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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Date	Name operator	Object	Chapter
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Summary

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 (m^3)
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 (mm^2) = object_area x (process_particle_pixel_size_mm)^2
Area excluded (mm^2) = 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/m^3

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

Concentration = nb. ind./m^3 = (object_annotation_category x acq_sub_part) / sample_tot_vol

2.2 Biovolume = Volume biomass of individus in the sampling/m^3

2.2.1 Plain biovolume

Radius of a circle = r (mm) = √ (Area (mm^2) / ∏)

Spherical Volume = V (mm^3) = 4/3 x ∏ x r^3

Biovolume = Bv (mm^3/m^3) = (Spherical Volume x acq_sub_part) / sample_tot_vol

2.2.2 Riddled biovolume

Radius of a circle = r (mm) = √ (Area excluded (mm^2) / ∏)

Spherical Volume = V (mm^3) = 4/3 x ∏ x r^3

Biovolume = Bv (mm^3/m^3) = (Spherical Volume x acq_sub_part) / sample_tot_vol

2.2.3 Ellipsoide biovolume

Spherical Volume = V (mm^3) = 4/3 x ∏ x [(Major(mm)/2) x (Minor(mm)/2) x (Minor(mm)/2)]

Biovolume = Bv (mm^3/m^3) = (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)

Export format	Options
◉ **General export** (configurable export for general purposes)	☑ Object Data (median,mean, x, y, ...) ☑ Process Data (software,version, ...) ☑ Acquisition Data (Resolution, ...) ☑ Sample Data (lat,long, date, ...) ☐ Historical Data ☐ Comments ☐ Use comma as decimal separator ☐ Internal Ids (including taxonomic source Id) Split in multiple files by NOT Active

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

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

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

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