Swansea University
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Livestock grazing impacts bee (Apoidea) pollination networks in saltmarshes of South Wales

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Summary

Saltmarsh habitats serve as crucial connective terrain for wildlife, yet they are exploited for livestock pasture. Halophytic saltmarsh herbs provide abundant flower resources for pollinators such as bees (Hymenoptera: Apoidea) and maintain a supply of nectar resources late in the flowering season. Several studies have demonstrated positive and negative impacts of grazing livestock management on grassland bee communities; however, the impacts of grazing on bees or the structure of their associated food plants in saltmarsh habitats is unknown.

The study aimed to test the hypothesis that grazing impacts bee populations by (1) increasing habitat heterogeneity, (2) increasing flower diversity, (3) reducing forb biomass, and (4) consuming flowers.

I compared mean values of bee populations and the structure of insect-pollinated plants in plots with different grazing intensities in Southwest Wales. Effects of grazing and insect-pollinated plant structure on bees were examined using GLMs.

Flower richness varied across sites and tended to be higher in more intensively grazed plots, though no significant effect of grazing on flower richness was detected. Bee community composition was primarily driven by the abundance of two mass-flowering species: *Tripolium pannonicum*, which decreased in biomass with grazing, and *Limonium vulgare*, which was largely absent under high grazing disturbance.

The results highlight the negative impact of grazing on dominant nectar-providing flowers, while also confronting the assumed value of saltmarsh flora for supporting local bee diversity. Significant reductions in grazing intensity and extensive rest periods on UK marshes are necessary for sustainable management of floral resources.

Lay summary

Saltmarshes are coastal grasslands that form at the interface between land and marine environments. Distributed along coastlines, saltmarshes are thus valued both as a wildlife habitat, and as a passageway connecting environments. Vegetation within saltmarsh habitats is typically composed of salt-tolerant shrubs, grasses, and herbs. The presence of nectar-producing flowers suggests that saltmarshes may serve as valuable foraging and nesting habitats for pollinators such as bees (Hymenoptera: Apoidea).

Saltmarshes are commonly exploited for farmland, especially for livestock pasturage. Grazing by livestock on grasslands can reshape plant communities through several mechanisms, including trampling, grazing, compaction of sediment, and nutrient deposition from animal defecation. Studies have demonstrated both positive and negative effects of grazing livestock management on grassland bees, primarily through changes in the composition of saltmarsh plant species. However, few papers have assessed how livestock grazing management impacts bee communities on saltmarshes and how the resulting changes in plant structure impacts food for bees.

The study aimed to test the hypothesis that grazing impacts bee populations by (1) increasing the variation in the height of flower structures, (2) increasing the number of flower species found in the area (known as flower diversity) (3) reducing the abundance of flowering plants, or (4) consuming only the flowers.

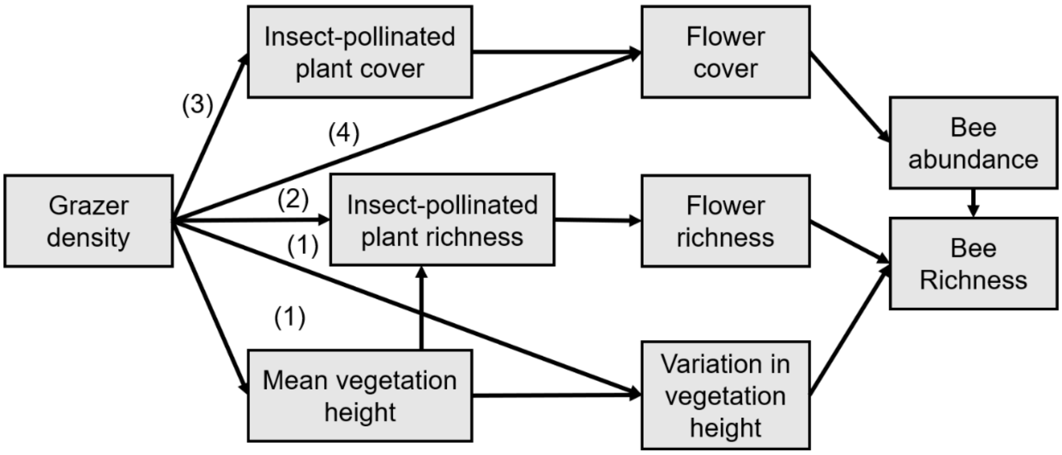

Figure 1.1 The potential mechanisms by which grazing affects bee communities. Numbers represent the tested hypotheses corresponding to each causal pathway.

I recorded aspects of the bee community, as well as the abundance of flowers and plants in plots at sites in Southwest Wales. The bee populations and the structure of insect-pollinated plants were compared against measurements of grazing intensity. The impact of plant structure on bees was then tested.

Animal grazing on grasslands typically inhibits grasses from dominating the plant community. When grasses are inhibited, a greater number of flower species can grow, typically increasing bee diversity, as there are more types of food plants to consume. In this study, the abundance of two flower species primarily influenced the number of bees; *T. pannonicum,* which declined in biomass with grazing, and *L. vulgare*- which was scarce in grazed marshes. The range of types of bee present (termed "functional richness") was generally low in saltmarshes. Consequently, fewer ecological roles that can be performed by bees could result in a decreased value in the plant-pollinator community. Low functional richness might have arisen because nectar was produced by plant species of only one flower type, or because the harsh saltmarsh environment imposes a strong natural limitation on which pollinators survive– known as abiotic filtering.

The results illustrate the negative impact of grazing on the flowering saltmarsh plants that provide the most nectar resources. Reductions in grazing intensity, and long periods of rest may be required to manage and restore important flower resources for bee populations where selected flowering plants are present.

Declarations

This work has not previously been accepted in substance for any degree and is not being concurrently submitted in candidature for any degree.

Signed: [redacted]

Date: 24/07/2024

This thesis is the result of my own investigations, except where otherwise stated. Other sources are acknowledged by footnotes giving explicit references. A bibliography is appended.

Signed: [redacted]

Date: 24/07/2024

I hereby give consent for my thesis, if accepted, to be available for electronic sharing

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The University's ethical procedures have been followed and, where appropriate, ethical approval has been granted.

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Date: 24/07/2024

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Acknowledgements

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Definitions or abbreviations

Abbreviation	Meaning
CB	Crymlyn Burrows ungrazed sample site
CR	Crofty grazed sample site
Grazed	Denotes a unit of space that has been used for pasture and is browsed by livestock
LU	Livestock Unit - the grazing equivalent of one adult dairy cow producing 3,000 kg of milk annually.
$LUha^{-1}$	Livestock Unit per hectare
LW	Llanelli Wetlands sample sites
LWG	Llanelli Wetlands grazed sample site
LWU	Llanelli Wetlands ungrazed sample site
NVC	National Vegetation Classification - acting as the main terrestrial habitat classification for UK Common Standards Monitoring and ecological assessments
PB	Pembrey grazed sample site
Ungrazed	Denotes a unit of space that was not grazed by livestock, irrespective of any wild herbivore activity.

Tables

Figures

1.0. Introduction

1.1. The ecological role of saltmarshes

Insect pollination is crucial for ecological health, facilitating the reproduction of approximately 75% of all flowering plant species (Eilers *et al.* 2011; Jordan *et al.* 2021). The value of pollination services has been estimated at US$267-657 billion per annum to the global agricultural economy (Porto *et al.* 2020). Bees (Hymenoptera: Apoidea) are recognised as highly efficient pollinators across many plant taxa because they actively collect and use pollen as their primary food source (Winfree, Gross & Kremen 2011). However, bee populations are suffering declines globally due to habitat fragmentation, disturbance, and agriculturalization, which drives losses of foraging and nesting resources (Sánchez-Bayo & Wyckhuys 2019). The impacts of anthropogenic exploitation on the biodiversity, stability, and functionality of marshes have highlighted a cause for concern (McKinley *et al.* 2022).

Saltmarshes are coastal grasslands that serve as wildlife corridors connecting terrestrial and aquatic environments (JNCC 2008; Natural Resources Wales 2020; Ladd 2021). Halophytic grasses, shrubs and densely flowering herbs typically dominate in UK marshes (Adam 1990; Fantinato *et al.* 2018b). Flowering herbs can be rich in pollen and nectar (Dmitruk *et al.* 2022), and thus, saltmarsh habitats could provide resources essential for connecting and maintaining bee populations (Davidson *et al.* 2020). However, the potential for saltmarsh habitats as pollinator habitat is often overlooked (Van Klink *et al.* 2016). Hence, understanding how saltmarsh habitats provide pollen resources to bees may be key to preserving pollinators.

1.2. Impact of livestock grazing on saltmarsh habitats

Saltmarshes in Wales have been exploited for livestock pasture since at least the Romano-British period (Allen & Fulford 1986; Kneafsey, Ilbery & Jenkins 2001; Chatters 2017). To date, livestock pasturage has been the most common use of saltmarsh habitat (Davidson *et al.* 2017; Muenzel & Martino 2018). Concerns arising from the intensive use of livestock in saltmarshes include a reshaping of plant community diversity and structure through trampling, selective defoliation, compaction of sediment, or nitrogen deposition resulting from animal defecation (Gedan, Silliman & Bertness 2009). More recently, the effects of grazing on microbial diversity and soil nutrient dynamics, as well as their consequences for carbon-nitrogen sequestration, have been explored (Zhou *et al.* 2017; Zhan *et al.* 2020; Zeying *et al.* 2023). Mounting support for negative impacts of land exploitation have highlighted the need for sustainable livestock management practices on the coastal fringe (Phelan, Shaw & Baylis 2011; Environment Agency 2022).

1.3. Grazing dynamics and pollinator conservation

Grazing intensity is a moderator of saltmarsh habitat properties (He & Silliman 2016). Saltmarshes left ungrazed typically result in unregulated plant succession and the dominance of competitive plant species. Respectively, in ungrazed brackish, lower, and higher saltmarshes, monocultures of *Phragmites australis*, *Atriplex portulacoides* and *Elytrigia atherica* are expected to dominate (Esselink *et al.* 2000; Bos *et al.* 2002; Wanner *et al.* 2014; Van Klink *et al.* 2016). The dominance of late-successional grasses is expected to threaten forb populations (Bos *et al.* 2002) and some invertebrate populations (van Klink *et al.* 2013). In contrast, grasslands that experience high grazing intensities display short, uniform swards with high species diversity and low habitat heterogeneity (Garrido *et al.* 2019). Extensive (or intermediate) grazing on saltmarshes is expected to prevent the encroachment of dominant shrubs and grasses, such as *E.altherica*, and promote flower-rich communities (Bakker *et al.* 2002).

Numerous studies report that high floral richness can benefit bee diversity by increasing the quality and quantity of foraging resources (nectar and pollen) (Dunne, Williams & Martinez 2002; Cardinale *et al.* 2006; Holzschuh *et al.* 2007). However, several studies on European saltmarshes have revealed that grazer-mediated declines of key flowering plants negatively impacted pollinating bee populations. Furthermore, increases in the richness of flowers due to grazing never compensated for the concurrent decline in flower abundance (Nolte, Esselink & Bakker 2013; Davidson *et al.* 2020). The studies contend that the positive relationship between grassland flower diversity and pollinator diversity may not be present in coastal systems (Fantinato *et al.* 2018a).

In such coastal systems, pollinator populations are proposed to be maintained by few animal-pollinated plant species, in contrast to the widely accepted view that high plant diversity benefits bees (Fantinato *et al.* 2018b). Possible mechanisms that facilitate the contrasting observations include differences in the attractiveness of inflorescences, disproportionate nectar distribution between plant species, selective pollination interactions and unbalanced sampling effort (Fantinato *et al.* 2018a). However, the mechanism producing the observed plant-pollinator networks is unknown. Understanding the links between saltmarsh floral communities and bee diversity will be crucial for the conservation of connective coastal bee habitats. Furthermore, emphasis on the functional role of grazer density as a mediator of plant-pollinator communities is required (Paine 1976).

1.4. Effects of livestock species

The impact of grazing on saltmarsh pollinator communities depends on the composition of grazing livestock (Van Klink *et al.* 2016). For example, sheep grazing often lowers bumblebee diversity (Carvell 2002), due to their high selectivity towards flowering legumes and forbs (Dumont *et al.* 2011). Experimental grazing on German saltmarshes found that sheep grazing may eradicate a key flowering plant, Sea aster *Tripolium pannonicum* from an ecosystem (Kiehl *et al.* 1996), having strong detrimental effects on the pollinator community (van Klink & van Schrojenstein Lantman 2015). In contrast, cattle grazing has been shown to prevent the growth of some dominant shrubs in Mediterranean grasslands, promoting floral diversity by maintaining open vegetation patches (Vulliamy, Potts S G. & Willmer 2006). Moderate trampling may also benefit ground-nesting bees by compacting or poaching ground substrates. However, trampling by denser herds may destroy flowering plants and bee nests (Nolte, Esselink & Bakker 2013; Scohier *et al.* 2013).

A study on saltmarsh pastures containing horses and cattle showed, the relative impacts of grazer species interacted with grazing intensity. At high stocking densities, trampling by horses primarily drove the destruction of T. *pannonicum*. Conversely, at low stocking density, cattle impacted *T. pannonicum* more heavily, as cattle selectively foraged for *T. pannonicum* over the less palatable grasses (Nolte, Esselink & Bakker 2013). Evidence for animal-mediated changes in plant communities is extensive, yet little evidence is presented to understand the interactive effects of grazing intensity on pollinator foraging resources and their impacts on coastal bee abundance and diversity.

The study aims to address this gap by assessing how grazing level impacts the diversity of insect-pollinated plant and bee communities in saltmarshes of Southwest Glamorgan, Wales. I tested whether grazers influence plant and bee biodiversity, as well as whether the influence of grazers on bees is direct or mediated through their effect on plants. I hypothesized that grazing has a positive impact on plant richness by reducing the limiting effects of superior plant competitor species on inferior competitors. Additionally, I sought to discriminate between alternative (but not necessarily exclusive) hypotheses about the role of grazers on bee biodiversity: (1) the effect of grazers on bees could be positive through increasing habitat heterogeneity and thus niche diversity, or (2) the effect of grazers on bees could be positive through their positive effect on plant diversity or (3) negative through reduction of flower prevalence, or (4) negative through reduction of insect-pollinated plant biomass which may be additionally modified through selective grazing of plant species (Figure 1.1).

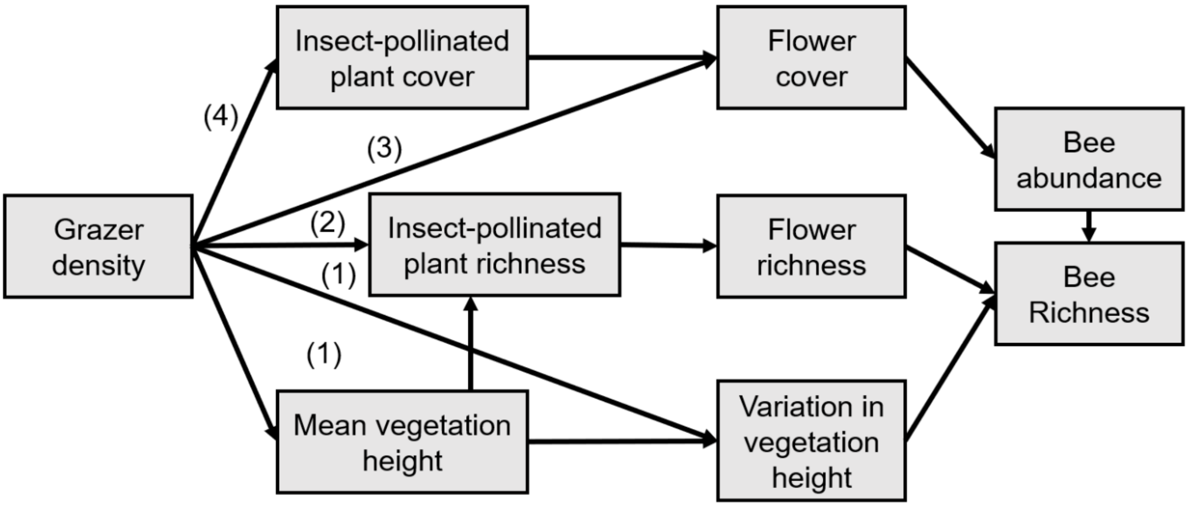

Figure 1.1 The potential mechanisms by which grazing affects Bee communities. Numbers represent the tested hypotheses corresponding to each causal pathway.

2.0. Methods

2.1. Study site description

Field data collection took place between April 14th 2023 and September 2nd 2023 in four saltmarsh sites in South Wales (UK); Data was collected from three ungrazed sites (Pembrey Saltings, Crymlyn Burrows, and Llanelli) and two grazed sites (Llanrhidian and Llanelli).

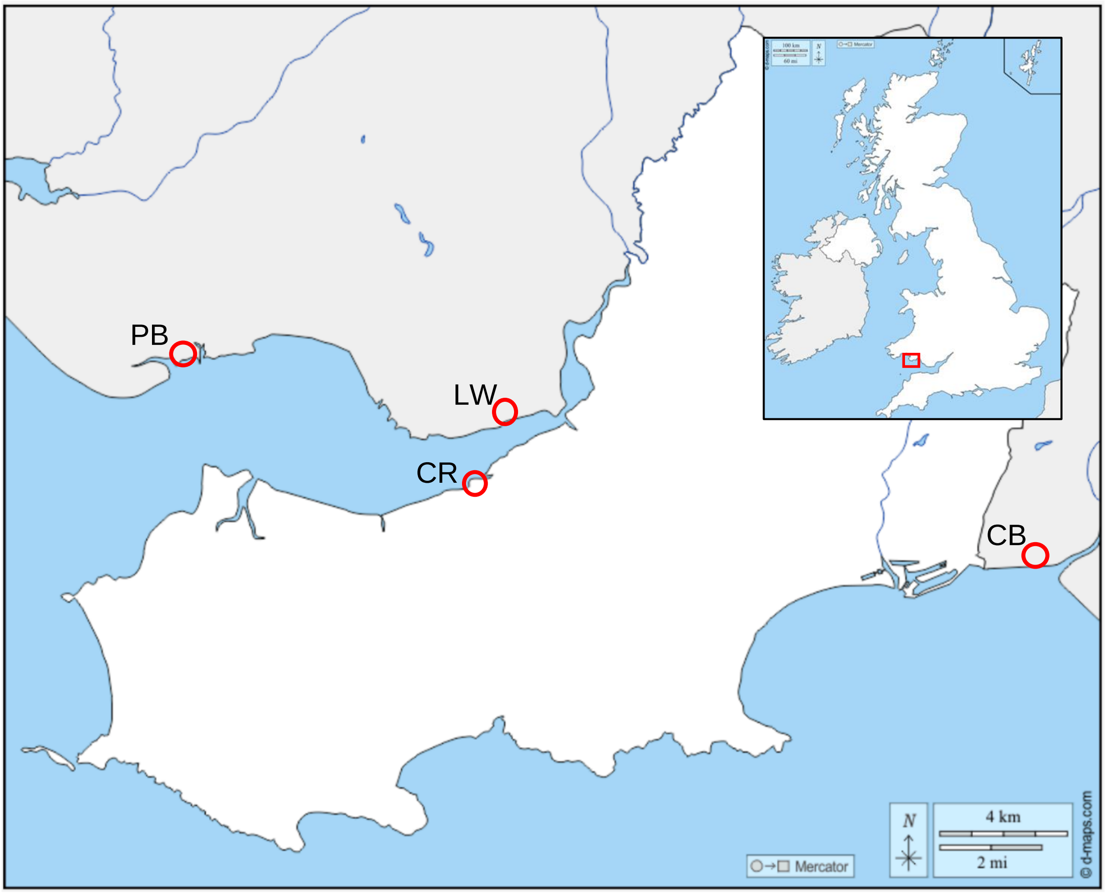

Figure 2.1. Main: Map of the Swansea region shaded in white, and four sites used in the study. Top right: Map of UK, shaded in white, with location of the Swansea region.

The surveyed sites are situated along the coast of the Bristol Channel, which experiences a hyper-tidal regime (Pye & Blott 2014). Three of the four sites are situated along the Loughor Estuary between Carmarthenshire and Swansea. The Loughor estuary is a coastal plain estuary with a spit enclosure and funnel shape

(Elliott & Gardiner 1981), reaching 16 km upstream of the mouth during spring tide (Bennett *et al.* 2023) and with spring and neap tidal ranges of 7.1 m and 3.3 m respectively (Robins 2009).

The 2.18 km^2 Llanrhidian Marsh runs along the south bank of the Bury estuary. Llanrhidian Marsh (CR) has experienced year-round intense grazing by sheep, horse and ponies for over 40 years, with the introduction of cattle three years prior to the study. Urban development borders the east of the site, and a mosaic of grazed semi-natural grasslands and small patches of semi-natural woodland borders the south.

Llanelli Wetlands (LW) contains an area of 0.93 km^2 located on the north bank, 8km inland of the estuary mouth. The marsh has been extensively grazed by cattle between May and November for over ten years (Davidson *et al.* 2020), except for a 0.07 km^2 area of ungrazed marsh, separated from the grazed marsh by a river (hence, the grazed and ungrazed sites were designated as LWG and LWU respectively). A mosaic of semi-natural wetland lakes and deciduous woodlands borders the sites.

Pembrey (PB) (area 0.86 km^2) occupies the north bank coastline at the mouth of the estuary, and the sites have remained ungrazed by livestock for at least 30 years (Davidson *et al.* 2020). The site in PB was bordered by coastal fixed dune grassland and deciduous dune woodland in the north. The southern face of the marsh beyond its marsh creek also contained fixed dune grassland.

Crymlyn Burrows saltmarsh (CB) (area 0.33 km^2) is formed on the western half of the River Neath mouth in north-eastern Swansea Bay. The border south and west of the CB site was majorly composed of coastal fixed dune grassland and dune shrubland, while the northern face of the marsh beyond its marsh creek was composed of wet deciduous woodland and fixed dune grassland (Pye & Blott 2014). Mean spring and neap tidal ranges are 8.6 m and 4.1 m, respectively (National Tidal Sea Level Facility, 2004), and the site has remained ungrazed by livestock for at least 30 years (Davidson *et al.* 2020), although it exhibits some areas heavily grazed by rabbit populations.

2.2. Sample area

Tidal dynamics and animal movements prevented the establishment of permanent transects. Thus, a total of 21 open rectangular sampling plots were identified on a map of the four sites using UK Ordinance Survey coordinates and Digimap software (Digimap 2023) (Figure 2.2). The sites each consisted of five of the 21 plots except for LW, which contained part grazed marsh (LWG) and part ungrazed marsh (LWU). For this site, six sampling plots were established, including three plots in LWG and three plots in LWU, thereby ensuring equal sampling effort for both grazed and ungrazed locations within the site. UK Ordinance Survey smartphone app (OS Locate, version 1.3.1) was used to locate plots and record transects.

A transect of 30 m was randomly placed in each plot during each site visit, along which all independent environmental variables were measured. A new transect was identified at each visit by locating the corner of the plot that was closest to the site entrance and generating a random value for the distance along the shape to the opposite corner of the plot. The distance along the shape was used as the starting point of the transect. Then, a random bearing between 0° and 360° from north was chosen as the direction to lay the transect. If the generated transect lay outside the plot or could not be sampled safely due to an intersection with a creek (>1 m width) or other obstruction, a new bearing was generated. The transect was measured from the starting point to the endpoint using a ball of string of length 30 m, marked at 5m intervals and anchored at the ends with two metal rods.

Ten sequential time windows, each two weeks long, were identified for the duration of the study. Each site was visited once within each time window. Sites were visited only on days forecast with the likelihood of rain below 20%.

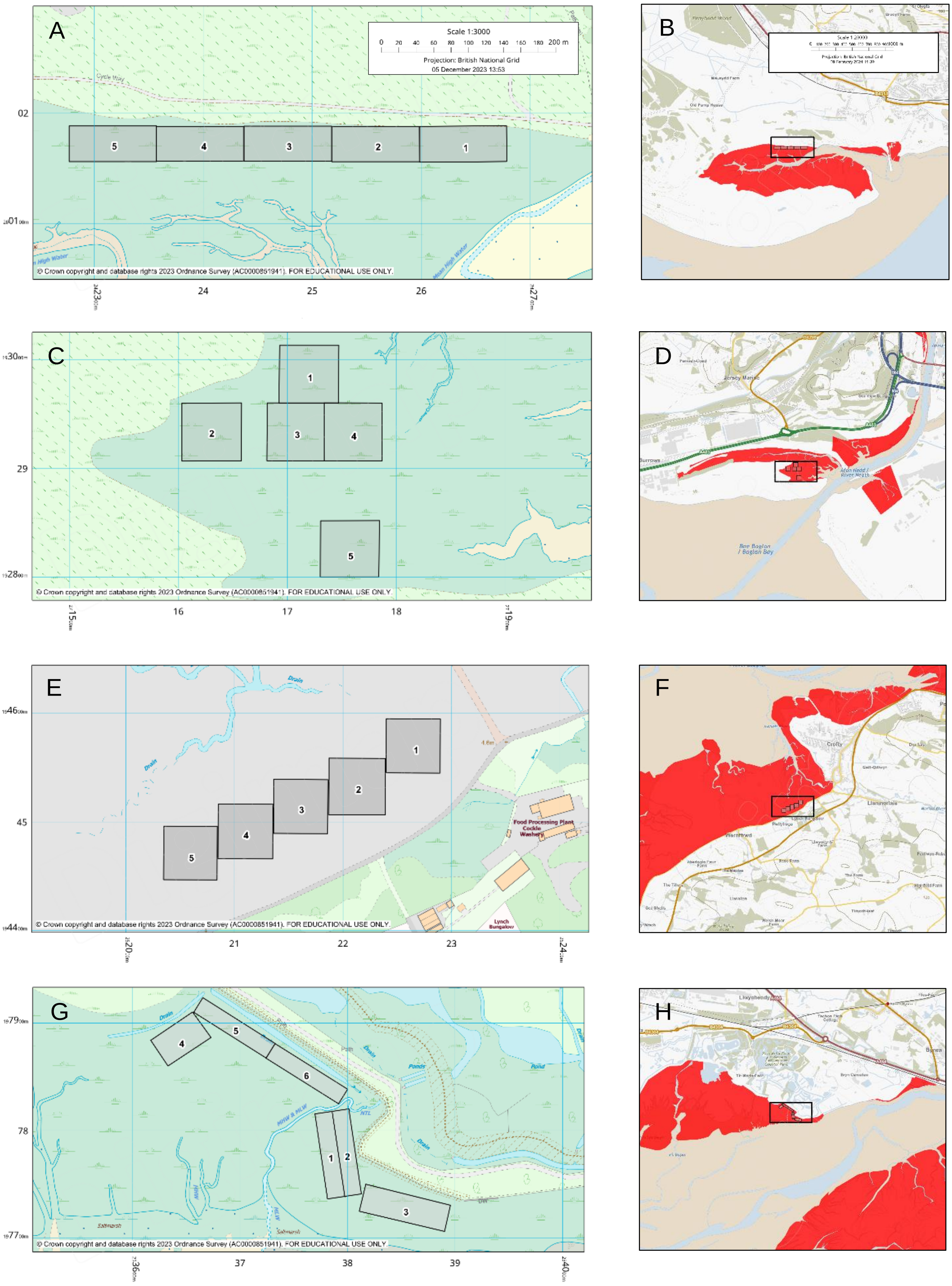

Figure 2.2. Map of study sites and arrangement of sampling plots. A and B = PB, C and D = CB, E and F = CR, G and H = LW (Where plots 1,2 and 3 are LWU, and plots 4,5 and 6 are LWG. Left: "Full colour" map of study site. Black outlines represent sampling plot borders. Right: "Vector Map District" map of area surrounding each study site. Red shaded area indicates saltmarsh habitat. Black rectangular outline represents location of corresponding full colour map to its left. Axis labels represent national grid Ordinance survey coordinates. Created on 5 April 2023, using OS MasterMap, Digimap Ordnance Survey Collection (Digimap 2023).

2.3. Plant cover

For every site visit, a transect of length 30 m was randomly placed within each plot. Four quadrats were placed every 10 metres along the transect. The cover of insect-pollinated plant and total floral cover was visually estimated in each quadrat. Plants were identified using Rose *et al.* (2006). Point sward height from ground level was measured to the nearest centimetre once at the bottom left corner and once at the top right corner of each quadrat with a 30 cm ruled rod (0.5 mm tolerance) (Joern 2005).

The percentage of submerged ground, bare ground and poached ground (ground indents clearly made by horses, ruminants, or rabbits, regardless of its status of colonisation) was recorded in each quadrat.

2.4. Grazing level

The number of grazing animals was counted per plot visit (See section A2.2). However, this could not estimate the impacts of inconspicuous grazers on grazing intensity. Thus, total seasonal grazing intensity was quantified using a function of livestock unit (LU) measurements and dung counts along the transect. LUs are reference units for different livestock species and life stages based on the nutritional or feed requirements of the animal, which facilitates calculation of stocking densities (Benoit & Veysset 2021). The number of dung piles in the space 1m to either side of the transect line was counted and classified visually into grazer species (Horses/Ponies, Cattle, Sheep, Geese, Ducks, Rabbits).

To calculate the seasonal stocking density of each transect, dung counts were multiplied by the LUs assigned per grazing species and life stage used by the UK government (Horse/Pony = 1, Cattle = 1, Sheep (lowland ewe/teg) = 0.12, Goose = 0.02, Duck = 0.01, Rabbit = 0.02) (Rural Payments Agency 2021).

2.5. Recording bees

Bees were sampled using a modified Pollard walk (Pollard & Yates 1993). The transect was walked at a speed of 0.33 m s^{-1}, recording any bees that landed on a flower in a visually estimated cube of 3x3x3 m ahead of the surveyor. The flower species that the bee was observed visiting was also recorded. Each bee was captured with a triangular sweep net (area 500 cm^2) and then transferred to a vial of ethyl acetate for identification in the lab. Each bee was identified to species or species complex level where possible using Falk (2016). One solitary bee was identified at the family level. If a bee escaped capture, it could not be identified and thus was not recorded. The transect was walked twice, leaving five minutes between walks for bees to resettle.

2.6. Statistical analyses

Collinearity between predictor variables was assessed using Spearman's correlation test. Strongly collinear variables were acknowledged during model interpretation.

Given the non-normal distribution of the data and the presence of unequal variances, GLMs were used to assess how the stocking density (derived from dung counts per transect) affected means of 1) flower cover, 2) insect-pollinated plant cover, 3) flower richness, 4) insect-pollinated plant richness, 5) vegetation height, 6) plant height heterogeneity (calculated as the coefficient of variation of all eight plant height measurements in a transect), 7) bee abundance and 8) bee richness. To visualize the impact of grazing on environmental variables, summaries of the response data were plotted as means ± 95% confidence intervals for each plot, with stocking density as a continuous predictor on the x-axis (Figure 3.3).

Predictors of 1) insect-pollinated plant abundance, 2) flower abundance, 3) insect-pollinated plant species richness, 4) mean plant height and 5) heterogeneity in insect-pollinated plant height were modelled against the response of bee abundance and richness using Generalised Linear Models (GLMs). Bee richness and bee abundance were modelled as count response variables using a Poisson distribution with a log link function. For each predictor, three models were fitted: 1) A model with the predictor alone, 2) an additive model including the predictor plus site as a categorical variable, and 3) an interaction model including the predictor, categorical variable site, and their interaction term. Model selection was based on ΔAIC comparisons among these three models. When ΔAIC between models exceeded five, indicating a substantially better fit, the model with the lowest AIC was chosen. Otherwise, the simpler model was preferred. This threshold is consistent with established recommendations (Burnham & Anderson 2002; Burnham *et al.* 2011; Stewart *et al.* 2023).

Dispersion parameters were checked to thresholds of between 0.5 and 2. When the dispersion was below 0.5, a negative binomial distribution was employed. Dispersion did not exceed 2. Then, Tukey's post-hoc test was used to show differences between sites. Poor weather conditions prevented surveys from being taken for LW and CR during time window seven (between 19/07/23 and 23/07/23), so window seven was removed from all analyses to avoid the influence of flowering period on the site variable.

All statistical analyses were performed in R-Studio version 4.3.1 (R Core Team 2023) with additional packages; bipartite (Dormann *et al.* 2008), corrplot (Sikmo 2021), cowplot (Wilke 2020), dplyr (Wickham *et al.* 2023b), FSA (Ogle *et al.* 2023), ggplot2 (Wickham 2016), ggpubr (Kassambara 2023), glmmTMB (Mollie *et al.*), lattice (Sarkar 2008), MASS (Venables & Ripley 2002), multcomp (Westfall 2008), psych (Revelle 2023), tidyr (Wickham *et al.* 2023a) and visreg (Patrick Breheny 2017).

3.0. Results

3.1. Bee and plant community

A total of 170 bees were recorded, with 130 observed at PB and 25 recorded at LWU. Sites CB, CR, and LWG had significantly lower bee abundance, with six, five, and four counts, respectively (Figure 3.1). Eight bee species were recorded, with the most common being *Apis mellifera,* (96 observations), followed by *Bombus* *lucorum/terrestris* complex (33 observations) and *Bombus pascuorum* (26 observations). Only one individual not belonging to the *Apis or Bombus* genera was observed (*Andrena sp*.).

