (zero) to view the extent of the model, which is now aligned properly in the space.

E. Check the `Resolution (m)` value again to be sure it is no longer a negative value and is within the appropriate size range. With `Resolution (m)` now positive, close

the `Build DEM` window by clicking `Cancel`, and proceed to *E2. Build DEM and Orthomosaic (Manual)* or *E3. Build DEM and Orthomosaic (Scripted).*

E2. Build DEM and Orthomosaic (Manual)

1. Right-click the `DEM & Orthomosaic` chunk, select `Process`, and then `Build DEM`. A new window called `Build DEM` will appear (Figure 33). Accept defaults for resolution and total size, and change settings according to Figure 33. Click `OK`.

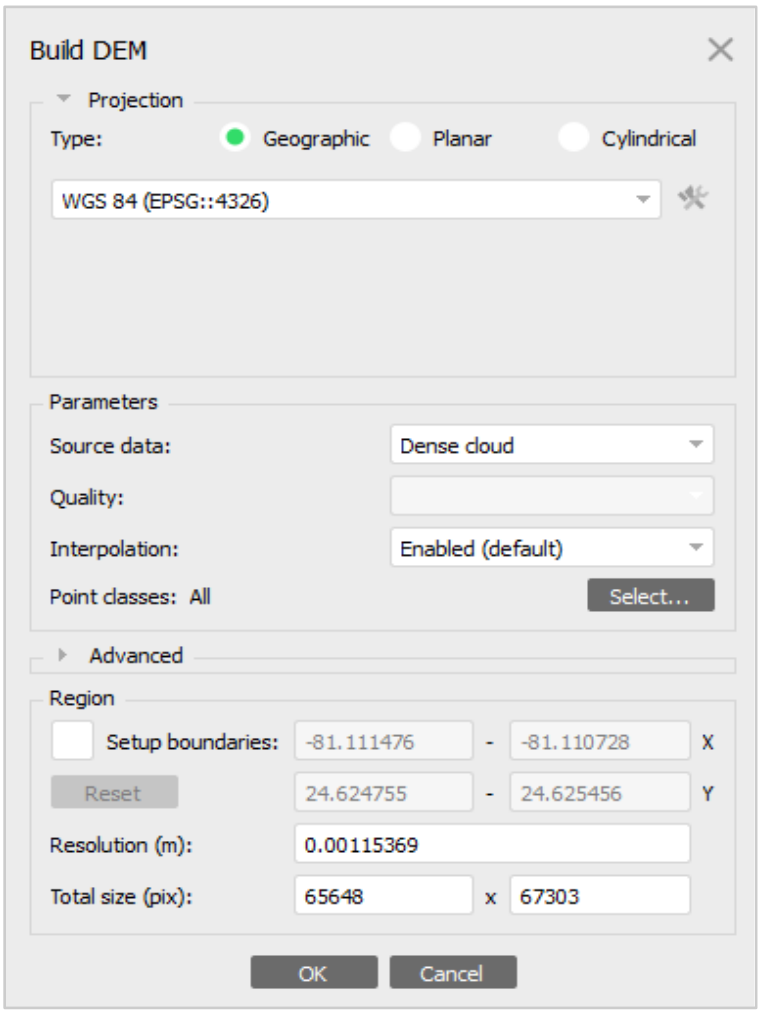


Figure 33. Build DEM window with settings to build DEM as described in step 1.

2. After the DEM has been built, check it by double-clicking on the generated DEM. Poorly generated DEMs may be all of the same color or have an extension of color off the model (Figure 34). Poorly generated DEMS with extensions of color can be fixed using the Draw tool.

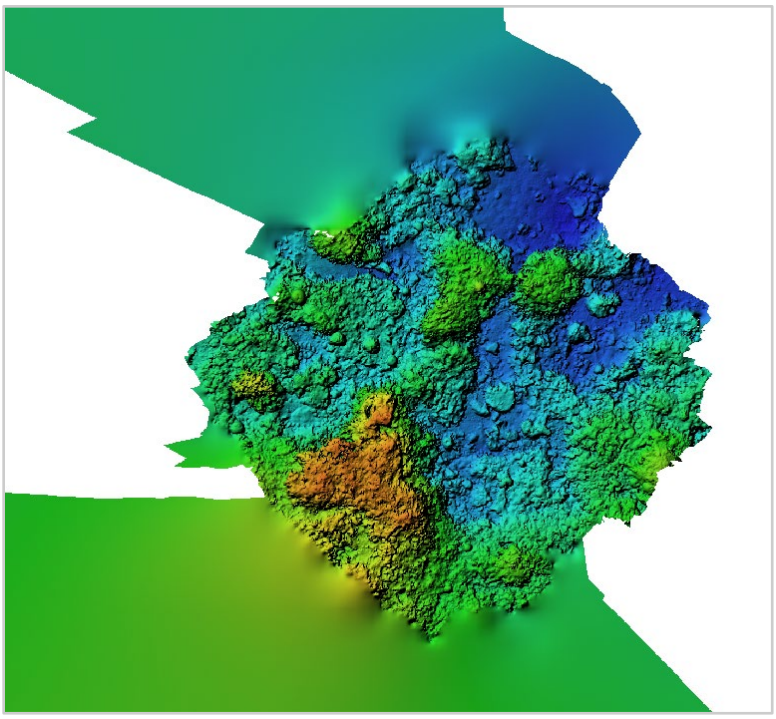


Figure 34. Example of poorly generated DEM with color extensions off the model.

A. Navigate to the Draw tool located next to the Rectangular Selection and Resize Region tools (Figure 35).

Figure 35. Location of the `Draw` icon in the main toolbar.

B. From the drop-down menu, select `Draw Polygon`. Continuously draw around the DEM model, making sure to exclude the smoothed portions that should be removed (Figure 36). Once the polygon has been drawn and the polygon lines connect at the starting point, a window named Shape Properties will appear. Click `OK` to save the polygon. Right-click on the polygon line, and from the context menu, select `Set Boundary Type`, then `Outer Boundary`. This sets the boundary to include anything inside the polygon when exporting the DEM or creating the orthomosaic.

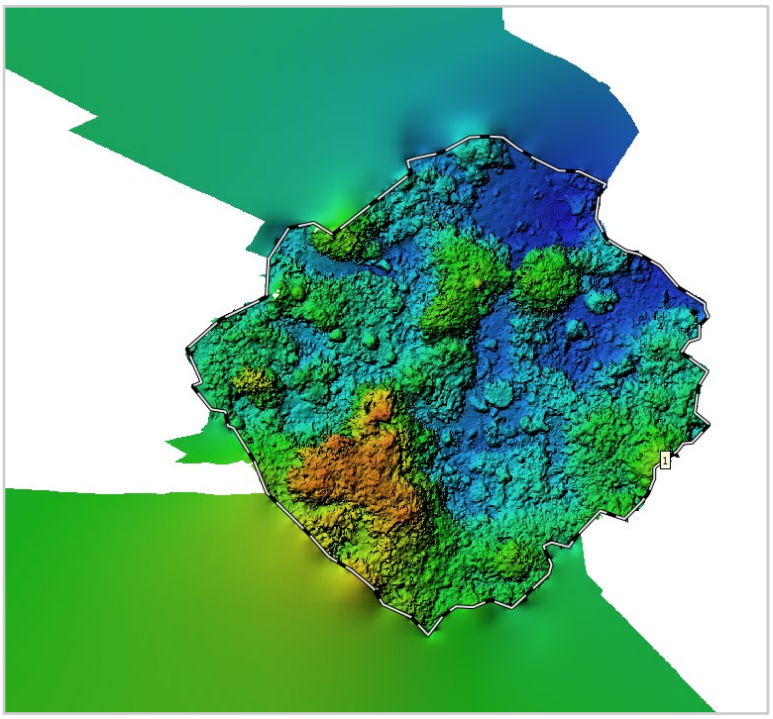


Figure 36. Example of poorly generated DEM with drawn polygon and set boundary.

3. Export the DEM by right-clicking the `DEM & Orthomosaic` chunk. Navigate to `Export`, then select `Export DEM` from the context menu. Save the file as TIFF/GeoTIFF (.tif) and name the file using the standardized naming convention with _DEM at the end (e.g., SOMB_R2-2_2022-08-25_DEM).
4. A new window named Export DEM - TIFF will appear. Accept defaults for `pixel size`, `no-data value`, and `total size (pix)`, and change settings according to Figure 37. Click `OK`.

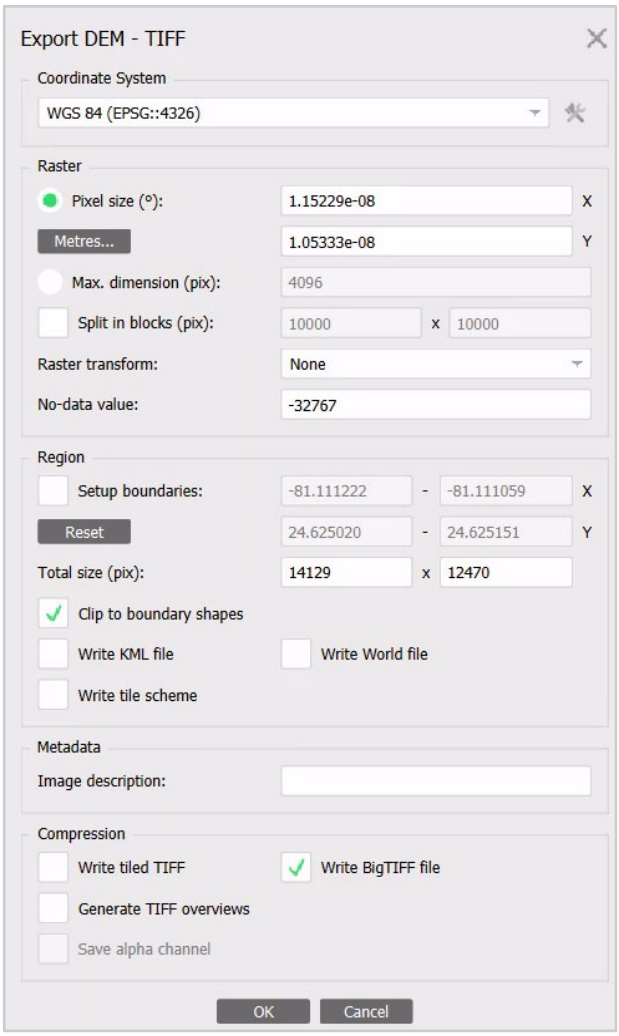


Figure 37. Export DEM - TIFF window with settings as described in step 4.

5. Once the DEM is finished exporting, navigate to the associated Metashape project folder (e.g., SOMB_R2-2_2022-08-25) to confirm the creation of the DEM TIFF file (e.g., SOMB_R2-2_2022-08-25_DEM.tif).
6. Return to Metashape, right-click on the `DEM & Orthomosaic` chunk, navigate to `Process`, and then select `Build Orthomosaic` from the context menu.
7. A new window called Build Orthomosaic will appear. Accept defaults for `pixel size`, and change settings according to Figure 38. Click `OK`.

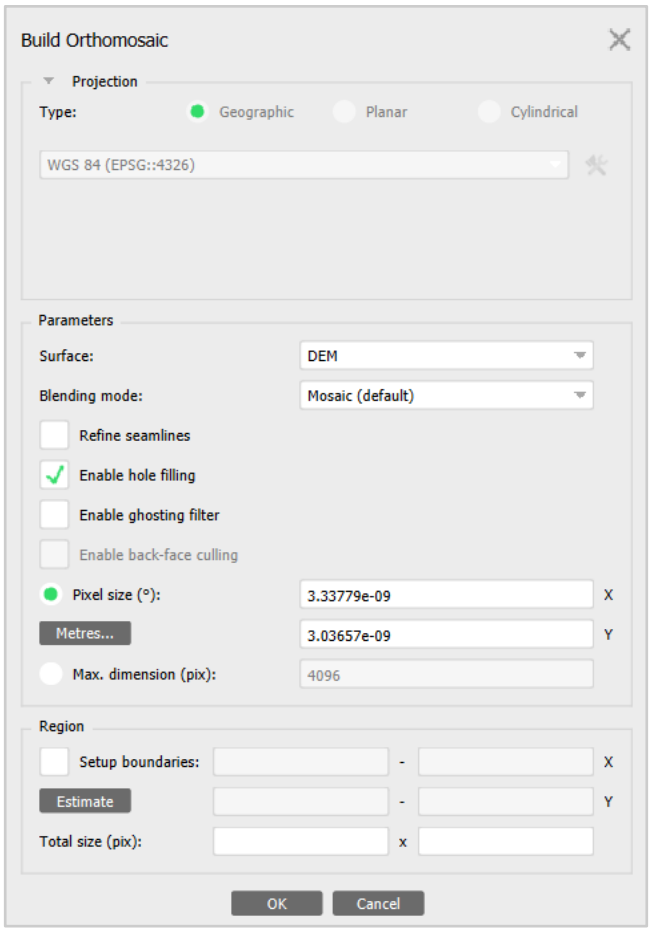


Figure 38. Build Orthomosaic window with settings as described in step 7.

8. Export the orthomosaic by right-clicking on the `DEM & Orthomosaic` chunk. Navigate to `Export`, then select `Export Orthomosaic` from the context menu. Save the file as TIFF/GeoTIFF (.tif), and name the file using the standardized naming convention with _Ortho at the end (e.g., SOMB_R2-2_2022-08-25_Ortho).
9. A new window called Export Othomosaic - TIFF will appear. Accept defaults for `pixel size` and `total size (pix)`, and change settings according to Figure 39. Click `OK`.
10. Once the orthomosaic is finished exporting, navigate to the associated Metashape project folder (e.g., SOMB_R2-2_2022-08-25) to confirm the creation of the orthomosaic TIF file (e.g., SOMB_R2-2_2022-08-25_Ortho.tif).

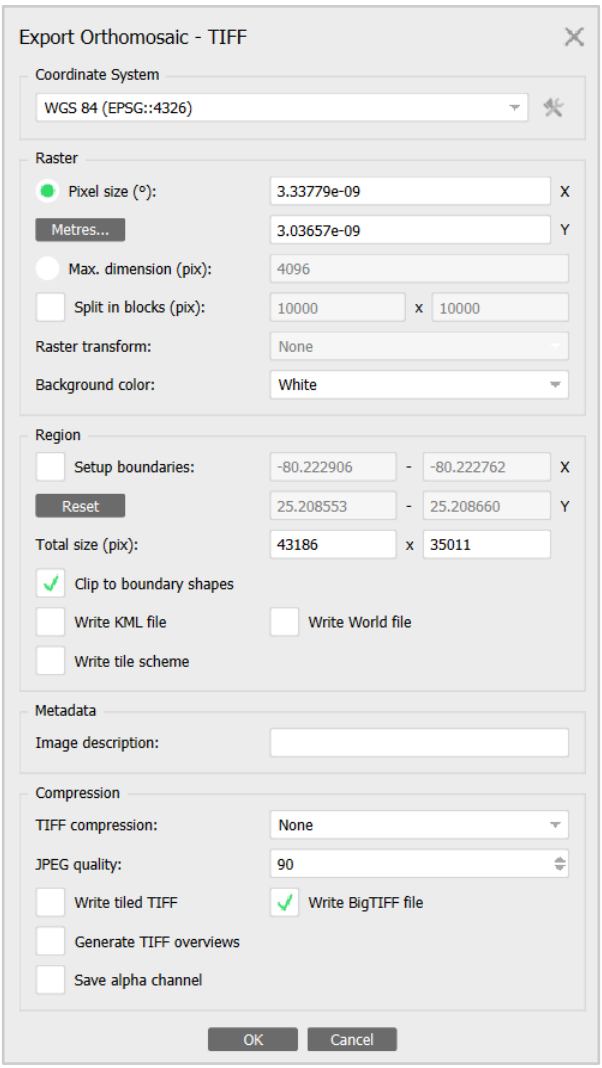


Figure 39. Export Orthomosaic - TIFF window with settings as described in step 9.

E3. Build DEM and Orthomosaic (Scripted)

1. Navigate to the topmost toolbar, and click on `Tools`, then `Run Script`.
    - To build the DEM and orthomosaic for one plot:
      Use script: MIR_Metashape_Processing_Part_III.py
      Type the following: `--input`, followed by the file path for the image folder (e.g., --input “E:\Raw_Imagery\SOMB_R2-2_2022-08-25_JPEG”).
      Click `OK` to start the build of the DEM and orthomosaic.
    - There are two ways to build DEMs and orthomosaics for multiple plots using a single batch processing script:

i. Use script: MIR_Metashape_Processing_Part_III.py
Type the following: `--input`, followed by the file paths to the folders containing the raw images to be processed (e.g., --input "E:\Raw_Imagery\SOMB_R2-2_2022-08-25_JPEG" "E:\Raw_Imagery\SOMB_R3-2_2022-09-26_JPEG"). When providing multiple paths, separate each path with a space only.

ii. Use script: MIR_Metashape_Processing_Part_III.py
Provide arguments as a text file that contains the paths for the image folders (e.g., --input "E:\Agisoft_Project_Data_Exports\ProcessingQueue.txt").
    - To avoid long queue times during DEM and orthomosaic generation, it is recommended to avoid batch processing more than six plots at a time.

Click `OK` to start the build of the DEMs and orthomosaics.

2. After the DEM and orthomosaic have been built, double-click on the generated DEM and follow steps 2 and 3 in *2E2. Build DEM and Orthomosaic (Manual)* to complete the process.
3. Navigate to the associated Metashape project folder (e.g., SOMB_R2-2_2022-08-25) to confirm the creation of two TIFF files. One will be the DEM (e.g., SOMB_R2-2_2022-08-25_DEM.tif), and the other will be the orthomosaic (e.g., SOMB_R2-2_2022-08-25_Ortho.tif).

E4. Completion of DEM and Orthomosaic Build

Once the DEM and orthomosaic are built (either manually or via script), the DEM & Orthomosaic chunk will show the creation of the DEM and orthomosaic in the Workspace pane (Figure 40). This marks the completion of the Metashape workflow.

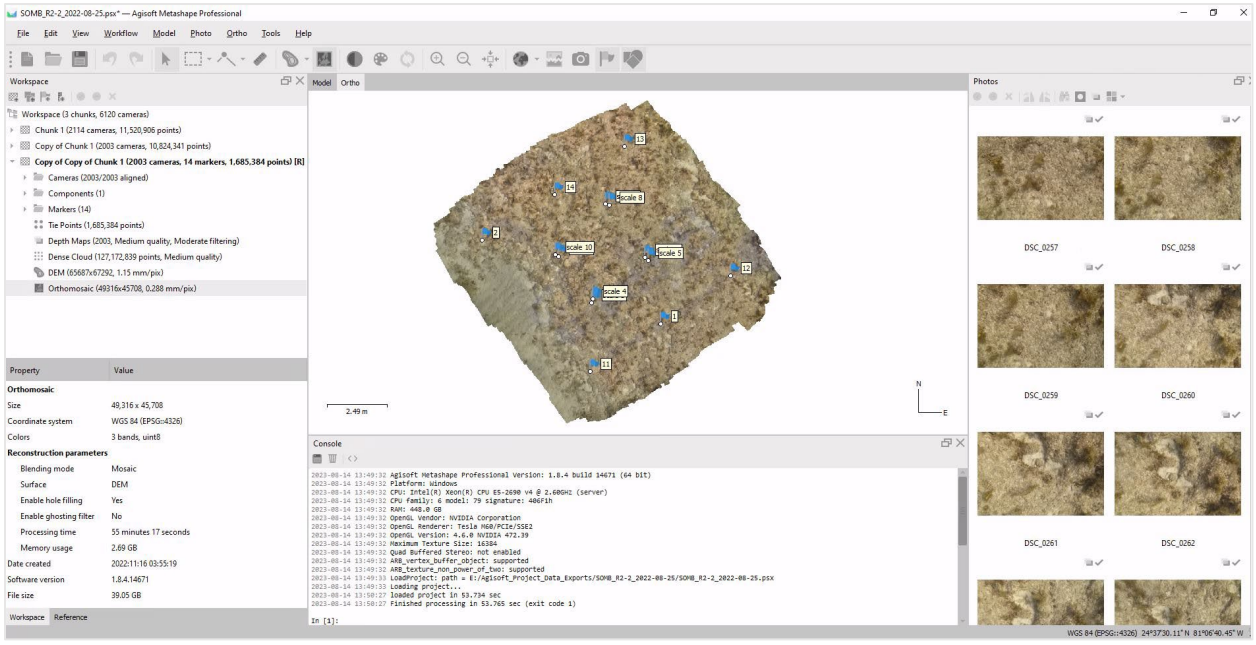


Figure 40. Completed DEMs and orthomosaics can be accessed via the Workspace pane.

F. Export 3D Model Data for Viscore

The DPC generated in Metashape is exported manually or via a script for use in the Viscore workflow. Data are exported as three files: .ply, .meta.json, and .cams.xml, and the.ply file is later converted to a Viscore-compatible format (.vml) for visualization in Viscore. The .meta.json and .cams.xml files (referred to as Cams files) are used to link raw images to the model.

F1. Export of .ply for Viscore (Manual)

1. Right-click on the `SPC & DPC – Optimized` chunk. Select `Export`, then `Export Points`. Save the file as Stanford PLY (.ply), and name the file using the standardized naming convention (e.g., SOMB_R2-2_2022-08-25).
2. A new window called Export Points - Stanford PLY will open. Change settings according to Figure 41, and click `OK`.

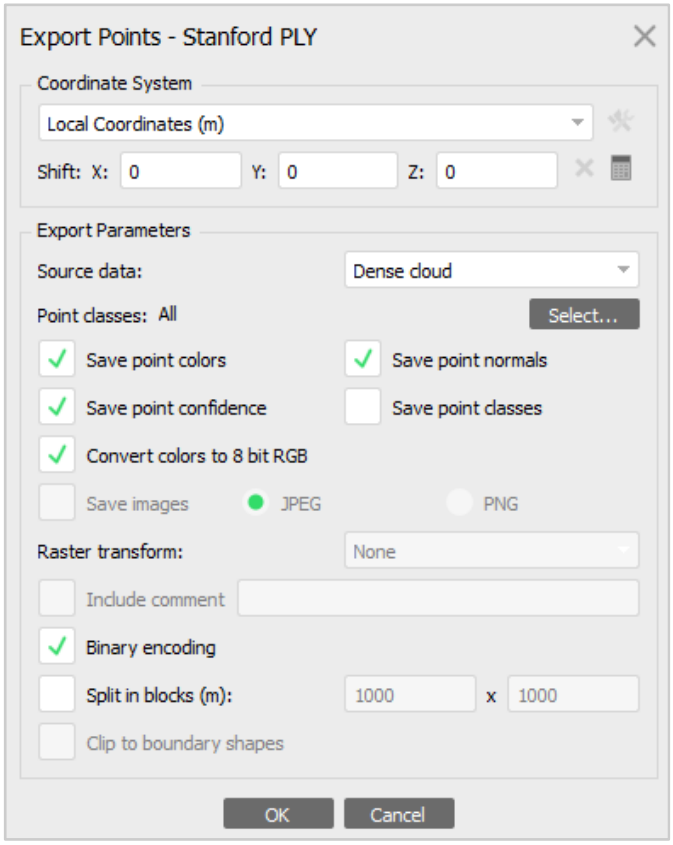


Figure 41. Export Points - Stanford PLY window with settings to export a .ply file as described in step 2.

3. To confirm creation of the .ply file, navigate to the associated Metashape project folder (e.g., E:\Agisoft_Project_Data_Exports\SOMB_R2-2_2022-08-25). There should be a 3D Object file with the naming convention in step 1 (e.g., SOMB_R2-2_2022-08-25.ply). This is the file that will be used to create a .vml file for use in Viscore.

F2. Export Camera Files for Viscore (Manual)

1. Select the `SPC & DPC – Optimized` chunk, then navigate to `Tools`, then `Run Script`.
   Use Script: extract_meta.py
   Leave the arguments field blank
   Press `OK` to start the export of the Cams files.
2. To confirm export of the camera files, navigate to the associated Metashape project folder (e.g., E:\Agisoft_Project_Data_Exports\SOMB_R2-2_2022-08-25). There should be an XML document (e.g., SOMB_R2-2_2022-08-25.cams.xml) and a JSON file (e.g., SOMB_R2-2_2022-08-25.meta.json) These are the files used to set the cameras of a model in Viscore.

F3. Export 3D Model Data for Viscore (Scripted)

3D model data for Viscore is exported automatically via the script used for *2C2. Optimization and Error Reduction of the SPC (Scripted).*

Alternative SfM Software Options

There are multiple SfM software options available for the generation of LAI. Below are some currently available alternatives to Metashape. The instructions here reference Agisoft Metashape Professional Version 1.8.4 and are not applicable to other software.

COLMAP
https://colmap.github.io/index.html

OpenDroneMap
https://opendronemap.org/

Pix4D
https://www.pix4d.com/try-software/

VisualSFM
http://ccwu.me/vsfm/

SECTION II. VISCORE

This section overviews the use of Viscore, a software platform used for the visualization and extraction of ecological data from LAI, in particular from point-based 3D models. Viscore provides an immersive visualization experience, while also providing a suite of functionality for the extraction of ecological data, including coregistration of time series imagery and orthoprojection (e.g., 2D map views) generation. Viscore also provides facile access to the raw imagery used to generate 3D models, enabling more detailed taxonomic analysis than would be available from 3D models or orthoprojections alone. Viscore is a custom software platform developed by Vid Petrovic and the Kuester Lab at UC San Diego, and the workflows described herein have been tested extensively by the Sandin Lab at the Scripps Institution of Oceanography, UC San Diego. NCCOS collaborates directly with both the Sandin and Kuester Labs and has recently worked in the development of additional Viscore workflows. The use of Viscore as described in this SOP pertains specifically to current NCCOS efforts in support of NOAA's M:IR restoration efforts in the Florida Keys, though it can be used more broadly by other projects for the study of benthic coral reef habitats.

This section outlines the following general workflows and tools in Viscore (Figure 42).

1. **Viscore Installation, Data Organization, and Preparation.** System configuration requirements and installation instructions are provided. Best practices and requirements for the management of data associated with the use of Viscore are described. Specific instructions detail the preparation and use of data generated in Metashape, including conversion of these data to the required Viscore format.
2. **Model Navigation and Overview of Tools.** Instructions for the navigation of 3D models, tools available, and important keystrokes in Viscore are described.
3. **Model Setup and Visualization Options.** Visualization options and suggested settings upon opening a model for the first time are provided in detail. Other key workflows that are described include linking of source imagery to 3D models for more detailed visualization, as well as the generation of multimedia.
4. **Prepare Model for Virtual Point Intercept (VPI) Preparation and Analysis.** Detailed steps are provided for the provisioning of scale and depth information to the 3D models prior to starting any analyses. Instructions for the use of the VPI tool for the estimation of benthic percent cover are provided in detail. Key steps include generation of the sample area, and generation and labeling of random point samples.

5. **Project Management and Creation of 2D Map Views with the Org Tool.** Project management and associated data organization activities can be accomplished in Viscore using the Org tool. 3D models collected at multiple locations (e.g., islands, reefs, sites, or plots), including associated VPI data and generated orthoprojections, can be managed via a single project file. Time series 3D models can also be similarly managed, and coregistration can be conducted via a semi-automated workflow. Top-down map views, or orthoprojected images, are generated directly from 3D DPCs in Viscore. Orthoprojections are exported from Viscore for later use in TagLab.

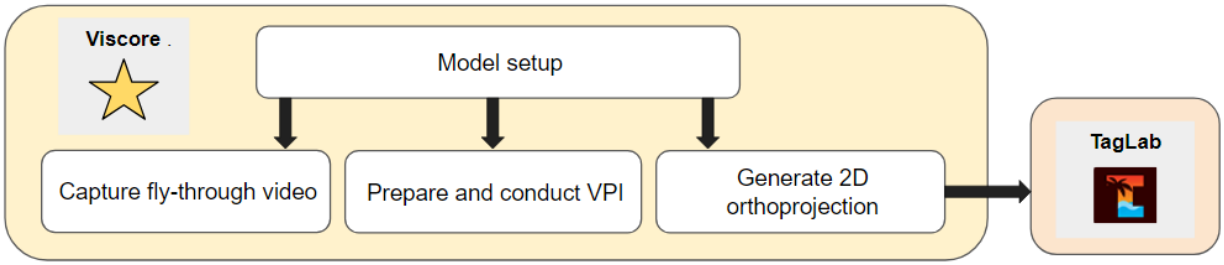


Figure 42. Diagram of Viscore workflows. After models have been prepared, three primary workflows are executed: fly-through videos, VPI analysis, and the generation of 2D orthoprojections for use in TagLab.

1. Preparation

Part 1 of this guide provides instructions for the installation of Viscore, as well as a description of the file formats and organization used by Viscore. Viscore has specific computational requirements that should be referenced prior to installation (*Appendix I.B.*). Before installing and using Viscore, it is important to change the default view in Windows Explorer to show file details and file name extensions (Figure 43).

1. Open a new File Explorer window from the computer's desktop (Figure 43).
2. Click on View pane at the top of the window (Figure 43A).
3. Check `File Name Extension` (Figure 43B).
4. Click on `Options` (Figure 43C).
5. In the Folder Options window under the tab View, click `Apply to Folders` (Figure 43D).
6. When finished, press `OK` (Figure 43E).

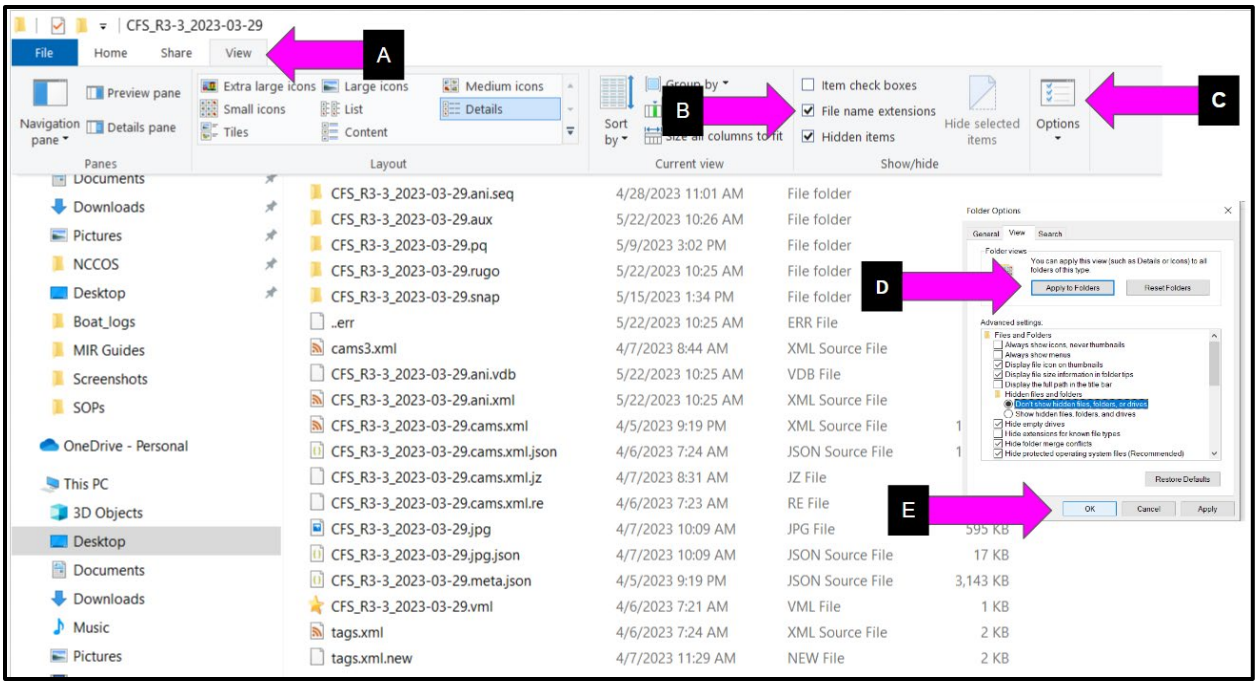


Figure 43. Steps to change the File Explorer settings to show file name extensions and file details. (A) Click the `View` tab at the top of the File Explorer window. (B) Check off `File Name Extensions`. (C) Select `Options`. (D) A new window will open, select `Apply to Folders`, then (E) `OK` to complete the process.

A. Installing Viscore

For NCCOS and M:IR staff, all software and dependencies will need prior approval and support from IT to install.

A1. Requirements

1. **Viscore installer**. Usually shared as a zipped folder (e.g., Viscore_NCCOS.zip). Unzip folder before use.
2. **Run-time libraries.** Microsoft Visual C++ redistributable installation files Vc_redistr_2015x64.exe and Vc_redistr_2010x86.exe.
3. **3D model data**. Usually, a small model is shared as a zipped folder (e.g., coral_test.zip), but any 3D model that has been prepped for Viscore use can be used to test installation success. Unzip this folder before use.
4. **Google Chrome**. Various Viscore tools utilize an internet browser (no internet connection required) and have been developed using Google Chrome. In most cases, other browsers will work but have not been extensively tested.
5. **Visual Studio Code**. Various components of data required and generated by Viscore are stored in large text files that are not easily viewed in standard text editors or programs such as Microsoft Word. Visual Studio Code is publicly available (https://code.visualstudio.com) and specifically designed for viewing these files and is highly recommended (though not technically required).

A2. Installation Instructions

1. Locate and extract the zipped Viscore installation folder (e.g., Viscore_NCCOS).
2. Inside the installation folder, find the file named `deploy-to-c.cmd` and double-click on the file to run the command.
3. The Command Prompt will open and start running the installation. The installation has finished when the Command Prompt shows `Press any key to continue`.
4. When finished, navigate to the computer's local C drive, and double check that there is a new folder named `vid` (Figure 44). If the Vid folder is not visible, it might be necessary to refresh Windows Explorer or run the deploy-to-c.cmd a second time. If users do not have write access to the drive, they should contact the owner of the administrator profile.

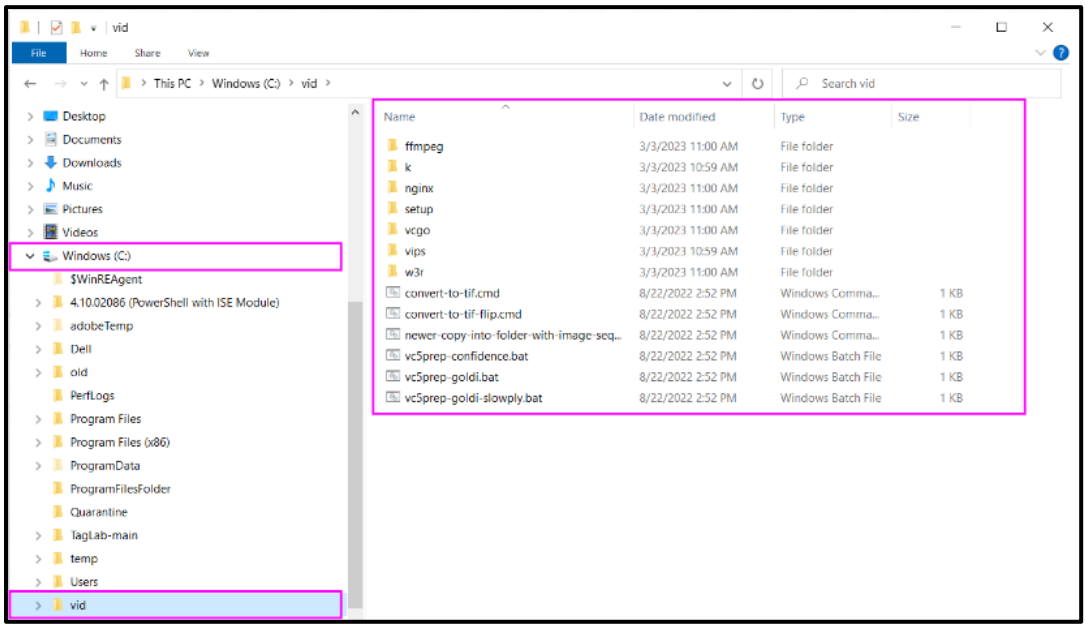


Figure 44. Contents within the Vid program folder.

5. Install the run-time libraries.
   - vc_redistr_2015x64.exe
   - vc_redistr_2010x86.exe
   - These run-time libraries are typically already installed on most computers. If an error message indicates that the program is already installed, no further action is needed. Continue to the next step.
6. Open a test dataset to confirm installation success. Models are opened using the .vml file, and Viscore must be set as the default program for this file type. Instructions for setting the default file type in Windows 10 are provided below (Figure 45). After setting Viscore as the default program to open .vml files, the .vml will now have a gold star icon.
   - Right-click on the .vml file and select `Open with` (Figure 45A).
   - Select `Choose another app` (Figure 45B).
   - Select `More apps` (Figure 45C).

- Check `Always use this app to open .vml files` (Figure 45D).
- Select `Look for another app on this PC` (Figure 45E).
- Navigate to the `vid` folder on the C drive and open the `vcgo` folder (e.g., C:\vid\vcgo) (Figure 45F).
- Select `vc5.exe` (Figure 45G).
- Click `Open` (Figure 45H).

7. After clicking `Open`, the model should automatically open (Figure 46). If it does not, return to the folder containing the model to be opened, and double-click the .vml file to launch the model.

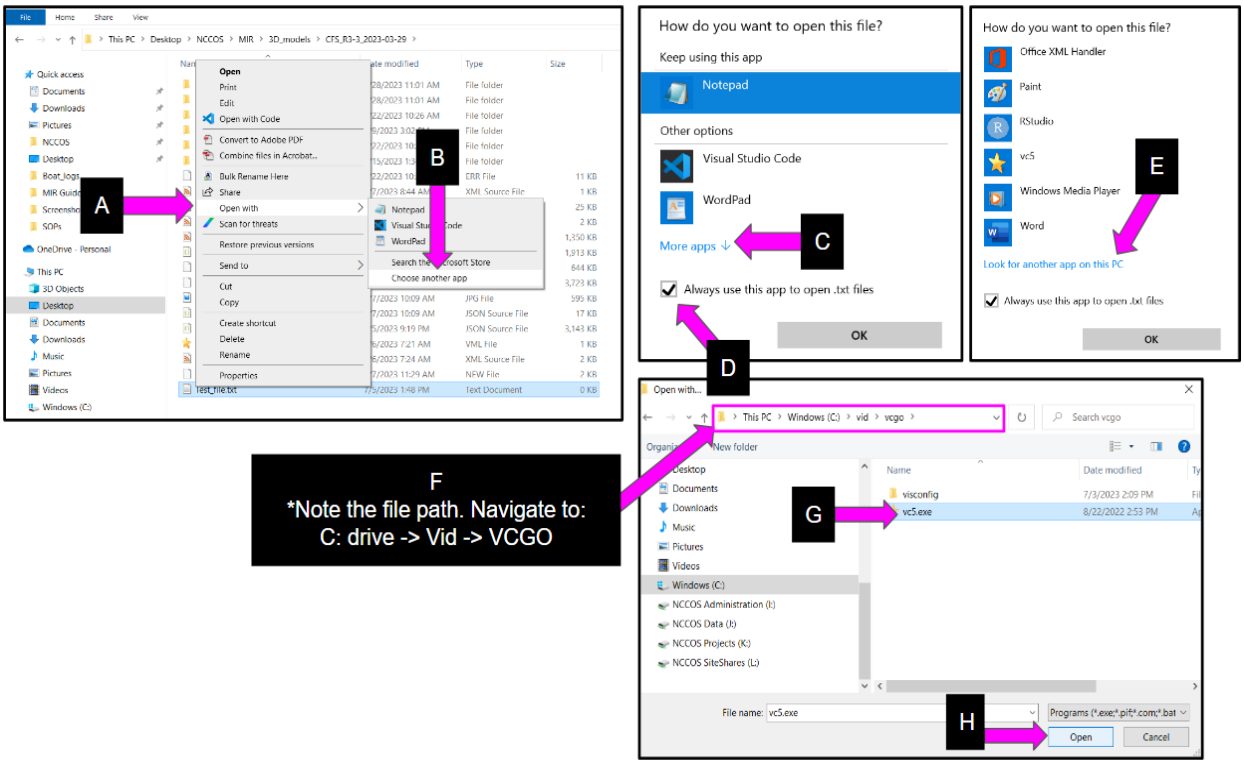


Figure 45. The steps required to set Viscore as the default program to open .vml files. (A) Right-click on the model's `.vml` to bring up the second window; click `Open` with. (B) Select `Choose another app`. (C) Click `More apps`, then (D) check off the box `Always use this app to open .vml files`. (E) Click `Look for another app on this PC`, and a new window will appear. (F) In the new window, navigate to the C drive where the Vid folder is located, open the folder `vcgo`, (G) select `vc5.exe`, then (H) click `Open` to complete the process.

8. When Viscore is opened, the Viscore Viewer will open along with a console window. The Viscore Viewer will briefly display configuration information while point data are loading (Figure 46A). The console window prints system information and is generally not used. Both windows can be accessed similarly to other Windows programs by hovering the cursor over the gold star in the task bar (Figure 46B). When opening a model, if there is a delay in loading the point data (beyond 10 s or so), click once somewhere in the black space of the

Viewer window to refresh the loading process (typical when opening large models, or when the data are stored on an enterprise server).

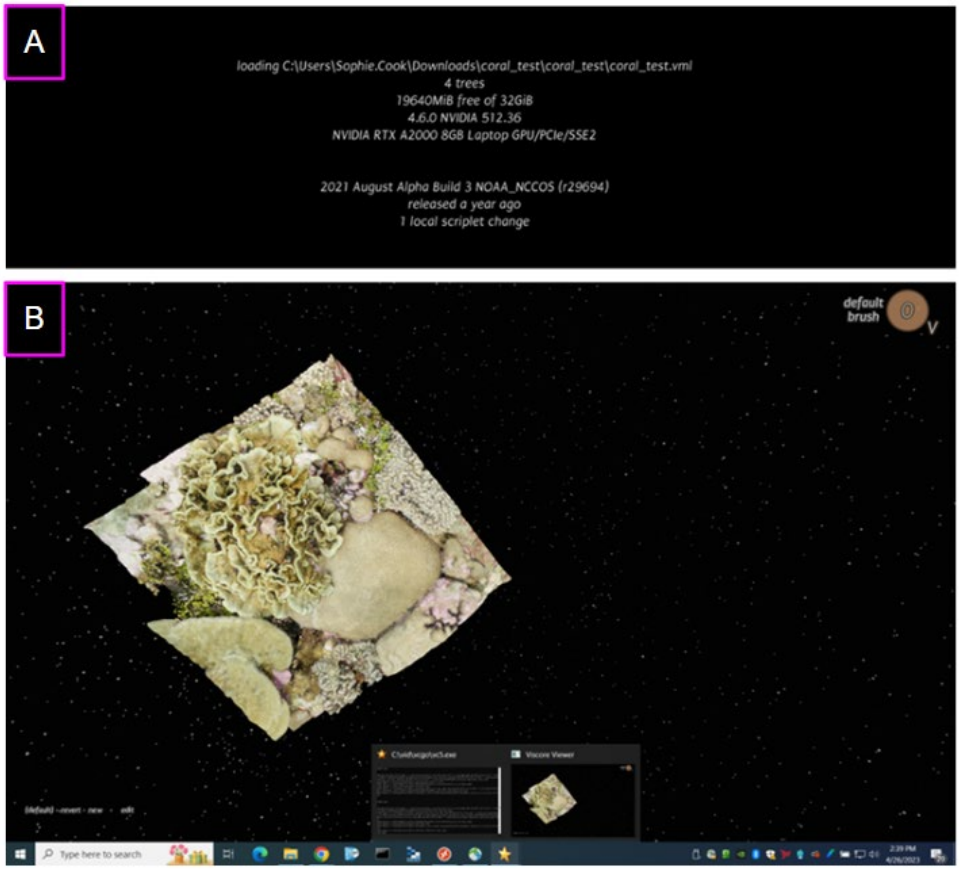


Figure 46. (A) When Viscore is opened, system configuration information will be briefly displayed while point data are loading. (B) Viscore opens in two windows, the interactive Viscore Viewer window and the console window, which displays system information and is otherwise not used.

9. To close Viscore, press the Esc key.
10. Enable GPU Utilization for Viscore. If the computer does not have a dedicated graphics card (i.e., it does not have NVIDIA or AMD), skip this section, and proceed to *1B. Viscore File Formats and Organization.*
    A. For computers with NVIDIA:
        - Open NVIDIA Control Panel (type `NVIDIA Control Panel` in taskbar to open and launch). Click on `Manage 3D settings`, then click on the Program Settings panel.
        - Under `1. Select a program to customize`, click `Add`, navigate to the C drive, and find the Vid folder. Open the `vcgo` folder, and select the file `vc5`.
        - Under `2. Select the preferred graphics processor for this program`, select NVIDIA or the desired graphics processor.
        - When finished, click `Apply`.
    B. For computers with other graphics cards (i.e., AMD):

- Open `Graphics settings` (type `Graphics settings` in taskbar to open and launch).
- Under `Graphics Performance Preference`, click `Browse`.
- Navigate to the C drive, and find the `vid` folder. Open the `vcgo` folder, and select the file `vc5`. Click `Add`.

11. If the graphics card is being utilized, it will appear in the system configuration information that is displayed when a model opens (Figure 47A).
12. Alternatively, verify GPU utilization via the Spacebar menu in the Viscore Viewer window.
    - Press the Spacebar to open the menu.
    - Using the arrow keys on the keyboard, navigate to `About` and click `Enter`.
    - Navigate to `System` to display the configuration. If the GPU is being utilized, it will be listed. If the computer does not have a GPU or if it is not being utilized, the CPU graphics card will be listed (Figure 47B).

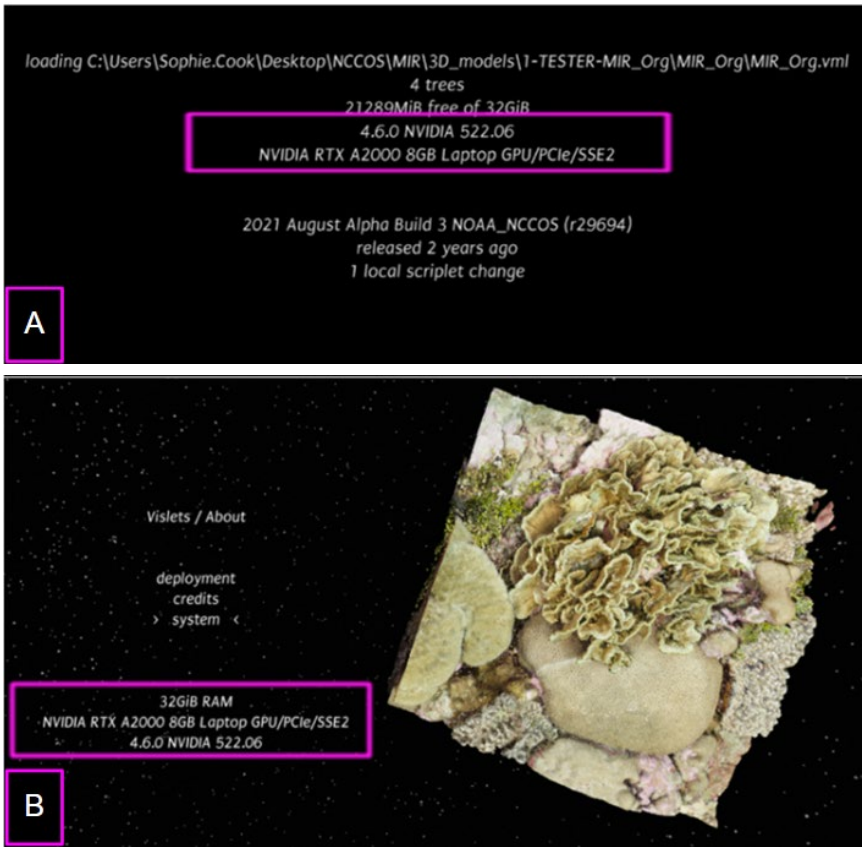


Figure 47. Examples of verifying if the graphics card is being utilized. (A) It can be verified by looking at the Viscore Viewer window when launching a .vml, or (B) by going to the submenu System via the Spacebar menu.

