

Space-time dynamics of natural enemies in a diversified strip cropping system during autumn

Vladimir Shlevkov Pronskiy

910107759080

FSE-80436

Wageningen University and Research Centre – Farming Systems Ecology

03/08/2016

Index

“Space-time dynamics of natural enemies in a diversified strip cropping system during autumn” (paper manuscript format)	1
Appendices	11
Basic Identification Key of Common Natural Enemies	11
R scripts	16
Personal R cheatsheet	16
Collinearity	21
GLMs Inter-plot	33
GLMs Inter-strip	38
Smoothed additive graphs (Araneae and Staphylinidae)	45
Smoothed additive graphs (Carabidae and Larvae)	59

Space-time dynamics of natural enemies in a diversified strip cropping system during autumn

Vladimir Shlevkov Pronskiy, Dirk van Apeldoorn, Felix Bianchi

Farming Systems Ecology, Wageningen University, PO Box 430, 6700 AK Wageningen, The Netherlands

Context: Diversified strip cropping systems are promising sustaining arthropod communities throughout autumn and winter periods, thus ecosystem services like pest control are ensured for the next growing season. However, it is still poorly understood how natural enemies of said arthropod communities (NEs) distribute in space and time in these agroecosystems prior to overwinter.

Objectives: To confirm that diversified strip cropping systems sustain NE communities during autumn, migration rates (individuals $\cdot$ m⁻¹ $\cdot$ d⁻¹) and directionality of NEs were studied. The three aims of the study were the assessment of NE preference for pre-overwintering sites depending on: 1) vegetation cover and management of crops and grass margins; 2) mixture and monoculture treatments; 3) other environmental factors such as weather and soil characteristics.

Methods: A diversified strip cropping system with rotation was chosen to study the movement of ground-dwelling NEs (Carabidae, Staphylinidae, their larvae and Araneae) among the strip cropping field and the monoculture/mixture treatments. The observation was conducted during September-November 2015 in an experimental farm in Wageningen, The Netherlands. Bi-directional pitfalls were used to sample the NEs a total of eight times. Variance analyses (with General Linear Models) and collinearity tests were performed to confirm the relation between strip and grass margin vegetation cover, soil management, weather and soil characteristics with the migration rates and directionality of NEs.

Results: The statistical analysis indicated similarities and positive correlation in migration rates between carabids and spiders, and between staphylinids and larvae. Carabids and spiders were negatively affected by soil disturbance, while staphylinids and larvae were not. Margins with stable vegetation cover acted as source of NEs into disturbed strips. Monoculture and mixture treatments did not show differences in migration rates nor directionality of NEs. Meteorological variables strongly influenced NE activity, but not soil pH or soil organic matter.

Conclusions: This study shows that diversified strip cropping systems sustain highly dynamic NE communities during autumn and before overwintering. Movement between strips was affected by soil disturbance but adjacent stable vegetation areas acted as a buffer maintaining the communities of NEs. Mixture treatment seemed redundant in terms of shelter and alternative food sources for pre-overwintering NEs in a diversified strip cropping system.

Keywords: *natural enemy, autumn, migration, directionality, crop diversity*

Introduction

Promoting ecological processes and dynamics is crucial for a sustainable agriculture (Malézieux, 2011). Thus, regarding pest suppression, fostering natural enemy (NE) populations is fundamental to reduce or avoid the use of pesticides, of which negative environmental impacts are broadly documented (Tilman et al., 2001). In order to ensure NE-based pest control, cropping systems must be designed taking their behaviour and dynamics into account. Monocultures host a low abundance and diversity of NEs that lead to regular pest outbreaks (Altieri et al., 1984). In contrast, systems that contain a higher diversity of crops, natural and/or semi-natural elements like hedges and grass margins may enhance NE communities, providing effective pest suppression (Kremen and Miles, 2012). Hence, crop diversification is a promising approach to stimulate this ecosystem service and to carry out Integrated Pest Management (IPM) practices (Sunderland and Samu, 2000).

There is a considerable amount of literature regarding spatial ecology of NEs, which include ground-dwelling and flying beetles, spiders and parasitoid wasps (summarized in [Bianchi et al., 2010](#)). However, the attention mainly goes to the spring and summer seasons, typical growing periods for the majority of crops and pest outbreaks in temperate regions ([Macfadyen et al., 2015](#); [Chaplin-Kramer et al., 2013](#)). Much less attention has been paid to overwintering period, which is important because it is a bottleneck for NE populations. For pest control purposes, their survival must be ensured for the effective control in the following growing season. Nearby natural and seminatural habitats such as forests, hedges, ditches, field margins and other landscape elements serve as refuge that act as source from which NEs can access the crop habitat during the growing season ([Bianchi et al., 2006](#)). Yet the preferences for overwintering sites of NEs within crop fields are poorly understood, being the studies more focused on crop-to-natural (and semi natural) movement ([Macfadyen et al., 2015](#); [Baveco et al., 2008](#)).

Successful pest suppressive cropping systems would benefit if a considerable amount of NEs were hosted within the fields during autumn and winter. This would allow a faster early colonization of crop habitats leading to a more effective pest control ([Sunderland and Ives, 2001](#)). In particular, diversified strip cropping systems (cultivation of two or more crops in adjacent strips, usually in seasonal rotation, with high crop diversity ([Labrie et al., 2015](#))), seem favourable to host overwintering populations because of their intrinsic habitat and ecotone variety, providing shelter and alternative food sources for NEs ([Langellotto and Denno, 2004](#)). Crop characteristics seem to be an important factor as different vegetation composition, structure and cover can affect NE movement behaviour ([Crist et al., 1992](#)) and their preference for the overwintering site ([Landis et al., 2000](#)). Habitat interfaces or ecotones (between crops and crop-to-non-crop areas) also influence NE movement due to higher diversity in food sources ([Allema et al., 2015](#)). Other factors affecting NE local movement and activity are crop management such as mowing, tillage and sowing ([Bugg, 1992](#); [Marrec et al., 2015](#); [Thorbeck and Bilde, 2004](#)), weather conditions ([Drake, 1994](#); [Bianchi et al., 2015](#)) and soil characteristics such as pH ([Paje and Mossakowski, 1984](#)). Although the environmental factors equally affect the NEs, strong differences in pre-overwintering movement patterns among taxa may be explained by their specific evolutionary histories and niches ([Danks, 2002](#); [Macfadyen et al., 2015](#)).

This study focuses on the NE local migration rate and directionality of movement to determine when and where do NEs go within a diversified strip cropping system prior to overwintering (autumn) in a Dutch agricultural landscape. Spatial scales studied are field (sum of all strips, figure 1), strip (each one with a specific crop and management operations, figure 2) and plot (monoculture or mixture segment of a strip, figures 1 and 2). The focus is on ground-dwelling predatory arthropods, which are less mobile than the flying ones, to allow a better study of their movement.

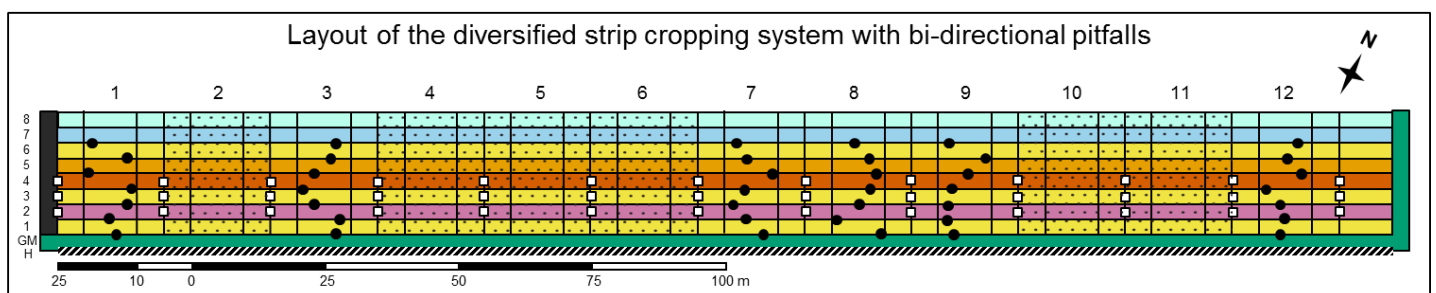


Figure 1: Representation of the observational set up in the diversified strip cropping system. The field contained 8 strips divided in 12 plots (clear plots: monoculture; shaded areas: mixtures), surrounding grass margins (GM), a strip of bare soil at the left edge (black strip), and a hedge (H). The location of bi-directional pitfalls of the inter-strip observation is indicated by black circles, while the ones for the inter-plot observation by white-filled squares.

