



ECOTAXA

HOW TO ANALYSE THE ECOTAXA TABLES EXPORTED FROM A ZOOSCAN/ZOOPROCESS PROJECT?

Quantitative Imaging Platform of Villefranche sur Mer (PIQv)

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Summary

1. Variables to utilize from	n the tables	2
1.1 Variables to utilize in	Object details (column called "object_XXXX")	2
1.2 Variables to utilize in	Sample details (column called "sample_XXXX")	2
1.3 Variables to utilize in	Process details (column called "process_XXXX")	2
1.4 Variables to utilize in	Acquisition details (column called "acq_XXXX")	2
2. Equations		2
2.1 Concentration = Num	ber of individus in the sampling/m³	2
2 2 Biovolume = Volume	hiomass of individus in the sampling/m ³	3

IMPORTANT NOTE:

Each lines of the table is 1 object (living or not living) scanned by the ZooScan Each columns of the table is 1 variable

1. Variables to utilize from the tables

1.1 Variables to utilize in Object details (column called "object_XXXX")

object_lat = GPS latitude of the sampling (decimal format)
object_lon = GPS longitude of the sampling (decimal format)
object_annotation_status = status of the images (unclassified, dubious, predicted or validated)

object_annotation_category = taxonomic name of the images object_area_exc = surface area of the objects excluded the empty spaces (holes) in pixel object_area = surface area of the objects included the empty spaces (holes) in pixel object_major = primary axis of the best fitting ellipse for the object in pixel object_minor = secondary axis of the best fitting ellipse for the object in pixel

1.2 Variables to utilize in Sample details (column called "sample_XXXX")

sample_tot_vol = initial volume filtered = volume of seawater filtered by the net (m³) sample_tow_nb = number of tow in the analyzed sample

1.3 Variables to utilize in Process details (column called "process_XXXX") process_particle_pixel_size_mm

1.4 Variables to utilize in Acquisition details (column called "acq_XXXX")

acq_id = origin of the object
acq_sub_part = sample fraction analysed into the ZooScan

2. Equations

IMPORTANT NOTE: You have to convert the pixel variables in metric form

Area (mm²) = object_area x (process_particle_pixel_size_mm)²

Area excluded (mm²) = object_area_exc x (process_particle_pixel_size_mm)²

Major (mm) = object_major x process_particle_pixel_size_mm

Minor (mm) = object_minor x process_particle_pixel_size_mm

2.1 Concentration = Number of individus in the sampling/m³

Number of recurrence for each taxonomic group in the variable object_annotation_category:

Concentration = nb. ind./m³ = (object_annotation_category x acq_sub_part) / sample_tot_vol

2.2 Biovolume = Volume biomass of individus in the sampling/m³

2.2.1 Plain biovolume

Radius of a circle = $r (mm) = V (Area (mm^2) / \Pi)$

Spherical Volume = $V (mm^3) = 4/3 x \prod x r^3$

Biovolume = Bv (mm³/m³) = (Spherical Volume x acq_sub_part) / sample_tot_vol

2.2.2 Riddled biovolume

Radius of a circle = $r (mm) = \sqrt{(Area excluded (mm^2) / \Pi)}$

Spherical Volume = $V (mm^3) = 4/3 \times \prod x r^3$

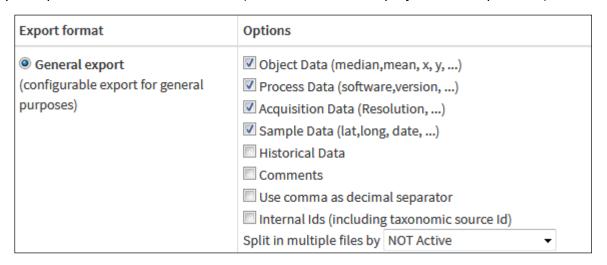
Biovolume = Bv (mm³/m³) = (Spherical Volume x acq_sub_part) / sample_tot_vol

2.2.3 Ellipsoide biovolume

Spherical Volume = $V (mm^3) = 4/3 \times \prod x [(Major(mm)/2) \times (Minor(mm)/2) \times (Minor(mm)/2)]$

Biovolume = Bv (mm³/m³) = (Spherical Volume x acq_sub_part) / sample_tot_vol

If you export the tables without filters (all the data from the project in 1 unique table)



You have to group the objects belonging to the same sample -> acq_id

You have to merge d1_XXX with d2_XXX (NB : the acq_sub_part is different between d1 and d2).

You have to group the objects belonging to the same category -> object_annotation_category

NB: check the validation status -> object_annotation_status (have to be validated)