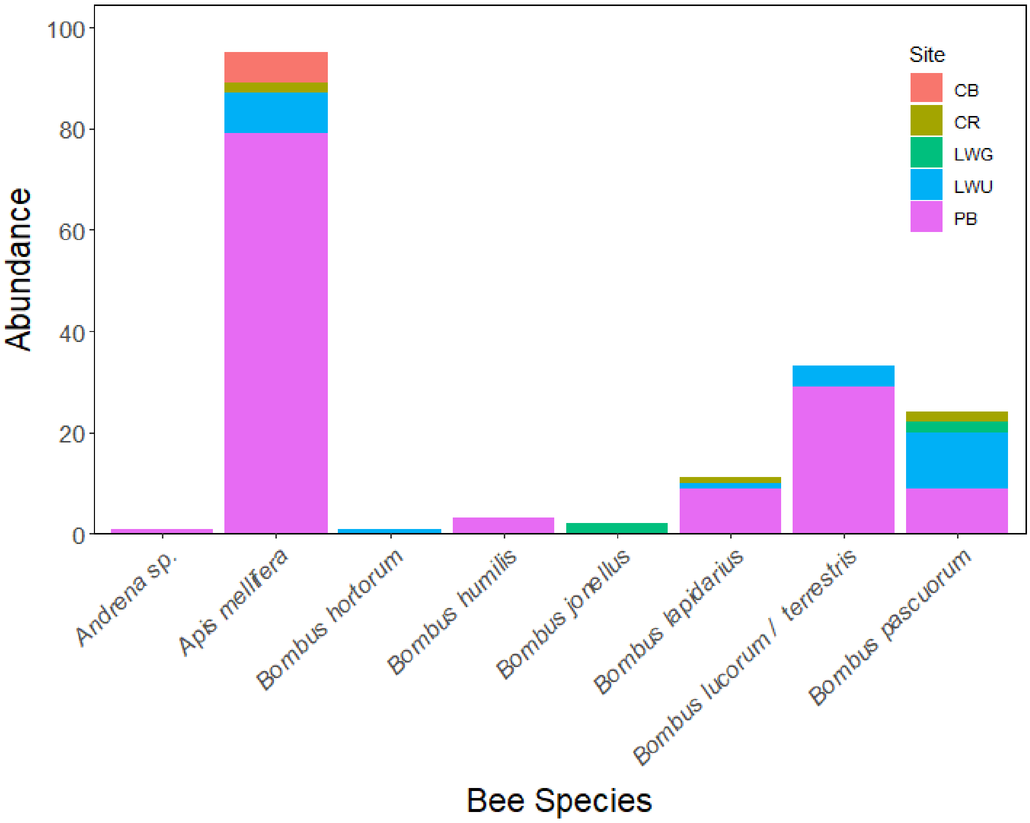

Figure 3.1. Abundance of bee species recorded (n = 170). Colour represents site of observation.

A total of 15 insect pollinated plant species were recorded across all plots. The species with the most widespread cover was *Tripolium pannonicum,* comprising a mean abundance of 7% across all plots (Figure A3.3). *T. pannonicum* flowered from 15/06/23, peaked at late June and continued flowering past the end of the sampling period at 24/9/23. Of the 15 insect pollinated plants, ten were observed flowering. Despite the high cover of *T. pannonicum*, the plant with highest flower abundance across all transects was *L. vulgare* (mean = 0.40%) which flowered from 15/06/23, peaked at late June and continued flowering past the end of the sampling period at 24/9/23 (Figure A3.4). The plant with the second highest flower abundance was *A. maritima* (mean = 0.25%). This plant flowered from 12/05/23 until the end of the sample period, peaking at late May (Figure A3.4). Of the ten plants observed flowering, five were visited by bees. The most visited flower was *L. vulgare* with 140 flower visits by seven species, and the second most visited flower was *T. pannonicum* with 23 visits by two species. Despite the high abundance of *A. maritima* flowers, *A. maritima* was only visited four times. All species exhibit polylectic feeding strategies except for one occurrence of *Bombus humilis* (an ogliolectic feeder) on Limonium flower. *Bombus pascuorum* showed the highest resource diversity, visiting four plant species (Figure 3.2).

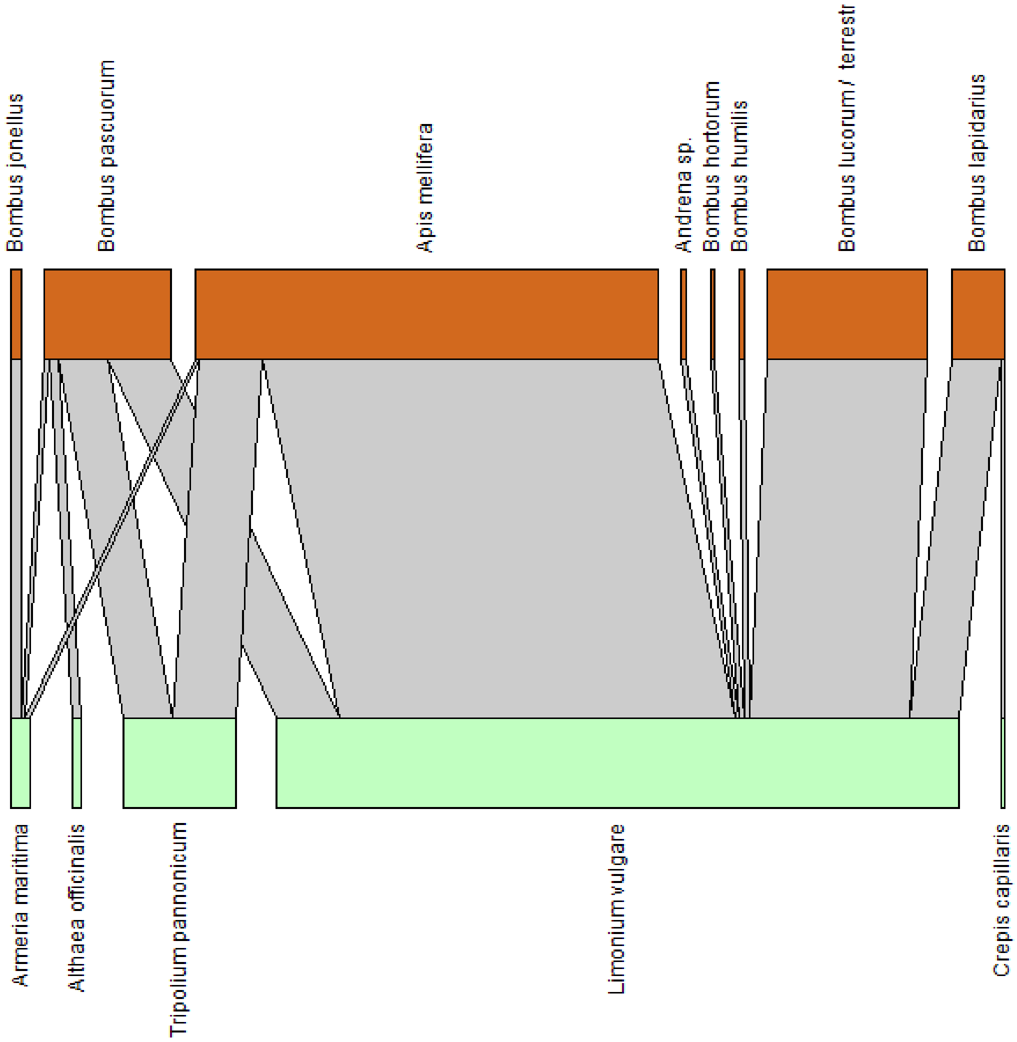

Figure 3.2. Plant-pollinator interaction network for all bee observations (n = 170). Upper orange bars represent bee species, with horizontal bar length proportional to their relative abundance. Bottom bars show plant species, with horizontal bar length indicating proportion of total bee visits received. Connector thickness reflects the frequency of interactions between individual bee and plant species.

3.2. Hypothesis 1: grazing impacts habitat heterogeneity

Table 1. General linear regression model outputs with livestock density and site as predictors. The “+” symbol indicates an additive model, and the “*” symbol indicates an interaction between sites. Model components describe the intercept, the gradient (shown as the predictor variable), additive components of each site shown as the site initial, and if the site interacted, the coefficient for each site was displayed as the gradient of CB, and then the differences in gradient for each site relative to CB.

Final model	Response variable	R code	Model component	Model Coefficient	Standard error	Model Z-value	Model P-value
m1a2	Flower richness	m1a2 <- glm(total.richness.fl ~ dung.livestock.density.total + site2, family = "poisson")	(Intercept)	-1.03	0.25	-4.12	<0.001
			dung.livestock.density.total	-0.02	0.02	-1.28	0.201
			site2cr	1.60	0.30	5.43	0.001
			site2lwg	0.64	0.34	1.87	0.062
			site2lwu	0.04	0.40	0.09	0.926
			site2pb	0.22	0.34	0.66	0.512
m1b1	Flower cover	m1b1 <- glm(mean.cover.fl.bi ~ dung.livestock.density.total, family = "binomial")	(Intercept)	-4.54	0.77	-5.88	<0.001
			dung.livestock.density.total	-0.04	0.21	-0.18	0.860
m1c1	Plant cover	m1c1 <- glm(mean.cover.ip.bi ~ dung.livestock.density.total, family = "binomial")	(Intercept)	-1.82	0.22	-8.16	0.000
			dung.livestock.density.total	0.02	0.04	0.39	0.695
m1d2	Mean vegetation height	m1d2 <- glm(mean.height ~ dung.livestock.density.total + site2, family = "gaussian")	(Intercept)	15.77	1.74	9.04	0.000
			dung.livestock.density.total	-0.02	0.22	-0.07	0.943
			site2cr	-5.60	2.90	-1.93	0.055
			site2lwg	11.06	2.85	3.88	0.000
			site2lwu	25.93	2.85	9.10	<0.001
			site2pb	5.64	2.47	2.28	0.023
m1e2	Coefficient of variation in vegetation height	m1e2 <- glm(cv ~ dung.livestock.density.total + site2, family = "gaussian")	(Intercept)	49.43	4.69	10.54	<0.001
			dung.livestock.density.total	-0.89	0.60	-1.47	0.144
			site2cr	24.50	7.80	3.14	0.002
			site2lwg	17.57	7.67	2.29	0.023
			site2lwu	-1.41	7.66	-0.18	0.854
			site2pb	25.16	6.63	3.79	<0.001
m1f2	Bee richness	m1f2 <- glm(bee.richness ~ dung.livestock.density.total + site2, family = "gaussian")	(Intercept)	0.04	0.10	0.44	0.660
			dung.livestock.density.total	0.02	0.01	1.41	0.162
			site2cr	-0.07	0.16	-0.46	0.647
			site2lwg	0.06	0.16	0.37	0.714
			site2lwu	0.37	0.16	2.35	0.020
			site2pb	0.58	0.13	4.31	<0.001
m1g2	Bee abundance	m1g2 <- glm(bee.abundance ~ dung.livestock.density.total + site2, family = "gaussian")	(Intercept)	0.13	0.25	0.52	0.604
			dung.livestock.density.total	0.03	0.03	0.80	0.425
			site2cr	-0.20	0.41	-0.48	0.636
			site2lwg	-0.04	0.41	-0.09	0.929
			site2lwu	0.80	0.41	1.96	0.052
			site2pb	1.09	0.35	3.10	0.002

The means of vegetation height appeared to decrease with grazing intensity in error bar plots in all sites except for CR, with a negative overarching relationship (Figure 3.3a). However, grazing intensity did not show any differences between gradients of grazing level on plant height with site, and grazing intensity did not impact mean vegetation height (Table 1, model m1d2). Mean vegetation height was higher in LWU than LWG. Furthermore, the grazed site CR had significantly lower vegetation height than all other sites (Table 1, model m1d2).

There was no visible impact of grazing intensity on the coefficient of variation in vegetation height in the error bar plot, and no impact of grazing density on variation of vegetation height (Table 1, model m1e2) (Figure 3.3b). Though, the coefficient of variation was much higher in CR and PB than all other sites, and LWG had a higher coefficient of variation than LWU.

3.3. Hypothesis 2: grazing impacts flower richness

Mean insect-pollinated plant richness and mean flower richness appeared to increase after 2.1 log(LSU) in error-bar plots (Figures 3.3c, d). Grazing intensity did not have any significant effect on flower richness (Table 1, model m1b1) or plant richness (Table 1, model m1a2), and there was no impact of site on the gradient. However, the most intensively grazed site had a significantly higher flower richness than all other sites (Table 1, model m1a2).

3.4. Hypothesis 3: grazing impacts flower prevalence

No visible trend of grazing intensity on means of flower cover was present in error-bar plots (Figures 3.3e) and there was no significant relationship present between grazing intensity and flower cover (Table 1, model m1b1). Furthermore, there was no impact of site on the relationship between flower abundance and insect-pollinated plant abundance (Figure A3.9).

3.5. Hypothesis 4: grazing impacts insect-pollinated plant cover

Error bar plots indicate a bimodal distribution between IP plant cover and grazing intensity, where IP plant cover reaches a minimum at 1.8 log(LSU) (Figure 3.3f). Though, no effects of grazing intensity were observed on insect pollinated plant cover, and site did not impact the relationship (Table 1, model m1c1).

3.6. Grazing impacts bee abundance and diversity.

Bee abundance and richness appeared to be higher in the ungrazed sites (Figure 3.3a and 3.3h). No impacts of grazing intensity were present within sites, and livestock density did not impact bee abundance. However, bee abundance was significantly higher in the PB site than in all other sites (Table 1, model m1g2). Furthermore, bee richness was significantly higher in PB and LWU than in all other sites (Table 1, model m1f2).

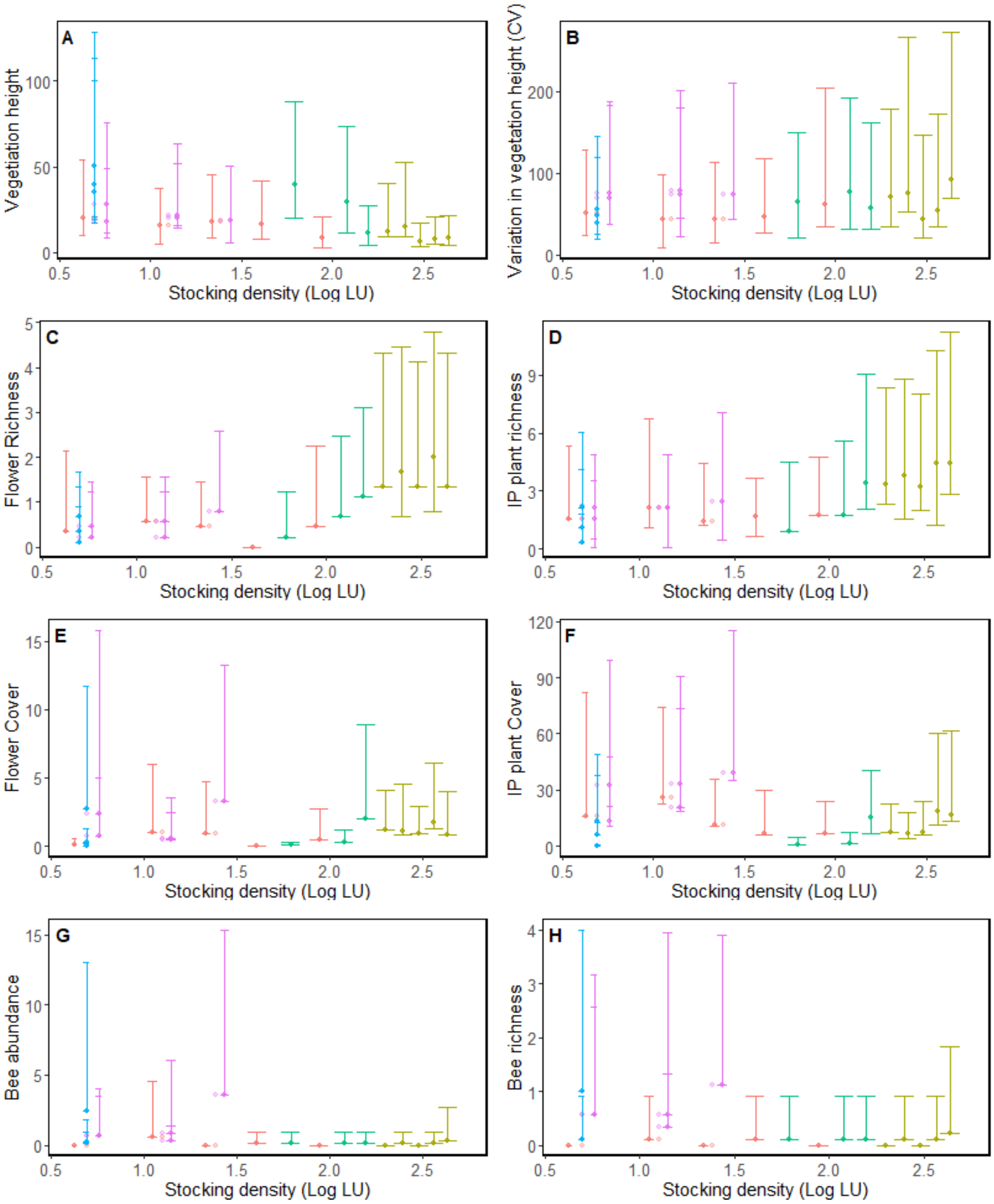

Figure 3.3. Summary means of plant and bee abundance attributes in plots with varying levels of stocking density. Stocking density in livestock units was estimated from Dung counts on plant and bee abundance attributes. Points represent means per plot. Bars represent 95% confidence intervals. Sites are offset horizontally to avoid point overlaying. Translucent points indicate the value of offset points. Colour represents site: Red = CB, Green = LWG, Mauve = PB, Blue = LWU, Brass = CR.

3.7. Hypothesis 1: Habitat heterogeneity impacts bee abundance

Table 2. General linear regression model outputs with bee abundance as a response variable. The "+" symbol indicates an additive model, and the "*" symbol indicates an interaction between sites. Model components describe the intercept, the gradient (shown as the predictor variable), additive components of each site shown as the site initial, and if the site interacted, the coefficient for each site was displayed as the gradient of CB, and then the differences in gradient for each site relative to CB.

Final model	Predictor	R code	Model component	Model Coefficient relative to CB	Model coefficient	Std error	Model Z-value	Model P-value
m2c2	Mean vegetation height	glm(bee.abundance ~ mean.height +site2, family = "poisson")	(Intercept)	-1.64	-1.64	0.43	-3.83	<0.001
			mean.height	-0.02	-0.02	0.01	-2.68	0.007
			cr	-0.32	-0.35	0.61	-0.53	0.594
			lwg	0.04	0.02	0.71	0.06	0.951
			lwu	2.48	2.46	0.49	5.10	<0.001
			pb	2.34	2.32	0.43	5.42	<0.001
m2d2	Coefficient of variation in vegetation height	glm(bee.abundance ~ cv +site2, family = "poisson")	(Intercept)	-1.44	-1.44	0.45	-3.21	0.001
			cv	-0.01	-0.01	0.00	-2.95	0.003
			cr	-0.05	-0.06	0.61	-0.09	0.931
			lwg	0.02	0.01	0.71	0.03	0.975
			lwu	1.92	1.91	0.45	4.23	<0.001
			pb	2.50	2.48	0.44	5.70	<0.001
m2a3	Flower richness	glm(bee.abundance ~ total.richness.fl * site2, family = "poisson")	(Intercept)	-2.63	-2.63	0.61	-4.28	<0.001
			total.richness.fl.site	1.07	1.07	0.55	1.95	0.051
			cr	0.66	1.73	1.01	0.65	0.517
			lwg	-1.96	-0.89	1.92	-1.02	0.308
			lwu	0.49	1.56	0.94	0.52	0.601
			pb	1.82	2.89	0.66	2.74	0.006
			total.richness.fl.site : cr	-1.23	-0.15	0.73	-1.68	0.093
			total.richness.fl.site : lwg	0.91	1.98	1.17	0.77	0.440
			total.richness.fl.site : lwu	1.90	2.97	0.92	2.07	0.039
			total.richness.fl.site : pb	0.40	1.48	0.59	0.68	0.496
m2b2	Flower cover	glm(bee.abundance ~ mean.cover.fl + site2, family = "poisson")	(Intercept)	-2.13	-2.13	0.41	-5.21	<0.001
			mean.cover.fl	0.18	0.18	0.02	8.88	<0.001
			cr	-0.30	-0.12	0.61	-0.49	0.621
			lwg	-0.27	-0.09	0.71	-0.38	0.701
			lwu	1.76	1.94	0.46	3.86	<0.001
			pb	1.79	1.97	0.44	4.07	<0.001

Bee abundance decreased with mean vegetation height, although this effect was small. The effect of mean vegetation height on bee abundance was lower in CR, and LWG, compared with CB and was significantly higher bee abundance were predicted in LWU and PB (Table 2, model m2c2), (Figure 3.4a).

Similarly, bee abundance decreased with variation in vegetation height. The effect of variation in vegetation height was insignificantly lower in CR and LWG compared to CB and significantly higher in LWU and PB compared to CB (Table 2, model m2d2) (Figure 3.4b).

3.8. Hypothesis 2: Flower richness impacts bee abundance

The Poisson GLM including an interaction term between flower richness and site revealed that Flower richness positively impacted bee abundance only in LWU. Only PB described a significantly higher bee abundance with flower richness than CB (Figure 3.4c), (Table 2, model m2a3). In contrast, CR described a declining trend of bee abundance with flower richness (Table 2, model m2a3).

3.9. Hypothesis 3: Flower cover impacts bee abundance

The additive model of flower cover impacting bee abundance showed that flower cover positively impacted bee abundance (Table 2, model m2b2) although the estimate for this effect was nine times higher in PB and LWU than in all other sites (Table 2, model m2b2). (Figure 3.4d).

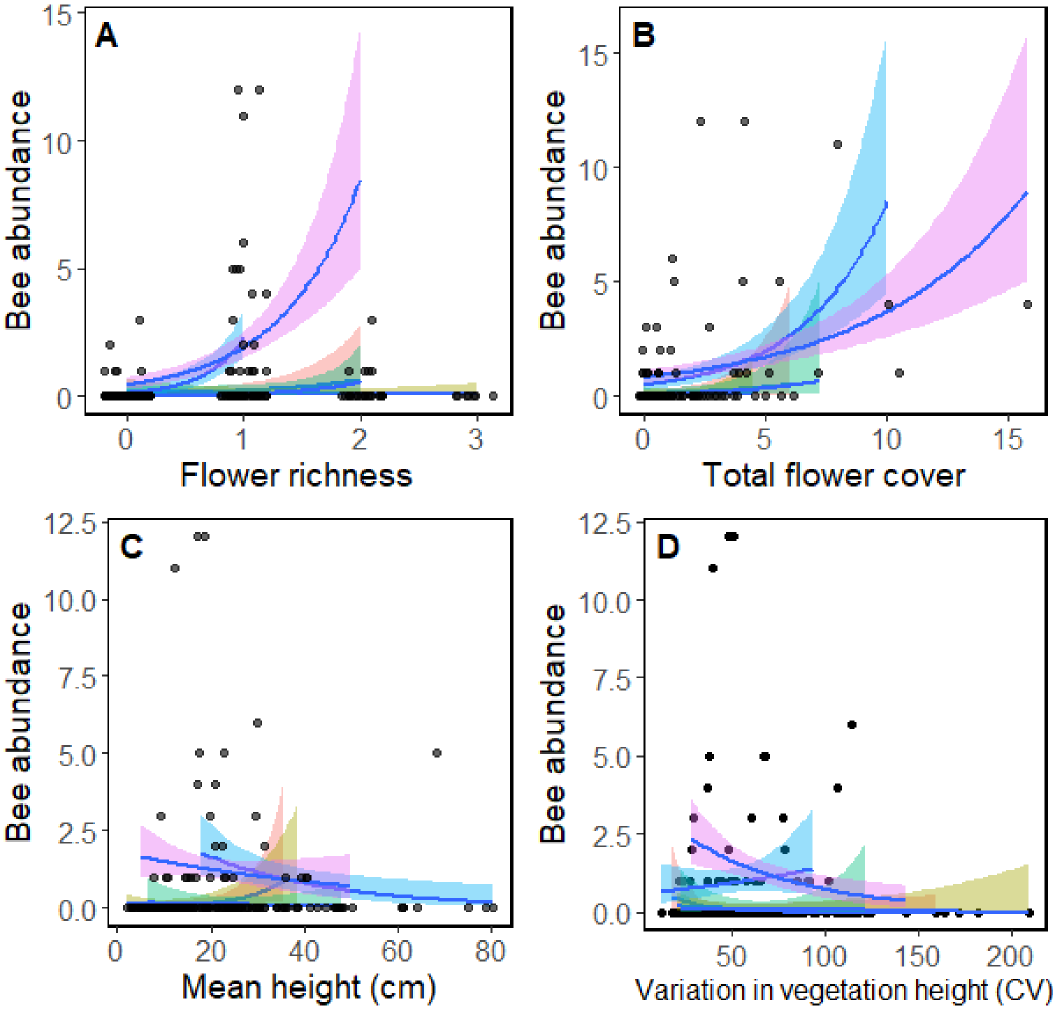

Figure 3.4. Effect of predictors on Bee abundance for each site. Lines represent Poisson distribution fit to the observed data. Shaded area represents 95% confidence intervals. Colour represents site: Red = CB, Green = LWG, Mauve = PB, Blue = LWU, Brass = CR. Points were horizontally offset to avoid point overlaying.

Table 3. General linear regression model outputs with bee richness as a response variable. The “+” symbol indicates an additive model, and the “*” symbol indicates an interaction between sites. Model components describe the intercept and the gradient (shown as the predictor variable). if the site interacted, the coefficient for each site was displayed as the gradient of CB, and then the differences in gradient for each site relative to CB.

Final model	Predictors	R code	Model component	Model Coefficient relative to CB	Model coefficient	Standard error	Model Z-value	Model P-value
m3c2	Mean vegetation height	glm(bee.richness ~ mean.height + site2, family = "poisson")	(Intercept)	-3.00	-3.00	0.73	-4.11	<0.001
			mean.height	-0.01	-0.01	0.01	-0.63	0.529
			cr	0.65	-2.35	0.87	0.75	0.454
			lwg	0.99	-2.01	0.92	1.08	0.280
			lwu	2.40	-0.60	0.82	2.94	0.003
			pb	2.68	-0.32	0.73	3.65	<0.001
m3d2	Coefficient of variation in vegetation height	glm(bee.richness ~ cv + site2, family = "poisson")	(Intercept)	-2.71	-2.71	0.75	-3.62	<0.001
			cv	-0.01	-0.01	0.01	-1.54	0.125
			cr	0.80	-1.91	0.87	0.92	0.356
			lwg	1.06	-1.66	0.92	1.15	0.249
			lwu	2.21	-0.51	0.77	2.87	0.004
			pb	2.84	0.12	0.74	3.83	<0.001
m3a2	Flower richness	glm(bee.richness ~ total.richness.fl + site2, family = "poisson")	(Intercept)	-3.82	-3.82	0.74	-5.17	0.000
			total.richness.fl.site	1.18	1.18	0.24	4.90	<0.001
			cr	-0.95	-4.77	0.94	-1.02	0.309
			lwg	0.44	-3.38	0.92	0.48	0.630
			lwu	2.32	-1.50	0.77	3.00	0.003
			pb	2.60	-1.22	0.73	3.55	<0.001
m3b2	Flower cover	glm(bee.richness ~ mean.cover.fl + site2, family = "poisson")	(Intercept)	-3.22	-3.22	0.71	-4.56	<0.001
			mean.cover.fl	0.17	0.17	0.03	6.14	<0.001
			cr	0.58	-2.65	0.87	0.67	0.505
			lwg	0.83	-2.39	0.91	0.91	0.363
			lwu	2.04	-1.18	0.77	2.65	0.008
			pb	2.23	-1.00	0.74	3.00	0.003
m3e3	Bee abundance	glm(bee.richness ~ bee.abundance * site2, data = beestats)	(Intercept)	-4.03	-4.03	1.13	-3.58	<0.001
			bee abundance	0.85	0.85	0.30	2.81	0.005
			cr	0.43	-3.61	1.44	0.30	0.767
			lwg	-34.10	-38.08	1.37E+07	0.00	1.000
			lwu	2.48	-1.55	1.21	2.06	0.040
			pb	2.93	-1.10	1.16	2.53	0.011
			interaction: cr	0.70	1.55	0.49	1.43	0.154
			interaction: lwg	37.20	38.08	1.37E+07	0.00	1.000
			interaction: lwu	-0.58	0.27	0.31	-1.88	0.060
			interaction: pb	-0.60	0.25	0.31	-1.97	0.049

3.10. Hypothesis 1: Habitat heterogeneity impacts bee richness

Bee richness was not influenced by vegetation height (Table 3, model m3c2), and site did not impact the relationship. Bee richness was not impacted by standard deviation of vegetation height (Table 3, model m3d2), although bee richness was generally higher in PB and LWU sites compared with all other sites (Table 3, model m3d2) (Figure 3.5a, 3.5b).

3.11. Hypothesis 2: Flower richness impacts bee richness

The model of flower richness impacting bee richness with site as an interaction term described an increase in bee richness with flower richness. A higher gradient was observed in ungrazed sites CB, LWU and PB for a given flower richness, although no effects were observed on grazed sites (Table 3, model m3a2) (Figure 3.5c).

3.12. Hypothesis 3: Flower cover impacts bee richness

Flower cover had a small positive effect on bee richness, although site did not interact with the relationship (Table 3, model m3b2) (Figure 3.5d).

3.13. Bee abundance impacts bee richness

Bee abundance significantly and positively impacted bee richness, although site interacted with the relationship- bee abundance was significantly less impactful on bee richness in LWU and in PB compared with other sites (Table 3, m3e3) (Figure 3.5e).

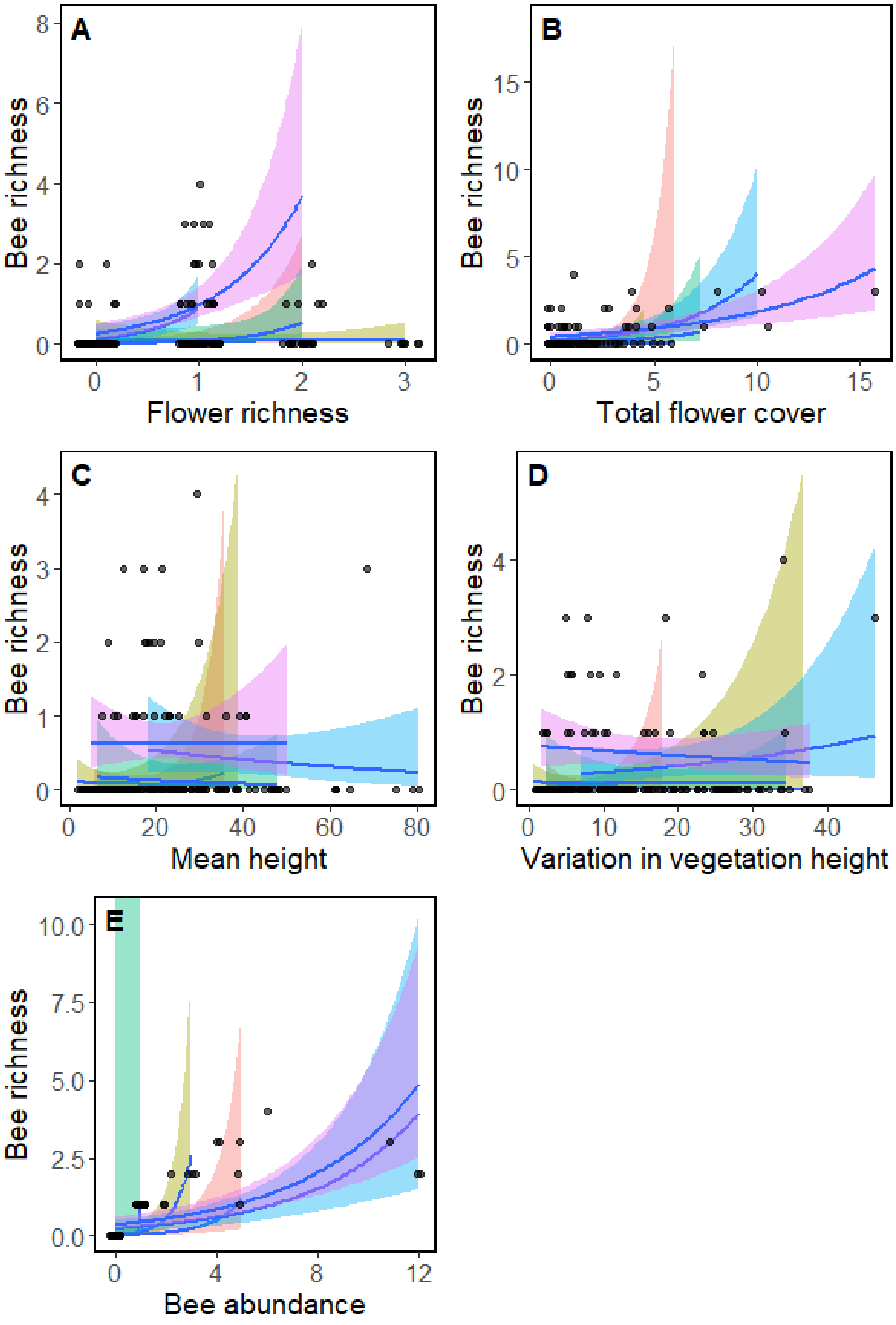

Figure 3.5. effect of predictors on Bee richness for each site. Lines represents Poisson distribution fit to the observed data. Shaded area represents 95% confidence intervals. Colour represents site: Red = CB, Green = LWG, Mauve = PB, Blue = LWU, Brass = CR. Points were horizontally offset to avoid point overlaying.

