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DEPARTMENT OF BIOLOGICAL, GEOLOGICAL, AND ENVIRONMENTAL SCIENCES · BiGeA

MASTER'S DEGREE IN
ENVIRONMENTAL ASSESSMENT AND MANAGEMENT

**Assessing the relationship
between bee/flower diversity and
vegetation structural heterogeneity
through UAV photogrammetry**

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Abstract

The ecosystem services provided by bees are very important, especially for agriculture. Factors as habitat fragmentation, intensive agriculture and climate change are contributing to the decline of bee populations. The use of remote sensing could be a useful tool for the recognition of sites with a high diversity, before performing a more expensive survey in the field.

In this study the ability of Unmanned Aerial Vehicles (UAV) images to estimate biodiversity at local scale has been analysed testing the concept of the Height Variation Hypothesis (HVH). This approach states that, the higher the vegetation height heterogeneity (HH) measured by remote sensing information, the higher the vertical complexity and the higher vegetation species diversity. In this thesis the concept has been brought to a higher level, in order to understand if the vegetation HH can be considered a proxy also of bee species diversity and abundance. We tested this approach in 30 grasslands in the South of the Netherlands where an intensive field data analysis (collection of bees and flowers diversity and abundance), together with a UAV campaign (collection of RGB images at high resolution) was carried out in 2021. The Canopy Height Model (CHM) of the grasslands were derived through the photogrammetry technique "Structure from Motion" (SfM) with a resolution of 10 cm, 25 cm, 50 cm. Successively, the HH assessed on the CHM (at different spatial resolution) using the Rao's Q heterogeneity index was correlated to the field data (bee abundance, species richness, diversity and flower species richness). The correlations were all positive and significant. Generally the highest R^2 values were found when the HH was calculated with CHM at 10 cm and correlated to bee species richness ($R^2 = 0.41$) and Shannon's H index ($R^2 = 0.38$). Using a lower spatial resolution the goodness of fit slightly decreases. In the correlation HH and flower species richness the R^2 ranged between 0.36 to 0.39 for the three spatial resolutions. Our results suggest that methods based on the concept behind the HVH, in this case deriving information of HH from UAV data, can be developed into valuable tools for large-scale, standardized and cost-effective monitoring of flower diversity and of the habitat quality for bees.

1 Introduction

1.1 Importance of biodiversity and bees

The biodiversity is a measure of how much the species composition varies in a community, constituting the structure of ecosystems, even though it includes also genetic levels (Kaennel Dobbertin, 1998). The correct functioning of an ecosystem depends on biodiversity (Cardinale et al., 2012), which is the combination of two components: species richness and evenness. Species richness represents how many species are present, while evenness refers to equitability among species evaluating how similar the abundances of present species are (Oldeland et al., 2010).

Intact ecosystems, with high biodiversity, provide many ecosystem services e.g. hosting pollinators leading to pest population reduction (Wratten et al., 2012), offering resistance against invasive species and hosting crop pollinators (Torresani et al., 2020). Biodiversity loss has an impact on ecosystems' functioning, leading to a reduction of their efficiency (Cardinale et al., 2012), for this reason biodiversity is measured as an indicator of ecosystem health (Rocchini et al., 2017).

In agricultural landscapes biodiversity decreased dramatically in the last decades, and in particular insect biodiversity is declining, resulting in the loss of benefits for crops and therefore also for humans (Raven and Wagner, 2021). The causes of this can be found in land use causing habitat fragmentation (Kleijn et al., 2008), in increasingly intensive agriculture and in climate change (Outhwaite et al., 2022). All these causes have affected the presence of niches for insects (Raven and Wagner, 2021).

Insect pollinators are essential to the maintenance of wild plant species, contributing to cultural ecosystem services, and agricultural yields (Breeze et al., 2011). Among the insects, bees provide ecosystem services such as honey and wax production (Carreck and Williams, 1998), but above all they play the most important role as pollinators (Potts et al., 2010). The 39% of world production of human edible crops is represented by insect pollinated crops, so this ecosystem service has a value of €153 billion a year (Gallai et al., 2009). In particular, the domesticated European Honeybee (*Apis mellifera*) is estimated to contribute 80% to pollination of insect pollinated agricultural crops (Breeze et al., 2011). This domesticated and managed species may however be dangerous for wild bees, due to the transfer of pathogens. It can also be observed a lack of nesting sites for wild bees that endangers them, and which can lead to diversity loss (Requier et al., 2019).

Bees are also undergoing a decline in abundance and species richness (Turley et al., 2022), and among the drivers that determine their pattern in the world there are the presence of xeric environments and solar radiation (Orr et al., 2021).

In order to improve ecosystem services provided by pollinator such as bees, and thus their biodiversity, it is important to monitor diversity and abundance and to implement conservation of pollinator habitat (Wratten et al., 2012).

The EU Showcase Project has been established, as indicated by the project, with the aim of *"showcasing synergies between agriculture, biodiversity and Ecosystem services to help farmers capitalising on native biodiversity"* (<https://showcase-project.eu/>). The project has, among its objectives, the task (1.4) of testing biodiversity indicators using landscape metrics.

1.2 Importance of remote sensing data

Thanks to Earth Observation through remote sensing we can investigate many characteristics of the earth (Reddy, 2021). Remote sensing allows to study earth's surface through large quantities of data at various spatial and temporal scale in a non invasive way (Willis, 2015). Therefore, especially since satellite sensors with fine resolution are available, it is possible to remotely monitor the ecosystems (Rocchini et al., 2004). Remote sensing data coupled with field study sites can provide an efficient tool capable of modelling and monitoring the biodiversity at various scales (Hakkenberg et al., 2018). Moreover, remote sensing allows monitoring and mapping in a less time-consuming and cheaper way in comparison to field sampling (Torresani et al., 2020). In addition, the use of remote sensing provides a huge amount of standardized data useful to estimating biodiversity (Tamburlin et al., 2021); on the contrary, using field data can cause problems in defining standardised data collecting procedures (Rocchini et al., 2017).

Remote sensing technology through Unmanned Aerial Vehicles (UAV) has been quickly developing and improving in the last few years, and it is being used in several sectors such as agro-forestry sector (Yin et al., 2019), mapping and monitoring and disaster management fields (Yang et al., 2022). In reference to agricultural sector, the use of UAV technology, for example drones, allows to achieve the goal of creating agricultural landscape with high biodiversity, surveying habitat characteristics (Librán-Embúid et al., 2020).

As for the field of ecology, which requires above all images at local scale but at the same time high resolution images, UAV seem to be one of the best solutions both because it is becoming more and more affordable for everyone (Anderson and Gaston, 2013) and because, through a low-altitude flight, they can capture images at a higher resolution than satellites (Turner et al., 2012). In general, the use of UAV, combined with the use of photogrammetry techniques and algorithms of "Structure from Motion" (SfM), can bring great benefit to the field of environmental sciences (Lisein et al., 2013). According to Schönberger and Frahm (2016), "*SfM is the process of reconstructing 3D structures from its projections into a series of images taken from different viewpoints*".

1.3 HVH - Height Variation Hypothesis

The Spectral Variation Hypothesis (SVH) was proposed and tested (Palmer et al., 2002), and it assumes that, in remotely sensed images, a higher heterogeneity in spectral response can be related to greater plant diversity, and therefore in general also to a greater spatial heterogeneity (Rocchini et al., 2004). When the spectral heterogeneity is high, it means that there are more ecological niches available for species (Torresani et al., 2019). In order to calculate the spectral variation, heterogeneity indices have to be used: the Rao's Q index has recently showed positive results (Torresani et al., 2020).

The concept of SVH can be transposed to Height Variation Hypothesis (HVH), focusing on the structural heterogeneity of vegetation. This hypothesis assumes that the more heterogeneous the heights of vegetation, the more complex structures exist, which create available niches providing a greater species diversity (Torresani et al., 2020). So, it can indirectly estimate species diversity (Tamburlin et al., 2021). In the same way as SVH, also for HVH it is necessary to calculate the height heterogeneity (HH), and it has to be based for example on Canopy Height Model (CHM) using an index that calculate the difference between pixels' values, like Rao's Q index (Torresani et al., 2020). In this study, HH has been calculated on CHM derived from UAV imagery which led to construction of a three-dimensional model through the SfM methodology.

The aim of this study is to test the relationship between the grassland HH derived from UAV RGB images (through SfM) and bee/flower abundance and diversity. Specifically, we assessed the HH using the Rao's Q heterogeneity index and we correlated it with information of bee abundance, richness and flower species richness collected in 30 study areas (grasslands located in the Netherlands).

