



SWUAV_BIO

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PROJECT SWUAV













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1. Introduction

Seaweed assemblages are present in rocky shores around the world, creating very productive ecosystems of high ecological and economic importance. These assemblages include a variety of structuring species that provide habitat, food and shelter for organisms from different trophic levels, supporting complex trophic webs important both ecologically and economically.

The SWUAV project aims to develop innovative, reliable yet expeditious, imagery tools to map the intertidal and assess seaweed biomass available in the field, using remotely sensed unmanned aerial vehicles (UAV) images.

Developed in the scope of the SWUAV Project, the SWUAV_BIO tool is a free open-source QGIS plugin that allows to map and quantify seaweed biomass.

The development of this tool was based on initial exploratory surveys, for the selection of sites and methodologies, followed by the collection of spectral signatures for each type of objects to classify. Next, aerial imagery acquired with UAV equipped with RGB and multispectral sensors were used to develop a QGIS plugin suitable for assessing biomass remotely. Aerial images and seaweed percentage cover data collected in the field, allowed the development of this new tool. The plugin was validated for *Fucus* spp. through ground truthing in the field.

The SWUAV_BIO plugin enables rapid surveys of large extensions of coastal intertidal regions, supporting the launching of future expedite rocky shores monitoring programs. It is, therefore, a valuable tool for rapid mapping and quantifying seaweed biomass, which improves the ability to increase the knowledge about local ecosystems and contributes to the sustainable management and conservation of marine habitats.

This tutorial was created to help the user to understand and apply the SWUAV_BIO open-source application, developed with and for QGIS software version 3.16.

2. Plugin Installation

2.1 QGIS download and installation (manual installation)

In order to run and use the plugin, it is necessary to install the QGIS software (Advanced mode). For that, the following steps must be taken:

- Download and install the QGIS version 3.16 (32 or 64 bits) from QGIS official page (https://qgis.org; the plugin was configured for this version). Next, choose Download and install OSGeo4W Network Installer.
- ii. Execute the QGIS installer with administrative rights (Run as administrator).
- iii. Choose Advanced Install.
- iv. Accept all the default options and in *Select Packages* in *Desktop* category, activate the *qgis-full: QGIS Full Desktop*.

2.2 SWUAV BIO plugin installation

In order to install the plugin, the next steps must be followed:

- i. Run QGIS 3.16
- ii. Menu Plugins/ Manage and Install Plugins/ Install from ZIP.
- iii. Insert location and name of the zip file of the plugin.
- iv. The plugin appears as a button in the menus (Figure 1).



Figure 1. SWUAV_BIO plugin icon.

3. The SWUAV_BIO interface

In this section, the interface of the plugin will be explained. The interface of the installed plugin is opened by clicking on the SWUAV_BIO button. Follow the steps below to understand the interface of the plugin (Figure 2).

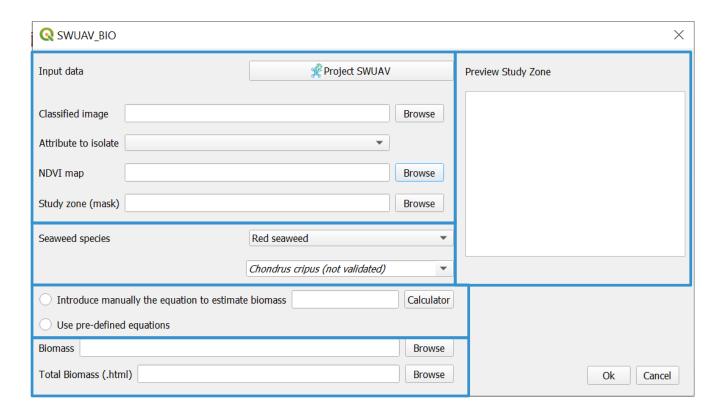


Figure 2. SWUAV_BIO plugin interface.

3.1 SWUAV_BIO plugin interface

The application is composed of five sections: i) the input section, where the user can open the input files for the study; ii) the seaweed species section, where the user chooses the seaweed species to study; iii) the equations section, where the user defines which equation is used to estimate the biomass (either the pre-defined equation, (validated for *Fucus* spp. only) or an equation introduced by the user); iv) the output section, where the user should define the output directories for the resulting biomass

raster and for a html page containing the statistics of the biomass areas; and v) the preview study zone section, where the input information will be presented and the user can delimit a study zone through drawing a polygon. These sections will be explained in detail in the next sub-chapters.

Notice that file, folder and path names should be short and without spaces. The *Browse* buttons open a browser where directories and files can be found, and new output files' directories can be created.

3.1.1 Input section

Input files

The SWUAV_BIO application requires two main inputs: the classified image (in which one of the classes corresponds to the studied seaweed) and the NDVI map, both of which have to be previously created.