B. Viscore File Formats and Organization

3D models and the raw imagery used to create them can require substantial storage. Additionally, with Viscore use, large numbers of files will be created. A robust data curation plan is strongly recommended to organize and securely store these data products. The approach to data organization and management described here is critical to execute various Viscore workflows, and the guidance provided should be followed as closely as possible. Given the large storage requirements associated with LAI, it is strongly advised to store Viscore 3D model data and raw imagery separately. Further, a large number of files are generated via Viscore workflows and standardized naming conventions appropriate to the project are critical. Data generated in Viscore will be saved within model-specific folders generated by Viscore within the project's folder.

The project organization provided below has been specifically developed for the proper use of Viscore.

B1. Project Organization Format

1. Create a project folder on the computer's desktop or documents folder (e.g., MIR_NCCOS).
2. Within the project folder (e.g., MIR_NCCOS), create a folder named `Viscore_models` to hold all Viscore 3D_models and derived data products.
    - Individual Viscore models are represented by a spatially contiguous set of images that are collected at a single site (or plot) at a single point in time and from which a single 3D model is generated. Each model is stored in a subfolder using the following standardized naming convention: Location_Plot-Subplot_YYYY-MM-DD format (e.g., the folder associated with a collection at plot R5-1 at the site Cheeca Rocks on January 9, 2023, would be labeled as CHCA_R5-1_2023-01-09 for the M:IR project).
    - This folder is distinct from Metashape project files, which should be stored elsewhere (e.g., Agisoft_Project_Data_Exports folder).
3. If it does not already exist, create a separate folder named `Raw_images` in the project folder (e.g., MIR_NCCOS) to store all of the imagery used to generate a given 3D model. The structure of the raw imagery folder should directly mirror the structure and naming conventions used in the Viscore models folder (e.g., for a model named CHCA_R5-1_2023-01-09, the name of the imagery folder should CHCA_R5-1_2023-01-09_JPEG within the Raw_image folder).

B2. Preparing Data for Viscore

1. To visualize and extract data from 3D models in Viscore, the following files are required (Figure 48):
    - **3D model data**. DPCs are exported from Metashape as a .ply file.
    - **Camera pose information (Cams files)**. Are exported from Metashape as .meta.json and .cams.xml files.
    - **Raw imagery.** Used to create a given 3D model. 3D model data and camera pose information are later used to link these raw images to the model.

2. Create a folder for the 3D model to be converted into Viscore format, and copy/move the .ply, .cams.xml and .meta.json files into this folder (Figure 48).

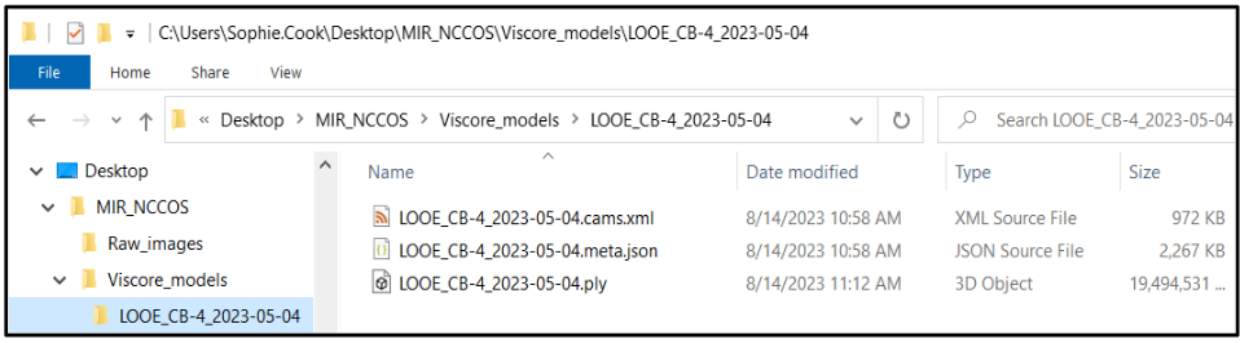


Figure 48. Example of the files that should be placed into a new folder for Viscore preparation. Folder structure is also shown in the left-hand pane. A project folder (e.g. MIR_NCCOS) contains folders for Raw_images and Viscore_models. Individual collections of models and images are then stored inside these folders with no additional nesting of folders.

3. Navigate to the `vid` folder on the C drive, and locate a file named `vc5prep-confidence.bat`. This file contains a script that will be used to convert the point data stored in the .ply file into the Viscore format.
4. Drag and drop the .ply file from the model folder (Figure 49A) onto the vc5prep-confidence.bat file. A Command Prompt will automatically open, and the file conversion process will begin. When the Command Prompt console reads `Press any key to continue`, the process is complete.
5. When the process has finished, the following will appear in the model folder:
   - A folder with the same name as the original .ply file, which contains the converted point data (Figure 49B).
   - A .vml file, which is used to open a given model in Viscore. If Viscore has previously been set as the default program, the .vml file will have a star icon next to it (Figure 49B). If a star does not appear, refer to step 6 under *1A2. Installation Instructions* before proceeding to the next step.

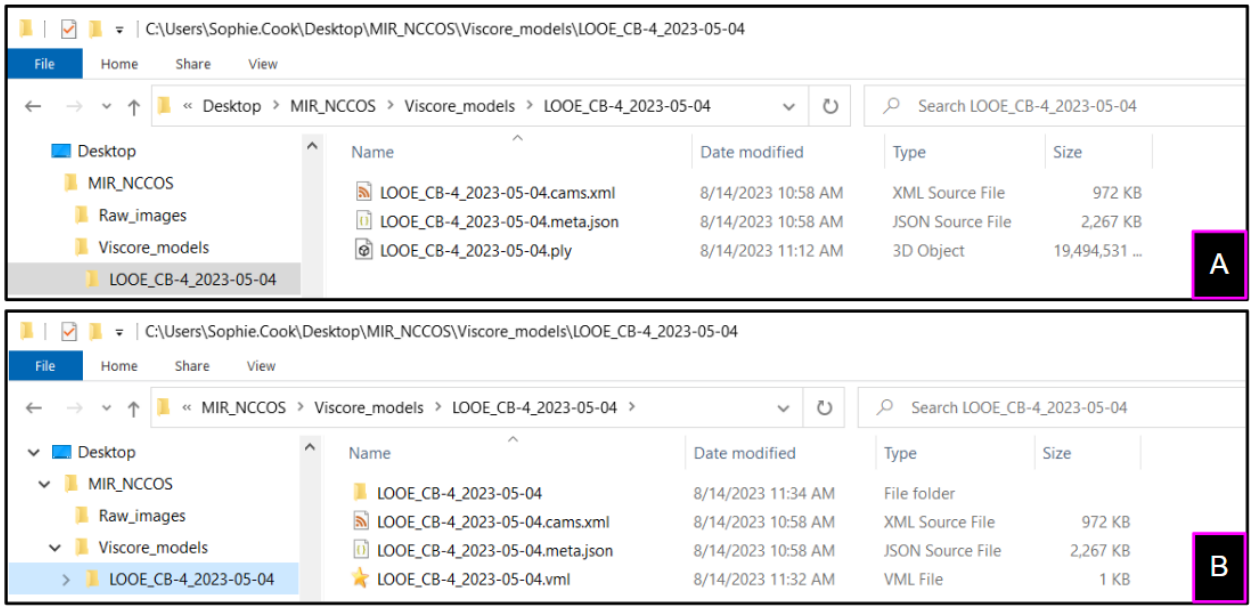


Figure 49. (A) The project folder prior to converting the .ply to a .vml and point data. (B) The newly created .vml and point data folder will have the same name as the original project folder (e.g., LOOE_CB-4_2023-05-04). Further, note the gold star icon next to the newly created .vml file.

6. Depending on the specific data curation plan being followed, the .ply file should either be moved back to the Metashape processing folder or deleted from the model folder. See *Appendix III.B.* for M:IR-specific data curation instructions.

B3. Viscore Data and File Types

As noted above, the .vml file and point data folder will retain the name of the .ply file from which they are generated. The point data folder contains hundreds to thousands of point data and associated files, all of which also retain the name of the original .ply file. When a model is opened for the first time, several additional new folders and files are automatically generated within the project folder, which also use the naming convention of the original .ply files (Figure 50A). As the model is set up (e.g., scale and orientation are provided) and other workflows are used, these data are automatically stored within the various folders previously generated by Viscore (Figure 50B). It is important to not change any of these file names, as they are used by Viscore to load and store data. If folder names are altered, Viscore will not be able to retrieve data stored within these folders, and in some cases, corruption or loss of data may occur.

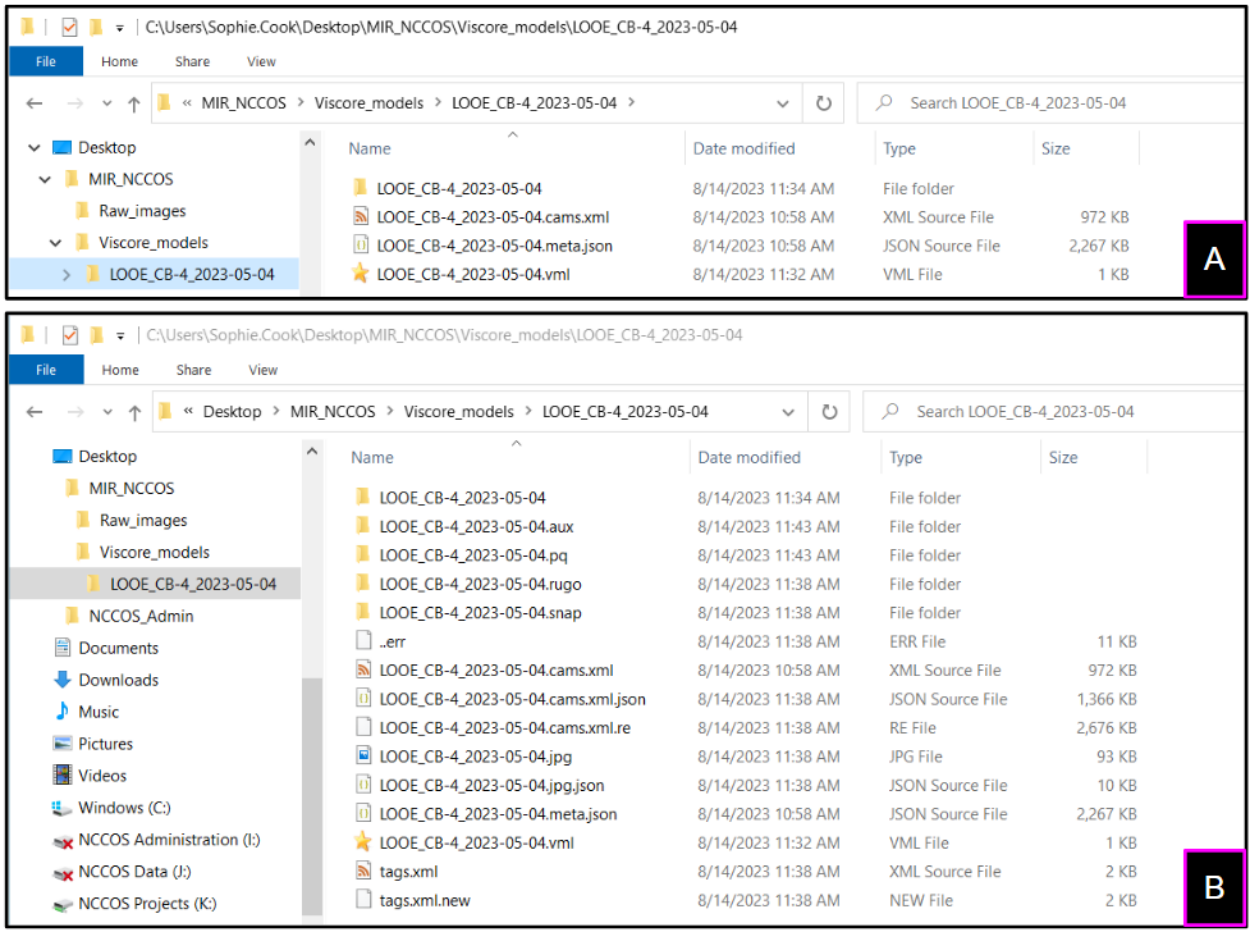


Figure 50. (A) The model folder's contents prior to opening the model for the first time and before any setup or workflows are applied. (B) The model folder's contents after the model has been opened or after any setup or workflows have been applied.

B4. Auxiliary Files and Folders

- .ani.seq (Folder)
  - This folder will be created when capturing an image sequence for a fly-through video. Depending on the version of Viscore being used, this folder may be called undefined.ani.seq or project-name.ani.seq. It will contain all of the screenshots that are put together for a video.
- .aux (Folder)
  - Houses auxiliary data including but not limited to scale and orientation data, exported orthoprojections, backups, etc.
- .pq (Folder)
  - Contains all data associated with the VPI tool, including the coordinates of the sample region (qbox.json), benthic classifications (qclasses.json), point coordinates (list all three), and classification data samples.cl.user.UserName.json.

- .rugo (Folder)
  - Contains all rugosity data. These include the box coordinates, transect sampling data, and the exported .csv file with coordinates for sampled points.
- .snap (Folder)
  - Contains all saved views.
- .ani.vdb and ani.xml (Files)
  - Associated with the fly-through video path, this file will be present only when a path containing at least three keyframes has been made.
- .jpeg (Files)
  - This is the saved default view for the model. Changing the default view changes this image.
- .cams.xml.json, .cams.xml.jsonz, .cams.xml.re (Files)
  - First created after opening a model in Viscore when the Cams files (.cams.xml and .meta.json files) containing image poses are present. These are transformed camera pose data for use in Viscore.
- Tags.xml (Files)
  - Contains the label and color scheme for tags of a model. Can be copied to another model to use the same tag classes and colors.

2. Model Navigation and Tools in Viscore

A. Navigation Instructions

It is recommended to visit Figure 155 under *Appendix I.B.* for reference on the use of particular mouse gesture buttons utilized throughout the remainder of the Viscore section *(Section II. Viscore*).

A1. Set the Navigation Target

- Double-click to create a navigation target.
- The view will center on the target.
- All navigation is based on target location. Continuously reset the target while navigating around the model.

A2. Rotate the Scene

- Imagine a screen-sized ball centered on the target (arcball-style control).
- Hold the left mouse button to drag the ball in the desired direction: dragging up/down rotates around the target's horizontal axis; dragging left/right rotates around the screen's vertical axis; dragging near the screen's edge in a clockwise/counterclockwise motion rotates around the axis perpendicular to the screen.

A3. Zoom In/Out

- Hold the right mouse button + drag.
- Push the mouse away to zoom out; pull the mouse in to zoom in.

A4. Pan the View

- Center-click (or simultaneous left-click + right-click) and drag.
- Note: Panning does not change the target position and navigation remains relative to the target. Panning extensively without resetting the navigation target may cause any rotating or zooming in/out to produce unexpected results.

B. Heads Up Display (HUD) and Spacebar Menu

Active tools (e.g., Ortho, Scaler, PQs, etc.) are accessed via the Viscore Heads up Display (HUD). Other tools can be added to the HUD (among other settings) via the Spacebar menu.

- HUD: accessed by hovering the cursor over the list of items on the right side of the Viscore Viewer (Figure 51).
  - Clicking on a tool in the HUD will turn it on or off (Figure 51).
  - When a tool is opened, an active menu for that tool will appear on the bottom-left side of the screen and display the menu options associated with that tool (Figure 51). Tools can also be turned off from the active menu in the bottom-left corner of the screen (Figure 51).
  - The primary tools available in the HUD that are utilized by this workflow are highlighted and briefly described in Figure 52.
  - For those tools with adjustable options, values can be changed as follows:
    - Increase a value, or scroll up through a list of categorical values: Position the cursor over the value, and left-click or scroll up to increase.
    - Decrease a value, or scroll down through a list of categorical values: Position the cursor over the value and right-click or scroll down to decrease.
    - For options with numeric values, mouse position and control are digit specific, e.g., positioning the mouse cursor over the digit 1 in 1.234 and clicking once or scrolling up will increase the value to 2.234, values in the first, second, third, etc. decimal places can be changed in the same manner.
- Spacebar menu: accessed by pressing the Spacebar on the keyboard.
  - Use arrow keys to navigate through submenus.
  - Use Enter to select or change submenu items.
  - Additional tools can be added to the HUD via the Scriptlets submenu found within the Spacebar menu (Figure 53A). Note that in the example provided in Figure 53B–C, the tool Ptconf was activated under the REPL submenu. However, other tools can also be found under the Core, App, and Misc submenus.

- When activating a tool, the options Now, VML, and Sys are used to turn on a tool and determine when that tool will be turned off (Figure 53D). Note that in Figure 53D, the Ptconf tool was activated to always turn on using the Now, VML, and Sys submenu options.
  - `Now`: select `Now:on` to turn a tool on for the active session. The tool will revert to off the next time the model is opened.
  - `VML`: when a given tool is set to `Vml:on`, that tool will remain turned on when the model currently in use is opened again. Alternately, when a given tool is set to `Vml:sys`, that tool will follow the setting in Sys.
  - `Sys`: when set to `Sys:on`, that tool will automatically be activated for any model opened on that computer.

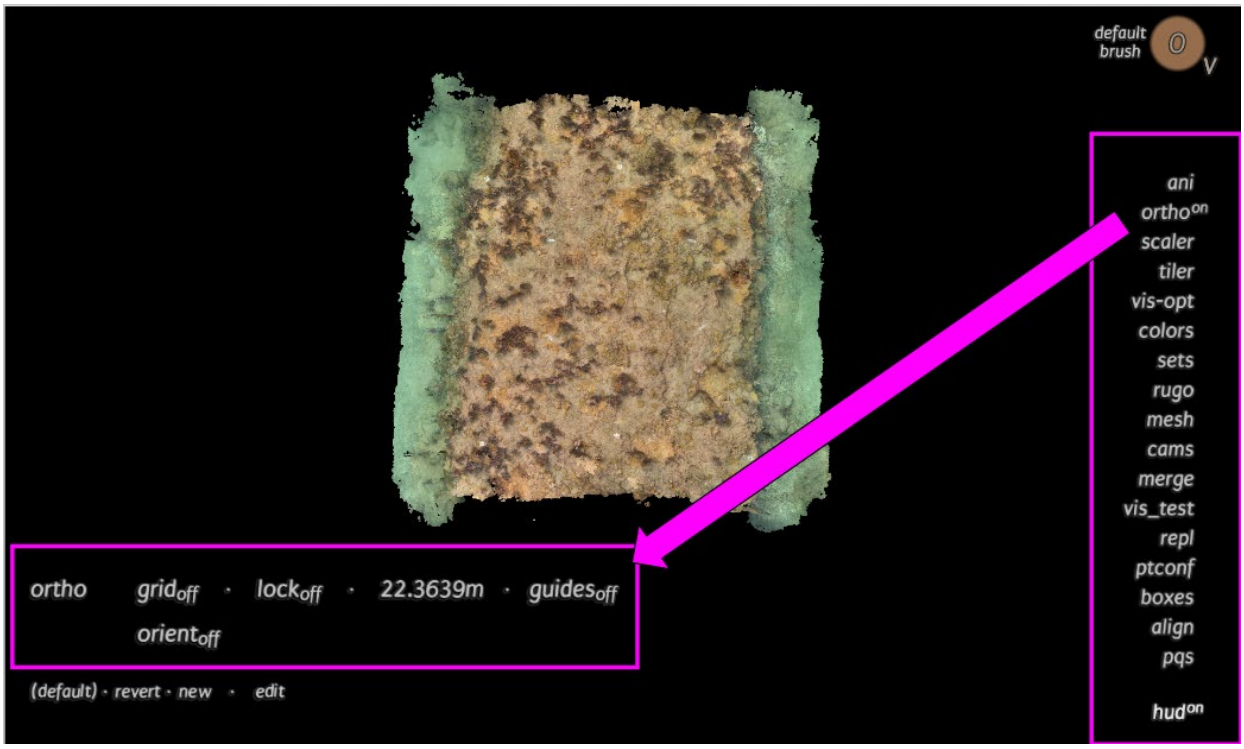


Figure 51. Example of where menu items from the HUD are located when turned on (i.e., hover over the right side of the screen to access the HUD, then click on the menu item to turn on). Once on, it will appear in the menu at the bottom-left corner of the screen.

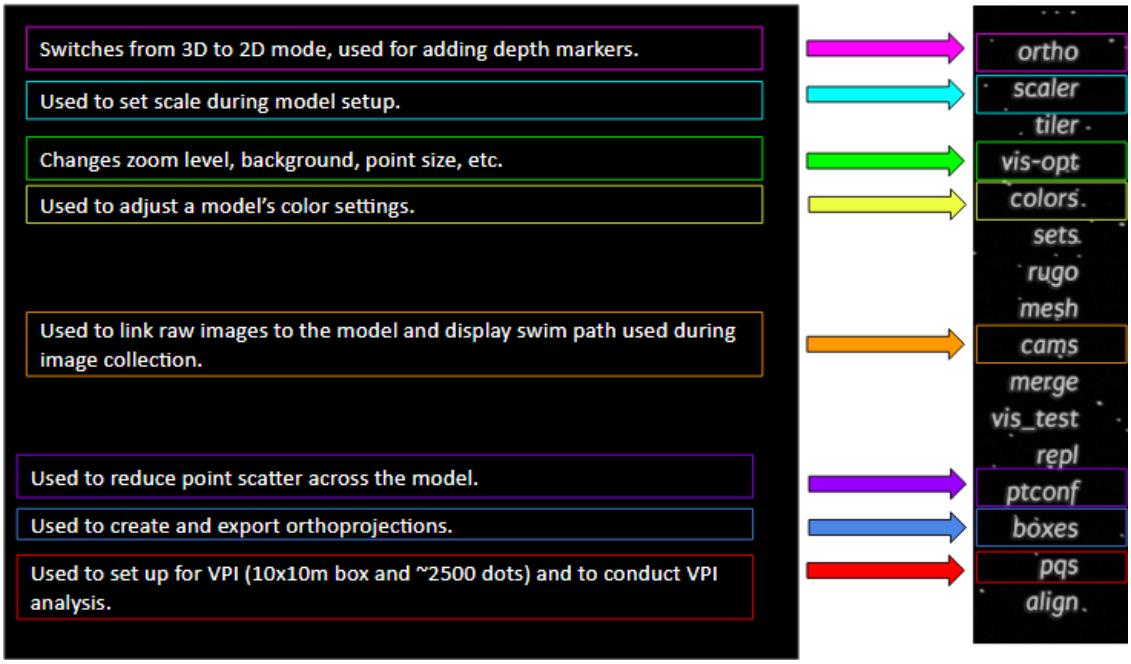


Figure 52. Example of HUD tools primarily used in this workflow.

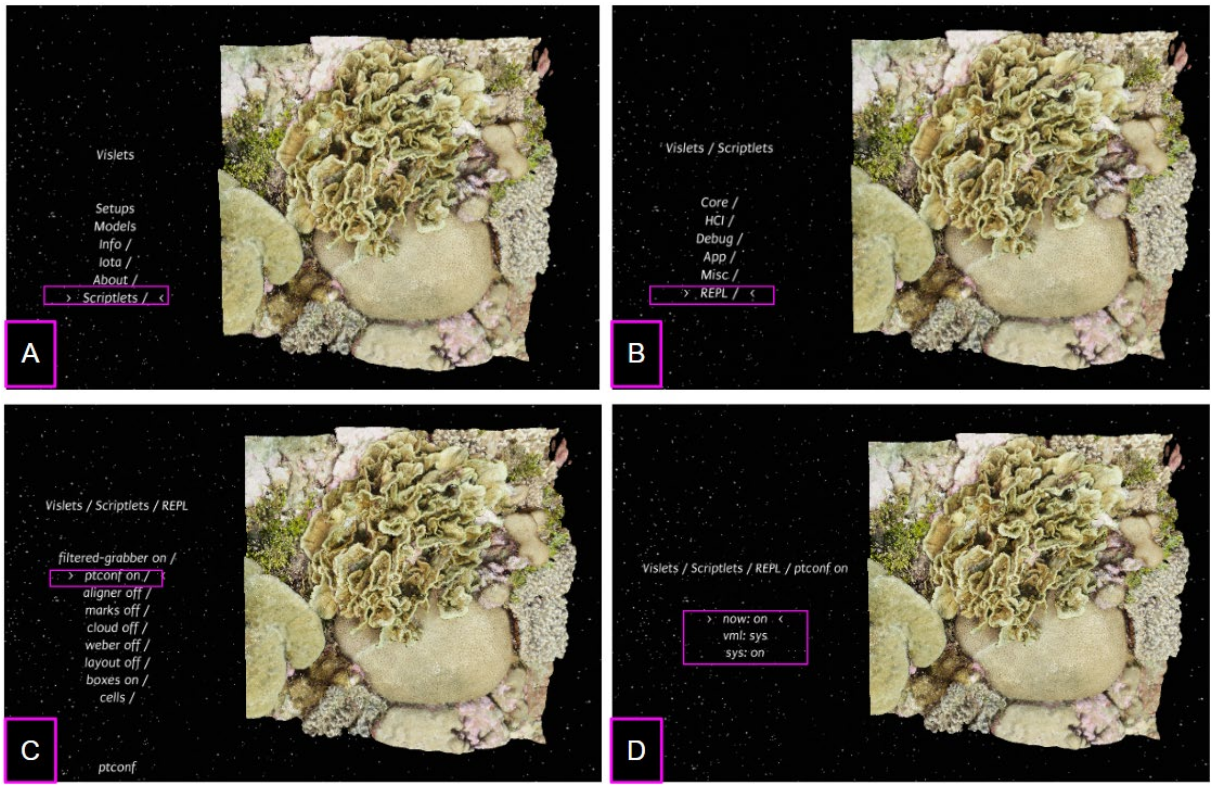


Figure 53. Example of using the Spacebar menu to permanently add a tool. Here the Ptconf tool is added. All tools can be found in the (A) Scriplets submenu, and Ptconf is located in the Repl submenu (B) and (C). After entering the Ptconf tool submenu (D), default tool settings can be set as required. In the case of commonly used tools, `sys` and `now` should be set to `on`, and `vml` should be set to `sys`.

C. Important Keystrokes

- Change the global point size: Ctrl + scroll.
  - Useful when point density varies across the model.
  - Point size can also be changed in the HUD under vis-opt.
- Switch between ortho mode (2D) and perspective mode (3D): Ctrl + X.
- Close and exit Viscore: Esc key.
  - Closing the Viewer window should be avoided as it can cause some processes to be corrupted.
- Enter/exit pseudo full-screen mode: F11.
  - Taskbar remains visible.
  - Use Shift + F to toggle standard full-screen mode.
- Undo: Ctrl + Z.
- Move the HUD display location: Hover over the HUD, and press and hold M.
  - Use the mouse to move the display.
  - Scroll to rescale display.
  - Press M a second time to set placement.
- Hide or display the HUD: Ctrl + H.
  - It is strongly recommended to not hide or close the HUD.
- Rotate model 90˚ when in Ortho mode: Arrow keys on keypad (See Figure 52 for further explanation of Ortho mode).

3. Model Setup and Visualization Options

When models are first opened in Viscore, key visual settings must be configured and saved. Complete 3A1–A6 below before closing the model to save these settings.

A. Open a Model for the First Time

1. To open a model, double-click on the `.vml` (with the gold star icon) found in the model's folder. If the model's .vml does not have a gold star icon, then Viscore has not been set as the default program for opening these files.
   - If Viscore has not been set as the default program to open .vml files, refer to *1A2. Installation Instructions* starting at step 6.
2. If it takes Viscore longer than 5–10 s to load the point data, click once somewhere in the black space of the Viscore Viewer window to refresh the loading process. The delay is expected when opening large models or when the data are stored on an enterprise server.
3. When a model is opened for the first time, it may not be in view. Pan across the Viewer window to locate the model.

A1. Adjust Zoom Settings

1. Turn on `vis-opt` in the HUD.
2. Reduce the value of `near` until the surface of the model can be zoomed into. Typically, a value of 0.500 will suffice. Values below 0.500 can cause glitchy visualization behavior (*Appendix II.B.*).
3. Increase the value of `far` until the model can be zoomed far enough away so that its entirety is in view and the HUD can be displayed without overlapping with the model. Typically, a value of 800 will suffice. Extreme values can cause glitchy visualization behavior, though the far parameter is less sensitive than near.

A2. Set Point Size

When a model is opened for the first time, the initial point size is likely too large, distorting the representation of the model and making navigation and interaction sluggish. Point size should immediately be reduced to provide a realistic view of the model (Figure 54A–B) and improve Viscore functionality.

1. Hold Ctrl + scroll down to reduce the point size until the model's features come into view.
2. Zoom in to a flat area on the model, and choose an object with hard boundaries (e.g., a coral colony or a large piece of rubble) (Figure 55A).
3. Scroll down again to continue to reduce point size (Ctrl + scroll down) until small gaps/holes appear between the points. The model will have a sparkly appearance (Figure 55B).
4. *Slowly* scroll up + Ctrl until the gaps close between the points and the boundaries of the coral colony or piece of rubble begin to grow. The goal is to fill the gaps between points without artificially increasing the size of objects (Figure 55C).
    - Be cautious when increasing point size, as making the points too large too fast will cause the computer's graphics card to overload and will crash the program or cause it to respond slowly.

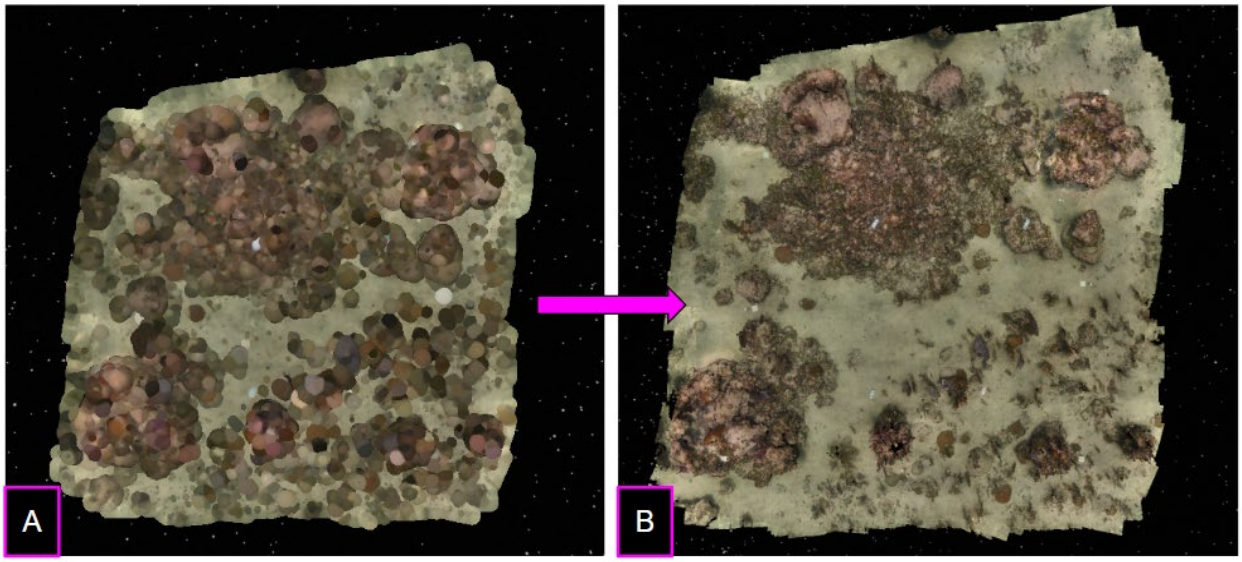


Figure 54. (A) Initial point size set too high. (B) Point size reduced to an appropriate level.

Figure 55. Example of an appropriate object to use as reference when reducing point size.In panel (A) point size is too large, and objects in the image look artificially inflated in size. In panel (B) point size is too small, resulting in a grainy appearance, with black space visible between points. Panel (C) shows point size set to an appropriate value.

A3. Adjust Point Confidence

Point clouds generated in and exported from Metashape contain metadata that store estimates of reconstruction precision for each point, known as point confidence (*Section I. Agisoft Metashape*). Areas with non-stationary items, such as upright fleshy algae and sea fans, are likely to have low-confidence points that appear to float above the surface of the model. Additionally, when oblique imagery is collected incorrectly, it can result in discolored and otherwise imprecise points. Point confidence values can be used to filter and hide these low-confidence and often undesirable points. However, adjusting the point confidence filter should be done with care, as filtering applies to the entire model. Due to differences in point density and reconstruction quality, the effects of filtering will not be consistent across the surface of the model, and in some cases, points that should be otherwise retained will be filtered out.

1. To hide low-confidence points, turn on `Ptconf` in the HUD.
2. If not available in the HUD, enable the tool via the Spacebar menu (*2B. Heads Up Display (HUD) and Spacebar Menu*).
3. Point confidence can be changed by scrolling over the value to the right of `min:` in the PtConf menu (Figure 56A–C).
4. Zoom out and change point confidence to get rid of any scattered points at the plot margins.
5. Zoom in to the surface of the model and adjust point confidence to get rid of noisy or messy points without removing any objects themselves (e.g., sea fans, gorgonians, etc.). Do this in several locations, finding the best value that removes bad points without getting rid of good ones.
6. In practice, setting Ptconf to 1 or 2 will tend to provide the best result. It is generally recommended to keep point confidence levels low, generally below a threshold of 3. Examples have been provided below to show how point confidence has been used to remove sea fans from the view of the model, but it should be noted that the high level of point confidence used is for demonstration purposes only (Figure 56A–D).

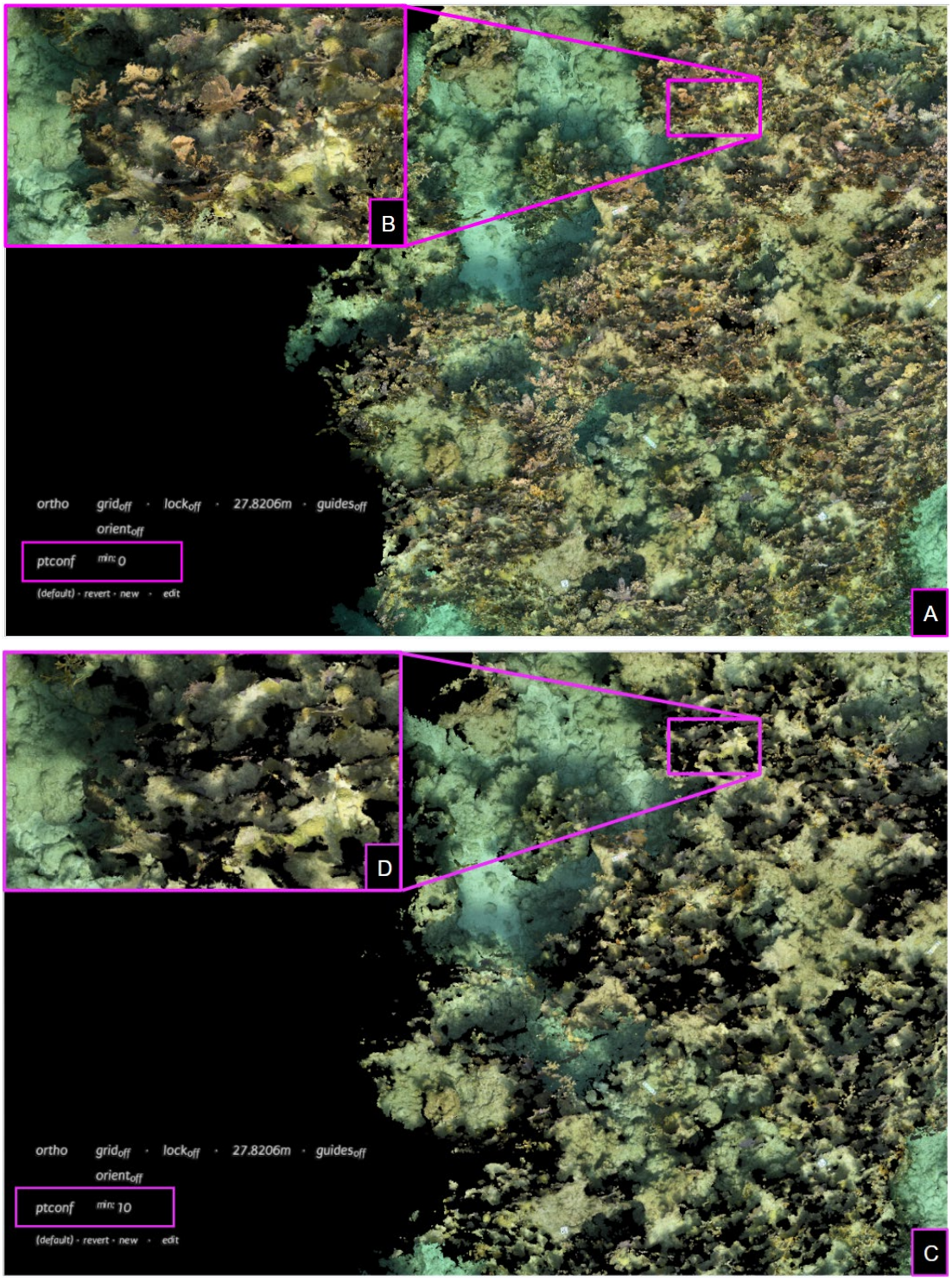


Figure 56. Example of Ptconf filter. (A) the model is shown zoomed out and (B) zoomed in to show further detail, without the point confidence filter applied. The same views are shown, (C) zoomed out and (D) zoomed in, with the point confidence filter set to a high value of 10 in order to clearly demonstrate the effects of the filter. Relatively low-confidence points on model margins are filtered from view (A vs. C) as are low-confidence points in the interior of the model, particularly for non-stationary portions of gorgonians and patches of upright macroalgae.

A4. Adjust Color

From the HUD, the Colors tool can be used to color-correct the model as needed (Figure 57).

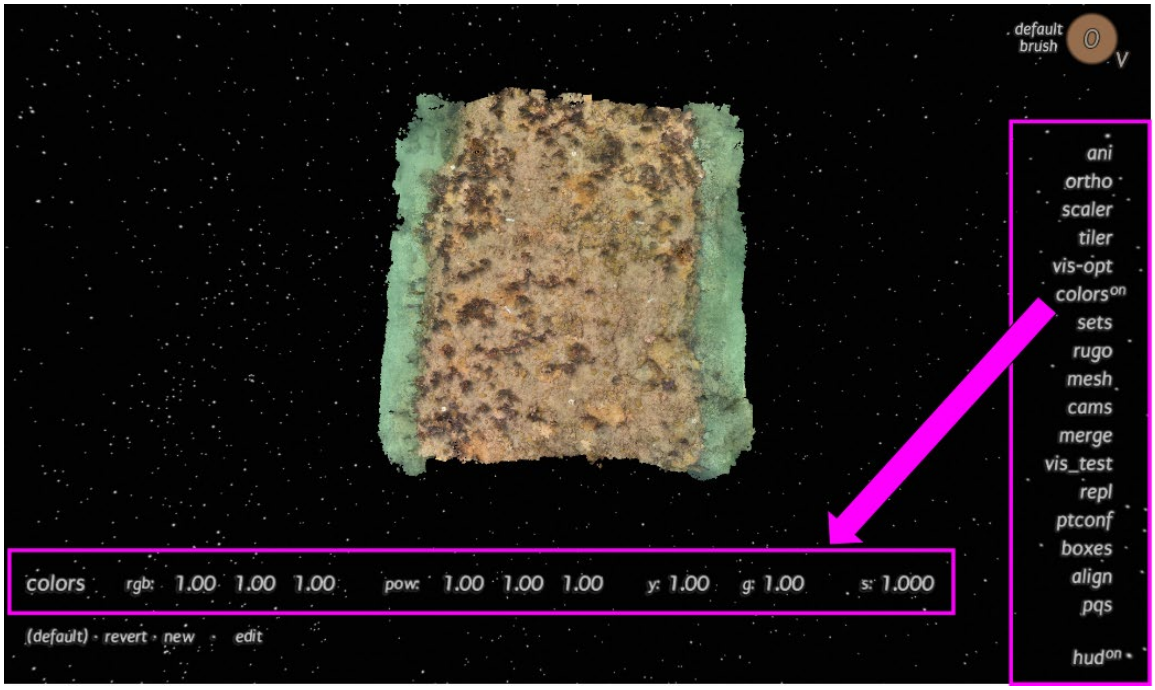


Figure 57. Colors menu turned on.

1. In the HUD, turn on `Colors`.
2. Adjust the values as needed (55):
   - `rgb`: Red, Green, Blue values.
   - `pow`: Power for Red, Green, Blue.
   - `y`: Increase exposure.
   - `g`: Decrease exposure.
   - `s`: Point size.
3. To save the color corrections, set or reset the default view as described in the next section.

A5. Set the Default View

The default view is the view that the model will display each time it is opened. Point size, vis-opt, and point confidence settings are also saved in the default view.

1. Position the model in a way that is in the center of the screen, at a zoom level such that the model fills up the majority of the Viscore Viewer (Figure 58A), and orient the model in a top-down view (Figure 58B).

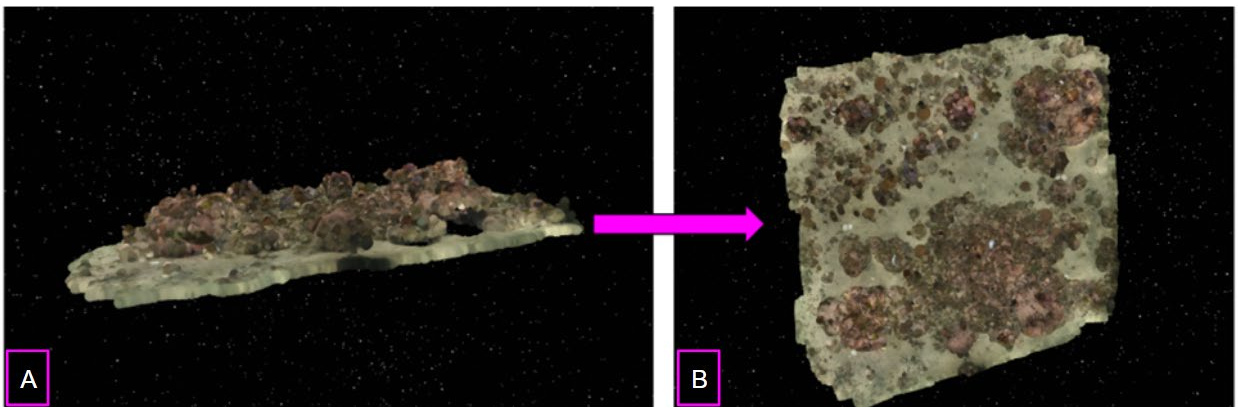


Figure 58. (A) The model view prior to orienting into a (B) top-down model view.

2. Locate the View menu in the bottom-left corner of the Viscore Viewer window (this tool is always on) (Figure 59A).
3. In the View menu `(default)` should be displayed. If `(default)` is not displayed, scroll up or down over the menu until `(default)` is displayed.
4. To set the default view, click `edit` to turn it on (Figure 59B).
5. Once `edit` is on, `overwrite` will appear (Figure 59C). Click `ok?` to save the current view as the default view (Figure 59D).
6. After the current view has been saved, turn `edit` off (Figure 59D).
7. At any time during model navigation, the default view can be accessed by changing the view to `(default)` and clicking `revert`.
8. Additional saved views can also be captured using the View menu, which is covered in the next section.

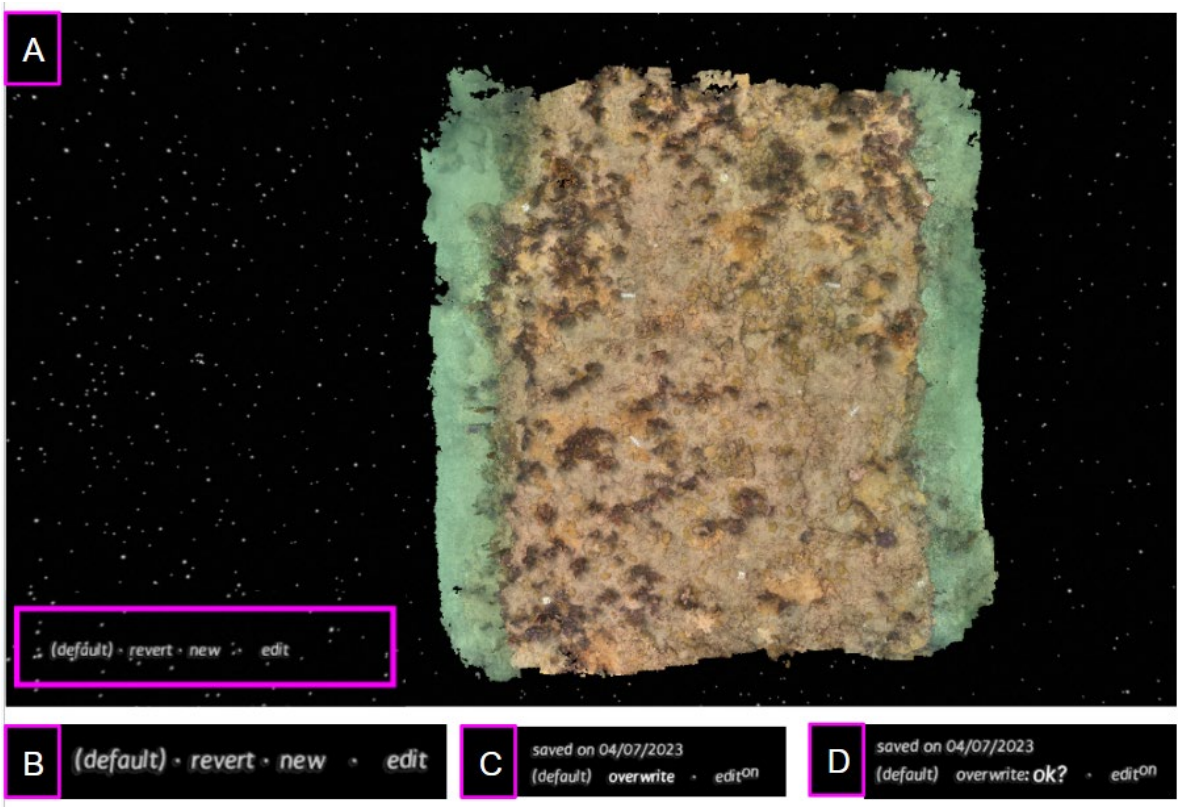


Figure 59. (A) Location of View menu. (B) Original View menu. (C) `Edit` is on to access `overwrite` option. (D) Click `ok` to overwrite the default view.

A6. Create Saved Views

Any current view displayed in the Viewer window can be captured and saved. Views are saved in the .snap folder as both .jpg and .json files. Views can also be used to save alternate visualization settings, as well as additional information such as any temporary markers that might be displayed at the time the view is saved (see *3A7. Marker Controls* for more information about using and saving temporary markers). The .jpeg is an image of the saved view, while the .json file contains important metadata, including any saved markers and visual settings. Views can be reloaded into the Viewer at any time using the View menu or by dragging and dropping them from the .snap folder into the Viewer window.

1. Once the model is in the desired view, ensure that `edit` is off in the View menu.
2. Click `new` (When capturing a new view, it does not matter what view is currently listed).
3. The first time a new view is captured, `view-1` will appear (Figure 60). Subsequent views will be captured as `view-2` and so on.
4. The view name can be changed by turning `edit` on and clicking `rename`. A cursor will appear at the end of the current view name. Edit as needed, and press Enter on the keyboard or click `ok` in the View menu options. Any files in the .snap folder associated with the renamed view will be automatically overwritten and renamed.
5. Any view will be saved in the model's .snap folder.

6. To overwrite a given view (including the default view), switch to that view in the View menu (or by drag and drop). Reposition the model as desired, turn `edit` on, and select `overwrite`.
7. Always make sure to turn `edit` off after making any changes to an existing view.

Figure 60. Menu after clicking `new` in View menu. New saved view, e.g., `view-1` will appear.