4.0. Discussion

4.1. Saltmarsh community

The structure and composition of landscapes play a crucial role in enhancing the richness and abundance of pollinator populations (Huston 1994; Potts *et al.* 2016). Heterogeneous plant communities provide a complementary mix of floral traits, which are essential for sustaining diverse pollinator assemblages (Potts *et al.* 2010). Here, the study provides support for a dependency of bee abundance on few plants with mass-flowering characteristics in a low-richness saltmarsh plant community (Davidson *et al.* 2020). There is partial support for a decline in flower abundance attributable to grazing pressure, and no evidence of grazing effects were present directly on bee abundance or indirectly through the vegetation structure pathway. However, I found low total and functional bee diversity across sites—dominated by generalist taxa such as *Apis mellifera*. Network analysis indicated that either strong abiotic filtering or non-specialised floral morphology may create ecologically redundant bee communities in South Wales saltmarshes (Biesmeijer *et al.* 2006; Winfree *et al.* 2009; Sponsler *et al.* 2023). Consequently, high floral abundance may not necessarily translate into improved pollinator diversity or resilience, with implications for the pollinator conservation value of saltmarshes (Rodwell, 2000; Baldock *et al.* 2015).

Of the 15 flowering species present, only five were visited by bees: *Limonium vulgare* (140 visits), *Tripolium Pannonicum* (23 visits), *Armeria Maritima* (four visits)*, Althaea officinalis* (two visits) *and Crepis capillaris* (one visit) (Figure A3.5), an indication of low pollen diversity (Ebeling *et al.* 2008). Furthermore, no flowers were visited between the start of the sampling period (13/4/23) and late May (29/05/23), supporting that nectar and pollen resources are provided only during summer and early autumn periods (Fantinato & Buffa 2019). Two flowering plants, *L. vulgare* and *T. pannonicum* exhibited mass-flowering characteristics (Figure A3.4). The presence of mass flowers centred around the late summer and early autumn makes saltmarshes a crucial late flowering habitat, provisioning a guaranteed source of nectar and pollen for bees during an annual period when flowering has ended for most of the surrounding plant communities, and thus floral resources are scarce (Adam 1990; Fantinato *et al.* 2018b)

4.2. Effects of grazing and flower richness on bees

Floral richness is widely recognised to promote pollinator diversity in grassland ecosystems by increasing nectar and pollen heterogeneity, which attracts both oligolectic and monotectic pollinators (Batáry *et al.* 2010; Lichtenberg *et al.* 2017). I recorded low bee richness and low flower richness across all sites. Both low bee richness and low flower richness likely masked any diversity links between grazer-plant-pollinator levels (Gillespie *et al.* 2024); thus, hypothesis (1) that grazing increased the diversity of bees through increases in flower richness on saltmarshes could not be validated. Despite this, I found positive impact of flower richness on bee richness in one ungrazed site (Pembrey) out of the five total sites. A positive relationship between floral diversity and bee diversity is coherent with more traditional views of a linked bee/flower diversity relationship (Potts *et al.* 2003). Here, the study challenges prior work reporting no link between floral and bee diversity in coastal systems (Fantinato *et al.* 2018a). I find that the mismatch between floral diversity and bee diversity does not extend to saltmarshes. Notwithstanding, the study supports the notion that few dominant flower species provide the available nectar resources in UK marshes (Lucas *et al.* 2017; Fantinato *et al.* 2018a). However, the structurally simple plant-pollinator community present on the sites suggests that saltmarshes host depauperate floral communities for bee populations. This could be attributed to the abiotic stressors presented in saltmarshes (Rodwell, 2000; Baldock *et al.* 2015).

All bees observed in this study were polylectic, with the honeybee *A. mellifera* comprising 58% of all observations. Fewer than 1% of total species belonged to non-*Bombus* and non-*Apis* genera. With few plant species in bloom — notably *Tripolium pannonicum* and *Limonium vulgare* — the diversity of available floral resources is highly constrained (Blaauw & Isaacs, 2014). Additionally, temporal constraints on nectar availability further limit community assembly (Sponsler *et al.* 2023). Such a narrow temporal flowering window disproportionately favours generalist, polylectic species capable of utilizing a variety of floral resources across multiple habitats (Waser *et al.* 1996; Wood *et al.* 2021). This could explain the predominance of the honeybee across sites, although landscape factors and occurrences of beekeeping remain to be accounted for (Torné-Noguera *et al.* 2016). The dominance of late-season flowers may support generalist bees during late-season dearth periods, but may preclude specialists, as many specialist species have narrower foraging windows and emerge earlier in the season, often timed to coincide with their specific host plants (Biesmeijer *et al.* 2006; Winfree *et al.* 2009; Sponsler *et al.* 2023).

The relatively open floral morphologies of the dominant plant species, combined with the absence of tubular flowers, can amplify favourability towards generalists, enabling exploitation of nectar resource by short-tongued, generalist foragers such as the honeybee and certain *Bombus spp*. (Fontaine *et al.* 2006; Müller, 1881; Hicks *et al.* 2016). The honeybee is known to forage aggressively and in high abundance, exerting competitive pressure on less dominant or specialised bees (Hudewenz & Klein, 2015; Page *et al.* 2024), especially during late-seasonal dearth periods (Wingnall *et al.* 2020). The absence of monolectic and oligolectic species from the assemblage suggests that the saltmarsh may function as a poor habitat for specialists, either due to the absence of host plants, due to competitive exclusion by dominant generalists such as the honeybee, or due to the absence of nesting resource (Biesmeijer *et al.* 2006; Winfree *et al.* 2009). The richness of saltmarsh flowers appeared to be higher in plots with intensive grazing (Figure 3.3c). However, the absence of a statistically significant relationship between grazing and flower abundance or richness, coupled with the absence of a visible effect of flower richness on bee species richness, creates uncertainty about whether grazing-induced increases in plant diversity will show landscape-level improvements of nectar provisions in marshes of South Wales (Joppa *et al.* 2010).

4.3. Effects of grazing and habitat heterogeneity on bees

Plant structural heterogeneity is a considerable driver of saltmarsh arthropod populations (Collinge, Prudic & Oliver 2003; Marini *et al.* 2008). The study tested variation in vegetation height along the transect scale and found no significant effect of grazing on the variation in vegetation height (Figure 3.3b). Furthermore, I observed no impact of variation in vegetation height on bee abundance or diversity. Hence, increasing structural heterogeneity may not be the explanation for increases in flower diversity. Therefore, hypothesis (2) that structural heterogeneity predicts bee abundance and diversity could not be validated (Figures 3.4b and 3.5b) (Ford *et al.* 2013). The study suggests that saltmarsh bees are instead predicted by plant composition, rather than structural variation, in accordance with some other arthropod groups (Schaffers *et al.* 2008).

The only flower species to show positive impacts of grazing disturbance was *Armeria maritima*, and it was only abundant in intensively grazed sites (Figure A3.10e), in accordance with other studies on saltmarshes of southwest Wales (Davidson *et al.* 2020). The compact, low rosettes of *A. maritima* make it considerably more resistant to grazing (Eisikowitch & Woodell 1975). Therefore, regular disturbance of vegetation allows *A. maritima* to persist in grazed plots where it would typically be succeeded by other species in ungrazed plots (Preston 1982). However, in this study, *A. maritima* was only visited by bees four times, despite being highly abundant and being predominantly bee-pollinated in other studies (Eisikowitch & Woodell 1975). the Intensively grazed site in CR was reduced to short turf (Figure 3.3a), indicative of intensive grazing levels (Nolte *et al.* 2014). The absence of shelter or vegetation structure may have resulted in increased aeolian or predator disturbance in CR and subsequent low foraging visitation rates by bees to *A. maritima* (Figure A3.5). However, this study did not disentangle the potential effect of flower species on the relationship between plant height and bee abundance. Alternatively, the disproportionately ignored species *A. maritima, L. maritima* and *C. officinalis* had small flowers (between 5-14 mm and up to 25 mm large inflorescences in *A. maritima*) and were sparsely clustered (Eisikowitch & Woodell 1975; Rose *et al.* 2006), making nectar collection more energetically demanding and less favourable compared with *L. vulgare* or *T. pannonicum* (Lucas *et al.* 2017).

Specialised solitary bees could benefit from visiting smaller flowers present on marshes. However, smaller solitary bees generally have limited foraging ranges (Gathmann & Tscharntke 2002). Furthermore, ground-nesting bees, particularly smaller species, generally avoid frequently disturbed, waterlogged substrates, as well as substrates composed of clay and silt, characteristics typical of UK marshes (Cane 1991) further filtering specialised bee species (Gathmann & Tscharntke 2002). The low abundance of solitary bees recorded in this study supports that suitable nesting resources for most bees are absent in saltmarshes despite offering some valuable foraging resources (Brunet & Minahan 2023). In this study, no impact of structural diversity on bee diversity was observed (Figure 3.5b). The low suitability of saltmarshes as nesting habitats for bees suggests that a relationship between structural diversity and bee diversity is unlikely to be detected.

4.3. Effects of grazing and flower abundance on bees

The main driver of bee abundance and richness in saltmarshes was flower abundance (Figure 3.4d). Flower abundance was mediated by the abundance of two dominant flowering plants, *L. vulgare* and *T. pannonicum*, which together comprised 95% of bee visits (Figure A3.5). Grazing did not impact total flower abundance (Figure 3.3e). However, flower abundance of both *L. vulgare* and *T. pannonicum* appeared to decrease in response to grazing (Figures 3.10a, b, c, d), subsequently reducing bee abundance in grazed sites (Figure 3.4a). This is in accordance with a previous study in southwest Wales (Davidson *et al.* 2020).

Tripolium pannonicum and *L. vulgare* plant and flower abundance decreased similarly in plots with higher grazing (Figure A3.10), suggesting that grazers mainly triggered reductions in flowering via reductions in plant biomass. This result supports hypothesis (4), that grazing reduces bee abundance via reductions in plant cover- and does not support hypothesis (3), that grazers impact nectar resources via selective removal of flowers only.

In this study, high sheep density may have been a core driver in reducing *T. pannonicum* plant abundance. Sheep experience a preference for forb plants (Scohier *et al.* 2013). Pastures grazed by sheep thus typically display a reduced abundance of forbs and, hence, a reduced abundance and diversity of nectar-dependent insect groups (Carvell 2002). However, *T. pannonicum* was still consistently present in grazed sites, supporting that *T. pannonicum* individuals resist heavy grazing pressure over long periods (Nolte, Esselink & Bakker 2013). Results differ from studies that find that *T. pannonicum* can be almost eradicated with intense sheep grazing (Kiehl *et al.* 1996; Van Klink *et al.* 2016).

The flowering plant *L. vulgare* was not present in CR. Plant bodies of *L. vulgare* are highly sensitive to grazing disturbance (Boorman 1967) and more palatable than *T. pannonicum* (Davidson *et al.* 2020). High sheep density may also explain the absence of *L. vulgare*. However, it does not explain the low abundance of *L. vulgare* in the ungrazed site CB. *Limonium vulgare* is more specialised to extreme edaphic factors than *T. pannonicum*, and thus *L. vulgare* abundance may be mainly driven by a combination of factors such as disturbance level, inundation frequency and soil moisture level (Boorman 1971; Hill *et al.* 1999). Hence, conservation management should focus on marshes where *L. vulgare* is abundant or has been abundant prior to reclamation.

Reducing grazing during the flowering period may have implications for improving *T. pannonicum* flower abundance (Pe'er *et al.* 2021). The findings suggest that sites with grazing intensities between 0.1 LUha^{-1} and 2.5 LUha^{-1} greatly reduces the abundance of nectar-rich mass-flowering species (Figure A3.10), whereas no grazing maintains high bee abundance and richness. It does not align with studies that suggest grazing intensity should be limited to 0.5 - 1.2. animal/ha (Batáry *et al.* 2010).

Grazing management techniques aimed towards improving forb biomass, such as rest periods, could subsequently enable flower production of *T. pannonicum* (and *L. vulgare* in marshes where *L. vulgare* is a predominant flower) (Carnevalli *et al.* 2006; Moran 2014; Chang *et al.* 2024). However, cessation during parts of the season may not be effective in low-productivity zones, as growth and succession rates are lower (Kindvall *et al.* 2022). Given that grazing affects *L. vulgare* plant biomass, cessation of grazing for more than one season is important to preserve the grazing-sensitive *L. vulgare* in sites where *L. vulgare* is present (Boorman 1971). Where cessation is not possible, grazing levels below 0.5 LUha^{-1} should be considered to limit the dominance of grasses and reduce the destruction of flowers and flowering plant biomass (Potts *et al.* 2009; Pe'er *et al.* 2021).

4.4. Effect of grazing on landscape resources

British vegetation can be classified into standardized UK National Vegetation Classification (NVC) communities. The UK NVC is a phytosociological classification used as a common standard to guide habitat monitoring and habitat assessment (Rodwell & Committee 2006). On the sites studied, *T. pannonicum* and *L. vulgare* appear to outcompete competitive plants at the ungrazed mid-marsh level of tidal disturbance. The NVC communities SM24 *Elymus pycnanthus* saltmarsh and S4 *Phragmites australis* swamp communities were observed in the upper levels of all ungrazed marshes (Davidson *et al.* 2020). These dominant grass communities are species-poor, and often monospecific (Pigott *et al.* 2000; Peter & Burdick 2010; Cleary *et al.* 2016). In contrast, the SM13 *Puccinellia maritima* saltmarsh and SM18 *Juncus maritimus* salt-marsh communities were found in the upper grazed marshes, displaying a heterogeneous and more diverse vegetation structure (Pigott *et al.* 2000).

The results hint that flower richness may be higher in plots with greater grazing disturbance in the upper-intermediate saltmarsh zone interface, where all plots were located (Figure 3.3c). Successive patterns of flower diversity on a saltmarsh can be explained by the 'dynamic equilibrium model' (Kondoh 2001). This model describes how the co-interaction of productivity and disturbance species determines species richness, whereby high levels of disturbance and low productivity (or inversely, low levels of disturbance and high productivity) create low species richness. In contrast, intermediately balanced levels of productivity and disturbance lead to higher species richness (Kondoh 2001). The tidal disturbance gradient in a salt marsh is sharp, exhibiting high disturbance at low altitudes and low disturbance at high altitudes, and low productivity at low altitudes and higher productivity at high altitudes (Adam 1990; Morris, Sundberg & Hopkinson 2013). The conservation value associated with grazing on saltmarshes may thus differ different in different marsh zones, as the dominant vegetation type changes along a gradient of tidal disturbance (Adam 1990).

Grazing may help balance the disturbance equilibrium in the upper marsh through biomass removal and compaction, allowing a larger abundance of flowering species to persist in this zone (Duffy *et al.* 2007). Thus, the ecosystem functionality of saltmarshes will be impacted differently at different scales (Sun *et al.* 2023). In the context of saltmarshes, grazing may reduce the establishment of monospecific grass communities and increase floral richness in the upper marsh, while also homogenising and reducing flower abundance in the mid marsh. Identifying how grazing impacts the flower-pollinator diversity patterns in the different marsh zones is out of the scope of this study. However, revealing how saltmarsh zonation patterns impact livestock disturbance models could help facilitate targeted management regimes aimed at promoting nectar resources (Esselink *et al.* 2000; Kondoh 2001).

5.0. Conclusion

Understanding the effects of grazing intensity on saltmarsh plant communities is crucial for conserving saltmarsh invertebrate habitats (Environment Agency 2022). This study examined the patterns of floral and bee diversity in coastal marshes, providing insights into the mechanisms by which grazing affects nectar availability.

This investigation revealed the potential negative impact of grazing on floral resources and the implications for floral heterogeneity. The study provided insights into the effect of changes in floral resources on bee abundance and diversity. While diverse flower assemblages provide diverse foraging resources for bees in productive grasslands, the suitability of coastal habitats as important nectar provisioners for specialist bees is challenged. Negative impacts of grazing on nectar provisions are evident through the removal of biomass of a few mass-flowering plants, as opposed to direct consumption of flowers. Thus, this study highlights the role of saltmarsh plant composition in driving bee abundance and diversity.

Currently, bee conservation strategies should focus on maintaining the dominant nectar-producing flowers on saltmarshes. Furthermore, conservation management should consider substantial reductions in grazing to preserve saltmarsh nectar resources. This study utilized inferences about community structures found at each site. However, it did not directly test for interactive effects along a disturbance gradient.

The mechanism governing the discrepancy in plant diversity relationships within coastal habitats remains poorly understood. Further research on how patterns of nectar resource partitioning develop in these systems is needed. Such insights could improve our understanding of landscape-level responses of pollinator communities to grazing and contribute to more effective strategies for conserving pollinators in coastal ecosystems.

6.0. References

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7.0. Appendices

A2.1. Plot arrangement

Plot locations had to meet the following criteria:

- Plots must start no further than 50m from the upper inland border of the marsh to ensure safe accessibility (identified on Digimap and confirmed during a pilot site visit)
- Plots must not contain water-filled creeks over 2 m in width
- Plots must be distributed across the marsh as evenly as possible
- Distance between plots must be small enough to complete data collection within six hours
- Plot locations must not intersect
- Plots should take the shape of a square of length 50 m and area 2500 m^2 Where landscape features prevent placement of this shape, a rectangle with the largest possible area up to 2500 m^2 is drawn

A2.2. Grazing level

While direct measurements of grazing intensity for enclosed pastures is possible, livestock in the intensively grazed site CR were not enclosed, and grazing by potential wild grazers would not be accurately represented. Furthermore, livestock could display spatial preferences for grazing patches due to variance in aeolian, vegetative or topographic gradients. Thus, local grazing intensity was quantified in each sample plot by counting grazers per plot per sample window. Grazers were counted within a visually estimated semi-circle of radius 400 m from the transect start point using binoculars. Grazer counts were multiplied by the LUs assigned per grazing species and life stage used by the UK government (Horse/Pony = 1, Foal = 0.7, Cattle = 1, Calf = 0.7, Sheep (lowland ewe/teg) = 0.12, Lamb (ewe follower) = 0.08, Goose = 0.02, Duck = 0.01, Rabbit = 0.02).

However, this quantification was unable to estimate potential differences in impacts of wild grazers on grazing intensity for each site. Furthermore, grazers were not present during some study windows, and thus grazing intensity will be underestimated for that window. Hence, dung count estimates of grazing intensity were preferred during the analysis.

To record total seasonal grazing intensity of livestock and to record grazing of potential influential, uncommon or inconspicuous animals, the number of dung piles in the space 1m to either side of the transect line were counted and classified into grazer species (Horses/Ponies, Cattle, Sheep, Geese, Ducks, Rabbits). One dung pile was defined as one patch with a high concentration of dung pellets at least 10 cm in diameter. Since waterfowl dung never reached lengths of 10 cm, each waterfowl dung was counted regardless of size. Dung from adults and juveniles could not be distinguished, so all dung were assumed to be deposited by adults.

A3.1. Estimates of grazing pressure

All dung in CB was created by rabbits, whereas most of the dung created in LWG was created by cattle, and dung from CR was from several wild bird and livestock species. Converting dung counts into stocking density (LU) significantly decreased the perceived values of grazing pressure in CB although CB box 2 still had LU comparable to LWG boxes.

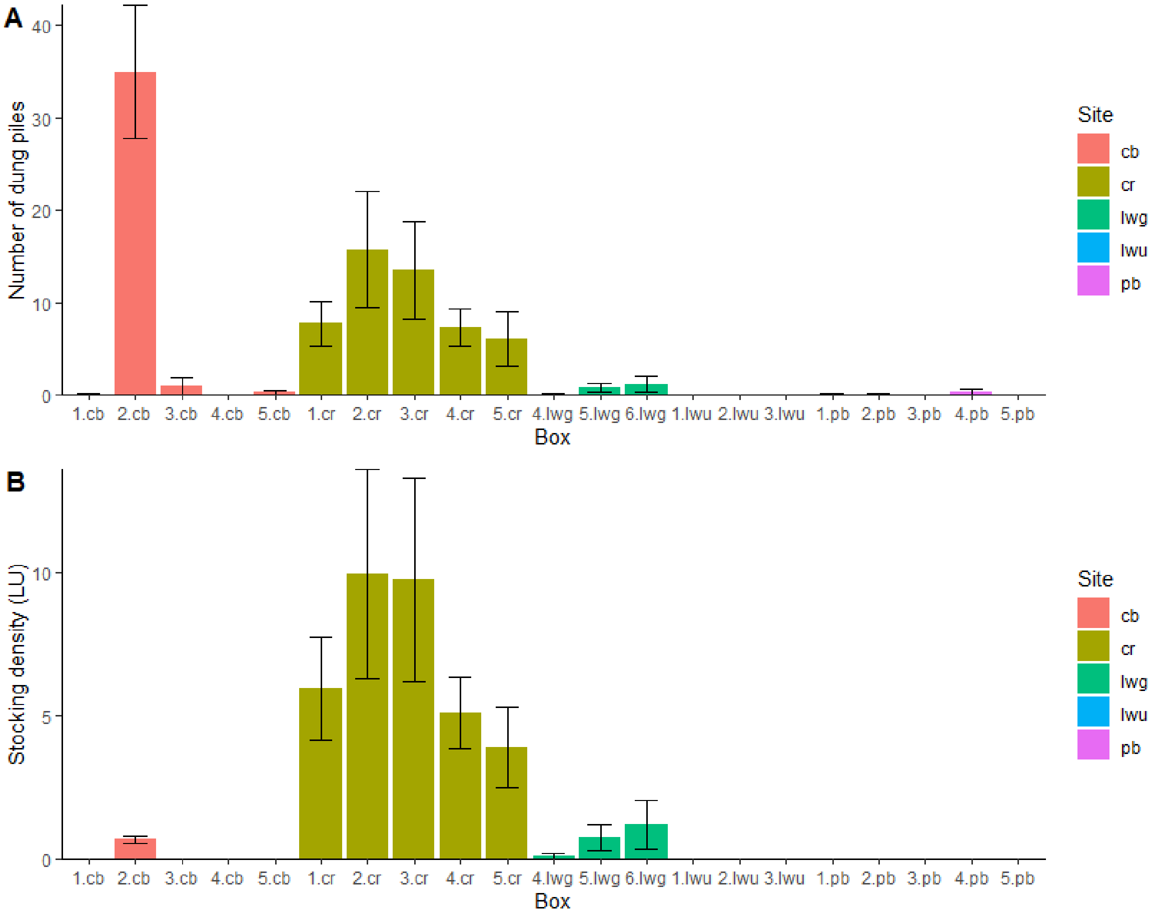


Figure A3.1. (a) mean number of dung piles per plot. (b) mean stocking density (LU) calculated from number of dung pats per plot. Colour represents site. Error bars represent standard errors.

Over 99% of grazers were observed at CR (mean = 49.24), whereas a total of only 26 grazer observations were recorded in LW (mean = 0.48).

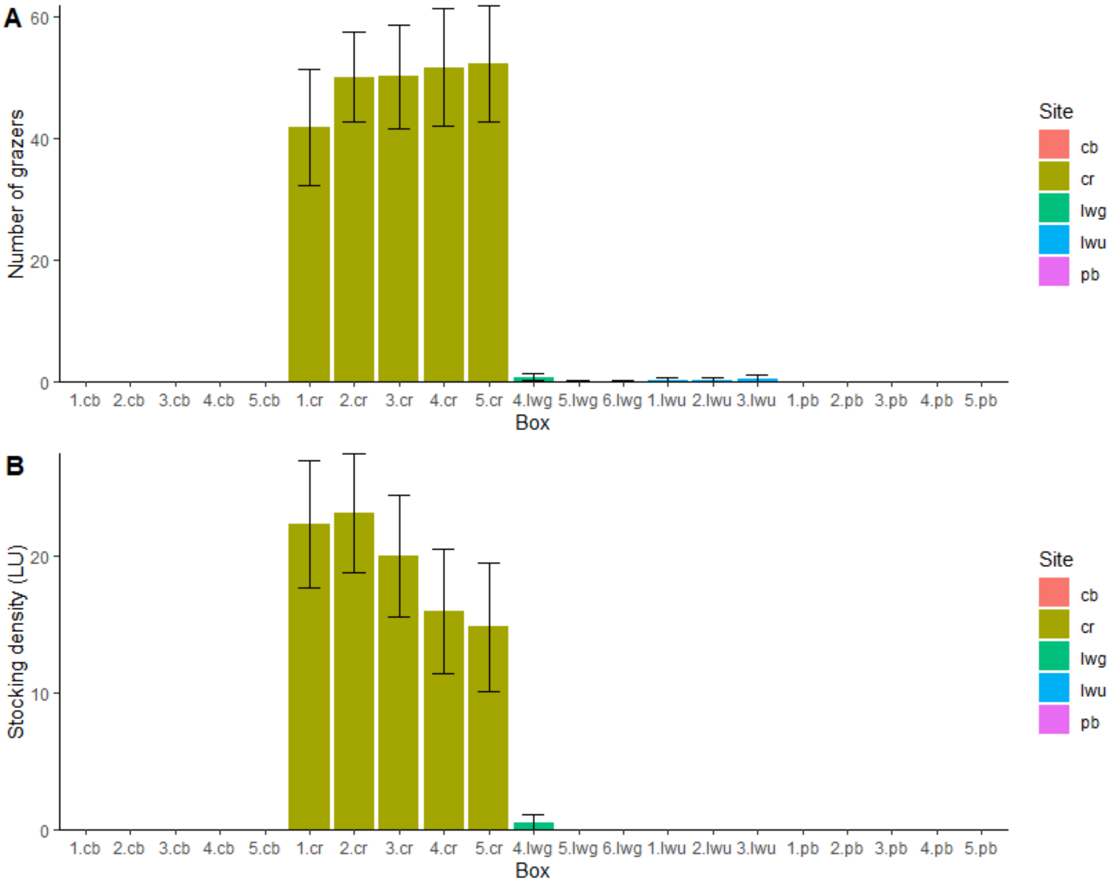


Figure A3.2. (a) mean number of grazers per plot. (b) mean stocking density (LU) calculated from number of grazers per plot. Colour represents site. Error bars represent standard errors**.**

A3.2. Bee and plant community analysis

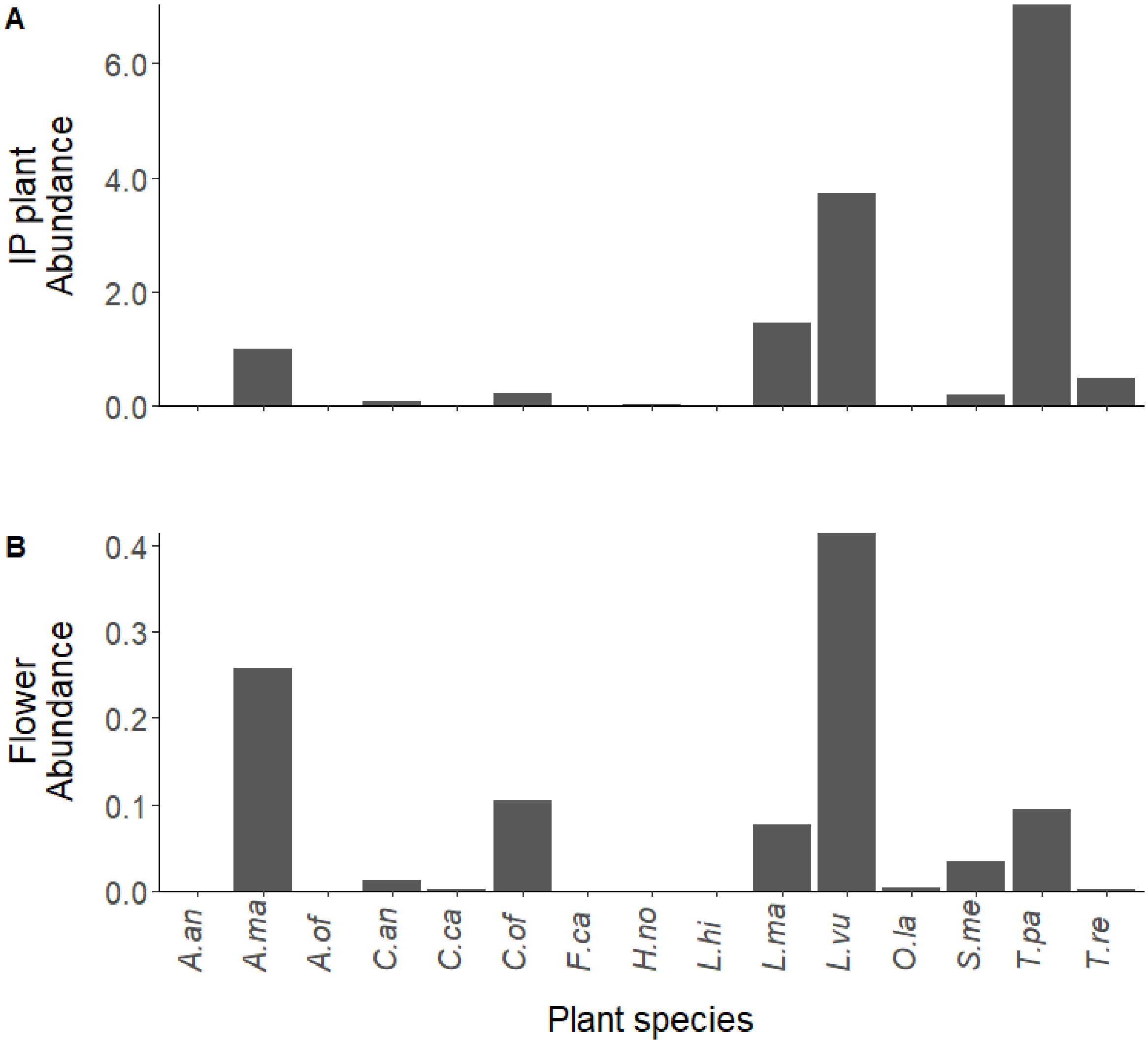


Figure A3.3. (a) Mean percentage abundance of each insect pollinated plant species across all quadrats in a transect. (b) Mean percentage abundance of flowers for each plant species across all quadrats in a transect. *A.an = A.anserina. A.ma = A.maritima, A.of = A.officinalis C.an = C.anglica, C.ca = C.capillaris, C.of = C.officinalis, F.cap = F.capreoloata, H.nod = H.nodiflorum, L.hi = L.hispidus, L.ma = L.maritima, L.vu = L.vulgare, O.la = O.lachenallii, S.me = S.media, T.pa = T.pannonicum, T.re = T.repens.*

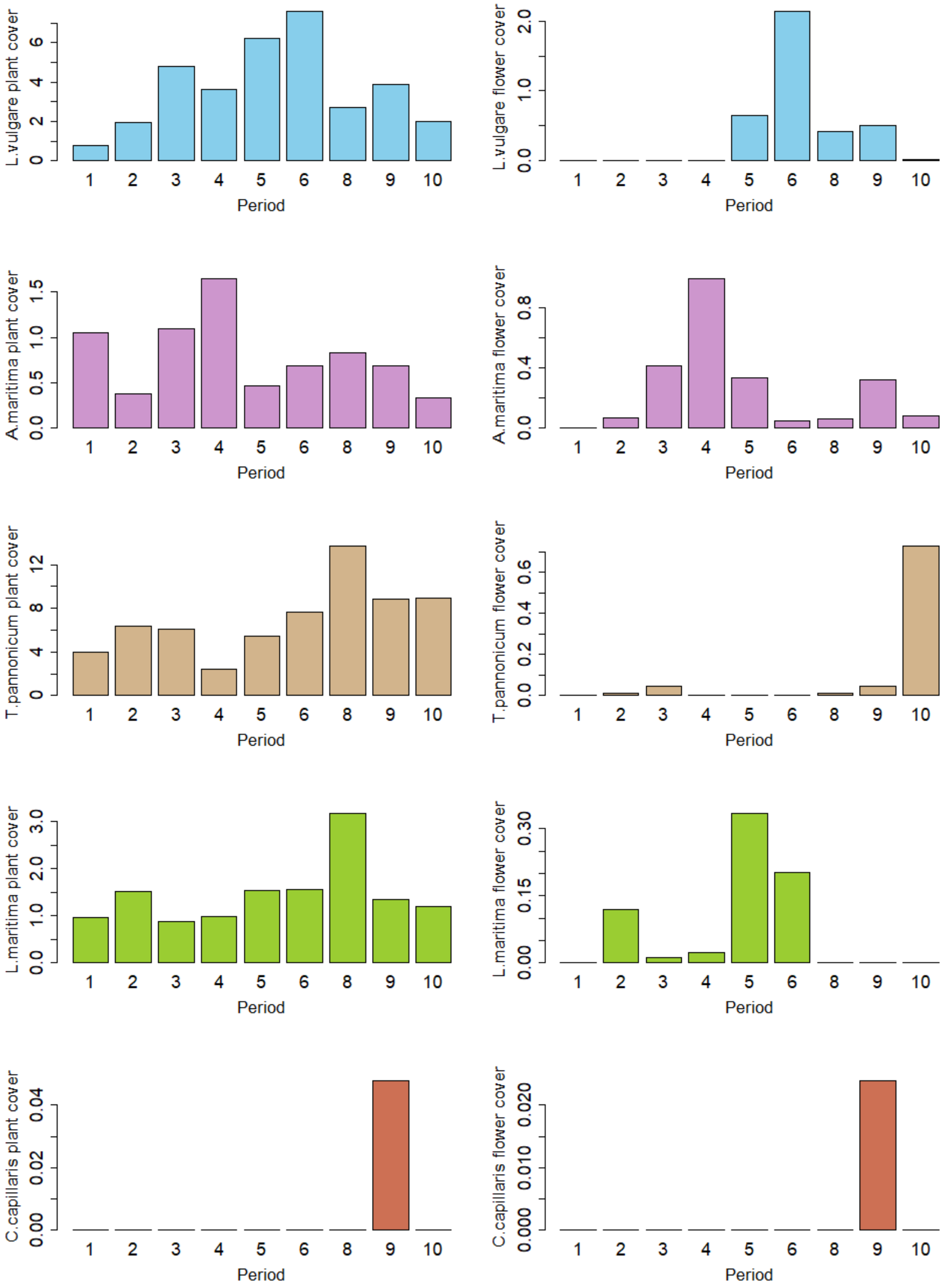


Figure A3.4. Mean abundance of plants (Left) and flowers (Right) over time for each flower species that was visited by at least one bee (Blue = *L.vulgare*, Pink = *A.maritima*, Tan = *T.pannonicum*, Green = *L.maritima*, Orange = *C.capillaris*) from early April until early September. Bars represent means per site visit at two-week time periods from 13/04/23 to 09/02/23.