The study has a threefold aim: first, to assess how the vegetation cover and management of crops (and grass margins) influence NE migration prior to overwintering. Second, to compare NE migration between mixture and monoculture treatments before overwinter. Third, to assess the influence of environmental heterogeneity (weather and soil characteristics) on NE migration.

	Summer crops		Winter crops	
8	Potato Toluca var. + mulches		Potato Toluca var. + mulches	
7	Flowers		Flowers	
6	lt. ryegrass + red clover	lt. ry. + Eng. rye + red clover + white clover + herbs	Winter OSR (01/10/15)	Winter OSR + white clover
5	Potato Toluca var.	Toluca + Ditta + Tiamo + Annabelle	lt. ryegrass + red clover (07/10/15)	lt. ry. + triticale + plantain + chicory + clover varieties*
4	Oil seed rape	Oil seed rape + clover	Oil seed rape	Oil seed rape + clover
3	lt. ryegrass + red clover	lt. ry. + Eng. rye + red clover + white clover + herbs	lt. ryegrass + red clover	lt. ry. + triticale + plantain + chicory + clover varieties*
2	Lennox	CCP + Faba	Triticale (05/10/15)	Triticale +w. wheat + rye + vetch + w. pea
1	lt. ryegrass + red clover	lt. ry. + Eng. rye + red clover + white clover + herbs	Triticale (05/10/15)	Triticale +w. wheat + rye + vetch + w. pea
GM				
H				

Figure 2: Crops in each strip (1 – 8), grass margin (GM) and hedge (H) during the observation. The dates indicate the moment of sowing the winter crop. Shaded areas correspond to the mixture treatment. Strip 7 was a constant strip of semi-wild flowers.

Materials and Methods

Study site

The study was conducted in 2015 between September 14th and November 26th in a strip cropping system with a total of 8 strips (figure 1), but strip 8 was excluded as it was part of an unrelated study. The study site was located at the Droevendaal Experimental Organic Farm of Wageningen University (51°59'30" N 5°39'5" E) in Wageningen, The Netherlands. The experimental field contained a strip cropping system experiment with a six-year rotation used for a variety of agrobiodiversity-related studies. The field had a total length of 240 m and a width of 18 m, split in 8 strips 3 m wide and with a semi-natural hedge separated by a 3 m wide grass strip at the Southwest side and a flower strip at the North-East. The field, and thus the strips, were divided in 12 transverse plots (20 m long). Each strip was cultivated with a specific crop and half of the plots were managed as monoculture while the other half as mixture (figure 1). In each plot, the central 10 m was the area of NEs sampling, while the 5 m sides were “buffers” to access the strips. Disturbances related to farming practices such as harvesting, mowing, tillage, harrowing and sowing were recorded. Some strips were moderately disturbed by harvesting (strips 2 and 4 on Sep. 9th), mowing (strip 6 on Sep. 22th, mixture plots of strip 3 on Sep. 23th). In other strips soil was highly disturbed by harvesting (strip 5 on Sep. 24th), tillage with rotary tiller (strips 1 and 6 on Sep. 29th), harrowing and sowing (strips 1, 2, 5 and 6 on Oct. 1st and 2nd). The upper part of the hedge was pruned on Sep. 28th. Nearby non-crop habitats (grass field margins, hedge) were taken into consideration for the analyses as well.

Weather variables

Temperature (°C), rain (mm) and humidity (%) were obtained from a local weather station (De Veenkampen). Soil pH ([H⁺]) and SOM (%) of the field were taken from the database of the Farming Systems Ecology department ([van Apeldoorn, 2015, unpublished dataset](#)).

Arthropod sampling

Bi-directional pitfalls were used to assess NE migration rates (individuals · m⁻¹ · day⁻¹) and directionality of their movement. The observation was designed as a generalized randomized block design to avoid spatial effects between traps. To study NE migration rates and directionality within the field and the Southwest grass margin the observations were set along the transverse (between strips or inter-strip observation) and longitudinal (between plots or inter-plot observation) axes of the field (figure 1). The inter-strip observation was arranged only in monoculture plots, as the aim was to detect influences of the vegetation cover and crop management on NE movement. The traps were placed along the edge of each strip in a randomized non-overlapping distribution to avoid interference between traps. The inter-plot set up was done in strips 2, 3 and 4 because they were considered representative of the monoculture/mixture treatments, allowing NE observation at three types of interface (monoculture-monoculture, monoculture-mixture and mixture-mixture).

NE migration rates and directionality were assessed using bi-directional pitfalls, consisting of a vertically placed black plastic barrier (150 x 24.5 cm) with two pitfall traps on each side at both ends of the barrier (4 pitfall traps per bi-directional pitfall) (figure 3). Pitfall traps consisted of two plastic cups (9 cm diameter, 14 cm deep), the outer one with holes at the bottom (for drainage) and the inner one, filled with 100 ml of water and soap mixture to break the water surface tension. Each pitfall was covered by a roof (14 cm diameter) to prevent flooding by rain and intrusion of debris and of larger animals. A total of 81 bi-directional pitfalls (324 pitfall traps) were placed to catch NEs a total of 8 times during the study period, being open for two days on Sep. 14th, Sep. 28th, Oct. 5th, Oct. 12th, and four days on Oct. 21th, Oct. 28th, Nov. 4th, Nov. 26th. The extra two days of the four last samplings were needed to increase the probability of catch, as arthropod activity is reduced with lower temperature ([Drake, 1994](#)). Hence, inter-strip observation consisted of 42 bi-directional pitfalls while the inter-plot set-up was done with 39. Between each sampling the pitfall traps were covered or removed and replaced due to crop management. Bi-directional pitfalls caught ground-dwelling arthropods coming from both directions, so the two pitfalls placed on one side of the barrier counted as a single sample. Thus 162 samples were a in each catch.

Identification

The collected specimens were identified to order and, in some cases, class and family levels. Narrowing down the identification to genus or species level was not needed as predation was treated as a common functional trait for many NE taxa. A stereo microscope was used for identification and the samples were stored in 70% ethanol at 4°C.

Statistical analysis

The caught NEs were considered as count data and the analyses were done using RStudio version 0.99.489 per each identified NE taxonomic group (Carabidae, Staphylinidae, Araneae and Larvae). Collinearity tests and Generalized Linear Models (GLM) were carried out to determine the variables that affected migration rates and directionality of NE movement in the strip cropping system. Collinearity tests were performed to assess correlations between NE migration rates and the following explanatory variables: catching date, crop treatment (monoculture/mixture), temperature (°C), rain (mm), humidity (%), soil pH ([H⁺]), SOM (%) and the analysed NE taxa (Carabidae, Araneae, Staphylinidae, Larvae).

To determine what variables had significant effects on the migration rates and directionality of NEs in the strip cropping system an analysis of variance was done. Three GLMs with negative binomial distribution were designed (related to strip and soil management characteristics, weather factors and soil characteristics at field level). The GLMs were selected after performing a model selection according to the Akaike Information Criterion (AIC), i. e. selecting the models with lower AIC number. Both inter-strip and inter-plot set-ups were analysed with the three GLMs. The first GLM (GLM.1) accounted for the directionality of NE movement by making the variable migration rate (individuals $\cdot$ m⁻¹ $\cdot$ day⁻¹) dependent of strip (or monoculture/mixture treatment for inter-plot set-up), direction of movement relative to strips, soil disturbance and catching date (the last two interacting with each other). In the inter-plot analysis GLM.1 was separately performed for each strip (2, 3 and 4). The second GLM (GLM.2) was designed to determine the effects of weather (temperature (°C), rain (mm) and humidity (%)) on the migration rates of NEs. An additional GLM (GLM.3) accounted for the effects of soil characteristics (soil pH ([H⁺]) and SOM (%)) on NE migration rates. Simplified coding of the GLMs were: GLM.1: NE taxon $\sim$ Strip (or Treatment) + Direction of movement + (Soil disturbance * Date); GLM.2: NE taxon $\sim$ (Temperature * Rain * Humidity) / Date; GLM.3: NE taxon $\sim$ (soil pH + SOM) * Date * Soil disturbance. The explanatory variables of GLM.2 were nested within the variable "Date". "Soil disturbance" was excluded for the analysis of strips 3, 4 and 7 as soil was not disturbed there.

The partition into three GLMs was done to avoid the overweighting of some exploratory variables that weakened the influences of other, which were also important to explain migration rates (e. g. weather) and spatial distribution of NEs (e. g. soil characteristics). "Strip" was chosen as exploratory variable over "crop" because some strips shared the same crop (1, 3 and 6 during summer period, and strips 1, 2 and 3, 4 at mid-autumn, figure 2). Strips indicated a constant position in space, while the crops changed due to rotation. Also, winter crops during the study time were barely germinating and lacking of vegetation cover.