2 Materials and Methods

2.1 Study area

The study area is located in the grasslands of Netherlands' south part, area with slightly hilly landscapes (example in figure 2), and consists in 30 areas. These 30 study sites (Figure 1) are part of the biodiversity experimental area network related to the EU Showcase Project, and their elevation ranges from 70 to 171 m asl. Different land use types are considered, from semi-natural grassland to intensive agriculture, so the sites differ in fertilization degree and in mowing frequency. In fact, some grasslands are nutrient-poor, others are intensively fertilized and cut in order to produce fodder. The sampling sites are located on various types of soils, from loess soil, to colluvial clay deposits, to lime-rich soils.

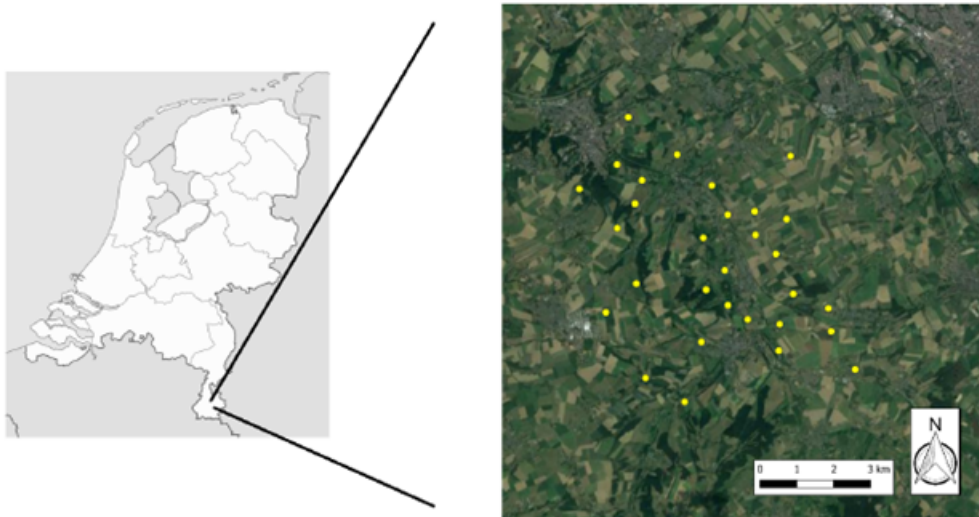


Figure 1: The 30 study sites are represented by yellow dots (Basemap: Google Earth map at August 2022)



Figure 2: Landscape in South Netherlands.

2.2 Field Sampling

The following scheme (figure 3) represents the methodology followed for the purpose of this study:

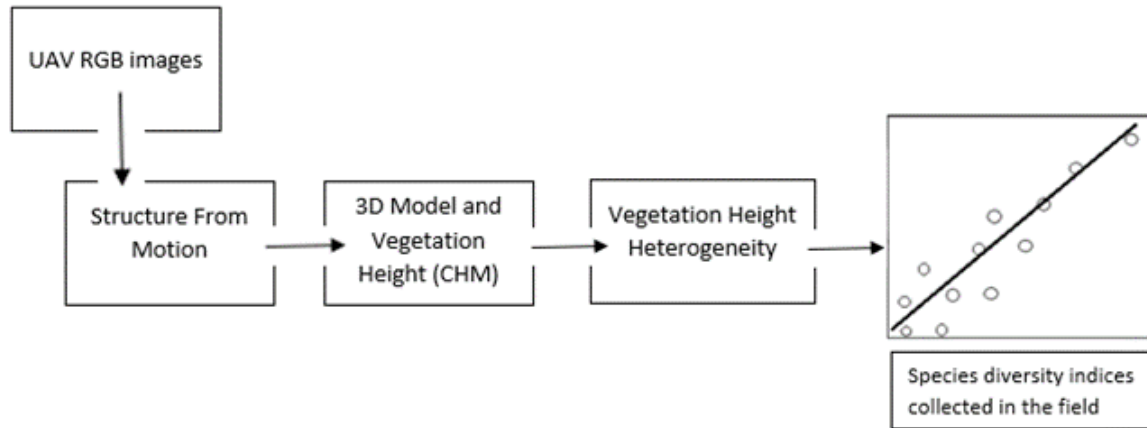


Figure 3: Scheme of used methodology.

As regards the field work, in each area was planned the setting up of a 150-meters-long transect that was subdivided in three sections of 50 m. The data collected concern bees and flowers, in particular their abundance and the species richness. See an example of grassland in figure 4.

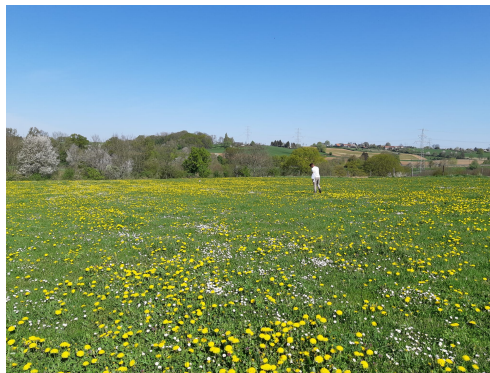


Figure 4: Example of grassland in a study site.

Field data collection took place between 12th and 31st May 2021, from 10 a.m. to 6 p.m.. The conditions under which bee data collection could take place were: dry environment, sunny for more than 50%, weak wind with a speed less than 2 on the Beaufort scale, and a minimum temperature of 15 degrees Celsius.

In order to count bees, transect walks was selected as a standardized sampling method (Westphal et al., 2008) in order to assess the presence, abundance and diversity of bee pollinators. The procedure requires an operator to walk slowly along the entire transect and in the meanwhile to count the bees that are in a 1-meter-buffer area around the trace of the transect. The identification of the species was made on site, and bees could be released, otherwise they were collected, taken to the laboratory and subsequently identified.

Bee species that have been found in the 30 areas are the following in alphabetical order:

Andrena cineraria, *Andrena dorsata*, *Andrena flavipes*, *Andrena gravida*, *Andrena haemorrhoea*, *Andrena humilis*, *Andrena labialis*, *Andrena nitida*, *Andrena ovatula*, *Andrena wilkella*, *Anthidium manicatum*, *Apis mellifera*, *Bombus hortorum*, *Bombus lapidarius*, *Bombus pascuorum*, *Bombus terrestris*, *Chelostoma florissomme*, *Eucera longicornis*, *Eucera nigrescens*, *Halictus scabiosae*, *Halictus tumulorum*, *Lasioglossum albipes*, *Lasioglossum calceatum*, *Lasioglossum lativentre*, *Lasioglossum leucozonium*, *Lasioglossum parvulum*, *Lasioglossum pauxillum*, *Lasioglossum spec.*, *Lasioglossum villosulum*, *Nomada fabriciana*, *Nomada flava*, *Nomada marshamella*, *Nomada panzeri*, *Nomada stigma*, *Osmia bicornis*, *Sphecodes gibbus*, *Sphecodes spec.*

In references to the flowers, they were counted using the method of Scheper et al. (2015), counting only the blossomed flowers.

The flowers were classified and the species recognised in the study grasslands are the following:

Alliaria petiolata, *Anthriscus sylvestris*, *Aquilegia vulgaris*, *Arenaria serpyllifolia*, *Belvis perennis*, *Capsella bursa-pastoris*, *Cardamine pratensis*, *Centaurea jacea*, *Cerastium fontanum subsp. vulgare*, *Cerastium glomeratum*, *Crepis biennis*, *Crepis vesicaria subsp. taraxacifolia*, *Cytisus scoparius*, *Euphorbia helioscopia*, *Fumaria officinalis*, *Galium aparine*, *Galium mollugo*, *Geranium dissectum*, *Geranium molle*, *Glechoma hederacea*, *Hieracium pilosella*, *Hypericum humifusum*, *Hypochaeris radicata*, *Lamium album*, *Lamium amplexicaule*, *Lamium purpureum*, *Leucanthemum vulgare*, *Lotus corniculatus*, *Medicago lupulina*, *Neottia ovata*, *Orchis militaris*, *Papaver rhoeas*, *Plantago media*, *Polygala comosa*, *Ranunculus acris*, *Ranunculus bulbosus*, *Ranunculus repens*, *Rhinanthus alectorolophus*, *Sanguisorba minor*, *Senecio vulgaris*, *Silene flos-cuculi*, *Silene latifolia*, *Sisymbrium officinale*, *Sonchus asper*, *Stellaria media*, *Taraxacum officinale*, *Tragopogon pratensis subsp. pratensis*, *Trifolium dubium*, *Trifolium pratense*, *Trifolium repens*, *Veronica anagallis-aquatica*, *Veronica arvensis*, *Veronica chamaedrys*, *Veronica filiformis*, *Veronica officinalis*, *Veronica serpyllifolia*, *Vicia hirsuta*, *Vicia sativa subsp. sativa*, *Viola arvensis*.