A7. Marker Controls

Markers are an integral part of efficiently navigating and utilizing various workflows in Viscore. Knowing how to select, deselect, add, and remove markers from a Viscore model will translate into more effective use and understanding of workflows outlined later in this guide. Markers are used by a variety of tools but can also be temporary. Figure 61 and Figure 62 show an overview of the markers menu and the controls available.

- Add a marker:
  - Alt + center-click (center-click may be accessed by clicking down on the scroll wheel, but be sure not to scroll) on any point/location in the model. A new marker will appear with its corresponding label, and a new menu will appear in the bottom-left corner of the screen (Figure 61).
- Select marker(s):
  - Left-click on the marker in its location *or*
  - Click select all markers in the bottom-left corner of the screen.
- Deselect a marker:

    - Left click on the marker *or*
    - Right click on the marker listed in the bottom-left corner of the screen.
    - Select `none` to deselect all selected markers
- Delete a marker:
    - With the marker selected, click `delete` in the bottom-left corner. If multiple markers are selected, clicking `delete` will remove all selected markers.
- Move a marker:
    - Right-click on marker + drag to move marker along the point cloud.
    - Center-click on marker + drag to move marker above or off the point cloud, or perpendicular to perspective. The marker can float in space as it will no longer be attached to a point on the point cloud. This is not recommended for most workflows described herein.
- Connect two or more markers (Figure 62):
    - Select markers individually (left-click) or all desired markers at once (Crtl + A).
- Disconnect two markers:
    - Deselect markers individually (left-click) or all markers at once (Ctrl + D).
- Rename or label markers:
    - Click on the marker's name next to `symbol` in the bottom-left corner menu (Figure 61), and type to change the symbol used for the maker. Press Enter to complete renaming.
    - A label can also be added by clicking next to the label and typing in the desired label. Press Enter to complete labeling.
- To make a marker the active navigation target (as opposed to double clicking somewhere on the model), left-click on the marker's name in the Marker menu (only previously selected will appear in the menu). This is a particularly useful and efficient method of navigating between markers.

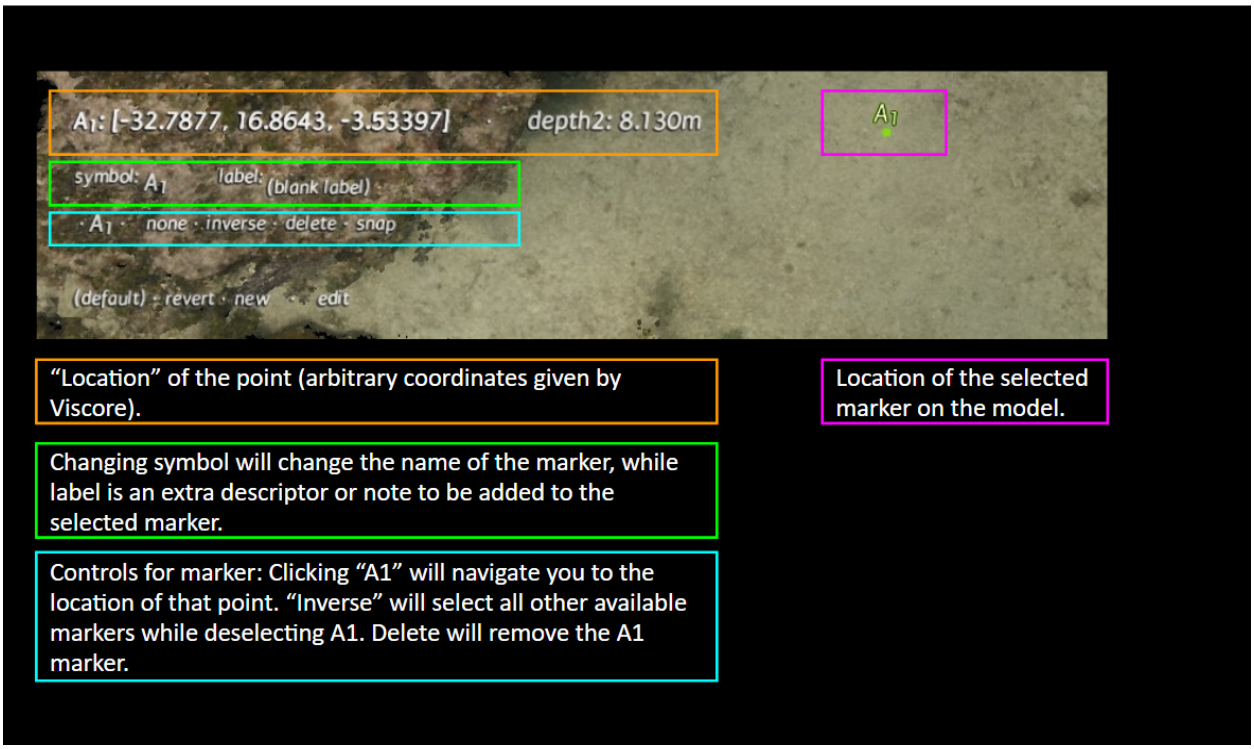


Figure 61. Marker menu in Viscore.

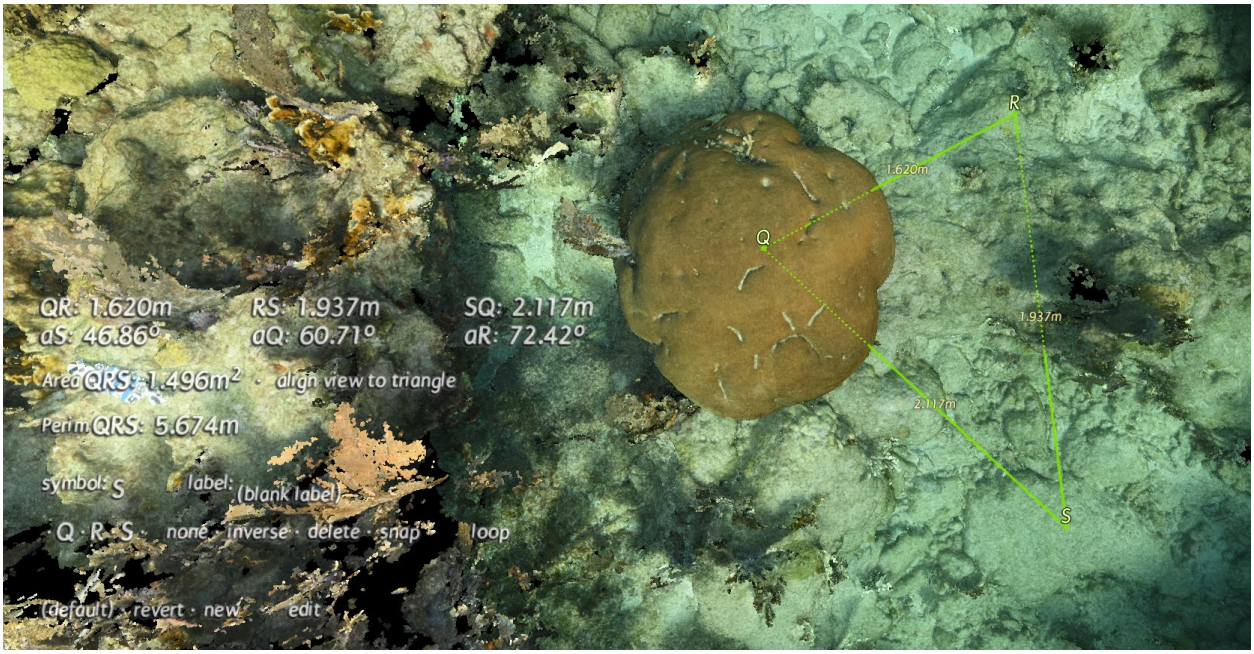


Figure 62. Example of multiple markers selected in Viscore.

A8. Link Raw Images

Viscore enables viewing of the raw imagery used to construct any location within the 3D model. Imagery can be displayed directly within the Viscore Viewer or in a separate window using an internet browser. To display images, the path to the image files must first be supplied to Viscore by dragging and dropping a raw image into the Viewer window. Any time images are moved to a different folder, the following steps will need to be repeated.

1. Turn on `cams` in the HUD**.**
2. In the Cams menu, click `none` (Figure 63A) to select the .cams file (e.g., NFH_CB-1_2022-06-10 in Figure 63B).
3. If the Cams tool is not available in the HUD or if clicking on `none` does nothing, the camera files (.meta.json and .cams.xml; see *1B. Viscore File Formats and Organization*) are missing and need to be copied/moved into the model folder. Viscore must be closed when Cams files are copied/moved into the model folder or restarted after doing so.
4. After selecting the correct .cams file, additional menu options will appear:
   - `drape`: allows the user to drape raw images over various locations in the model to see the raw image that corresponds to that location in the model.
   - `dots`: shows locations where pictures were taken in relation to the model.
   - `path`: shows the path connecting sequential images (e.g., dots above) as they were collected by the diver.

Figure 63. (A) Before and (B) after selecting the .cams file.

A9. Drape Raw Images in the Viscore Viewer Window

1. Turn on `cams`, and under the Cams menu, turn on `drape`.
2. Double center-click with the mouse on any location within the model. A black checkerboard will appear along with text indicating that the image is missing under the Cams menu (Figure 64).

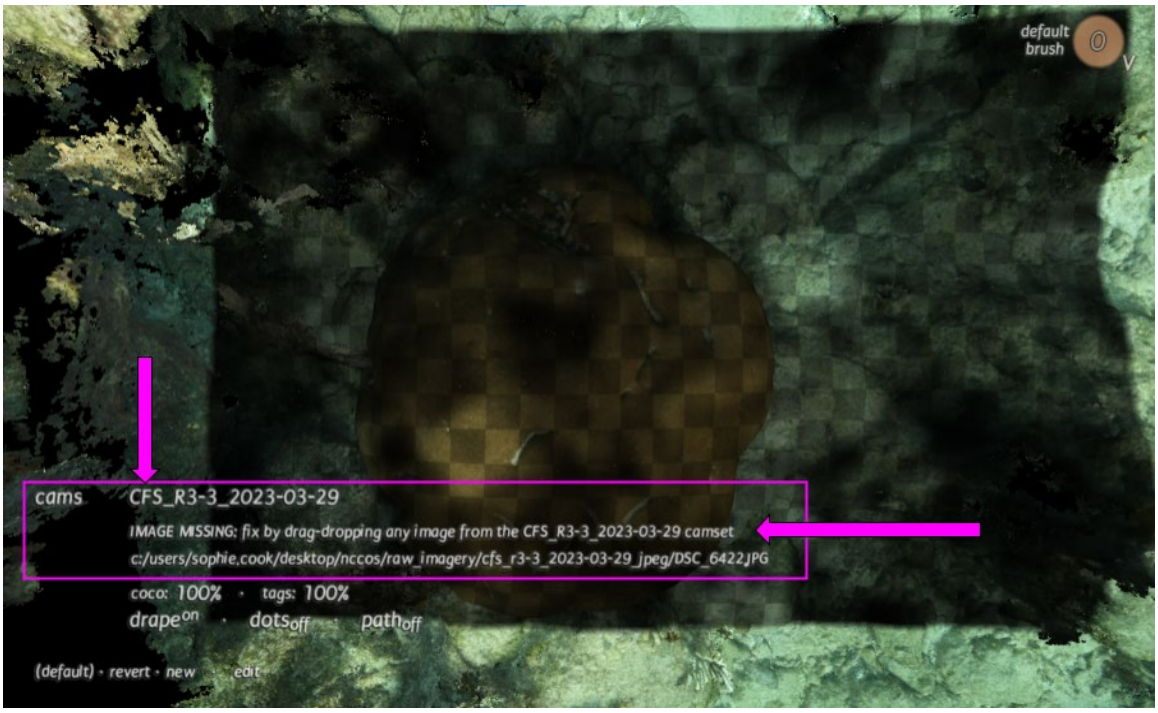


Figure 64. Checkerboard will appear if raw images are not linked. Note the `IMAGE MISSING` message in the Cams menu.

3. Open the corresponding raw image folder, and drag and drop any raw image from the raw image folder into the Viscore Viewer window.
    - Only images used to construct models are listed in the Cams files and can be used to set the raw image file path. It is generally recommended to select an image in the middle of the image sequence from the raw imagery folder. Often, the first or last handful of images collected by divers are random scenery photos or action shots that were not used for model construction but were otherwise not deleted.
4. After the raw image has been dragged and dropped, the Cams menu in the bottom-left corner will update, and the black checkered box will be replaced with a raw image (Figure 65).
5. Change `tags` to `0%` (Figure 65).

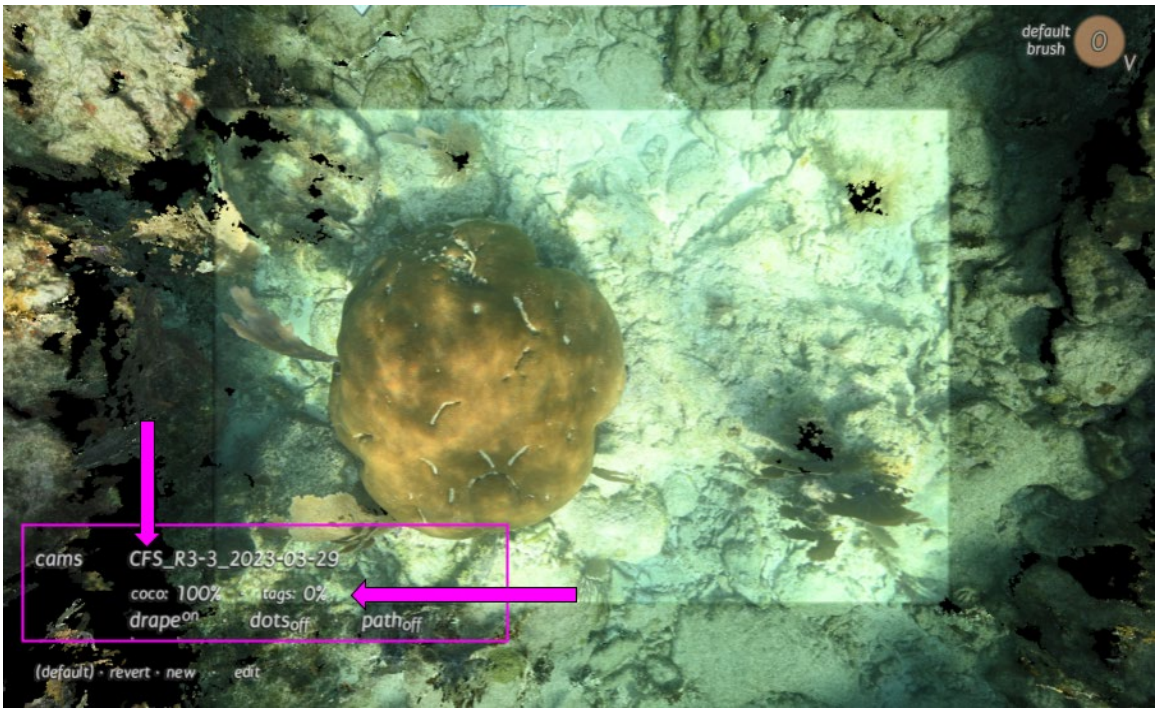


Figure 65. Checkerboard disappears, and the raw image associated with the model area is displayed. Note the Tags menu to change raw image display.

6. Double center-click on any location in the model to view raw images associated with that point or location in the model. Hold right-click + scroll through images as they were collected in sequence.
7. Alternately, hold Alt + center-click to drop a temporary marker at any location in the model. Hold right-click + scroll to move through all raw images associated with that location of the model. Reposition the marker (right-click + drag) to view raw images at other locations.

A10. Drape Raw Images in a Browser Window (Viscore iView)

Viscore enables raw images to be viewed with the iView tool via an internet browser window. No internet connection is required to the use the browser tool; however, a Viscore model must be open to establish a local connection between Viscore and the browser (Figure 66). A variety of Viscore tools are made available via internet browser (e.g., analyses such as VPI). Importantly, these tools have been developed and tested using Google Chrome; therefore, it is strongly recommended to use this as the default browser for all Viscore workflows.

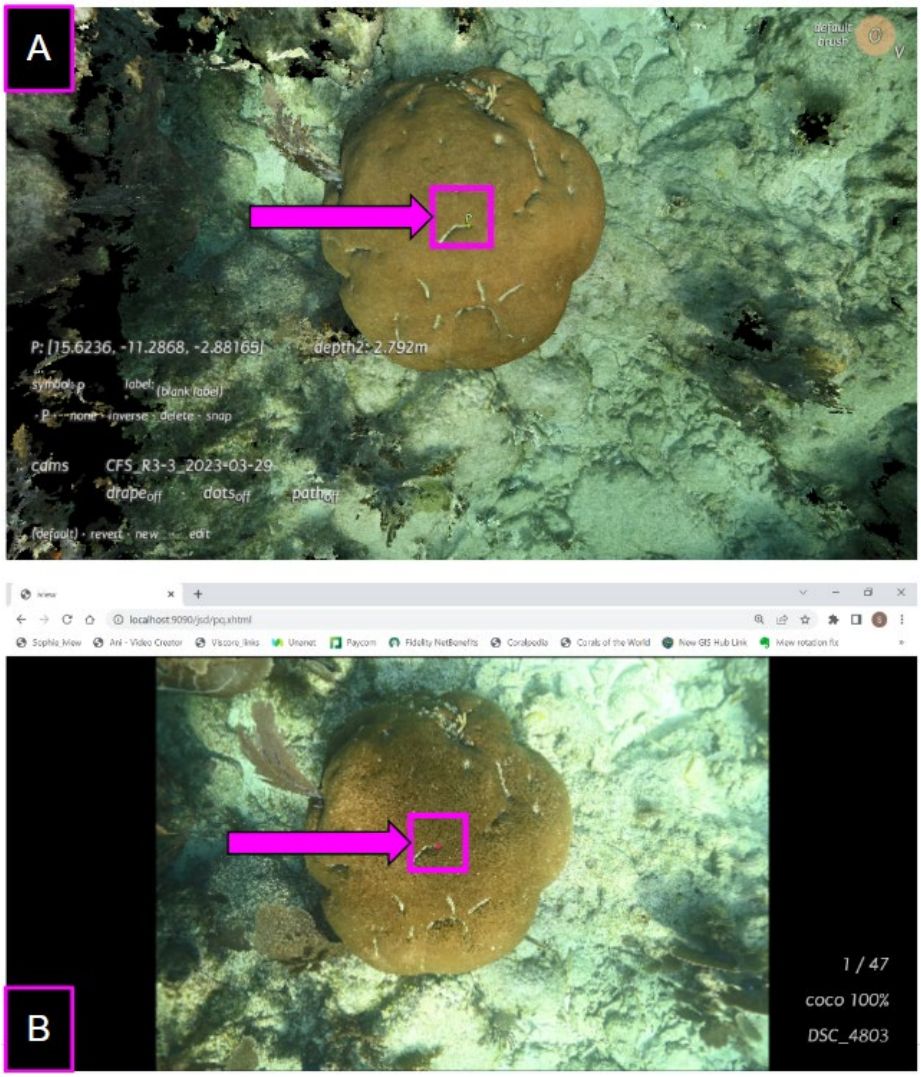


Figure 66. (A) Example of dropped marker in desired location on Viscore model in the Viscore Viewer window. Note the location of the dropped marker P in the Viscore Viewer and how it corresponds to the (B) pink point on the raw image in iView.

1. Open a Google Chrome browser window, and enter the following link: http://localhost:9090/jsd/pq.xhtml
   The message "waiting" will likely appear, or the screen will be blank until the steps below are completed.
2. In the Viscore Viewer window, hold Alt + center-click to drop a temporary marker on the desired location of the Viscore model. The image associated with that location in the model should appear in iView/the browser window (Figure 66A–B).
   - Note: Sometimes it is necessary to jitter the dropped marker before it will appear in the browser. To do so, right-click + hold on the marker and move it slightly. The browser window will update. In some cases, it may be necessary to refresh the browser window.

3. iView controls:
    - View multiple images that correspond to the same dropped marker:
        - Press Spacebar.
        - Hold right-click + scroll.
        - Scroll over the first number in the bottom-left corner (e.g., 1/10).
        - Press the N key to go to the next photo.
        - Press the B key to go to the previous photo.
    - Use scroll wheel to zoom in and out.
    - Left-click + drag to pan.
    - Right-click + drag a corner of the image to rotate.
    - To reposition the target or view the raw image associated with another location on the model, double-click on another location in the photo. The marker in the Viscore Viewer will automatically adjust to this new location. Alternatively, return to the Viscore model in the Viewer window, and reposition the marker to the new desired location (right-click + drag the marker).
    - The URL associated with any image in iView can be bookmarked and saved for quick access. The appropriate model must first be loaded in the Viewer window in order for iView bookmarks to function properly.

B. Creating Fly-Through Videos in Viscore

Viscore allows users to create virtual tours, or fly-through videos, of 3D models that can be exported as .mp4 video files and are useful for communication and outreach purposes.

1. Navigate to the model's folder and double-click on the `.vml` to open the model in the Viscore Viewer.
2. During fly-through capture, various options in the HUD can be turned on or off for different visualizations in a fly-through video.
    - **Markers**: Any selected markers will be captured in the fly-through, including any labels or displayed distances between markers (markers are described in further detail in *3A7. Marker Controls*
    - **Path and Dots**: Turn on `cams` in the HUD, then turn on `path` and/or `dots` under the Cams menu (the Cams menu is described in further detail in *3A8. Link Raw Images*).
    - **General size of the model**: Turn on `pqs` in the HUD (used to conduct VPI, PQs is described in further detail in *4B1. Prepare VPI Quad and Samples*).
    - **Scale**: Turn on `scaler` in the HUD; scale bar lengths will appear (scaler is described in further detail in *4A1. Set Scale*).
    - **Depth markers/orientation:** Turn on `ortho` and `orient`, then use the Down arrow key to show depth markers from side angle (ortho and orient are described in further detail in *4A2. Set Model Orientation*).

- If the slice size is too small, the depth markers may not be visible. Hold Alt + scroll up until the depth markers appear.

3. In Google Chrome, enter the following link and press Enter: http://localhost:9090/jsd/ani.xhtml. The view should appear similarly to Figure 67.
   - Note: as with iView, a Viscore model must be open to establish a local connection between Viscore and the browser.

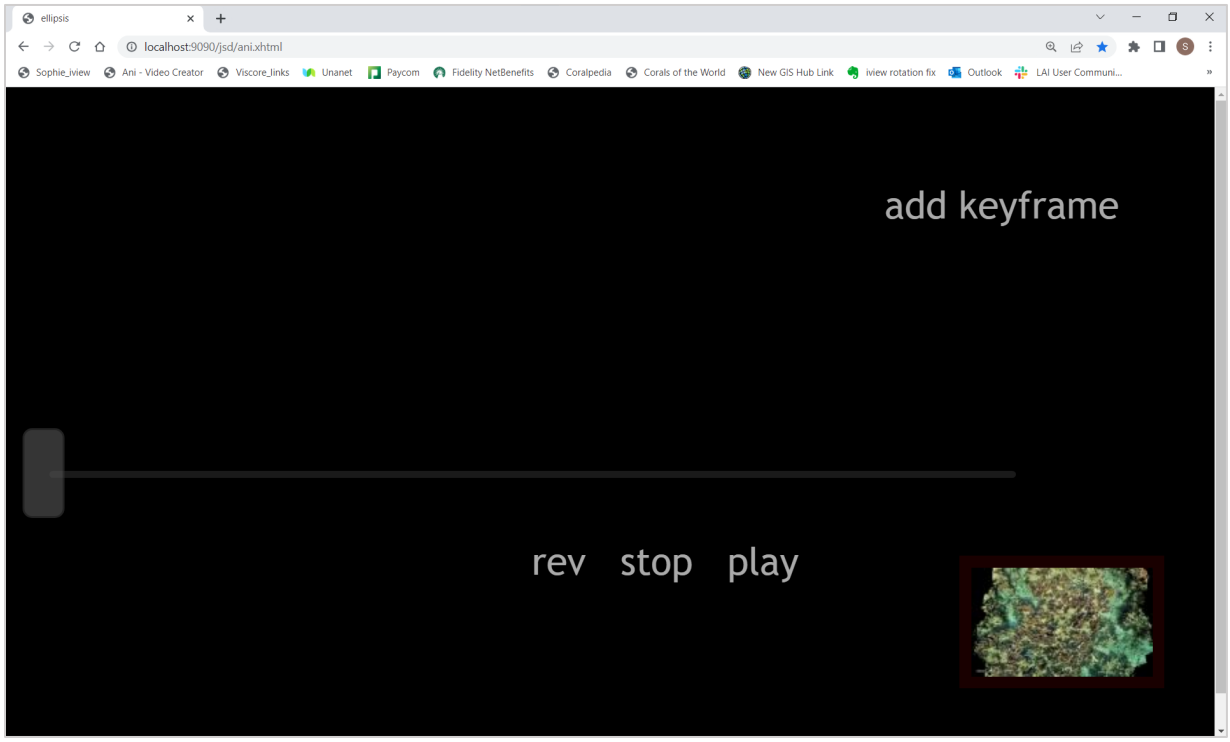


Figure 67. An example of the browser window appearance after entering the Ani tool URL. A preview of the model open in Viscore will show in the bottom-right corner.

4. Navigate to the model in Viscore. Set up the model the way it should be shown in the video. For example, to generate a top-down view, orient the model in a top-down view.
5. Switch to the browser window and click `add keyframe` (Figure 67).
6. After at least one frame has been selected in the internet browser, `ani` will appear in the Viscore Viewer HUD. The following menu items can be used (Figure 68):
   - `kf`: keyframe number, corresponding to the keyframe in the browser.
   - `t`: elapsed time.
   - `f`: specific video frame (default frame rate is 24 fps).
   - Video resolution (displayed next to `f)`: resolution at which the video sequence will be captured. Recommended to set at `1080p`.
   - Leave `q`, `s`, `360`, and `stereo` with the default values.
7. Repeat steps 4–6 until all of the keyframes for the video have been acquired.
8. To adjust the length of time it takes the virtual camera to travel between each keyframe in the video, press the + or – sign over the keyframe in the browser.

9. Keyframes can be deleted by hitting the `X` over the keyframe. The order of the keyframes can be changed by dragging a keyframe to another spot in the browser.
10. To preview the video:
    - Browser:
        i. Click play to watch the video in the navigator window in the bottom-right corner of the internet browser (hover the cursor over the navigator window in the bottom-right corner to make it bigger), or view from the Viscore Viewer window.
        ii. Click on the thumbnail for a specific keyframe, or manually drag the slider between keyframes.
    - Viewer: Select play in the Ani menu.
11. Set the Ani menu to the following settings (Figure 68):
    - To start the video at the first keyframe, set `kf` to `0`. Otherwise, specify the desired keyframe.
    - Similarly set `t` and `f` to `0` to start at the beginning of the sequence. Otherwise specify the desired values.
    - Set video quality to `1080p`. Videos can alternatively be exported in 2K or 4K resolution by selecting 2160p or 4320p, respectively. File size will be very large for 2K and 4K videos.
    - Turn on `cap` to begin capturing the video.

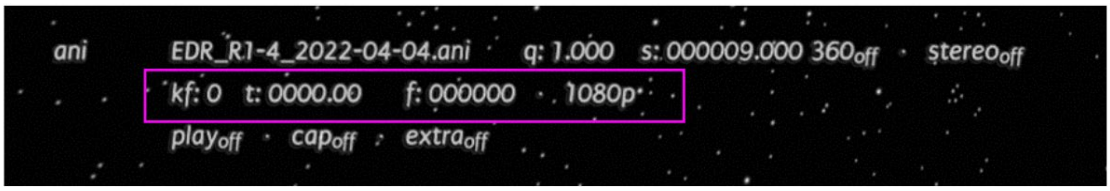


Figure 68. Example of correct settings under the Ani menu before exporting a video. Default video resolution is specific to the resolution of the screen being used and can be changed by clicking on the text to the right of the frame rate setting f (e.g., 1080p).

12. Once Viscore has finished capturing images for the video, go to the model folder, and open the newly created folder .ani.seq (in some cases, undefined.seq).
13. In the Vid folder on the C drive, locate the file named `newer-copy-into-folder-with-image-sequence-and-run-to-make-video.cmd`, and copy it into the model's ani.seq folder.
14. Double-click on the `newer-copy-into-folder-with-image-sequence-and-run-to-make-video.cmd` to run the video rendering process. A Command Prompt terminal will open. When the video is finished, `Press any key to continue` will appear in the Command Prompt.
15. The final video will appear as video2.mp4 in the ani.seq folder.
16. For M:IR-specific instructions on saving and storing fly-through videos, refer to *Appendix III.B.*

4. Basic Analysis in Viscore

A. Prepare Model for Analysis

Before quantitative data can be extracted from 3D models in Viscore, model scale and orientation with respect to the sea surface must be established. First, scale is set using a series of scale bars that are deployed during image collection and should be visible in the reconstructed 3D model. Next, the orientation of the plot with respect to the sea surface is determined using a series of depth measurements collected during imaging in the field, which are also visible in the final 3D model. After these measurements have been provided to Viscore, quantitative information can be extracted (e.g., depth measurements of temporary markers as well as the distance between any two markers) and data analyses can be conducted (e.g., VPI). The following sections provide instructions for adding scale and orientation to 3D models in Viscore.

A1. Set Scale

The scale should be set using all available scale bars that are well reconstructed. If a scale bar is poorly reconstructed, it will not provide accurate scale and should not be used to set model scale. See Figure 69 for an example of a poorly reconstructed scale bar that should not be used and Figure 70 for an example of a scale bar with good reconstruction that should be used to set scale.

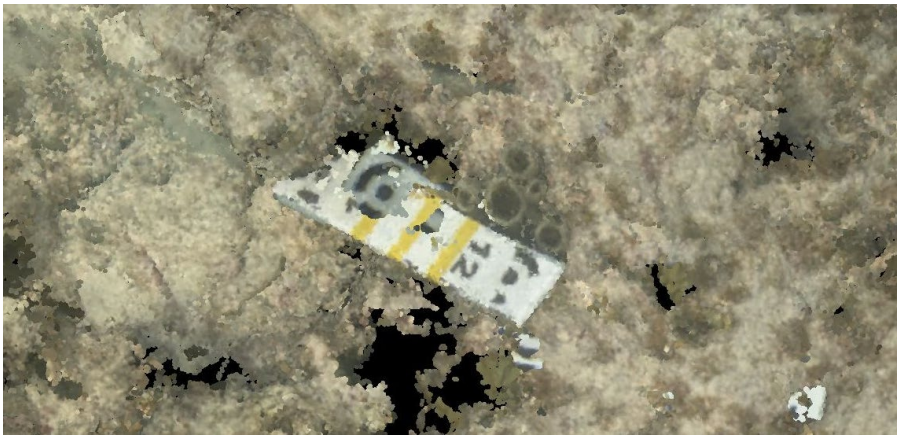


Figure 69. Example of a poorly reconstructed scale bar that should not be used to set scale.

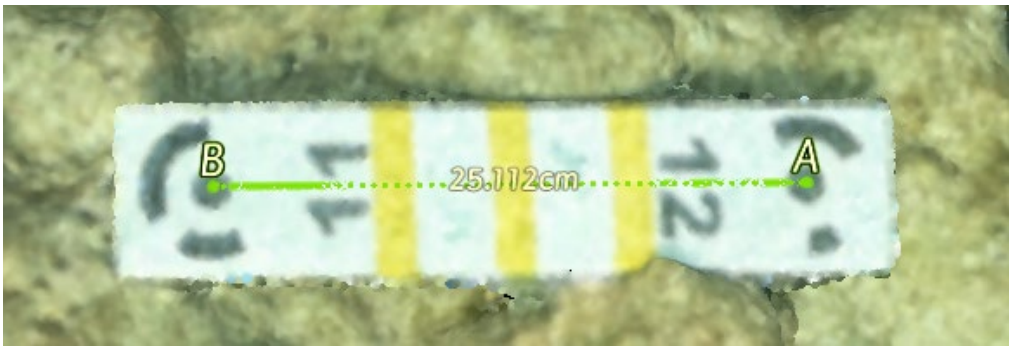


Figure 70. Example of good reconstruction of a scale bar as well as two markers being used to set scale. Note that before the scale is set, the markers and line between are green.

1. Pick a clearly imaged scale bar on the model and zoom in so to see it in closer view (Figure 70).
2. If zooming in does not allow a close enough view of the scale bar, turn on `vis-opt` and make the `near` value smaller (*3A1. Adjust Zoom Settings*).
3. Using Alt + center-click, add markers to the center of each black circle on the scale bar (Figure 70).
4. The bottom-left corner of the screen shows an option that says `add ##` (#s correspond to the letter of the marker being used; here, markers A and B have been assigned by Viscore, e.g., in Figure 71, the screenshot has `add` A_sB_s). Click `add ##` to add the markers. The color of the markers and the line between them will change from green to pink, which signifies that the markers have been added to the Scaler menu (Figure 72).

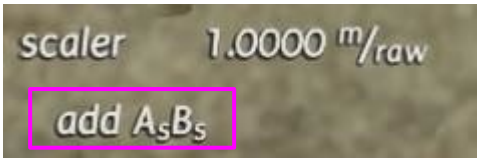


Figure 71. Highlighted menu option to add markers to the Scaler tool.

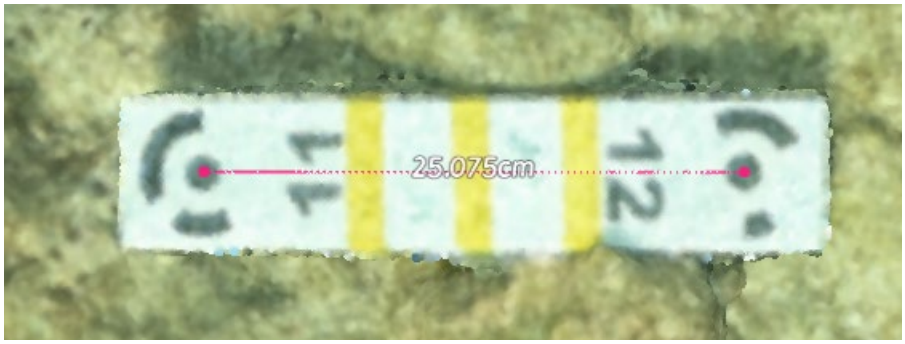


Figure 72. Example of two markers being used to set scale. Note that when the markers have been added to the Scaler tool, the markers and line between are pink. The distance has also changed as error has been accounted for after entering the scale bar distance for all four scale bars.

5. Confirm the length of scale bars using the field metadata sheet (e.g., column Q of MIR SfM Metadata sheet for M:IR users). Locate the scale bar distance that corresponds to the model being used. Enter this value in meters by clicking on or scrolling over the numbers next to the added markers (Figure 73).

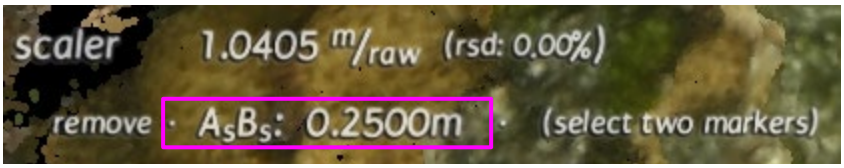


Figure 73. Example of markers with associated scale length in meters.

6. Repeat steps 3–5 three more times for all well-constructed scale bars.
7. Turn the `scaler` off when finished.

A2. Set Model Orientation

Most quantitative workflows rely on depth and orientation of the model with respect to the plane of the sea surface. To provide this information, depth measurements collected in the field must be added to at least four locations in the model.

1. Similar to setting markers for the scale bars, zoom in on one of the depth markers around the perimeter of the plot. Hold Alt + center-click to add a Viscore marker to the center of the depth marker (Figure 74).

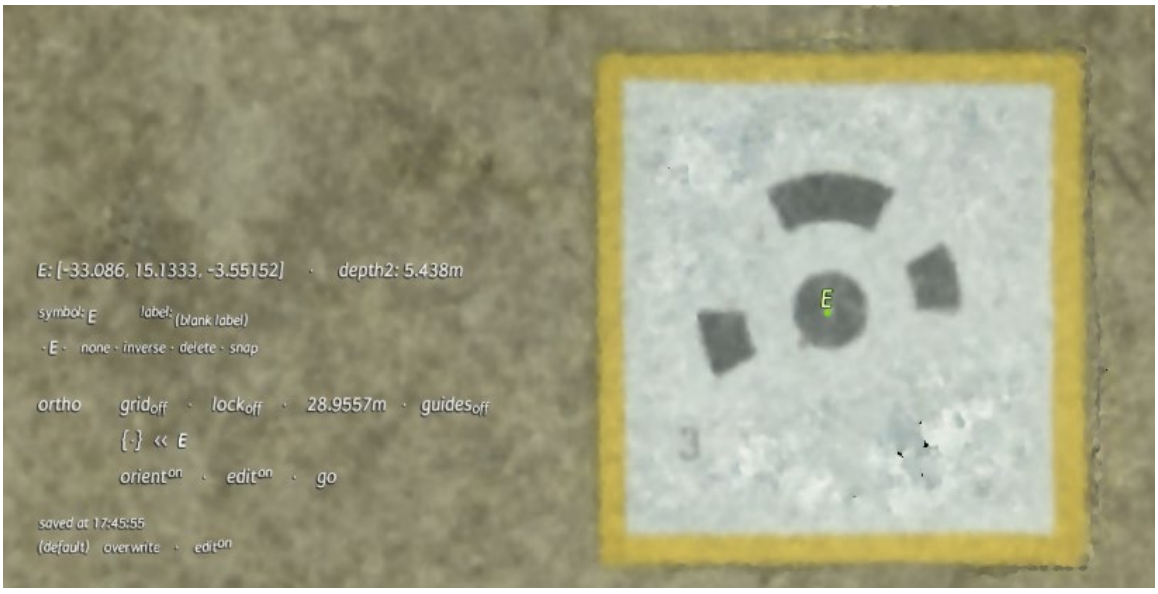


Figure 74. Example of setting depth markers.

2. Repeat this for all depth markers visible in the model. A minimum of four depth markers are required.
3. In the HUD, click `ortho` to turn it on, or use Ctrl + X.

4. When Ortho is turned on, often only a portion of model is visible (Figure 75A). This is due to the thickness and/or the position of the cross-sectional view. To make the entire model visible, hold Alt + scroll up until the entire model is visible (Figure 75B). Scaled red guidelines showing the cross-section thickness will be visible to aid the process. If the model remains partially or completely out of view, it is because the cross-section is not positioned around the model. To change the position of the cross-section, scroll up or down. To further explore these viewing options, try making a thin cross and changing the model's position.

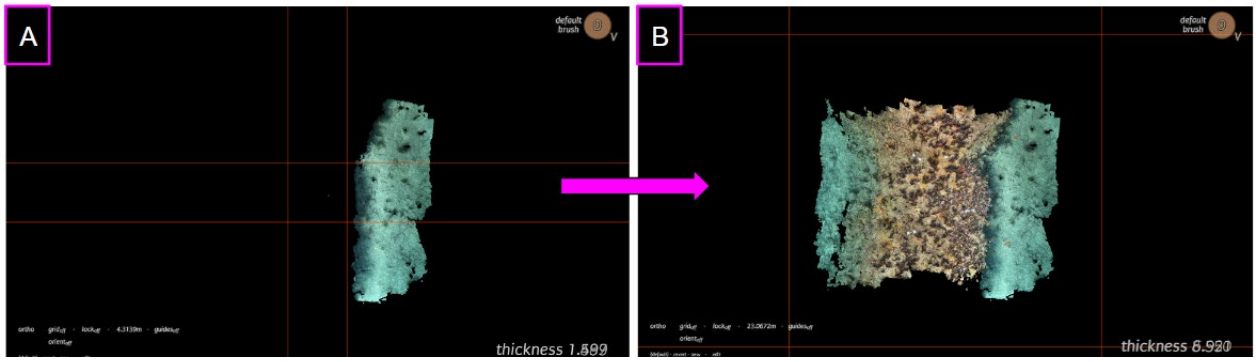


Figure 75. (A) The model is in partial view prior to (B) expanding the crosshatch to encompass the entire model.

5. In the bottom-left corner of the screen, under `ortho`, turn on `orient` and `edit`.
6. After markers have been added to all (six) depth markers, click the double arrows to add all of the markers to the Ortho grab set brackets (Figure 76).

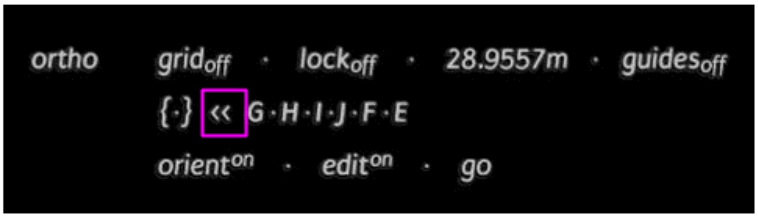


Figure 76. Click on the double arrows to add depth markers to brackets.

7. After markers are added to the grab set, they become assigned to the Ortho tool. The markers change from green to blue and receive default depth values of `10 m` (Figure 77).

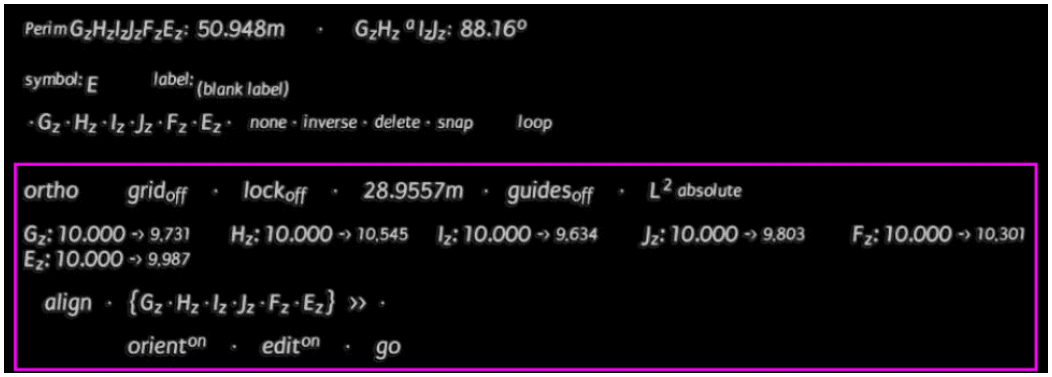


Figure 77. Example of how the Ortho menu changes once depth markers have been added prior to setting the corresponding depths.

8. Locate the metadata file that includes the depths collected in the field (*Section I. Agisoft Metashape*).
9. Enter the depths that correspond to each marker in meters by scrolling over or clicking on the value to the left of the arrow (in the example shown in Figure 78, the value to be scrolled over is `10.000`). The digit over which the cursor is placed will be the number that is changed and scrolling past 9 for any digit will increase the digit to the right by a unit of 1. Complete this for all six depth markers.
    - The number on each marker must be legible in order to identify which markers correspond to the depths collected in the field. If numbers are not legible, it may help to reduce the point size. If adjusting point size does not improve the visibility of the marker numbers, search for any marker with visible numbers and reference the field data sheet (*Section I. Agisoft Metashape*). Using this field data sheet and the marker numbers that are legible on the Viscore model, orient the model to match that of the data sheet, then add in the depths for the markers without visible numbers. Alternatively, Drape in the Cams menu or iView can be used to view the raw imagery associated with a given marker and will often contain a useful view of the depth marker number.

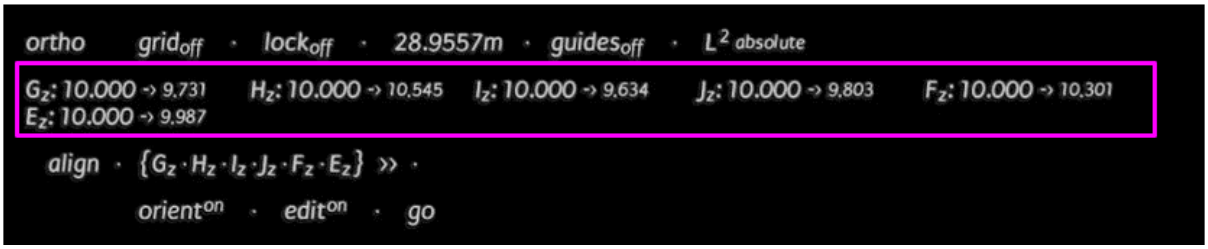


Figure 78. Enter the depths that correspond to each marker in meters. The first number next to the marker's assigned letter, to the left of the arrow, is the value to be adjusted. Hover the cursor over the value, and either click or scroll over the value to change accordingly.

10. Once the correct depth has been entered for all depth markers, click `align` in the Ortho menu.
11. Turn `edit` off to avoid changing any of the depth values in later workflows.
12. Press the Down arrow key to ensure the depth markers are pointing up toward the sea surface (Figure 79).
13. If no depth markers with lines pointing towards the surface are shown, turn `orient` off then back on again. Or, ensure the slab size is wide enough by holding Alt + scrolling up.
14. Further, if the markers are pointing downward (i.e., opposite from what is shown in Figure 79), see *Appendix II.B.* for troubleshooting.

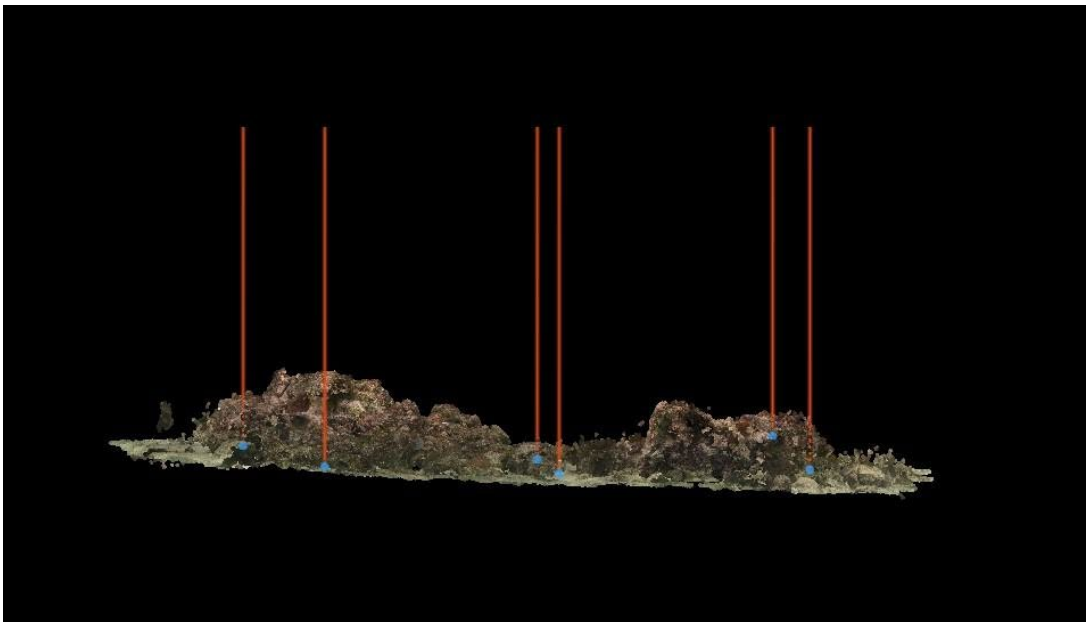


Figure 79. Example of model with depth markers pointing in the correct direction (i.e., “up”).

B. Estimating Benthic Cover with the VPI Tool

Benthic cover (%) is estimated using VPI in Viscore and is displayed in the HUD and internally within Viscore as the PQs tool. Point samples are generated in a stratified random manner from the top-down perspective (relative to the sea surface) within a user-defined area and with a user-defined sampling density. For the M:IR project, a 10 × 10 m sample area (i.e., quadrat or quad) is placed in the center of the plot and is sampled with 2,500 points. A separate browser window (e.g., Google Chrome) and link are used to view the raw images and label sampled points using a list of predetermined taxonomic labels. Primary labels are used to annotate benthos to genus or species level or other taxonomic groupings (i.e., turf), while descriptor labels can be used to include occurrences of disease, predation, and bleaching. The sections below guide the user with setting up a model for VPI, provide instructions for conducting VPI, and assist the user with potential difficulties when conducting VPI.