Results

Identified arthropod taxa

A total of 15,006 NEs were trapped and identified. The major NE taxa found were Carabidae (2117 individuals) and Staphylinidae (1984) (order Coleoptera), larvae of both families (2150, considered as a group apart due to their reduced mobility) and order Araneae (2693). Coccinellidae, Hymenoptera (mainly parasitoid wasps) and Chilopoda were found but they were excluded from the analysis. Other non-NE were also identified (Aphididae, Crysomelidae, Dermaptera, Formicidae, Heteroptera, Isopoda and Opilionidae) but were excluded from the analysis.

Activity of taxa along time

Common migration rates were found between carabids and spiders and between staphylinids and larvae in both inter-strip and inter-plot observations (table 1). Carabids and spiders significantly decreased their activity, being more pronounced in the beetles to the point of virtually disappearing in the last date. Staphylinids showed mixed migration rates along the study period, while larvae increased their activity at mid period (figure 3).

Directionality of movement per taxon

The results of GLM.1 for the inter-strip set-up indicated significant immigration of carabids towards strips 6 and 7 ($p < 0.05$). At mid-period onwards carabids emigrated from the grass margin towards strip 1 (figure 3), although it was not significant enough in the GLM.1. Spiders showed a tendency for leaving strips 2, 5 and 6 (disturbed) and strips 3, 4 (with stable vegetation cover) ($p < 0.05$). Staphylinids and larvae did not show significance preference towards any specific strip. Migration rates of all NE taxa at the interface between strips 3 and 4 were lower than at the rest of strip edges (figure 3). Regarding inter-plot set-up staphylinids had a correlation of 11% with mixture treatment in strip 4, while in strip 3 larvae showed 16%. However, GLM.1 indicated no significant differences in NE movement between monoculture and mixture treatments. NE activity between the plots was 100 ± 50 spiders $100\text{m}^{-1}\cdot\text{day}^{-1}$; 70 ± 25

Correlation between explanatory variables and NE migration rates (%)									
Explanatory variables	Inter-strip				Inter-plot				Model used for an. var.
	Carabidae	Araneae	Staph.	Larvae	Carabidae	Araneae	Staph.	Larvae	
Time	-52.5	-19*	4	11	-54	-24.5	7	25.5	GLM.1
Disturbance	-25.5	-13.5	19.5	21	-21	-16.5	-5	14*	
Treatment	-	-	-	-	1	7.5	1.5	8.5	
Temperature	36	14.5	-5.5	-1.5	41.5	15	-2	2.5	GLM.2
Rain	32	26.5	-21.5*	-28	49	34	-19	-18	
Humidity	-17.5	-7.5	-5*	-3.5	-7	-7.5	10.5	7.5	
Soil pH	-5.5	22	7.5	0.5	-1.5	2.5	2.5	8.5	GLM.3
SOM	-7.5	2.5	2	-17	1	-4	8	-6	
Carabidae	-	26.5	11	8	-	21	-1	-5.5	
Araneae	-	-	5	-6.5	-	-	2	-4	
Staph.	-	-	-	26	-	-	-	22	

Table 1: Bold numbers indicate significance of the explanatory variable in the corresponding GLM ($p < 0.05$). * p -value between 0.10 and 0.05. The levels for “Treatment” factor were monoculture and mixture, coded in the R script as 1 and 2 respectively, thus positive correlation indicates migration tendency towards mixture treatment. This variable was excluded from inter-strip set-up because it was done in monoculture only. “Staph.” indicates Staphylinidae.

staphylinids $100\text{m}^{-1} \cdot \text{day}^{-1}$ and 70 ± 50 larvae $100\text{m}^{-1} \cdot \text{day}^{-1}$. Carabids had an activity at a rate of 70 ± 50 individuals $\cdot 100\text{m}^{-1} \cdot \text{day}^{-1}$.

Effects of soil disturbance on NE activity

Heavy soil disturbance resulting in the total loss of vegetation cover occurred in strips 1, 2, 5 and 6 negatively correlated with carabid and spider migration rate (although without significance in GLM.1), but positively for larvae's (table 1). Staphylinids positively correlated to soil disturbances in the inter-strip set-up, but negatively in the inter-plot one. Migration rates of staphylinids and larvae in strips 1, 2, 5 and 6 increased right after heavy soil disturbances, while decreased for carabids (same strips) and spiders (strip 2 only). Subsequently, carabid migration rates decreased along time in all strips (figure 3).

Weather and soil

As seen in table 1, the effects of weather on NE movement (analysed with collinearity tests and GLM.2) showed positive influences of temperature and rain on carabid and spider migration rates. However the effects on the migration rates of staphylinids and larvae were the opposite. Humidity was negatively correlated with all the NE taxa in the inter-strip observation, but it was positive for staphylinids and larvae in the inter-plot set-up. Temperature dropped along the study period, being the correlation with time of -61%. Soil pH was negatively correlated with carabids and positively for the rest of the groups in both set-ups, being significant only for spiders in the inter-strip observation ($p < 0.05$) (table 1). SOM had mixed influences in the taxa migration rates, but it was positive at inter-strip and negative at inter-plot ($p < 0.05$) set-ups for spiders.

Intraguild influences

As shown in table 1, collinearity test indicated that carabid migration rates were positively correlated with the rest of the groups in the inter-strip observations, while at inter-plot set up it was positive only with spiders. Staphylinid and larvae migration rates were positively correlated in both set ups. Spiders showed negative correlation with larval and low positive correlation with staphylinid migration rates in both set-ups.

Migration rates and directionality of NEs between strips along time

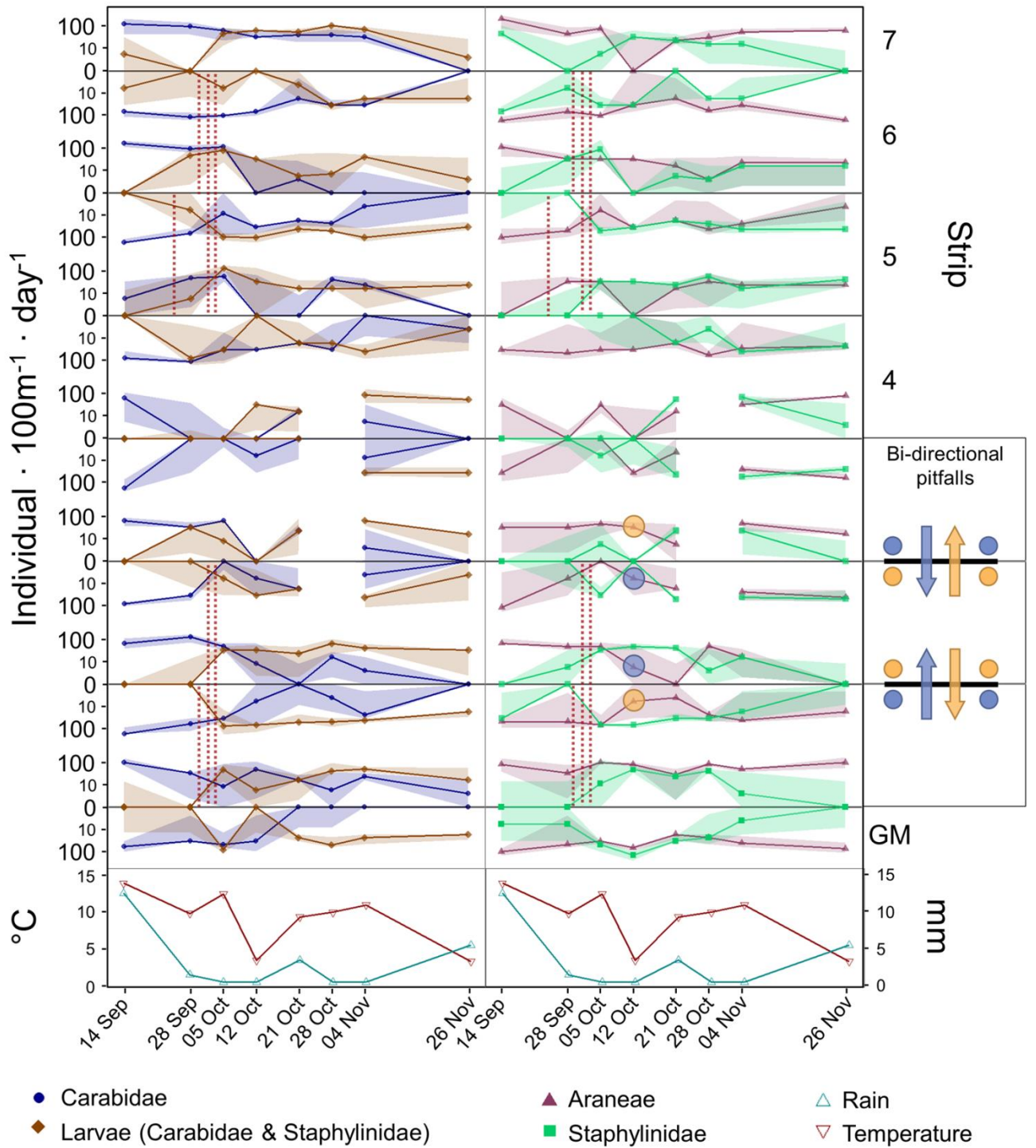


Figure 3: Space and time representation of the migration rates and directionality of each NE taxon among strips. The dots represent the median of individuals $\cdot 100\text{m}^{-1} \cdot \text{day}^{-1}$, while shaded area is the variance (CI 75%). The scale is logarithmic for the better visualization of data. No sampling was done in strips 3 and 4 on 28th October due to farm operations. Heavy soil disturbance events in strips 1, 2, 5 and 6 are indicated by vertical dashed lines. The lower panels show temperature and rain at the study site along time. The lateral panel depicts a schematic of the sampling of bi-directional pitfalls at two strip edges (2 and 3): immigrating NEs towards strip 2 are indicated with blue arrows and circles, while emigrating from strip 2 are indicated with golden ones.