In table 1 (Appendix section) can be seen the field data that, among others, have been directly collected: flower species richness, bee species richness, namely how many unique species were counted, and bee abundance that refers to the total number of counted organisms. Subsequently, the following indices have been calculated: bee Shannon's H index and bee Simpson's S index. All the data are linked to each study sites. The 30 areas are named for the localities near which they are located (e.g. GU1 is located at the Gulpen village).

The Shannon's H index in the 1 equation is an index of species diversity and takes account of both abundance of species and evenness of population (Shannon, 1948).

$$H = - \sum_{i=1}^q p_i \times \log p_i \quad (1)$$

Where:

H = Shannon's index

q = number of species

p_i = relative proportion of species i

The Simpson's S index in the 2 equation studies species diversity evaluating the probability of drawing two individuals belonging to the same species (Gregorius and Gillet, 2008).

$$S = 1 - \sum_{i=1}^n p_i^2 \quad (2)$$

Where:

S = Simpson's index

n = total number of individuals belonging to a particular species

p_i = relative proportion of species i

2.3 UAV Data Acquisition

Together with the gathering of field data, a collection of remote sensing images has been started. Drones, namely UAV - unmanned aerial vehicle, were used to collect remotely images in order to test biodiversity at local scale.

A RGB Zenmuse X5 camera (16.0 MP, 17.3 x 13.0 mm sensor) was mounted on the drone (model DJI Matrice 210 RTK) which was equipped with RTK gps. In figure 5 the UAV used in the field campaign can be observed. The flight of the drones was handled by two technicians part of the Netherlands Plant Eco-phenotyping Centre NPEC, who also made contact with the airport authority of Maastricht airport in order to obtain the necessary permit.



Figure 5: The UAV used in field to capture images with RGB camera.

As we can see in figure 6, plates were placed at strategic points in the grasslands used as ground points for UAV, so that, when processing images, overlapping and alignment could be carried out. A fundamental step was to capture the white for to calibrate colours. With regard to the flight height, it was set at 20 meters from the ground, without considering changes in soil morphology.

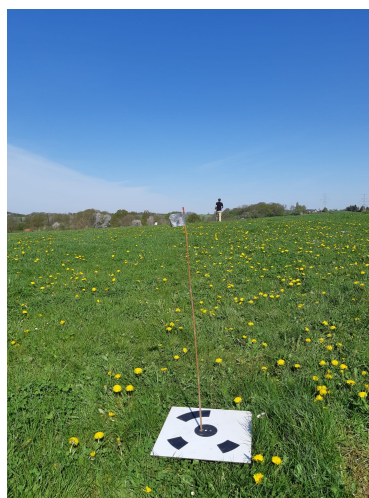


Figure 6: Plates used as ground points for drones allowing the overlapping of images.

2.4 UAV Data Processing

As the image processing phase started, Agisoft Metashape Professional software was used for free trial for UAV photogrammetric processing. By overlapping and aligning the hundreds of images captured with the RGB camera on drone, it was possible to create a 3D image of each study site. This process is called "Structure From Motion". Specifically, the 3D image (in this case namely the height of the vegetation) can be created because the UAV captures numerous images almost continuously, and manages to photograph the vegetation from various angles.

The steps in Agisoft Metashape Professional software to create DEM - Digital Elevation Model - and DTM - Digital Terrain Model - are the following:

- Alignment of photos and creation of a 3D point cloud derived from the features within the images. High accuracy has been set;
- creation of dense cloud and export it in .las format;
- build DEM by using default setting in Metashape and export it in .tiff format;
- build DTM, previously classifying the ground points.

These steps were performed on all 30 areas. The reference system used is WGS84 zone 32N, and the GPS coordinates were automatically obtained from the Ground Control Points placed in field and visible in the images.

We also tested an alternative way of creating DSM - Digital Surface Model - and DTM starting with dense cloud (.las format) in R environment. Examples of dense cloud visualization can be seen in Figure 7 and in Figure 8.

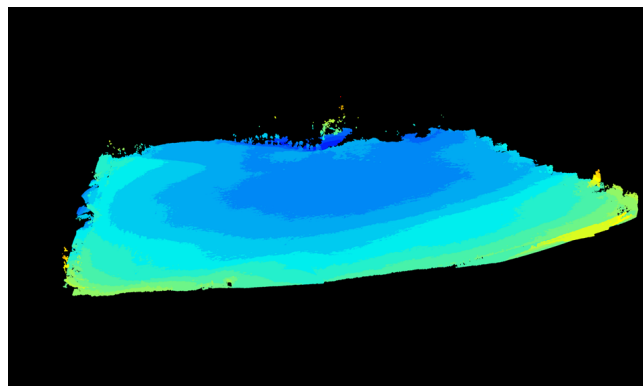


Figure 7: Example of the dense cloud display in R, without zoom.

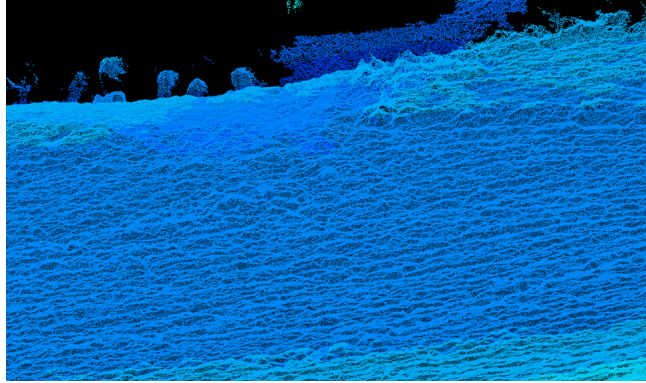


Figure 8: Example of the dense cloud display in R, with zoom.

The DTM has been derived as a raster considering the lowest points in a sub area of 0.1 m and using the `dsmtin` algorithm in the `rasterize_canopy` function of the `lidR` package. Given the sometimes very low vegetation, in this case it is more appropriate to calculate DSM and DTM in R environment.

Both DSM and DTM were calculated using three different resolutions: 10 cm, 25 cm, 50 cm. As a difference between DEM and DTM it was possible to calculate the CHM - Canopy Height Model - representing the height of vegetation.

This is the script created and used for this purpose, example of 10 cm resolution for EL1 area:

```
library(lidR)
library(raster)

setwd("F:/DC")
# open .las file
pc <- readLAS("F:/DC/EL1_DC.las")
# select the lowest point in a sub-area of 0.1 m
thinned = decimate_points(pc, lowest(0.1))
# create raster with lowest points representing dtm
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
# create dsm from dense cloud
dsm <- rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
# create chm
chm<-dsm-dtm
```

The whole script for the 10 cm resolution can be viewed in the Appendix section.

Simultaneously, buffer areas of one meter width have been created in the GIS environment. The starting point were the already defined paths on which the transects were placed in the grasslands. The buffer function in geoprocessing tools allowed to build them.

After creating the buffer areas and CHMs, the latter were cut on the first with a suitable R script. It has been used the `crop` and the `mask` function. To apply this functions in iterative mode on all 30 CHMs, it has been used a `for` loop, as can be seen in following code part, referring to the 10 cm resolution:

```
library(raster)

####CHM crop####
lista_chm<-list.files("F:/CHM_10", full.names = T)
lista_shp<-list.files("F:/test", recursive = T, pattern = "buffer1m.shp",
  full.names = T)

lista_final<-matrix(ncol = 2)
lista_final<-data.frame(lista_final)
listadimezzo<-list()
for (i in 1:length(lista_chm)) {
  raster_chm<-raster(lista_chm[[i]])
  shp_area<-shapefile(lista_shp[i])
  titolo_s<-paste(unlist(strsplit(lista_chm[[i]], split = '/', fixed = T)
    ) [2], sep = "" )
  titolo_s<-paste(unlist(strsplit(titolo_s, split = '_', fixed = T)) [1],
    sep = "" )
  #titolo_s<-paste(unlist(strsplit(titolo_s, split = '.', fixed = T)
    [1], sep = "" )
  chm_cropped<-crop(raster_chm, extent(shp_area))
  chm_cropped2<-mask(chm_cropped, shp_area)
  listadimezzo[i]<-chm_cropped2
}
setwd("F:/chm_10cm_buffer1m")
saveRDS(listadimezzo, "chm10cm_buffer1m.rds")
```

2.5 HH calculation - Rao's Q Index

The heterogeneity index measures diversity. In this case, the focus is on the height of vegetation, for this reason height heterogeneity (HH) has been derived and it has been calculated using Rao's Q index (Rao, 1982) on remote sensing images processed at CHM raster. So, the pixel's values represent the canopy height previously found.