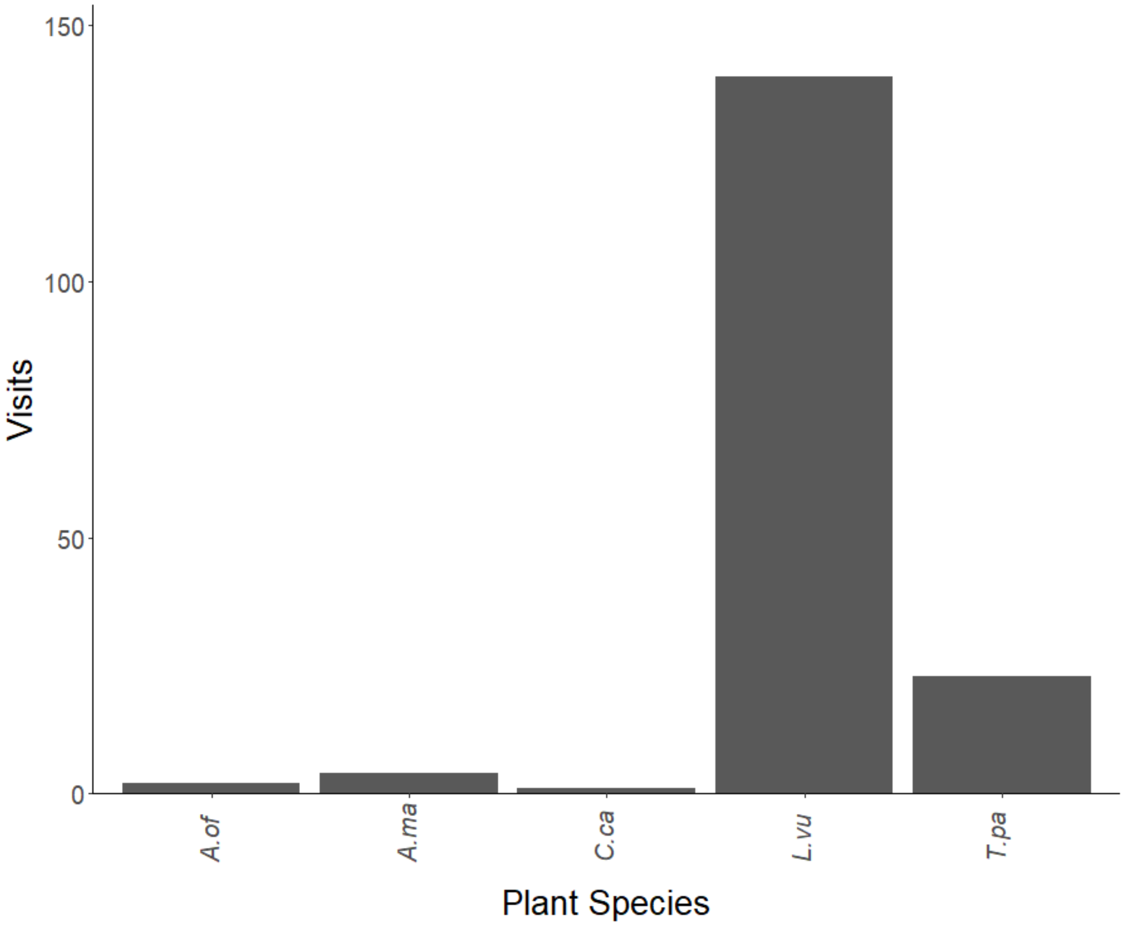
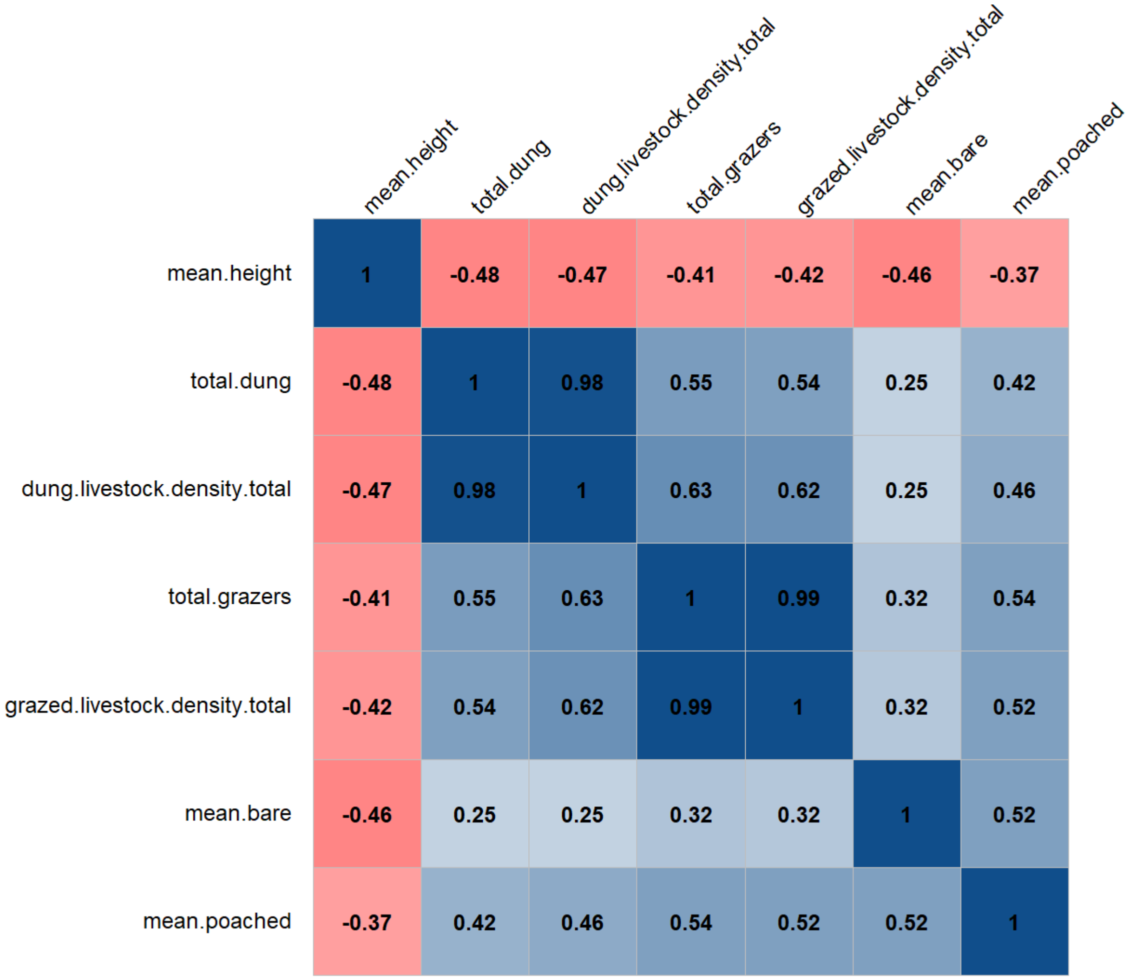


Figure A3.5. Total count of bee visits of each insect pollinated plant species. *A.ma = A.maritima, A.of = A.officinalis C.an = C.anglica, C.ca = C.capillaris, , L.vu = L.vulgare, T.pa = T.pannonicum.*

Raw grazer and dung counts were included in the correlation tests in addition to livestock densities. The Pearsons correlations test shows all grazing values are significant with the total dataset, except for the correlation between dung values and bare ground. While grazer counts and grazer LSU did not have a correlation coefficient larger than 0.2 when paired with dung counts, the correlation was increased to 0.37 and 0.41 respectively when paired with dung LSU. The grazer counts significantly correlated with poached ground and bare ground (ρ= 0.35 and 0.46) respectively, however the correlation value declined to (ρ = 0.25 and 0.34) when converted to grazer LSU. Not including count/LSU conversions, the highest correlation was with bare and poached ground (ρ = 0.55).

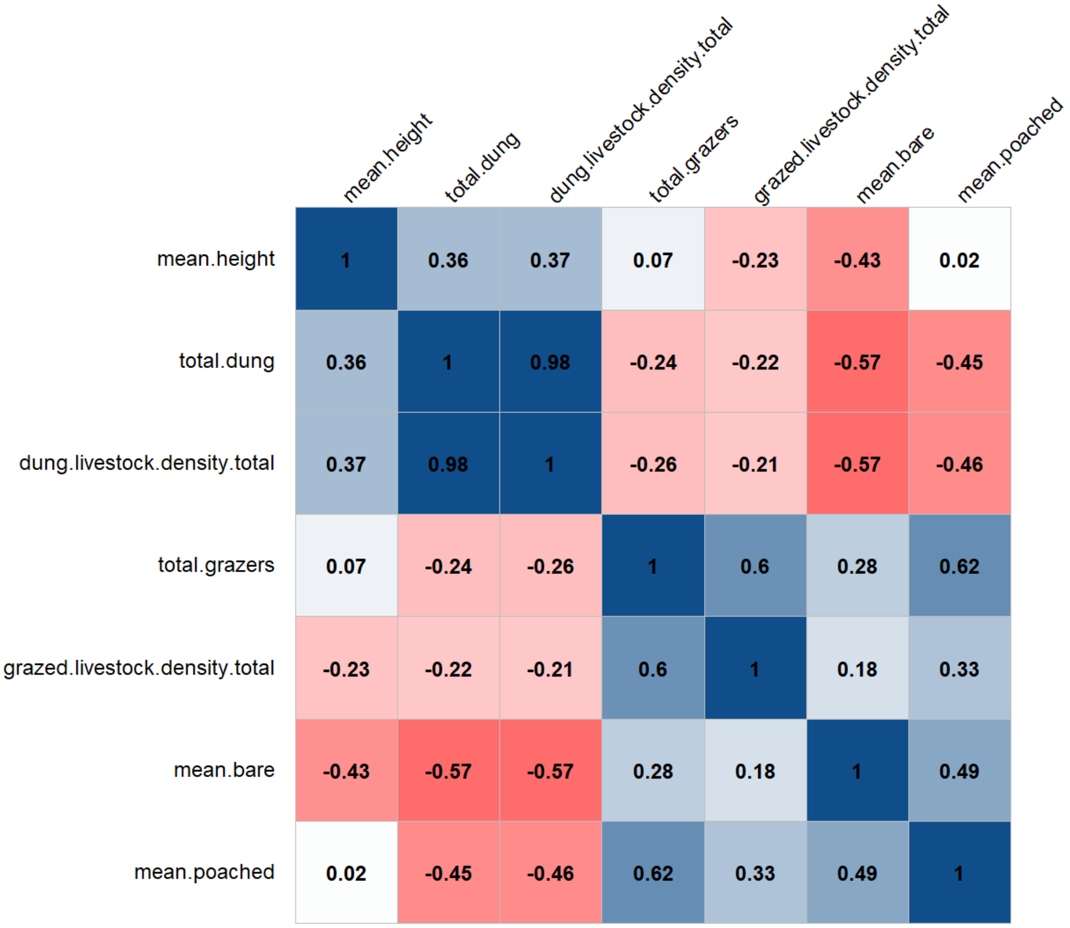
A3.3. Predictor correlation tests



	mean.height	total.dung	dung.livestock.density.total	total.grazers	grazed.livestock.density.total	mean.bare	mean.poached
mean.height	1	-0.48	-0.47	-0.41	-0.42	-0.46	-0.37
total.dung	-0.48	1	0.98	0.55	0.54	0.25	0.42
dung.livestock.density.total	-0.47	0.98	1	0.63	0.62	0.25	0.46
total.grazers	-0.41	0.55	0.63	1	0.99	0.32	0.54
grazed.livestock.density.total	-0.42	0.54	0.62	0.99	1	0.32	0.52
mean.bare	-0.46	0.25	0.25	0.32	0.32	1	0.52
mean.poached	-0.37	0.42	0.46	0.54	0.52	0.52	1

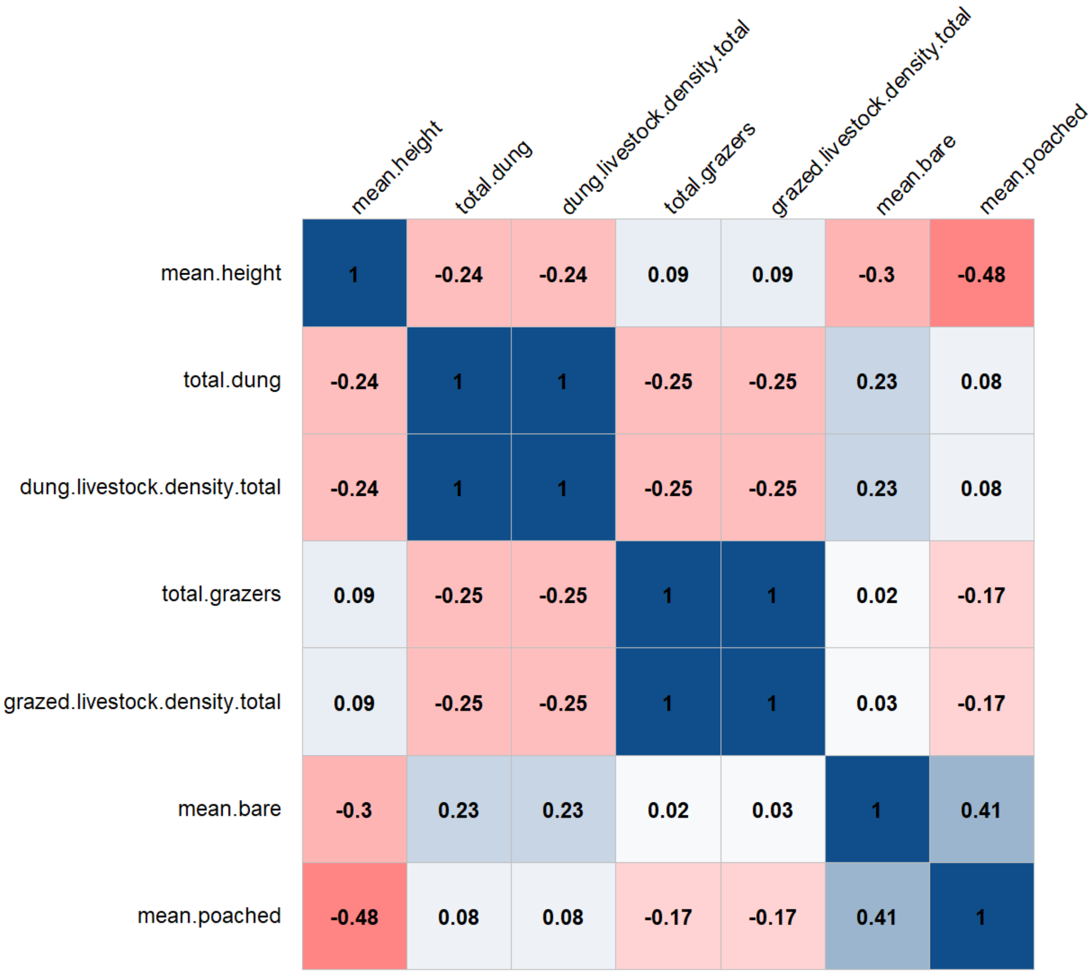
Figure A3.6. Spearman's correlation coefficients of grazing estimates for each variable combination in the total dataset. Blue = positive correlation coefficients, white = no correlation, Red = negative correlation coefficients.

Dung livestock density in the Crofty site showed a negative correlation with total number of grazers. Bare and poached ground are negatively correlated with dung. Bare and poached ground were highly correlated, however they were not used in the analysis since bare ground presence may facilitate easier recognition of poached ground by the surveyor, so it is difficult to entangle these values. Most grazing values are significantly correlated, however, the main fixed variables (dung livestock density, grazed livestock density and mean vegetation height) did not correlate above $\rho = 0.37$, so can be treated as independent explanatory variables. Correlation tests with LWG data did not produce any significant correlations.



	mean.height	total.dung	dung.livestock.density.total	total.grazers	grazed.livestock.density.total	mean.bare	mean.poached
mean.height	1	0.36	0.37	0.07	-0.23	-0.43	0.02
total.dung	0.36	1	0.98	-0.24	-0.22	-0.57	-0.45
dung.livestock.density.total	0.37	0.98	1	-0.26	-0.21	-0.57	-0.46
total.grazers	0.07	-0.24	-0.26	1	0.6	0.28	0.62
grazed.livestock.density.total	-0.23	-0.22	-0.21	0.6	1	0.18	0.33
mean.bare	-0.43	-0.57	-0.57	0.28	0.18	1	0.49
mean.poached	0.02	-0.45	-0.46	0.62	0.33	0.49	1

Figure A3.7. Spearman's correlation coefficients of grazing estimates for each variable combination for data collected in CR. Blue = positive correlation coefficients, white = no correlation, Red = negative correlation coefficients.



	mean.height	total.dung	dung.livestock.density.total	total.grazers	grazed.livestock.density.total	mean.bare	mean.poached
mean.height	1	-0.24	-0.24	0.09	0.09	-0.3	-0.48
total.dung	-0.24	1	1	-0.25	-0.25	0.23	0.08
dung.livestock.density.total	-0.24	1	1	-0.25	-0.25	0.23	0.08
total.grazers	0.09	-0.25	-0.25	1	1	0.02	-0.17
grazed.livestock.density.total	0.09	-0.25	-0.25	1	1	0.03	-0.17
mean.bare	-0.3	0.23	0.23	0.02	0.03	1	0.41
mean.poached	-0.48	0.08	0.08	-0.17	-0.17	0.41	1

Figure A3.8. Spearman's correlation coefficients of grazing estimates for each variable combination for data collected in LWG Blue = positive correlation coefficients, white = no correlation, Red = negative correlation coefficients.

A3.4. Further analysis of the impact of grazing on flower cover.

To test the impact of grazing intensity on flower cover, a general linear model with poisson distribution was employed with insect-pollinated plant cover predicting flower cover, and grazing presence as an interactive effect. The model described that the intercept of the flower abundance and insect-pollinated plant abundance relationship did not differ in each site (P > 0.05), and there was no interaction of site on the relationship (Figure A3.9).

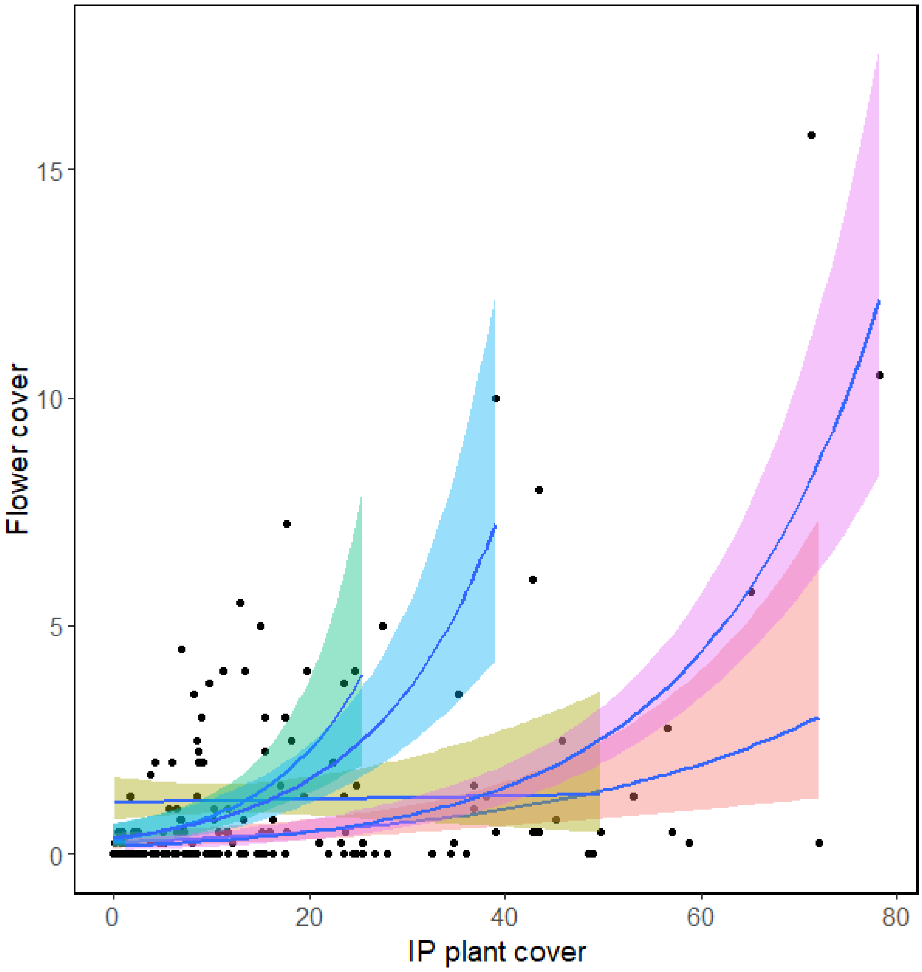


Figure A3.9. Effects of insect pollinated plant cover on flower cover for each site. Points represent transect data. Lines represent poisson distribution ANCOVA fit to the observed data. Shaded area represents 95% confidence intervals. Colour represents site: Red = CB, Green = LWG, Mauve = PB, Blue = LWU, Brass = CR.

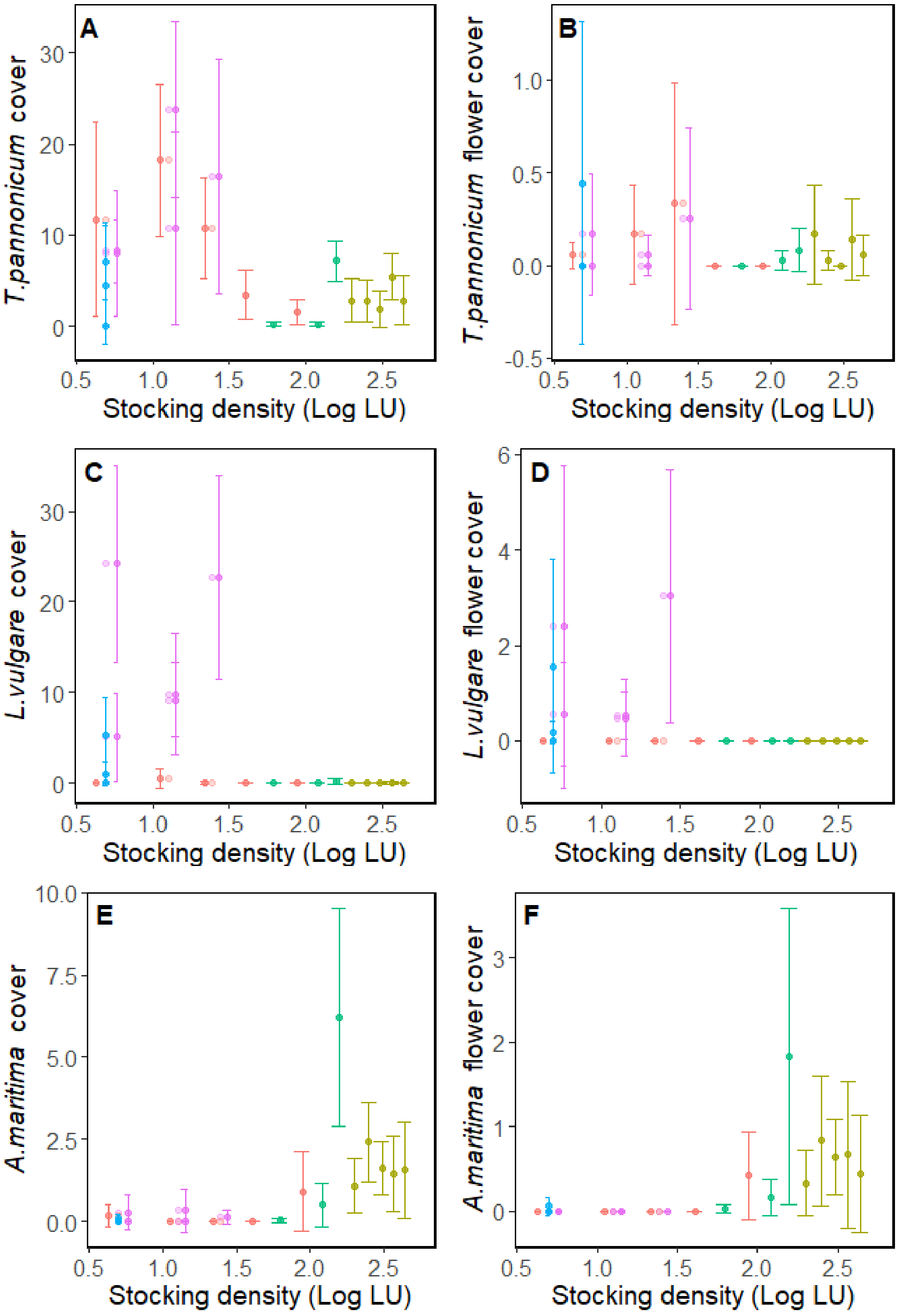


Figure A3.10. effect of stocking density estimated from Dung livestock units on plant species cover attributes. Points represent means per plot. Bars represent 95% confidence intervals. Points are scattered per site to avoid point overlaying. Translucent points indicate the value of scattered points. Colour represents site: Red = CB, Green = LWG, Mauve = PB, Blue = LWU, Brass = CR.

A3.5. Statement of expenditure

Student Name: Benjamin Lam
Student Number: 981599
Project Title: Livestock grazing impacts Bee (Apoidea) - pollination networks in the saltmarshes of Southwest Wales

Category	Item	Description	Cost
Travel	Public transport tickets	Bi-weekly travel to study sites	£192.34
	Car fuel	Bi-weekly travel to study sites	£16.12
Consumables	Clipboard	Write data into datasheets in the field	£1.00
	Net head	Capture bees to collect abundance data	£8.80
	Black net	Capture bees to collect abundance data	£7.75
	White net	Capture bees to collect abundance data	£7.75
	Net handle	Capture bees to collect abundance data	£7.50
	Plaster of Paris jars	Kill bee specimens for identification	£2.55
	Ethyl acetate	Kill bee specimens for identification	£3.20
	Plastazote store box (16”x11”)	Store bee specimens	£65.42
	38x.35 Continental steel nylon pins	Store bee specimens	£5.20
	38x.50 Continental steel nylon pins	Store bee specimens	£5.20
	Spring action pinning forceps	Prepare bee specimens	£15.75
	Pinning stage	Prepare bee specimens	£14.95
	String	Transect marker	£5.17
	Delivery charge	Delivery of consumables	£12.30
	VAT	VAT for purchasing consumables	£28.81
Total			£399.21

I hereby certify that the above information is true and correct to the best of my knowledge.

[redacted]

[redacted]

Signature (Supervisor)

Signature (Student)

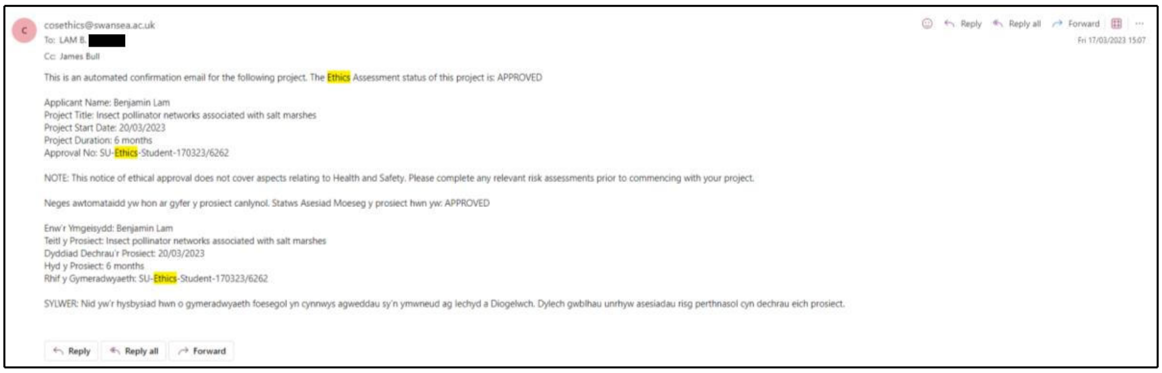
A3.6. Statement of contributions of Co-Authors

The authors below have certified that:

1. They meet the criteria for authorship in that they have participated in the conception, execution or interpretation of at least that part of the publication in their field of expertise;
2. They take public responsibility for their part of the publication, except for the responsible author who accepts overall responsibility for the publication;
3. There are no other authors of the publication according to these criteria:
4. Potential conflicts of interest have been disclosed to (a) granting bodies, (b) the editor or publisher of journals or other publications, and (c) the head of the responsible academic unit, and
5. They agree to the use of the publication in the student's thesis and to its availability online in the University's Open Access Repository and for inter-library loan, and for the title and summary to be made available to outside organisations consistent with any limitations set by publisher requirements.

Contributor Role	**Persons involved**
Conceptualization	JCB, WEH
Data Curation	BTL
Formal analysis	BTL
Funding Acquisition	n/a
Investigation	BTL
Methodology	BTL, JCB, WEH
Project Administration	BTL, JCB
Resources	JCB, WEH
Software	BTL, JCB
Supervision	JCB, WEH
Validation	JCB
Visualization	BTL, JCB, WEH
Writing – Original Draft Preparation	BTL
Writing – Review & Editing	BTL, JCB, WEH

A3.7. Ethics Approval



cosethics@swansea.ac.uk
To: LAM B. [redacted]
Cc: James Bull
Fri 17/03/2023 15:07

This is an automated confirmation email for the following project. The Ethics Assessment status of this project is: APPROVED

Applicant Name: Benjamin Lam
Project Title: Insect pollinator networks associated with salt marshes
Project Start Date: 20/03/2023
Project Duration: 6 months
Approval No: SU-Ethics-Student-170323/6262

NOTE: This notice of ethical approval does not cover aspects relating to Health and Safety. Please complete any relevant risk assessments prior to commencing with your project.

Neges awtomataidd yw hon ar gyfer y prosiect canlynol. Statws Asesiad Moeseg y prosiect hwn yw: APPROVED

Enw'r Ymgeisydd: Benjamin Lam
Teitl y Prosiect: Insect pollinator networks associated with salt marshes
Dyddiad Dechrau'r Prosiect: 20/03/2023
Hyd y Prosiect: 6 months
Rhif y Gymeradwyaeth: SU-Ethics-Student-170323/6262

SYLWER: Nid yw'r hysbysiad hwn o gymeradwyaeth foesegol yn cynnwys agweddau sy'n ymwneud ag Iechyd a Diogelwch. Dylech gwblhau unrhyw asesiadau risg perthnasol cyn dechrau eich prosiect.

A3.8. Health and Safety and Risk assessments

Science fieldwork risk assessment (PGR)

You must not carry out fieldwork until this risk assessment has been approved by your Supervisor.

***☒College of Science.**

Student's name	**Benjamin Lam**	Email	[redacted]
Student number	[redacted]	**✓ UG**	**☐ PGT ☐ PGR**
Supervisor's name	**Dr. James Bull and Dr. Wendy Harris**	Email	[redacted] [redacted]
Student Contact number		[redacted]	
Next of kin		Heather Lam	
Next of kin contact number		[redacted]	
Maximum number of participants (on any fieldtrip)		2	
Name of field assistant(s) – Lone working is only permitted in exceptional circumstances, with the agreement of your Supervisor.		none	
Brief outline of the research / fieldwork activity:			
Insect-pollinator networks associated with salt marshes: **Sampling of vegetation flora, bee (Insecta; Hymenoptera) community composition and environmental conditions in grazed and ungrazed saltmarsh landscapes across the South-West Wales area (Swansea and Gowerton) using in-vivo direct observation, capture/release with handheld nets, and specimen capture and killing along straight 30 m transects.**			
List of methods to be used. Add additional methods if required.			
Method 1 Identification of 100m sampling square, and randomly choose a 30m transect within. If the transect crosses a large creek, choose a different random transect. Method 2 Direct observation of bee species among vegetation along a 30m transect using quadrats			

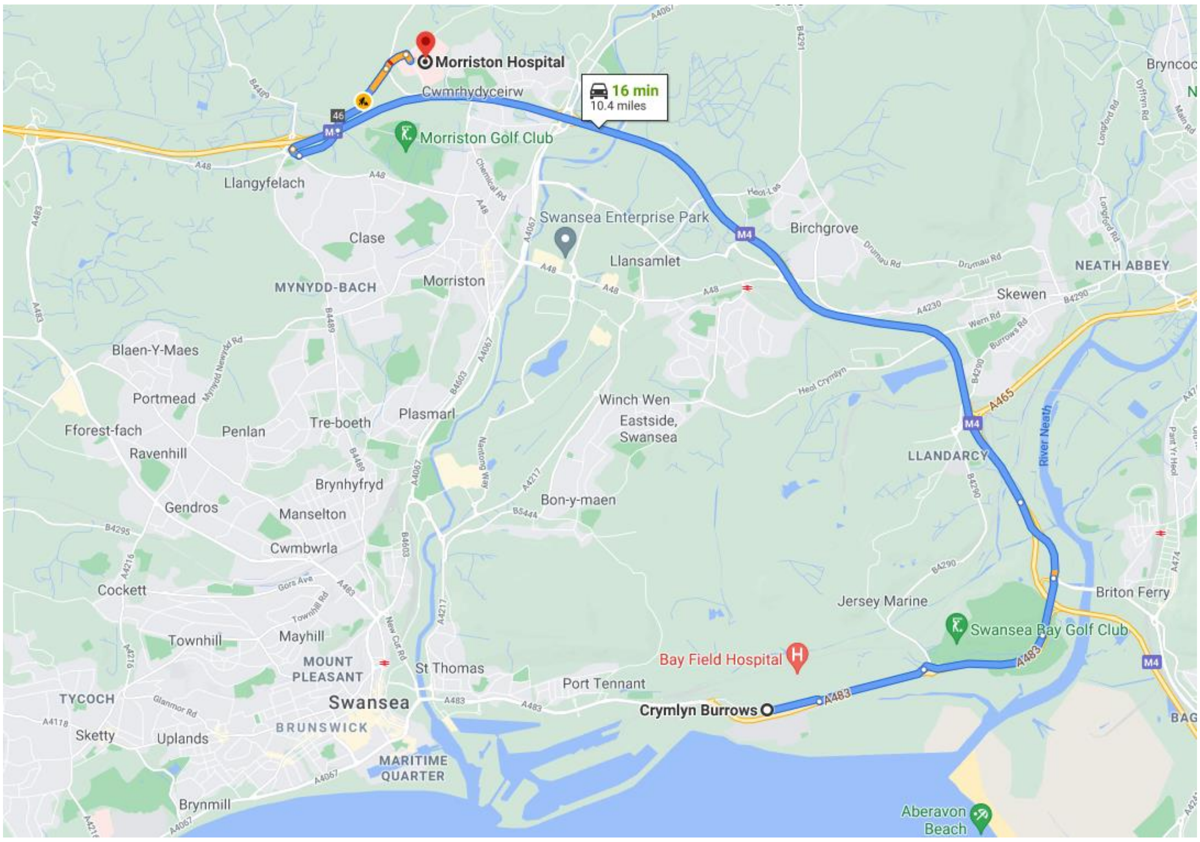
Method 3
Capture/identification/release of inconspicuous bee individuals using a hand net and pots, within the same survey as above. Capture and killing of inconspicuous bee individuals using ethyl acetate in pots.