B1. Prepare VPI Quad and Samples

1. Turn on `ortho` and `orient`.
2. Turn on `pqs` in the HUD.
3. Select `make quad` in the PQs menu (Figure 80).

Figure 80. Turn on `orient`, then click `make quad` from the PQs menu.

4. A bright pink box will appear on the model. Move and resize the quad so that it covers the desired sample area.
   - To move the quad: center-click on the `C` dot + drag to move in the desired direction.
   - To rotate the quad: center-click on the corner with `TR` + drag to rotate the box in the desired direction.
5. Ensure the quad encompasses the entire depth of the model (Figure 81).
   - Press the Down arrow key.
   - Using the `C` dot to move the quad, drag the quad up or down in the desired direction. The pink quad should encompass the top and bottom of the model.
   - When finished, press the Up arrow key to return to the top-down view.

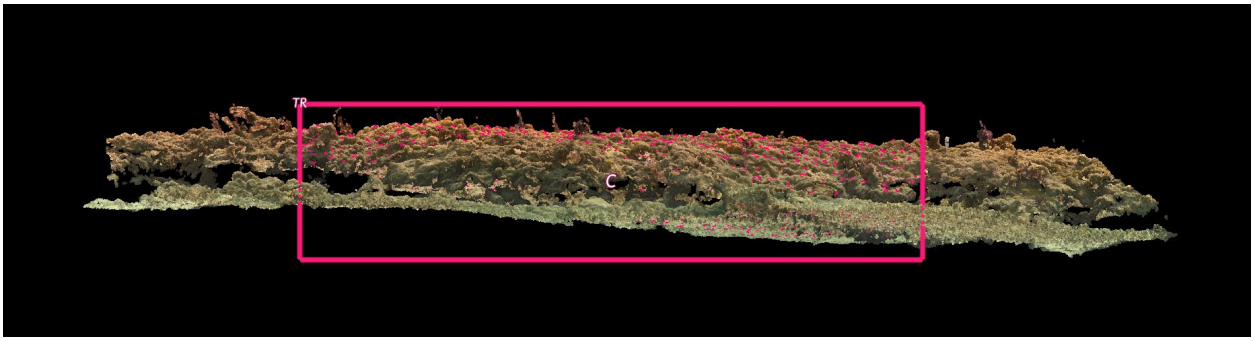


Figure 81. Example of checking the side view of the model to ensure the box placement encompasses depth of model.

6. Adjust the settings in the PQs menu to the following (Figure 82).
   - `Quad-dim: 10.0 m.`
   - `Count: 2500.`

Figure 82. Example of correct settings before preparing a VPI sample.

7. When the location of the quad is satisfactory and the sampling parameters have been set, click `prepare`.
8. While the samples (i.e., points) are being prepared for the PQs quad, avoid other computational tasks until the process has finished. Doing so may interrupt the process and result in a redo.
9. Proceed to the next step when the sampling has finished. The process is complete when the model stops moving on its own and the sampled points and quad are displayed (Figure 83).

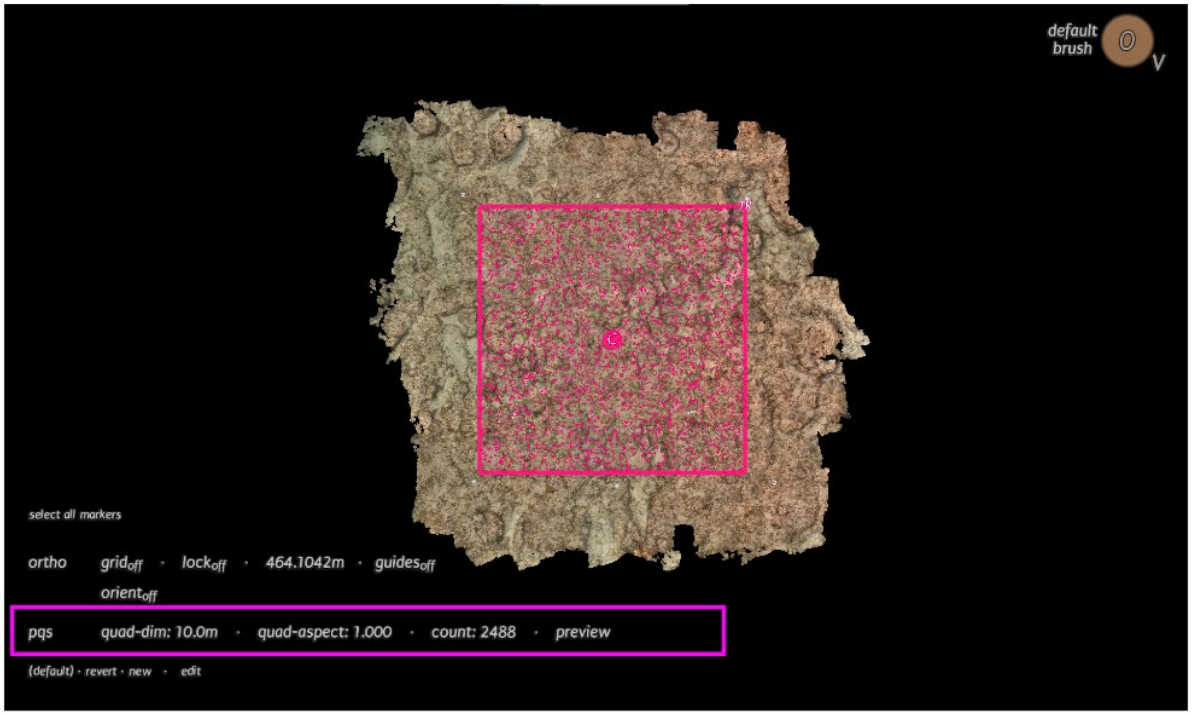


Figure 83. Example of finished quad and samples.

10. Check the final sample count by clicking on `count` in the PQs menu (Figure 83). The number of points successfully sampled will often be lower than the specified count as a result of unsuccessful sampling in data-sparse regions of the model.
11. Replace the qclasses file. A project-specific list of taxonomic IDs used for labeling points is saved in a Viscore model's .pq folder and determines what buttons will be shown and used for VPI in the browser. Before conducting VPI for the first time, the default qclasses file will need to be replaced with one that corresponds to the associated project.

B2. Prepare the Viewer for VPI

Before labeling points in the browser, the model in the Viscore Viewer window needs to be set up so that it can be referred to in cases where the views provided by the raw imagery in the browser window are ambiguous (as explained in *4B5. Labeling Points* and addressed in *Appendix II.B.*). To expedite this process, set up the Viewer window as follows:

1. Turn `ortho` on.
2. Ensure `edit` is off to avoid changing any of the depth values.
3. When conducting VPI, it is important to view the model from the top-down perspective at which points were sampled, as there can be ambiguity in point placement on individual raw images. To view the top-down view as defined by the depth measurements, turn on `orient` in the Ortho menu.
4. In the HUD, turn on `cams`.
   - Click `none` in the Cams menu, so that it switches to the .cams file that corresponds to the model.
   - Turn off `drape`, `dots`, and `path` as they will obscure views of the 3D model.
5. Select the `C` dot in the middle of the model by clicking on the `C` marker once with the left mouse button.
   - As with temporary markers, when the C marker is selected, it will appear in the Marker menu (Figure 84).
   - As points are progressed through in the browser, the C marker will move to the location of the respective point in the Viscore Viewer window.

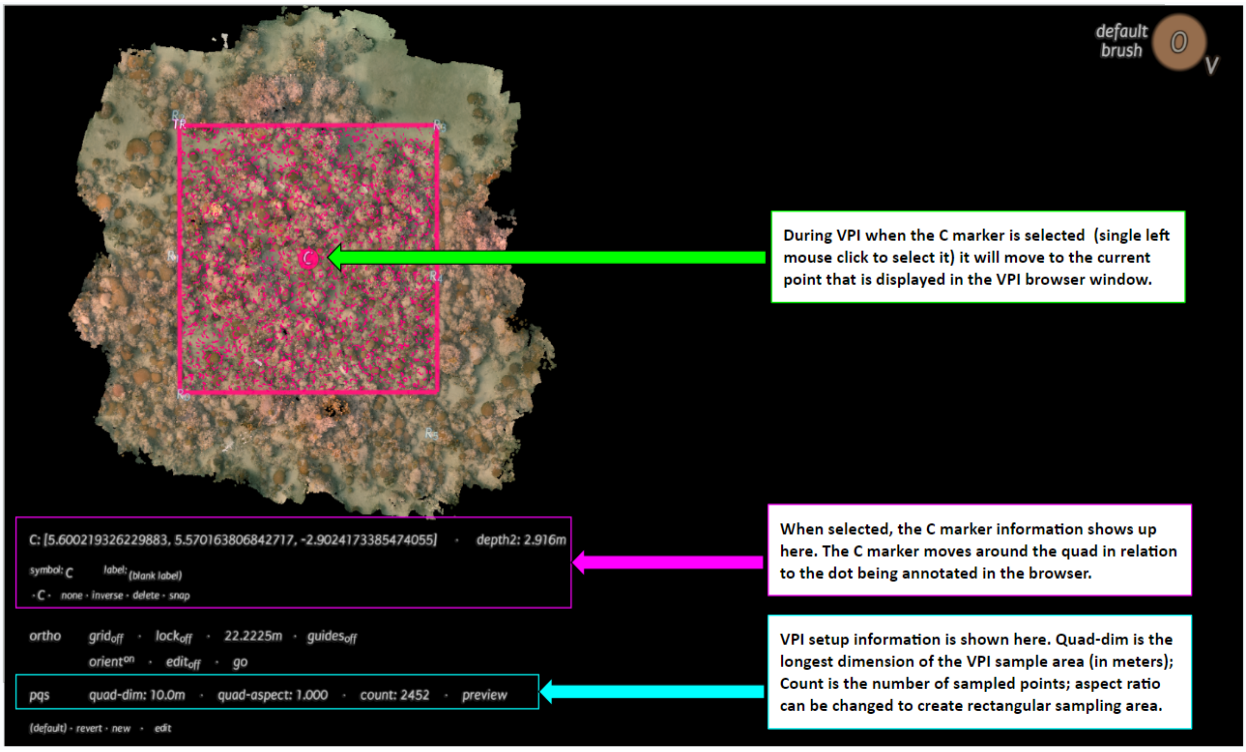


Figure 84. Overview of PQs menu items in Viscore Viewer window.

B3. Conducting VPI

A browser window is used to conduct VPI in conjunction with the 3D model concurrently open in the Viscore Viewer window. The controls for viewing raw images and annotating sample points are all conducted in the browser window accessed through the VPI URL. Controls for conducting VPI are covered in Figure 85, and instructions are further outlined in the section below.

1. With the model open and prepared for VPI in the Viewer window, open a new window in Google Chrome or another preferred browser if Google Chrome is not available. Copy and paste the VPI URL below into the address bar. Reminder: this link works only when a model is open in Viscore.
   http://localhost:9090/jsd/pq.xhtml#0/1/USER_NAME${"class_filter":["GROUP_HERE"]}
   - Change `USER_NAME` in the URL to the desired username.
   - Bookmark this changed URL in the browser to `VPI_USER_NAME`.
     - It is important use this same bookmarked URL each time VPI is conducted to ensure generated data are saved.
   - Press refresh in the browser, and double check that the username is in the browser URL.
     - The buttons at the bottom of the screen may temporarily disappear, this is normal.
   - A list of buttons with taxonomic groupings and a raw photo associated with the sampled point on the model will be displayed in the browser window (Figure 85).

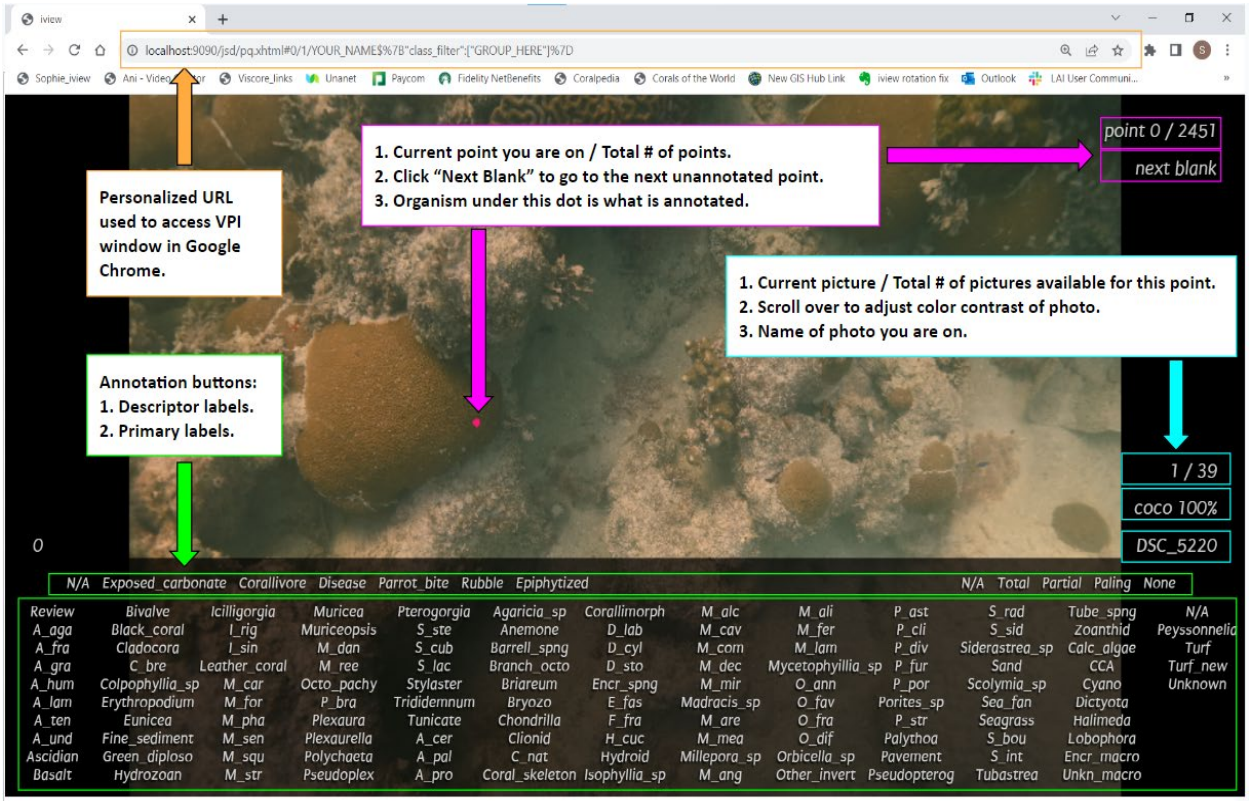


Figure 85. Overview of VPI browser window, with raw image and taxonomic labels displayed in browser window.

B4. VPI Controls

There are multiple ways to maneuver the photos in the browser. For the controls with multiple methods, we recommend using the fastest method in the list below. However, the user-preferred control will be discovered as models are completed in VPI. Note, many of these controls are similar to the iView tool.

- View multiple images that correspond to the same point:
  - Space bar: will flip through the photos.
  - Hold right-click + scroll.
  - Scroll over the first number in the bottom-left corner.
  - Click the N key on the keyboard to progress to the next photo.
  - Click the B key on the keyboard to return to the previous photo.
- Image controls:
  - Use scroll wheel to zoom in and out.
  - Left-click + drag to pan.
  - Left-click + drag to rotate.
- Progressing to the next point:
  - Double-click on any class label.
  - Right arrow key.
  - Scroll up over the point number in the top-right corner.
  - Left-click on next blank in the top-right corner of the browser window.
  - Click the V key on the keyboard.
  - Change the point number in the browser.
- Returning to the previous point:
  - Left arrow key.
  - Scroll down over the point number in the top-right corner.
  - Right-click on next blank in the top-right corner of the browser window.
  - Click the C key on the keyboard.

B5. Labeling Points

Flip through the first 5–10 photos associated with a given point, and pay attention to where the pink point lands. The point should land in the same place each time and should not make large bounces (e.g., from one benthic organism to another), nor should the entire benthos rotate (i.e., photo rotation is normal and to be expected; the problem occurs when the objects themselves rotate changing the entire view). If this error occurs, see *Appendix II.B.* before completing the remainder of this section.

1. Flip through the first couple of photos (usually 5–10 will suffice unless a better view is needed), and annotate what the pink point lands on by double-clicking the button that corresponds to the benthic organism identified (these buttons are at the bottom of the browser screen; Figure 85). Labels displayed in the browser are abbreviated and the full label can be shown by hovering the mouse over a given label.
2. Continue through the points until the end of the dataset.

- When a session is finished (i.e., if data are being processed in more than one sitting), it is not necessary to save the data as Viscore automatically records the data in the samples.cl.user.UserName.json file in the model's .pq folder and can be accessed in subsequent sessions. It is necessary only to close down the model and browser window when done.
- For subsequent sessions: reopen the model and VPI URL in a browser window, and return to the stopping point of a previous session by clicking `next blank` in the browser. This will bring up the last point that was not annotated or to any points labeled as Review.

3. Once VPI is finished for the selected model, back up the data extracted from the model.
   - The model's .pq folder contains a file named as: samples.cl.user.UserName.json. This file holds all of the extracted data and should be backed up. If the model has been modified at all (e.g., PQ quad or samples were changed) the model data should also be backed up accordingly).

B6. Reviewing Points

1. Points that were not labeled or were labeled as Review are grouped together by Viscore and can be reviewed together. Starting at point 0, left-click `next blank` in top-right corner to progress to the next unlabeled or Review point, and provide a label if one can be determined. Keep clicking `next blank` until complete.
2. To review previous annotations made for a specific ID, subset that group by changing `GROUP_HERE` highlighted in the URL browser below, to the annotation to be reviewed (must be the exact name of the button). For example, to review all of the *Siderastrea_sp*, do the following:
   - Change the URL in the browser
     - from:
     http://localhost:9090/jsd/pq.xhtml#0/1/USER_NAME${"class_filter":["GROUP_HERE"]}
     - to:
     http://localhost:9090/jsd/pq.xhtml#0/1/USER_NAME${"class_filter":["Siderastrea_sp"]}
   - When reviewing all points in the dataset by subsetting a particular button, start at point 0 by changing the number next to `#` in the browser to `0`. Otherwise, points may be missed at the beginning of the sampled set of points.
     - http://localhost:9090/jsd/pq.xhtml#0/1/USER_NAME${"class_filter":["Siderastrea_sp"]}
   - Press Enter, then refresh the browser window. A new button will appear under the `next blank` button in the upper-right corner of window, with the name of the button that was added to the URL. Left-mouse click on the name of the subset button to progress to the next point labeled *Siderastrea_sp* (or whatever button is being reviewed). Right-click will return to the previous point.
   - When finished reviewing a subset of annotations, change `Siderastrea_sp` (or whatever button is being used for review) back to `GROUP_HERE`, press Enter, then

refresh. The browser screen will return to the default settings without the subset button.

5. Project Management with the Viscore Org Tool

Viscore's Org tool allows 3D models from multiple locations or collection dates to be accessed using a single .vml for a project. The Org tool provides functions for time series analysis, including a semi-automated coregistration (i.e., spatial alignment of time series data from the same location) tool to align time series, and the replication of sample areas across these time series. A major advantage of Org is that any changes made to 3D models—or any data extracted from them—are stored and organized via a single Org project rather than through multiple individual model folders. For the purposes of this section, 3D models loaded into an Org project are referred to as layers.

The workflows outlined below are similar to those previously described; however, there are some differences in how Viscore operates when utilizing Org. The sections below describe 1- *basic setup and use of projects in Org*, 2- *how to conduct VPI in an Org project*, 3- *coregistration of time series data*, and 4- *generating orthoprojections*.

A. Basics of Org

A1. Start a New Project

1. New Org projects are created using a host 3D model (i.e., layer) to which additional models can be added as new layers. The host layer can be any model with an existing point dataset and .vml; no other information (e.g., scale and depth) is required for the host layer. Ideally, the host layer should be a small dataset (e.g., coral_test) that is not otherwise used for analysis. The Org project folder should contain a .vml and point data.
2. Rename the model folder and .vml to whatever the Org project should be named (e.g., M:IR project uses MIR_Org).
    - Open the .vml, set the point size, adjust zoom settings with Vis-opt menu, and reset the default view. No scaling or orientation is needed.
3. To turn the host model into an Org project, enable the Org tool via the Spacebar menu (Figure 86, also reference *2B. Heads Up Display (HUD) and Spacebar Menu* for further information).
    - Press Spacebar to access the menu, then navigate with the arrows on the keyboard to `scriplets > misc > org`.
    - Then turn `now` and `vml` on. `Sys` must remain off to prevent Org projects from automatically being created when opening other 3D models. The screen should display `now: on`, `vml: on`, and `sys: off` as shown in Figure 86.

Figure 86. Example of accessing the Org tool via the Spacebar menu.

4. The Org tool will now appear in the HUD. Click on `org` in the HUD to turn it on.
5. A major function of Org is the ability to switch between 3D models or layers using the layer selection options. The Org tool is designed to organize projects by 1- *location (e.g., reef or island)*, 2- *site or plot*, and 3- *collection date*. Different islands, sites, or time points are selected or loaded by clicking on the appropriate field. Viscore assumes layers are named in the location_date_plot format. If the host layer lacks this information in its name, a newly opened Org project will display `undefined` or `none` for these fields (Figure 88). Regardless, it is recommended to replace labels for any entries in these fields with the field titles:
    A. Open Google Chrome, and navigate to the following link: http://localhost:9090/jsd/index.xhtml. Click on `web multiview setup`, then click the link named `Org_sets spreadsheet`.
        - Note: This link will work only with an Org project open. It may be necessary to refresh the browser if the links do not appear.
    B. The column `layer` displays the name of the host layer .vml and cannot be changed. Under the columns `island`, `site`, and `time`, replace `undefined` or `NONE` with the names of the organizational structure to be used. For instance, for the M:IR project, the entries of `NONE` in the `island`, `site`, and `time` columns would be changed to `Site`, `Plot`, and `Year`, respectively (Figure 89).

Figure 87. Org menu. When creating a new Org project, the Layer Selection menu will display `undefined`, `default` or `none`.

org_sets

localhost:9090/jsd/spread.xhtml#org_sets

layer ↑	island	site	time
boxo-100pct coral_test/	NONE	NONE	NONE

Figure 88. Org_sets spreadsheet used to organize layer data.

A2. Add Additional Layers

Before a given model can be loaded into an Org project, it must first be scaled and oriented in Viscore in single layer mode. If the model has already been set up with scale and orientation, proceed with the section below; if not, visit *4A. Prepare Model for Analysis*.

1. Open the Org project by double-clicking on the Org project `.vml`.
2. Locate the folder for the model to be added to the Org project. Drag and drop the entire model folder into the Viscore Viewer (Figure 89). In the center of the Viscore Viewer, `vml loading` will appear and quickly disappear.

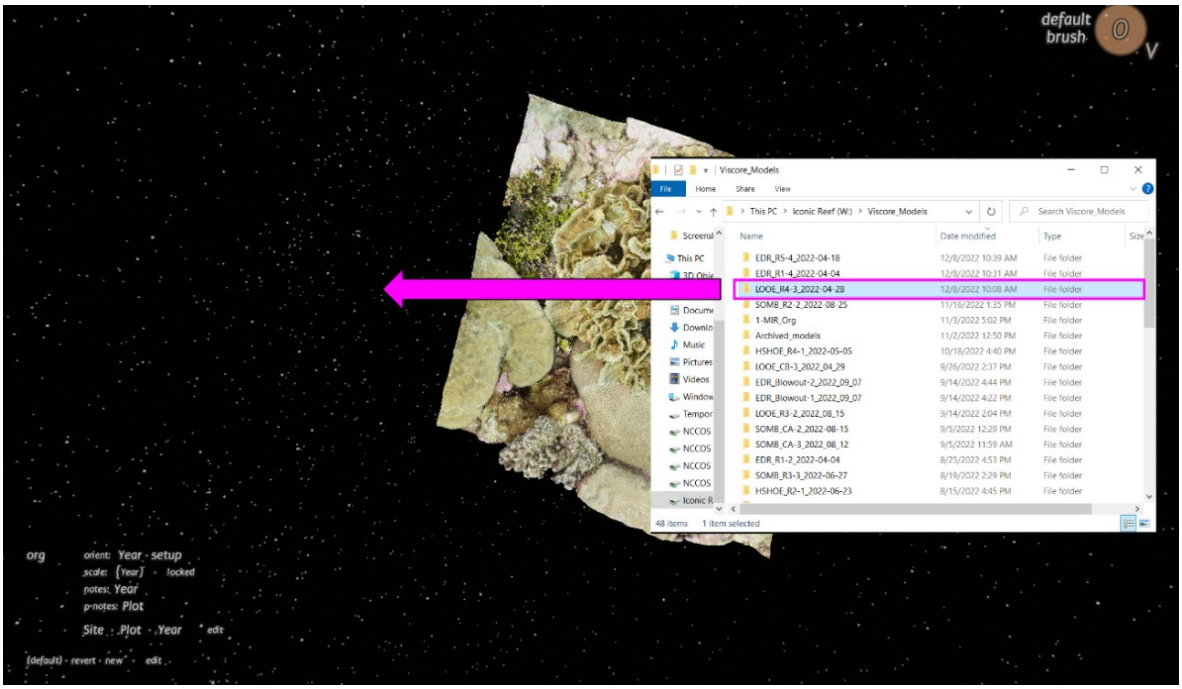


Figure 89. Drag and drop the model folder into the Viewer window.

3. When a new layer is added, the Org layer selection will automatically revert to the host layer. Cycle through the layer selection option in the Org menu to find the recently added site(s).
    - Note: In some instances (e.g., when there is a naming issue), the layer will not appear as an option in Org. This is corrected in the following step.
4. Depending on the naming convention used for naming 3D models, layers will need to be renamed using the Org_sets spreadsheet. This is also an opportunity to rename layers for any needed corrections or for any other reason. Changing names in the Org_sets spreadsheet will change the way that Org displays and organizes this layer, but no changes will be made to the original 3D model. (For example, when using the M:IR naming convention, plot name and collection data will appear in reverse order under the Org menu, as shown in Figure 90, and must be edited using the layers spreadsheet shown in Figure 91.)

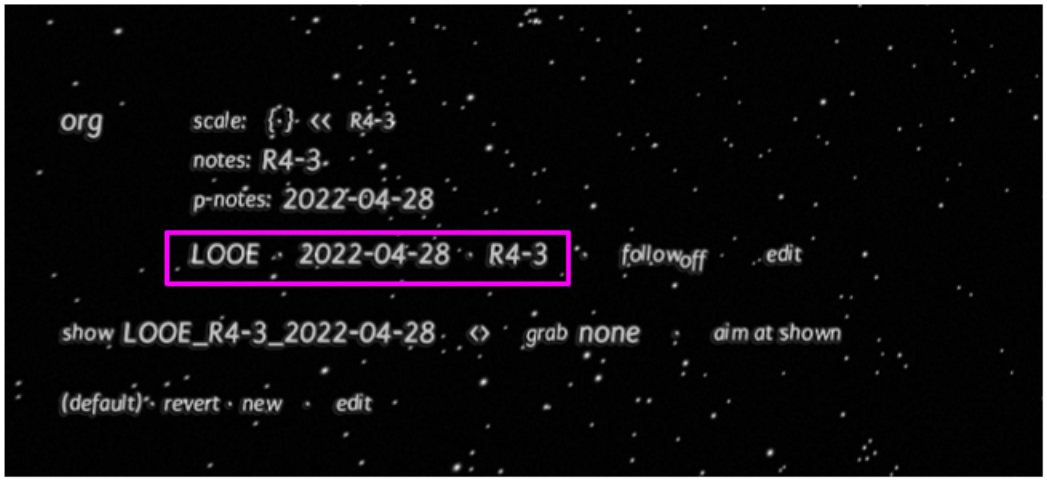


Figure 90. Example of layer name incorrectly ordered.

5. Reopen or refresh the Org_sets spreadsheet. Layers that have been added to the Org project will now appear.
6. Correct entries in the fields `island`, `site`, and `time` as needed (Figure 91).

layer	island	site	time
CFN_R7-4_2022-07-06	CFN	R7-4	2022-07-06
CFS_R1-1_2022-07-06	CFS	R1-1	2022-07-06
CFS_R3-4_2022-06-23	CFS	R3-4	2022-06-23
CHCA_CB-1_2022-06-20	CHCA	CB-1	2022-06-20
CHCA_CC-1_2022-06-20	CHCA	CC-1	2022-06-20
CHCA_R3-1_2022-06-28	CHCA	R3-1	2022-06-28
CHCA_R6-1_2022-06-20	CHCA	R6-1	2022-06-20
EDR_Blowout-1_2022_09_07	EDR	Blowout-1	2022-09-07
EDR_Blowout-2_2022_09_07	EDR	Blowout-2	2022-09-07
EDR_CE-2_2022-05-06	EDR	CE-2	2022-05-06
EDR_CE-3_2022-05-06	EDR	CE-3	2022-05-06
EDR_R1-2_2022-04-04	EDR	R1-2	2022-04-04
EDR_R1-4_2022-04-04	EDR	2022-04-04	R1-4
EDR_R8-4_2022-05-06	EDR	R8-4	2022-05-06

Figure 91. An example of how a layer's name will appear in the Org_sets sheet prior to being fixed. Note the prior and subsequent layer names that are correctly ordered. Make the highlighted one look like the others. Be sure to avoid any hanging spaces.

7. After renaming layers, return to the Viscore Viewer window. The Org layer selection will again revert to the host layer.
8. Use the Org layer selection to navigate back to the layer that was just added.
9. Any time a layer is not in view:
   - Pan to bring it into view.
   - Switch layers back and forth in Org, as Org will automatically display the selected layer.

- If the selected layer in Org is not visible in the Viewer, `aim at shown` will appear in the Org menu. Select `aim at shown` to bring the layer into view (the layer must also be listed under `show` in the bottom-left corner of the Viewer).

A3. Set Scale and Orientation

1. With the desired layer selected in the Org menu, click on the double arrows (`<<`) next to `scale` in the Org menu (Figure 92A). `Locked` will now appear next to the set of arrows to show the scale has been set. (Figure 92B).

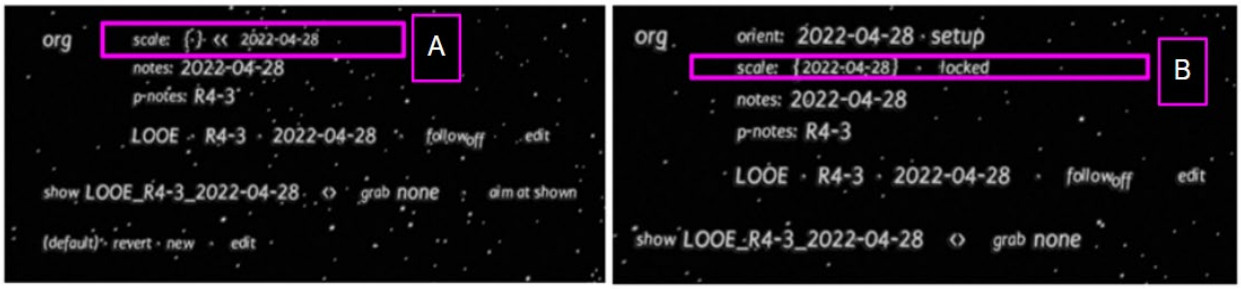


Figure 92. (A) Before and (B) after scale is set.

2. Under the Org menu, next to `orient`, click `setup`, `confirm?` (`confirm?` appears after `setup` has been clicked).
3. The Ortho menu will automatically open. Click `align` (Figure 93).

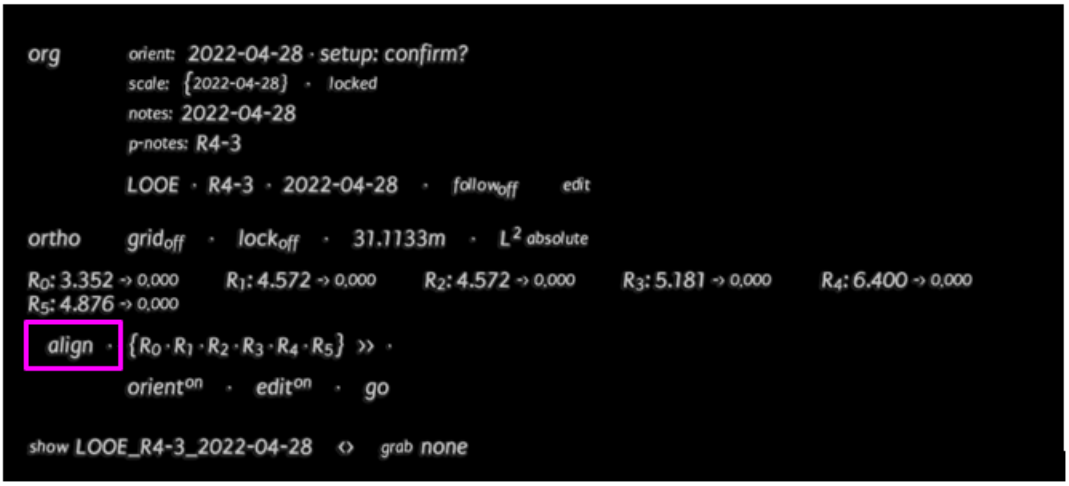


Figure 93. Click `align` as highlighted above to continue orientation setup.

4. At the top of the Org menu next to `orient`, click `apply` then `confirm?` when it appears (Figure 94).

Figure 94. Click `apply` as shown above to finish orientation setup in Org.

5. Turn on `edit` under the Org menu and `locked` will now appear next to `orient` (Figure 95). This confirms that the orientation for the layer has been set. Be sure to turn `edit` off when finished!

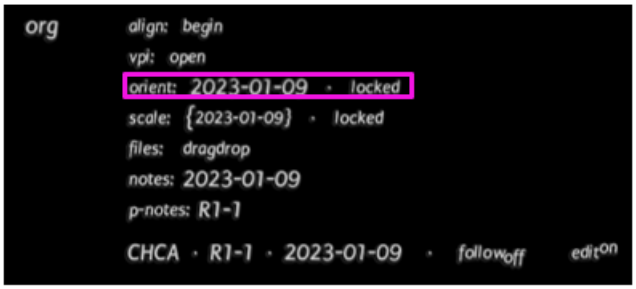


Figure 95. Seeing `locked` as shown above signifies the orientation setup is complete.

A4. Adjust Point Size and Color

Point size in Org is set using the Colors tool. Point size is layer-specific and must be individually set for each layer. Do not use Ctrl + scroll to change point size in an Org project as this changes the point size for all layers in the project and can produce unexpected results.

1. With the desired layer selected in the Org menu (Figure 96A), the active layer should automatically be displayed in `show` and `grab` at the bottom of the Viewer window (Figure 96B). If it is not, change the layer name in the Org layer selection until the correct layer is also displayed in the `show` option. It is important that no layer is selected in `grab` when setting point size.
2. Turn on `colors` from the HUD (Figure 96C).
3. Use options `rgb`, `g`, and `y` to change the color of the selected layer as needed (Figure 96D and *3A4. Adjust Color*).
4. Use `s` to change the point size to an appropriate level for the layer (Figure 96D). If in doubt of correct point size level, refer to *3A2. Set Point Size* from earlier in this guide for examples of appropriate point size levels.

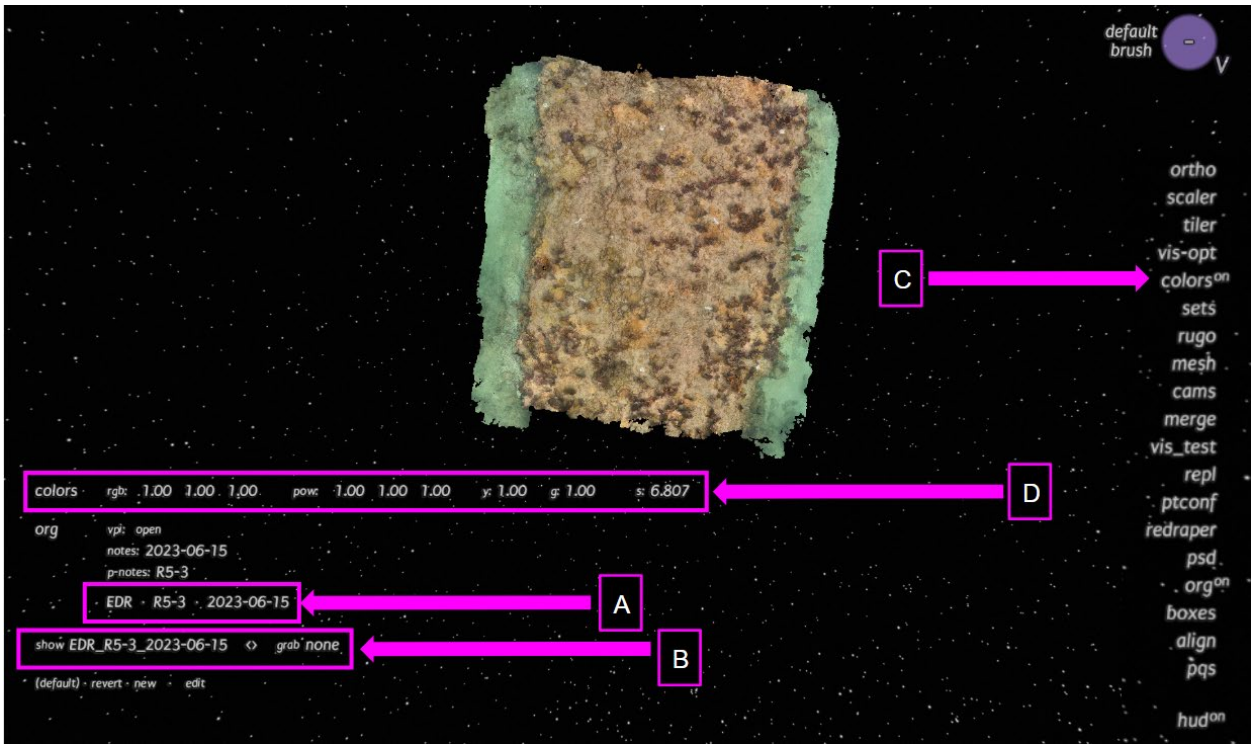


Figure 96. Example of (A) layer selection in the Org menu. (B) The selected layer will automatically appear in `show`. In order to change point size and point colors for the selected layer, make sure that `grab` is set to `none`. (C–D) Turn on the Colors tool and adjust settings as needed.

A5. Import Cams Files and Link Raw Images

1. Select the layer whose Cams files need to be imported.
2. Under the Org Menu, next to the layer name, click `edit` to turn it on. Next to `files`, click `dragdrop` to turn on the drag-drop feature (Figure 97).
3. Drag and drop the entire layer folder for the layer whose Cams files are being imported.
4. The Org Menu will display `searching for` and `loading` the corresponding files. Once import is finished, the status will change to: `found _ folders, _ camfiles, _ pq files`, and a new option, `import cams`, will appear (Figure 98). `Import VPI layers` will also appear if pre-existing VPI data are available (Importing VPI data is covered later in *5C1. Import Existing VPI Data*).
5. Click `import cams` then `confirm?`.

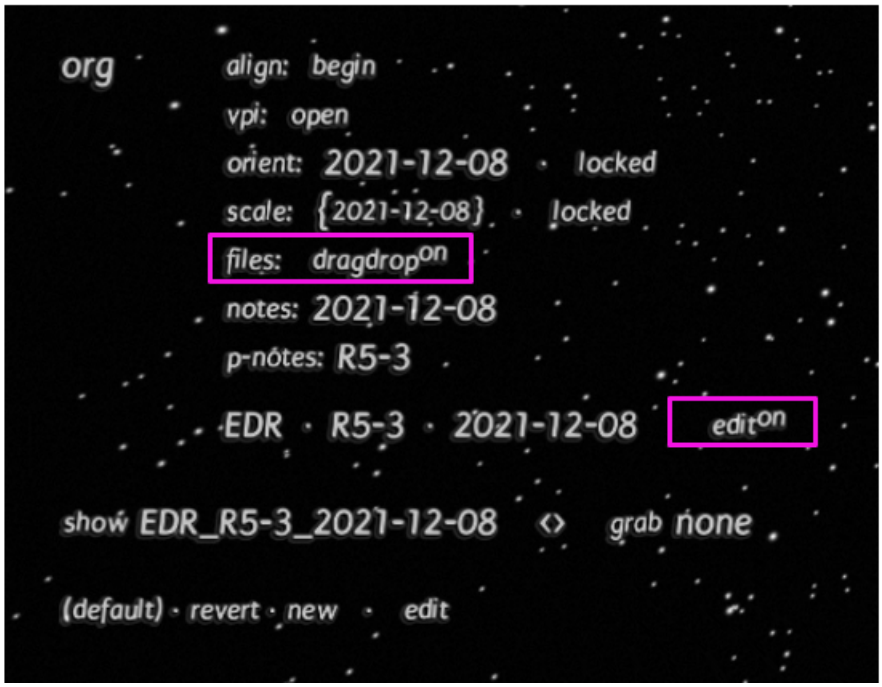


Figure 97. Example of turning on `edit` and `dragdrop` for a layer.

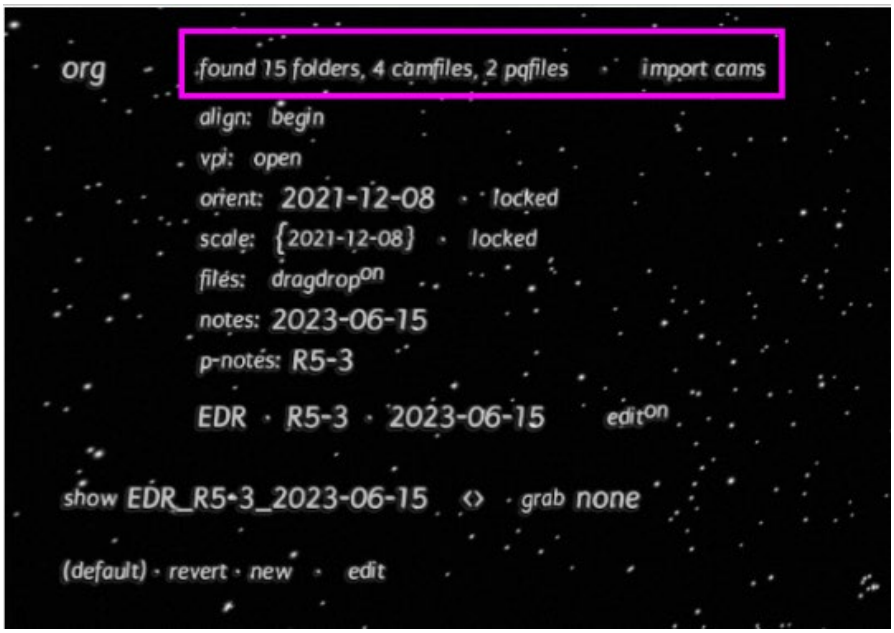


Figure 98. Example of importing Cams files and the menu prompts.

6. A status message indicating the Cams files are loading will appear briefly in the center of the screen. For layers created from a large number of raw images, this may take up to several minutes. A status message will also indicate that Cams are being reloaded for any other layers that have already been added to the Org project. The Cams files for the layer will now be added to the Org folder.

7. Alternatively, copy and paste the .cams.xml and .meta.json files from the original model folder into the Org project folder.
8. Turn on `cams`. The layer selected in Org should automatically be displayed in the Cams menu.
9. If the selected layer is not displayed, click on the layer displayed in the Cams menu until the correct layer name appears. Alternatively, the Cams menu should automatically change to match the selected layer in Org, and switching the layer back and forth should update the layer displayed in the Cams menu. If the layer cannot be selected, restart Viscore before proceeding to the next step.
10. Once the correct .cams file can be selected, setting image paths, draping raw images in the Viscore Viewer window, and displaying the images in the browser (iView) follow the same instructions described *in 3A8. Link Raw Images*, *3A9. Drape Raw Images in the Viscore Viewer Window* and *3A10. Drape Raw Images in a Browser Window (Viscore* iView).

A6. Loading Model Data

The Org tool organizes projects and stores metadata and derived data products. 3D model data associated with individual layers remain in whatever folders they are stored in and not with the Org project. If the point data associated with individual layers are subsequently moved or the drive letter is changed, which is very common when using external hard drives, the location of the data must be reestablished as follows:

1. Each time an Org project is reopened, layer data will need to be loaded before it can be selected.
    - Navigate to the desired layer in the Org menu.
    - Press `load site`, and all layers from that site will appear.
    - If model data have been moved or the drive letter where the data are stored has changed, which is typical when using external hard drives, the file path must be reset by dragging and dropping the model folder(s) again.
    - If the layer still does not appear, follow *5A2. Add Additional Layers.*

B. Time Series Coregistration

Semi-automated tools are available for the coregistration of 3D models collected at the same location at different points in time. Coregistration allows sampling areas to be directly replicated through time to facilitate temporal comparisons. The approach used in the M:IR project when working with multiple time points is shown in Figure 99.

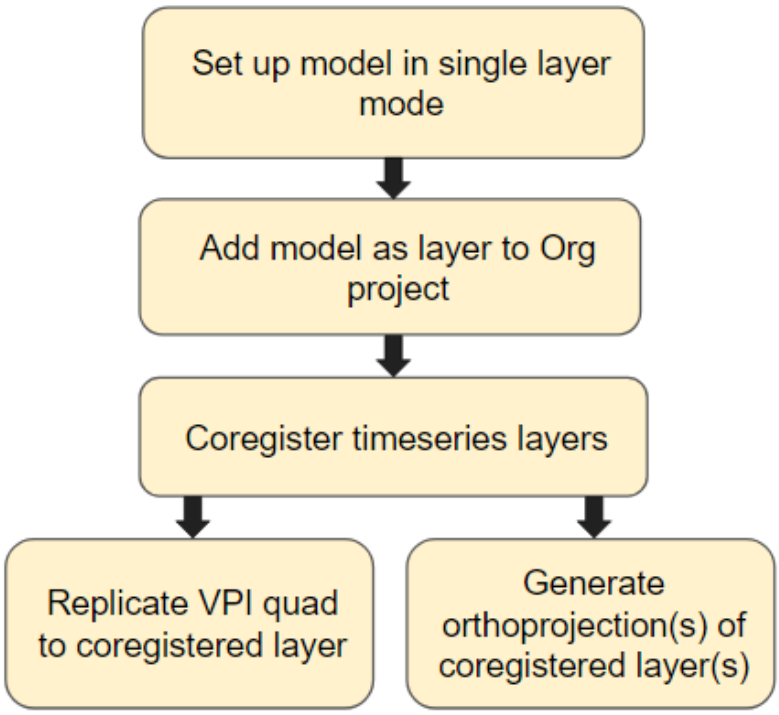


Figure 99. Example of M:IR workflow when working with multiple time points.

B1. Coregistration

This guide describes the process for sequential coregistration, where layers are coregistered to the immediately preceding time point, known as the reference layer. After coregistration, the scale of any group of coregistered layers can be defined as an average across time points or can be based on any one time point. The reference plane can be based on the depth measurements from any layer from a group of coregistered layers; however, depth measurements can only be applied from one layer at a given time. There is some flexibility to this process; however, here, we describe the coregistration workflow as it is implemented for NCCOS projects.

1. Open the Org project and load both layers to be coregistered.
2. Check that the orientation and scale are locked for the reference layer and the layer to be coregistered.
   - If `locked` does not appear next to both scale and orientation for a particular layer, turn on `edit` to view scale and orientation setup. If locked does not appear, lock the scale and orientation following the steps in *5A3. Set Scale and Orientation*. Turn `edit` off when finished.
3. In the layer selection, select the layer to be coregistered to the reference layer, and turn on `edit` (Figure 100A).
   - The reference layer is usually the first time point, and the layer to be coregistered is usually the second time point.
4. In the Org menu, click `align`, then `begin`, then `confirm?` (Figure 100B).