The Rao's Q index (equation 3) can be used for measuring heterogeneity from remote sensing data (Rocchini et al., 2017). According to Rocchini et al. (2017), the Rao's Q index, in an image of N pixels, considers the distance between the values (in this case the heights in CHM raster are used) of pixel i and pixel j , and multiplies it by the relative abundance of both pixel i and pixel j , obtaining $d \times 1/N^2$. Then the sum for all pixel pairs is calculated. Hence, unlike other indices, the Rao's Q takes into account both the value and the abundance of pixels.

$$Q_{rs} = \sum_{i=1}^{F-1} \sum_{j=i+1}^F d_{ij} \times p_i \times p_j \quad (3)$$

Where:

Q_{rs} = Rao's Q index (rs= remote sensing)

F = study plot

p = relative abundance of a pixel value

d_{ij} = distance between i pixel value and j pixel value

Having the CHMs one meter wide and 150 meters long, the Rao's Q index has been calculated on them in R, using a `for loop` on every before-cropped CHM. The code used is the following:


```

####Rao's Q index####
listadimezzo<-readRDS("F:/chm_10cm_buffer1m/chm10cm_buffer1m.rds")

#create data.frame where to save the results
matrix_final_s<-matrix(ncol = 2)
df_final<-data.frame(matrix_final_s)
colnames(df_final)<-c("Rao's Q", "nome_area")

#A for loop for Rao's Q calculation
for(i in 1:length(listadimezzo)){
  mat_s_2<-listadimezzo[[i]]
  mat_s1<-getValues (mat_s_2)
  a<-as.data.frame(mat_s1)
  b<-na.omit(a)
  c<-as.matrix(b)
  mat_s<-as.numeric(c)

  n_s<-length(mat_s)
  n2_s<-n_s^2
  distm_s<-as.matrix(dist(mat_s))

  sumdist_s<-sum(distm_s)
  rao_ndvi_s<- sumdist_s/n2_s

  df_final[[i,1]]<-rao_ndvi_s
  df_final[[i,2]]<-names(listadimezzo[[i]])
}

df_final

setwd("F:/rao_chm_10cm")
saveRDS(df_final, "rao_chm10cm_buffer1m.rds")

```

The results of this calculation of Rao's Q index are visible in table 2 (Appendix section).

3 Results

In order to assess whether images with high pixel diversity, therefore with high values of diversity in the height of vegetation, can be representative of high diversity of bees and flowers, correlation graphs have been created. For the analysis, the field-based variables such as bee abundance, bee species richness, bee Shannon's H index, bee Simpson's S index and flower species richness have been correlated by linear regression analysis to the height heterogeneity of vegetation, expressed through the Rao's Q index values calculated on CHM. In addition, the correlation was studied using different spatial resolutions, respectively 10 cm, 25 cm and 50 cm, obtained by processing CHM at different resolutions. On each graph are annotated the R^2 and the p -value.

3.1 Resolution 10 cm

In figure 9 it can be seen the linear regression analysis showing the relationship between Rao's Q values in 10 cm resolution, representing height heterogeneity calculated on drone-acquired images, and four field-based indices concerning bees: bee abundance, bee species richness, bee Shannon's H index, bee Simpson's S index.

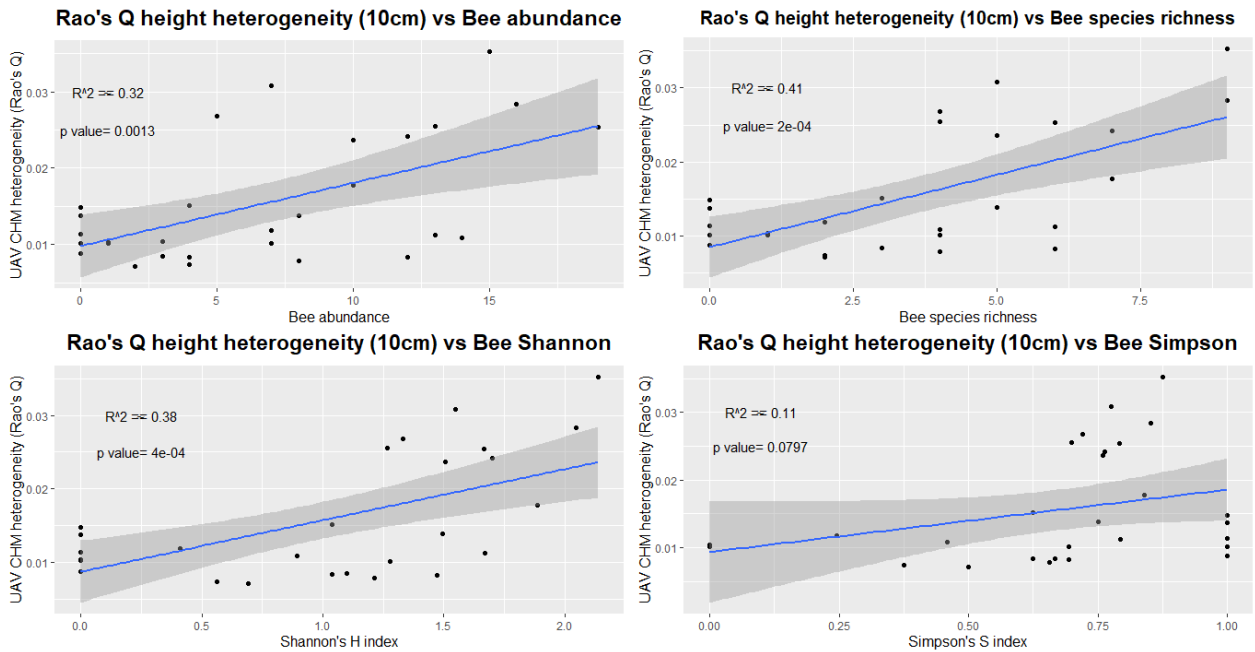


Figure 9: Relationship between height heterogeneity and bee's species abundance and diversity indices, 10 cm resolution.

It can be noted that the greatest correlation can be found with the bee species richness variable ($R^2 = 0.41$) and the bee Shannon's H index ($R^2 = 0.38$), showing a positive and significant correlation, since the p -value are respectively 0.0002 for bee species richness and 0.0004 for bee Shannon's H index, therefore they remain below the threshold of 5% and even 1%. The variable bee abundance shows a slightly lower ($R^2 = 0.32$) but, however, still significant correlation with a p -value of 0.0013 (still less than 5% and than 1%). Bee Simpson's S index has a extremely low correlation and not significant, showing $R^2 = 0.11$ and a higher than 5% p -value (0.0797), so it is not so rare that under assumption of null hypothesis similar results can be obtained.

Figure 10 shows that the correlation between height heterogeneity and flower species richness is also moderate ($R^2 = 0.36$), and significant with a p -value $< 1\%$ (p -value = 0.0006).

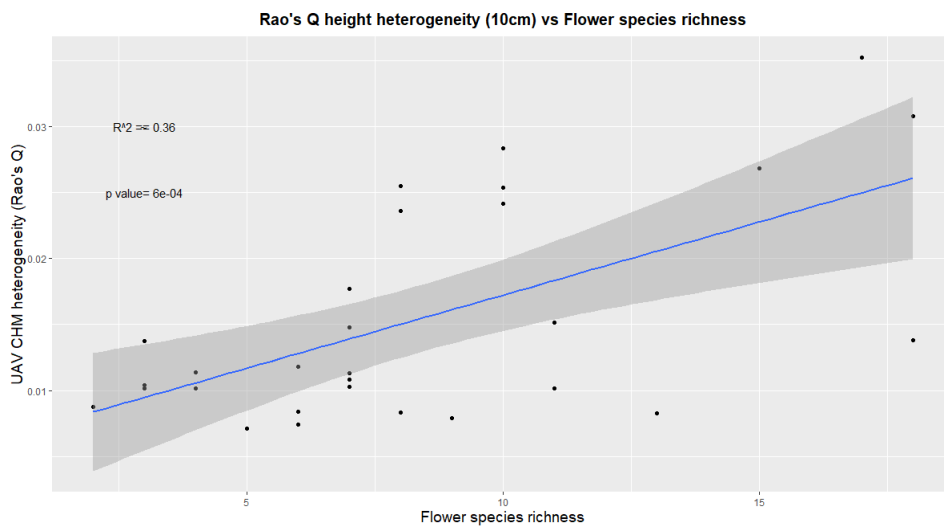


Figure 10: Relationship between height heterogeneity and flower species richness, 25 cm resolution.