Method 4
Identification of plant species and vegetative structure of the 2x2m plot by direct observation or removal of specimen samples.

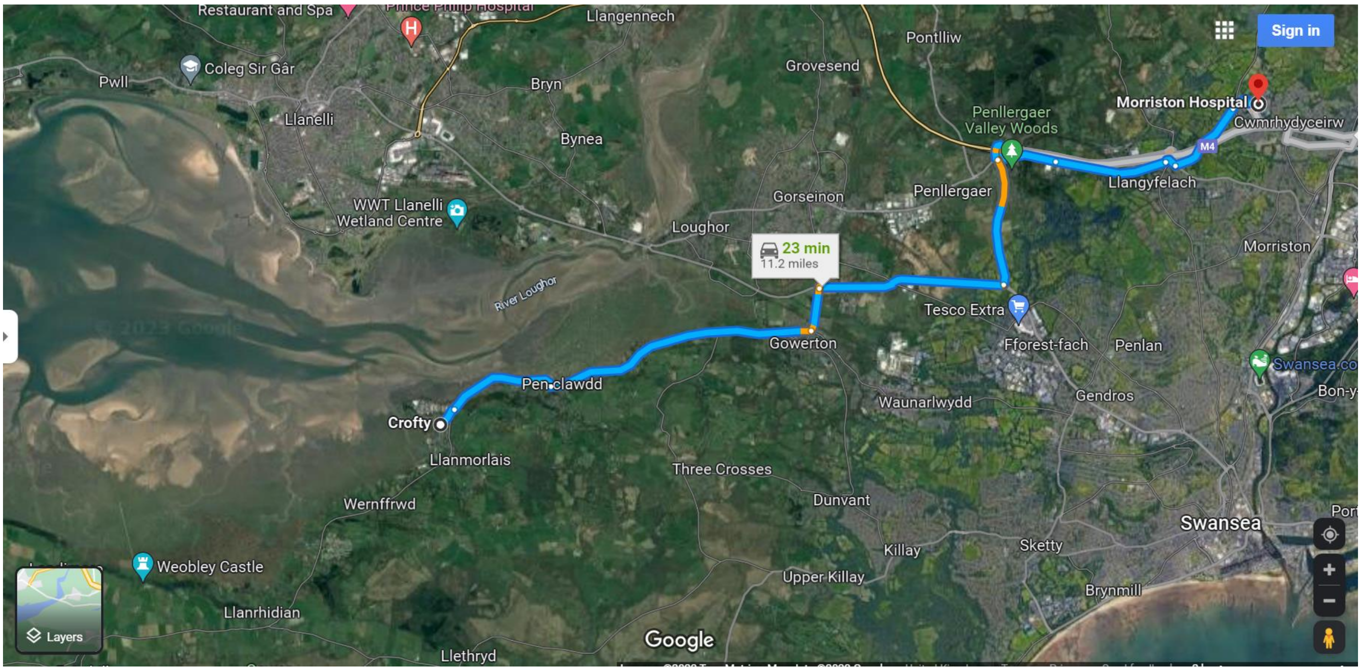
Ethics approval number			
Date of activity - Start:	15/3/2023	End:	1/9/2023
Location of activity (site name, region etc.):		Crymlyn burrows SSSI, Swansea. Llanrhidian saltmarsh, Swansea. Llanelli Wetlands, Llanelli. Pembrey saltings, Pembrey.	
UK Map Reference or LAT LON (if outside UK)		Crymlyn: SS 713 929 Llanrhidian: SS 513 953 Llanelli: SS 524 973 Pembrey: SN 428 000.	
What 3 words Reference (what3words.com)		Crymlyn: ///prickly.dogs.bitter Llanrhidian: ///wades.farmed.bulldozer Llanelli: /// removers.consonant.systems Pembrey: /// regress.exchange.ports	
Nearest hospital with A&E (incl. postcode for use with a satnav / app)		Morriston hospital - SA6 6NL (Crymlyn, Llanrhidian, Llanelli) Glangwili General Hospital - SA31 2AF (Pembrey)	
Approx. distance from field site?		Crymlyn: 9.4 miles Llanrhidian: 11.2 miles Llanelli: 12.8 Pembrey: 16.1 miles	
Is there mobile phone coverage?		☒Yes ☐No	
If there is no phone reception, how will you summon help?		SafeZone app with emergency contact to Swansea university security using mobile data.	
Contact Name for Check-in / Safe return (Ensure that they know where you are going, your expected return time, your Supervisor's name).		Name & Contact details: Heather Lam [redacted] [redacted]	
Frequency of check-ins / Communication Plan (e.g. start and end of each day)		Check in with Contact (Heather) and bay campus security via SafeZone app at start and end of the day.	

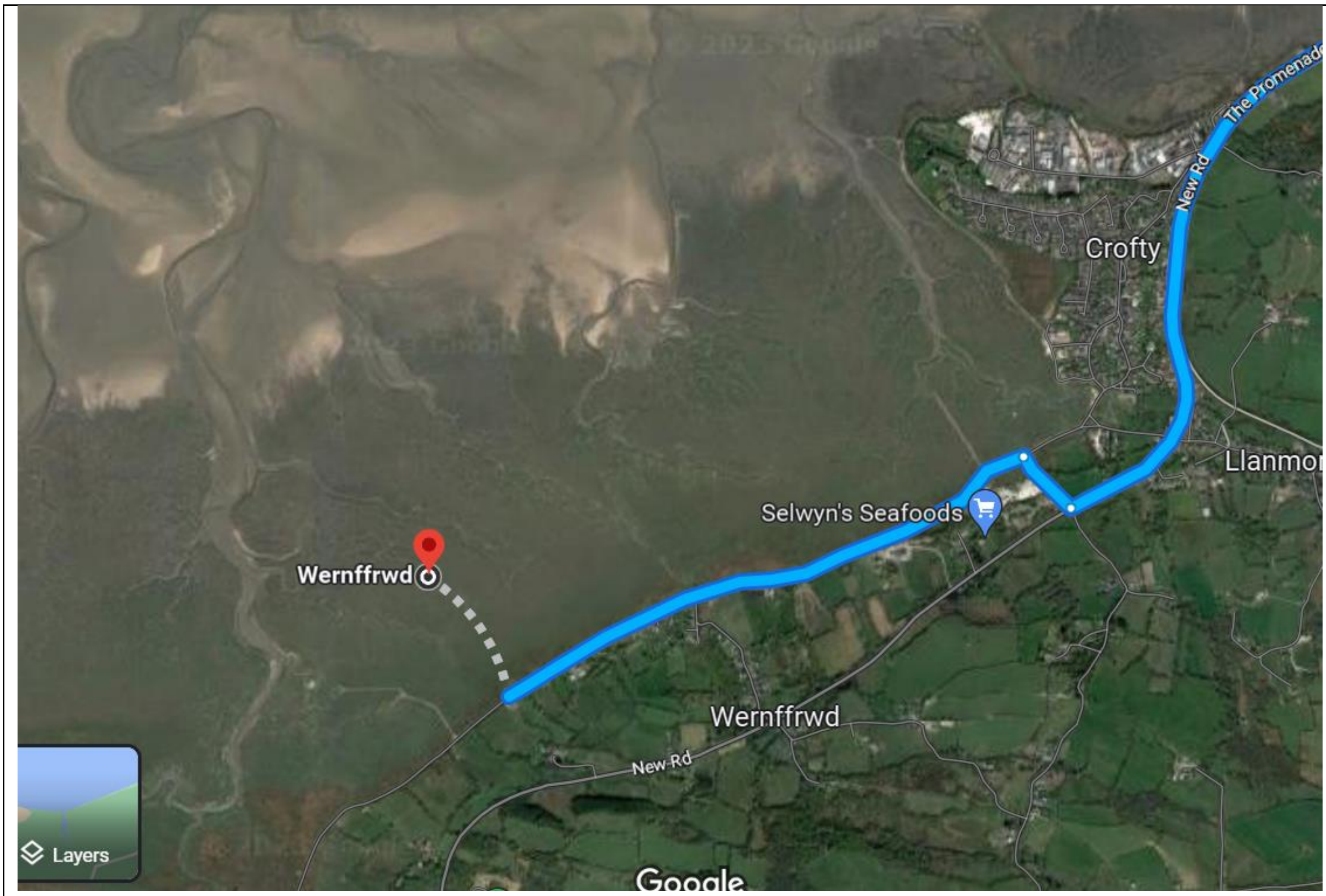
Map of field site (Identify route to nearest hospital with an A&E Department)

Crymlyn Burrows:



Llanrhidian:

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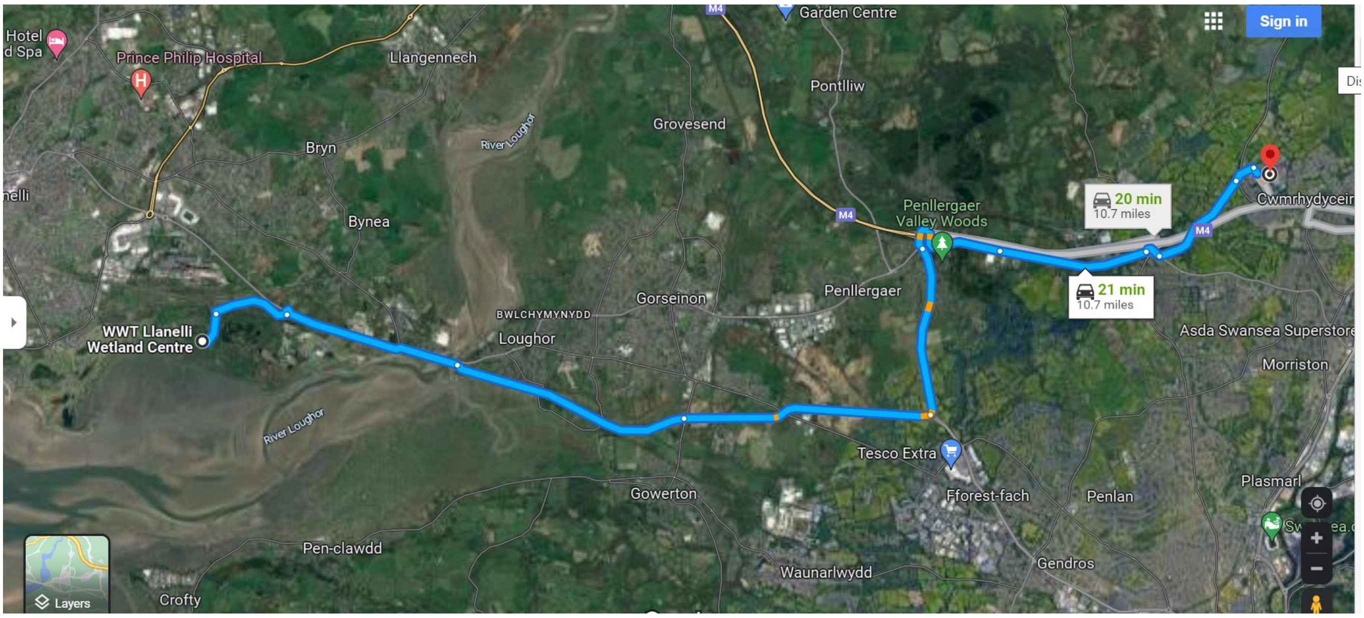
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Penllergaer
Gorseinon
BWLCHYMYNYDD
Loughor
WWT Llanelli Wetland Centre
Asda Swansea Superstore
Morriston
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Gendros
Layers
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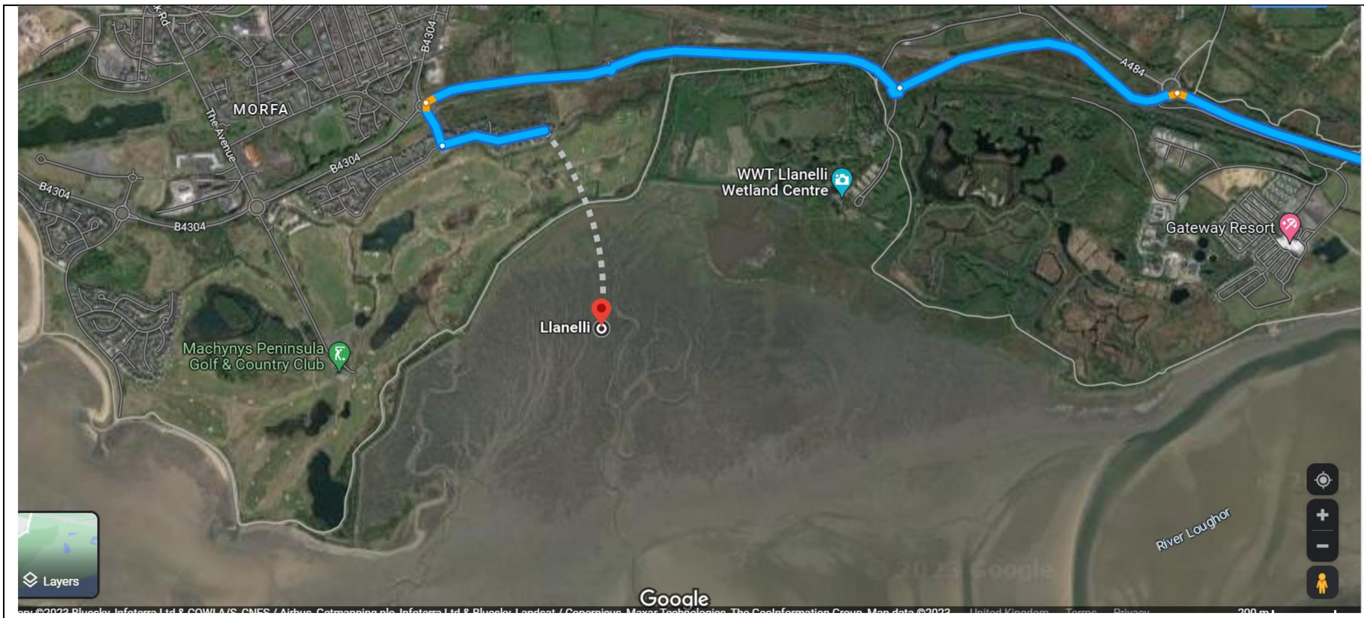
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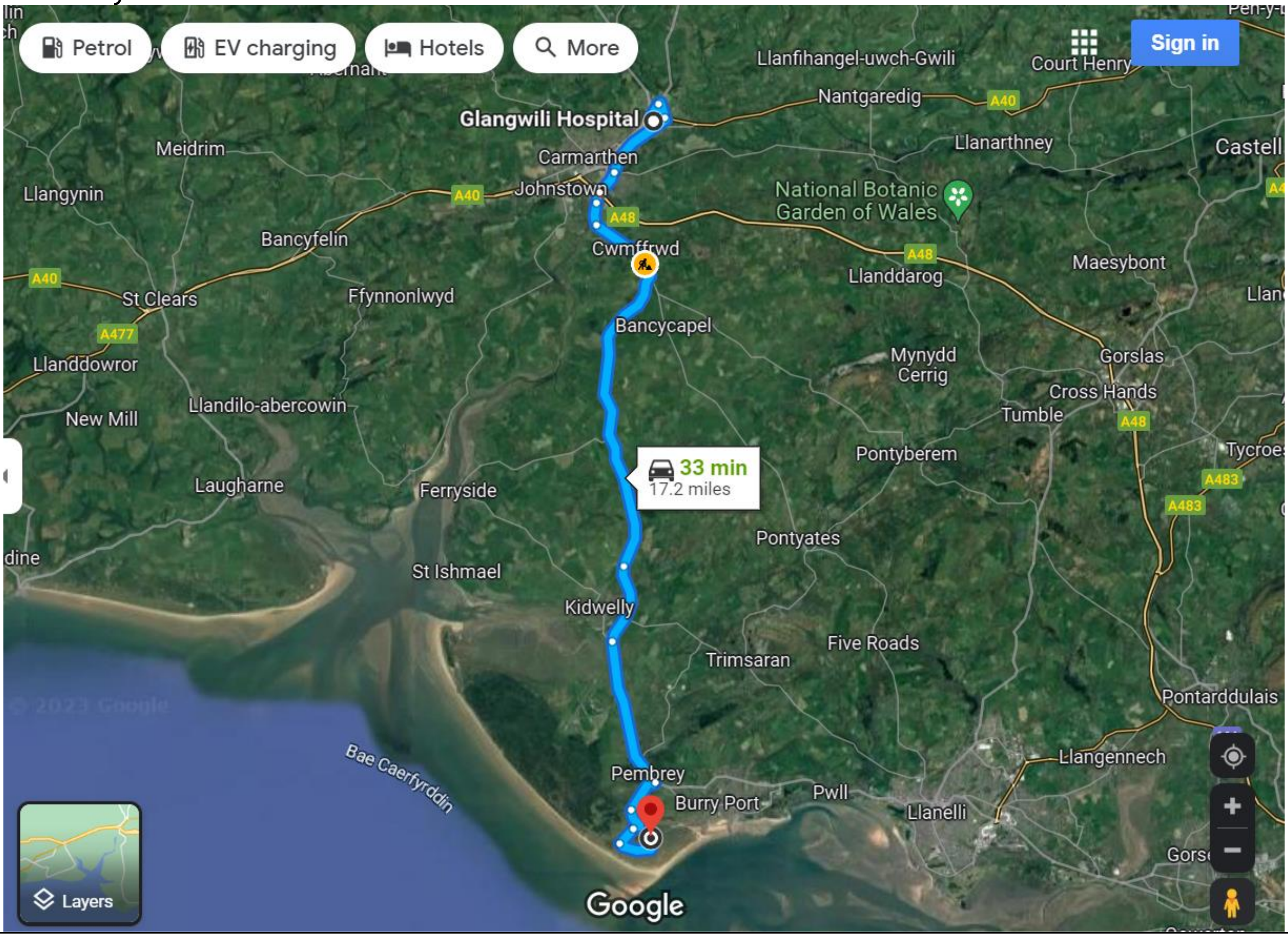
Wetland Centre
Gateway Resort
Machynys Peninsula
Golf & Country Club
Llanelli
River Loughor
Layers
Google

Pembrey


Petrol
EV charging
Hotels
More
Sign in
Llanfihangel-uwch-Gwili
Court Henry
Nantgaredig
A40
Glangwili Hospital
Llanarthney
Castell
Meidrim
Carmarthen
Johnstown
Llangynin
A40
A48
National Botanic
Garden of Wales
Bancyfelin
Cwmffrwd
A48
Llanddarog
Maesybont
A40
St Clears
Ffynnonlwyd
Bancycapel
A477
Llanddowror
Mynydd
Cerrig
Gorslas
Cross Hands
Tumble
New Mill
Llandilo-abercowin
A48
Pontyberem
Tycroes
33 min
17.2 miles
Laugharne
Ferryside
A483
A483
Pontyates
St Ishmael
Kidwelly
Five Roads
Trimsaran
Pontarddulais
Bae Caerfyrddin
Llangennech
Pembrey
Burry Port
Pwll
Llanelli
Layers
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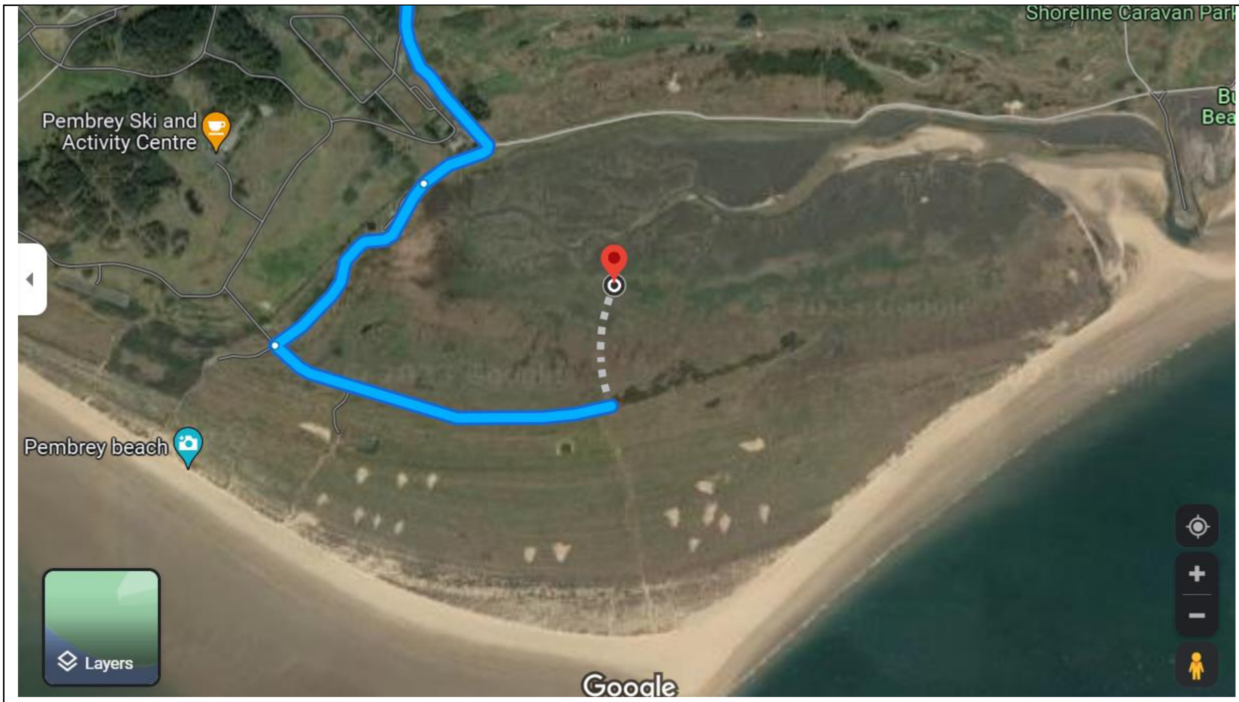

Fieldwork Risk Assessment Form Fill in the grid with the appropriate information. Extend the table as required. See Appendix 1 - Fieldwork Risk Assessment – Guidance Document. See Appendix 2 - Examples of some hazards associated with fieldwork.								
Step 1	*Step 2*	*Step 3*						
Description of hazard	**Who may be harmed and how**	**S**	**L**	**R**	**Controls / actions required** (to eliminate / reduce the risk)	**S**	**L**	**R**
Travelling to/from fieldwork site	Accident using bicycle injury to self and/or others and/or equipment. Falling from platform when boarding train / Bus	3	2	6	○ Use public and certified bus ○ Ensure the seating plan for the mode of transport is in-line with Covid-19 requirements ○ Stay away from platform, beware of other pedestrians. Do not board train if there are obstacles in doorway. Keep bicycle locked in bike carriage.	2	1	2
Slippery and/or uneven surfaces	Slips, trips and falls; falling over causing bruises, cuts and broken bones	1	3	3	○ Wear strong and sensible footwear. ○ Take care, especially on wet surfaces and loose screes. ○ Be aware of other potential trip hazards. Adjust or abandon route if necessary.	1	2	2
Steep slopes	Slipping and falling	2	2	4	○ Stay on marked paths where possible.	2	1	2

					o Be aware of and do not stand on cliff edges. Adjust or abandon route if necessary.			
Weather (cold and wet)	Hypothermia	3	1	3	o Wear warm and waterproof clothing. o Carry spare clothing. o Carry survival bag/blanket. Carry food and warm drink.	3	1	3
Weather (hot and sunny)	Hyperthermia	3	2	6	o Wear a sun hat and loose-fitting clothing. o Keep hydrated. Carry plenty of water. Drink regularly. o Be aware of sources of drinking water. o Wear sunscreen (high SPF) Wear sunglasses Stop off at shaded places when available	3	1	3
Designation of research site	Compliance requirement	2	1	2	o Understand the site's status and any requirements e.g. Site of Special Scientific Interest (SSSI), Special Protection Area (SPA), Private Land etc. Obtain any permissions required e.g. Natural Resources Wales, Environment Agency, Landowner etc.	1	1	1
Heavy bags and equipment	Strain from carrying too much.	2	1	2	o Don't try and carry more than you can manage.	2	1	2
Animals and plants	Bites, stings and scratches	2	3	6	o Keep first aid kit at hand. o Wear garden gloves when handling vegetation. o Look out for brambles, thorns and biting/stinging animals. o Avoid contact with poisonous plants. o Educate on what poisonous plants look like e.g. stinging nettle, Poison hemlock, and Wolfsbane. o Cover skin in areas of severe insect infestation. o Wear thick clothing that covers all body skin unless it is hot. o Check regularly for ticks and take care removing them.	2	2	4

					o Seek immediate expert help if bitten by venomous animal. o Do not attempt to “pet” animals you are unfamiliar with. Monitor for symptoms of Lyme Disease if exposed to ticks.			
	Bee stings	2	2	4	o Educate on what to do when a bee stings. o Have emergency services at hand in the case of allergic reaction. Bring sterile tweezers to remove stings, and an ice pack to reduce swelling. o Do not directly handle bees. o Carefully transfer bee from net to pot using standard method keeping hands well away from bees. o Wear gloves around bees	2	2	4
	Mobilization of invasive species	2	1	2	o Do not remove, break or replace any invasive species e.g. rosa rugosa, sea buckthorn, Japanese knotweed.	2	1	2
	Disturbance of protected species	3	2	6	o Avoid areas where signs of birds may be nesting. o Avoid trampling of wild grassland and flora o Keep to paths.	3	1	3
	Kicks or bites from aggressive domestic grazers	3	2	6	o Do not approach domestic grazers. Especially those with young o Always ensure there is an escape route between you and the animal. Do not allow yourself to be cornered from escape. o watch for warning signs of animal aggression o Move slowly and calmly at all times. o Do not turn your back on a cow	3	1	3
Infection	Contamination of scratches, bites or grazes	3	2	6	o Clean skin wounds carefully with clean water and/or antiseptic wipes/cream. o Carry simple first-aid kit.	3	1	3
Illness	Food poisoning or gastro-intestinal infection from eating	3	1	3	o Wash hands before eating or preparing food.	3	1	3

	or drinking contaminated food/water				o Don’t drink from streams and rivers			
Ethyl Acetate use	Poisoning or accidental inhalation, leading to unconsciousness and resulting in potential drowning in the saltmarsh field.	3	2	6	o Label killing jars “poison” o Do not sniff jars or deliberately inhale fumes. o Never test a killing jar by smelling its contents. o Bury or burn old jars that do not kill quickly. o Do not use near open flame or cigarettes o Wash face, hands and any exposed skin thoroughly after handling o Use only outdoors o Keep container tightly closed o Wear protective gloves/protective clothing o Keep cool o Response: Get medical attention/advice if you feel unwell Inhalation o IF INHALED: Remove victim to fresh air and keep at rest in a position comfortable for breathing o Call a POISON CENTER or doctor/physician if you feel unwell Skin o IF ON SKIN (or hair): Take off immediately all contaminated clothing. Rinse skin with water/shower Eyes o IF IN EYES: Rinse cautiously with water for several minutes. Remove contact lenses, if present and easy to do. Continue rinsing If eye irritation persists o Keep container tightly closed Store locked up Disposal Dispose of contents/container to an approved waste disposal plant Hazards not otherwise classified (HNOC)	3	1	3
Fences and stiles	Injury from tripping. Minor cuts/bruises	2	1	2	o Take care at all times.	2	1	2

	from sharp surfaces. Shock from electric fences.				o Look out for sharp surfaces, barbed wire and electric fences. Avoid where possible.			
					o			
Water	Deep water – risk of drowning. Cold water – risk of thermal shock and hypothermia. Moving Water – risk of entrapment (strainers), falls, flash flooding and current. Tidal water – risk of entrapment, rip tides, cut-off by tide, waves.	3	3	9	o Avoid going near water o Do not cross streams without assessment of risk, wear backpacks on one strap only. o Consider what lies beneath the water. o Wear appropriate footwear. o Know the tide times for the day(s) you will be working o Plan a contingency for tides into your work plan. Avoid getting cut-off by rising tide or waves. o Beware of flash floods o Do not walk further than the upper saltmarsh o Observer on bank who is aware of emergency procedures and will provide support as required	2	2	4
Tidal Environments, saltmarshes, mudflats, estuaries.	Entrapment in mud, fast flowing water in gullies, hypothermia following accidental exposure to water, pollution, litter and debris leading to cuts and physical injuries.	3	3	9	o Wear strong, sturdy walking boots. o Avoid going near streams, creeks, mud and water in general. o Have security on SafeZone app to ping your location if needed. o Be aware of entrapment risk from estuarine mud and saltmarsh environments – know what to do if trapped. o Appropriate PPE o Be aware that there may be hazards (rubbish, debris etc.) hidden in the mud.	2	2	4
Tidal Isolation	isolation by rising water, hypothermia and drowning	3	3	9	o Plan and know the tidal times and tidal range for the day(s) of sampling. o Plan route beforehand using a terrain map.	2	2	4

					○ Be aware of any entrapment points, rip currents, races or gullies. ○ Do not use potentially isolating parts of the site during incoming tide. ○ Know the tide times for the day(s) you will be working ○ Plan a contingency for tides into your work plan. Avoid getting cut-off by rising tide or waves. ○ Beware of flash floods ○ Do not walk further than the upper saltmarsh ○ Observer on bank who is aware of emergency procedures and will provide support as required ○ Set a notification and turn back when the predicted tide direction changes.			
Coronavirus	People can catch COVID-19 from others who have the virus. These people may be symptomatic or asymptomatic. Worst case, this may be fatal, illness of varying degrees. Refer to NHS website for symptoms. <u>Vulnerable individuals - Some people are at increased risk</u> Infection can spread by inhaling small droplets in the air (spread from people nearby through breathing, coughs and sneezes).	2	3	6	○ Comply with Country / Local coronavirus restrictions. Wales: https://gov.wales/covid-19-alert-levels ○ Do not attend fieldwork if you have coronavirus symptoms (New and continuous cough / high temperature / loss or change of taste or smell) ○ Do not attend fieldwork if someone in your household has coronavirus symptoms, or you have been told to self-isolate by Test, Trace and Protect. ○ Check for updates: https://myuni.swansea.ac.uk/coronavirus-student-faqs/ **Hands / Face / Space / Fresh air** ○ Wash hands frequently and always before eating / drinking. Use hand sanitizer or soap and water. Avoid	2	1	2

	Touching shared equipment or high touch points that has been contaminated – then touching the mouth/ eyes/ nose can also cause transmission of the virus.				touching your face with unwashed hands. ○ Cover your nose and mouth with a tissue or your elbow (not your hands) when you cough or sneeze. ○ Do not share equipment with people who are not in your household / use disinfectant wipes between use if this cannot be avoided. ○ Wear face covering when using public transport / public spaces / enclosed areas (e.g. transport) ○ Maintain 2 metres social distancing from people who are not in your household. ○ Where 2 metres social distancing cannot be avoided, minimise activity time, try to work side-by-side or back-to-back (not face to face), wear a face covering. ○ Consider safe ways to travel, where possible avoid sharing cars with people who are not in your household. ○ Keep enclosed spaces well ventilated (e.g. vehicles).			
Isolation/ Lone working	Lone worker has no visual nor audible communication with someone who can summon assistance in the event of an accident, emergency or illness.	3	2	6	○ Keep emergency contact at all times ○ Ensure mobile data and cell service are both working ○ Use safezone app to notify security on field. ○ Keep first aid kit at all times ○ Ensure water and food is packed at all times	3	1	3

Risk (R) = (SxL): LOW (1-2), MODERATE (3-5), HIGH (6-9).

Coronavirus: Whilst coronavirus remains in circulation you must include this hazard in your risk assessment.