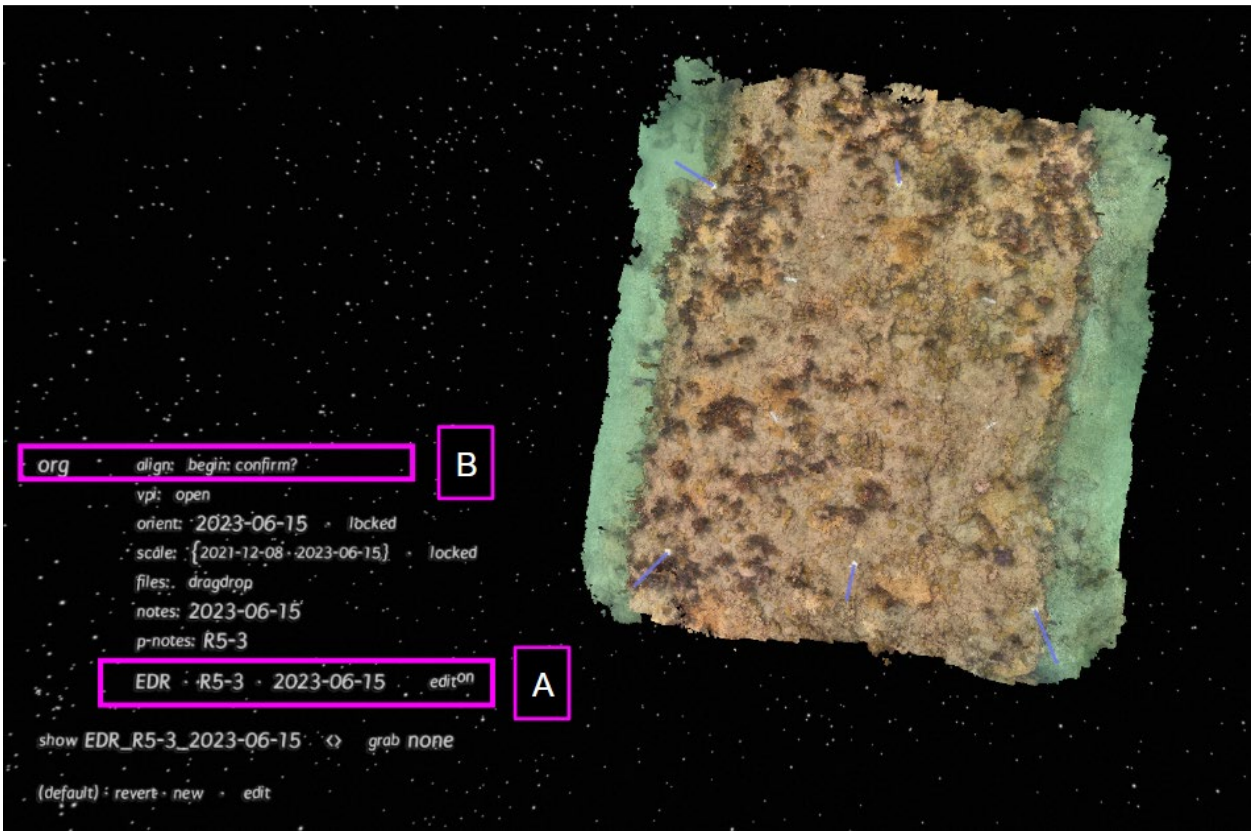


Figure 100. Example of menu items that were used to begin the alignment process. (A) Before starting the alignment process, ensure the layer to be coregistered is shown under the Org menu and that `edit` is on. (B) To start the alignment, click on `align`, `begin`, then `confirm?`

5. In the Org menu next to `align:`, `wrt` will now appear followed by the name of the reference layer (i.e., the previous time point, in Figure 101A the `wrt` layer is `2021-12-08`). If the reference layer is not shown next to `wrt` , change the layer to the appropriate reference layer (necessary when there are more than two time points in a time series).
6. The `mix` option in the Show/Grab tool will automatically turn on. When the color comparison function is set to `colo`, blue and red color filters will appear over each layer (Figure 101B). The blue is the `show` layer (reference layer, Figure 101C), and the red is the `grab` layer (layer to be aligned or coregistered) (Figure 101D).

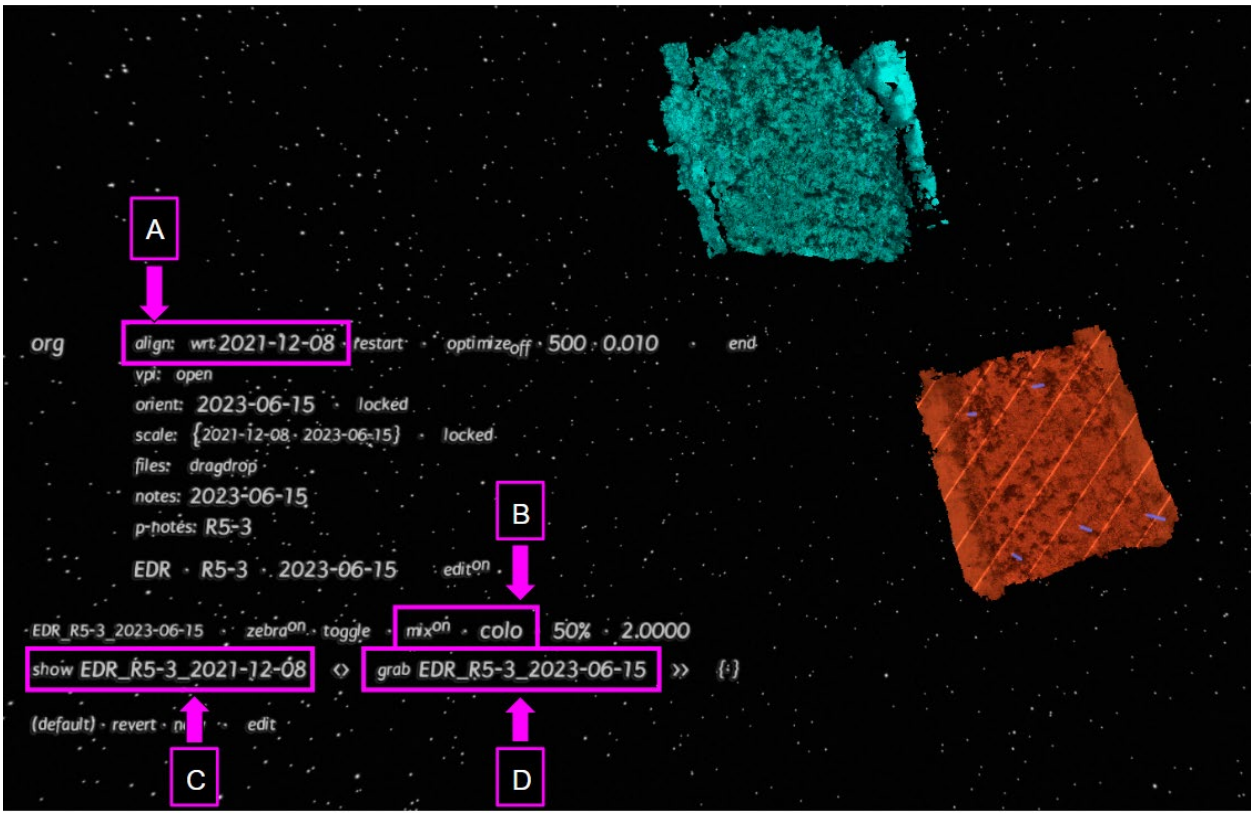


Figure 101. Coregistration tools. (A) The selected layer in Org is aligned to the layer specified next to `wrt`. (B) `The mix` tool will automatically appear during alignment, and the option `colo` can be used to aid layer visualization during or after coregistration. (C) The model selected in `show` will be displayed with a blue filter (in this case, the layer above), and (D) the model selected in `grab` will be displayed with a red filter (in this case, the layer below with diagonal lines). The individual layers can also be differentiated by switching between the show and grab layers via the `Toggle` tool or mouse thumb buttons. After coregistration is complete, overlapping regions of the layers will be colored gray.

7. Click `restart` then `confirm?`. This step guesses the initial alignment, and a new process listed as `traversal %` will appear at the top of the Org menu. When `traversal %` is no longer displayed in the Org menu, two markers, `A1` and `B1`, appear on the layers, and the layers will have lined up with one another (Figure 102).

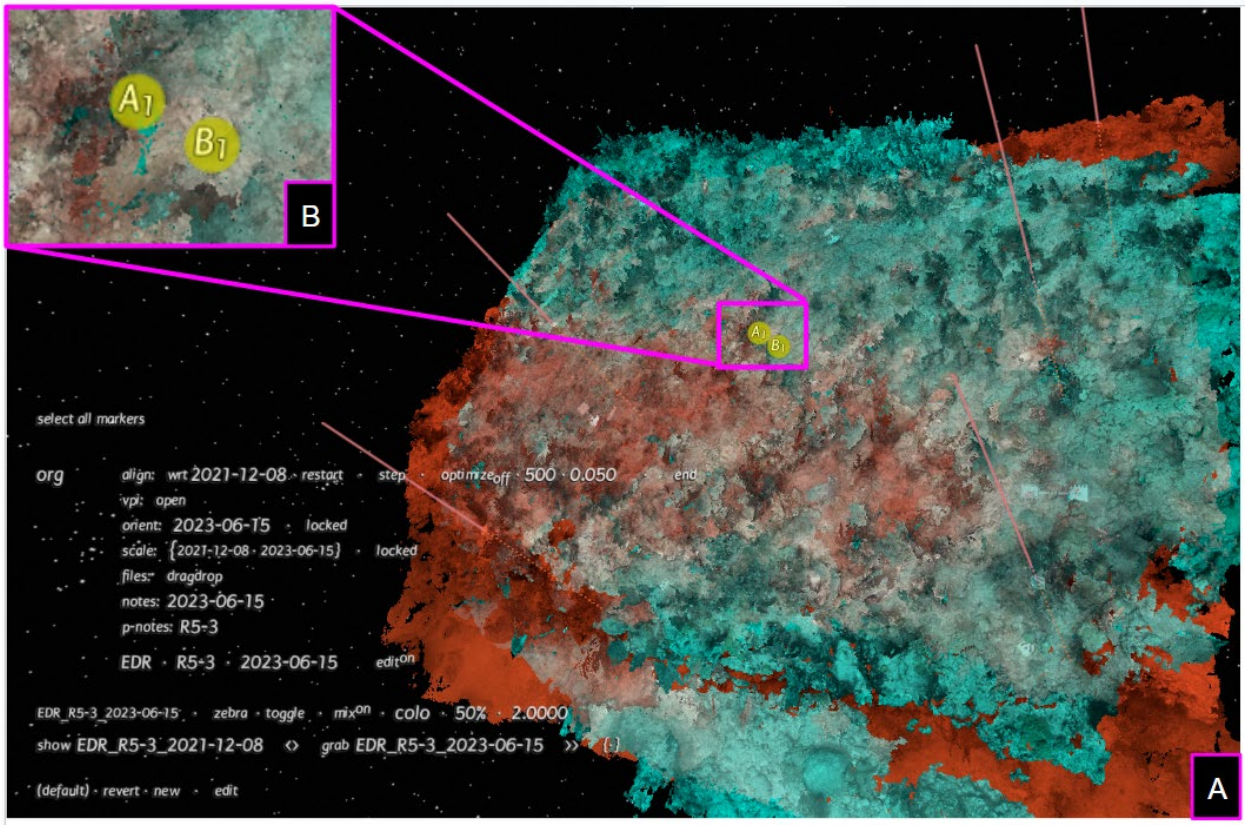


Figure 102. Example of when the traversal step has finished. (A) Note how the two layers are now lined up with one another with the red and blue filters over them, and the (B) markers `A1` and `B1` that appear (zoomed in for further detail). The individual layers can also be differentiated by switching between the show and grab layers via the `Toggle` tool or mouse thumb buttons.

8. The layers will now be provisionally aligned (Figure 102). In some cases, the alignment will be close to correct; however, in other cases, there will be large differences in tilt or rotation. Regardless, the next steps involve refining the coregistration using the `A1` and `B1` markers as follows:
    - Flip back and forth between layers using the mouse thumb buttons. Click the upper thumb button to switch between layers, or press the down thumb button to view both at the same time.
        - Note: If a mouse with thumb buttons is not available, use the Toggle option that is part of the Show/Grab tool. When a layer is selected in both `show` and `grab`, `toggle` will appear above the Show/Grab menu. When Toggle is turned on, the symbol between show and grab will change from <> to an arrow, → that points to the layer that is displayed. Click on the arrow to switch the layer that is displayed. Turn `toggle` off to display both layers.
        - Turn `zebra` off to remove the moving diagonal lines across the layers if the filter is visually distracting.

- Locate a common morphological feature or known landmark that is present at the same location in both time points and has not changed. Examples include fixed coral heads or rebar markers (Figure 103A–D). Examples of features that should not be used include non-stationary items or those that can be expected to change considerably between surveys, such as sponges, scale bars, depth markers, or macroalgae.
- Use the side thumb buttons on the mouse (or the Toggle arrows) to flip to the reference layer where the marker `A1` is shown. Select the `A1` marker (one left mouse click), and move the marker (right-click + drag) to the chosen morphological feature or landmark. Then zoom in and further place the marker in a more precise location, e.g., a crack or crevice present on a live coral colony or dead coral head (Figure 103A–B).
- Use the side thumb buttons on the mouse (or the Toggle arrows) to flip to the coregistered layer where the marker `B1` is shown. Select the `B1` marker (one left mouse click), and move the marker (right-click + drag) to the same morphological feature or landmark that was chosen for marker `A1` in the previous step but is also present in the second time point or layer. Then zoom in and further place the marker in a more precise location, e.g., a crack or crevice present on a live coral colony or dead coral head (Figure 103C–D).
- When finished with the marker placement for both `A1` and `B1`, click `step` then `confirm?`. The layer being coregistered should shift to more closely align to the reference layer. In rare cases, the alignment might become worse, but in either case, proceed to the next step.

9. Two new markers labeled `A2` and `B2` will appear. Repeat the same process used in step 8, placing the markers `A2` and `B2` on a second chosen landmark located at least partway across the plot from the first landmark. After `step` then `confirm?` are clicked, the layer to be coregistered should now be even more closely aligned to the reference layer. Use thumb buttons, or the Toggle arrows to flip between layers to view the alignment).

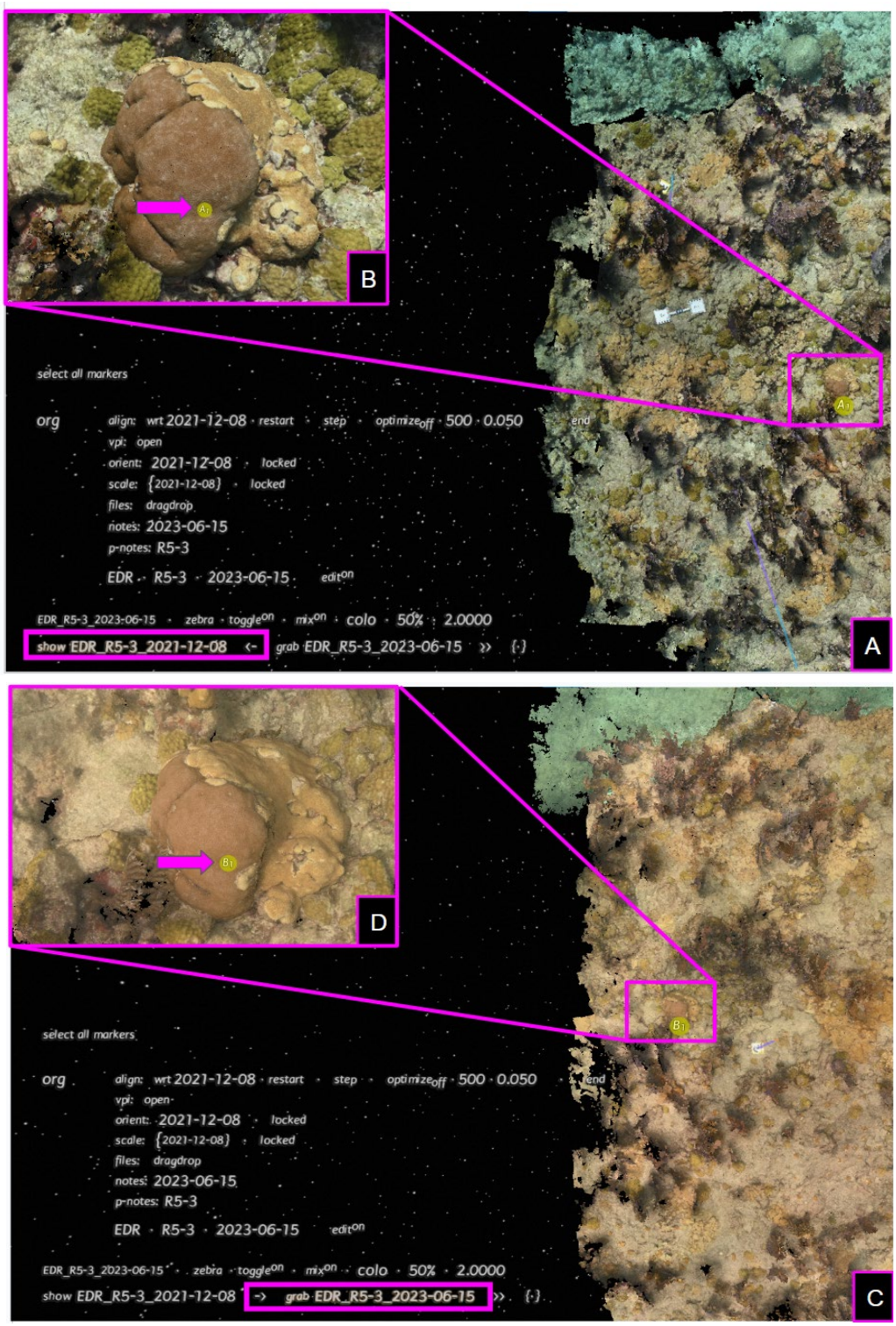


Figure 103. (A–D) Example of dragging the A1 and B1 markers along both layers to a chosen landmark that is present in both time points. (A) Shows the reference layer and A1 marker location zoomed out, and (B) shows the same area zoomed in. (C) Shows the registered layer and B1 marker location zoomed out, and (D) shows the same area zoomed in.

10. Complete the coregistration by optimizing. In the Org menu, two numbers are displayed next to `optimize`:
    - The first number is the number of tie lines to be used to coregister the layers. Set this value to `1000`.
    - The second number is the maximum length of the tie lines. The larger the number, the easier it is to connect the layers, generally speaking. Begin with this number set to `0.500`, increasing or decreasing as needed to achieve the best alignment.
11. Click `optimize`$_{off}$ to turn `optimize` on.
12. `Optimizing…%` will now appear above the Org menu. The percentage of tie lines successfully connecting to both models will be displayed.
    - While the alignment is being optimized, zoom in to various parts of the layer and toggle between the following views: 1- *the two layers individually* (upper thumb button or use Toggle) and 2- *both layers shown simultaneously with the color filter* (lower-thumb button or use Toggle). Travel across the layer, toggling between these views to monitor the optimization process.
13. Coral reefs are dynamic environments, and coregistration should not be expected to be perfect, especially when plots are altered due to prodigious growth or damage (e.g., due to storms). As a result, the goal is not for a 100% alignment, but the best overall alignment for the plot. In some cases, making the tie lines longer will result in a closer alignment.
14. When the `%` next to `optimizing` stabilizes (e.g., is not changing more than 1–3%) and optimization seems adequate (after switching between various views of the layer in step 12), click `end`.
15. To check the alignment:
    - Ensure one layer is listed under `show` and the other layer is listed under `grab`.
    - Using the thumb buttons on the side of the mouse, or the Toggle arrows, switch between the two layers to check that the layers seem to line up with one another.
    - Be sure to check multiple views, i.e., turn the aligned layers on their sides. If changes to the alignment are needed, return to step 10 and adjust the number and length of tie points to re-optimize the layer. Continue until the layers are adequately aligned.

B2. Comparing Timeseries

The Mix options in the Show/Grab tool are used to compare coregistered layers to each other. Mix is automatically enabled when layers are selected in both the Show and Grab options. Mix is used in conjunction with the Org tool for comparing layers, is used during coregistration, and in some cases, to aid layer navigation.

To compare layers (multiple time points for a single site):

1. In the Org menu, navigate to one of the layers to be compared. That layer will automatically appear under `show` in the bottom-left corner (Figure 104A), while `grab` will display `none`. Click on `grab` to switch from `none` to the secondary layer to be viewed (Figure 104B).

2. Click the upper thumb button to switch between layers or press the down thumb button to view both layers at the same time. Alternatively, turn `toggle` on, and click on the arrow between `show` and `grab` to change which one is displayed. Turn `toggle` off to display both layers.

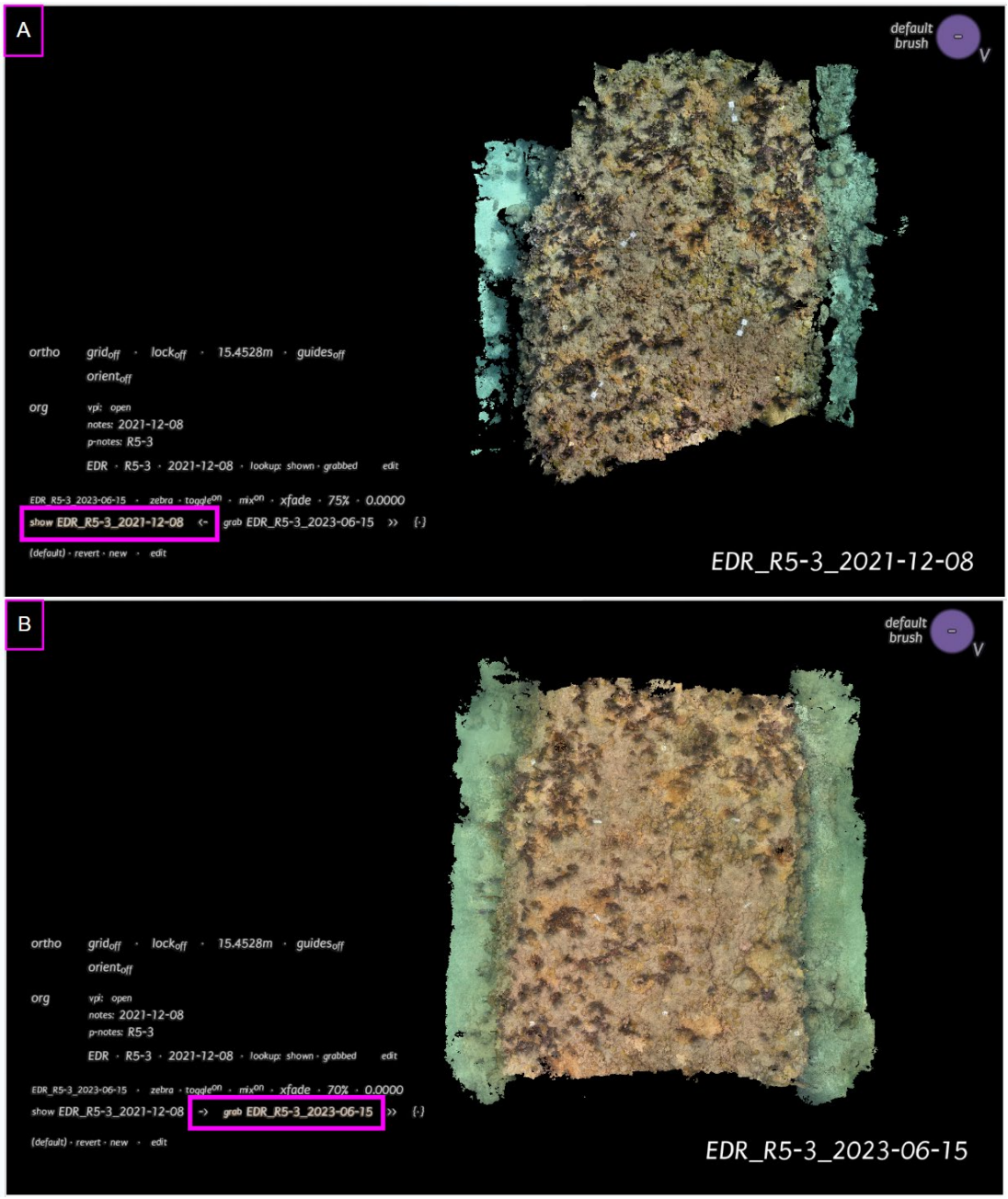


Figure 104. (A) `Show` layer and (B) `Grab` layer shown individually. In the Show/Grab tool, the arrow points to the name of the layer being displayed, which is also highlighted and displayed in the bottom-right corner of the screen.

3. Click on `mix` to turn it on from the Show/Grab Menu (Figure 105A).
4. The first Mix option, `xfade`, will appear as the first filter in the list (Figure 105B). To change to other filters, scroll over or click on `xfade` to view the additional options. Scroll over the `%` to change the intensity of the filter gradient (Figure 105C).

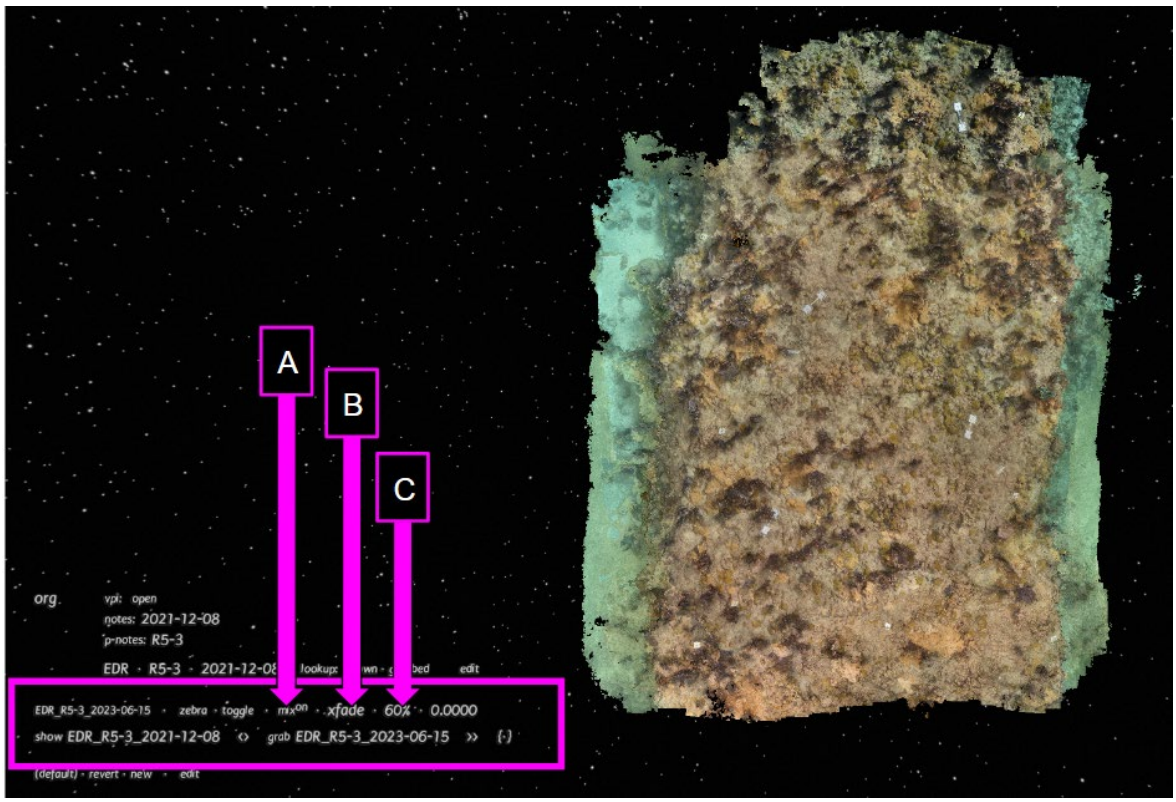


Figure 105. (A) Example of turning `mix` on, seeing (B) `xfade` first appear (C) and using the `%` to change intensity of the filter. In this example, both layers are shown simultaneously with the Xfade filter on.

5. Some of the useful filter options under `mix` are listed and shown below.
   - `xfade`. Xfade is used to make layers semi or fully transparent and is used when both layers are visible (and Toggle is turned off). Adjusting the `%` will change the transparency of Xfade (Figure 105). When xfade is set to 100%, only the layer in `show` is visible, and when set to 0% only the layer in `grab` is visible. When set to 50% both layers are equally visible. When only one layer is displayed, the value of xfade has no effect.
   - `color`. See the change between two years. Adjusting the `%` will alter the intensity of the color gradient between layers, and can be useful to highlight slight differences between layers. Red or blue will show growth or loss depending on the layers selected in the Show/Grab tool (Figure 106).
   - `wipe`. Adjusting the `%` will change how much of each layer is shown (Figure 107).

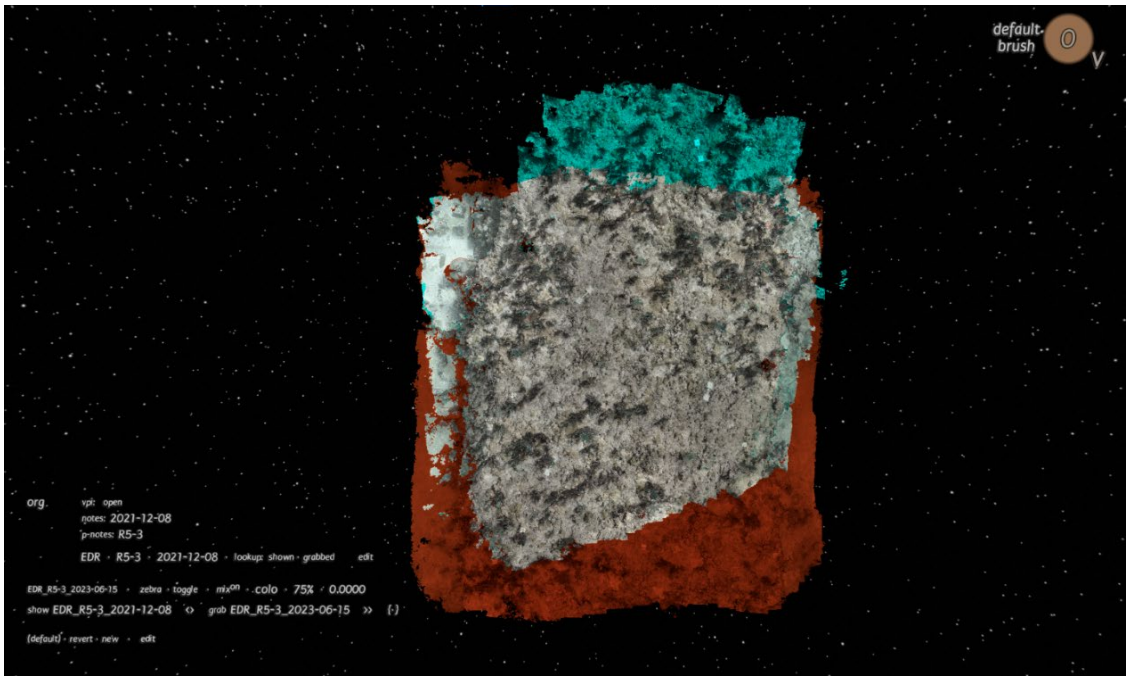


Figure 106. Both layers shown with `colo` filter on. The way the `show` and `grab` layers are selected in this example, blue exhibits growth, while red exhibits loss. The individual layers can also be differentiated by switching between the show and grab layers to see what color corresponds to each individual layer by using the Toggle tool or mouse thumb buttons. Note that there is very little change in the center of the layer by the lack of red and blue, and the blue and red on the edges in this example show the difference in layer overlap from year to year.

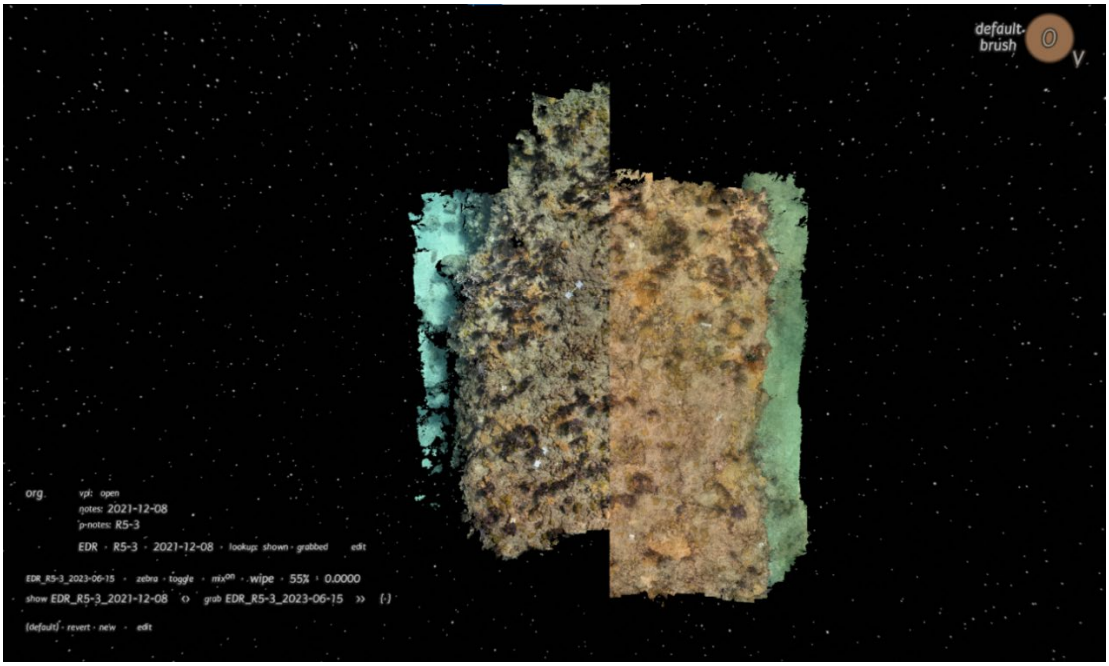


Figure 107. Both layers shown with `wipe` filter on. Left half is the layer in `show`, and right half is in `grab`. Notice the difference in layer overlap between the top and bottom halves.

C. VPI in Org Projects

C1. Import Existing VPI Data

If VPI data were generated for a given 3D model before that model was added to Org as a layer (i.e., VPI was done in single layer mode, e.g., as referenced in *4B. Estimating Benthic Cover with the VPI tool*), the VPI data can be manually added to the Org project. If no pre-existing data are associated with the model or layer in question, ignore this section, and proceed to *5C2. Add a New VPI Quad and Samples in Org* below.

In an Org project, the VPI workflow is accessed from Org's submenu `VPI`. However, in older versions of Viscore, `VPI` may instead be displayed as `PQs`. For instance, in the instructions below, the prompts `VPI: open` or `import VPI`, may instead appear as `PQs open` or `import PQs`.

1. In the Org menu, navigate to the desired layer.
2. Under the Org menu, turn `edit` and `dragdrop` on. Drag and drop the layer's entire folder into the Viscore Viewer window. Click `import VPI layer` then `confirm?`
3. As with the Cams files, the loading of the VPI data will appear in the center of the screen and may take a moment to load.
4. Turn off `dragdrop` and `edit` when done to prevent accidentally changing of other settings.
5. These data can now be opened directly from the Org project for review or to continue analysis. Continue to *5C4. VPI in Org* to conduct VPI in Org.

C2. Add a New VPI Quad and Samples in Org

VPI samples can also be generated and processed directly inside an Org project. If VPI data do not already exist for a site, a new quad and samples can be generated by following these instructions. Viscore will automatically archive any pre-existing data.

1. To create a new VPI sample for a layer in Org, navigate to the desired layer in the Org menu.
2. Click `VPI: open` then `confirm?`. The PQs menu will automatically open and appear below the Org menu.
4. Click on `make quad`. A bright pink box will appear over the layer. Under the PQs menu, click `preview` to lock the layer in a top-down view. Position the quad as needed and generate sample as indicated in *4B1. Prepare VPI Quad and Samples.*
5. After generating samples, turn VPI off by clicking `VPI: close`. Otherwise, proceed to section *4B3. Conducting VPI* to conduct VPI in an Org project.

C3. Replicate VPI Quad in a Time Series

If two layers have been coregistered and any earlier time point has a pre-existing VPI sampling area, that region can be replicated and resampled for the subsequent time points.

1. Select the layer to which the sample area will be copied to.
2. Click `VPI: open` then `confirm?`.
3. Switch to the layer with the existing sample area in the Org Menu.
4. Click `initialize opened VPI from this box` and then `confirm?`.
5. The Org menu will switch from the first to the second time point (i.e., the time point to which the sample area was copied to). The menu items will appear similarly to what is shown in Figure 108.

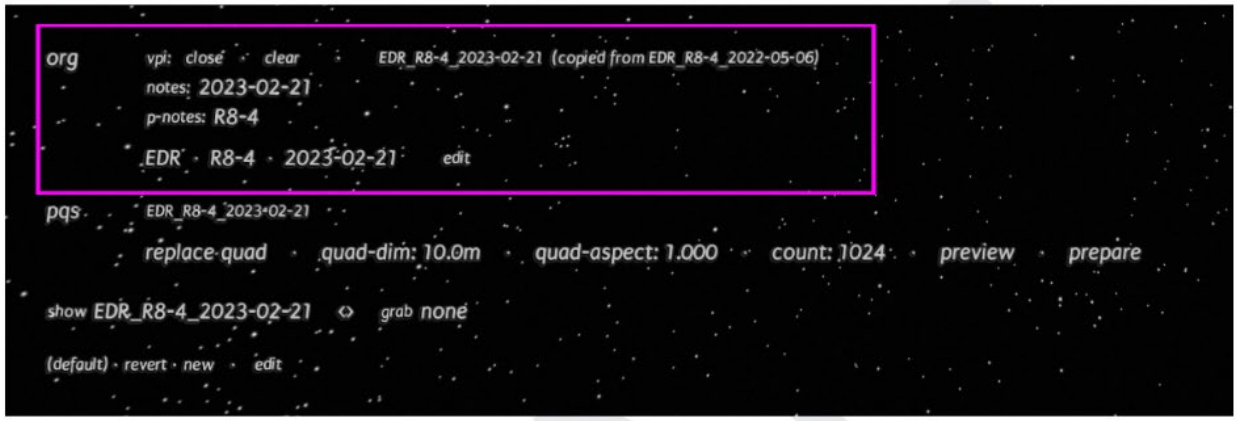


Figure 108. Note in the Org menu that the subsequent time point is shown and that it states which layer the PQs quad was copied from.

6. After the quad is copied, sample points can be generated as covered in *4B1. Prepare VPI Quad and Samples*.
7. When finished with the layer, click `VPI: close` under the Org menu, or proceed to conduct VPI.

C4. VPI in Org

Once VPI data have been imported or generated for a model or layer, VPI can be conducted.

1. Navigate to the desired layer to conduct VPI. Click `load site` to bring the site into Org.
2. Under the Org menu, click `VPI: open` then `confirm?` to load the PQs quad and samples associated with the layer.
3. The PQs menu will automatically open, and VPI can be conducted following the instructions provided in *4B2. Prepare the Viewer for VPI* and *4B3. Conducting VPI*.
4. When finished with VPI for a given session, click `VPI: close` before selecting another layer or doing any other operations in Org.

D. Generating Orthoprojections

Orthoprojections are orthorectified 2D maps projected from the surface of 3D point clouds in Viscore. Orthoprojections of the DPC generated in Viscore are similar to orthomosaics created with Agisoft Metashape (*Section I. Agisoft Metashape*). However, DPC orthoprojections (hereafter simply referred to as orthoprojections) exported from Viscore tend to be slightly less visually detailed, but more geometrically accurate, and are thus preferred for analysis. Orthoprojections are generated in Viscore and imported into TagLab to derive coral size structure and, when time series data are available, measure the growth of individual coral colonies (*Section III. TagLab*). Orthoprojections are created with the Boxes tool located in the HUD. Within the model or Org project's Mapcap folder, multiple files will be made during the orthoprojection process, each of which contains specific information within the name of the file (Figure 109). The .small files save the view that was used to capture the orthoprojection; specifically, the .jpg can be used as a bookmark by dragging and dropping it into the Viscore Viewer window. The final file is the .color.ppm file, containing the orthoprojection, which will need to be converted into TIF format so that the file is compatible with TagLab. The instructions here are provided in the context of an Org project with coregistered time series layers using the Boxes tool. However, orthoprojections can be generated with the Boxes tool from a single-layer instance of Viscore, or from Org projects that do not have time series.

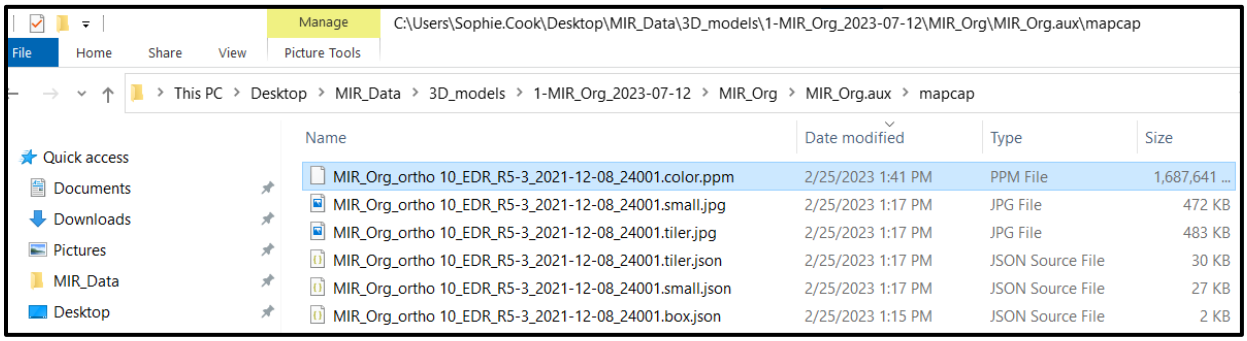


Figure 109. In the Org project Mapcap folder, multiple files will be made during the orthoprojection process. Each file contains the name of the project used (in this example, it's MIR_Org), the name of the box used for the capture area (in this example, it's ortho 10), the name of the layer orthoprojected (EDR_R5-3_2021-12-08), the pixel resolution of the exported map (24001), and the file extension (e.g., .color.ppm). The file highlighted in blue is the file converted in later steps to TIF format.

D1. Specify the Export Region (Used for Initial Time Point)

The section below describes the process for exporting an orthoprojection of the first model or layer in a time series. The export region, created using the Boxes tool in the HUD, captures the original study area by placing a box where the VPI quad and samples were placed, with a 1-m buffer. Orthoprojections of subsequent time points or coregistered layers should adhere to the instructions outlined in the next section (*5D2. Create an Orthoprojection of a Subsequent Time Point*).

1. Navigate to the layer to be orthoprojected in Org. Click `load site` then `ok?` to bring the site into Org. Ensure the corresponding site, plot/subplot, and year are shown under the Org menu.

2. Set the layer to the top-down view.
    - Under the Org menu, click `VPI: open` then `confirm?` to launch the PQs menu. This is to ensure that the orthoprojection to be exported is centered in the same area as the original VPI sample area (e.g., quad).
    - Under the PQs menu, click `preview`. This will set the layer to the top-down view.
        - Note: Ortho works differently in Org; thus, the preview option within the PQs menu is used to orient the layer in a top-down view.
3. In the HUD, turn `boxes` on.
4. Next to `boxes`, click `new` then `current ortho?`.
        - Note: To see the layer in its entirety, the cross-section thickness may need to be adjusted the cross-section thickness size by holding Alt + scrolling up until the layer comes into view.
5. Change the width and the height of the box to `12 × 12 m`, for depth change to `6 m`, or however large the box needs to be to encompass the entire layer.
    - Values can be changed by scrolling over or clicking on (left-click increases; right-click decreases) the numbers next to `w` (width), `h` (height), and `d` (depth) under the Boxes menu in the bottom-left corner of the Viscore Viewer window (Figure 110A).
    - To check if the depth is appropriate, press the Down arrow key to see the side view of the layer. The red box should encompass the entirety of the layer (Figure 111).
    - Ensure that there are no dots following the last digit(s) of the number(s) for each dimension (e.g., If `. . .` appears after a dimension number, click on `. . .` then `round` when it appears).

Figure 110. Example of Boxes menu options and prompts shown during orthoprojection export. (A) Box dimensions are set using `w`, `h`, and `d` before turning `map-export` on. `New` and `edit` are used to change and save box names (this example uses `box 1`). After `map-export` is turned on in (A), options to set map resolution (`mm/px`) and the resulting image dimensions will appear, as shown in (B). In this example, setting the resolution to `0.500 mm/px` results in an image measuring `24000 x 24000` pixels. Clicking `capture` (B) will begin the map export process, and the `pt-size` option must be set in (C) based on visual inspection of different image tiles by scrolling over `preview tile`. Finalize map export by clicking `capture` in (C) and return to the main Viscore Viewer window after map export, or at any time, by clicking `end preview`.

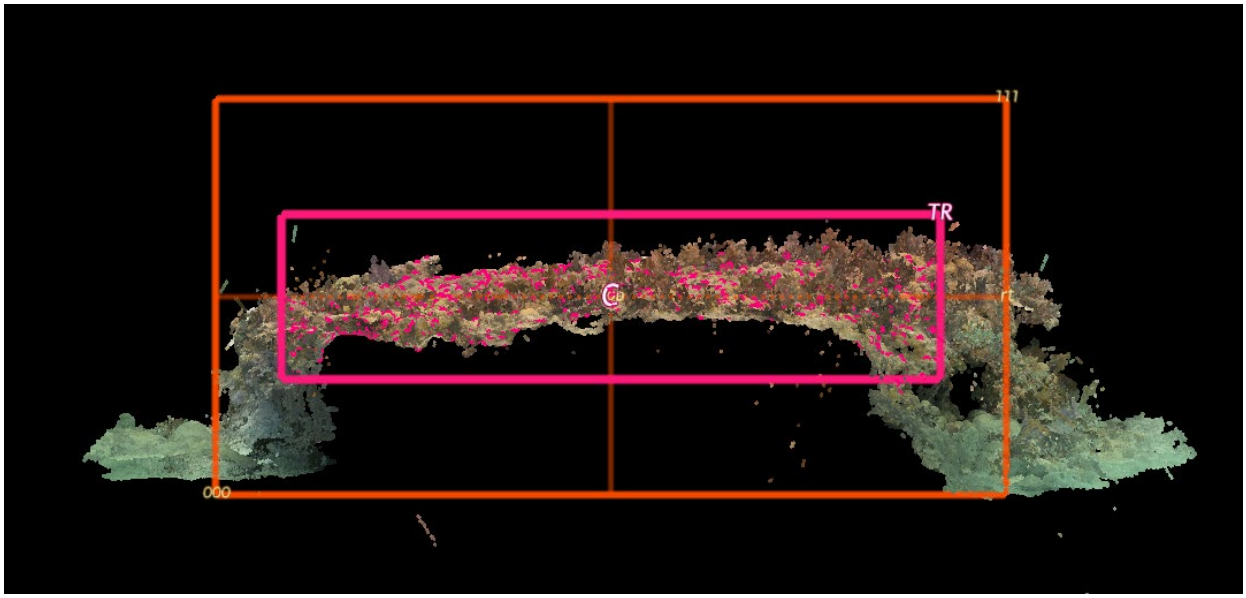


Figure 111. Ensure the box encapsulates the entire height/depth of the layer.