Discussion

This study provides an insight of the complex spatial dynamics of ground-dwelling NEs in a diversified strip cropping system during autumn in a Dutch landscape, prior to overwintering. The evidence provided by nearly 9.000 NE specimens collected in eight catches showed particular NE activity patterns.

Among all the explanatory variables tested, time was the most important variable determining the migration rates of the studied NEs. Carabids and spiders decreased their activity, which could be explained by their innate pre-overwintering behaviour. However it is more likely that environmental factors played a more important role because both groups were sensitive to temperature and rain decline and to soil-disturbance events. Spiders tended to emigrate from the disturbed strips 1, 2, 5 and 6, while carabids immigrated into strips 6 and 7. Carabid migration into strip 6 could be explained by the mortality of large numbers during soil disturbance (as similarly observed by [Shearin et al., 2007](#)), leaving only immigration from strip 7 (stable vegetation cover) as the only possibility. The same effect was observed after disturbance of strip 1, which was followed by immigration from the grass margin (stable vegetation cover). This spillover effect from grass margins was also observed by [Bianchi et al. \(2006\)](#) and [Holland et al. \(2012\)](#). Thus, after soil disturbances, the grass margin and the semi-wild flower strip behaved as a buffer against the disruption of NE communities, helping to recolonize the field during autumn. Spiders showed a more complex spatial dynamic, probably due to their high mobility through ground and air (by ballooning). On the contrary, staphylinids and larvae increased their activity after the disturbances in strips 1, 2, 5 and 6. Tillage and sowing may have unearthed soil-biota preys but, if that was the case, all the NEs were expected to migrate into those strips. Hence, it is more likely that staphylinids and larvae were unearthed, being residents on the upper layer of soil. The decrease in migration rates of both taxa after rains could be explained by the water clogging of disturbed strips. Staphylinids and larvae were more independent from time and temperature than carabids and spiders, probably because the first layer of soil provided a shelter against weather.

Mixture and monoculture plots showed no significant difference of NE migration despite of the distinct vegetation composition in each one. This lack of difference cannot be attributed to crop management as the analysis was done on a heavily disturbed strip (2) and strips with stable vegetation cover (3 and 4). Although monoculture-mixture edges are habitat interfaces, which affect NE movement ([Allema et al., 2015](#); [Bommarco and Fagan, 2002](#)), they seemed to be redundant in terms of shelter and alternative preys in a highly diversified strip cropping system.

The effects of soil characteristics (pH and SOM) among NEs migration rates were mixed. Spiders showed affinity for the patches with higher pH, although the reasons remain unclear. SOM had little effect on the NEs, but spiders were positively correlated to this variable in the inter-strip set-up and negatively in the inter-plot one. A more detailed analysis of spatial dynamics of spiders would clarify these observations.

Each NE group behaved in a distinctive manner showing that it is not reliable to analyse population dynamics when they are aggregated. However, high correlation of migration rates between carabids and spiders and between staphylinids and larvae allow a certain level of predictability. That is, in order to study the activity of several NE taxa, it is possible to choose a few as indicators of the migration rates and habitat preferences of other NE groups.

Regarding the use of bi-directional pitfalls this observational set up did not provide population densities, which would help confirming the preferred pre-overwintering sites of NEs. A separate sampling per strip and crop for overwintering NE in the soil was executed but, due to unusually wet weather conditions of 2015-2016 winter, the sampling had to be terminated. Other inherent limitations of the study relied on the null isolation of the field from the surrounding ecosystem, which contributed to unknown factors difficult to monitor and analyse. Inter-annual variability is an important limitation for this kind of studies, requiring extended replications in time.

Therefore it is suggested to 1) monitor vegetation cover throughout the catching period as it may provide links between NE activity and level of shelter (and of alternative food sources); 2) to replicate the observation in time and in different diversified cropping systems to confirm the presented results and 3) to compare it to conventional monoculture systems to increase the amount of evidence that complex agricultural landscapes improve NE-mediated crop control (Rusch et al., 2016) providing enough shelter and food resources to sustain biological pest control all year round. All this increasing knowledge on NE inter-field dynamics will help to the understanding of fundamental agroecological phenomena in off-season arable lands and to provide practical information to design more effective pest suppressive agroecosystems.

The key findings of this study are that (i) soil disturbance is a stronger determining factor of NE migration rates and directionality than vegetation cover, (ii) not all NEs are negatively affected by heavy soil disturbance in a diversified strip cropping system (staphylinids and larvae remain, while carabids immigrate from adjacent margins with stable vegetation cover), (iii) in a diversified strip cropping system there are no differences of NE activity between monoculture and polyculture treatments, and (iv) NE migration within a diversified strip cropping system is influenced by meteorological variables.

Acknowledgements

I thank Dirk van Apeldoorn and Felix Bianchi for the supervision and feedbacks on the observational set up and on the analyses with R software; Dine Volker for the invaluable help at the field and providing the necessary materials; Bas Allema for assistance in insect identification; Jan Jansen for the tips on data management with R software and Shantonu Abe Chatterjee for the help during fieldwork.

References

- Allema, B., van der Werf, W., van Lenteren, J., Hemerik, L. and Rossing, W. (2014). Movement Behaviour of the Carabid Beetle *Pterostichus melanarius* in Crops and at a Habitat Interface Explains Patterns of Population Redistribution in the Field. *PLoS ONE*, 9(12), p.e115751.
- Altieri, M., Letourneau, D. and Risch, S. (1984). Vegetation diversity and insect pest outbreaks. *Critical Reviews in Plant Sciences*, 2(2), pp.131-169.
- Baveco, J., Bianchi, F., van der Werf, W. and Goedhart, P. (2008). Mapping the ecosystem service of pest control associated with forest in agricultural landscapes; a proof of concept. *Landscape Management for Functional Biodiversity IOBC wprs Bulletin*, 34, pp.21-23.
- Bianchi, F., Booij, C. and Tscharrntke, T. (2006). Sustainable pest regulation in agricultural landscapes: a review on landscape composition, biodiversity and natural pest control. *Proceedings of the Royal Society B: Biological Sciences*, 273(1595), pp.1715-1727.
- Bianchi, F., Schellhorn, N., Buckley, Y. and Possingham, H. (2010). Spatial variability in ecosystem services: simple rules for predator-mediated pest suppression. *Ecological Applications*, 20(8), pp.2322-2333.
- Bianchi, F., Walters, B., ten Hove, A., Cunningham, S., van der Werf, W., Douma, J. and Schellhorn, N. (2015). Early-season crop colonization by parasitoids is associated with native vegetation, but is spatially and temporally erratic. *Agriculture, Ecosystems & Environment*, 207, pp.10-16.
- Bommarco, R. and Fagan, W. (2002). Influence of crop edges on movement of generalist predators: a diffusion approach. *Agricultural and Forest Entomology*, 4(1), pp.21-30.
- Bugg, R. (1992). Using cover crops to manage arthropods on truck farms. *HortScience*, 27(7), pp.741-745.
- Chaplin-Kramer, R., de Valpine, P., Mills, N. and Kremen, C. (2013). Detecting pest control services across spatial and temporal scales. *Agriculture, Ecosystems & Environment*, 181, pp.206-212.