3.2 Resolution 25 cm

In figure 11 correlations between Rao's Q and bee diversity indices within 25 cm resolution are visible. Again the correlations are positive and significant for bee abundance, bee species richness and bee Shannon's H index. The greatest and most significant correlation, as in the previous case, is found with the bee species richness variable, shown by a $R^2 = 0.4$ and a $p - value = 0.0002$. Then follows the Bee Shannon's H index, which shows a very similar correlation ($R^2 = 0.37$) and is still significant ($p - value = 0.0005$). Bee abundance variable proves a lower but still moderate correlation with a $R^2 = 0.31$ that is also still significant ($p - value = 0.0018$). As in the former order, bee Simpson's S index reveals a very low correlation ($R^2 = 0.13$), even though slightly higher than in the 10 cm resolution, and moreover not significant ($p - value = 0.0577$).

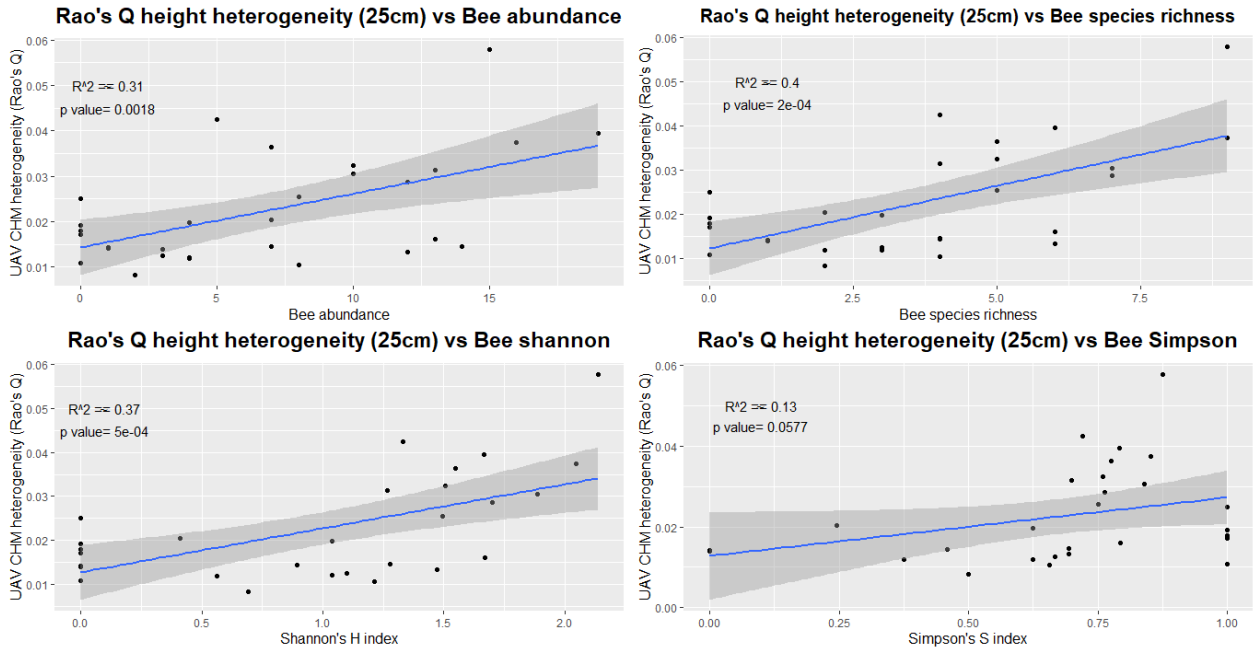


Figure 11: Relationship between height heterogeneity and bee's species abundance and diversity indices, 25 cm resolution.

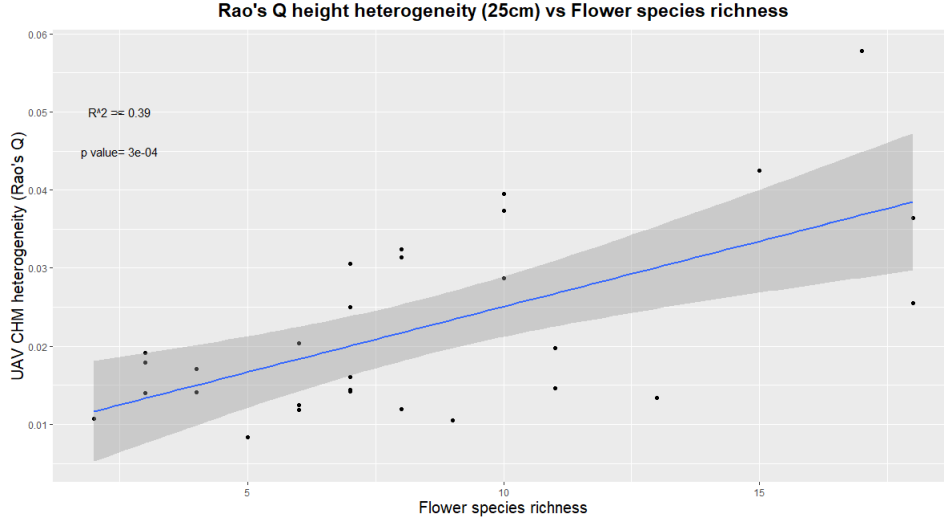


Figure 12: Relationship between height heterogeneity and flower species richness, 25 cm resolution.

The correlation between height heterogeneity and flower species richness within 25 cm resolution, shown in figure 12, is also quite high and significant ($R^2 = 0.39$ and $p - value = 0.0003$).

3.3 Resolution 50 cm

Always according to the trend of previous resolutions, correlations follow the same order of importance and in most cases evidence a decrease in R^2 as resolution of CHM decreases. An exception is the Simpson's S index, whose correlation with HH increases slightly with the decrease in resolution, and at the same time increases the significance: in any case the correlations always remains low. Also for the flower species richness R^2 shows that the best resolution is not 10 cm, but in this case is the 25 cm resolution.

In the case of 50 cm resolution, visible in figure 13, bee species richness and bee Shannon's H index reveal the stronger positive relation with HH (bee species richness shows $R^2 = 0.4$ as in the 25 cm resolutions, and bee Shannon's H index shows $R^2 = 0.36$) with an acceptable level of significance (respectively, $p - value$ are 0.0002 and 0.0006). Bee abundance reveals a moderate and significant correlation ($R^2 = 0.33$ and $p - value = 0.0011$).

Instead, bee Simpson's S index points out low correlation ($R^2 = 0.14$), which, furthermore, is not so significant ($p - value = 0.0453$).

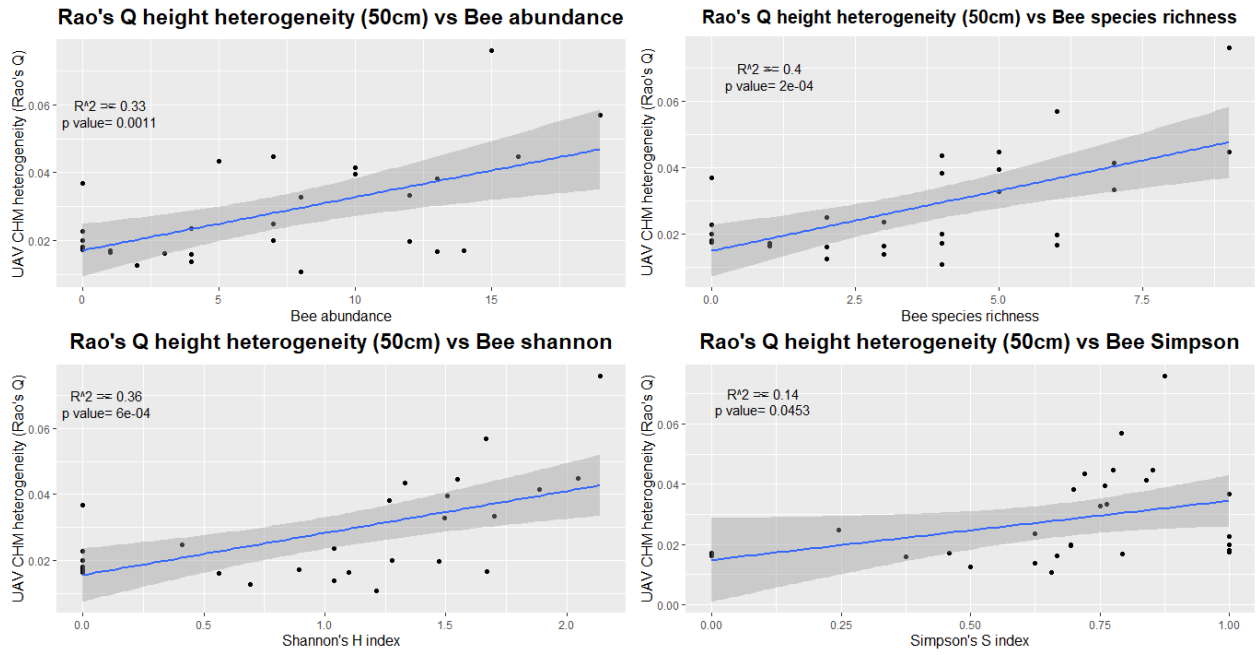


Figure 13: Relationship between height heterogeneity and bee's species abundance and diversity indices, 50 cm resolution.