6. After dimensions have been set, click `save as new` then `ok?`. To rename the box, click `edit`, `rename`, then click on the current box name before typing the new name to save the new box as. Then click `save`, and turn `edit` off.
7. Close the PQs quad so it is no longer in view by clicking `VPI: close` then `confirm?` from the Org menu.
8. Under the Boxes menu, turn `map-export` on (Figure 110A).
9. Change the pixel spatial resolution by setting the value next to `map` to the desired value (e.g., for the M:IR project, this value should be `0.500 mm/px`, Figure 110B).
10. Make sure `tags` and `depths` are off. Then click `capture` (Figure 110B).
11. In the bottom-left corner of the screen, a new context menu will appear (Figure 110C). Scroll over `preview tile` until landing on an image in which the benthos can be clearly viewed (may be necessary to scroll over preview tile for a while to stop seeing black space; this is normal if the box expands past the edges of the layer). Adjust pt size until the point size is appropriate for the layer. Leave `pt-skirt` at the default of `3.00` (Figure 110C).
12. Repeat the previous step for a couple more preview tiles to ensure the correct point size has been selected for the layer. For example, there should not be holes between the points, and corals should not look enlarged.
    - Larger holes in the imagery should be disregarded. Point size should only be increased so that the holes between the points are filled (e.g., to reduce the sparkly or fish net appearance); but not increased so much that corals look inflated or bubbly.
    - For clarification on appropriate point size, refer to *3A2. Set Point Size* from earlier in this guide.
13. When the point size seems accurate after scrolling through multiple preview tiles, click `capture` (Figure 110C) then `confirm?` when it appears. Viscore will capturing tiled views of the dense point cloud to create the orthoprojection. This process is computationally intensive, and it is strongly advised to avoid using other programs during orthoprojection generation to avoid an incomplete or corrupted export.
14. To exit the window when Viscore is finished capturing, click `end preview` (Figure 110C) then `confirm?` when it appears to go back to the main Viscore Viewer window.
15. The orthoprojection can now be converted to TIF format, as outlined in *5D3. Convert to TIF.*

D2. Create an Orthoprojection of a Subsequent Time Point

When two layers have been coregistered, the subsequent time point is orthoprojected using the same coordinates (e.g., box) that was used for the first time point. This ensures that the original study area is replicated for subsequent time points, and that the exported time series maps retain their spatial coregistration.

1. Locate the .aux folder within the Org project folder. Open the folder `mapcap`, find the .color.ppm file created for the first time point, and note the name of the box used to create the orthoprojection (Figure 109).
2. In the Org project, navigate to the layer (secondary time point) to be orthoprojected.

3. Turn on `boxes` from the HUD. In the Boxes menu, scroll over the box names (e.g., `ortho 1` or `box 1` as shown in Figure 110) to select the box used to export the earlier time point. For instance, in the example show in Figure 109 the name of the box is ortho10. The box should replicate the same area of the first time point that was orthoprojected (i.e., the area encompassed by the quad that was sampled for VPI).
4. Click `preview from above` to set the layer in a top-down view, and ensure the slice thickness size encompasses the entire model by holding Alt + scrolling up. Refer to step 4 in *4A2. Set Model Orientation*.
5. To export the orthoprojection, follow the same instructions as outlined above in *5D1. Specify the Export Region (Used for Initial Time Point)* starting at step 8.

D3. Convert to TIF

Orthoprojections are exported as a .ppm file and then converted to TIF format for further use (e.g., for TagLab). During map export, Viscore generates a variety of associated metadata files that follow the same naming conventions. It is strongly advised to refrain from changing any of these names.

1. Locate the .aux folder within the Org project folder. Open the folder `mapcap`, and find the file created (the one that corresponds to the name of the layer orthoprojected) with the extension `.color.ppm`.
2. On the computer's C drive, open the folder `vid` and locate the script file named `convert-to-tif-flip.cmd`. Drag and drop the `.color.ppm` file onto this script to convert it into a .TIF.
3. The Command Prompt will open and begin processing. Do not close the Command Prompt window until `Press any key to continue` appears, which indicates the process has finished (Figure 112).
    - This process may take some time. If the process appears to fail in the Command Prompt, check that the file path of the .color.ppm file does not contain any spaces and that it is not exceptionally long (i.e., the orthoprojection is within many nested folders, creating an unusually long file path).
4. The converted TIF file will be located in the model's .aux folder, in the mapcap folder and will have the same name as the original .color.ppm file. This is the file to be uploaded into TagLab projects as outlined in the next section in this series (*Section III. TagLab*).

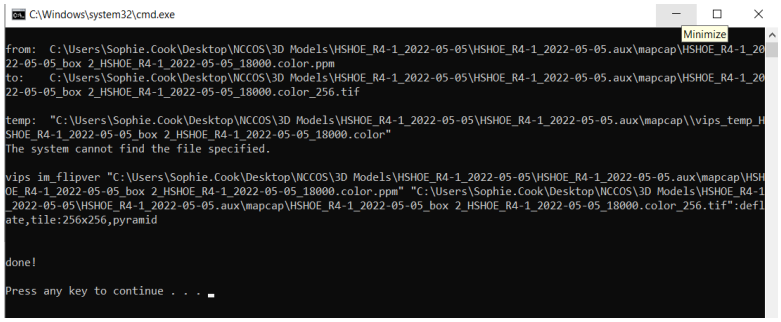


Figure 112. The process has finished when it shows `Press any key to continue.`

SECTION III. TAGLAB

This section describes the use of TagLab to calculate the size of individual coral colonies and assess colony condition, and, when time series information is available, colony fates such as growth or shrinkage, survivorship, and recruitment can also be tracked. Using TagLab, coral colonies (also referred to as regions of interest, or ROIs) are outlined via a process known as segmentation, and, when scale is provided, the size of each coral can be calculated. Segmentation can be conducted manually; however, AI-enhanced workflows allow semi-automated and fully automated segmentation of colonies, increasing the rate at which data can be generated and, importantly, improving the accuracy of segmented colonies (Pavoni et al., 2022). The workflows described here have been tailored to support evaluation of coral reefs as part of active NCCOS projects, and this SOP is not a comprehensive summary of the functionality and capabilities of TagLab. TagLab was developed by the Visual Computing Lab, Consiglio Nazionale delle Ricerche, (Pisa, Italy). For additional information, please refer to the TagLab website http://taglab.isti.cnr.it and associated publications (Pavoni et al., 2021; Pavoni et al., 2022).

The TagLab workflow is summarized in five stages (Figure 113).

1. **Installation and Navigation.** Steps to install TagLab and required dependencies are provided. An overview of launching and navigating the software, common keystrokes, and instructions for the use of segmentation and annotation tools are described in detail.
2. **Project Setup.** Orthoprojections are imported into TagLab as maps, and a project file is created. Project-specific labels are created or imported into the project, and the study area is designated via the placement of a grid.
3. **Segment and Annotate Coral Colonies.** Users systematically segments and annotates coral colonies from all target taxa within a user-defined study area.
4. **Match Coral Colonies Across Time Series.** Time series orthoprojections are required for this section, which can be uploaded simultaneously or separately into an existing TagLab project as maps. After colonies have been segmented in each of the available time points, individual coral colonies are matched, allowing calculation of change in colony area. Once corals are matched, the matches and fates are reviewed through a quality assurance and quality control (QAQC) process.
5. **Export Data.** Data are exported for further analysis in statistical software.

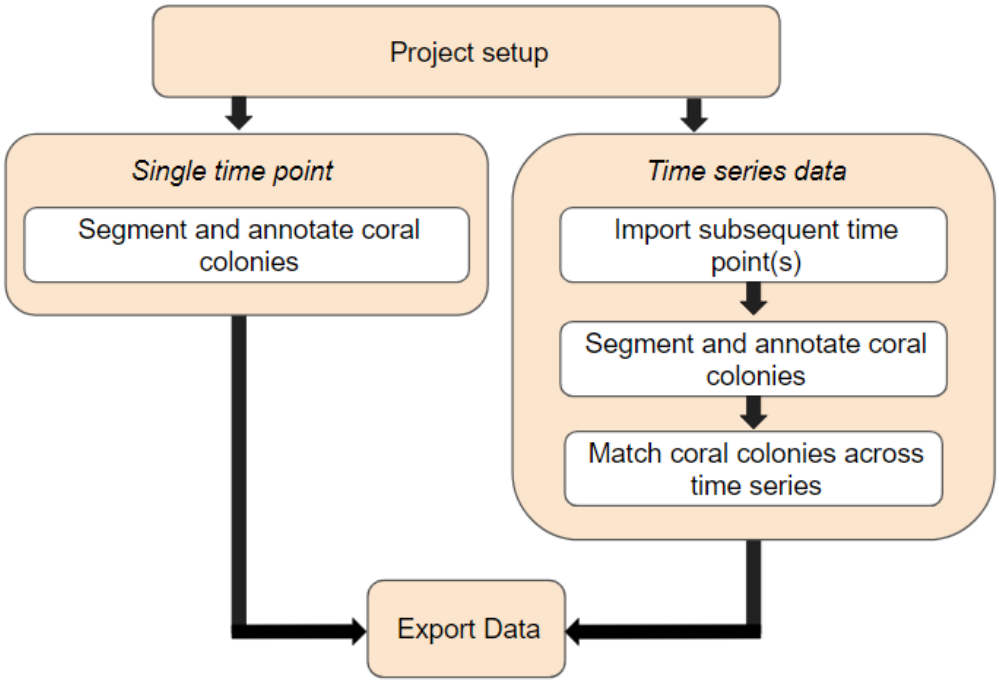


Figure 113. Diagram of the TagLab workflow stages following software installation and navigation.

1. Basics of TagLab: Installation to Navigation

This section provides instructions for installing, launching, and updating TagLab; descriptions and functions of menus and tool panes; map navigation; keystrokes and commonly used shortcuts; and segmentation tools. TagLab has specific computational requirements that should be referenced prior to installation (*Appendix I.C.*).

A. TagLab Installation

Various software packages and dependencies associated with the Python programming language and software must be installed prior to the installation or use of TagLab. *It is important to allow all downloads outlined in* 1A1–A4 *to finish before proceeding to* 1A5. Finalize TagLab Installation**.** The instructions below are for Microsoft operating systems. For Linux or macOS operating systems, refer to the official installation instructions: https://github.com/cnr-isti-vclab/TagLab/wiki/Install-TagLab.

For NCCOS and M:IR staff, all software and dependencies will need prior approval and support from IT to install.

A1. Download Python Version Required by TagLab

1. Download and install a 64-bit version of Python 3.8.x, 3.9.x, or 3.10.x from https://www.python.org/downloads/ (please refer to the TagLab installation website for up to date installation requirements). If Python was previously installed, skip to step three to

confirm that the correct version is installed. In the event that an alternate version of Python is installed, it may be necessary to remove the previous installation and install the required version.

2. When installing Python, select `Add Python to PATH` and select `Disable PATH length limit` before leaving the setup prompts (Figure 114).

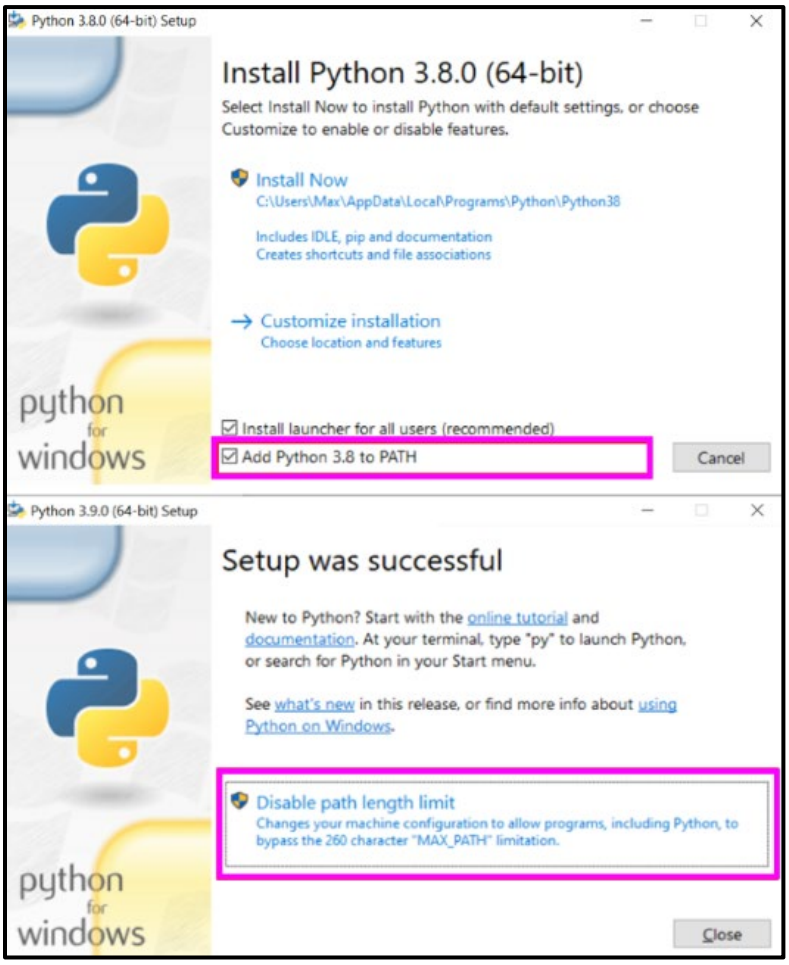


Figure 114. Example of prompts and options to be selected when installing Python.

3. To check if installation was successful or if Python is already installed and TagLab compatible, open the Command Prompt, and type `python --version` and click Enter. The installed version of Python will appear in the Command Prompt (Figure 115).

Figure 115. Command Prompt returning the version of Python installed.

4. Alternatively, if Python is already installed, the Python version can be checked by searching `Python` in the desktop taskbar (Figure 116).

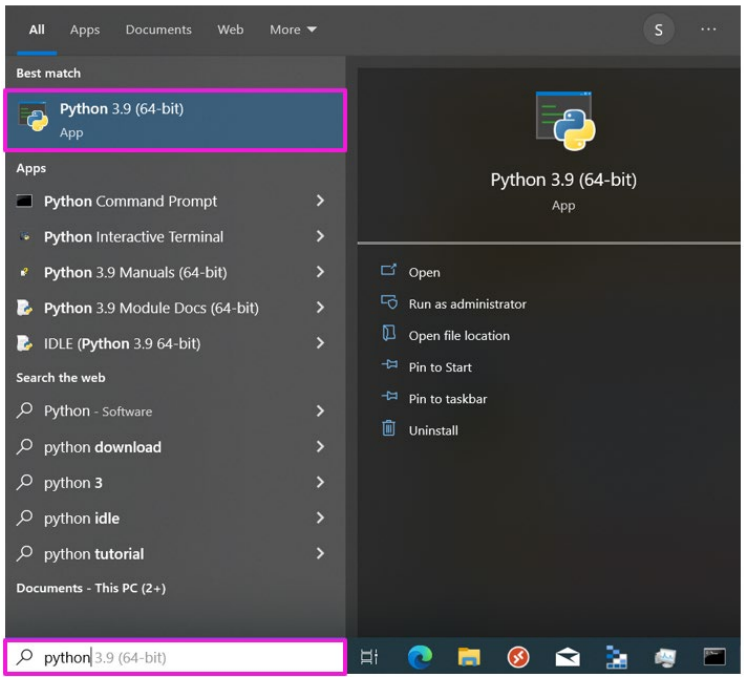


Figure 116. Using taskbar to search for Python version.

A2. Download Microsoft C++ Build Tools Suite

1. Go to: https://visualstudio.microsoft.com/visual-cpp-build-tools/ and click `Download Build Tools` (Figure 117).

2. Launch the installer, and then select `Desktop development with C++` and then select the options as shown in Figure 118. Click `Install`.

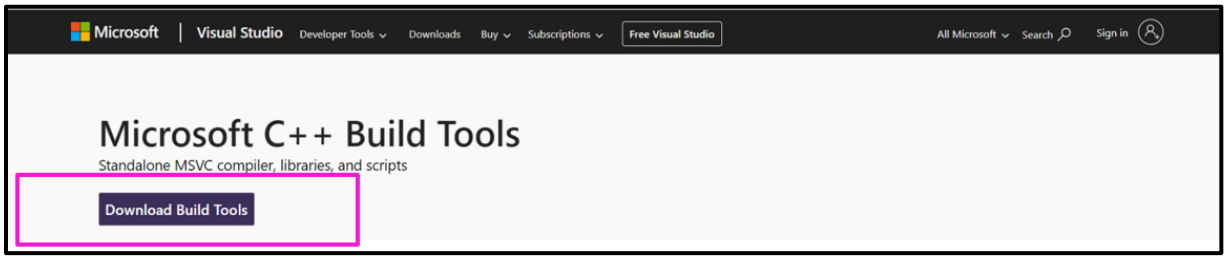


Figure 117. Select `Download Build Tools`.

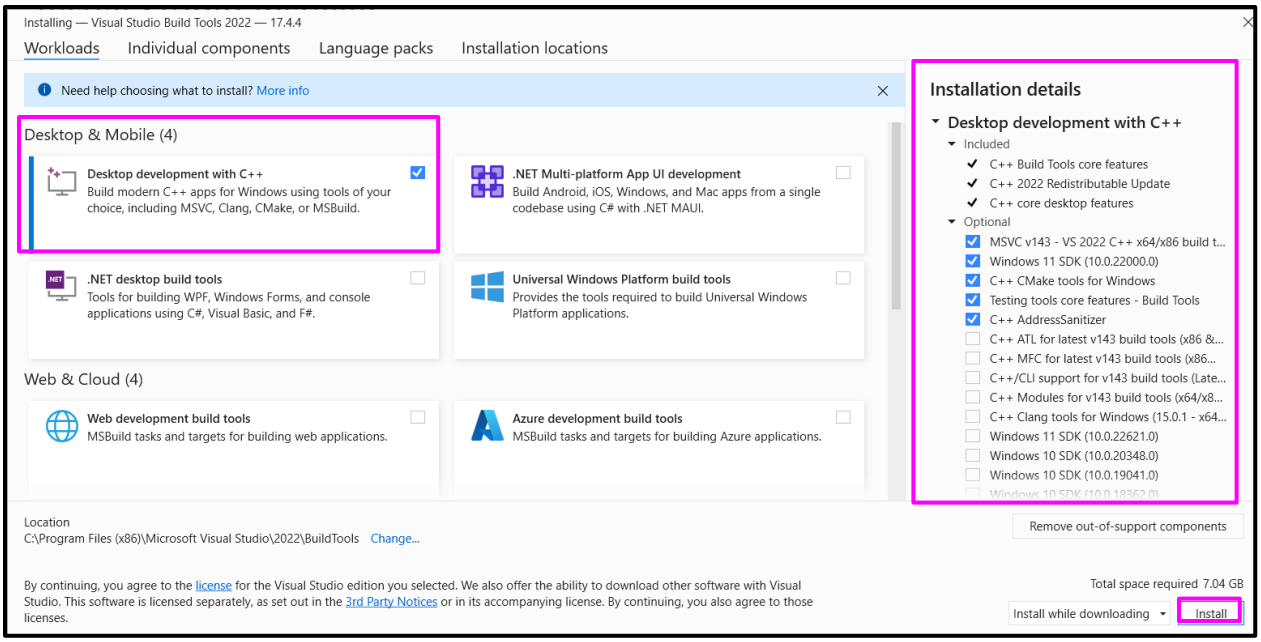


Figure 118. Ensure the options in the pink boxes are checked before clicking `install`.

A3. Download TagLab

1. Go to: https://github.com/cnr-isti-vclab/TagLab, and click the green button `Code` to open the drop-down menu. Click `Download ZIP` to download the TagLab package (Figure 119).

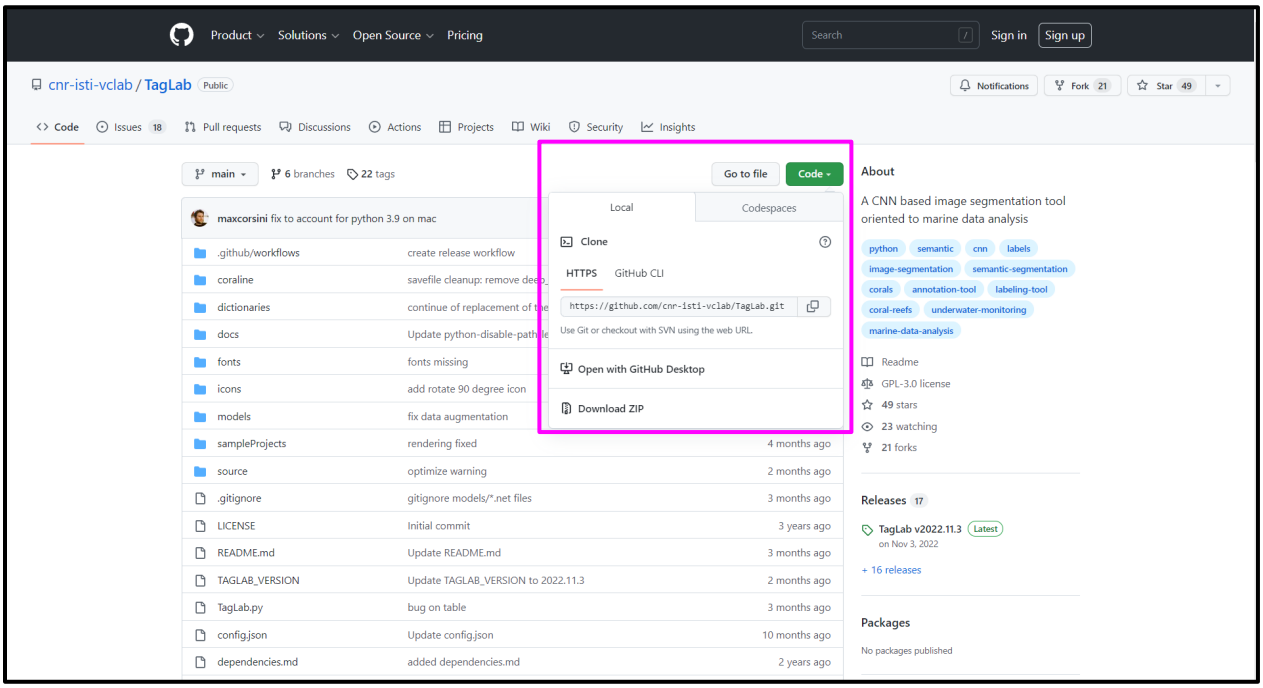


Figure 119. Example of where to locate and download TagLab on GitHub.

A4. Download CUDA Toolkit

1. Go to the TagLab installation page (https://github.com/cnr-isti-vclab/TagLab/wiki/Install-TagLab) and download the recommended version of the CUDA Toolkit.
2. To check if installation was successful or if CUDA is already installed: check the current CUDA version to ensure it corresponds to the TagLab-compatible version listed in step 1. Open the Command Prompt, and type `nvcc --version` and press Enter. The version of CUDA installed will appear in the Command Prompt console (Figure 120).

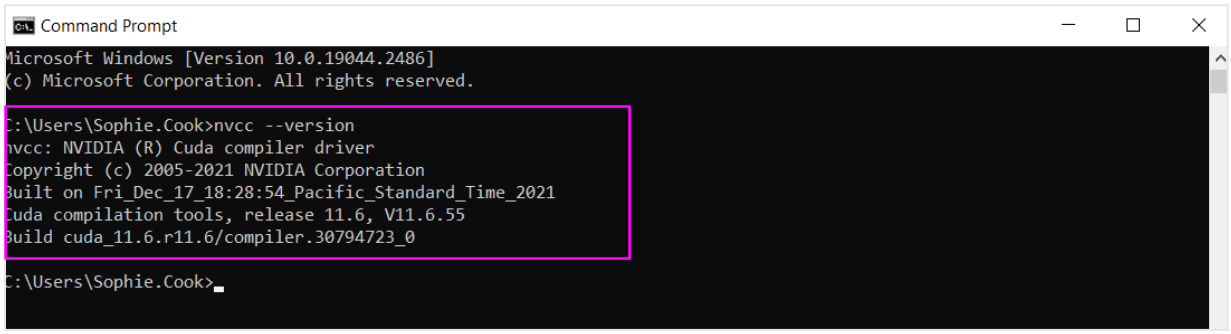


Figure 120. Example of the Command Prompt returning the version of NVIDIA CUDA installed.

Important: Before proceeding to 1A5, ensure all installations and downloads listed above from 1A1–A4 have finished.

A5. Finalize TagLab Installation

1. Unzip the downloaded TagLab folder to the C drive.
2. Open the Command Prompt, and follow the instructions below:
   - Change the working directory by typing `cd` followed by the file to the location of the unzipped TagLab-main folder, then press Enter. (e.g., cd C:\TagLab-main, Figure 121).

Figure 121. Command Prompt and changing working directory.

   - Type `install.py`, then press Enter. This step may take a while. Do not close the Command Prompt until the process has finished (process is finished when it returns to > in the Command Prompt).
   - If prompted to install additional dependencies, please refer to the developer's website for additional details: https://github.com/cnr-isti-vclab/TagLab/wiki/Install-TagLab.
   - Verify that installation was successful by launching TagLab in the next section.

B. Launch and Update TagLab

B1. Launch TagLab

1. Open the Command Prompt, and change the working directory to the C drive where the TagLab-main folder is located (e.g., cd C:\TagLab-main; Figure 121) in the Command Prompt, then press Enter.
2. Type `TagLab.py`, and press Enter in the Command Prompt to launch TagLab.

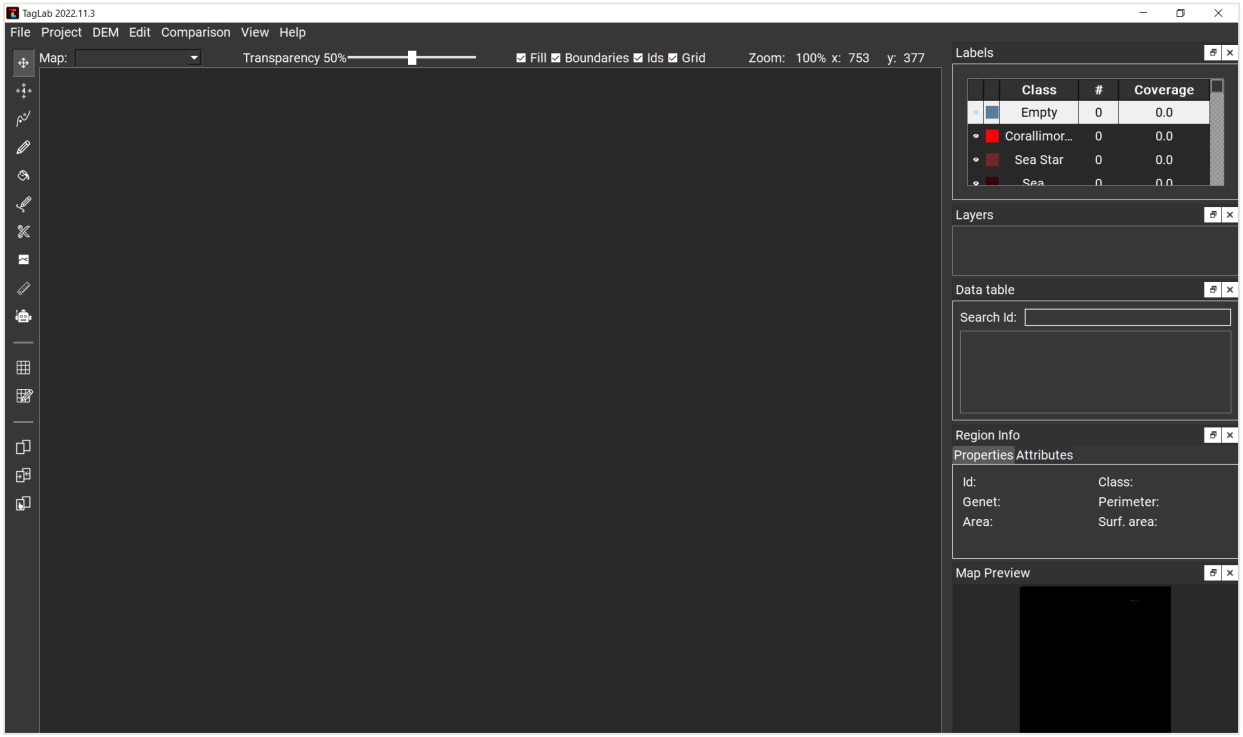


Figure 122. TagLab installation has been successful when this window appears.

B2. Update TagLab

After launching TagLab, a message may appear in the Command Prompt to install the newest version of TagLab (Figure 123). These updates are mandatory and must be run in the Command Prompt before TagLab can be launched. If prompted with an update message, type `update.py` in the Command Prompt, press Enter, and allow the process to finish in the Command Prompt. When the update is complete, launch TagLab.

To launch TagLab without updating, momentarily disconnect from the internet, launch TagLab, then reconnect to the internet as needed.

```
C:\TagLab-main> TagLab.py
New version available. Please, launch update.py
```

Figure 123. Example of required TagLab update in the Command Prompt.

C. Menus and Panes in TagLab

C1. Menu Panes Found in Main Window

The main TagLab window and associated menu panes are outlined below to familiarize the user with the software interface (Figure 124 and Figure 125).

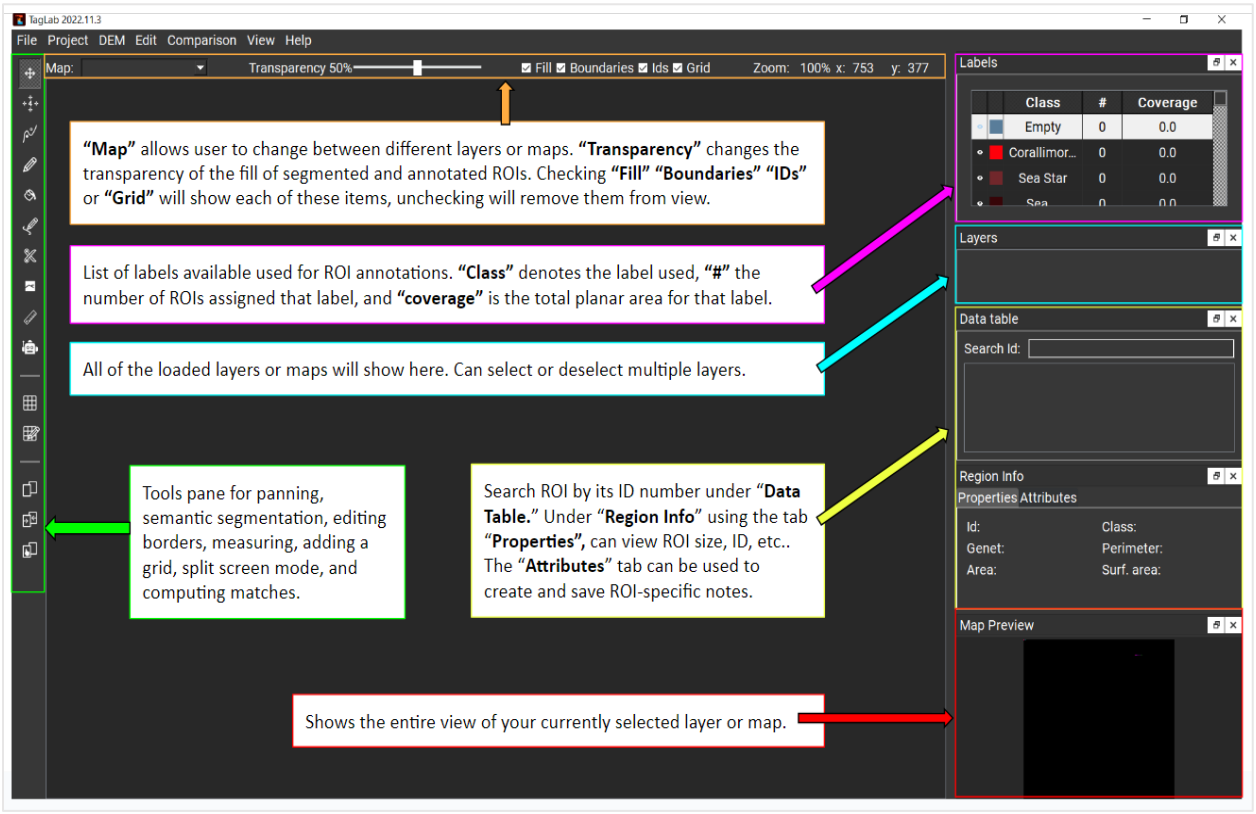


Figure 124. Overview of menu panes in TagLab.

Tools Pane in Detail

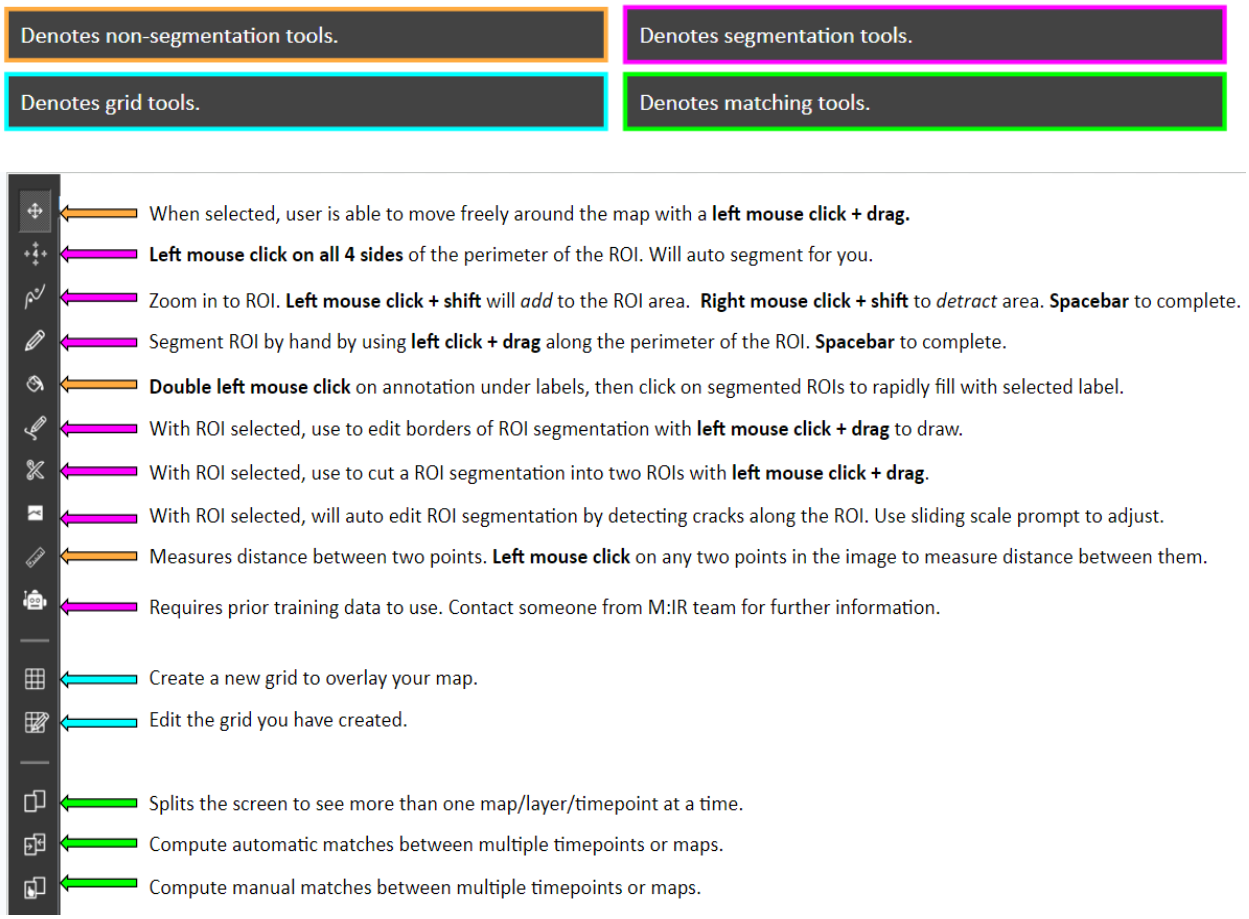


Figure 125. Overview of Tools pane in TagLab.

D. Navigation

D1. Pan

- Select the Pan tool  from the Tools pane on the left side of the window.
- Ctrl + left mouse drag will allow panning while a segmentation tool is selected.

D2. Zoom

Place the cursor in the area to be zoomed into. Scrolling up on the mouse wheel will zoom in; scrolling down will zoom out.

E. Keystrokes and Shortcuts

E1. Overview of Available Keystrokes and Shortcuts

Useful keystrokes can be accessed via the Help menu in the main TagLab window but have also been highlighted below (Figure 126).

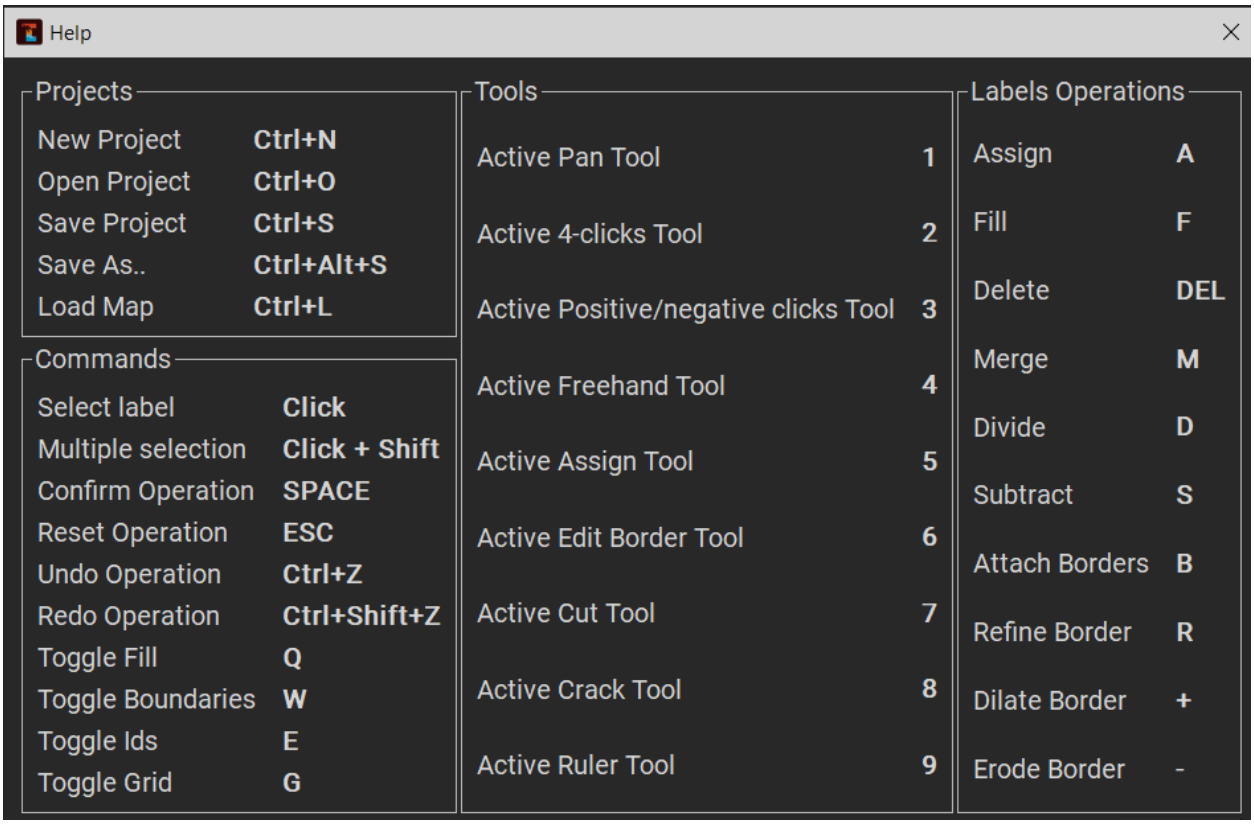


Figure 126. The Help Menu is accessed as a drop-down menu at the top of the TagLab window.

E2. Commonly Used Shortcuts for the Segmentation and Annotation of ROIs

- Undo: Crtl + Z.
- Finish segmentation: Click Spacebar. Outline will switch from black to white.
- Select ROI: Double-click on/inside segmentation.
- Select multiple ROIs at once: hold Shift + left- click on segmentations.
- Deselect ROI: Double-click outside segmentation or press Esc key.
- Merge ROIs into one: Select multiple ROIs by holding Shift + left-click on ROIs. Once the ROIs have been selected, press M to merge multiple ROIs into one.
- Delete segmentation: Select segmentation, then click Delete or right-click > select `Delete Labels` from the context menu.
- Change annotation/label: Select annotated ROI, then double-click on desired annotation from Labels pane in upper-right corner of the window.

F. Segmentation Tools in Detail

F1. Tools for Segmentation

Below are descriptions of the primary tools used in the segmentation workflows: 1- *Freehand/Manual Segmentation*, 2- *Positive/Negative Clicks Segmentation*, 3- *Edit Borders tool* and 4- *Cut Segmentation*. Additional tools for segmentation are described in the next section, *1F2. Other Tools in Detail*). For each tool, first select the corresponding icon in the Tools pane on the left side of the TagLab window, then follow the instructions as outlined below.

Freehand/Manual Segmentation

1. Zoom in on the coral colony as far as possible but with the entirety in view.
2. Left-click + drag the cursor *continuously* along the edges of the coral colony to trace the colony outline. The beginning/end of the segmentation must cross over itself to complete the segmentation (Figure 127).

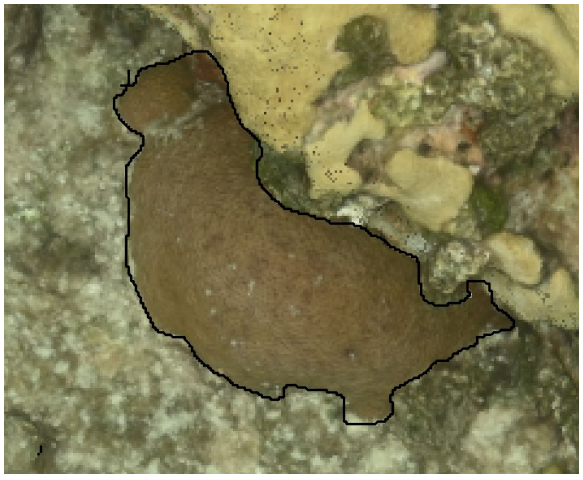


Figure 127. Example of segmentation using the Manual tool.

3. The coral colony can also be traced with multiple partial segments. Ensure that all segments overlap one another (Figure 128) to complete the full segmentation. Press Spacebar to finish the segmentation.

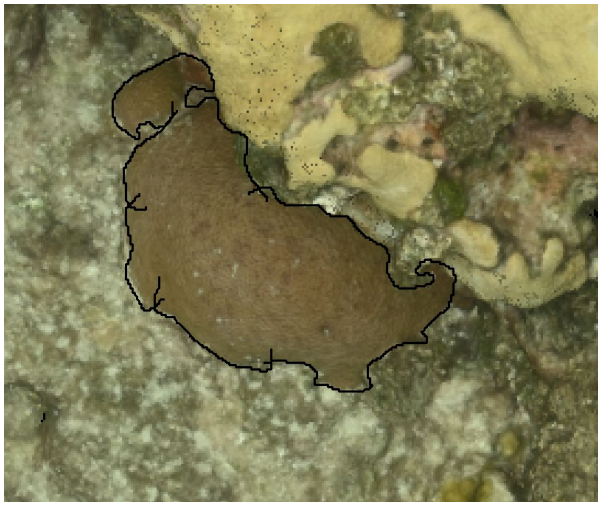


Figure 128. Example of tracing a coral colony in segments using the Manual tool.

4. Once the segmentation is complete and the spacebar is pressed, the segmentation will change from black to white and the coral colony will be assigned an ID number.
5. To merge multiple completed segmentations into a single segmentation with one ID number (i.e., to combine two or more enclosed, separate segmentations into one) hold Shift + double-click on the finished segmentations to select them, then click M on the keyboard to merge.

Positive/Negative Clicks Segmentation

Preferred tool for the segmentation of ROIs as it is accurate and efficient.

1. Zoom in on the coral colony as far as possible but with the entirety of the colony in view.
2. Hold Shift + left-click on a representative area of the coral colony. After a brief pause, a green dot will appear and the coral colony will be partially or completely segmented (Figure 129).

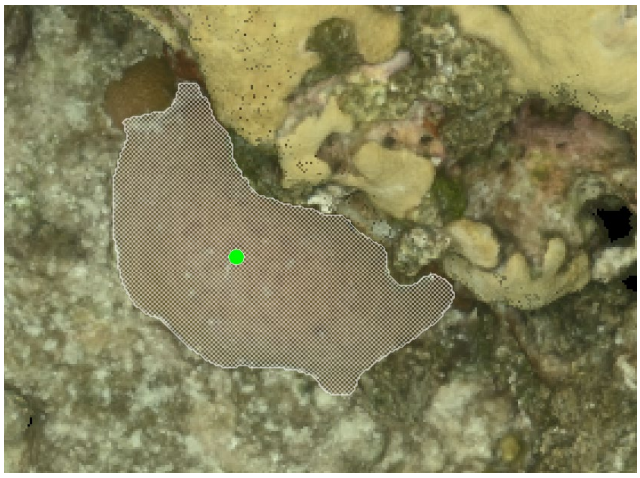


Figure 129. Example of first segmentation.

3. To add areas to the segmentation, hold Shift + left-click on area(s) to be added (Figure 130).

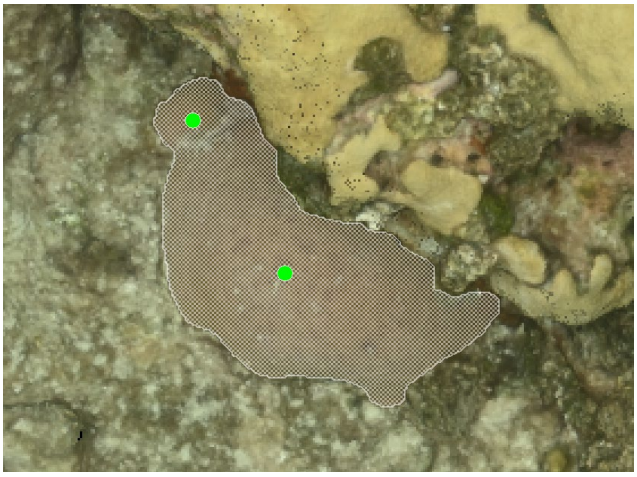


Figure 130. Example of secondary segmentation.

4. To remove areas from the segmentation, hold Shift + right-click on area(s) to be removed. A red dot will appear in removed areas (Figure 131).

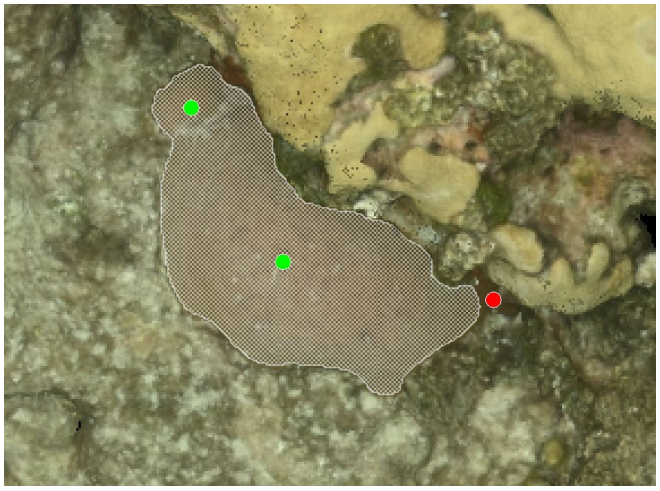


Figure 131. Example of removing areas from segmentation.

5. When the segmentation looks accurate, press Spacebar to finish.
6. The segmented coral colony will be assigned an ID number with a white perimeter (Figure 132).

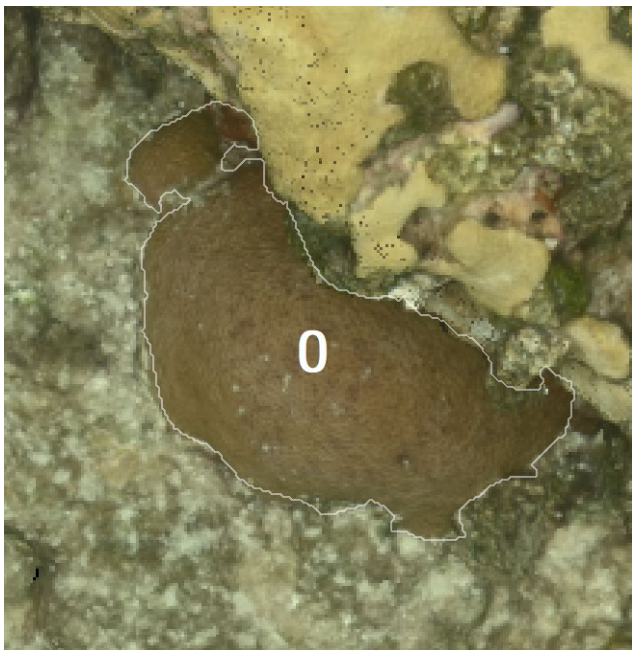


Figure 132. Example of completed segmentation with the white border and ID number.