- Crist, T., Guertin, D., Wiens, J. and Milne, B. (1992). Animal Movement in Heterogeneous Landscapes: An Experiment with Eleodes Beetles in Shortgrass Prairie. *Functional Ecology*, 6(5), pp.536-544.
- Danks, H. (2002). The range of insect dormancy responses. *European Journal of Entomology*, 99, pp.127-142.
- Drake, V. (1994). The influence of weather and climate on agriculturally important insects: an Australian perspective. *Australian Journal of Agricultural Research*, 45(3), pp.487-509.
- Holland, J., Oaten, H., Moreby, S., Birkett, T., Simper, J., Southway, S. and Smith, B. (2012). Agri-environment scheme enhancing ecosystem services: A demonstration of improved biological control in cereal crops. *Agriculture, Ecosystems & Environment*, 155, pp.147-152.
- Kremen, C. and Miles, A. (2012). Ecosystem Services in Biologically Diversified versus Conventional Farming Systems: Benefits, Externalities, and Trade-Offs. *Ecology and Society*, 17(4).
- Labrie, G., Estevez, B. and Lucas, E. (2016). Impact of large strip cropping system (24 and 48 rows) on soybean aphid during four years in organic soybean. *Agriculture, Ecosystems & Environment*, 222, pp.249-257.
- Landis, D., Wratten, S. and Gurr, G. (2000). Habitat Management to Conserve Natural Enemies of Arthropod Pests in Agriculture. *Annual Review of Entomology*, 45(1), pp.175-201.
- Langellotto, G. and Denno, R. (2004). Responses of invertebrate natural enemies to complex-structured habitats: a meta-analytical synthesis. *Oecologia*, 139(1), pp.1-10.
- Lockeretz, W. (2007). *Organic farming*. Cambridge, MA: CABI.
- Macfadyen, S., Hopkinson, J., Parry, H., Neave, M., Bianchi, F., Zalucki, M. and Schellhorn, N. (2015). Early-season movement dynamics of phytophagous pest and natural enemies across a native vegetation-crop ecotone. *Agriculture, Ecosystems & Environment*, 200, pp.110-118.
- Malézieux, E. (2011). Designing cropping systems from nature. *Agronomy for Sustainable Development*, 32(1), pp.15-29.
- Marrec, R., Badenhausser, I., Bretagnolle, V., Börger, L., Roncoroni, M., Guillon, N. and Gauffre, B. (2015). Crop succession and habitat preferences drive the distribution and abundance of carabid beetles in an agricultural landscape. *Agriculture, Ecosystems & Environment*, 199, pp.282-289.
- Paje, F. and Mossakowski, D. (1984). pH-preferences and habitat selection in carabid beetles. *Oecologia*, 64(1), pp.41-46.
- Rusch, A., Chaplin-Kramer, R., Gardiner, M., Hawro, V., Holland, J., Landis, D., Thies, C., Tschardtke, T., Weisser, W., Winqvist, C., Woltz, M. and Bommarco, R. (2016). Agricultural landscape simplification reduces natural pest control: A quantitative synthesis. *Agriculture, Ecosystems & Environment*, 221, pp.198-204.
- Shearin, A., Reberg-Horton, S. and Gallandt, E. (2007). Direct Effects of Tillage on the Activity Density of Ground Beetle (Coleoptera: Carabidae) Weed Seed Predators. *Environmental Entomology*, 36(5), pp.1140-1146.
- Sunderland, K. and Samu, F. (2000). Effects of agricultural diversification on the abundance, distribution, and pest control potential of spiders: a review. *Entomologia Experimentalis et Applicata*, 95(1), pp.1-13.
- Thorbek, P. And Bilde, T. (2004). Reduced numbers of generalist arthropod predators after crop management. *Journal of Applied Ecology*, 41(3), pp.526-538.
- Tilman, D., Fargione, J., Wolff, B., D'Antonio, C., Dobson, A., Howarth, R., Schindler, D., Schlesinger, W., Simberloff, D. and Swackhamer, D. (2001). Forecasting Agriculturally Driven Global Environmental Change. *Science*, 292(5515), pp.281-284.

Appendices

Basic identification key of common Natural Enemies

Vladimir Shlevkov Pronskiy

Student MSc. Organic Agriculture, FSE group

- 1: 3 pairs of legs -> class **INSECTA** (2)
>3 pairs of legs -> (13)
- 2: Winged (can be covered) -> (3)
Wingless -> (18)
- 3: 1 pair of wings -> order **DIPTERA** (flies, *non-NE*)
2 pairs of wings -> (4)
- 4: Forewings are thicker and cover the hindwings -> (5)
Uncovered wings -> (23)
- 5: Pair of articulated pincers on the end of abdomen (**cerci**) -> order **DERMAPTERA** (earwigs, *non-NE*)
No cerci -> (6)
- 6: Long jumping hind legs, saddle-shaped **pronotum** (in the **thorax**) -> order **ORTHOPTERA**
(grasshoppers and crickets, *non-NE*)
Others -> (7)
- 7: Forewings completely leathery or horny (**elytra**) -> order **COLEOPTERA** (8)
Forewings partly leathery or horny with a membranous tip, piercing suction beak -> order **HETEROPTERA** (30)
- 8: Elytra completely (or almost completely) cover the abdomen -> (9)
Abdomen largely uncovered -> family **STAPHYLINIDAE** (rove beetles, *NE*)
- 9: Filiform antennae (11 segments), 5 segmented **tarsi**, lobed extended hind **trochanters** -> family **CARABIDAE** (ground beetles, *NE*)
Others -> (10)
- 10: Elytra usually brightly coloured with punctuated pattern, usually round-shaped body -> family **COCCINELIDAE** (lady beetles, *NE*)
Others -> (11)
- 11: 4 segmented tarsi, last one deeply embedded in 3st -> family **CHRYSOMELIDAE** (leaf beetles, *non-NE*)
Others -> (12)

- 12: Antennae ended in hand-like segments, usually spiked **tibiae** -> family **SCARABEIDAE** (dung beetles, *non-NE*)
Other *non-NE* beetles, see more detailed identification keys.
- 13: 4 pairs of legs -> class **ARACHNIDA** (14)
>4 pairs of legs -> (16)
- 14: Head and **thorax** fused, differentiated and non-segmented **abdomen** -> order **ARANEAE** (spiders, *NE*)
Head, thorax and abdomen fused -> (15)
- 15: Segmented body, usually very long legs -> order **OPILIONES** (harvestmen, *non-NE*)
Non-segmented body, tiny, relatively short legs, round shaped body -> subclass **ACARINA** (ticks and mites, *diverse**)
- 16: 7 pairs of legs, tail with numerous small plates (**telson**) -> order **ISOPODA** (woodlice, *non-NE*)
>7 pairs of legs -> subphylum **MYRIAPODA** (17)
- 17: 2 pair of legs per segment, no antennae, long body that can get coiled for defense of when dead -> class **DIPLOPODA** (millipedes, *non-NE*)
1 pair of legs per segment, strong fangs, long antennae -> class **CHILOPODA** (centipedes, *NE*)
- 18: Tiny, with springing organ (**furcula**) at the end of abdomen -> subclass **COLLEMBOLA** (springtails, *non-NE*)
Without furcula -> (19)
- 19: Long soft body -> (20)
Body with complete exoskeleton -> (21)
- 20: Three pairs of segmented legs at the front, five pairs of fleshy **prolegs** at the back -> **larvae** of order **LEPIDOPTERA** (caterpillars, *non-NE*)
No fleshy prolegs, with jaws -> **larvae** of orders **COLEOPTERA** and **NEUROPTERA** (*NE*)
- 21: Suction beak, hind end of abdomen with pair of "horns" (**cornicles**), pear shaped body -> family **APHIDIDAE** (plant lice, *non-NE*)
Others -> (22)
- 22: Strongly elbowed antennae, waist of one or two segments -> family **FORMICIDAE** (ants, *non-NE*)
Antennae generally filiform, but can be elbowed, females with **ovipositor** -> **WASPS** (several families of Hymenoptera, *diverse**)
- 23: Wide coloured wings (with tiny scales), coiled mouthparts -> order **LEPIDOPTERA** (butterflies and moths, *non-NE*)
Wings with venation -> (24)
- 24: Suction beak, hind end of abdomen with pair of "horns" (**cornicles**), pear shaped body -> family **APHIDIDAE** (plant lice, *non-NE*)
Others -> (25)

- 25: Suction beak, forewings with uniform texture, short antennae -> suborder **HOMOPTERA** (cicadas, froghoppers and leafhoppers, *non-NE*)
Others -> (26)
- 26: Large wings with numerous small cells covering the whole abdomen at rest, very long antennae -> family **CRYSOPIDAE** (lacewings, *diverse**)
Forewings larger than hindwings, with waist -> (27)
- 27: Very hairy body -> **BEES** and **BUMBLEBEES** (several families of order Hymenoptera, *non-NE*)
Non hairy body -> (28)
- 28: Without ovipositor -> **WASPS** (several families of Hymenoptera, *diverse**)
Females with long ovipositor, can be hidden under/inside abdomen -> (29)
- 29: Tiny, long non-elbowed antennae, forewings with distinctive venation -> family **CYNIPIDAE** (gall wasps, *non-NE*)**
Forewings usually with *stigma*, antennae can be very long, short and/or elbowed -> **PARASITOID WASPS** (diverse families of Hymenoptera, *NE*)**
- 30: Strong and curved 3 or 4-segmented suction beak, antennae can be elbowed after 1st segment -> family **REDUVIIDAE** (assassin bugs, *NE*)
Rest of heteropteran bugs -> diverse families of order **HETEROPTERA** (bugs, *non-NE*)

*NE and non-NE species can be found in this group, see more detailed identification guides.