Are you working near water?	Yes
If **yes**, please address the following questions:	
What, if any, is the degree of immersion (i.e. none, boat, wade, swim etc.)	Up to one foot on saltflats.
What is the nature of the wet environment (river, beach, still water etc.)	Creek/salt marsh/beach

Can you and your field assistant(s) swim?	☒Yes ☐No		
In moving water, specify any additional hazards to consider regarding the rate of flow, tides, water temperature etc.	Tidal Isolation from mainland. Fast water flow in creeks Freezing water temperatures Boggy, quicksand-type sediment		
I will assess flow rate and risk on-site before entering the water and monitor throughout the experiment.	**Mandatory**		
If applicable: What are the tidal times for the dates(s) of activity?	Date(s)	High water	Low water
Is the water polluted? If yes, what protection measures are you taking?	☐Yes ☒No		
Work in or around water is potentially dangerous. Additional personal protective equipment (PPE) is required. You and your assistant(s) need to know how to use these items.			
PPE Buoyancy aid	☐Yes ☒No		
Throw Line	☐Yes ☒No		
Wet suit / dry suit / waders / boots required (specify)?	☒Yes ☐No. Specify: Wellington boots		
Other (specify):	☐Yes ☒No. Specify:		

National Emergency Tel: 999. University Switchboard [redacted] *(non-emergency).*

All required research permission and permits obtained? Give details:	☒Yes ☐No. Give details: permission from site warden and land owners.

Working method statement
Detail here the field methods you will be using and any controls / actions you will take to reduce the risk. Include Standard Operating Procedures or append references as appropriate. Sit or stand on the saltmarsh for multiple hours per day, record bee abundances in 2x2m plots (marked out with 10mm diameter poles), via direct observation for 1hour at a time. *Make your way to the sampling locations using main established paths, avoid steep areas. Use buddy system and SafeZone app to notify contacts of location. Wear sun lotion, and bring extra to re-apply hourly. wear warm clothing during cold period. Bring a suitable supply of water, and do not stay out in the sun too long to avoid sun/heat stroke.* Recording cryptic bees via capture/release with a net and sampling pots. *Educate on what to do when a bee stings. Have emergency services at hand in the case of allergic reaction. Bring sterile tweezers to remove stings, and an ice pack to reduce swelling. Do not directly handle bees. Carefully transfer bee from net to pot using standard method keeping hands well away from bees. Wear gloves near bees.* Recording plants in vivo, using keys. Unidentifiable specimens removed from site in poly-pockets.

Wear full-body clothing, with no skin showing to avoid tick and other arthropod bites. Be wary of overheating however and find shady locations to rest. Be aware of potential poisonous plants on site including stinging nettle, Poison hemlock, and Wolfsbane.

Sampling in boggy saltmarsh with deep creeks and cryptic pools potentially several feet deep.
Tread carefully. Wear strong, sturdy walking boots or wellington boots. Have campus security on call if a fall takes place on Crymlyn. Have emergency services on call if a fall takes place outside of campus. Keep first aid kit at hand. Wear garden gloves when handling vegetation

Sampling of saltmarsh with large grazers
Avoid areas with a high density of large animals, do not approach grazers and know what to do when met with an aggressive or threatening animal.

Sampling in the salt marsh and near the beach. *Avoid going near streams, creeks, mud and water in general. Do not enter the beach. The spit and saltmarsh risks isolation from the mainland during incoming tide. Be aware of the tide times before entering the field. Avoid spending too much time in these areas, especially during high tide. Have security on SafeZone app to ping your location if needed. Avoid treading in muddy substrate, and know what to do when you get stuck.*

Personal checks (student):

In signing this form, I agree that:

✓ I consent to this information being shared in accordance with the General Data Protection Regulations.

✓ I have assessed the risks associated with the activity. I will put in place the controls / activities identified in the risk assessment. I understand that no research activity can be totally risk free.

✓ I have discussed with my Supervisor any disability or medical condition that may affect my Health and Safety in the field. I will discuss with them any additional controls or reasonable adjustments that I require.

✓ I will notify my **contact** that I will be in the field, I will communicate with them according the agreed communication plan. I will take with me appropriate contact numbers and means for summoning help.

✓ I have established the location of the nearest hospital with an accident and emergency department. I have included the post code for the hospital as this may assist if using a sat. nav.

✓ I have a plan in the event that mobile phones will not work on site either due to reception or failure of equipment.

☒ I have a map and compass for location and navigation in the field (tick only if required).

✓ I am familiar with the use of all field equipment and will work within the approved method statements.

✓ I will secure written permission to access the field site and will carry with me a copy of the agreement including any permits to collect samples.

✓ I will ensure that all participants are suitably equipped and capable of working **safely** in the field.

✓ I will brief my field assistant(s) and advised them of emergency procedures. I will discuss the work plan, risks and safety arrangements with the field assistant(s) as part of my briefing.

✓ I will access the site with due care (following the Country Code).

✓ I will engage politely and professionally with any members of the public with whom I interact during fieldwork and take the time to explain to them what I am doing if this is appropriate.

✓ I will work safely in a manner respectful of others.

✓ I will log all accidents and "near-misses" using the adverse event system (https://www.swansea.ac.uk/about-us/safety-and-security/health-and-safety/report-it/) and ensure that my Supervisor is informed.

I will work safely, implementing the controls identified within the risk assessment. In the event that my methods change or that the environment changes I will dynamically re-assess the risk and cease the activity if the environment or activity becomes unsafe or if conditions move beyond the scope of this assessment. **✓Yes** **☐No.** To be signed **after** discussion with your Supervisor:

Student signature	**Date of assessment**
[redacted]	13/03/2023

Supervisor checks:

Directly test and challenge the student before approval – in the event of a <u>NO</u> answer to any of these questions the student must review the assessment with their Supervisor and then re-test:

Has the student personally assessed the risks associated with this activity? ☐**Yes** ☐**No** ☐**Not applicable**

Has the student identified appropriate controls / actions to reduce risk so far as is reasonably practicable? ☐**Yes** ☐**No**

Are additional controls and/or reasonable adjustments in place for *participants* that have a medical condition or disability? ☐**Yes** ☐**No** ☐**Not applicable**

Is lone working permitted? ☐**Yes** ☐**No**. *If yes*, are you complying with the Lone Working Policy Arrangements? ☐**Yes** ☐**No**

Is the level of risk acceptable for this student activity to take place? ☐**Yes** ☐**No**

Does the student know what actions to take in the event of a foreseeable emergency? ☐ **Yes** ☐**No**

Have you given the student the opportunity to ask questions about the activity? ☐**Yes** ☐**No**

Have you checked that the student understands what they are doing and why, the controls required to reduce risks and actions to take in the event of an emergency? ☐**Yes** ☐**No**

Are you satisfied that the risks have been appropriately assessed and suitable controls have been identified, such that the student can work safely within the remit of the assessment? ☐**Yes** ☐**No**

If you have answered no to any of the questions, do not sign the form approving this activity.

Supervisor's signature	**Date of approval**
[redacted]	13/03/2023

Students travelling overseas, for University business purposes, must comply with the International Travel Policy and take with them a copy of the Swansea University Travel Cover Summary document.

Appendix 1 - Fieldwork Risk Assessment – Guidance Document

- This form supports the fieldwork risk assessment form above.

Carrying out a risk assessment:

STEP 1 – Identify the hazards. A hazard is anything that has the potential to cause harm. Examples: e.g. fast flowing water / falling rocks / carrying heavy items. Think about the fieldwork that you are going to do (activities and environment) and think about what may cause you, or others, harm. Record these in column 1. Appendix 2 lists a few the common hazards associated with fieldwork.

STEP 2 – Consider who may be harmed and how.

For each hazard, consider who may be harmed and how – maybe yourself, other fieldworker, or members of the public. Some fieldwork participants may be "vulnerable workers", (e.g. they have a disability / ill-health / new or expectant parent / young person U18 / new to the job), reasonable adjustments and/or additional controls may be required - this should also be recorded on your risk assessment.

Example: Weather, (cold and wet) – (who) all participants, (how) may cause hypothermia.

Example: (who) the participants collecting samples near the rock face, below cliffs (how) falling rocks may cause cut, bruises and broken bones.

Record these in column 2.

STEP 3 –Evaluate the risk

Severity (S): For each hazard estimate the potential severity of harm on a scale from 1 to 3. Record this on the form.

1 LOW: temporary discomfort or very minor injury treatable on the scene.

2 MEDIUM: more serious non-emergency injury requiring medical attention/hospital, medium-term impact to health and well-being with full recovery

3 HIGH: Serious injury or death, high risk of permanent or long-term damage to health or well-being.

Likelihood (L): For each hazard estimate the likelihood that harm will occur on a scale of 1 to 3. Record this on the form.

1 UNLIKELY BUT POSSIBLE: this event does not happen in the normal course of events but could – these events are often those with very serious consequences or those resulting from a chain of events.

2 MODERATELY LIKELY: this event is not a typical or frequent occurrence but could occur given specific conditions (e.g. very high spring tides).

3 VERY LIKELY: this event could happen very easily without correct planning.

Risk (R): For each hazard, calculate the risk. Risk = Severity (S) x Likelihood (L).

Record this on the form.

	Likelihood		
Severity	Unlikely - 1	Moderate - 2	Very likely - 3
Low - 1	1	2	3
Medium - 2	2	4	6
High - 3	3	6	9

Risk – 1-2 Low Risk, 3-5 Moderate Risk, 6-9 High Risk.

Controls / Actions required

This is the most important part of your risk assessment. You're not expected to eliminate all risks, but you need to do everything 'reasonably practicable' to protect yourself and others from harm. Seriously consider what controls / actions you need to take to reduce the risk (particularly those with the highest risk). Example: Cold and wet weather may cause hypothermia. Controls / Actions: Wear warm and waterproof clothing / Carry spare clothing / Carry survival bag/blanket / Carry food and warm drink.

- Record these controls / actions on the form. This is not just a paperwork exercise. The actions you have identified, to reduce the risk of harm, must be carried out when you are in the field, to keep you and others safe and to comply with the law.

Recalculate the risk with the controls / actions in place.

For each hazard

- Is the harm less **severe** or the same? *Record on the sheet*
- Is the harm less **likely** to occur or the same? *Record on the sheet*
- Then calculate the **risk**. Risk = Severity x Likelihood. *Record on the sheet.*

Is the risk reduced to an acceptable level to proceed with your activity? If not, contact your Supervisor for advice.

(This online risk assessment should not be used by Postgraduate students who already follow the University Field Safety Policy Arrangements and use the associated documentation).

Appendix 2 - Examples of hazards associated with fieldwork

(Modified from Dr Geraint Owen & Geologists' Association South Wales)

Important: This is not a complete list, you need to consider the hazards association with your specific work and environment. This may also change with the location, time of day and weather.

HAZARD (Something with the potential to cause harm)	**How may you be harmed?** (harm to health / injury caused by hazard*)	**CONTROLS / ACTION(S) REQUIRED** (to eliminate / reduce the risk)
Travelling to/from fieldwork site	Accident using chosen mode of transport – injury to self and/or others and/or equipment	o Identify the safest mode of travel to get to your destination o Ensure the seating plan for the mode of transport is in-line with Covid-19 requirements o Use modes of transport with the lowest carbon impact on the environment. o Ensure the mode of transport has the appropriate insurances, licences and any other accreditations required (as required) o Check the mode of transport is road/sea-worthy prior to use
Slippery and/or uneven surfaces	Slips, trips and falls; falling over causing bruises, cuts and broken bones	o Wear strong and sensible footwear. o Take care, especially on wet surfaces and loose screes. o Be aware of other potential trip hazards. o Adjust or abandon route if necessary.
Steep slopes	Slipping and falling	o Stay on marked paths. o Be aware of and do not stand on cliff edges. o Adjust or abandon route if necessary.
Weather (cold and wet)	Hypothermia	o Wear warm and waterproof clothing. o Carry spare clothing. o Carry survival bag/blanket. o Carry food and warm drink.
Weather (hot and sunny)	Hyperthermia	o Wear a sun hat and loose-fitting clothing. o Keep hydrated. Carry plenty of water. Drink regularly. o Be aware of sources of drinking water. o Wear sunscreen (high SPF) o Wear sunglasses
Falling rock	Cuts, bruises, broken bones	o Wear a hard hat and high visibility jacket when working close to rock faces especially under cliffs. o Be aware of other people above and below you.
Designation of research site	Compliance requirement	o Understand the site's status and any requirements e.g. Site of Special Scientific Interest (SSSI), Special Protection Area (SPA), Private Land etc.

		○ Obtain any permissions required e.g. Natural Resources Wales, Environment Agency, Landowner etc.
Specimen collecting	Rock splinters from hammering; hitting hands with hammer; strain from carrying too much	○ Take care when hammering. ○ Wear protective goggles and gloves. ○ Don’t try and carry more than you can manage.
Animals and plants	Bites, stings and scratches	○ Look out for brambles, thorns and biting/stinging animals. ○ Avoid contact with poisonous plants. ○ Cover skin in areas of severe insect infestation. ○ Use insect repellent if appropriate. ○ Check regularly for ticks and take care removing them. ○ Seek immediate expert help if bitten by venomous animal. ○ Do not attempt to “pet” animals you are unfamiliar with. ○ Monitor for symptoms of Lyme Disease if exposed to ticks.
	Mobilisation of invasive species	○ Understand whether your research has the ability to mobilise invasive species, this may be species of plant or animal e.g. Japanese knotweed, killer shrimp ○ Design your method of work in a way to avoid the risk of this occurring
	Disturbance of protected species	○ Understand whether your work may disturb protected species in the area, this may include plants and animals ○ Design your method to minimise disturbance e.g. after nesting season or when migratory species are not present. ○ Protected species licence may be required if impacts are unavoidable
Farm animals	Trampling, goring and butting. Ingesting contaminated matter.	○ Be aware of any farm animals and keep clear. ○ Be aware of animal waste and wash hands after fieldwork or before eating in the field.
Infection	Contamination of scratches or grazes	○ Clean skin wounds carefully with clean water and/or antiseptic wipes/cream. ○ Carry simple first-aid kit.
Illness	Food poisoning or gastro-intestinal infection from eating or drinking contaminated food/water	○ Wash hands before eating or preparing food. ○ Don’t drink from streams and rivers; use water purification tablets/filter if water must be obtained from such source. ○ Keep strict hygiene regime in campsite.
Roads and traffic	Being knocked over leading to cuts,	○ Take care when crossing roads.

	bruises, broken bones, internal traumas and death	○ Always walk at the roadside towards oncoming traffic. ○ Be alert at all times. ○ Wear high-visibility clothing if working alongside roads.
Fences and stiles	Injury from tripping. Minor cuts/bruises from sharp surfaces. Shock from electric fences.	○ Take care at all times. ○ Look out for sharp surfaces, barbed wire and electric fences. Avoid where possible.
Driving between sites	Accident and injury from distraction when looking for sites or following a car.	○ Take care at all times. ○ Confirm next location before setting off. ○ Lead car to drive at safe speed to allow others to follow.
Woodland	Slips, trips, falls. Falling branches and deadwood.	○ Take care when working under trees – be aware of deadwood. ○ Work carefully to avoid trips and falls from uneven forest floor (roots etc.).
Peat Bogs	Risk of entrapment, cold, wet – hypothermia risk, risk of immersion in pools uneven surfaces leading to injury	○ Work carefully avoid deep pools and bogs. ○ Learn procedure for exiting a bog if trapped. ○ Take care carrying equipment over bog surface. ○ Bring warm clothes, dry clothes in case of accidental immersion as required. ○ Take care when coring – use correct manual handling technique (e.g. lift with legs).
Water	Deep water – risk of drowning. Cold water – risk of thermal shock and hypothermia. Moving Water – risk of entrapment (strainers), falls, flash flooding and current. Tidal water – risk of entrapment, rip tides, cut-off by tide, waves. Uneven riverbed – entrapment and fall	○ Avoid exposure to cold water or deep water ○ Carry warm clothes and dry clothes in the event of accidental emersion. ○ Do not cross streams without assessment of risk, wear backpacks on one strap only. ○ Assess water before entering – if flow rate is faster than a brisk walk do not enter. ○ Consider what lies beneath the water. ○ Wear appropriate footwear. ○ Know the tide times for the day(s) you will be working ○ Plan a contingency for tides into your work plan. Avoid getting cut-off by rising tide or waves. ○ Establish if the river is prone to flash flooding ○ Observer on bank who is aware of emergency procedures and will provide support as required (**Mandatory**)
Water sampling (bankside)	Weil's Disease (leptospirosis) Slips and falls from bank Pollution	○ Dress and cover all cuts, wash hands and exposed areas. Monitor for symptoms. ○ Do not sample from undercut riverbanks ○ Take care on wet and slippery surfaces ○ No lone working ○ Wear PPE (buoyancy aid?)

	Accidental immersion, cold shock, physical injury and drowning	○ Observer on bank who is aware of emergency procedures and will provide support as required (**Mandatory**)
Water sampling (in-water)	Weil's Disease (leptospirosis) Slips and falls from bank Slips and falls in water Entrapment in riverbed Biologicals (jelly fish, weaver fish etc.) Pollution Accidental immersion – hypothermia, physical injury cold shock, drowning	○ Dress and cover all cuts, wash hands and exposed areas. Monitor for symptoms. ○ Do not sample from undercut riverbanks ○ Take care on wet and slippery surfaces ○ No lone working ○ Wear PPE (buoyancy aid?) ○ Observer on bank who is aware of emergency procedures and will provide support as required (**Mandatory**) ○ Establish ingress and egress points before sampling.
Tidal Environments, saltmarshes, mudflats, estuaries.	Entrapment in mud, isolation by rising water, fast flowing water in gullies, hypothermia following accidental exposure to water, pollution, litter and debris leading to cuts and physical injuries.	○ Plan and know the tidal times and tidal range for the day(s) of sampling. ○ Be aware of any entrapment points, rip currents, races or gullies. ○ Be aware of entrapment risk from estuarine mud and saltmarsh environments – know what to do if trapped. ○ Appropriate PPE ○ Be aware that there may be hazards (rubbish, debris etc.) hidden in the mud. Wear suitable footwear.
Coronavirus	People can catch COVID-19 from others who have the virus. These people may be symptomatic or asymptomatic. Worst case, this may be fatal, illness of varying degrees. Refer to NHS website for symptoms. <u>Vulnerable individuals - Some people are at increased risk</u> Infection can spread by inhaling small droplets in the air (spread from people nearby through	• Comply with Country / Local coronavirus restrictions. Wales: https://gov.wales/covid-19-alert-levels • Do not attend fieldwork if you have coronavirus symptoms (New and continuous cough / high temperature / loss or change of taste or smell) • Do not attend fieldwork if someone in your household has coronavirus symptoms, or you have been told to self-isolate by Test, Trace and Protect. • Check for updates: https://myuni.swansea.ac.uk/coronavirus-student-faqs/ **Hands / Face / Space / Fresh air** • Wash hands frequently and always before eating / drinking. Use hand sanitizer or soap and water. Avoid touching your face with unwashed hands. • Cover your nose and mouth with a tissue or your elbow (not your hands) when you cough or sneeze.

	breathing, coughs and sneezes). Touching shared equipment or high touch points that has been contaminated – then touching the mouth/ eyes/ nose can also cause transmission of the virus.	• Do not share equipment with people who are not in your household / use disinfectant wipes between use if this cannot be avoided. • Wear face covering when using public transport / public spaces / enclosed areas (e.g. transport) • Maintain 2 metres social distancing from people who are not in your household. • Where 2 metres social distancing cannot be avoided, minimise activity time, try to work side-by-side or back-to-back (not face to face), wear a face covering. • Consider safe ways to travel, where possible avoid sharing cars with people who are not in your household. • Keep enclosed spaces well ventilated (e.g. vehicles).
Lone working	Lone worker has no visual nor audible communication with someone who can summon assistance in the event of an accident, emergency or illness.	• Lone working must not be undertaken where there is a reasonably foreseeable risk that the work might result in an adverse event or emergency, which would be sufficiently serious to require a second person to be available to summon help or provide assistance. • Lone working will only be agreed in exceptional circumstances. The Supervisor must comply with the University Lone Working Policy Arrangements.
Waste and recycling	Compliance requirement: Clean Neighbourhoods and Environment Act 2005	• Consider any resulting wastes and how they will be managed when undertaking your fieldwork incl. disposing to appropriate bins • Leaving waste is considered as fly tipping and can be prosecuted