Edit Border

Used when a segmentation for an ROI needs its borders further refined.

1. Select a previously segmented coral colony (border will be white).
2. Left-click + drag the cursor to draw a line (or multiple lines) to edit borders. Ensure the beginning and the end of the line cross over the previously created segmentation (Figure 133).

Figure 133. Example of editing the border of a previously made segmentation.

3. Create a *concave* curve or segment along the edges of the coral colony's segmentation to *delete* parts from the segmentation (Figure 134A), and press Spacebar to finish (Figure 134B).

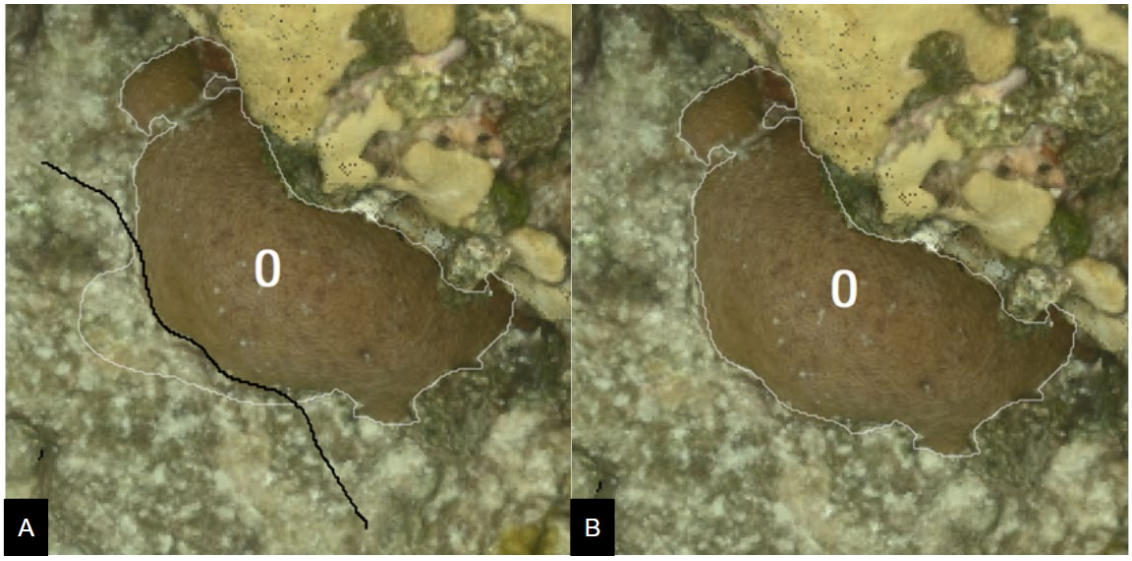


Figure 134. (A) Segmentation to remove an area (black line) and (B) the result after pressing Spacebar.

4. Create a *convex* curve or segment along the edges of the coral colony's segmentation to *add* parts to the segmentation (Figure 135A), and press the Spacebar to finish (Figure 135B).

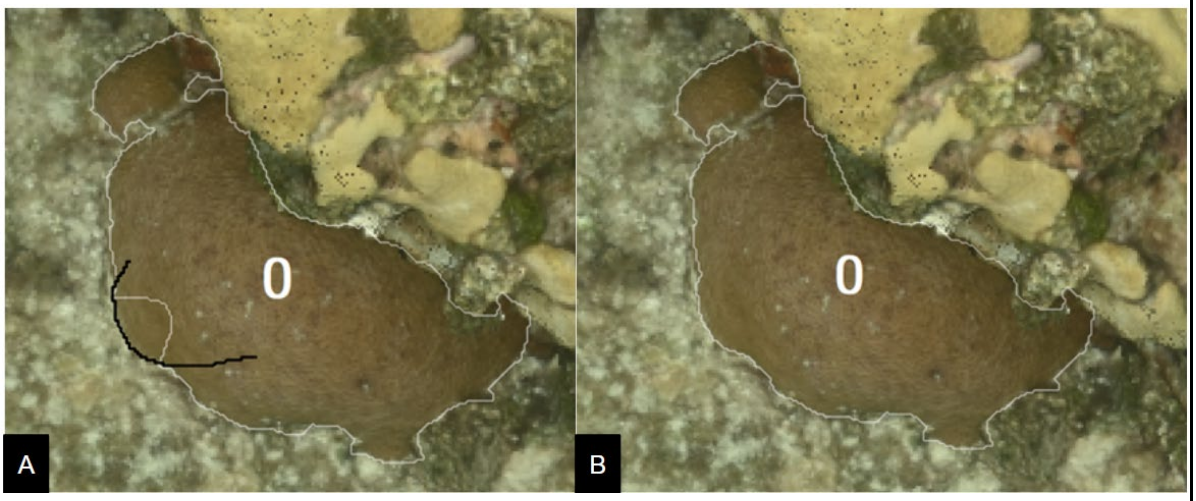


Figure 135. (A) Segmentation to add an area (black line) and (B) the result after pressing Spacebar.

Cut Segmentation

Used for scenarios when an ROI should be divided into multiple ROIs rather than one.

1. Select a previously segmented coral colony (border will be white).
2. Left-click + drag to draw a line to separate the segmentation into two (or more) parts (Figure 136A).
3. Press Spacebar to finish (Figure 136B). The segmentation will be separated into multiple ROIs and will be assigned separate ID numbers.

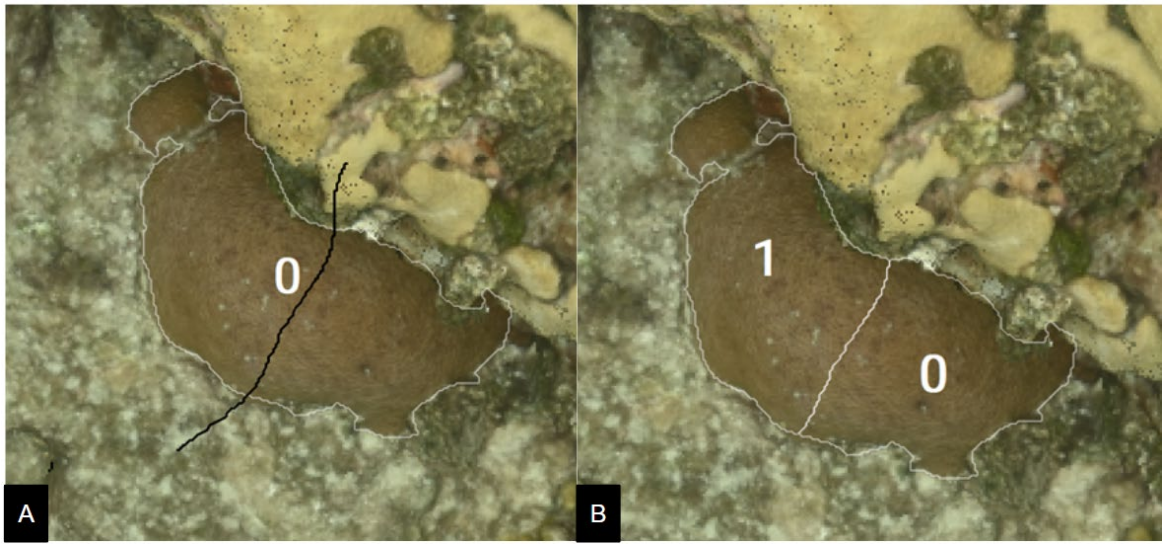


Figure 136. (A) Segmentation to cut one coral colony into two (black line) and (B) the result after pressing Spacebar.

F2. Other Tools in Detail

Four Clicks Segmentation

Effective semi-automatic segmentation tool.

1. Zoom in on the coral colony as far as possible but with its entirety in view.
2. With the tool selected, a white cross will appear.
3. Shift + left-click at the four outermost edges of the coral colony (Figure 137). A red X will appear after each click.

Figure 137. Using the cross to designate four clicks.

4. After the fourth click, the segmentation will automatically finish, a white segmentation will appear, and the coral colony will be assigned an ID number. It may be necessary to use the Edit Border tool to improve the segmentation (Figure 138).

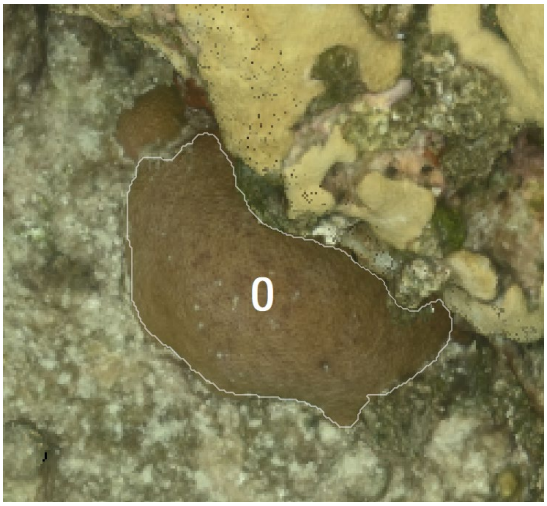


Figure 138. Example of a finished segmentation.

Assign Class

Assign a taxonomic class label to each ROI.

1. With the tool selected, select a desired label from the class list in the Labels Pane.
2. Double-click on a segmented coral colony to add the class label annotation. The segmented coral colony will be filled with the color corresponding to the selected class from the Labels pane (Figure 139).

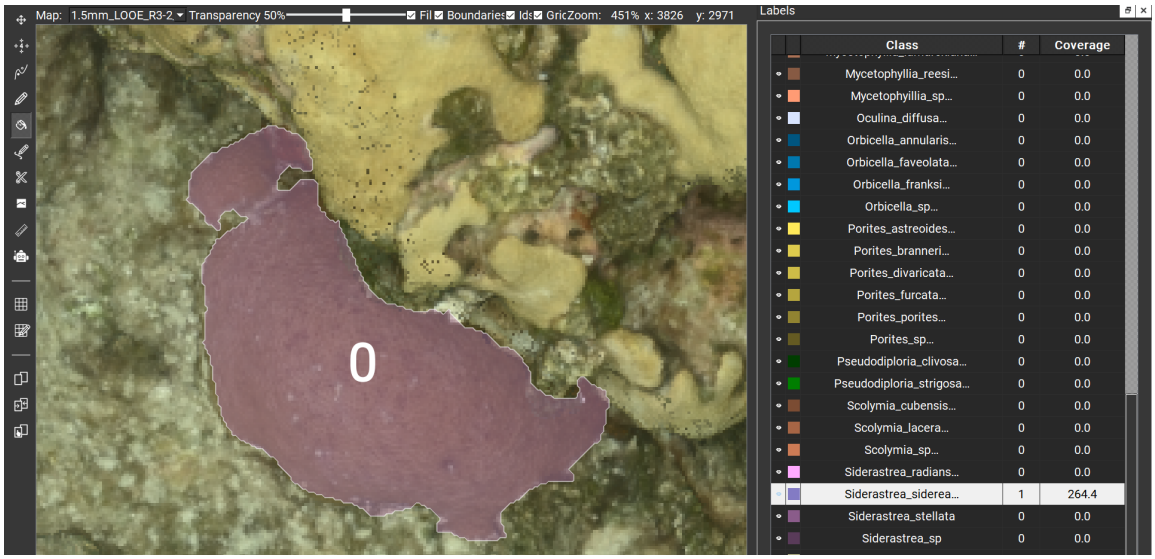


Figure 139. Example of annotating or assigning a label to a coral colony.

2. Preparation for TagLab Workflow

Data should generally be separated by maps (.tif files), TagLab projects (.json files), and exported data (can have various formats, e.g., .csv and .tif) (See *Appendix III.C.* for M:IR-specific data download and organization standards). A labels dictionary is uploaded into the project and is used for project-specific annotation needs. During project setup, the TIF files, separated by time points as maps, are uploaded into TagLab to create a new TagLab project. TagLab projects are saved as .json files and are named after the study site (e.g., M:IR follows the naming convention: Site_Plot-Subplot). When the data generation is complete in TagLab, data can be exported as .png, .csv, and .tif files.

A. Set Up a Project

A1. Launch TagLab

1. Launch TagLab from the Command Prompt (*1B1. Launch TagLab*).

A2. Import or Add a Dictionary with Project-Specific Labels

1. In the top of the TagLab window, click `Project`, and select `Labels Dictionary Editor` from the drop-down menu.
2. A new window will appear (Figure 140).

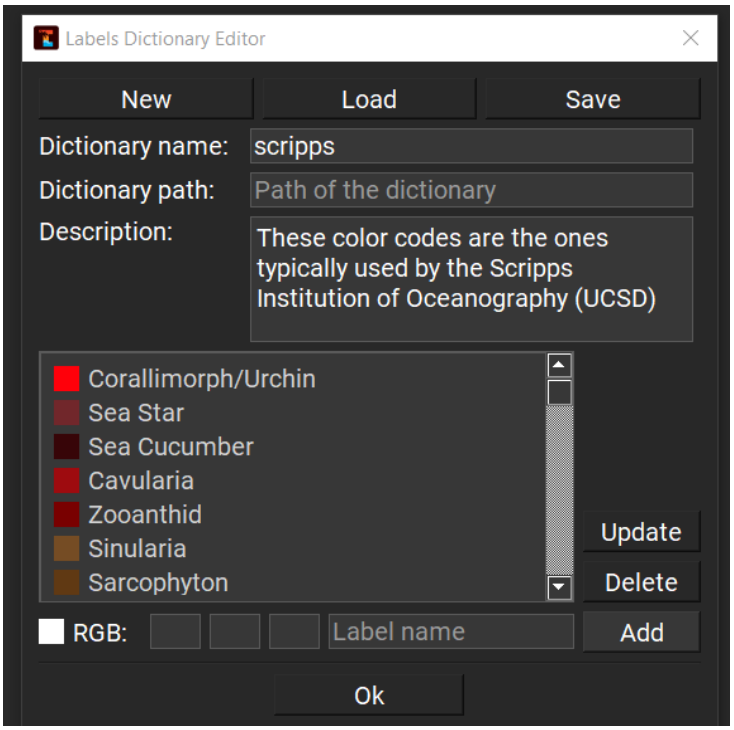


Figure 140. Scripps is the default dictionary, which needs to be changed to project-specific labels.

3. If using a pre-existing labels or dictionary, e.g., M:IR Project:
    - Click `Load` in the Labels Dictionary Editor window. Navigate to the TagLab project folder (or where the pre-existing labels file lives), and locate the .json file with the project-specific labels (e.g., MIR_Labels_MOST_RECENT_DATE). Select this file, and click `Open`.
    - A second window will appear, click `Replace` (Figure 141) and then `Ok` under the Labels Dictionary Editor window (Figure 142A). The labels will now appear in the top-right corner of the TagLab window under the Labels pane (as shown by the pink arrow in Figure 142B).

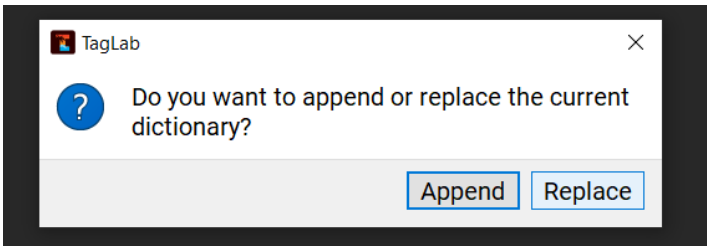


Figure 141. Example of prompt when replacing Labels Dictionary.

4. If not using a pre-existing labels dictionary, it will be necessary to create one:
    - In the Labels Dictionary Editor window, click `new`, then enter the fields as specified by the project (e.g., Dictionary name, description, etc.). Add new labels to the dictionary as specified below.
5. To add a new label to a pre-existing or new dictionary:
    - In the Labels Dictionary Editor window, click the white box next to `RGB`. A new window will appear with colors and settings. Select the desired color, then click `Ok`. Return to the Labels Dictionary Editor window, write the desired label name in the empty field `Label name`, and select `Add`.
    - When finished, press `Save`. The dictionary will be saved as a .json file and can be uploaded into subsequent/new projects). The updated labels will appear in the top-right corner of the TagLab window under the Labels pane (as shown by the pink arrow in Figure 142B).

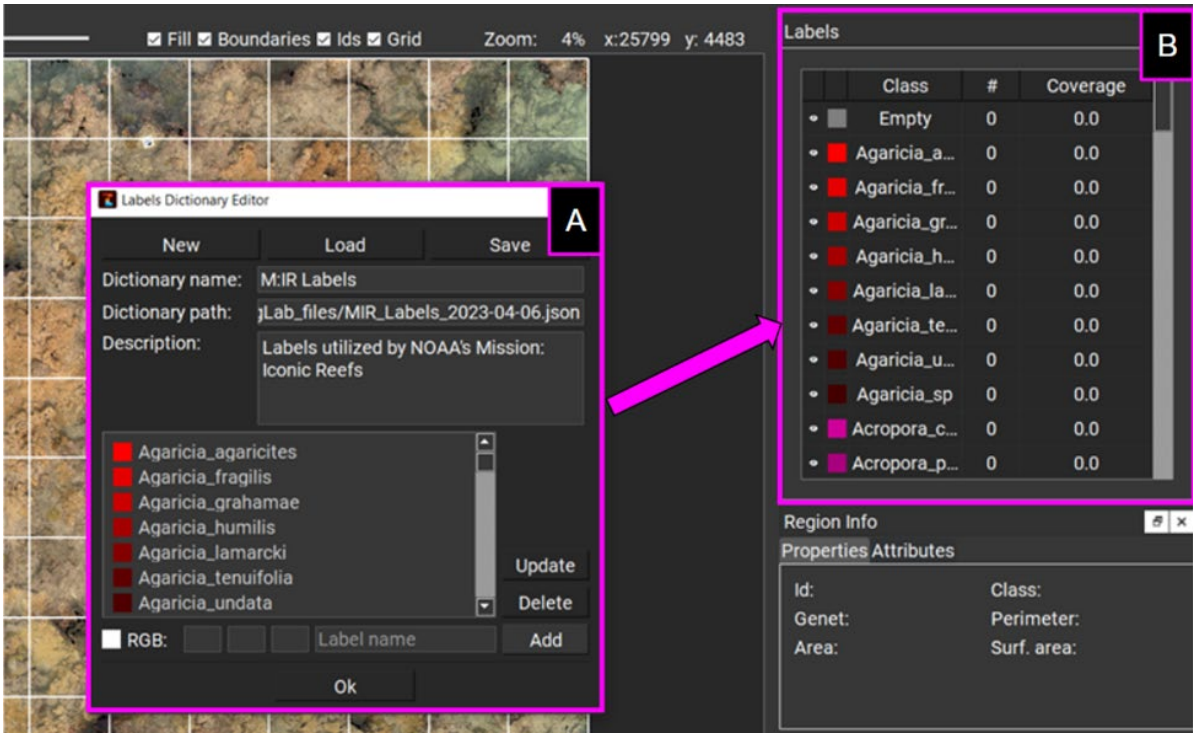


Figure 142. (A) Labels Dictionary Editor window used to add or modify a labels dictionary and (B) location of project-specific labels when added to a TagLab project.

A3. Add a New Map to TagLab

1. At the top of the TagLab window, click `Project` > Add `new map`. A Map Settings window will appear (Figure 143).

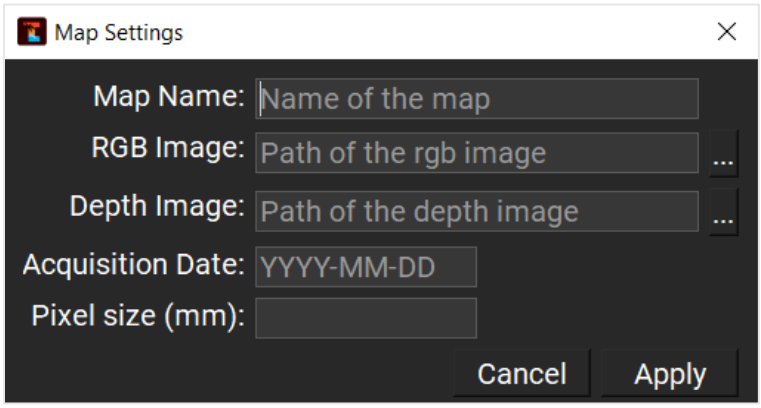


Figure 143. Example of prompt when adding a new map.

2. Enter each item as follows.
    A. `Map name`**:** Use the project-specific naming convention of the model/layer being worked with. (e.g., M:IR uses Site_Plot_Timepoint NFH_CB-1_2022-06-10).
    B. `RGB Ie`: Click the three dots (`...`) to search for the TIF file that corresponds to the model/layer being worked with.
    C. `Depth Image`: Leave blank.
    D. `Acquisition Date`: Enter the date the imagery was acquired. M:IR-specific note: use the date at the end of the map name (e.g., for NFH_CB-1_2022-06-10, enter 2022-06-10).
    E. `Pixel size (mm)`: Enter the spatial extent of a single pixel (i.e., ground sampling distance) as specified during orthoprojection export from Viscore (or Metashape, etc.; *Section I. Agisoft Metashape* and *Section II. Viscore*). For the M:IR project, maps are exported at a pixel resolution of 0.5 unless otherwise specified.
3. When finished, click `Apply`.
4. The map will now show up in the Map drop-down menu at the top of the TagLab window.

A4. Add a New Grid

1. Locate and click grid icon  in the Tools pane.
2. A new window will appear. Enter the items as shown in Figure 144:

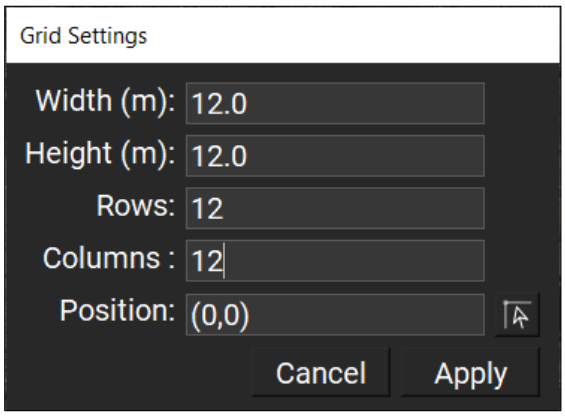


Figure 144. Correct dimensions for grid placement.

3. A 12 x 12m will be generated, with a one cell (each 1-m^2) buffer around the core study area where percent cover was also estimated (*Section II. Viscore*). The grid should take up the entire map if the orthoprojection was exported with the correct resolution in Viscore (Figure 145).

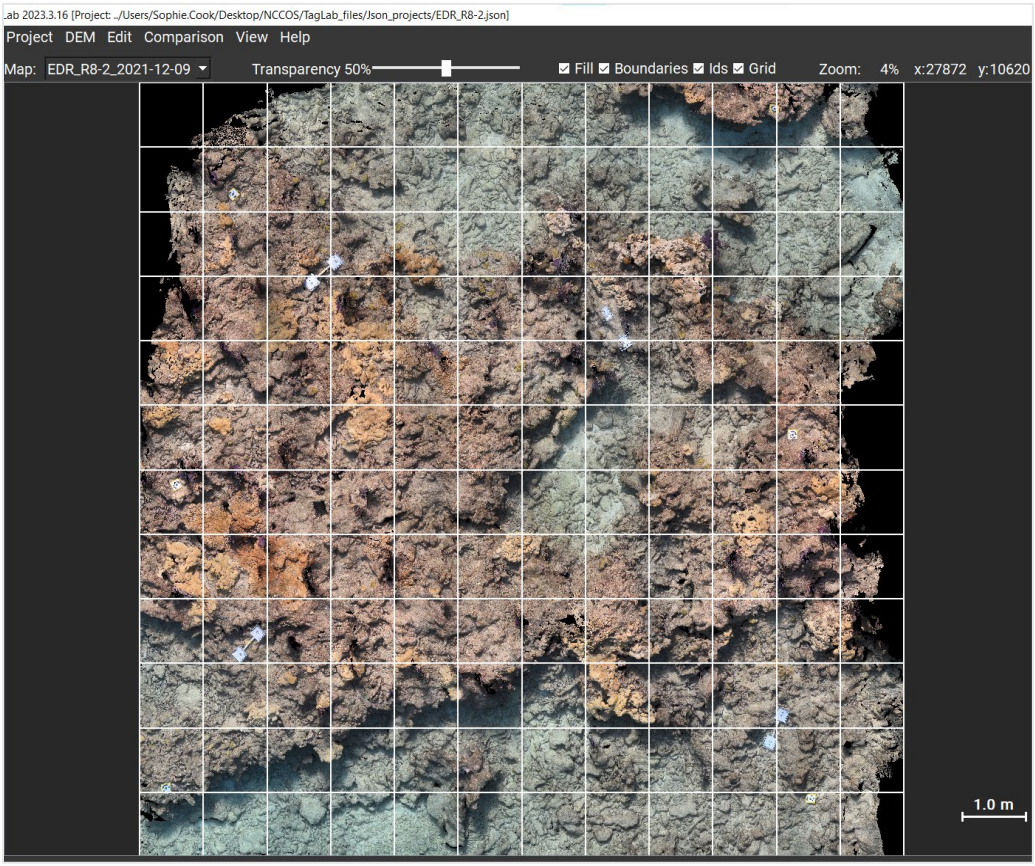


Figure 145. Example of correct grid placement. Note how the grid encompasses the entire map.

4. Trace all coral colonies inside the inner 10 × 10 m grid (Figure 146).

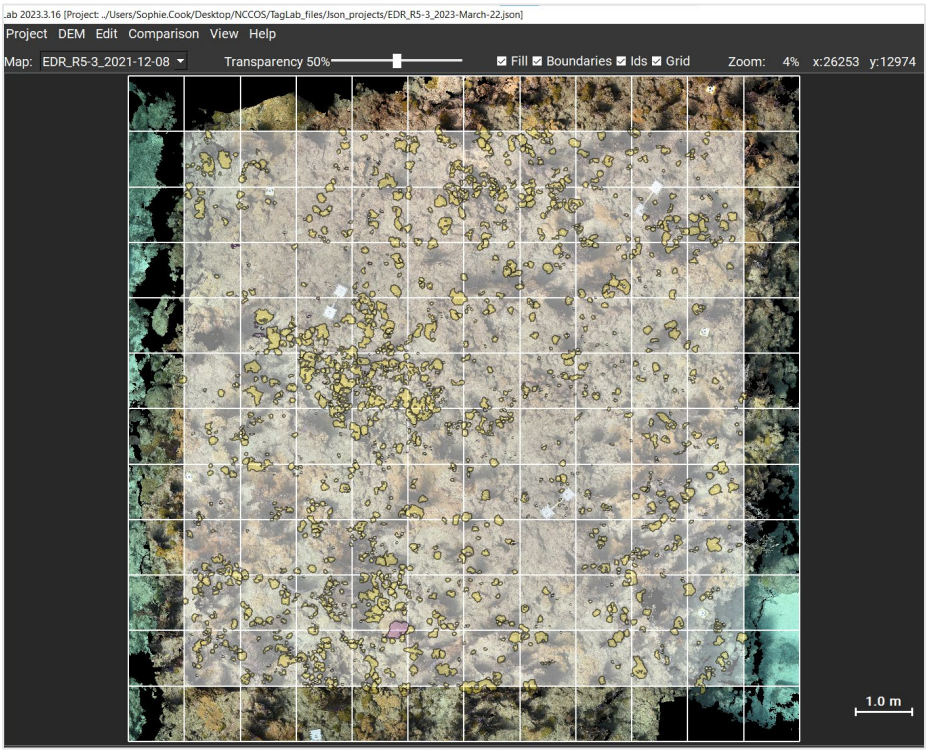


Figure 146. Example of the grid cells to be traced and a finished map (10 × 10 m) with a 1-m buffer for reference.

A5. Save Project

1. Before moving forward with tracing, click `File` at the top of the window, and select `Save As`. Name the project to match the project's predetermined naming standards (e.g., M:IR uses Site_Plot-Subplot).

3. ROI Annotation, Segmentation, and Matching

The workflow outlined below incorporates the use of both TagLab and Viscore. TagLab is used to annotate and segment ROIs in the orthoprojection or map created from the 3D model in Viscore, while the raw imagery associated with the 3D model is referenced in Viscore iView throughout the annotation and segmentation process. Raw imagery is utilized at every step of segmentation and annotation to ensure 1- *annotations are correct as raw imagery provides the most accurate view(s) for taxonomic identification,* 2- *the borders of the segmentations are as accurate as possible, with any dead or epiphytized portions removed,* and 3- *all corals that exist within each grid cell have been traced.*

As additional time points are added, the annotation and segmentation process is replicated for each available map. When two or more time series maps have been completed, coral colonies can be tracked

through time using the TagLab matching feature. When ROI matches and fates (e.g., growth, survivorship, and recruitment) have been reviewed, the data are exported.

A. Annotate and Segment ROIs

A1. General Guidelines for Tracing

- Raw imagery should be referenced in Viscore iView and deferred to in every single step of annotation and segmentation of ROIs.
- Utilize the Grid tool to create a designated study area and to keep track of tracing progress.
- Bleached or diseased portions should remain within segmentations as the coral tissue is still considered alive.
- Portions of coral colonies with turf or macroalgae should be excluded from segmentations as these regions of the colony are considered dead.
- Trace all visible hard corals greater than 3 cm in diameter. Corals smaller than this are difficult to size and accurately identify; and alternate approaches to quantify recruitment should be used instead (not included in this SOP).
- If a coral colony is covered by another organism (e.g., a sea fan blocks the view of the coral) or its entirety is not completely within view in the map, select the coral colony and navigate to the Region Info pane. Under the Attributes tab, write a note that the coral colony is occluded.
- If a sandy patch is larger than 1 m^2 (the size of one grid cell), trace the sandy bottom, and annotate it as softbottom from the labels list.
- When finished with a map, double check that no corals remain labeled as Empty and are properly annotated.

  It is important to be as precise as possible when tracing. However, extensive fine tuning of colonies can be extremely time consuming and often results in miniscule changes to total coral colony area (< 1%). Users are encouraged to experiment at the outset of a project to determine the level of detail appropriate to the resolution of their maps, and the ecological questions of interest.

A2. Open TagLab Project

If using a TagLab project that has already been prepared, continue with the section below. To set up a project from scratch, return to *2A. Set Up a Project* before completing this section.

1. Launch TagLab in a new window.
2. With TagLab open, click `File` and then `Open Project` to navigate to the saved project (which should be saved as a .json file in the Project Files folder. Alternatively, if the project has been recently opened, it will be shown under the file drop-down menu. Select the relevant project to open.
   - If TIF files have moved from their original location after the initial setup of a TagLab project, TagLab will ask for the TIFs associated with each time point or map. It is important to follow the prompts and to upload the time points in order as prompted by TagLab.

A3. View Raw Imagery in Viscore iView

Raw imagery should be utilized throughout the entire process of segmentation and annotation in TagLab. Raw images linked to the 3D model in Viscore are viewed in a separate browser window called iView (*Section II. Viscore*). These raw images are then compared to the ROIs in the 2D maps in TagLab to create accurate segmentations and annotations.

1. Open the TagLab project on one monitor and open the corresponding model in Viscore on a second monitor (Figure 147).
2. Under the HUD in Viscore, turn `ortho` on. Under the Ortho menu, turn `grid` and `orient` on.
3. Turn `cams` on, and ensure raw images are linked (*Section II. Viscore*).
4. Orient the model in Viscore to match the 2D map orientation in TagLab. Find and match the location of the first grid cell in TagLab (Figure 147A) to the location of the model in Viscore (Figure 147B). Place a temporary marker in the grid cell in Viscore (Alt + center-click).

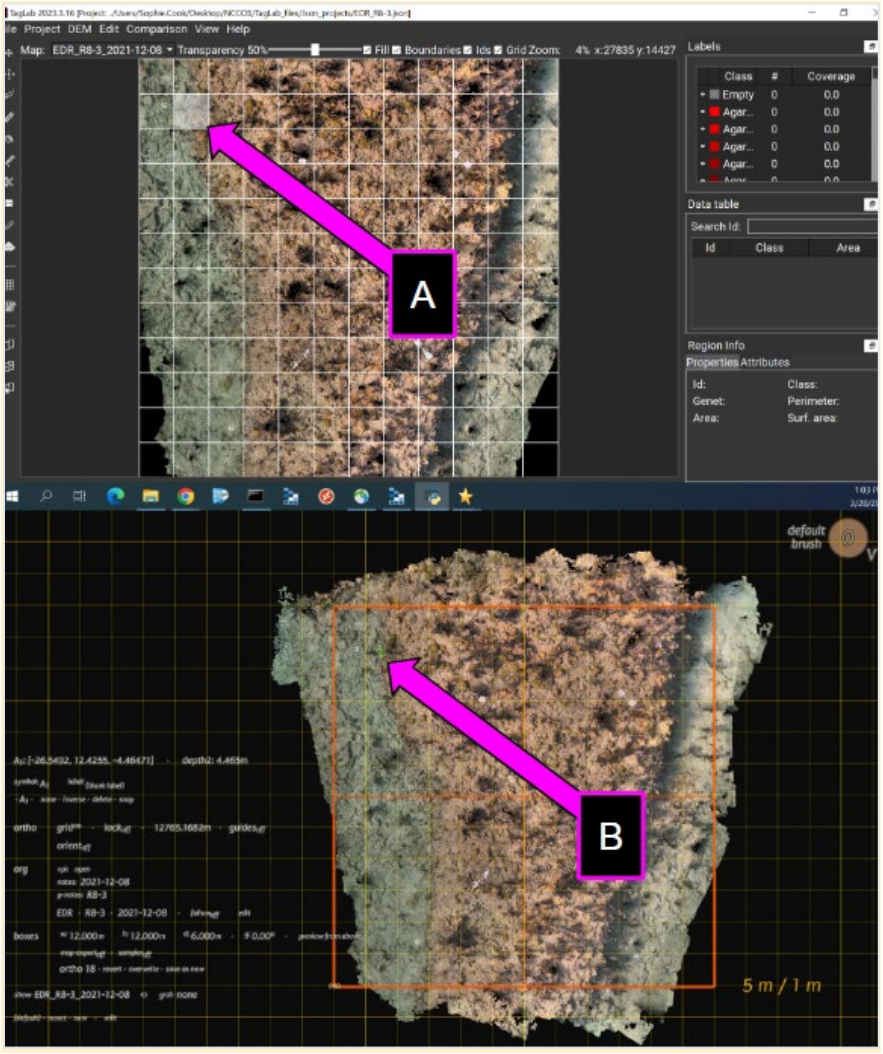


Figure 147. Example of split screen with (A) TagLab and (B) Viscore open on separate monitors. Pink arrows denote the same location shown in both software.

5. Go to the following link in Google Chrome to access iView, and view the raw images associated with the dropped point on the model in Viscore: http://localhost:9090/jsd/pq.xhtml (Figure 148A–B).
6. The raw imagery displayed in iView is used as reference to create annotations and segmentations in TagLab (Figure 149A–B).
7. To navigate through the photos and change the location of the pink point in the image shown in iView, the controls are as follows:
    - Double-clicking above, below, left, or right of the point in the image or the image boundaries will move in that direction on the model and bring up the image associated with that location.
    - Double-clicking on any object in the image (e.g., a coral) will bring up all images associated with that spot.
    - Tapping the Space bar will flip to the next image.
    - For more information regarding the display of imagery with iView see *Section II. Viscore*.

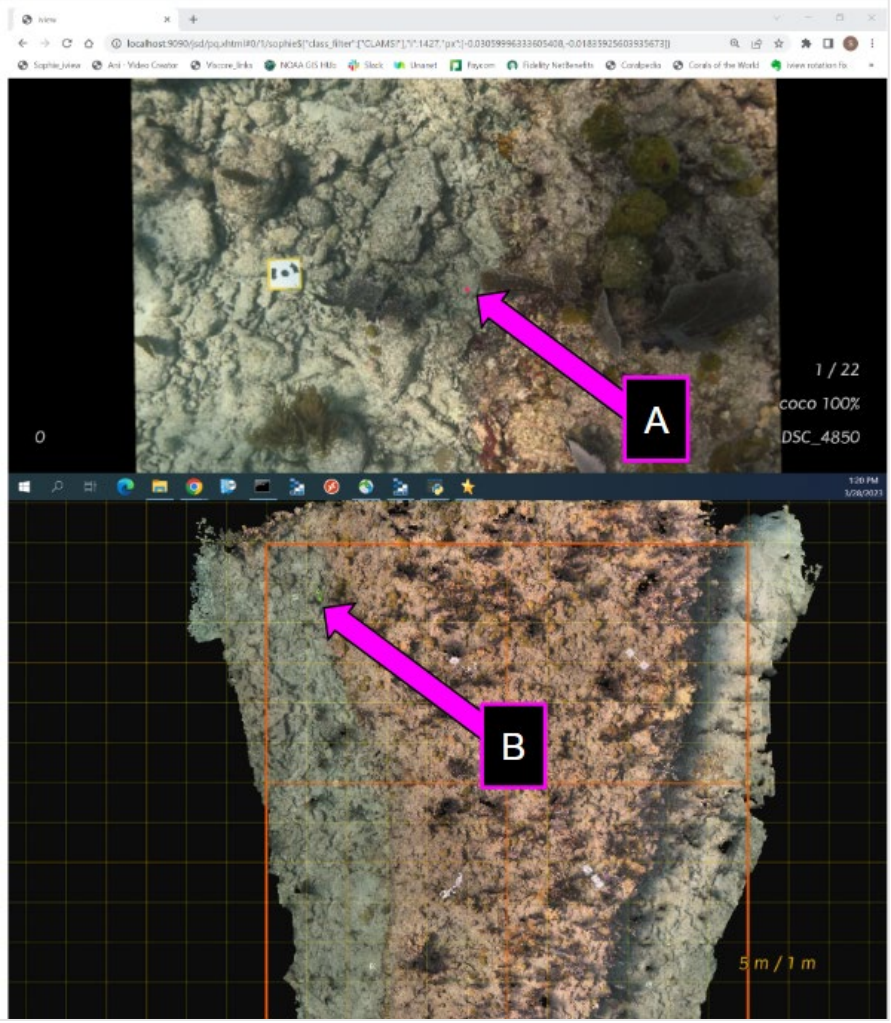


Figure 148. Example of split screen showing (A) iView and raw images on one monitor and (B) Viscore open on a separate monitor. Pink arrows denote the same location in both the raw image in iView and the model in Viscore.

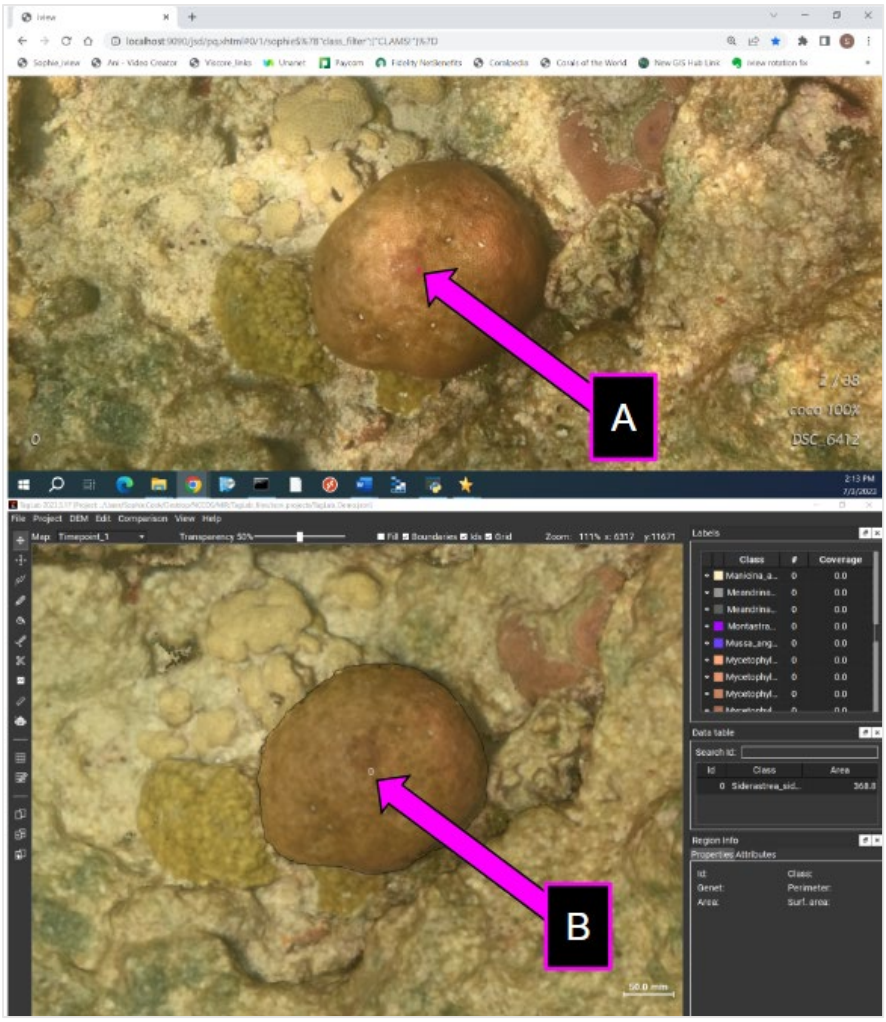


Figure 149. Example of split screen with (A) iView and (B) TagLab open on separate monitors. The pink point on the raw image in iView corresponds to the same location in the traced ROI in TagLab.

A4. Annotate and Segment ROIs in the Designated Study Area

1. Refer to *1F. Segmentation Tools in Detail* for additional information on the use of segmentation tools.
2. In order to constrain efforts and maintain searching efficiency, restrict the segmentation and annotation process to one 1-m^2 cell at a time.
3. Within the current 1-m^2 cell, segment and annotate every hard coral species before progressing to the next cell in a column or row, including any portion of a colony that extends into adjacent cells.
    - *Important*: Ensure that not only the orthoprojection (i.e., map) is being used to segment and annotate ROIs but also the raw imagery associated with the model in Viscore iView.
    - It is recommended to use the Positive/Negative Clicks tool to segment all colonies with regular or semi-regular boundaries, while the Manual tool is preferred for corals with complex borders, or to edit complex portions of colonies. For colonies with complex boundaries, the Positive/Negative Clicks tool will often work, but users are cautioned to

not try to force the tool if it does not produce a close first segmentation, as it will often be faster to manually complete the segmentation rather than spending time adding or removing areas that were not initially recognized by the tool.

- Be sure to provide taxonomic IDs to each segmented ROI using annotations from the project's labels dictionary (e.g., M:IR labels dictionary) listed in the Labels pane.

4. When a cell is finished, turn on the Active/Deactivate Grid Operations tool  . Right-click on the finished cell, and select `mark cell as complete`. This will help keep track of which cells have been completed and will mark which cell to return to the next time the TagLab project is opened (i.e., the next cell in the row or column that is not filled).
5. Continue until all 100 cells in the inner 10 × 10 m grid have been completed (Figure 150).

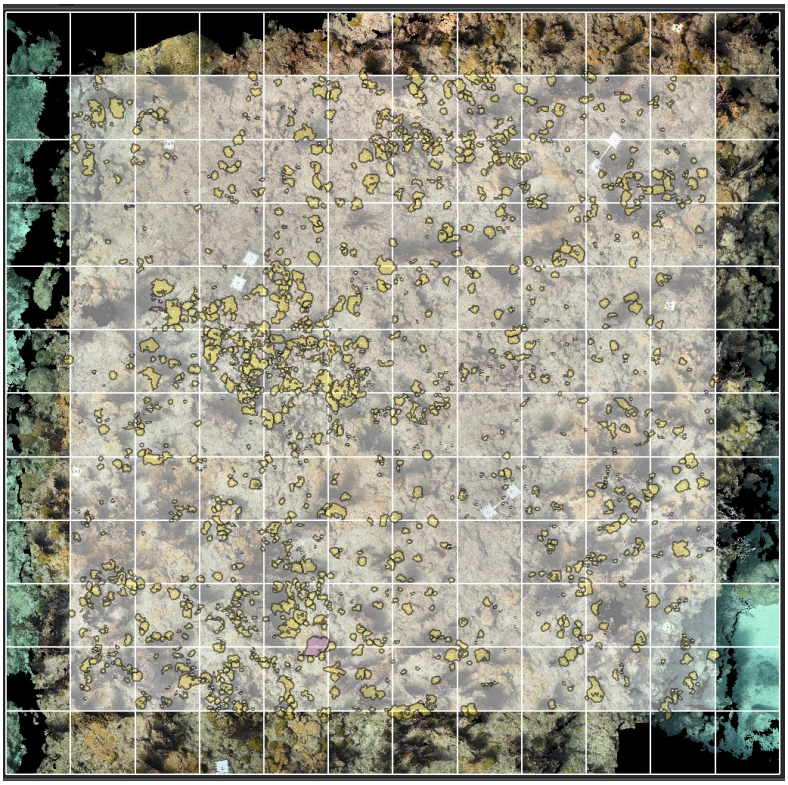


Figure 150. Example of a finished 100-m^2 plot in TagLab.

6. Upon completion of the project, ensure that no segmented corals remain labeled as `Empty`. Locate the Data Table pane on the right side of the TagLab window. Click on the column heading `Class` to sort the labels alphabetically. Scroll down to see if `Empty` is on the list (Figure 151).

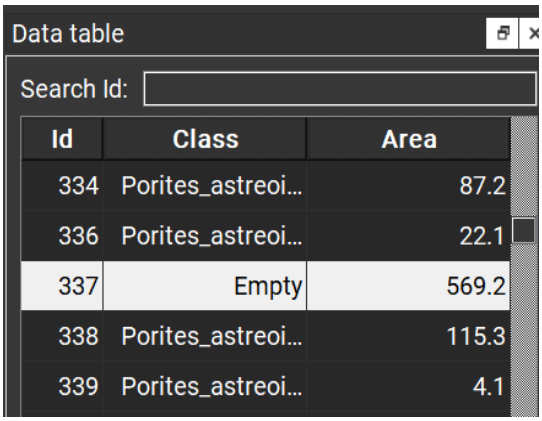


Figure 151. Example of Empty label from labels list.

7. If there are any IDs with Empty labels (Figure 151), the ROIs labeled as `Empty` will need to be annotated with the correct label. Zoom in close to the map—anywhere on the map will do, but be sure to zoom in close enough to see an ROI up close. Then, under the Data Table pane, double-click on the ID labeled `Empty` to automatically pan to the location of the unlabeled coral colony (Figure 152).