Figure 14 shows linear regression analysis between height heterogeneity and flower species richness for a 50 cm resolution. As it can be expected given the previous cases, the correlation is quite high ($R^2 = 0.36$) and significant ($p\text{ value} = 0.0006$).

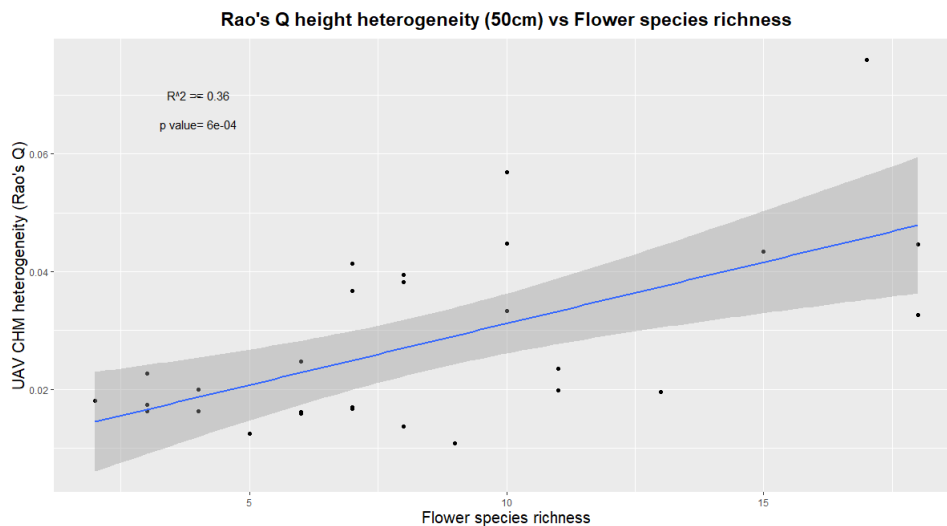


Figure 14: Relationship between height heterogeneity and flower species richness, 50 cm resolution.

4 Discussion

In this study, the Height Variation Hypothesis was tested at multiple spatial resolutions, looking for the relationship between the field variables, measured to express the richness of diversity of a site, and the Height Heterogeneity extrapolated from remotely detected RGB images. In order to calculate the HH it has been used the Rao's Q index.

Observing correlations in different spatial resolutions, the resolution showing the best correlations, as regards the bees, is in most cases the highest (10 cm). This is probably due to the better ability to investigate the different heights in the context of grasslands. A similar behavior is noted in the study of Torresani et al. (2020), in which HVH is also tested, but in forest environments: depending on the type of considered ecosystem, it is necessary to choose the CHM with the resolution most capable of reflecting the structure and heterogeneity of the ecosystem under analysis.

The question of the resolution is still debated, in fact there are cases where high resolutions lead to a greater accuracy, as in the case study of Torresani et al. (2020). On the other hand sometimes too high resolutions risk having too many details that create a disturbance to the analysis: this can happen for example if the pixels are smaller than the object under analysis (Nagendra and Rocchini, 2008). On the other hand, too coarse resolutions are not able to perceive the differences that are sought.

Within each resolution, the same trend of field-based variables is recognised: the strongest correlation is always between HH and bee species richness.

Given the results of the study, it can be argued that the diversity of bees can be predicted by remote local analysis through the heterogeneity index, in this case Rao's Q, confirming the HVH. However, it should also be added that HVH is dependent on the scale at which the image is analysed, because the correlation between bees field data and remote data tends to decrease with decreasing resolution. In fact, in most cases it can be observed that the correlation is higher in 10 cm resolution, while it is a bit lower in the resolutions 25 cm and 50 cm.

Regarding the relationship between HH and flower species richness, it seems to be decisive in all spatial resolution. Thereby according to this study the structural diversity derived from RGB images does also imply a greater flower species richness. Note that, in the case of flowers, the resolution showing the best correlation between HH and flower species richness is the 25 cm resolution, while 10 cm and 50 cm are slightly lower, even though always quite high. This can be explained by what was explained earlier, namely

that in HVH is essential to choose the imagery resolution better capable of capturing the heterogeneity.

It should be noted that it is the first time that such a study has been done using Unmanned Aerial Vehicles, then using the technique of photogrammetry. In fact, through photogrammetry it was possible to evaluate the height of vegetation, by deriving CHM, and then to find the correlation between the diversity of heights in the vegetation and biodiversity. The use of LiDAR data may be appropriate for having more information on three-dimensional structure and therefore on structural diversity (Torresani et al., 2020). However, the use of RGB images remains more available and affordable for initial analysis.

Only the Rao's Q index has been used in this study, although other heterogeneity indices could be used. However, Rao's Q has been chosen because it showed good results in various studies, such as those of Torresani et al. (2019), of Marzialetti et al. (2020) and Khare et al. (2019). Looking at the results of this study, it can be said that the use of the Rao's Q index makes it possible to extrapolate the level of diversity from digital imagery and can be easily linked to field observations. Promising results for this index have been also obtained in the study of Rocchini et al. (2017), in which the advantages for its use in remote sensing images were illustrated.

As stated before, among all the considered field variables, what correlates best with HH is the bee species richness, in all the spatial resolutions. This means that the structural heterogeneity in the grasslands is linked to the diversity of bees. Moreover, given the high correlation between height diversity and flower species richness, the relationship could mean that the greater the heterogeneity of heights, the greater the diversity of flowers and therefore the greater the diversity of bees. This relationship is supported by the study of Gerner and Sargent (2022), in which is illustrated how, in yards, the richness of floral species can be used as a proxy for the diversity and also abundance of bees.

5 Conclusion

The aim of this study was to correlate the diversity measured in the field with the diversity of heights of vegetation through the use of the Rao's Q index. Heterogeneity data was calculated on drone-detected images using photogrammetry. The results show a good correlation, in particular with the bee species richness and the flower species richness. The study therefore confirms HVH, arguing that the HH calculated on the CHM at 10 cm can be a good proxy for the bee species richness, while the HH calculated on the CHM at 25 cm is a good proxy for the flower species richness.

But photogrammetry also shows disadvantages, for example it is not so accurate as LiDAR technology. Thus, among the things that can be improved in such a study is the use of LiDAR sensor mounted on a drone. Moreover, surveys could be carried out on other areas in other countries, as well as the analysis of the presence of other species, such as butterflies.

6 Bibliography

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A Appendix

A.1 Code: CHM

```
library(lidR)
library(raster)

setwd("F:/DC")
# open .las file
pc <- readLAS("F:/DC/EL1_DC.las")
# select the lowest point in a sub-area of 0.1 m
thinned = decimate_points(pc, lowest(0.1))
# create raster with lowest points representing dtm
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
# create dsm from dense cloud
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
# create chm
chm<-dsm-dtm
setwd("F:/CHM_10")
# save chm
writeRaster(chm, "chm_EL1_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/EY1_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_EY1_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/EY2_DC.las")
thinned = decimate_points(pc, lowest(0.1))
```

```

dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_EY2_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/EY3_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_EY3_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/EY4_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_EY4_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/FR1_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm

```

```

setwd("F:/CHM_10")
writeRaster(chm, "chm_FR1_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/FR2_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_FR2_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/FR3_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_FR3_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/FR4_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_FR4_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/GE3_DC.las")

```



```

thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_GE3_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/GU1_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_GU1_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/GU2_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_GU2_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/GU3_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)

```

```

chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_GU3_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/GU4_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_GU4_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/MA2_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_MA2_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/MA3_DC.las") # qui ho caricato il file .las
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_MA3_0.1-10.tiff")

setwd("F:/DC")

```

```

pc <- readLAS("F:/DC/PA2_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_PA2_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/RA4_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_RA4_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/SG3_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_SG3_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/SI1_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())

```

```

dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_SI1_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/SI2_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_SI2_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/VA1_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_VA1_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/VA2_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_VA2_0.1-10.tiff")

```

```

setwd("F:/DC")
pc <- readLAS("F:/DC/VA3_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_VA3_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/VA4_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_VA4_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/WA1_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_WA1_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/WY1_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)