A3.9. R-Code for statistical analysis

```
########################################################################
#############
#
#
#    Document Title:  MRes thesis, analysis of results
#    Produced for Thesis: Livestock grazing impacts Bee (Apoidea) - pollination
networks   in  the   saltmarshes  of  Southwest  Wales
#    Author: Benjamin Lam 981599
#    Date: 19/05/2025
#    Data sources: (1) Transect environmental dataset, (2) Transect Bee counts
dataset, stored as CSV files
#
#
########################################################################
#############
########################################################################
#############
# insert data
########################################################################
#############

#clear environment
rm(list = ls())

#import environmental data
mbees <- read.csv("environment.raw.24.04.05.1.0.goodmaritimabund.csv", header
= TRUE)
summary(mbees)
View(mbees)

#import bee counts
mbc <- read.csv("walks.raw.23.09.27.1.2.realplants.csv", header = TRUE)
summary(mbc)


#get packages
library(corrplot)
library(cowplot)
library(dplyr)
library(FSA)
library(ggplot2)
library(ggpubr)
library(glmmTMB)
library(lattice)
```

```
library(MASS)
library(multcomp)
library(psych)
library(tidyr)
library(visreg)
library(bipartite)




#################################################################
#############
# Formatting data
#################################################################
#############


#summary of environment
summary(mbees)

#remove data from pilot study
mbees <- mbees %>%
  filter(!(site == 'cb' & date == '04/04/2023' ))

#remove data from pilot study - boxes 1-6 in llanelli only
mbees <- mbees %>%
  filter(!(site == 'lw' & box <8))


#turn all site boxes into number from 1-5 (or 1-6 for LW)

mbees$box <- ifelse(mbees$box==6,5,mbees$box)
summary(mbees$box[mbees$site == "cb"])
mbees$box <- ifelse(mbees$box==9,1,mbees$box)
mbees$box <- ifelse(mbees$box==10,2,mbees$box)
mbees$box <- ifelse(mbees$box==11,3,mbees$box)
mbees$box <- ifelse(mbees$box==12,4,mbees$box)
mbees$box <- ifelse(mbees$box==13,5,mbees$box)
mbees$box <- ifelse(mbees$box==14,6,mbees$box)
summary(mbees$box)
#1, 2, 3 are ungrazed. 4, 5, 6 are grazed

#same for walks.raw
mbc$box <- ifelse(mbc$box==6,5,mbc$box)
summary(mbc$box[mbc$site == "cb"])
mbc$box <- ifelse(mbc$box==9,1,mbc$box)
mbc$box <- ifelse(mbc$box==10,2,mbc$box)
```

```
mbc$box <- ifelse(mbc$box==11,3,mbc$box)
mbc$box <- ifelse(mbc$box==12,4,mbc$box)
mbc$box <- ifelse(mbc$box==13,5,mbc$box)
mbc$box <- ifelse(mbc$box==14,6,mbc$box)
summary(mbc$box)

#separate lw into lwu and lwg and make a new factor set site2
mbees$site2 <- mbees$site
mbees$site2 <- ifelse(mbees$site == "cb", "cb",
            ifelse(mbees$site == "pb","pb",
                ifelse(mbees$site == "cr", "cr",
                    ifelse(mbees$box ==1 , "lwu",
                        ifelse(mbees$box ==2 , "lwu",
                            ifelse(mbees$box ==3 , "lwu","lwg"))))))
str(mbees$site2)
mbc$site2 <- mbc$site
mbc$site2 <- ifelse(mbc$site == "cb", "cb",
           ifelse(mbc$site == "pb","pb",
               ifelse(mbc$site == "cr", "cr",
                   ifelse(mbc$box ==1 , "lwu",
                       ifelse(mbc$box ==2 , "lwu",
                           ifelse(mbc$box ==3 , "lwu","lwg"))))))
str(mbc$site2)

#create new column grouping by grazing presence
mbees$graze01 <- ifelse(mbees$site2 == "cr", "grazed",
              ifelse(mbees$site2 == "pb","ungrazed",
                  ifelse(mbees$site2 == "lwg", "grazed",
                      ifelse(mbees$box == "lwu" , "ungrazed",
                          ifelse(mbees$box ==2 , "grazed",
                              "ungrazed")))))
mbc$graze01 <- ifelse(mbc$site2 == "cr", "grazed",
            ifelse(mbc$site2 == "pb","ungrazed",
                ifelse(mbc$site2 == "lwg", "grazed",
                    ifelse(mbc$box == "lwu" , "ungrazed",
                        ifelse(mbc$box ==2 , "grazed",
                            "ungrazed")))))


#create new column with values of coefficient of variation.
mbees$cv <- mbees$sd.height / mbees$mean.height * 100


#format columns
mbees$date <- as.Date(mbees$date, format = "%d/%m/%Y")
mbees$site <- as.factor(mbees$site)
mbees$site2 <- as.factor(mbees$site2)
mbees$box <- as.numeric(mbees$box) ; mbees$box <- as.factor(mbees$box)
```

```
mbees$weather <- as.factor(mbees$weather)
mbees$wind.speed <- as.numeric(mbees$wind.speed)
mbees$total.richness.fl.site <- as.integer(mbees$total.richness.fl.site)
mbees$total.richness.ip.site <- as.integer(mbees$total.richness.ip.site)
mbees$bee.richness <- as.integer(mbees$bee.richness)
names(mbees)[names(mbees) == "mean.pocahced"] <- "mean.poached"
mbees$dung.livestock.density.total <-
as.numeric(mbees$dung.livestock.density.total)

#same for walks.raw
mbc$date <- as.Date(mbc$date, format = "%d/%m/%Y")
mbc$site <- as.factor(mbc$site)
mbc$box <- as.factor(mbc$box)
mbc$id <- as.factor(mbc$id)
mbc$species <- as.factor(mbc$species)
mbc$flower <- as.factor(mbc$flower)
mbc$Pinned <- as.factor(mbc$Pinned)
mbc$Species.confirmed.in.the.lab <- as.factor(mbc$Species.confirmed.in.the.lab)
mbc$site2 <- as.factor(mbc$site2)



# create new column block season
# Define breaks for the cut function
breaks <- c(as.Date("2023-04-12"), as.Date("2023-04-30"), as.Date("2023-05-14"),
as.Date("2023-05-28"), as.Date("2023-06-11"), as.Date("2023-06-
25"),as.Date("2023-07-09"), as.Date("2023-07-23"), as.Date("2023-08-06"),
as.Date("2023-08-20"),Inf)
# Create a new column with factors based on the date
mbees$block <- cut(mbees$date, breaks = breaks, labels = c("1", "2", "3", "4", "5",
"6", "7", "8", "9", "10"))
mbees$block <- as.numeric(mbees$block)
summary(mbees$block)

#create data for binomial GLMs
mbees$mean.cover.ip.bi <- as.numeric(mbees$mean.cover.ip)/100
mbees$mean.cover.fl.bi <- as.numeric(mbees$mean.cover.fl)/100



# exclude the time block where I could not sample all sites
# (19/07/23, pembrey, 21/07/23, crymlyn)
nrow(mbees)
mbees <- subset(mbees, mbees$date!= "2023-07-21");
mbees <- subset(mbees, mbees$date!= "2023-07-19")
nrow(mbees)

attach(mbees)
```

```
##################################################################
###
#    Bee networks
##################################################################
###


#create total species network
mbcnet <- mbc

interaction_df <- mbcnet %>%
  dplyr::group_by(flower, species) %>%
  dplyr::summarise(visits = n(), .groups = "drop") %>%
  tidyr::pivot_wider(
    names_from = species,
    values_from = visits,
    values_fill = list(visits = 0)
  )
interaction_matrix <- interaction_df %>%
  tibble::column_to_rownames("flower") %>%
  as.matrix()
print(interaction_matrix)

#plot network
plotweb(interaction_matrix, col.high="chocolate", col.low="darkseagreen1",
y.lim=c(-1,2.5), text.rot=90)

###
#
#create site-level subsets
mbcnet <- droplevels(mbcnet)
dfm_cb <- mbcnet[mbcnet$site == 'cb', ] ; dfm_pb <- mbcnet[mbcnet$site == 'pb',
]; dfm_cr <- mbcnet[mbcnet$site == 'cr', ] ; dfm_lwg <- mbcnet[mbcnet$site2 ==
'lwg', ] ; dfm_lwu <- mbcnet[mbcnet$site2 == 'lwu', ];
#dfm_lwu <- dfm_lw[dfm_lw$box %in% c('1', '2','3'), ] ; dfm_lwu <-
droplevels(dfm_lwu)
#dfm_lwg <- dfm_lw[dfm_lw$box %in% c('4', '5','6'), ] ; dfm_lwg <-
droplevels(dfm_lwg)
summary(dfm_lwg)

###

#create Llanelli ungrazed species network

interaction_df <- dfm_lwu %>%
  dplyr::group_by(flower, species) %>%
```

```
  dplyr::summarise(visits = n(), .groups = "drop") %>%
  tidyr::pivot_wider(
    names_from = species,
    values_from = visits,
    values_fill = list(visits = 0)
  ) ; interaction_matrix2 <- interaction_df %>% # turn matrix into numeric format for plotting
  tibble::column_to_rownames("flower") %>%
  as.matrix() ; print(interaction_matrix2)
  plotweb(interaction_matrix2, col.high="chocolate", col.low="darkseagreen1", y.lim=c(-1,2.5), text.rot=90) #plot network

  ###

  #create Llanelli grazed species network

  interaction_df <- dfm_lwg %>%
    dplyr::group_by(flower, species) %>%
    dplyr::summarise(visits = n(), .groups = "drop") %>%
    tidyr::pivot_wider(
      names_from = species,
      values_from = visits,
      values_fill = list(visits = 0)
    ) ; interaction_matrix3 <- interaction_df %>% # turn matrix into numeric format for plotting
    tibble::column_to_rownames("flower") %>%
    as.matrix() ; print(interaction_matrix3)
  plotweb(interaction_matrix3, col.high="chocolate", col.low="darkseagreen1", y.lim=c(-1,2.5), text.rot=90) #plot network

  ###

  #create crofty species network

  interaction_df <- dfm_cr %>%
    dplyr::group_by(flower, species) %>%
    dplyr::summarise(visits = n(), .groups = "drop") %>%
    tidyr::pivot_wider(
      names_from = species,
      values_from = visits,
      values_fill = list(visits = 0)
    ) ; interaction_matrix4 <- interaction_df %>% # turn matrix into numeric format for plotting
    tibble::column_to_rownames("flower") %>%
    as.matrix() ; print(interaction_matrix4)
  plotweb(interaction_matrix4, col.high="chocolate", col.low="darkseagreen1", y.lim=c(-1,2.5), text.rot=90) #plot network
```

```
  #create pembrey species network

  interaction_df <- dfm_pb %>%
    dplyr::group_by(flower, species) %>%
    dplyr::summarise(visits = n(), .groups = "drop") %>%
    tidyr::pivot_wider(
      names_from = species,
      values_from = visits,
      values_fill = list(visits = 0)
    ) ; interaction_matrix5 <- interaction_df %>% # turn matrix into numeric format
for plotting
    tibble::column_to_rownames("flower") %>%
    as.matrix() ; print(interaction_matrix5)
  plotweb(interaction_matrix5, col.high="chocolate", col.low="darkseagreen1",
y.lim=c(-1,2.5), text.rot=90) #plot network

  #create crymlyn species network

  interaction_df <- dfm_cb %>%
    dplyr::group_by(flower, species) %>%
    dplyr::summarise(visits = n(), .groups = "drop") %>%
    tidyr::pivot_wider(
      names_from = species,
      values_from = visits,
      values_fill = list(visits = 0)
    ) ; interaction_matrix6 <- interaction_df %>% # turn matrix into numeric format
for plotting
    tibble::column_to_rownames("flower") %>%
    as.matrix() ; print(interaction_matrix6)
  plotweb(interaction_matrix6, col.high="chocolate", col.low="darkseagreen1",
y.lim=c(-1,2.5), text.rot=90) #plot network

par(mfrow = c(2,2))
plotweb(interaction_matrix2, col.high="chocolate", col.low="darkseagreen1" ) #plot
network
plotweb(interaction_matrix3, col.high="chocolate", col.low="darkseagreen1" ) #plot
network
plotweb(interaction_matrix4, col.high="chocolate", col.low="darkseagreen1" ) #plot
network
plotweb(interaction_matrix5, col.high="chocolate", col.low="darkseagreen1" ) #plot
network

par(mfrow = c(1,1))
par(mar = c(5, 20, 4, 2))
plotweb(interaction_matrix, text.rot = 90, y.lim = c(-0.05, 2.1), col.high="chocolate",
col.low="darkseagreen1",  lab.face = "italic") #plot network
plotweb(interaction_matrix6, col.high="chocolate", col.low="darkseagreen1"  )
#plot network
```

```
########################################################################
###
#     Dung livestock density impacts environment
########################################################################
###

#generate model graphs
p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = log(1+mean.cover.fl),
fill = site2)) +
  geom_point(color = "olivedrab") +
  labs(x = "Stocking density (Log LU)", y = "Flower cover") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1))
pa <- p + geom_smooth(method = "glm", method.args = list(family = "gaussian"),
se = T,);pa# + ylim(0, 0.20)


# 3.6.1
p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = mean.cover.ip, fill =
site2)) +
  geom_point(color = "olivedrab") +
  labs(x = "Stocking density (Log LU)", y = "IP plant cover") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1))
pb <- p + geom_smooth(method = "glm", method.args = list(family =
"quasipoisson"), se = T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"));pb

#
p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = total.richness.fl.site, fill
= site2)) +
  geom_point(color = "olivedrab") +
  labs(x = "Stocking density (Log LU)", y = "Flower richness") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1))
pc <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
```

```
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"));pc

#
p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = mean.height, fill =
site2 )) +
  geom_point(color = "olivedrab") +
  labs(x = "Stocking density (Log LU)", y = "Plant height") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1))
pd <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#
p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = cv, fill = site2 )) +
  geom_point(color = "olivedrab") +
  labs(x = "Stocking density (Log LU)", y = "Variation in vegetation height (CV)") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1))
pe <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"));pe

#
p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = bee.abundance, fill =
site2 )) +
  geom_point(color = "olivedrab") +
  labs(x = "Stocking density (Log LU)", y = "Bee abundance") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1))
pf <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"));pf

#
p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = total.richness.ip.site,
fill = site2)) +
```

```
  geom_point(color = "olivedrab") +
  labs(x = "Stocking density (Log LU)", y = "IP plant richness") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1))
pg <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"));pg

#
p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = bee.richness, fill =
site2)) +
  geom_point(color = "olivedrab") +
  labs(x = "Stocking density (Log LU)", y = "Bee richness") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1))
pg <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"));pg



#plotting
plot_grid(pd, pe, pc, pg, pa, pb, pf, pg, nrow = 4, ncol = 2)




p <- ggplot(mbees, aes(x = (as.numeric(bee.richness)), y =
(as.numeric(bee.abundance))  )) +
  geom_point() +
  labs(x = "Bee richness", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qa <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))



#

p <- ggplot(mbees, aes(x = total.richness.fl.site, y = bee.richness  )) +
```

```
  geom_point(color = "red") +
  labs(x = "Flower richness", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qb <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#

p <- ggplot(mbees, aes(x = mean.cover.fl, y = bee.richness  )) +
  geom_point(color = "olivedrab3") +
  labs(x = "Total flower cover", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qc <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#

p <- ggplot(mbees, aes(x = mean.height, y = bee.richness  )) +
  geom_point(color = "grey") +
  labs(x = "Mean height", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qd <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#

p <- ggplot(mbees, aes(x = sd.height, y = bee.richness  )) +
  geom_point(color = "skyblue") +
  labs(x = "Variation in veg height", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qe <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))



#
```

```
p <- ggplot(mbees, aes(x = grazed.livestock.density.total, y = bee.richness  )) +
  geom_point(color = "black") +
  labs(x = "Grazer livestock density", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qh <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#

p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = bee.richness  )) +
  geom_point(color = "black") +
  labs(x = "Dung livestock density", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qi <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#plotting
plot_grid(qe,qb,qc,qd,qa,qh,qi, nrow = 3, ncol = 3)


#################################################################
#############
#     Environment impacts bee abundance
#################################################################
#############

#generate model graphs
p <- ggplot(mbees, aes(x = (as.numeric(bee.richness)), y =
(as.numeric(bee.abundance))  )) +
  geom_point() +
  labs(x = "Bee richness", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qa <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))



#

p <- ggplot(mbees, aes(x = total.richness.fl.site, y = bee.abundance  )) +
```

```
  geom_point(color = "red") +
  labs(x = "Flower richness", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qb <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#

p <- ggplot(mbees, aes(x = mean.cover.fl, y = bee.abundance  )) +
  geom_point(color = "olivedrab3") +
  labs(x = "Total flower cover", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qc <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#

p <- ggplot(mbees, aes(x = mean.height, y = bee.abundance  )) +
  geom_point(color = "grey") +
  labs(x = "Mean height", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qd <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#

p <- ggplot(mbees, aes(x = sd.height, y = bee.abundance  )) +
  geom_point(color = "skyblue") +
  labs(x = "Variation in veg height", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qe <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))



#
```

```
p <- ggplot(mbees, aes(x = grazed.livestock.density.total, y = bee.abundance  )) +
  geom_point(color = "black") +
  labs(x = "Grazer livestock density", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qh <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#

p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = bee.abundance  )) +
  geom_point(color = "black") +
  labs(x = "Dung livestock density", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qi <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#plotting
plot_grid(qe,qb,qc,qd,qa,qh,qi, nrow = 3, ncol = 3)
plot_grid(qe,qb,qc, nrow = 1, ncol = 3)


###################################################################
#############
#     Environment impacts bee abundance By Site
###################################################################
#############

#generate model graphs
p <- ggplot(mbees, aes(x = abs(total.richness.fl.site), y = abs(bee.abundance), fill
= site2 )) +
  geom_blank(size = 1) +
  labs(x = "Flower richness", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
rb <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  annotate("text", x = -Inf, y = Inf, label = "A", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1)) +
```

```
  scale_y_continuous(limits = c(0, NA)) +  geom_jitter(width = 0.2, height = .0, alpha = 0.6); rb



#

p <- ggplot(mbees, aes(x = mean.cover.fl, y = bee.abundance, fill = site2 )) +
  geom_blank() +
  labs(x = "Total flower cover", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
rc <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se = T,)+
  annotate("text", x = -Inf, y = Inf, label = "B", fontface = "bold", color = "Black", size = 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(panel.background = element_blank(), axis.line = element_line(color = "black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text = element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size = 1))+
  geom_jitter(width = 0.2, height = .0, alpha = 0.6) + scale_y_continuous(limits = c(0, NA)); rc



#

p <- ggplot(mbees, aes(x = abs(mean.height), y = abs(bee.abundance), fill = site2 )) +
  geom_blank() +
  labs(x = "Mean height (cm)", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
rd <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se = T,)+
  annotate("text", x = -Inf, y = Inf, label = "C", fontface = "bold", color = "Black", size = 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(panel.background = element_blank(), axis.line = element_line(color = "black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text = element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size = 1))+
  geom_jitter(width = 0.2, height = .0, alpha = 0.6) + scale_y_continuous(limits = c(0, NA)); rd




#

p <- ggplot(mbees, aes(x = cv, y = bee.abundance, fill = site2 )) +
```

```
  geom_point() +
  geom_jitter(width = 0.2, height = 0, alpha = 0.6) +  # Add jittered points
  labs(x = "Variation in vegetation height (CV)", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 12))
re <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  annotate("text", x = -Inf, y = Inf, label = "D", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1), axis.title.x = element_text(size = 12) );re


#

p <- ggplot(mbees, aes(x = grazed.livestock.density.total, y = bee.abundance, fill =
site2 )) +
  geom_point() +
  labs(x = "Grazed livestock density", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
rh <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1))
#

p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = bee.abundance, fill =
site2 )) +
  geom_point() +
  labs(x = "Dung livestock density", y = "Bee abundance") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
ri <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = c(1.3, 0.5),
axis.text = element_text(size = 12), panel.border = element_rect(color = "black", fill
= NA, size = 1), legend.text = element_text(size = 12),legend.title =
element_blank() ,legend.key.size = unit(1.7, "lines"))


#plotting
plot_grid(rb,rc,rd,re, nrow = 3, ncol = 2)
```

```
#################################################################
#############
#     Environment impacts bee richness
#################################################################
#############

#generate model graphs
p <- ggplot(mbees, aes(x = (as.numeric(bee.abundance)), y =
(as.numeric(bee.richness))  )) +
  geom_point() +
  labs(x = "Bee abundance", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qa <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))



#
p <- ggplot(mbees, aes(x = total.richness.fl.site, y = bee.richness  )) +
  geom_point(color = "red") +
  labs(x = "Flower richness", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qb <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#
p <- ggplot(mbees, aes(x = mean.cover.fl, y = bee.richness  )) +
  geom_point(color = "olivedrab3") +
  labs(x = "Total flower cover", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qc <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#
p <- ggplot(mbees, aes(x = mean.height, y = bee.richness  )) +
  geom_point(color = "grey") +
  labs(x = "Mean height", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
```

```
qd <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#
p <- ggplot(mbees, aes(x = sd.height, y = bee.richness  )) +
  geom_point(color = "skyblue") +
  labs(x = "Variation in veg height", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qe <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))



#
p <- ggplot(mbees, aes(x = grazed.livestock.density.total, y = bee.richness  )) +
  geom_point(color = "black") +
  labs(x = "Grazer livestock density", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qh <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#
p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = bee.richness  )) +
  geom_point(color = "black") +
  labs(x = "Dung livestock density", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
qi <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"))


#plotting
plot_grid(qe,qb,qc,qd,qa,qh,qi, nrow = 3, ncol = 3)



########################################################################
#############
#     Environment impacts bee richness By Site
```

```
#################################################################
#############

#generate model graphs
p <- ggplot(mbees, aes(x = total.richness.fl.site, y = bee.richness, fill = site2 )) +
  geom_blank() +
  labs(x = "Flower richness", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
rb <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  annotate("text", x = -Inf, y = Inf, label = "A", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  geom_jitter(width = 0.2, height = .0, alpha = 0.6) + theme(panel.background =
element_blank(), axis.line = element_line(color = "black"),  axis.title =
element_text(size = 14), legend.position = "none", axis.text = element_text(size =
12), panel.border = element_rect(color = "black", fill = NA, size = 1))


#

p <- ggplot(mbees, aes(x = mean.cover.fl, y = bee.richness, fill = site2 )) +
  geom_blank() +
  labs(x = "Total flower cover", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
rc <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  annotate("text", x = -Inf, y = Inf, label = "B", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  geom_jitter(width = 0.2, height = .0, alpha = 0.6) + theme(panel.background =
element_blank(), axis.line = element_line(color = "black"),  axis.title =
element_text(size = 14), legend.position = "none", axis.text = element_text(size =
12), panel.border = element_rect(color = "black", fill = NA, size = 1))

#

p <- ggplot(mbees, aes(x = mean.height, y = bee.richness, fill = site2 )) +
  geom_blank() +
  labs(x = "Mean height", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
rd <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  annotate("text", x = -Inf, y = Inf, label = "C", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  geom_jitter(width = 0.2, height = .0, alpha = 0.6) + theme(panel.background =
element_blank(), axis.line = element_line(color = "black"),  axis.title =
element_text(size = 14), legend.position = "none", axis.text = element_text(size =
12), panel.border = element_rect(color = "black", fill = NA, size = 1))
```

```
#

p <- ggplot(mbees, aes(x = sd.height, y = bee.richness, fill = site2 )) +
  geom_blank() +
  labs(x = "Variation in vegetation height", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 13))
re <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  annotate("text", x = -Inf, y = Inf, label = "D", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  geom_jitter(width = 0.2, height = .0, alpha = 0.6) + theme(panel.background =
element_blank(), axis.line = element_line(color = "black"),  axis.title =
element_text(size = 14), legend.position = "none", axis.text = element_text(size =
12), panel.border = element_rect(color = "black", fill = NA, size = 1))

#

p <- ggplot(mbees, aes(x = bee.abundance, y = bee.richness, fill = site2 )) +
  geom_blank() +
  labs(x = "Bee abundance", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
rh <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  annotate("text", x = -Inf, y = Inf, label = "E", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  geom_jitter(width = 0.2, height = .0, alpha = 0.6) + theme(panel.background =
element_blank(), axis.line = element_line(color = "black"),  axis.title =
element_text(size = 14), legend.position = "none", axis.text = element_text(size =
12), panel.border = element_rect(color = "black", fill = NA, size = 1))

#

p <- ggplot(mbees, aes(x = dung.livestock.density.total, y = bee.richness, fill =
site2 )) +
  geom_blank() +
  labs(x = "Dung livestock density", y = "Bee richness") +
  theme (axis.text = element_text(size = 14), axis.title = element_text(size = 15))
ri <- p + geom_smooth(method = "glm", method.args = list(family = "poisson"), se
= T,)+
  geom_jitter(width = 0.2, height = .0, alpha = 0.6) + theme(panel.background =
element_blank(), axis.line = element_line(color = "black"),  axis.title =
element_text(size = 14), legend.position = c(0.8, 0.65), legend.title =
element_blank(), axis.text = element_text(size = 12), panel.border =
element_rect(color = "black", fill = NA, size = 1), legend.text = element_text(size =
12), legend.key.size = unit(1.4, "lines"))

#plotting
plot_grid(rb,rc,rd,re,rh, nrow = 3, ncol = 2)
```

```
######################################################################
###
#     Dung livestock density impacts environment by site error bar plot
######################################################################
###


#create subsets of only one site each
mbees <- droplevels(mbees)
df_cb <- mbees[mbees$site == 'cb', ] ; df_pb <- mbees[mbees$site == 'pb', ]; df_cr
<- mbees[mbees$site == 'cr', ] ; df_lw <- mbees[mbees$site == 'lw', ]
df_lwu <- df_lw[df_lw$box %in% c('1', '2','3'), ] ; df_lwu <- droplevels(df_lwu)
df_lwg <- df_lw[df_lw$box %in% c('4', '5','6'), ] ; df_lwg <- droplevels(df_lwg)
summary(df_lwg)


#do this categorized by transect
lsu_means <- aggregate(dung.livestock.density.total ~ box + site2, mbees, mean)
mbees <- merge(mbees, lsu_means, by = c("box", "site2"), suffixes = c("",
".mean"))
mbees$dung.livestock.density.total.mean <-
as.factor(mbees$dung.livestock.density.total.mean)
mbees$dung.livestock.density.total.mean <-
as.numeric(mbees$dung.livestock.density.total.mean)

# Calculate means by Dung_Livestock_Unit
oasmeans         <- aggregate(mean.height ~ dung.livestock.density.total.mean +
site2 + box, mbees, mean)
# Calculate asymmetrical confidence intervals
oasci_lower <- aggregate(mean.height ~ dung.livestock.density.total.mean + site2
+ box, mbees, function(x) quantile(x, 0.025))
oasci_upper <- aggregate(mean.height ~ dung.livestock.density.total.mean + site2
+ box, mbees, function(x) quantile(x, 0.975))
# Create the plot
oas <- ggplot(oasmeans, aes(x = log(dung.livestock.density.total.mean + 1), y =
mean.height, color = site2)) +
  geom_point(alpha = 0.3) +  # Plot individual points
  geom_errorbar(aes(ymin = oasmeans$mean.height-oasci_lower$mean.height,
ymax = oasmeans$mean.height+oasci_upper$mean.height),
                position = position_dodge(width = 0.2), width = 0.1) +  # Add
asymmetrical error bars
  geom_point(position = position_dodge(width = 0.2), alpha = 0.7) +  # Plot mean
line
```

```
  labs(x = "Stocking density (Log LU)", y = "Vegetiation height", fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "A", fontface = "bold", color = "black", size
= 5, hjust = -0.5, vjust = 1.5) +  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"),
        panel.background = element_blank(),
        axis.line = element_line(color = "black"),
        axis.title = element_text(size = 14),
        legend.position = "none",
        axis.text = element_text(size = 12),
        panel.border = element_rect(color = "black", fill = NA, size = 1))
print(oas)



# Calculate means by Dung_Livestock_Unit
obsmeans <- aggregate(cv ~ dung.livestock.density.total.mean + site2 + box,
mbees, mean)
# Calculate asymmetrical confidence intervals
obsci_lower <- aggregate(cv ~ dung.livestock.density.total.mean + site2 + box,
mbees, function(x) quantile(x, 0.025))
obsci_upper <- aggregate(cv ~ dung.livestock.density.total.mean + site2 + box,
mbees, function(x) quantile(x, 0.975))
# Create the plot
obs <- ggplot(obsmeans, aes(x = log(dung.livestock.density.total.mean + 1), y =
cv, color = site2)) +
  geom_point(alpha = 0.3) +  # Plot individual points
  geom_errorbar(aes(ymin = obsmeans$cv-obsci_lower$cv, ymax =
obsmeans$cv+obsci_upper$cv),
                position = position_dodge(width = 0.2), width = 0.1) +  # Add
asymmetrical error bars
  geom_point(position = position_dodge(width = 0.2), alpha = 0.7) +  # Plot mean
line
  labs(x = "Stocking density (Log LU)", y = "Variation in vegetation height (CV)", fill
= "Site") +
  annotate("text", x = -Inf, y = Inf, label = "B", fontface = "bold", color = "black", size
= 5, hjust = -0.5, vjust = 1.5) +  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"),
        panel.background = element_blank(),
        axis.line = element_line(color = "black"),
        axis.title = element_text(size = 14),
        legend.position = "none",
        axis.text = element_text(size = 12),
        panel.border = element_rect(color = "black", fill = NA, size = 1))
print(obs)



# Calculate means by Dung_Livestock_Unit
```

```
ocsmeans         <- aggregate(total.richness.fl.site ~
dung.livestock.density.total.mean + site2 + box, mbees, mean)
# Calculate asymmetrical confidence intervals
ocsci_lower <- aggregate(total.richness.fl.site ~ dung.livestock.density.total.mean
+ site2 + box, mbees, function(x) quantile(x, 0.025))
ocsci_upper <- aggregate(total.richness.fl.site ~ dung.livestock.density.total.mean
+ site2 + box, mbees, function(x) quantile(x, 0.975))
# Create the plot
ocs <- ggplot(ocsmeans, aes(x = log(dung.livestock.density.total.mean + 1), y =
total.richness.fl.site, color = site2)) +
  geom_point(alpha = 0.3) +  # Plot individual points
  geom_errorbar(aes(ymin = ocsmeans$total.richness.fl.site-
ocsci_lower$total.richness.fl.site, ymax =
ocsmeans$total.richness.fl.site+ocsci_upper$total.richness.fl.site),
                position = position_dodge(width = 0.2), width = 0.1) +  # Add
asymmetrical error bars
  geom_point(position = position_dodge(width = 0.2), alpha = 0.7) +  # Plot mean
line
  labs(x = "Stocking density (Log LU)", y = "Flower Richness", fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "C", fontface = "bold", color = "black", size
= 5, hjust = -0.5, vjust = 1.5) +  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"),
        panel.background = element_blank(),
        axis.line = element_line(color = "black"),
        axis.title = element_text(size = 14),
        legend.position = "none",
        axis.text = element_text(size = 12),
        panel.border = element_rect(color = "black", fill = NA, size = 1))
print(ocs)

#

plot(total.richness.fl.site~ dung.livestock.density.total.mean, data = ocsmeans)

par(mfrow = c(5,4))
hist( df_cr$total.richness.ip.site[df_cr$box == 1], main = "1",  xlab = "IP richness",
col = "tan",)
hist( df_cr$total.richness.ip.site[df_cr$box == 2], main = "2",  xlab = "IP richness",
col = "tan",)
hist( df_cr$total.richness.ip.site[df_cr$box == 3], main = "3",  xlab = "IP richness",
col = "tan",)
hist( df_cr$total.richness.ip.site[df_cr$box == 4], main = "4",  xlab = "IP richness",
col = "tan",)

hist( df_lwu$total.richness.ip.site[df_lwu$box == 1], main = "1",  xlab = "IP
richness", col = "turquoise",)
hist( df_lwu$total.richness.ip.site[df_lwu$box == 2], main = "2",  xlab = "IP
richness", col = "turquoise",)
```

```
hist( df_lwu$total.richness.ip.site[df_lwu$box == 3], main = "3",  xlab = "IP
richness", col = "turquoise",)
frame()

hist( df_lwg$total.richness.ip.site[df_lwg$box == 4], main = "4",  xlab = "IP
richness", col = "darkgreen",)
hist( df_lwg$total.richness.ip.site[df_lwg$box == 5], main = "5",  xlab = "IP
richness", col = "darkgreen",)
hist( df_lwg$total.richness.ip.site[df_lwg$box == 6], main = "6",  xlab = "IP
richness", col = "darkgreen",)
frame()

hist( df_cb$total.richness.ip.site[df_cb$box == 1], main = "1",  xlab = "IP richness",
col = "red",)
hist( df_cb$total.richness.ip.site[df_cb$box == 2], main = "2",  xlab = "IP richness",
col = "red",)
hist( df_cb$total.richness.ip.site[df_cb$box == 3], main = "3",  xlab = "IP richness",
col = "red",)
hist( df_cb$total.richness.ip.site[df_cb$box == 4], main = "4",  xlab = "IP richness",
col = "red",)

hist( df_pb$total.richness.ip.site[df_pb$box == 1], main = "1",  xlab = "IP richness",
col = "magenta",)
hist( df_pb$total.richness.ip.site[df_pb$box == 2], main = "2",  xlab = "IP richness",
col = "magenta",)
hist( df_pb$total.richness.ip.site[df_pb$box == 3], main = "3",  xlab = "IP richness",
col = "magenta",)
hist( df_pb$total.richness.ip.site[df_pb$box == 4], main = "4",  xlab = "IP richness",
col = "magenta",)



ocs <- ggplot(mbees, aes(x = log(dung.livestock.density.total.mean + 1),
                         y = total.richness.fl.site,
                         color = site2,
                         group = interaction(site2, box))) +
  geom_boxplot(alpha = 0.6, outlier.shape = NA, position = position_dodge(width =
0.2)) +  # Add boxplot
  geom_jitter(alpha = 0.3, position = position_jitterdodge(jitter.width = 0.2,
dodge.width = 0.2)) +  # Jittered points for visibility
  labs(x = "Stocking density (Log LU)",
       y = "Flower Richness",
       color = "Site") +
  annotate("text", x = -Inf, y = Inf,
           label = "C",
           fontface = "bold",
           color = "black",
           size = 5,
```

```
          hjust = -0.5,
          vjust = 1.5) +  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"),
        panel.background = element_blank(),
        axis.line = element_line(color = "black"),
        axis.title = element_text(size = 14),
        legend.position = "none",
        axis.text = element_text(size = 12),
        panel.border = element_rect(color = "black", fill = NA, size = 1))

print(ocs)


#





# Calculate means by Dung_Livestock_Unit
odsmeans         <- aggregate(total.richness.ip.site ~
dung.livestock.density.total.mean + site2 + box, mbees, mean)
# Calculate asymmetrical confidence intervals
odsci_lower <- aggregate(total.richness.ip.site ~ dung.livestock.density.total.mean
+ site2 + box, mbees, function(x) quantile(x, 0.025))
odsci_upper <- aggregate(total.richness.ip.site ~ dung.livestock.density.total.mean
+ site2 + box, mbees, function(x) quantile(x, 0.975))
# Create the plot
ods <- ggplot(odsmeans, aes(x = log(dung.livestock.density.total.mean + 1), y =
total.richness.ip.site, color = site2)) +
  geom_point(alpha = 0.3) +  # Plot individual points
  geom_errorbar(aes(ymin = odsmeans$total.richness.ip.site-
odsci_lower$total.richness.ip.site, ymax =
odsmeans$total.richness.ip.site+odsci_upper$total.richness.ip.site),
                position = position_dodge(width = 0.2), width = 0.1) +  # Add
asymmetrical error bars
  geom_point(position = position_dodge(width = 0.2), alpha = 0.7) +  # Plot mean
line
  labs(x = "Stocking density (Log LU)", y = "IP plant richness", fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "D", fontface = "bold", color = "black", size
= 5, hjust = -0.5, vjust = 1.5) +  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"),
        panel.background = element_blank(),
        axis.line = element_line(color = "black"),
        axis.title = element_text(size = 14),
        legend.position = "none",
        axis.text = element_text(size = 12),
        panel.border = element_rect(color = "black", fill = NA, size = 1))
```

```
print(ods)



# Calculate means by Dung_Livestock_Unit
oesmeans          <- aggregate(mean.cover.fl ~ dung.livestock.density.total.mean +
site2 + box, mbees, mean)
# Calculate asymmetrical confidence intervals
oesci_lower <- aggregate(mean.cover.fl ~ dung.livestock.density.total.mean +
site2 + box, mbees, function(x) quantile(x, 0.025))
oesci_upper <- aggregate(mean.cover.fl ~ dung.livestock.density.total.mean +
site2 + box, mbees, function(x) quantile(x, 0.975))
# Create the plot
oes <- ggplot(oesmeans, aes(x = log(dung.livestock.density.total.mean + 1), y =
mean.cover.fl, color = site2)) +
  geom_point(alpha = 0.3) +  # Plot individual points
  geom_errorbar(aes(ymin = oesmeans$mean.cover.fl-oesci_lower$mean.cover.fl,
ymax = oesmeans$mean.cover.fl+oesci_upper$mean.cover.fl),
                position = position_dodge(width = 0.2), width = 0.1) +  # Add
asymmetrical error bars
  geom_point(position = position_dodge(width = 0.2), alpha = 0.7) +  # Plot mean
line
  labs(x = "Stocking density (Log LU)", y = "Flower Cover", fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "E", fontface = "bold", color = "black", size
= 5, hjust = -0.5, vjust = 1.5) +  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"),
        panel.background = element_blank(),
        axis.line = element_line(color = "black"),
        axis.title = element_text(size = 14),
        legend.position = "none",
        axis.text = element_text(size = 12),
        panel.border = element_rect(color = "black", fill = NA, size = 1))
print(oes)



# Calculate means by Dung_Livestock_Unit
ofsmeans          <- aggregate(mean.cover.ip ~ dung.livestock.density.total.mean +
site2 + box, mbees, mean)
# Calculate asymmetrical confidence intervals
ofsci_lower <- aggregate(mean.cover.ip ~ dung.livestock.density.total.mean +
site2 + box, mbees, function(x) quantile(x, 0.025))
ofsci_upper <- aggregate(mean.cover.ip ~ dung.livestock.density.total.mean +
site2 + box, mbees, function(x) quantile(x, 0.975))
# Create the plot
ofs <- ggplot(ofsmeans, aes(x = log(dung.livestock.density.total.mean + 1), y =
mean.cover.ip, color = site2)) +
  geom_point(alpha = 0.3) +  # Plot individual points
```

```
  geom_errorbar(aes(ymin = ofsmeans$mean.cover.ip-ofsci_lower$mean.cover.ip,
ymax = ofsmeans$mean.cover.ip+ofsci_upper$mean.cover.ip),
                position = position_dodge(width = 0.2), width = 0.1) +  # Add
asymmetrical error bars
  geom_point(position = position_dodge(width = 0.2), alpha = 0.7) +  # Plot mean
line
  labs(x = "Stocking density (Log LU)", y = "IP plant Cover", fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "F", fontface = "bold", color = "black", size
= 5, hjust = -0.5, vjust = 1.5) +  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"),
        panel.background = element_blank(),
        axis.line = element_line(color = "black"),
        axis.title = element_text(size = 14),
        legend.position = "none",
        axis.text = element_text(size = 12),
        panel.border = element_rect(color = "black", fill = NA, size = 1))
print(ofs)


# Calculate means by Dung_Livestock_Unit
ogsmeans          <- aggregate(bee.abundance ~ dung.livestock.density.total.mean
+ site2 + box, mbees, mean)
# Calculate asymmetrical confidence intervals
ogsci_lower <- aggregate(bee.abundance ~ dung.livestock.density.total.mean +
site2 + box, mbees, function(x) quantile(x, 0.025))
ogsci_upper <- aggregate(bee.abundance ~ dung.livestock.density.total.mean +
site2 + box, mbees, function(x) quantile(x, 0.975))