**Identification of gall and parasitoid wasps is difficult, this guide is an approximation to determine these groups. See more detailed identification guides for more accuracy.

Figures

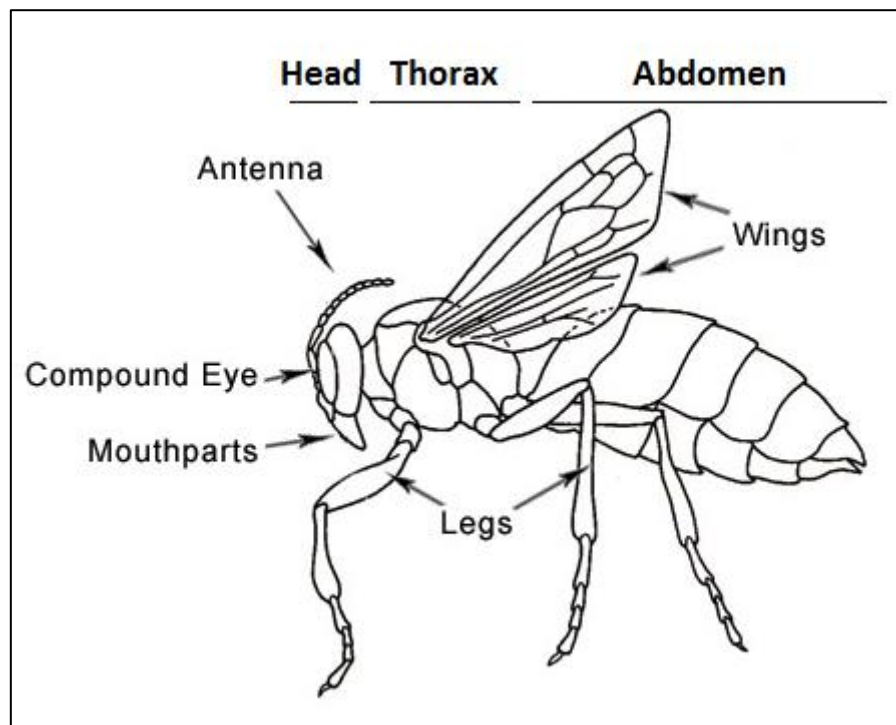


Fig 1: Basic insect anatomy (modified from Purdue University)

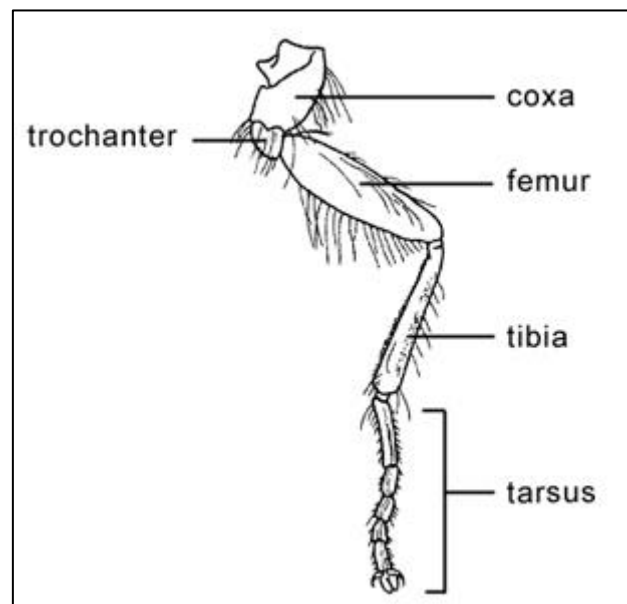


Fig 2: Anatomy of an insect leg (modified from Purdue University)

Glossary

Abdomen: 3rd and last section of the body, following the thorax.

Cercus (pl. cerci): pair of articulated organs at the end of the abdomen.

Cornicle: pair of small backward-pointing dorsal tubes at the end of the abdomen.

Elytron (pl. elytra): hardened forewings which cover the 2nd pair of wings or hindwings and the abdomen.

Furcula: forked jumping organ at the end of the abdomen of springtails (or. Collembola).

Ovipositor: laying egg organ at the end of the abdomen.

Proleg: small, stumpy or fleshy ventral structures found in caterpillars (larvae of or. Lepidoptera) used for mobility.

Pronotum: dorsally enlarged 1st segment of thorax in class Insecta.

Tarsus (pl. tarsi): foot, consisting of 1 to 5 segments, usually ended in 1 or 2 claws.

Telson: last segment of abdomen in crustaceans.

Thorax: midsection of the body which carries the legs and the wings (when present).

Tibia (pl. tibiae): leg segment between femur and tarsi.

Trochanter: leg segment between coxa (which connects to the body) and femur.

References

Chinery, M. (1986). *Collins guide to the insects of Britain and Western Europe*. London: Collins.

Choate, P. M. (2003). *Introduction to the Identification of Beetles (Coleoptera)*

Luff F., Martin. *The Carabidae (ground beetles) of Britain and Ireland*. Royal Entomological Society 2nd Ed (2007)

Purdue University, (2015). *Insect Anatomy*. [online] Extension.entm.purdue.edu. Available at: http://extension.entm.purdue.edu/401Book/default.php?page=insect_anatomy [Accessed 1 Dec. 2015].

van Lenteren, J. (2011). The state of commercial augmentative biological control: plenty of natural enemies, but a frustrating lack of uptake. *BioControl*, 57(1), pp.1-20.

R scripts

Personal R cheatsheet

```
#-----  
# Personal R cheatseet (notes, tricks and tips)  
# Vladimir Shlevkov Pronskiy  
# v.shlevkov@gmail.com  
# Started on 01/03/16  
#-----  
# INDEX:  
## To find each trick below: Ctrl+F and copypaste the indexed title  
## (Index per alphabetic order, tricks per chronological order)  
#  
# Add a column to an existing data frame  
# Aggregate  
# Build a matrix  
# Getting information of a dataset  
# Hashtag  
# Interaction plot  
# Looking at the data (extracting basic information)  
# Lots of graph types  
# Merging two data frames by a common column  
# Naming rows and columns  
# Pivoting tables  
# Regression lines for exponential models + graph setting  
# Remove percentiles (e. g. to get rid of outliers)  
# Removing NA's from data frame  
# Rename a column  
# Replacing 0 to NA  
# Replacing NA to 0  
# Row sum  
# Save as jpeg  
# Subsetting  
# Test models  
# To close all graphs windows  
#  
# More tricks on these websites  
#  
#  
#  
#-----  
  
# Aggregate per factor  
Newdata      <-      aggregate(cbind(Data$var1,      Data$var2, Data$var3)~Factor,  
data=Data,FUN=mean)  
colnames(Newdata) <- c("factor","var1","var2","var3")
```

```

# Also valid to aggregate per various factor
Newdata <- aggregate(cbind(Data$var1,
Data$var2,Data$var3)~Factor1*Factor2*Factor3,
                    data=Data,FUN=mean)
colnames(Newdata) <- c("factor1","factor2","factor3","var1","var2","var3")

# Build a matrix
B <- matrix(c(2, 4, 3, 1, 5, 7), nrow=3, ncol=2)
colnames(B) <- c("one", "two")
rownames(B) <- c("a", "b", "c")

# Looking at the data (extracting basic information)

datainfo <- within(data, {
  var1 <- factor(var1)
  var2 <- factor(var2)
  var3 <- factor(var3)
})

summary(datainfo)

#Also:
summary(mydata)

# To see sd of factors:
sapply(mydata, sd)

# Hashtag
## Hashtag preceding a string/code indicates R not to read or run the code. If
you want to
## prevent R from reading certain codes you can put hashtag instead of erasing
it. Useful for
## titles, text and comments.

# Getting information of a dataset
## list objects in the working environment
ls(object)
# list the variables in mydata
names(mydata)
## list the structure of mydata
str(mydata)
## list levels of factor v1 in mydata
levels(mydata$v1)
## dimensions of an object
dim(object)
## class of an object (numeric, matrix, data frame, etc)