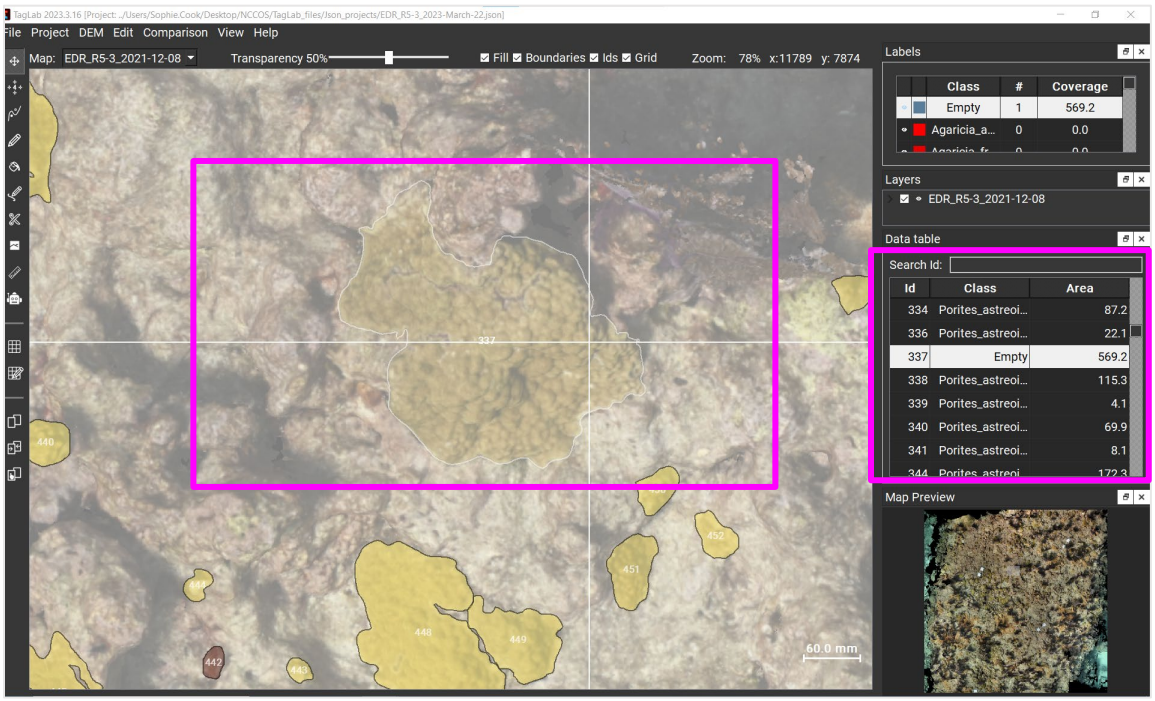


Figure 152. Example of using Empty label from Labels pane as a tool for locating missed annotations.

8. Change the annotation as needed by selecting a label from the Labels pane, ensuring that raw imagery is used to make an accurate ID.
9. Save the project with the current date (e.g., Site_Plot-Subplot_Year), and back up data as needed (For M:IR users, back up data to the W drive).

B. Add and Segment Subsequent Time Points

Before maps from subsequent time points are uploaded into TagLab, the original model from which the orthoprojection was created will need to be coregistered to the initial time point. While TagLab has coregistration tools, those instructions are not provided in this SOP as this workflow uses maps that were previously coregistered in Viscore (*Section II. Viscore*).

1. At the top of the TagLab window, under the Project menu, select `Add New Map`.
2. Follow the instructions as outlined in *2A3. Add a New Map to TagLab*, ensuring that the correct subsequent time point is added to the project.
3. When finished, the subsequent time points/maps will appear in the Map drop-down menu.
4. Change to the new year in the Map drop-down menu. Add a new 12 × 12 m grid, and segment the study area as outlined previously in this guide.

C. Match Coral Colonies

When two successive time points have been fully annotated, colonies can be matched. The Compute Automatic Matches tool automatically matches colonies that overlap by at least 50%. Afterward, any missing matches can be manually matched, and any errors from the automatic matching can be corrected. Additionally, TagLab allows genet tracking, and during manual matching any ramets belonging to the same genet can be identified and provided a genet ID.

1. Under the Tools pane, enable split screen mode by clicking on the Split Screen tool  .
2. Under the Map drop-down menu, ensure the earlier time point/map is displayed in the left drop-down, with the subsequent time point in the right drop-down.
3. Under the Tools pane, click the Compute Automatic Matches tool  .
4. A Comparison Table will appear on the right side of the TagLab window, with each row listing the matched ROIs IDs, the genet ID, the area for each ROI (if present in both time points), and the fates under the `Action` and `Split/Fuse` columns. These data in the Comparison Table are used when matches and fates are reviewed in the next section.
5. It is very important to not rerun the Compute Automatic Matches tool after the initial computation as it will overwrite any subsequent editing.

4. QAQC: Review Matches and Fates

After matching has been completed, it is important to perform a QAQC check to ensure that no colonies were missed or incorrectly matched. First, existing matches are visually checked to ensure that matches have been assigned to the correct ROIs and to check for any colonies that may have been accidentally missed during initial segmentation (Figure 153). Second, the fates of corals (i.e., if a coral died or was born) must be confirmed for each time point using the Comparison Table in TagLab (Figure 154) as a final QAQC process. Detailed fate tracking may not be necessary depending on the project objective. Otherwise, when using the Automatic Matching tool, data must be reviewed.

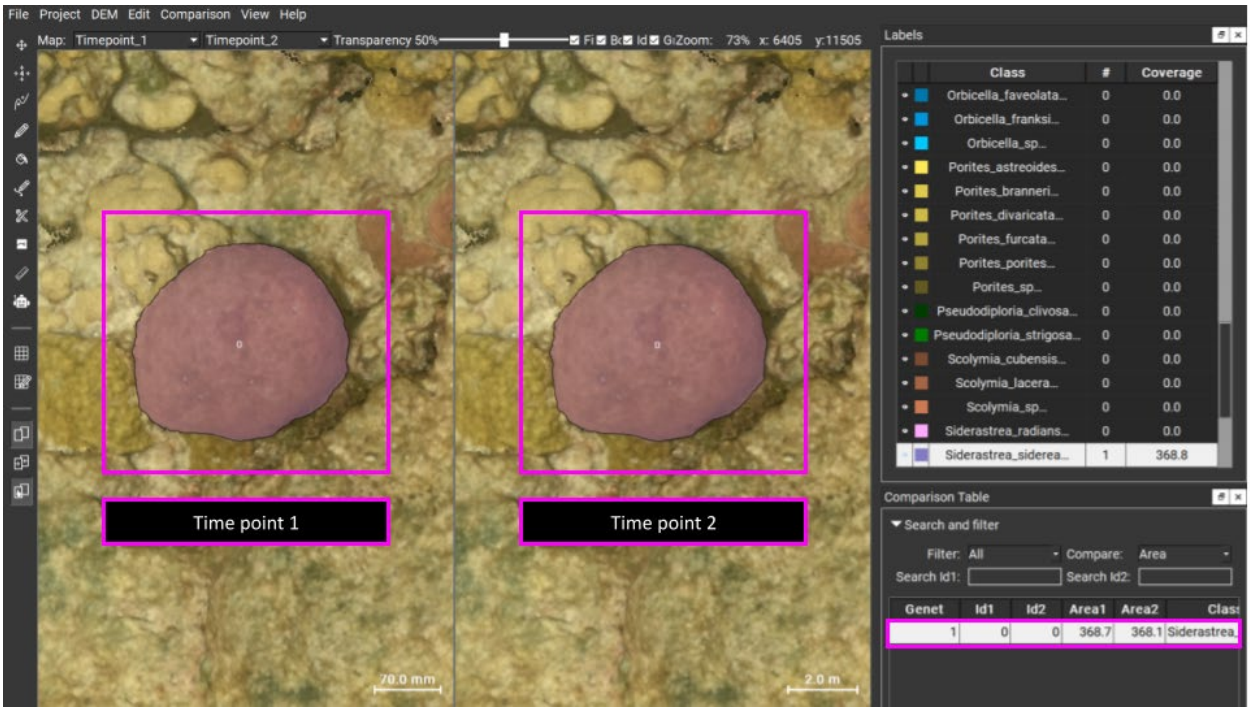


Figure 153. Example of tracking two ROIs through time and where they are listed in the Comparison Table.

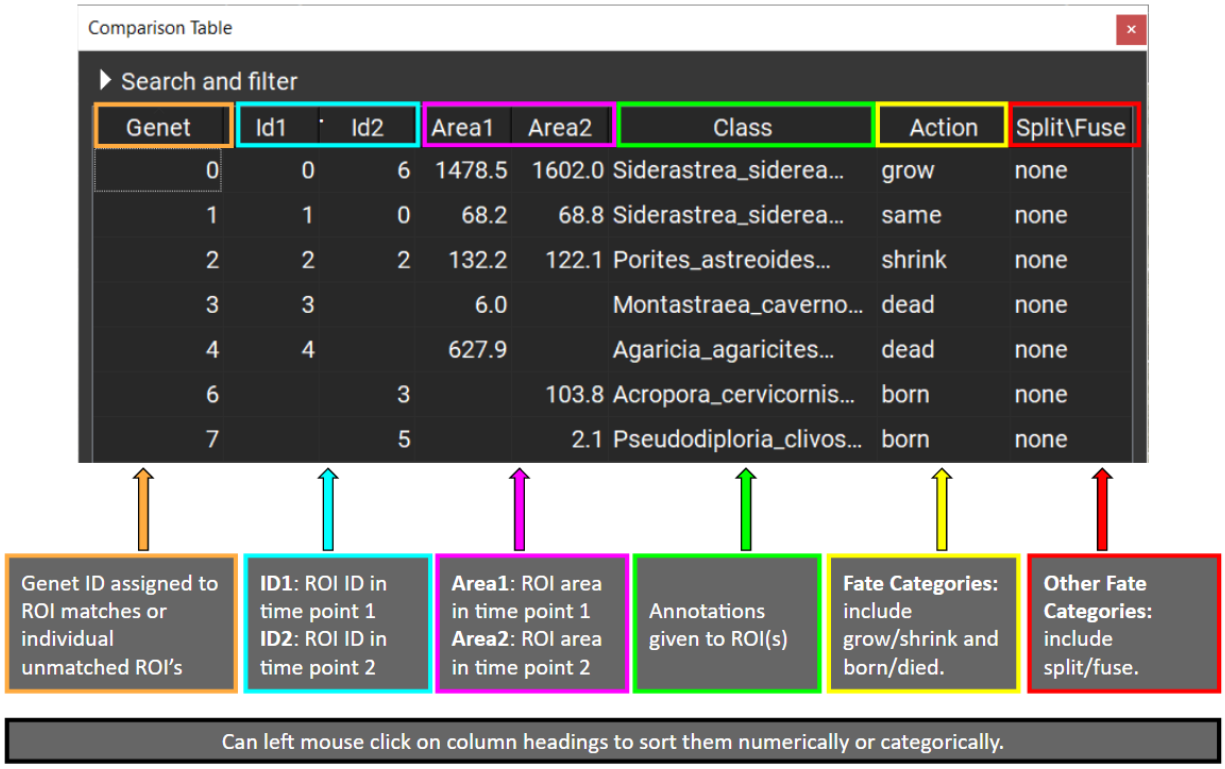


Figure 154. Explanation of columns in the Comparison Table used for matching and fate tracking.

A. Review ROI Matches

The algorithm utilized by TagLab searches for overlap between ROIs from two time points to create a match. In cases where ROIs or segmented coral colonies experience partial mortality or undergo fission or fusion, false automatic matches can be made if there is a change in overlap between the two ROIs. For this reason, automatic matches should be carefully reviewed.

1. Under the Tools pane, click on the Split Screen tool  . In the Map drop-down menu ensure the earlier time point/map is on the left with the subsequent time point/map on the right.
2. Under the Tools pane, click on the Add Manual Matches tool  to enable the manual matching feature.
    - *Important*: Comments added to the `Notes` field in the `Attributes` tab can only be saved in editing mode. To add a note, first turn on `Add Manual Matches`, add the note, and then turn off `Add Manual Matches` to resume reviewing matches.
3. Start visually inspecting matches by moving through the grid one cell at a time to ensure that all coral colonies within each cell have been traced and properly matched.
    A. The corals have been matched together if: double-clicking on a coral colony in the first time point automatically selects the same coral in the subsequent time point. When a colony has been selected, the perimeter of the segmentation will turn white, and its row will be automatically selected in the `Comparison Table` on the right.
    B. If two corals have not been matched but should be matched:
        - Select both coral colonies to be matched (hold Shift + left-click on each segmentation).
        - Press Spacebar.
        - In the `Comparison Table` on the right side, the two IDs will be matched together.
    C. If a coral was missed/not segmented in one of the time points:
        - Use the raw imagery to trace and annotate the coral. Then manually match the two ROIs as outlined above.
    B. If a coral colony experienced fission or fusion in one of the time points, ramets can be tracked with a genet ID:
        - Select the ramets and the genet from each of the time points (hold Shift + left-click on each segmentation).
        - Press Spacebar.
        - Check in the `Comparison Table` that all of the matched ROIs have the same genet ID.

B. Track Alternate ROI Fates

When two or more corals (i.e., ROIs) are matched through time, TagLab calculates and assigns a fate to the ROI under the Action column in the Attributes Table. TagLab considers a coral to be born if there is no matching coral in the previous time point, and considers a coral to be dead if there is no matching coral in the subsequent time point. Not having a match in the previous or subsequent time point does not necessarily mean the coral was born or it died, as the corals may have moved into or out of the plot area in the time interval between image collections due to variable environmental conditions such as storms. For this reason, born/dead assignments should be confirmed; otherwise, an alternate fate should be recorded for each ROI.

B1. List of Alternate Coral Fates to Note

When reviewing the born/dead assignment, the following categories of alternate coral fates should be noted in the Attributes tab of the Region Info table:

- **Emigrated**: corals that were present in the first time point but dislodged or otherwise removed from the substrate and unable to be identified in the second time point. During analysis, these colonies should be treated differently from colonies that can are confirmed to have died in place.
- **Immigrated**: corals present in the second time point that were not present in the first time point. These are largely coral fragments that have rolled or are otherwise displaced from outside the plot into a location where they did not initially recruit. Such corals are generally larger than juvenile corals.
- **Moved**: corals that can be visually confirmed to have moved from one location in the study area to another. This can be difficult to determine sometimes, but using coral shape, size, and distinguishing features can help.
- **Other potential notes**: add any other relevant information regarding the fate or analysis of the ROI. For example, there may be evidence of the presence of a coral in both time points; but there is a hole in the model in one time point, and the coral cannot be accurately traced—this should be noted.

B2. Track Alternate Fates

1. Under the Tools pane, click on the Split Screen tool  to enable split screen mode.
2. Use the Map drop-down menu to display the first time point on the left, and the subsequent time point on the right.
3. Turn `Add Manual Matches` off.
    - *Important*: As noted above, `Add Manual Matches` must be turned off to add and save comments added to the `Notes` field in the `Attributes` tab.

4. To identify corals that immigrated into the study area between the time points, sort column `Area1` from smallest to largest (click on column heading to switch) in the `Comparison Table`. The first rows of the table will show any corals that are in time point 2 and not matched to a coral in time point 1 (i.e., no measurement will be listed under column `Area1`).
    - Double-click each row with an unmatched coral and confirm the fate of the coral based on the specified project goals.
    - To add a note for a coral under the `Attributes` tab (e.g., to confirm if a coral immigrated or moved), double-click the coral, and then type the alternate fate in the `Notes` field. If this table is not displayed, go to the View drop-down menu at the top of the TagLab window, then select `Region Info`.
5. To identify corals that emigrated outside of the study area between the time points, sort column `Area2` from smallest to largest (click on column heading to switch) in the `Comparison Table`. The first rows of the table will show any corals that are in time point 1 and not matched to a coral in time point 2 (i.e., no measurement will be listed under column `Area2`).
    - Double-click each row with an unmatched coral and confirm the fate of the coral to the degree warranted by the project's goals.
    - To add a note for a coral under the `Attributes` tab (e.g., to confirm if a coral emigrated or moved), double click the coral, and then type the alternate fate in the `Notes` field. If this table is not displayed, go to the View drop-down menu, then select `Region Info`.
6. To track corals that moved from one cell location to another and are present in both time points (that did not immigrate nor emigrate), *temporarily* turn `Add Manual Matches` on, match the corals, then turn `Add Manual Matches` off**.**
    - To add a note for a coral under the `Attributes` tab (e.g., to confirm if a coral moved), double-click the coral, and then type the alternate fate in the `Notes` field. If this table is not displayed, go to the View drop-down menu, then select `Region Info`.

5. Data Export

A. General Data Export

1. In the top of the TagLab window, click on the File drop-down menu then `Export`.
2. Choose how the annotations should be exported (e.g., as a data table, GeoTiff, or labeled image) from the secondary menu.
3. For M:IR-specific instructions regarding data export, see *Appendix III.C.*

B. Data Export for Reviewed Matches

1. In the top pane of the TagLab window, click on the Comparison drop-down menu. Click `Compute Genets`. This step provides an ID to each coral (i.e., one ID number for two matched corals).
    A. `Export Matches`: exports data for every unmatched ROI and every matched ROI combination (i.e., if split/fuse or multiple ROIs are matched to multiple ROIs from one time point to the next).
        - Click on the Comparison drop-down menu. Select `Export Matches`.
    B. `Export Genets`: exports data for each genet of matched or unmatched ROIs. If there are multiple ROIs per time point per genet there will be multiple values in the cell.
        - Click on the Comparison drop-down menu. Select `Export Genet Data as CSV`. If there are multiple ROIs per time point per genet, there will be multiple values in the cell.

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Appendices

Appendix I. Computer Hardware Requirements

A. Metashape

Processing models in Metashape with image sets containing thousands of high-quality images requires significant computing power. Metashape takes advantage of GPU acceleration for various reconstruction steps and requires a large amount of memory with increasing numbers of images. Increasing the number of CPU cores and the quality and number of GPUs can significantly decrease processing time (Sandin et al., 2023). For a complete list of recommended specifications, refer to the official Metashape documentation. For image sets of this size, the current recommended minimum computer hardware includes:

- High-speed 10-Core CPU
- One or two high-end GPUs (e.g., NVIDIA xx70+ series)
- 64 GB RAM (128 GB RAM recommended)
- Solid state drive (SSD)

B. Viscore

- Windows Operating System (Required)
- At least 16 GB RAM (Recommended)
- SSD (Recommended)
- Dedicated graphics card (strongly recommended - NVIDIA or AMD)
- Viscore can be operated with integrated graphics chips (Intel); however, this will result in a reduction in performance or unexpected behavior in some features.
- A mouse with scroll wheel, dedicated center button, and thumb buttons (highly recommended; e.g., the mouse Logitech MxAnywhere 2S; Figure 155). Keystrokes and workarounds are provided where possible.
- Secondary monitor or desktop (recommended). In lieu of a second monitor, the multiple desktop function can also be used.

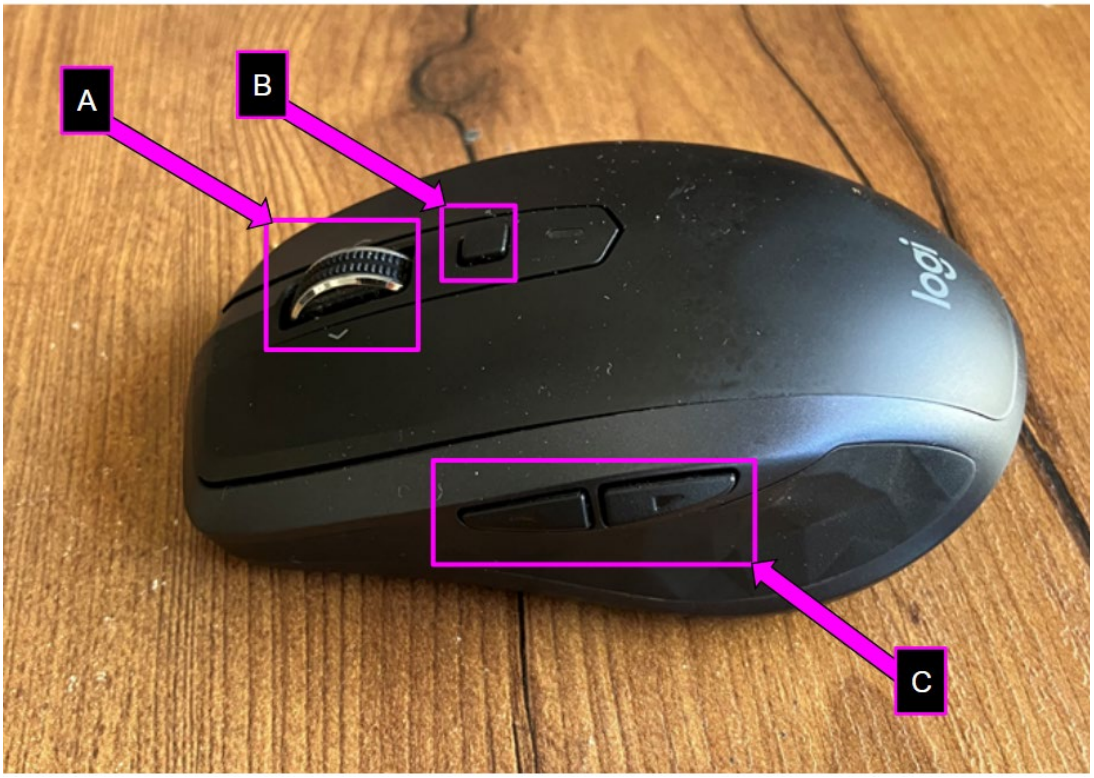

Figure 155. Example of mouse with gesture buttons. Logitech MxAnywhere 2S. (A) Mouse scroll wheel that can also be pushed left or right to quickly switch between desktop screens when programmed to do so. (B) Center button. (C) Upper and lower thumb buttons. Photo credit: Sophie Cook (CSS, Inc./NOAA NCCOS).

C. TagLab

TagLab runs on Linux, Windows, and MacOS. To run TagLab, the main requirement at the time of publication is 64-bit Python 3.7.x, 3.8.x or 3.9.x. For more information, please refer to TagLab's official website for recommendations.

- At the time of publication, GPU accelerated functions are not supported on MacOS or any machine that does not have a CUDA-enabled NVIDIA graphics card. To use CUDA, the NVIDIA CUDA Toolkit will need to be installed; currently, versions 9.2, 10.1, 10.2, 11.0, 11.1, 11.3, and 11.6 are supported. If the computer does not have an NVIDIA graphics card (or if MacOS is being used), the CPU will be used instead.
- Secondary desktop or monitor (recommended).

Appendix II. Troubleshooting

A. Metashape

Photos Are Undetected

When a Metashape project file and its associated folder archive are moved to a new location (e.g., from the working drive to a storage drive), the project file will lose the file path for the imagery used to create the model. Undetected photos will show an error that states `Preview not available` (Figure 156).

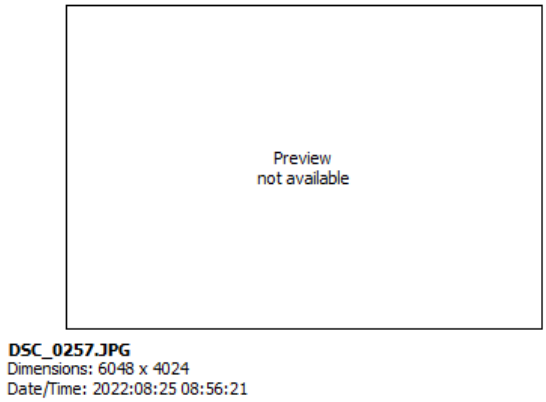

Figure 156. Undetected photos will receive an error indicating that the preview of the image is not available due to photo location.

1. Navigate to the Workspace pane, and click the drop-down arrow of the selected chunk.
2. Click the `Cameras` drop-down arrow, and right-click on a single camera (e.g., plot image; i.e., DSC_0257). Select `Change Path` from the context menu.
3. A new window will appear named Relocate Photos. Under `Apply to`, choose `All cameras`, and click `OK`.
4. A File Explorer window will appear. Navigate to the imagery folder associated with the photos (e.g., E:/Raw_Imagery/SOMB_R2-2_2022-08-25_JPEG), and double-click on the image folder. Click on the image file available, and click `Open`. Now all images associated with the plot have been relinked to the Metashape project.

Loop Script Error

When a .txt. file is created to process two or more plots at the same time (e.g., MIRMetashapeProcessing_PartI.py), it is important to remove quotation marks around the file paths and be sure there is no additional spacing between paths. It is also important to be sure that there is no spacing after the last file path copied into the .txt file. If there is a space after the last file path, a

processing error will appear in Metashape (Figure 157). This error means that Metashape is attempting to search for the next plot to process but cannot find it because there is a line with no text.

```
2023-04-03 17:50:08 export_path: Agisoft_Project_Data_Exports\
2023-04-03 17:50:08 Traceback (most recent call last):
2023-04-03 17:50:08   File "W:/Agisoft_Project_Data_Exports/MIRmetashapeprocessing_PartI-LOOP_v4.py", line
58, in <module>
2023-04-03 17:50:08     os.makedirs(export_path)
2023-04-03 17:50:08   File "C:\Program Files/Agisoft/Metashape Pro/python\lib\os.py", line 223, in makedirs
2023-04-03 17:50:08     mkdir(name, mode)
2023-04-03 17:50:08 PermissionError: [WinError 5] Access is denied: 'Agisoft_Project_Data_Exports\\'
2023-04-03 17:50:08 Error: [WinError 5] Access is denied: 'Agisoft_Project_Data_Exports\\'
```

Figure 157. Metashape error when .txt file for SPC generation of two or more plots has space after the last file path.

B. Viscore

Common Issues When Learning to Navigate Models in Viscore

I was using my mouse scroll wheel when my model disappeared.

- Scroll in the opposite direction until the model reappears. Or hold Alt + scroll to bring the model back into view.
- *Alternate*: Press `revert` next to `(default)` to bring the model back into view.

When I turned Ortho mode on, my model disappeared.

- Hold the Alt + scroll up on the mouse scroll wheel to increase the size of the red crosshatch until it encompasses the entire model.
- *Alternate:* Turn `orient` on under the Ortho menu, and the entire model will appear.

My model continues to spin even after I stopped moving it.

- Left-click once anywhere on the model to stop it from spinning.

Common Issues When Setting Up a Model for the First Time

I opened a model for the first time, and now I cannot find it.

- Zoom out until the model appears. Bring the model to the center of the Viewer window, and set the default view (`Edit > Overwrite > OK`) to avoid losing the model in space in later stages.

I started model set-up but, now I cannot find my model.

- If the default view has been set, click `revert` next to (`default`), or refer to instructions in the step above.

I cannot zoom in far enough to set the model's scale bars/depth markers/etc.

- In the HUD, turn on `vis-opt`. Under the `near` setting, lower the number to increase the parameters for the zoom level. Try zooming into the model again, and the model should come into closer view.

- *Alternate:* Set one scale bar, then zoom in again to see if the scale value can be adjusted further so that it is more accurate (i.e., ensure each marker is in the center point of the scale's markers).

I adjusted the near setting in Vis-opt, but I continue to zoom through the model into space.

- In the HUD, turn on `vis-opt`. Under the `near` setting, increase the value to above `1.0` m. This should decrease the zoom-level parameters and thus avoid zooming through the model.

My markers are all connected or keep connecting to other undesired markers.

- Deselect the undesired markers. Revisit *3A7. Marker Controls* for further instruction on the use of markers.

My depth markers point down after orienting the model.

- It may be necessary to slightly adjust a few of the depth marker values (e.g., if the value is 10.000, adjust in small increments 10.001, 10.002, etc.) and then to re-set the orientation. First try adjusting the value for one depth marker then a second to see if the orientation rights itself.
- *Alternate:* Sometimes a user will accidentally set the markers from the underside of the plot (i.e., they may not realize the plot is flipped upside down when first opening it in Viscore if the plot is flat, predominately pavement or sand bottom, etc.). Ensure the plot is right side up, delete previous markers, and redo orientation setup.

Common Issues When Conducting VPI

My VPI point does not consistently fall on the same location of the benthos as I scroll through images.

- If a VPI point does not land in the same place on the bottom as photos are flipped through in the browser, refer to the 3D model in the Viscore Viewer window to confirm the true location of that point. When the VPI tool is active, a marker labeled `C` will appear in the center of the VPI box. When the Cams menu is turned on and `drape` is off, the C marker will automatically progress to the position of the point currently displayed in the browser window. To check where the current point lands on the 3D model, first make sure that the C marker is selected, and the model is in Ortho mode (necessary to ensure that points are from the top-down direction from which they were sampled). After the marker is selected it might be necessary to refresh the browser window to update the location of the marker to the current point. Zoom in to the C marker, and use colors and morphological features to determine what item that point has fallen on. Then return to the VPI browser and scroll through the images to find the view indicated in the Viewer window, confirm the identity of the benthos under that point, and label the point accordingly. See section *4B2. Prepare the Viewer for VPI* for further instruction on setting up the Viscore Viewer for VPI analysis.

My annotation buttons have disappeared in the VPI window (browser window).

- Press the Refresh button. If any menu items were adjusted or changed in the Viewer window then it was the likely cause (e.g., Cams was accidentally turned off, the C dot was deselected, etc.).
- *Alternate*: press the back button in the browser window to return. This likely occurred after accidentally double-clicking somewhere in the iView window.

I see Pacific taxa when opening my VPI URL in the browser window for the first time.

- Replace the qclasses file in the model's folder. Navigate to the .pq folder within the model folder. Find the file named qclasses, and rename it to Pacific_qclassses. Locate the project's pertinent qclasses file (this is project specific), and put it into the model's .pq folder. Ensure the name is qclasses; otherwise, the buttons will not be shown in the browser window.

Other Confounding Cases in Viscore

The model seems to be sparkling and/or looks like a fish net.

- Adjust point size to make the points bigger.

The model bounces when I zoom in or out.

- Adjust the near setting accordingly under `vis-opt`.

The HUD is not in the right corner of the screen when I open a model in Viscore.

- Press the Spacebar in the Viscore Viewer, and navigate using the arrow keys to `Scriplets > HCI > new HUD layout` and ensure `Now`, `Vml`, and `Sys` are turned on.

The version of Viscore I am using seems to be missing features or is a different version entirely.

- Double check that the correct version of Viscore is being used. If the correct version is installed, try re-downloading and re-installing Viscore.

C. TagLab

Common Issues

I already created a TagLab project, but when I reopen the project, it asks me for the TIF file(s).

- This likely signifies that the original TIF files were moved. Following the menu prompts, reload the TIF files from their new location, ensuring they match the exact file name that is asked for (e.g., 2023 maps are loaded with 2023 TIFs).

The images in iView are dark, and I cannot get a clear view of the coral I am tracing.

- Adjust the color contrast of the model in Viscore to brighten the model, then refresh the browser in iView (*Section II. Viscore*).
  1. Turn on `Colors`, located in the HUD.
  2. Adjust the `y` value to increase the brightness of the model.

3. Return to the photo in iView, refresh the page, and click through more photos with the adjusted contrast to see if an accurate annotation and segmentation can be made.

Appendix III. NCCOS and M:IR-Specific Instructions

In the below appendices, various software and applications are required to access NCCOS data including Remote Desktop, NOAA NCCOS Microsoft Azure Virtual Machine, and Microsoft Azure Storage Explorer. Installation and access will need prior approval and support from IT.

A. Metashape

Access Remote Desktop

3D reconstruction in Metashape is computationally intensive and requires sufficient capacity. NCCOS uses the NOAA NCCOS Microsoft Azure Virtual Machine (VM) for computational capacity. The VM is accessed through the Remote Desktop application. NCCOS team-specific instructions follow.

1. Navigate to the Windows search bar, type `Remote Desktop`, and open the application.
2. A separate window will open with a list of computer icons indicating the VMs available for use. Choose `NCCOS AVD Iconic Reef - High End GPU` by clicking on the computer icon `Desktop (IRPool1)`. The pop-up window will require login credentials (e.g., common access card PIN). The application will open a new window with a bar on the top that reads `Desktop (IRPool1)`. After login, the VM will show a new desktop screen.
    - If working remotely, the NCCOS VPN must be active in order to access the VM.

Download Raw Images

Image files for each plot (e.g., SOMB_R2-2_2022-08-25_JPEG) are uploaded onto Microsoft Azure Storage Explorer (ASE). Navigate to the Windows search bar, type `Microsoft Azure Storage Explorer`, and open the application. Pin ASE to the taskbar of the virtual desktop (IRPool1). Access to the storage account associated with the M:IR project is required. If the Subscription drop-down menu (Figure 158) does not contain the nccosiconicreef storage account with the associated blob containers and file shares, access will need to be requested.

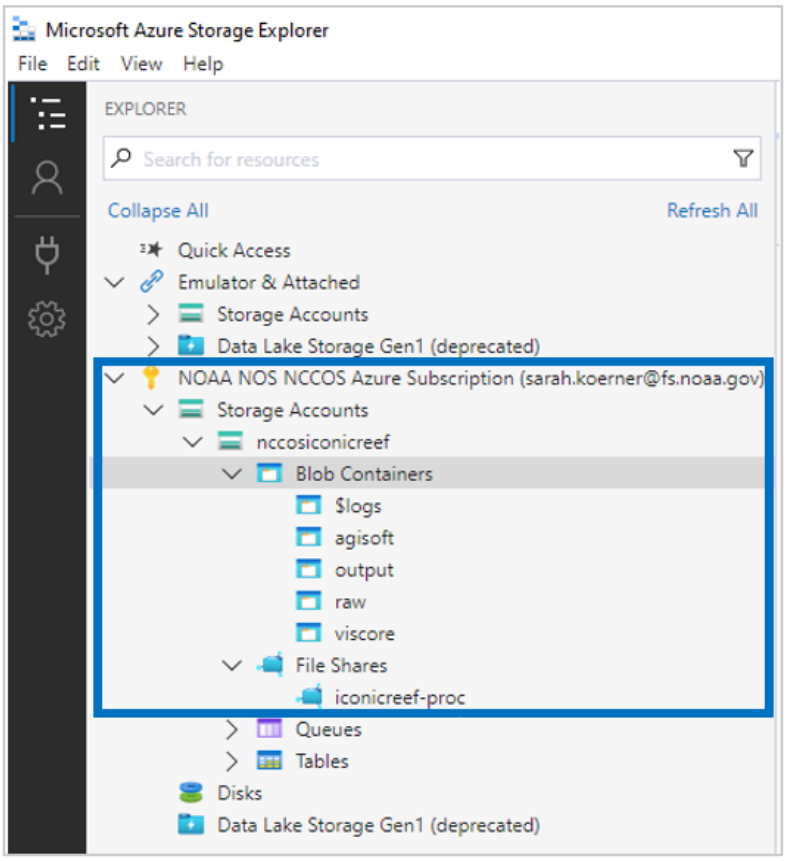

Figure 158. Microsoft ASE window. The blue box indicates nccosiconicreef storage account with associated blobs and file shares.

1. To download the image files for a plot, navigate to `NOAA NOS NCCOS Azure Subscription > Storage Accounts > nccossiconicreef > Blob Containers > raw`.
2. The associated image files will be stored in a folder with the same naming convention as the transcribed field data sheet (e.g., SOMB_R2-2_2022-08-25_JPEG).
3. Download the plot image folder by clicking on the image folder name and then selecting the Download option in the toolbar on the top of the window. A separate window will appear asking where the image folder should be downloaded to. Select `iconic reef (E:)`, then `Raw_Imagery`.
4. When the download is complete, the Activities pane on the bottom of the ASE window will show a green check mark and a breakdown of the download. The breakdown will include transfer locations (i.e., from Azure to E drive), the number of items (files) transferred, and the start time and duration of the transfer.
5. Navigate to `E:/Raw_Imagery`, and check that the naming convention for the downloaded image folder is correct (i.e., dashes and underscores are in the correct locations, and the plot name matches the M:IR SfM Metadata sheet, e.g., SOMB_R2-2_2022-08-25_JPEG). Be sure the file name is correct, for uncorrected naming errors carry through the naming conventions of all files hereafter.

Metashape Data Transfer

Considering NCCOS uses a VM (e.g., IRPool1) and local drive (e.g., iconic reef [E:]) to build models in Metashape, the plot imagery and Metashape project files need to be transferred to the appropriate file shares once the Metashape workflow is complete.

The NCCOS team uses blob containers, a low-cost cloud storage solution, as a repository for raw imagery and Metashape project files not immediately in use. ASE is required to access and transfer data to blob containers.

Navigate to the ASE application pinned to the taskbar of the virtual desktop (e.g., IRPool1). If it is not pinned, navigate to the Windows search bar, type `Microsoft Azure Storage Explorer` and open the application.

Transfer Raw Imagery to a Blob Container

1. To upload image files for a plot, navigate to `NOAA NOS NCCOS Azure Subscription > Storage Accounts > nccossiconicreef > Blob Containers > raw`.
2. Upload the image folder by selecting the `Upload` option in the toolbar on the top of the window. Choose `Upload Folder` from the drop-down menu.
3. A separate window will appear, asking where the plot image folder should be uploaded from. Under `Selected Folder`, click on the `No folder selected` box (or the `...` to the right). A new File Explorer window will appear. Navigate to `E:/Raw_Imagery`, and select the image folder to be uploaded (e.g., SOMB_R2-2_2022-08-25_JPEG).
4. When the upload is complete, the Activities pane on the bottom of the ASE window will show a green check mark and a breakdown of the upload. The breakdown will include transfer locations (i.e., from E drive to raw blob container), the number of items (files) transferred, and the start time and duration of the transfer.
5. Complete a final confirmation of data transfer by comparing the number of images in the folder on iconic reef (E:) to the number of items (files) transferred to the raw blob.

Transfer Metashape Project Files to a Blob Container

1. To upload Metashape project files for a plot, navigate to `NOAA NOS NCCOS Azure Subscription > Storage Accounts > nccossiconicreef > Files Shares > iconicreef-proc`. This is the Iconic Reef (W) drive.
2. Navigate to the project folder named `Agisoft_Project_Data_Exports`. The project folder associated with the Metashape project (e.g., SOMB_R2-2_2022-08-25) will be uploaded to this folder (Figure 159).

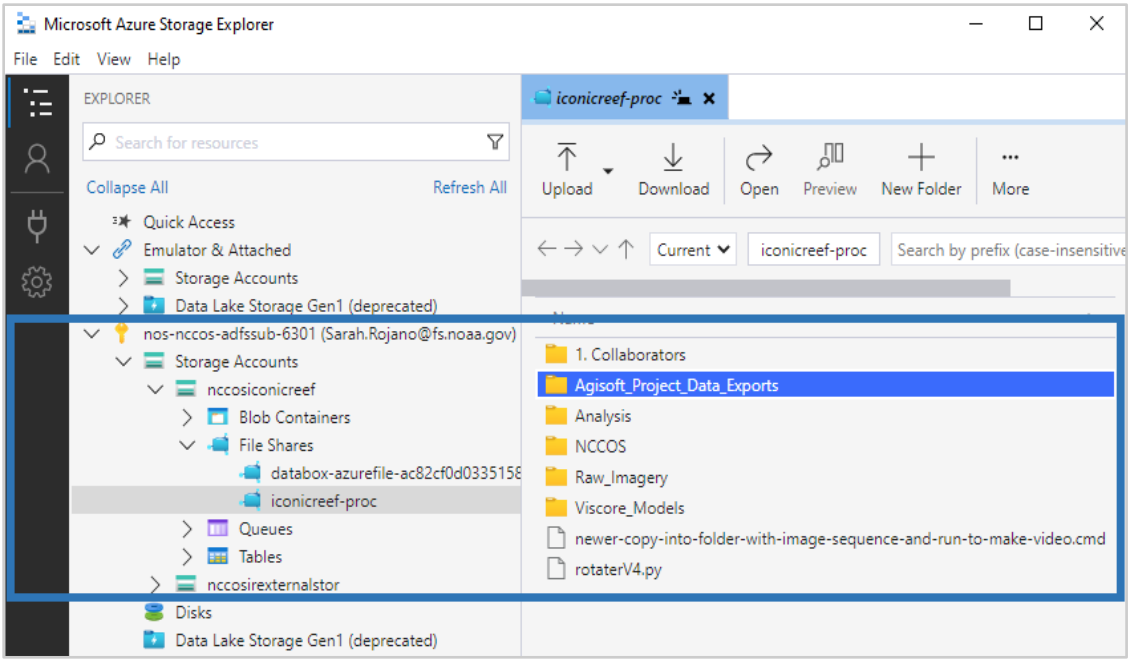

Figure 159. ASE window. The blue box indicates nccosiconicreef storage account with the Iconic Reef (W) drive (iconicreef-proc) and the Agisoft_Project_Data_Exports folder where Metashape project folders are stored.

3. Upload the project folder by selecting the `Upload` option in the toolbar on the top of the window. Choose `Upload Folder` from the drop-down menu.
4. A separate window will appear, asking where the image folder should be uploaded from. Under `Selected Folder`, click on the `No folder selected` box (or the `...` to the right). A new File Explorer window will appear. Navigate to `E:/Agisoft_Project_Data_Exports` and select the project folder to be uploaded (e.g., SOMB_R2-2_2022-08-25).
5. When the upload is complete, the Activities pane on the bottom of the ASE window will show a green check mark and a breakdown of the upload. The breakdown will include transfer locations (from E drive to W drive), the number of items (files) transferred, and the start time and duration of the transfer.
6. Navigate to the `W:/Agisoft_Project_Data_Exports` folder to confirm the upload was successful. Complete a final confirmation of data transfer by checking that the properties of the folder on Iconic Reef (W:) match the properties of the folder on iconic reef (E:).
    - Right-click on the folder `W:/SOMB_R2-2_2022-08-25`, and select `Properties` from the context menu. A window named SOMB_R2-2_2022-08-25 Properties will appear. In a separate window, repeat this step for the folder E:/SOMB_R2-2_2022-08-25.
    - Compare the `Contains` information for both folders to confirm that W:/SOMB_R2-2_2022-08-25 matches E:/SOMB_R2-2_2022-08-25. Both folders should have the same number of files and folders. If the folder properties do not match, delete the folder on Iconic Reef (W), and repeat steps 1–5.

Completion of Metashape Data Transfer

Once the plot imagery and Metashape project files have been transferred to the Iconic Reef (W) drive, the folders can be removed from the iconic reef (E) drive. Navigate to the `iconic reef (E)` drive, and delete the project and image folders for the plot (e.g., SOMB_R2-2_2022-08-25) from their respective places (e.g., Agisoft_Raw_Data Exports and Raw_Imagery).

B. Viscore

Access and Download M:IR Data

The following examples are specific to M:IR NOAA partners and illustrate the inclusion of cloud computing into the workflow. Access to this workflow is strictly controlled by user-specific permissions and limited to project collaborators. M:IR data can be accessed via 1- *NOAA NCCOS Microsoft Azure Virtual Machine (VM)* and 2- *Microsoft Azure Storage Explorer (ASE)*. The VM is most commonly used to prepare model data and to store the final data products used for analysis. ASE is utilized for downloading data onto a local machine (e.g., to the computer's desktop) from the VM via shared NCCOS drives or blob containers. When downloading data from ASE, it is likely that model data have already been converted to Viscore format and the model has already been set up beforehand. While there are numerous ways to access and download M:IR data, the options available to M:IR users are described in further detail below.

Prepare Model Data on Azure Virtual Machine

This option is for preparing a model from scratch after exporting files from an Agisoft Metashape project.

1. Navigate to the Windows search bar, type `Remote Desktop`, and open the application. Choose `NCCOS AVD Iconic Reef - High End GPU` by clicking on the computer icon `Desktop (IRPool1)`.
2. Navigate to the E drive or iconicreef-proc shared drive.
3. Open the folder `Agisoft_Project_Exports`, and navigate to the model's folder to be converted into a Viscore model (e.g., HSHOE_R4-1_2022-05-05).
4. Within the model's folder, create an empty folder with the corresponding naming convention (e.g., HSHOE_R4-1_2022-05-05).
5. Copy and paste the meta.json and cams.xml files into the folder.
6. Drag and drop the .ply file into the newly created model folder.
7. Visit *1B2. Preparing Data for Viscore* to prepare the model's point data, then return to steps 8–10 below.
8. After preparation of the .vml file, return the .ply to the model's pertinent folder under Agisoft_Project_Exports.
9. Open ASE on the VM (IRPool1), and navigate to the file share `iconicreef-proc`.

10. Locate the folder `Viscore_Models`. Find the newly created model folder in the `Agisoft_Project_Exports` folder that contains the .vml file, meta.json, cams.xml, and newly generated point data folder. Upload the entire model folder to `Viscore_Models` on the W drive using ASE.
11. When the transfer has finished, compare the model folder on both the W and E drives to ensure that all files have transferred.

Download Data from NCCOS File Shares on Azure Storage Explorer

This option is for those who wish to download a previously prepared model to a local desktop or machine from NCCOS file shares. The user must have full access to NCCOS file shares. This example is specific to the M:IR project.

1. Navigate to ASE, double-click on `nccosiconic reef > File Shares`, then `iconicreef-proc` to open the shared drive.
2. Open the folder `Viscore Models`, and locate the folder of the model to be worked with.
3. Click `Download` to download into the Viscore Models folder on the local desktop.
4. Return to the main folder in the file share `iconicreef-proc`, and open the folder `Raw_Imagery`.
5. Locate the folder that corresponds to the model being used.
6. Click `Download` to download into the Raw Imagery folder on the local machine.
7. Open up the model (double-click on .vml to open in Viscore Viewer), and check that the model has been scaled and oriented.
    - If the model has been set up with scale and orientation, basic analyses such as VPI may be conducted.
    - If the model has not been scaled and oriented, see *I. Viscore 4A1. Set Scale* and *4A2. Set Model Orientation* for further guidance.

Download Data from Blob Containers on Azure Storage Explorer

This option is for those downloading a previously prepared model to a local desktop or machine that does not have full access to NCCOS file shares. In this scenario, the user accesses data on blob containers via shared access signature (SAS) tokens on ASE. All SAS tokens are requested by the NCCOS team on behalf of project partners and are specific to individual users.

1. Navigate to ASE, and double-click on `nccosiconic reef` then `Blob Containers`.
2. Open the blob container `Viscore`, and locate the folder of the model being used.
    - Click `Download` on the top pane to download the model data into the Viscore Models folder to the local machine.

3. Return to the main Blob Containers folder, open the blob container `Raw`, and locate the folder that corresponds to the model being used.
    - Click `Download` to download into the Raw_Imagery folder on the local machine.
4. Open up the model (i.e., double-click on .vml to open in Viscore Viewer), and check that the model has been scaled and oriented.
    - If the model has been set up with scale and orientation, basic analyses such as VPI may be conducted.
    - If the model has not been scaled and oriented, see *4A1. Set Scale* and *4A2. Set Model Orientation* for further guidance.

Saving and Backing Up the Fly-Through Video

1. Rename the video to match the naming convention of the model (e.g., CFN_R7-4_2022-07-06).
2. Cut and paste the video to the folder `1- Site Fly-Through` under Raw_Imagery on the W drive (file path to folder is W:\Raw_Imagery\1- Site Fly-Through).
3. Upload the video to the model's corresponding folder on the M:IR Google Drive.

Tips and Tricks for Hard to Identify Points in VPI:

- Label as `Review`, then return to it during another session. It is possible that it becomes recognizable later as subsequent points and images may help with identification.
- Label as `Review`, and leave it for someone from the M:IR team to ID during the analysis phase.
- If the point lands on a marker, scale bar, or other human-made object (e.g., trash), label it as `N/A`.
- If the imagery is too dark or if the point lands on a dark crevasse in the image:
    - Adjust the contrast of the photo by returning to the model in Viscore.
    - Turn on `Colors`, located in the HUD.
    - Adjust the `y` value to increase the brightness of the model.
    - Return to the photo in the browser window, refresh the page, and click through more photos with the adjusted contrast to see if an accurate ID can be made.
    - If an accurate ID still cannot be made based on the photos available, label it as `Unknown`.

C. TagLab

Data Organization and Download

M:IR data found on the shared drive follow the organization outlined below and can be accessed via 1- *NOAA NCCOS Microsoft Azure Virtual Machine (VM)* and 2- *Azure Storage Explorer (ASE)*. For M:IR data, either download and backup data on ASE, or directly work with the data on the shared drive (Iconic Reef W drive) on the VM.

M:IR data are organized and separated by three folders:

- **Maps**: contain the .tif files.
- **Project Files**: contain the .json files generated from TagLab projects and the labels dictionary.
- **Exported Data**: contain the colony segmentation data exported from TagLab.

M:IR Project Naming Conventions

Before moving forward with tracing, under the File menu at the top of the window pane, click `Save As`, then name the project to match the project's predetermined naming standards (e.g., Site_Plot-Subplot). The date of imagery collection is omitted as this project file will hold the 2D maps for the initial and subsequent time points associated with the Site_Plot-Subplot.

Data Export

Export the data to the folder `Exported_Data` on the W drive under the folders `Analysis > TagLab` (e.g., file path: W:\Analysis\TagLab\Exported_data on the shared Iconic Reef W drive or to ASE). Ensure the naming convention matches the name of the project, e.g., Site_Plot-Subplot_Timepoint.

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Richard Spinrad, *Under Secretary for Oceans and Atmosphere*

National Ocean Service
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