# Create the plot
ogs <- ggplot(ogsmeans, aes(x = log(dung.livestock.density.total.mean + 1), y =
bee.abundance, color = site2)) +
  geom_point(alpha = 0.3) +  # Plot individual points
  geom_errorbar(aes(ymin = ogsmeans$bee.abundance-
ogsci_lower$bee.abundance, ymax =
ogsmeans$bee.abundance+ogsci_upper$bee.abundance),
                position = position_dodge(width = 0.2), width = 0.1) +  # Add
asymmetrical error bars
  geom_point(position = position_dodge(width = 0.2), alpha = 0.7) +  # Plot mean
line
  labs(x = "Stocking density (Log LU)", y = "Bee abundance", fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "G", fontface = "bold", color = "black", size
= 5, hjust = -0.5, vjust = 1.5) +  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"),
        panel.background = element_blank(),
        axis.line = element_line(color = "black"),
        axis.title = element_text(size = 14),
        legend.position = "none",
        axis.text = element_text(size = 12),
        panel.border = element_rect(color = "black", fill = NA, size = 1))
```

```
print(ogs)


# Calculate means by Dung_Livestock_Unit
ohsmeans         <- aggregate(bee.richness ~ dung.livestock.density.total.mean +
site2 + box, mbees, mean)
# Calculate asymmetrical confidence intervals
ohsci_lower <- aggregate(bee.richness ~ dung.livestock.density.total.mean + site2
+ box, mbees, function(x) quantile(x, 0.025))
ohsci_upper <- aggregate(bee.richness ~ dung.livestock.density.total.mean + site2
+ box, mbees, function(x) quantile(x, 0.975))
# Create the plot
ohs <- ggplot(ohsmeans, aes(x = log(dung.livestock.density.total.mean + 1), y =
bee.richness, color = site2)) +
  geom_point(alpha = 0.3) +  # Plot individual points
  geom_errorbar(aes(ymin = ohsmeans$bee.richness-ohsci_lower$bee.richness,
ymax = ohsmeans$bee.richness+ohsci_upper$bee.richness),
                position = position_dodge(width = 0.2), width = 0.1) +  # Add
asymmetrical error bars
  geom_point(position = position_dodge(width = 0.2), alpha = 0.7) +  # Plot mean
line
  labs(x = "Stocking density (Log LU)", y = "Bee richness", fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "H", fontface = "bold", color = "black", size
= 5, hjust = -0.5, vjust = 1.5) +  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"),
        panel.background = element_blank(),
        axis.line = element_line(color = "black"),
        axis.title = element_text(size = 14),
        legend.position = "none",
        axis.text = element_text(size = 12),
        panel.border = element_rect(color = "black", fill = NA, size = 1))
print(ohs)


#plot the graphs of dung livestock
plot_grid(oas, obs, ocs, ods, oes, ofs, ogs, ohs, nrow = 4, ncol = 2)


#####################################################################
#############
#     DUNG LIVESTOCK error plant specific
#####################################################################
#############


##########flower cover
# Calculate means by Dung_Livestock_Unit
```

```
oameans <- aggregate(t.pannonicum.flo.av ~ dung.livestock.density.total.mean +
site2 + box, mbees, mean)
oboase <- aggregate(t.pannonicum.flo.av ~ dung.livestock.density.total.mean +
site2 + box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
oa <- ggplot(oameans, aes(x = log(dung.livestock.density.total.mean+1), y =
t.pannonicum.flo.av, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = oameans, aes(y =  t.pannonicum.flo.av, ymin =
t.pannonicum.flo.av - oboase$t.pannonicum.flo.av, ymax =  t.pannonicum.flo.av +
oboase$t.pannonicum.flo.av, color = site2), position = position_dodge(width = 0.2),
width = 0.1) +  # Add standard error bars
  geom_point(data = oameans, aes(y = t.pannonicum.flo.av), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Stocking density (Log LU)", y = expression(italic("T.pannonicum")* "
flower cover"), fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "B", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.3, vjust = 1.5)+  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"))+  # Adjust plot margins
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));oa

#ip plant cover
# Calculate means by Dung_Livestock_Unit
obmeans <- aggregate(t.pannonicum.ip.av ~ dung.livestock.density.total.mean
+site2 + box, mbees, mean)
obse <- aggregate(t.pannonicum.ip.av ~ dung.livestock.density.total.mean +site2 +
box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
ob <- ggplot(obmeans, aes(x = log(dung.livestock.density.total.mean+1), y =
t.pannonicum.ip.av, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(aes(y = obmeans$t.pannonicum.ip.av, ymin =
obmeans$t.pannonicum.ip.av - obse$t.pannonicum.ip.av, ymax =
obmeans$t.pannonicum.ip.av + obse$t.pannonicum.ip.av, color = site2), position =
position_dodge(width = 0.2), width = 0.1) +  # Add standard error bars
  geom_point(data = obmeans, aes(y = t.pannonicum.ip.av), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Stocking density (Log LU)", y = expression(italic("T.pannonicum")* "
cover"), fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "A", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"))+  # Adjust plot margins
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
```

```
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));ob



##########flower cover
# Calculate means by Dung_Livestock_Unit
ocmeans <- aggregate(l.vulgare.flo.av ~ dung.livestock.density.total.mean + site2
+ box, mbees, mean)
ocoase <- aggregate(l.vulgare.flo.av ~ dung.livestock.density.total.mean + site2 +
box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
oc <- ggplot(ocmeans, aes(x = log(dung.livestock.density.total.mean+1), y =
l.vulgare.flo.av, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = ocmeans, aes(y =  l.vulgare.flo.av, ymin =  l.vulgare.flo.av
- ocoase$l.vulgare.flo.av, ymax =  l.vulgare.flo.av + ocoase$l.vulgare.flo.av, color =
site2), position = position_dodge(width = 0.2), width = 0.1) +  # Add standard error
bars
  geom_point(data = ocmeans, aes(y = l.vulgare.flo.av), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Stocking density (Log LU)", y = expression(italic("L.vulgare")* " flower
cover"), fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "D", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"))+  # Adjust plot margins
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));oc

#ip plant cover
# Calculate means by Dung_Livestock_Unit
odmeans <- aggregate(l.vulgare.ip.av ~ dung.livestock.density.total.mean +site2 +
box, mbees, mean)
odse <- aggregate(l.vulgare.ip.av ~ dung.livestock.density.total.mean +site2 + box,
mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
od <- ggplot(odmeans, aes(x = log(dung.livestock.density.total.mean+1), y =
l.vulgare.ip.av, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(aes(y = odmeans$l.vulgare.ip.av, ymin = odmeans$l.vulgare.ip.av
- odse$l.vulgare.ip.av, ymax = odmeans$l.vulgare.ip.av + odse$l.vulgare.ip.av,
color = site2), position = position_dodge(width = 0.2), width = 0.1) +  # Add
standard error bars
  geom_point(data = odmeans, aes(y = l.vulgare.ip.av), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
```

```
  labs(x = "Stocking density (Log LU)", y = expression(italic("L.vulgare")* " cover"), fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "C", fontface = "bold", color = "Black", size = 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"))+  # Adjust plot margins
  theme(panel.background = element_blank(), axis.line = element_line(color = "black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text = element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size = 1));od



##########flower cover
# Calculate means by Dung_Livestock_Unit
oemeans <- aggregate(a.maritima.flo.av ~ dung.livestock.density.total.mean + site2 + box, mbees, mean)
oeoase <- aggregate(a.maritima.flo.av ~ dung.livestock.density.total.mean + site2 + box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
oe <- ggplot(oemeans, aes(x = log(dung.livestock.density.total.mean+1), y = a.maritima.flo.av, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = oemeans, aes(y =  a.maritima.flo.av, ymin = a.maritima.flo.av - oeoase$a.maritima.flo.av, ymax =  a.maritima.flo.av + oeoase$a.maritima.flo.av, color = site2), position = position_dodge(width = 0.2), width = 0.1) +  # Add standard error bars
  geom_point(data = oemeans, aes(y = a.maritima.flo.av), position = position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Stocking density (Log LU)", y = expression(italic("A.maritima")* " flower cover"), fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "F", fontface = "bold", color = "Black", size = 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"))+  # Adjust plot margins
  theme(panel.background = element_blank(), axis.line = element_line(color = "black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text = element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size = 1));oe

#ip plant cover
# Calculate means by Dung_Livestock_Unit
ofmeans <- aggregate(a.maritima.ip.av ~ dung.livestock.density.total.mean +site2 + box, mbees, mean)
ofse <- aggregate(a.maritima.ip.av ~ dung.livestock.density.total.mean +site2 + box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
of <- ggplot(ofmeans, aes(x = log(dung.livestock.density.total.mean+1), y = a.maritima.ip.av, color = site2)) +
```

```
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(aes(y = ofmeans$a.maritima.ip.av, ymin =
ofmeans$a.maritima.ip.av - ofse$a.maritima.ip.av, ymax =
ofmeans$a.maritima.ip.av + ofse$a.maritima.ip.av, color = site2), position =
position_dodge(width = 0.2), width = 0.1) +  # Add standard error bars
  geom_point(data = ofmeans, aes(y = a.maritima.ip.av), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Stocking density (Log LU)", y = expression(italic("A.maritima")* "
cover"), fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "E", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"))+  # Adjust plot margins
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));of


##########flower cover
# Calculate means by Dung_Livestock_Unit
ogmeans <- aggregate(l.maritima.flo.av ~ dung.livestock.density.total.mean + site2
+ box, mbees, mean)
ogoase <- aggregate(l.maritima.flo.av ~ dung.livestock.density.total.mean + site2 +
box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
og <- ggplot(ogmeans, aes(x = log(dung.livestock.density.total.mean+1), y =
l.maritima.flo.av, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = ogmeans, aes(y =  l.maritima.flo.av, ymin =
l.maritima.flo.av - ogoase$l.maritima.flo.av, ymax =  l.maritima.flo.av +
ogoase$l.maritima.flo.av, color = site2), position = position_dodge(width = 0.2),
width = 0.1) +  # Add standard error bars
  geom_point(data = ogmeans, aes(y = l.maritima.flo.av), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Stocking density (Log LU)", y = expression(italic("l.maritima")* " flower
cover"), fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "F", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"))+  # Adjust plot margins
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));og

##########ip cover
# Calculate means by Dung_Livestock_Unit
ogmeans <- aggregate(l.maritima.ip.av ~ dung.livestock.density.total.mean + site2
+ box, mbees, mean)
```

```
ogoase <- aggregate(l.maritima.ip.av ~ dung.livestock.density.total.mean + site2 +
box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
oh <- ggplot(ogmeans, aes(x = log(dung.livestock.density.total.mean+1), y =
l.maritima.ip.av, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = ogmeans, aes(y =  l.maritima.ip.av, ymin =
l.maritima.ip.av - ogoase$l.maritima.ip.av, ymax =  l.maritima.ip.av +
ogoase$l.maritima.ip.av, color = site2), position = position_dodge(width = 0.2),
width = 0.1) +  # Add standard error bars
  geom_point(data = ogmeans, aes(y = l.maritima.ip.av), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Stocking density (Log LU)", y = expression(italic("l.maritima")* " IP plant
cover"), fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "F", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"))+  # Adjust plot margins
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));oh


##########flower cover
# Calculate means by Dung_Livestock_Unit
ogmeans <- aggregate(c.officinalis.flo.av ~ dung.livestock.density.total.mean +
site2 + box, mbees, mean)
ogoase <- aggregate(c.officinalis.flo.av ~ dung.livestock.density.total.mean + site2
+ box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
oi <- ggplot(ogmeans, aes(x = log(dung.livestock.density.total.mean+1), y =
c.officinalis.flo.av, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = ogmeans, aes(y =  c.officinalis.flo.av, ymin =
c.officinalis.flo.av - ogoase$c.officinalis.flo.av, ymax =  c.officinalis.flo.av +
ogoase$c.officinalis.flo.av, color = site2), position = position_dodge(width = 0.2),
width = 0.1) +  # Add standard error bars
  geom_point(data = ogmeans, aes(y = c.officinalis.flo.av), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Stocking density (Log LU)", y = expression(italic("c.officinalis")* " flower
cover"), fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "F", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"))+  # Adjust plot margins
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));oi
```

```
##########ip cover
# Calculate means by Dung_Livestock_Unit
ogmeans <- aggregate(c.officinalis.ip.av ~ dung.livestock.density.total.mean +
site2 + box, mbees, mean)
ogoase <- aggregate(c.officinalis.ip.av ~ dung.livestock.density.total.mean + site2
+ box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
oj <- ggplot(ogmeans, aes(x = log(dung.livestock.density.total.mean+1), y =
c.officinalis.ip.av, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = ogmeans, aes(y =  c.officinalis.ip.av, ymin =
c.officinalis.ip.av - ogoase$c.officinalis.ip.av, ymax =  c.officinalis.ip.av +
ogoase$c.officinalis.ip.av, color = site2), position = position_dodge(width = 0.2),
width = 0.1) +  # Add standard error bars
  geom_point(data = ogmeans, aes(y = c.officinalis.ip.av), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Stocking density (Log LU)", y = expression(italic("c.officinalis")* " IP
plant cover"), fill = "Site") +
  annotate("text", x = -Inf, y = Inf, label = "F", fontface = "bold", color = "Black", size
= 5, hjust = 0-0.5, vjust = 1.5)+  # Add figure letter
  theme(plot.margin = margin(5, 5, 0, 0, "mm"))+  # Adjust plot margins
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));oj



plot_grid(ob,oa,od,oc,of,oe, nrow = 3, ncol = 2)

#plot_grid(og, oh, nrow = 3, ncol = 2)



##################################################################
#############
#     Bee abundance error
##################################################################
#############

#########bee richness
#do this categorized by transect
lsu_means_rich <- aggregate(bee.richness ~ box + site2, mbees, mean)
```

```
mbees <- merge(mbees, lsu_means_rich, by = c("box", "site2"), suffixes = c("",
".mean"))
mbees$bee.richness.mean <- as.factor(mbees$bee.richness.mean)
# Calculate means by Dung_Livestock_Unit
ooameans <- aggregate(bee.abundance ~ bee.richness.mean + site2 + box,
mbees, mean)
ooase <- aggregate(bee.abundance ~ bee.richness.mean + site2 + box, mbees,
function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
ooameans$bee.richness.mean2 <- as.numeric(ooameans$bee.richness.mean,
digits = 5)
ooa <- ggplot(ooameans, aes(x = (bee.richness.mean), y = bee.abundance, color
= site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = ooameans, aes(y =  bee.abundance, ymin =
bee.abundance - ooase$bee.abundance, ymax =  bee.abundance +
ooase$bee.abundance, color = site2), position = position_dodge(width = 0.2),
width = 0.1) +  # Add standard error bars
  geom_point(data = ooameans, aes(y = bee.abundance), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Bee richness", y = "Bee abundance", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));ooa



#########flower richness
#do this categorized by transect
mbees$total.richness.fl <- as.numeric(mbees$total.richness.fl)
lsu_means_flrich <- aggregate(total.richness.fl ~ box + site2, mbees, mean)
mbees <- merge(mbees, lsu_means_flrich, by = c("box", "site2"), suffixes = c("",
".mean"))
# Calculate means by Dung_Livestock_Unit
oobmeans <- aggregate(bee.abundance ~ total.richness.fl.mean + site2 + box,
mbees, mean)
oobse <- aggregate(bee.abundance ~ total.richness.fl.mean + site2 + box, mbees,
function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
oob <- ggplot(oobmeans, aes(x = (total.richness.fl.mean), y = bee.abundance,
color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = oobmeans, aes(y =  bee.abundance, ymin =
bee.abundance - oobse$bee.abundance, ymax =  bee.abundance +
oobse$bee.abundance, color = site2), position = position_dodge(width = 0.2),
width = 0.1) +  # Add standard error bars
```

```
  geom_point(data = oobmeans, aes(y = bee.abundance), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Flower richness", y = "Bee abundance", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));oob



#########flower cover
#do this categorized by transect
mbees$mean.cover.fl <- as.numeric(mbees$mean.cover.fl)
lsu_means_cov <- aggregate(mean.cover.fl ~ box + site2, mbees, mean)
mbees <- merge(mbees, lsu_means_cov, by = c("box", "site2"), suffixes = c("",
".mean"))
# Calculate means by Dung_Livestock_Unit
oocmeans <- aggregate(bee.abundance ~  site2 + mean.cover.fl.mean + box,
mbees, mean)
oocse <- aggregate(bee.abundance ~ site2 + mean.cover.fl.mean + box, mbees,
function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
ooc <- ggplot(oocmeans, aes(x = (mean.cover.fl.mean), y = bee.abundance, color
= site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = oocmeans, aes(y =  bee.abundance, ymin =
bee.abundance - oocse$bee.abundance, ymax =  bee.abundance +
oocse$bee.abundance, color = site2), position = position_dodge(width = 0.2),
width = 0.1) +  # Add standard error bars
  geom_point(data = oocmeans, aes(y = bee.abundance), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Flower cover", y = "Bee abundance", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));ooc



#########mean height
#do this categorized by transect
mbees$mean.height <- as.numeric(mbees$mean.height)
lsu_means_heig <- aggregate(mean.height ~ box + site2, mbees, mean)
mbees <- merge(mbees, lsu_means_heig, by = c("box", "site2"), suffixes = c("",
".mean"))
# Calculate means by Dung_Livestock_Unit
oodmeans <- aggregate(bee.abundance ~  site2 + mean.height.mean + box,
mbees, mean)
```

```
oodse <- aggregate(bee.abundance ~ site2 + mean.height.mean + box, mbees,
function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
ood <- ggplot(oodmeans, aes(x = (mean.height.mean), y = bee.abundance, color
= site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = oodmeans, aes(y =  bee.abundance, ymin =
bee.abundance - oodse$bee.abundance, ymax =  bee.abundance +
oodse$bee.abundance, color = site2), position = position_dodge(width = 0.2),
width = 0.1) +  # Add standard error bars
  geom_point(data = oodmeans, aes(y = bee.abundance), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Mean height", y = "Bee abundance", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));ood



######### sd dev height
#do this categorized by transect
mbees$sd.height <- as.numeric(mbees$sd.height)
lsu_means_heig <- aggregate(sd.height ~ box + site2, mbees, mean)
mbees <- merge(mbees, lsu_means_heig, by = c("box", "site2"), suffixes = c("",
".mean"))
# Calculate means by Dung_Livestock_Unit
ooemeans <- aggregate(bee.abundance ~  site2 + sd.height.mean + box, mbees,
mean)
ooese <- aggregate(bee.abundance ~ site2 + sd.height.mean + box, mbees,
function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
ooe <- ggplot(ooemeans, aes(x = (sd.height.mean), y = bee.abundance, color =
site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = ooemeans, aes(y =  bee.abundance, ymin =
bee.abundance - ooese$bee.abundance, ymax =  bee.abundance +
ooese$bee.abundance, color = site2), position = position_dodge(width = 0.2),
width = 0.1) +  # Add standard error bars
  geom_point(data = ooemeans, aes(y = bee.abundance), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Variation in vegetation height", y = "Bee abundance", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));ooe
```

```
#########grazer livestock density
#do this categorized by transect
mbees$grazed.livestock.density.total <-
as.numeric(mbees$grazed.livestock.density.total)
lsu_means_grazer <- aggregate(grazed.livestock.density.total ~ box + site2,
mbees, mean)
mbees <- merge(mbees, lsu_means_grazer, by = c("box", "site2"), suffixes = c("",
".mean"))
# Calculate means by Dung_Livestock_Unit
oofmeans <- aggregate(bee.abundance ~  site2 +
grazed.livestock.density.total.mean + box, mbees, mean)
oofse <- aggregate(bee.abundance ~ site2 + grazed.livestock.density.total.mean +
box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
oof <- ggplot(oofmeans, aes(x = (log(grazed.livestock.density.total.mean+1)), y =
bee.abundance, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = oofmeans, aes(y =  bee.abundance, ymin =
bee.abundance - oofse$bee.abundance, ymax =  bee.abundance +
oofse$bee.abundance, color = site2), position = position_dodge(width = 0.2), width
= 0.1) +  # Add standard error bars
  geom_point(data = oofmeans, aes(y = bee.abundance), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Log(Grazer livestock density)", y = "Bee abundance", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));oof


#########dung livestock density
#do this categorized by transect
mbees$dung.livestock.density.total <-
as.numeric(mbees$dung.livestock.density.total)
lsu_means_dung <- aggregate(dung.livestock.density.total ~ box + site2, mbees,
mean)
mbees <- merge(mbees, lsu_means_dung, by = c("box", "site2"), suffixes = c("",
".mean"))
# Calculate means by Dung_Livestock_Unit
oogmeans <- aggregate(bee.abundance ~  site2 +
dung.livestock.density.total.mean + box, mbees, mean)
oogse <- aggregate(bee.abundance ~ site2 + dung.livestock.density.total.mean +
box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
oog <- ggplot(oogmeans, aes(x = (log(dung.livestock.density.total.mean+1)), y =
bee.abundance, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
```

```
  geom_errorbar(data = oogmeans, aes(y =  bee.abundance, ymin = 
bee.abundance - oogse$bee.abundance, ymax =  bee.abundance + 
oogse$bee.abundance, color = site2), position = position_dodge(width = 0.2), 
width = 0.1) +  # Add standard error bars
  geom_point(data = oogmeans, aes(y = bee.abundance), position = 
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Log(livestock density)", y = "Bee abundance", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color = 
"black"),  axis.title = element_text(size = 14), legend.position = c(1.3, 0.5), 
axis.text = element_text(size = 12), panel.border = element_rect(color = "black", fill 
= NA, size = 1), legend.text = element_text(size = 12), legend.key.size = unit(1.5, 
"lines"));oog
plot_grid(ooa,oob,ooc,ood,ooe,oof,oog, nrow = 3, ncol = 3)

################################################################
##############
#     Bee richness error
################################################################
##############


#########flower richness
#do this categorized by transect
mbees$total.richness.fl <- as.numeric(mbees$total.richness.fl)
lsu_means_flrich <- aggregate(total.richness.fl ~ box + site2, mbees, mean)
mbees <- merge(mbees, lsu_means_flrich, by = c("box", "site2"), suffixes = c("", 
".mean"))
# Calculate means by Dung_Livestock_Unit
oobmeans <- aggregate(bee.richness ~ total.richness.fl.mean + site2 + box, 
mbees, mean)
oobse <- aggregate(bee.richness ~ total.richness.fl.mean + site2 + box, mbees, 
function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
oob <- ggplot(oobmeans, aes(x = (total.richness.fl.mean), y = bee.richness, color = 
site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = oobmeans, aes(y =  bee.richness, ymin =  bee.richness - 
oobse$bee.richness, ymax =  bee.richness + oobse$bee.richness, color = site2), 
position = position_dodge(width = 0.2), width = 0.1) +  # Add standard error bars
  geom_point(data = oobmeans, aes(y = bee.richness), position = 
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Flower richness", y = "Bee richness", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color = 
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text = 
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size 
= 1));oob
```

```
#########flower cover
#do this categorized by transect
mbees$mean.cover.fl <- as.numeric(mbees$mean.cover.fl)
lsu_means_cov <- aggregate(mean.cover.fl ~ box + site2, mbees, mean)
mbees <- merge(mbees, lsu_means_cov, by = c("box", "site2"), suffixes = c("",
".mean"))
# Calculate means by Dung_Livestock_Unit
oocmeans <- aggregate(bee.richness ~  site2 + mean.cover.fl.mean + box,
mbees, mean)
oocse <- aggregate(bee.richness ~ site2 + mean.cover.fl.mean + box, mbees,
function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
ooc <- ggplot(oocmeans, aes(x = (mean.cover.fl.mean), y = bee.richness, color =
site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = oocmeans, aes(y =  bee.richness, ymin =  bee.richness -
oocse$bee.richness, ymax =  bee.richness + oocse$bee.richness, color = site2),
position = position_dodge(width = 0.2), width = 0.1) +  # Add standard error bars
  geom_point(data = oocmeans, aes(y = bee.richness), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Flower cover", y = "Bee richness", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));ooc



#########mean height
#do this categorized by transect
mbees$mean.height <- as.numeric(mbees$mean.height)
lsu_means_heig <- aggregate(mean.height ~ box + site2, mbees, mean)
mbees <- merge(mbees, lsu_means_heig, by = c("box", "site2"), suffixes = c("",
".mean"))
# Calculate means by Dung_Livestock_Unit
oodmeans <- aggregate(bee.richness ~  site2 + mean.height.mean + box, mbees,
mean)
oodse <- aggregate(bee.richness ~ site2 + mean.height.mean + box, mbees,
function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
ood <- ggplot(oodmeans, aes(x = (mean.height.mean), y = bee.richness, color =
site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = oodmeans, aes(y =  bee.richness, ymin =  bee.richness -
oodse$bee.richness, ymax =  bee.richness + oodse$bee.richness, color = site2),
position = position_dodge(width = 0.2), width = 0.1) +  # Add standard error bars
```

```
  geom_point(data = oodmeans, aes(y = bee.richness), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Mean height", y = "Bee richness", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));ood



######### sd dev height
#do this categorized by transect
mbees$sd.height <- as.numeric(mbees$sd.height)
lsu_means_heig <- aggregate(sd.height ~ box + site2, mbees, mean)
mbees <- merge(mbees, lsu_means_heig, by = c("box", "site2"), suffixes = c("",
".mean"))
# Calculate means by Dung_Livestock_Unit
ooemeans <- aggregate(bee.richness ~  site2 + sd.height.mean + box, mbees,
mean)
ooese <- aggregate(bee.richness ~ site2 + sd.height.mean + box, mbees,
function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
ooe <- ggplot(ooemeans, aes(x = (sd.height.mean), y = bee.richness, color =
site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = ooemeans, aes(y =  bee.richness, ymin =  bee.richness -
ooese$bee.richness, ymax =  bee.richness + ooese$bee.richness, color = site2),
position = position_dodge(width = 0.2), width = 0.1) +  # Add standard error bars
  geom_point(data = ooemeans, aes(y = bee.richness), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Variation in vegetation height", y = "Bee richness", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));ooe



#########grazer livestock density
#do this categorized by transect
mbees$grazed.livestock.density.total <-
as.numeric(mbees$grazed.livestock.density.total)
lsu_means_grazer <- aggregate(grazed.livestock.density.total ~ box + site2,
mbees, mean)
mbees <- merge(mbees, lsu_means_grazer, by = c("box", "site2"), suffixes = c("",
".mean"))
# Calculate means by Dung_Livestock_Unit
```

```
oofmeans <- aggregate(bee.richness ~  site2 + grazed.livestock.density.total.mean
+ box, mbees, mean)
oofse <- aggregate(bee.richness ~ site2 + grazed.livestock.density.total.mean +
box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
oof <- ggplot(oofmeans, aes(x = (log(grazed.livestock.density.total.mean+1)), y =
bee.richness, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = oofmeans, aes(y =  bee.richness, ymin =  bee.richness -
oofse$bee.richness, ymax =  bee.richness + oofse$bee.richness, color = site2),
position = position_dodge(width = 0.2), width = 0.1) +  # Add standard error bars
  geom_point(data = oofmeans, aes(y = bee.richness), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Log(Grazer livestock density)", y = "Bee richness", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = "none", axis.text =
element_text(size = 12), panel.border = element_rect(color = "black", fill = NA, size
= 1));oof


#########dung livestock density
#do this categorized by transect
mbees$dung.livestock.density.total <-
as.numeric(mbees$dung.livestock.density.total)
lsu_means_dung <- aggregate(dung.livestock.density.total ~ box + site2, mbees,
mean)
mbees <- merge(mbees, lsu_means_dung, by = c("box", "site2"), suffixes = c("",
".mean"))
# Calculate means by Dung_Livestock_Unit
oogmeans <- aggregate(bee.richness ~  site2 + dung.livestock.density.total.mean
+ box, mbees, mean)
oogse <- aggregate(bee.richness ~ site2 + dung.livestock.density.total.mean +
box, mbees, function(x) 1.96*(sd(x) / sqrt(length(x))))
# Create the plot
oog <- ggplot(oogmeans, aes(x = (log(dung.livestock.density.total.mean+1)), y =
bee.richness, color = site2)) +
  geom_point(alpha = 0.3, aes(color = site2)) +  # Plot individual points
  geom_errorbar(data = oogmeans, aes(y =  bee.richness, ymin =  bee.richness -
oogse$bee.richness, ymax =  bee.richness + oogse$bee.richness, color = site2),
position = position_dodge(width = 0.2), width = 0.1) +  # Add standard error bars
  geom_point(data = oogmeans, aes(y = bee.richness), position =
position_dodge(width = 0.2), alpha=0.7) +  # Plot mean line
  labs(x = "Log(livestock density)", y = "Bee richness", fill = "Site") +
  theme(panel.background = element_blank(), axis.line = element_line(color =
"black"),  axis.title = element_text(size = 14), legend.position = c(1.3, 0.5),
axis.text = element_text(size = 12), panel.border = element_rect(color = "black", fill
= NA, size = 1), legend.text = element_text(size = 12), legend.key.size = unit(1.5,
"lines"));oog
```

```
plot_grid(oob,ooc,ood,ooe,oof,oog, nrow = 2, ncol = 3)




#######################################################################
#############
#    Bee abundance GLMs
#######################################################################
#############


# Merge the two ID columns
beestats <- mbees
beestats$merged <- paste(mbees$site2, mbees$box, sep = "_")

# Display the result
print(beestats$merged)
View(beestats)
attach(beestats)

#show means of livestock density groups
dungmeans <- tapply(dung.livestock.density.total, merged, mean) ; dungmeans

#total.richness.fl
m2a1 <- glm(bee.abundance ~ total.richness.fl,         data = beestats, family =
"poisson") ; summary(m2a1) #try a glm see what happens
m2a2 <- glm(bee.abundance ~ total.richness.fl + site2, data = beestats, family =
"poisson") ; summary(m2a2) #try a glm see what happens
m2a3 <- glm(bee.abundance ~ total.richness.fl * site2, data = beestats, family =
"poisson") ; summary(m2a3) #try a glm see what happens
anova(m2a1, m2a2, m2a3)
residual_deviance <- summary(m2a2)$deviance
residual_df <- summary(m2a2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion # good (dispersion parameter between 0.5 and 2.5)


#mean.cover.fl
m2b1 <- glm(bee.abundance ~ mean.cover.fl,         data = beestats, family =
"poisson") ; summary(m2b1) #try a glm see what happens
m2b2 <- glm(bee.abundance ~ mean.cover.fl + site2, data = beestats, family =
"poisson") ; summary(m2b2) #try a glm see what happens
m2b3 <- glm(bee.abundance ~ mean.cover.fl * site2, data = beestats, family =
"poisson") ; summary(m2b3) #try a glm see what happens
anova(m2b1, m2b2, m2b3)
```

```
residual_deviance <- summary(m2b2)$deviance
residual_df <- summary(m2b2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion

#mean.height
m2c1 <- glm(bee.abundance ~ mean.height,          data = beestats, family =
"poisson") ; summary(m2c1) #try a glm see what happens
m2c2 <- glm(bee.abundance ~ mean.height + site2, data = beestats, family =
"poisson") ; summary(m2c2) #try a glm see what happens
m2c3 <- glm(bee.abundance ~ mean.height * site2, data = beestats, family =
"poisson") ; summary(m2c3) #try a glm see what happens
anova(m2c1, m2c2, m2c3)
residual_deviance <- summary(m2c2)$deviance
residual_df <- summary(m2c2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion

#cv
m2d1 <- glm(bee.abundance ~ cv,          data = beestats, family = "poisson") ;
summary(m2d1) #try a glm see what happens
m2d2 <- glm(bee.abundance ~ cv + site2, data = beestats, family = "poisson") ;
summary(m2d2) #try a glm see what happens
m2d3 <- glm(bee.abundance ~ cv * site2, data = beestats, family = "poisson") ;
summary(m2d3) #try a glm see what happens
anova(m2d1, m2d2, m2d3)
residual_deviance <- summary(m2d2)$deviance
residual_df <- summary(m2d2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion




#######################################################################
#############
#     Bee richness GLMs
#######################################################################
#############

#total.richness.fl
m3a1 <- glm(bee.richness ~ total.richness.fl,          data = beestats, family =
"poisson") ; summary(m3a1) #try a glm see what happens
m3a2 <- glm(bee.richness ~ total.richness.fl + site2, data = beestats, family =
"poisson") ; summary(m3a2) #try a glm see what happens
m3a3 <- glm(bee.richness ~ total.richness.fl * site2, data = beestats, family =
"poisson") ; summary(m3a3) #try a glm see what happens
```

```
anova(m3a1, m3a2, m3a3)
residual_deviance <- summary(m3a2)$deviance
residual_df <- summary(m3a2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion

#mean.cover.fl
m3b1 <- glm(bee.richness ~ mean.cover.fl,         data = beestats, family =
"poisson") ; summary(m3b1) #try a glm see what happens
m3b2 <- glm(bee.richness ~ mean.cover.fl + site2, data = beestats, family =
"poisson") ; summary(m3b2) #try a glm see what happens
m3b3 <- glm(bee.richness ~ mean.cover.fl * site2, data = beestats, family =
"poisson") ; summary(m3b3) #try a glm see what happens
anova(m3b1, m3b2, m3b3)
residual_deviance <- summary(m3b2)$deviance
residual_df <- summary(m3b2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion

#mean.height
m3c1 <- glm(bee.richness ~ mean.height,         data = beestats, family =
"poisson") ; summary(m3c1) #try a glm see what happens
m3c2 <- glm(bee.richness ~ mean.height + site2, data = beestats, family =
"poisson") ; summary(m3c2) #try a glm see what happens
m3c3 <- glm(bee.richness ~ mean.height * site2, data = beestats, family =
"poisson") ; summary(m3c3) #try a glm see what happens
anova(m3c1, m3c2, m3c3)
residual_deviance <- summary(m3c2)$deviance
residual_df <- summary(m3c2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion

#cv
m3d1 <- glm(bee.richness ~ cv,         data = beestats, family = "poisson") ;
summary(m3d1) #try a glm see what happens
m3d2 <- glm(bee.richness ~ cv + site2, data = beestats, family = "poisson") ;
summary(m3d2) #try a glm see what happens
m3d3 <- glm(bee.richness ~ cv * site2, data = beestats, family = "poisson") ;
summary(m3d3) #try a glm see what happens
anova(m3d1, m3d2, m3d3)
residual_deviance <- summary(m3d2)$deviance
residual_df <- summary(m3d2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion

#bee.abundance
m3e1 <- glm(bee.richness ~ bee.abundance,         data = beestats, family =
"poisson") ; summary(m3e1) #try a glm see what happens
```

```
m3e2 <- glm(bee.richness ~ bee.abundance + site2, data = beestats, family =
"poisson") ; summary(m3e2) #try a glm see what happens
anova(m3e1, m3e2)
residual_deviance <- summary(m3e2)$deviance
residual_df <- summary(m3e2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion


#################################################################
#############
#     Dung livestock density GLMs
#################################################################
#############

#total.richness.fl
m1a1 <- glm(total.richness.fl ~ dung.livestock.density.total,          data = beestats,
family = "poisson") ; summary(m1a1) #try a glm see what happens
m1a2 <- glm(total.richness.fl ~ dung.livestock.density.total + site2, data =
beestats, family = "poisson") ; summary(m1a2) #try a glm see what happens
m1a3 <- glm(total.richness.fl ~ dung.livestock.density.total * site2, data = beestats,
family = "poisson") ; summary(m1a3) #try a glm see what happens
anova(m1a1, m1a2, m1a3)
residual_deviance <- summary(m1a2)$deviance
residual_df <- summary(m1a2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion
posthoc <- glht(m1a2, linfct = mcp(site2 = "Tukey")) ; summary(posthoc)


#mean.cover.fl
m1b1 <- glm(mean.cover.fl.bi ~ dung.livestock.density.total,          data = beestats,
family = "binomial") ; summary(m1b1) #try a glm see what happens
m1b2 <- glm(mean.cover.fl.bi ~ dung.livestock.density.total + site2, data =
beestats, family = "binomial") ; summary(m1b2) #try a glm see what happens
m1b3 <- glm(mean.cover.fl.bi ~ dung.livestock.density.total * site2, data =
beestats, family = "binomial") ; summary(m1b3) #try a glm see what happens
anova(m1b1, m1b2, m1b3)
residual_deviance <- summary(m1b3)$deviance
residual_df <- summary(m1b3)$df.residual
dispersion <- residual_deviance / residual_df
dispersion


#mean.cover.ip
m1c1 <- glm(mean.cover.ip.bi ~ dung.livestock.density.total,          data = beestats,
family = "binomial") ; summary(m1c1) #try a glm see what happens
```

```
m1c2 <- glm(mean.cover.ip.bi ~ dung.livestock.density.total + site2, data =
beestats, family = "binomial") ; summary(m1c2) #try a glm see what happens
m1c3 <- glm(mean.cover.ip.bi ~ dung.livestock.density.total * site2, data =
beestats, family = "binomial") ; summary(m1c3) #try a glm see what happens
anova(m1c1, m1c2, m1c3)
residual_deviance <- summary(m1c1)$deviance
residual_df <- summary(m1c1)$df.residual
dispersion <- residual_deviance / residual_df
dispersion
posthoc <- glht(m1c2, linfct = mcp(site2 = "Tukey")) ; summary(posthoc)


#mean.height
m1d1 <- glm(mean.height ~ dung.livestock.density.total,        data = beestats,
family = "gaussian") ; summary(m1d1) #try a glm see what happens
m1d2 <- glm(mean.height ~ dung.livestock.density.total + site2, data = beestats,
family = "gaussian") ; summary(m1d2) #try a glm see what happens
m1d3 <- glm(mean.height ~ dung.livestock.density.total * site2, data = beestats,
family = "gaussian") ; summary(m1d3) #try a glm see what happens
anova(m1d1, m1d2, m1d3)
residual_deviance <- summary(m1d2)$deviance
residual_df <- summary(m1d2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion
posthoc <- glht(m1d2, linfct = mcp(site2 = "Tukey")) ; summary(posthoc)


#cv
m1e1 <- glm(cv ~ dung.livestock.density.total,        data = beestats, family =
"gaussian") ; summary(m1e1) #try a glm see what happens
m1e2 <- glm(cv ~ dung.livestock.density.total + site2, data = beestats, family =
"gaussian") ; summary(m1e2) #try a glm see what happens
m1e3 <- glm(cv ~ dung.livestock.density.total * site2, data = beestats, family =
"gaussian") ; summary(m1e3) #try a glm see what happens
anova(m1e1, m1e2, m1e3)
residual_deviance <- summary(m1e2)$deviance
residual_df <- summary(m1e2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion
posthoc <- glht(m1e2, linfct = mcp(site2 = "Tukey")) ; summary(posthoc)

#bee.richness
m1f1 <- glm(bee.richness ~ dung.livestock.density.total,        data = beestats,
family = "gaussian") ; summary(m1f1) #try a glm see what happens
m1f2 <- glm(bee.richness ~ dung.livestock.density.total + site2, data = beestats,
family = "gaussian") ; summary(m1f2) #try a glm see what happens
m1f3 <- glm(bee.richness ~ dung.livestock.density.total * site2, data = beestats,
family = "gaussian") ; summary(m1f3) #try a glm see what happens
```

```
anova(m1f1, m1f2, m1f3)
residual_deviance <- summary(m1f2)$deviance
residual_df <- summary(m1f2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion
posthoc <- glht(m1f2, linfct = mcp(site2 = "Tukey")) ; summary(posthoc)

#bee.abundance
m1g1 <- glm(bee.abundance ~ dung.livestock.density.total,       data = beestats,
family = "gaussian") ; summary(m1g1) #try a glm see what happens
m1g2 <- glm(bee.abundance ~ dung.livestock.density.total + site2, data =
beestats, family = "gaussian") ; summary(m1g2) #try a glm see what happens
m1g3 <- glm(bee.abundance ~ dung.livestock.density.total * site2, data =
beestats, family = "gaussian") ; summary(m1g3) #try a glm see what happens
anova(m1g1, m1g2, m1g3)
residual_deviance <- summary(m1g2)$deviance
residual_df <- summary(m1g2)$df.residual
dispersion <- residual_deviance / residual_df
dispersion
posthoc <- glht(m1g2, linfct = mcp(site2 = "Tukey")) ; summary(posthoc)




#####################################################################
#############
#
#    END
#
#####################################################################
#############
```