Classified image: input the classified image

Attribute to isolate: choose the attribute corresponding to the seaweed species

NDVI map: input the NDVI map

Study zone

The study zone can be defined by two procedures: i) input a shapefile with the study zone(s) or ii) define the study zone manually in the *Preview Study Zone* window.

For the first option:

Study zone (mask): input the shapefile with the study zone(s).

For the second option:

When the user adds the classified image and the NDVI map directories, these images automatically open in *Preview Study Zone*, so the user can define manually a rectangle delimiting the study area (Figure 3). The application will automatically create a temporary shapefile.

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Example:

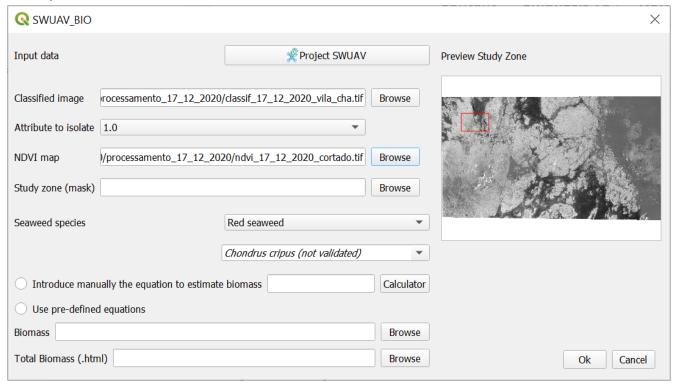


Figure 3. Study zone delimitation (red rectangle) using the *Preview Study Zone*.

3.1.2 Seaweed species selection

The user can choose between three types of seaweed: Red seaweed, Green seaweed and Brown seaweed (Figure 4), and between two species for each type.

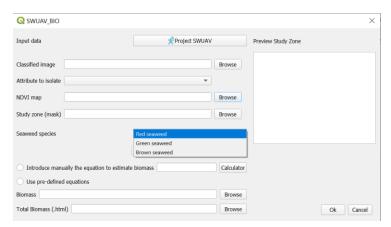


Figure 4. SWUAV_BIO seaweed species options: Red seaweed, Green seaweed, and Brown seaweed.

Red seaweed: Chondrus crispus and Osmundea pinnatifida (Figure 5).

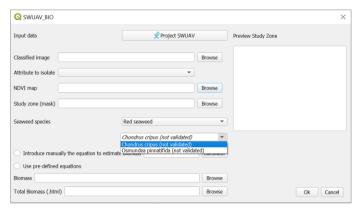


Figure 5. Red seaweed options.

Green seaweed: Codium spp. and Ulva spp. (Figure 6).

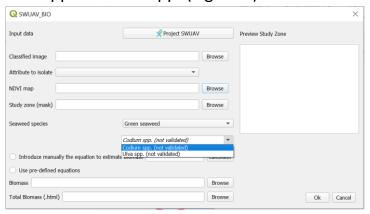


Figure 6. Green seaweed options.

Brown seaweed: Fucus spp. and Laminaria ochroleuca (Figure 7).

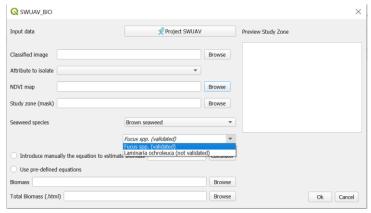


Figure 7. Brown seaweed options.

The user must choose one species to estimate its biomass (g DWm⁻²).

3.1.3 Equations to estimate the biomass from NDVI

The dry biomass (gDW m⁻²) can be estimated from NDVI values considering the following equations (validated for *Fucus* spp.), for the three types of species (Figure 8).

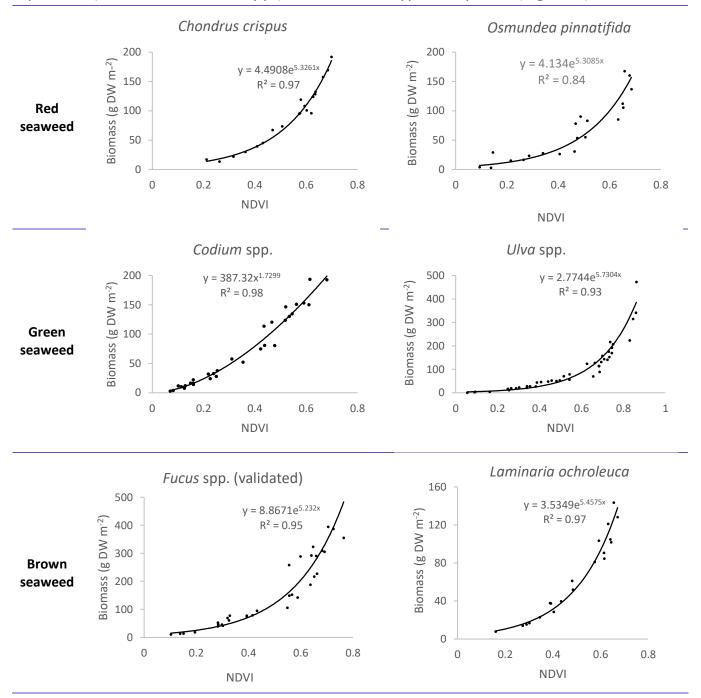


Figure 8. NDVI vs. biomass relationships and respective equations for the seaweed species included in the plugin.