```

```

class(object)
## print mydata
mydata
## print first 10 rows of mydata
head(mydata, n=10)
## print last 5 rows of mydata
tail(mydata, n=5)

# Pivoting tables
install.packages('rpivotTable')
library(rpivotTable)

Pivoted_table <- rpivotTable(data, rows="name", cols=c("whatever name", "another
name"))

# Naming rows and columns
## Rows
row.names(data)[n°] <- "name"
row.names(data)[n°] <- "other name"

## Columns
colnames(data)[n°] <- "name"
### or when various names
colnames(data) <- c("name", "other name")

# Subsetting
## Multiple ways to subset (keep/drop variables; select per observation)
## See http://www.statmethods.net/management/subset.html

# Lots of graph types
## http://docs.ggplot2.org/current/
## http://docs.ggplot2.org/dev/vignettes/qplot.html

# Regression lines for exponential models + graph settings
#1
abline(lm(Freq~ID), col="red", lwd=1.5)

#2
exponential.model <- lm(log(ID)~ Word)
summary(exponential.model)
zipflaw <- seq(0, 30, 0.1)
Counts.exponential2 <- exp(predict(exponential.model, list(ID=zipflaw)))
plot(ID, Freq, pch=19)
lines(zipflaw, Counts.exponential2, lwd=2, col = "red", xlab = "Word", ylab =
"Freq")

# Removing NA's from data frame
data[rowSums(is.na(data)) == 0,]

# Replacing 0 to NA:

```

```

df[df == 0] <- NA

# Replacing NA to 0:
df[is.na(df)] <- 0

# Merging to data frames by a common column (will be merged by
# column with same name):
myfulldata = merge(mydata1, mydata2)

# Save plot(model) as jpeg (analogous with png, pdf, etc - just change the
function. Some arguments
# don't work depending on the function used!)
jpeg(file= 'directory\\filename.jpeg', width = 800, height = 600, quality = 100)
plot(model)
dev.off()

# Add a column to an existing data frame
data["new_column_name"] <- n°
# (n° or NA or whatever we want to put)
# but careful as it will add it with the same observation in the
# whole column!

# To close all graphs windows
graphics.off()

# Remove percentiles (e. g. to get rid of outliers)
library(scales)
newdata<- squish(data, quantile(data,c(.05, .95), na.rm=T))

# Row sum
Newdata <- as.data.frame(rowSums(data[c("var1", "var2", "var3")],na.rm = TRUE))

# Rename a column
dataframe <- rename(data, c("x"="ics", "y"="why", "z"="zed"))
# or
colnames(data)[n°_of_column] <- "name"
colnames(data) <- "name" # This when dataframe has only 1 column

# Interaction plot

interaction.plot(data$x, data$group, data$y,
                fun = mean,
                xlab = deparse(substitute(x)),
                ylab = deparse(substitute(y)),
                trace.label = deparse(substitute(group)))

# Test models
require(pscl)
vuong(m1,m2)

```

```
# More tricks on these websites
##
https://en.wikibooks.org/wiki/R\_Programming/Working\_with\_data\_frames#Attaching\_
data
## http://www.cookbook-r.com/
## For fundamental and R analysis statistics and codes see books: Crowley ("The
R Book");
## Zuur et al ("Mixed Effects Models and Extensions in Ecology with R")
```

Collinearity

```
# -----
# Script for data analysis: COLLINEARITY
# From Zuur et al Mixed Effects Models and Extensions in Ecology
# with R pg 535
# Vladimir Shlevkov 26/03/2016
# vladimir.shlevkovpronskiy@wur.nl
# -----
# Glossary :
#   x = number of strip
#   d = direction of NE movement
#       n = pitfall placed in the north face of the edge/trap so = from north
#       (to south)
#       s = pitfall placed in the south face of the edge/trap so = from south
#       (to north)
#
# Schematic of the functioning of bi-directional pitfalls:
#
#
#           *      *
#----- strip 4           ^
#           *      *       | N
#
#           *      *
#----- strip 3
#           *      *
#
#           *      *
#----- strip 2
#           *      * s -----> NEs towards strip 3
#
#           *      * n -----> NEs towards strip 1
#----- strip 1
#           *      *
#
# Reminder Dates of catches:
# Date 1: 14/09/2015
# Date 2: 28/09/2015
# Date 3: 05/10/2015
# Date 4: 12/10/2015
# Date 5: 21/10/2015
# Date 6: 28/10/2015
# Date 7: 04/11/2015
# Date 8: 26/11/2015
#
#-----

setwd("Directory")
```

```

# clean up workspace
rm(list=ls())
graphics.off()
gc(FALSE)
cat("\014")

# Some of collinearity functions need the AED package (not in R, nor CRAN nor
longer provided by
# http://www.highstat.com/book2.htm) by the latter provides alternative free
software code:
source("Directory")

# Work with Mega is it has all the Mega per strip and date + soil + environment
data
Mega <- read.csv("Megadata.csv", header=T, sep=";", dec=".", fill=T, skip=3)

# Defining type of variable
Mega$Id <- as.numeric(Mega$Id)
Mega$Date <- as.Date(Mega$Date, "%d/%m/%Y")
Mega$Strip <- as.factor(Mega$Strip)
Mega$Plot <- as.factor(Mega$Plot)
Mega$Disturbance <- as.factor(Mega$Disturbance)
Mega$Direction <- as.character(Mega$Direction)
Mega$Column <- as.factor(Mega$Column)
Mega$Treatment <- as.factor(Mega$Treatment)
Mega$Treatment.num <- as.factor(Mega$Treatment.num)
Mega$FieldX <- as.numeric(Mega$FieldX)
Mega$FieldY <- as.numeric(Mega$FieldY)
Mega$RD_X <- as.factor(Mega$RD_X)
Mega$RD_Y <- as.factor(Mega$RD_Y)
Mega$ID2 <- as.factor(Mega$ID2)
Mega$Quadrant <- as.numeric(Mega$Quadrant)
Mega$Edge <- as.factor(Mega$Edge)
Mega$Days <- as.numeric(Mega$Days)
Mega$NEs <- as.numeric(Mega$NEs)
Mega$IntNEs <- as.numeric(Mega$IntNEs)
Mega$Carabidae <- as.numeric(Mega$Carabidae)
Mega$Staphylinidae <- as.numeric(Mega$Staphylinidae)
Mega$Araneae <- as.numeric(Mega$Araneae)
Mega$Larvae <- as.numeric(Mega$Larvae)
Mega$Coccinelidae <- as.numeric(Mega$Coccinelidae)
Mega$Chilopoda <- as.numeric(Mega$Chilopoda)
Mega$Hymenoptera <- as.numeric(Mega$Hymenoptera)
Mega$TotalNEs <- as.numeric(Mega$TotalNEs)
Mega$TotalIntNEs <- as.numeric(Mega$TotalIntNEs)
Mega$TotalCar <- as.numeric(Mega$TotalCar)
Mega$TotalSta <- as.numeric(Mega$TotalSta)
Mega$TotalAra <- as.numeric(Mega$TotalAra)
Mega$TotalLar <- as.numeric(Mega$TotalLar)
Mega$TotalCoc <- as.numeric(Mega$TotalCoc)
Mega$TotalChi <- as.numeric(Mega$TotalChi)

```

```

Mega$pH <- as.numeric(Mega$pH)
Mega$pH_log <- as.numeric(Mega$pH_log)
Mega$OM_x <- as.numeric(Mega$OM_x)
Mega$Ntot <- as.numeric(Mega$Ntot)
Mega$pH_fit_KCl <- as.numeric(Mega$pH_fit_KCl)
Mega$pH_fit_KCl_log <- as.numeric(Mega$pH_fit_KCl_log)
Mega$nw_correct <- as.numeric(Mega$nw_correct)
Mega$g_m2 <- as.numeric(Mega$g_m2)
Mega$Tun <- as.numeric(Mega$Tun)
Mega$Tvai <- as.numeric(Mega$Tvai)
Mega$Humidity <- as.numeric(Mega$Humidity)
Mega$RD <- as.numeric(Mega$RD)
Mega$TundG <- as.numeric(Mega$TundG)

# Dividing samples by the trap length (NE/m)
## Take variables to be divided and divide them:
myvars <- c("NEs", "IntNEs", "Carabidae", "Staphylinidae", "Araneae", "Larvae",
            "TotalNEs", "TotalIntNEs", "TotalCar",
            "TotalSta", "TotalAra", "TotalLar",
            "TotalCoc", "TotalChi", "TotalHym")
MegaNEs <- Mega[myvars]
MegaNEs<-sweep(MegaNEs, MARGIN=2, STATS= 1.5, FUN="/")
## Merge divided variables with original dataset:
Mega <- cbind(Mega,MegaNEs)
## Eliminate old non-divided variables:
Mega <- Mega[c(-22:-37)]

# Subsetting for inter-strip (n/s sides of trap) movement
MegaS.s <- subset(Mega,Direction == "s" & Edge == "inter" & Solution ==
"normal")
MegaS.s <- na.omit(MegaS.s)

MegaS.n <- subset(Mega,Direction == "n" & Edge == "inter" & Solution ==
"normal")
MegaS.n <- na.omit(MegaS.n)

# Subsetting for inter-plot (w/e sides of trap) movement
MegaB.w <- subset(Mega,Direction == "w" & Edge == "buffer")
MegaB.w <- MegaB.w[c(-9:-16)]
MegaB.w <- na.omit(MegaB.w)

MegaB.e <- subset(Mega,Direction == "e" & Edge == "buffer")
MegaB.e <- MegaB.e[c(-9:-16)]
MegaB.e <- na.omit(MegaB.e)

#-----
## Factors to work with:
### NEs/day: IntNEs, Carabidae, Staphylinidae, Araneae, Larvae
###
### Soil variables: Strip, Plot, pH, pH_log, OM_x, Ntot, pH_fit_KCl,
###                pH_fit_KCl_log, nw_correct, g_m2