```

```

dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_WY1_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/WY2_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_WY2_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/WY3_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_WY3_0.1-10.tiff")

setwd("F:/DC")
pc <- readLAS("F:/DC/WY4_DC.las")
thinned = decimate_points(pc, lowest(0.1))
dtm <- rasterize_canopy(thinned, algorithm = dsmtin(), res = 0.1)
dtm<-raster(dtm)
dsm <-rasterize_canopy(pc, res = 0.1, dsmtin())
dsm<-raster(dsm)
chm<-dsm-dtm
setwd("F:/CHM_10")
writeRaster(chm, "chm_WY4_0.1-10.tiff")

```

A.2 Code: Correlation between HH and diversity indices graphs

```
####library####
require(lidR)
library(raster)
library(readr)
library(magrittr)
library(gtools)
library(stringr)
library(ggplot2)
library(lubridate)
library(ggpubr)
library(tidyverse)
library(gridExtra)

####Import field data and Rao's Q data, previously merged in a
  spreadsheet
rao_field<-read.table("F:/tutti_uav_campo_definitivo_grahl.csv", sep=",",
  header = T )
View(rao_field)
rao_field<-rao_field[-(1),]
class(rao_field$bee_abundance)

rao_field$rao10cm<-as.numeric(rao_field$rao10cm)
rao_field$rao25cm<-as.numeric(rao_field$rao25cm)
rao_field$rao50cm<-as.numeric(rao_field$rao50cm)

####10cm####

####bee abundance####
####Derive information about correlation
sommario_lidar<-summary(lm(rao_field$bee_abundance ~ rao_field$rao10cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
```

```

r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot1_10<-ggplot(data=rao_field, aes(x=bee_abundance, y=rao10cm)) +
  geom_point() +
  geom_smooth(method='lm')+
  labs(x="Bee_abundance", y="UAV_CHM_heterogeneity_(Rao's_Q)", title="Rao
    's_Q_height_heterogeneity_(10cm)_vs_Bee_abundance") +
  theme(plot.title = element_text(hjust=0.5, vjust=2, size=17, face='bold
    '))+
  theme(axis.title = element_text(size = 15))+
  annotate("text",label=p3, x=1, y=0.025)+
  annotate("text",label=r2_lidar, x=1, y=0.030)

####bee_species_richness####
sommario_lidar<-summary(lm(rao_field$bee_species_richness ~ rao_field$
  rao10cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot2_10<-ggplot(data=rao_field, aes(x=bee_species_richness, y=rao10cm))
  +
  geom_point() +
  geom_smooth(method='lm')+
  labs(x="Bee_species_richness", y="UAV_CHM_heterogeneity_(Rao's_Q)",
    title="Rao's_Q_height_heterogeneity_(10cm)_vs_Bee_species_richness")
  +
  theme(plot.title = element_text(hjust=0.5, vjust=2, size=15, face='bold
    '))+

```



```

theme(axis.title = element_text(size = 14))+
annotate("text",label=p3, x=1, y=0.025)+
annotate("text",label=r2_lidar, x=1, y=0.030)

####bee_shannon####
sommario_lidar<-summary(lm(rao_field$bee_shannon ~ rao_field$rao10cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot3_10<-ggplot(data=rao_field, aes(x=bee_shannon, y=rao10cm)) +
  geom_point() +
  geom_smooth(method='lm')+
  labs(x="Shannon's H_index", y="UAV_CHM_heterogeneity (Rao's Q)", title=
    "Rao's Q_height_heterogeneity (10cm) vs Bee Shannon") +
  theme(plot.title = element_text(hjust=0.5, vjust=2, size=17, face='bold
  '))+
  theme(axis.title = element_text(size = 15))+
  annotate("text",label=p3, x=0.25, y=0.025)+
  annotate("text",label=r2_lidar, x=0.25, y=0.030)

####bee simpson####
sommario_lidar<-summary(lm(rao_field$bee_simpson~ rao_field$rao10cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot4_10<-ggplot(data=rao_field, aes(x=bee_simpson, y=rao10cm)) +

```

```

geom_point() +
geom_smooth(method='lm')+
labs(x="Simpson's S index", y="UAV CHM heterogeneity (Rao's Q)", title=
  "Rao's Q height heterogeneity (10cm) vs Bee Simpson") +
theme(plot.title = element_text(hjust=0.5, vjust=2, size=17, face='bold
  '))+
theme(axis.title = element_text(size = 15))+
annotate("text",label=p3, x=0.1, y=0.025)+
annotate("text",label=r2_lidar, x=0.1, y=0.030)

####flower species richness####
sommario_lidar<-summary(lm(rao_field$flower_species_richness ~ rao_field$
  rao10cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot5_10<-ggplot(data=rao_field, aes(x=flower_species_richness, y=rao10cm
  )) +
geom_point() +
geom_smooth(method='lm')+
labs(x="Flower species richness", y="UAV CHM heterogeneity (Rao's Q)",
  title="Rao's Q height heterogeneity (10cm) vs Flower species
  richness") +
theme(plot.title = element_text(hjust=0.5, vjust=2, size=17, face='bold
  '))+
theme(axis.title = element_text(size = 15))+
annotate("text",label=p3, x=3, y=0.025)+
annotate("text",label=r2_lidar, x=3, y=0.030)

####create mutiplot####
grid.arrange(plot1_10, plot2_10, plot3_10, plot4_10, nrow=2, ncol=2)

```

```

plot10bee<-grid.arrange(plot1_10, plot2_10, plot3_10, plot4_10, nrow=2,
  ncol=2)
plot(plot10bee)

####25cm####

####bee abundance####
sommario_lidar<-summary(lm(rao_field$bee_abundance ~ rao_field$rao25cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot1_25<-ggplot(data=rao_field, aes(x=bee_abundance, y=rao25cm)) +
  geom_point() +
  geom_smooth(method='lm')+
  labs(x="Bee_abundance", y="UAV_CHM_heterogeneity_(Rao's_Q)", title="Rao
  's_Q_height_heterogeneity_(25cm)_vs_Bee_abundance") +
  theme(plot.title = element_text(hjust=0.5, vjust=2, size=17, face='bold
  '))+
  theme(axis.title = element_text(size = 15))+
  annotate("text",label=p3, x=1, y=0.045)+
  annotate("text",label=r2_lidar, x=1, y=0.050)

####bee_species_richness####
sommario_lidar<-summary(lm(rao_field$bee_species_richness ~ rao_field$
  rao25cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)

```

```

p3<-(paste(p1, pval, sep = ""))

plot2_25<-ggplot(data=rao_field, aes(x=bee_species_richness, y=rao25cm))
  +
  geom_point() +
  geom_smooth(method='lm')+
  labs(x="Bee_species_richness", y="UAV_CHM_heterogeneity_(Rao's_Q)",
       title="Rao's_Q_height_heterogeneity_(25cm)_vs_Bee_species_richness")
  +
  theme(plot.title = element_text(hjust=0.5, vjust=2, size=15, face='bold
  '))+
  theme(axis.title = element_text(size = 14))+
  annotate("text",label=p3, x=1, y=0.045)+
  annotate("text",label=r2_lidar, x=1, y=0.050)

####bee_shannon####
sommario_lidar<-summary(lm(rao_field$bee_shannon ~ rao_field$rao25cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot3_25<-ggplot(data=rao_field, aes(x=bee_shannon, y=rao25cm)) +
  geom_point() +
  geom_smooth(method='lm')+
  labs(x="Shannon's_H_index", y="UAV_CHM_heterogeneity_(Rao's_Q)", title=
  "Rao's_Q_height_heterogeneity_(25cm)_vs_Bee_shannon") +
  theme(plot.title = element_text(hjust=0.5, vjust=2, size=17, face='bold
  '))+
  theme(axis.title = element_text(size = 15))+
  annotate("text",label=p3, x=0.1, y=0.045)+
  annotate("text",label=r2_lidar, x=0.1, y=0.050)

####bee simpson####

```

```

sommario_lidar<-summary(lm(rao_field$bee_simpson~ rao_field$rao25cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot4_25<-ggplot(data=rao_field, aes(x=bee_simpson, y=rao25cm)) +
  geom_point() +
  geom_smooth(method='lm')+
  labs(x="Simpson's S_index", y="UAV_CHM_heterogeneity (Rao's Q)", title=
    "Rao's Q_height_heterogeneity (25cm) vs Bee Simpson") +
  theme(plot.title = element_text(hjust=0.5, vjust=2, size=17, face='bold
  '))+
  theme(axis.title = element_text(size = 15))+
  annotate("text",label=p3, x=0.1, y=0.045)+
  annotate("text",label=r2_lidar, x=0.1, y=0.050)

####flower species richness####
sommario_lidar<-summary(lm(rao_field$flower_species_richness ~ rao_field$
  rao25cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot5_25<-ggplot(data=rao_field, aes(x=flower_species_richness, y=rao25cm
  )) +
  geom_point() +
  geom_smooth(method='lm')+