The equations were computed in the SWUAV_BIO application. The user has two options:

To use the pre-defined equations:

Select Use pre-defined equations

To introduce a new equation:

Select Introduce manually the equation to estimate biomass

In the second option, the equation must be manually introduced (Figure 9), which can be done with the help of the calculator, accessible through the *Calculator* button (Figure 10).

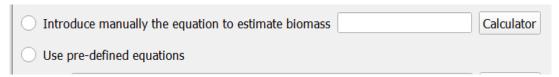


Figure 9. Options to introduce the equation.

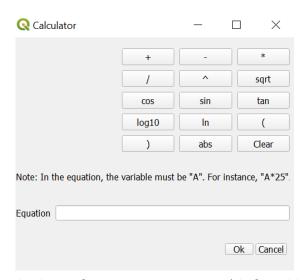


Figure 10. Calculator for a new equation (defined by the user).

The *Calculator* graphic interface allows to build an equation using mathematical operators. Notice that, since the NDVI map will be the dependent variable of the equation, the NDVI map should be referred to as *A*, when the user writes the equation. The equation will be added to the line edit in the main interface, when clicking *Ok*.

3.1.4 Outputs

The SWUAV_BIO application (work flow summarized in Figure 11) returns two different outputs: a raster with the biomass estimation (g DWm⁻²) and a *html* file with the statistics of the biomass raster (Figure 12a, where the *Sum* variable, in the red rectangle, represents the total biomass or standing stock (gDW) for the defined study zone).

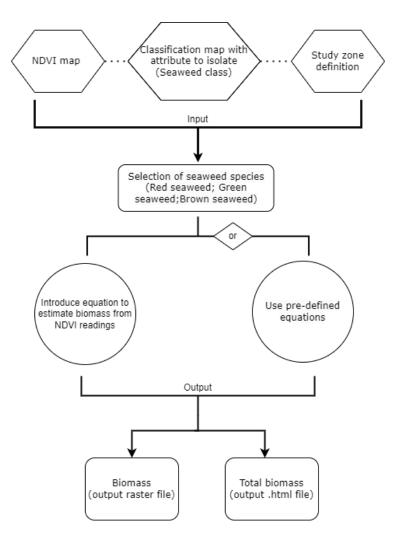


Figure 11. SWUAV BIO summarized work flow.

The user must define the output directories (Figure 12b) and wait until the application returns the results (which can take several minutes, depending on the study area and hardware, and may produce a *not responding* message next to the plugin name, which can be neglected). The raster file will be automatically added to the project. Both raster and html file will be saved in the folder(s) previously defined by the user.

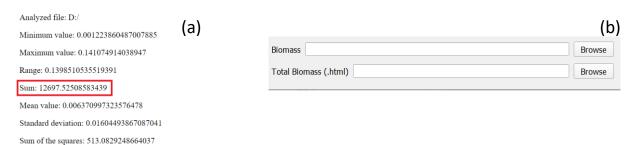


Figure 12. Outputs of the plugin.

Given the several steps required to implement the SWUAV_BIO plugin presented in this tutorial, residual errors will be generated with a cumulative effect. These errors are related with the NDVI to biomass estimation and the classification process (e.g. the error of the estimated area for the target class), and should be considered when interpreting the SWUAV_BIO outputs. Previous validation of the *Fucus* spp. data from northern Portugal has underestimated the biomass in 36% relatively to in-situ field data. Therefore, the inspection of the classification performance by class, combined with the photointerpretation of the RGB imagery and knowledge of the terrain, is essential for data interpretation (for more details see Borges et al. in press).

4. Report errors

4.1 How can I report an error?

If you find an error of the SWUAV_BIO plugin you can report your error/bug through the plugin's Github repository (https://github.com/swuavproject) or directly contact the researchers of the project (https://swuav.ciimar.up.pt/contacts).

4.2 Where is the source code of the SWUAV_BIO plugin?

The source code of the SWUAV_BIO plugin is hosted in the Github repository (https://github.com/swuavproject). The code is open-source and free. All suggestions for improvement are welcome and will be considered by the developer and the research team.

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