```

```

labs(x="Flower_species_richness", y="UAV_CHM_heterogeneity_(Rao's_Q)",
      title="Rao's_Q_height_heterogeneity_(25cm)_vs_Flower_species_richness") +
theme(plot.title = element_text(hjust=0.5, vjust=2, size=17, face='bold
  '))+
theme(axis.title = element_text(size = 15))+
annotate("text",label=p3, x=2.5, y=0.045)+
annotate("text",label=r2_lidar, x=2.5, y=0.050)

####create multiplot####
grid.arrange(plot1_25, plot2_25, plot3_25, plot4_25, nrow=2, ncol=2)
plot25bee<-grid.arrange(plot1_25, plot2_25, plot3_25, plot4_25, nrow=2,
  ncol=2)
plot(plot25bee)

####50cm####

####bee abundance####
sommario_lidar<-summary(lm(rao_field$bee_abundance ~ rao_field$rao50cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot1_50<-ggplot(data=rao_field, aes(x=bee_abundance, y=rao50cm)) +
  geom_point() +
  geom_smooth(method='lm')+
  labs(x="Bee_abundance", y="UAV_CHM_heterogeneity_(Rao's_Q)", title="Rao
    's_Q_height_heterogeneity_(50cm)_vs_Bee_abundance") +
  theme(plot.title = element_text(hjust=0.5, vjust=2, size=17, face='bold
    '))+
  theme(axis.title = element_text(size = 15))+
  annotate("text",label=p3, x=1, y=0.055)+
  annotate("text",label=r2_lidar, x=1, y=0.060)

```

```

####bee_species_richness####
sommario_lidar<-summary(lm(rao_field$bee_species_richness ~ rao_field$
  rao50cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot2_50<-ggplot(data=rao_field, aes(x=bee_species_richness, y=rao50cm))
  +
  geom_point() +
  geom_smooth(method='lm')+
  labs(x="Bee_species_richness", y="UAV_CHM_heterogeneity_(Rao's_Q)",
    title="Rao's_Q_height_heterogeneity_(50cm)_vs_Bee_species_richness")
  +
  theme(plot.title = element_text(hjust=0.5, vjust=2, size=15, face='bold
  '))+
  theme(axis.title = element_text(size = 14))+
  annotate("text",label=p3, x=1, y=0.065)+
  annotate("text",label=r2_lidar, x=1, y=0.07)

####bee_shannon####
sommario_lidar<-summary(lm(rao_field$bee_shannon ~ rao_field$rao50cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot3_50<-ggplot(data=rao_field, aes(x=bee_shannon, y=rao50cm)) +

```

```

geom_point() +
geom_smooth(method='lm')+
labs(x="Shannon's H index", y="UAV CHM heterogeneity (Rao's Q)", title=
  "Rao's Q height heterogeneity (50cm) vs Bee Shannon") +
theme(plot.title = element_text(hjust=0.5, vjust=2, size=17, face='bold
  '))+
theme(axis.title = element_text(size = 15))+
annotate("text",label=p3, x=0.1, y=0.065)+
annotate("text",label=r2_lidar, x=0.1, y=0.07)

####bee simpson####
sommario_lidar<-summary(lm(rao_field$bee_simpson~ rao_field$rao50cm))
sommario_lidar
#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
  digits = 2))))
p1<-paste ( "p value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot4_50<-ggplot(data=rao_field, aes(x=bee_simpson, y=rao50cm)) +
  geom_point() +
  geom_smooth(method='lm')+
  labs(x="Simpson's S index", y="UAV CHM heterogeneity (Rao's Q)", title=
    "Rao's Q height heterogeneity (50cm) vs Bee Simpson") +
  theme(plot.title = element_text(hjust=0.5, vjust=2, size=17, face='bold
    '))+
  theme(axis.title = element_text(size = 15))+
  annotate("text",label=p3, x=0.1, y=0.065)+
  annotate("text",label=r2_lidar, x=0.1, y=0.07)

####flower species richness####
sommario_lidar<-summary(lm(rao_field$flower_species_richness ~ rao_field$
  rao50cm))
sommario_lidar

```



```

#add Rsquared to the plot####
r2_2_lidar<- round(sommario_lidar$r.squared, digits = 2)
r2_lidar<-as.character(bquote(~R^2 == .(round(sommario_lidar$r.squared,
      digits = 2))))
p1<-paste ( "p_value=")
pval<- round(sommario_lidar$coefficients[2,4], digits = 4)
p3<-(paste(p1, pval, sep = ""))

plot5_50<-ggplot(data=rao_field, aes(x=flower_species_richness, y=rao50cm
  )) +
  geom_point() +
  geom_smooth(method='lm')+
  labs(x="Flower_species_richness", y="UAV_CHM_heterogeneity_(Rao's_Q)",
    title="Rao's_Q_height_heterogeneity_(50cm)_vs_Flower_species_
    richness") +
  theme(plot.title = element_text(hjust=0.5, vjust=2, size=17, face='bold
    '))+
  theme(axis.title = element_text(size = 15))+
  annotate("text",label=p3, x=4, y=0.065)+
  annotate("text",label=r2_lidar, x=4, y=0.07)

####create a multiplot####
grid.arrange(plot1_50, plot2_50, plot3_50, plot4_50, nrow=2, ncol=2)
plot50bee<-grid.arrange(plot1_50, plot2_50, plot3_50, plot4_50, nrow=2,
  ncol=2)
plot(plot50bee)

```

A.3 Tables

Area	Flower sp.richness	Bee Shannon	Bee Simpson	Bee sp.rich.	Bee abundance
EL1	3	0	0	1	1
EY1	10	2.046738533	0.851562500	9	16
EY2	10	1.69878299	0.763888889	7	12
EY3	18	1.494175138	0.750000000	5	8
EY4	6	1.098612289	0.666666667	3	3
FR1	7	1.671595278	0.792899408	6	13
FR2	3	0	0	1	3
FR3	13	1.473502385	0.694444444	6	12
FR4	7	0	0	1	1
GE3	11	1.039720771	0.625000000	3	4
GU1	3	0	1	0	0
GU2	7	0.895332666	0.459183673	4	14
GU3	15	1.33217904	0.720000000	4	5
GU4	8	1.039720771	0.625000000	3	4
MA2	4	0	1	0	0
MA3	18	1.549826046	0.775510204	5	7
PA2	5	0.693147181	0.500000000	2	2
RA4	11	1.277034259	0.693877551	4	7
SG3	6	0.410116318	0.244897959	2	7
SI1	3	0	1	0	0
SI2	9	1.213007566	0.656250000	4	8
VA1	8	1.265856752	0.698224852	4	13
VA2	2	0	1	0	0
VA3	7	0	1	0	0
VA4	7	1.886696785	0.840000000	7	10
WA1	6	0.562335145	0.375000000	2	4
WY1	8	1.504788284	0.760000000	5	10
WY2	10	1.666875697	0.792243767	6	19
WY3	17	2.13833306	0.875000000	9	15
WY4	4	0	0	1	1

Table 1: Field data collected: Flower species richness, Bee Shannon’s H index, Bee Simpson’s S index, Bee species richness, Bee abundance, and the corresponding area.

Area	Rao's Q 10 cm	Rao's Q 25 cm	Rao's Q 50 cm
EL1	0.0105195	0.0160477	0.017904
EY1	0.028346	0.03788	0.044727
EY2	0.024152	0.028666	0.03334
EY3	0.013814	0.025517	0.032705
EY4	0.008403	0.012511	0.016177
FR1	0.011285	0.016116	0.016684
FR2	0.010375	0.013978	0.016301
FR3	0.008269	0.013376	0.01959
FR4	0.010255	0.014225	0.017032
GE3	0.01513	0.01972	0.023563
GU1	0.01017	0.017889	0.017372
GU2	0.010841	0.014413	0.017035
GU3	0.026804	0.042463	0.043444
GU4	0.008315	0.011974	0.01367
MA2	0.011366	0.01714	0.019967
MA3	0.030803	0.036427	0.044678
PA2	0.007114	0.008313	0.01255
RA4	0.010128	0.014602	0.019869
SG3	0.011826	0.020401	0.024811
SI1	0.013737	0.019176	0.022755
SI2	0.007877	0.01051	0.010816
VA1	0.025505	0.031433	0.038253
VA2	0.008772	0.010756	0.018065
VA3	0.014802	0.024977	0.036779
VA4	0.017729	0.03053	0.041415
WA1	0.00739	0.011823	0.015951
WY1	0.023621	0.032447	0.039496
WY2	0.02536	0.039512	0.056926
WY3	0.035236	0.057827	0.075962
WY4	0.010171	0.014166	0.016359

Table 2: Rao's Q index values of the 30 areas, divided by resolution.