```

```

###
### Atmospheric variables: Tun (temperature, °C), Humidity (%),
###                               RD (rain, mm)
###
### Soil variables: pH_log ([H+]), OM_x (SOM, %)
#-----

## Defining settings for different collinearity panel types (panel.cor,
panel.smooth and panel.hist):
# Settings for panel.panel.cor (correlation)
panel.cor <- function(x, y, digits=2, prefix="", cex.cor)
{
  usr <- par("usr"); on.exit(par(usr))
  par(usr = c(0, 1, 0, 1))
  r = (cor(x, y))
  txt <- format(c(r, 0.123456789), digits=digits)[1]
  txt <- paste(prefix, txt, sep="")
  if(missing(cex.cor)) cex <- 0.7/strwidth(txt)
  text(0.5, 0.5, txt,cex = cex)
}
# To have proportional correlation numbers then (cex = cex * abs(r))

# Settings for panel.smooth
panel.smooth<-function (x, y, col = "black", bg = NA, pch = 18,
                        cex = 0.8, col.smooth = "red", span = 2/3, iter = 3,
...)
{
  points(x, y, pch = pch, col = col, bg = bg, cex = cex)
  ok <- is.finite(x) & is.finite(y)
  if (any(ok))
    lines(stats::lowess(x[ok], y[ok], f = span, iter = iter),
          col = col.smooth, ...)
}

# Settings for panel.hist
panel.hist <- function(x, ...)
{
  usr <- par("usr"); on.exit(par(usr))
  par(usr = c(usr[1:2], 0, 1.5) )
  h <- hist(x, plot = FALSE)
  breaks <- h$breaks; nB <- length(breaks)
  y <- h$counts; y <- y/max(y)
  rect(breaks[-nB], 0, breaks[-1], y, col="cyan2", ...)
}

#-----

### Collinearity inter-strip (S), s/n
# Carabidae S.s
Coll <- cbind(MegaS.s$Date,MegaS.s$Strip,MegaS.s$Plot,
              MegaS.s$pH_log,MegaS.s$OM_x,

```

```

MegaS.s$Disturbance,
MegaS.s$Tun,MegaS.s$Humidity,
MegaS.s$RD,MegaS.s$Carabidae)
colnames(Coll) <- c("Date","Strip", "Plot", "[H+]", "SOM","Disturbance",
"Temperature", "Humidity", "Rain", "Carabidae")

# Running collinearity + automatically saving the scatterplot
png(file = 'Directory\\Name.png', width = 800, height = 600,res=100)
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,font.labels = 2,gap = 0.5, main="Carabidae S.s")
dev.off()
graphics.off()

# Carabidae S.n
Coll <-
cbind(MegaS.n$Date,MegaS.n$Strip,MegaS.n$Plot,MegaS.n$pH_log,MegaS.n$OM_x,
MegaS.n$Disturbance,
MegaS.n$pH_,MegaS.n$Tun,MegaS.n$Humidity,
MegaS.n$RD,MegaS.n$Carabidae)
colnames(Coll) <- c("Date","Strip", "Plot", "[H+]", "SOM","Disturbance",
"Temperature", "Humidity", "Rain", "Carabidae")

# Running collinearity + automatically saving the scatterplot
png(file = 'Directory\\Name.png', width = 800, height = 600,res=100)
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,font.labels = 2,gap = 0.5, main="Carabidae S.n")
dev.off()
graphics.off()

# Araneae S.s
Coll <-
cbind(MegaS.s$Date,MegaS.s$Strip,MegaS.s$Plot,MegaS.s$pH_log,MegaS.s$OM_x,
MegaS.s$Disturbance,
MegaS.s$pH_,MegaS.s$Tun,MegaS.s$Humidity,
MegaS.s$RD,MegaS.s$Araneae,MegaS.s$Carabidae)
colnames(Coll) <- c("Date","Strip", "Plot", "[H+]", "SOM","Disturbance",
"Temperature", "Humidity", "Rain", "Araneae", "Carabidae")

# Running collinearity + automatically saving the scatterplot
png(file = 'Directory\\Name.png', width = 800, height = 600,res=100)
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,font.labels = 2,gap = 0.5, main="Carabidae S.n")
dev.off()
graphics.off()

# Araneae S.n
Coll <-
cbind(MegaS.n$Date,MegaS.n$Strip,MegaS.n$Plot,MegaS.n$pH_log,MegaS.n$OM_x,

```

```

MegaS.n$Disturbance,
MegaS.n$pH_,MegaS.n$Tun,MegaS.n$Humidity,
MegaS.n$RD,MegaS.n$Araneae,MegaS.n$Carabidae)
colnames(Coll) <- c("Date","Strip", "Plot", "[H+]", "SOM","Disturbance",
"Temperature", "Humidity", "Rain", "Araneae", "Carabidae")

# Running collinearity + automatically saving the scatterplot
png(file = 'Directory\\Name.png', width = 800, height = 600,res=100)
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,font.labels = 2,gap = 0.5, main="Carabidae S.n")
dev.off()
graphics.off()

# Staphylinidae S.s
Coll <-
cbind(MegaS.s$Date,MegaS.s$Strip,MegaS.s$Plot,MegaS.s$pH_log,MegaS.s$OM_x,
MegaS.s$Disturbance,
MegaS.s$pH_,MegaS.s$Tun,MegaS.s$Humidity,
MegaS.s$RD,MegaS.s$Staphylinidae,MegaS.s$Carabidae)
colnames(Coll) <- c("Date","Strip", "Plot", "[H+]", "SOM","Disturbance",
"Temperature", "Humidity", "Rain", "Staphylinidae",
"Carabidae")

# Running collinearity + automatically saving the scatterplot
png(file = 'Directory\\Name.png', width = 800, height = 600,res=100)
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,font.labels = 2,gap = 0.5, main="Carabidae S.n")
dev.off()
graphics.off()

# Staphylinidae S.n
Coll <-
cbind(MegaS.n$Date,MegaS.n$Strip,MegaS.n$Plot,MegaS.n$pH_log,MegaS.n$OM_x,
MegaS.n$Disturbance,
MegaS.n$pH_,MegaS.n$Tun,MegaS.n$Humidity,
MegaS.n$RD,MegaS.n$Staphylinidae,MegaS.n$Carabidae)
colnames(Coll) <- c("Date","Strip", "Plot", "[H+]", "SOM","Disturbance",
"Temperature", "Humidity", "Rain", "Staphylinidae",
"Carabidae")

# Running collinearity + automatically saving the scatterplot
png(file = 'Directory\\Name.png', width = 800, height = 600,res=100)
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,font.labels = 2,gap = 0.5, main="Carabidae S.n")
dev.off()
graphics.off()

```

```

# Larvae S.s
Coll
cbind(MegaS.s$Date,MegaS.s$Strip,MegaS.s$Plot,MegaS.s$pH_log,MegaS.s$OM_x,
      MegaS.s$Disturbance,
      MegaS.s$pH_,MegaS.s$Tun,MegaS.s$Humidity,
      MegaS.s$RD,MegaS.s$Larvae,MegaS.s$Carabidae)
colnames(Coll) <- c("Date","Strip", "Plot", "[H+]", "SOM","Disturbance",
                  "Temperature", "Humidity", "Rain", "Larvae", "Carabidae")

# Running collinearity + automatically saving the scatterplot
png(file = 'Directory\\Name.png', width = 800, height = 600,res=100)
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,font.labels = 2,gap = 0.5, main="Carabidae S.n")
dev.off()
graphics.off()

# Larvae S.n
Coll
cbind(MegaS.n$Date,MegaS.n$Strip,MegaS.n$Plot,MegaS.n$pH_log,MegaS.n$OM_x,
      MegaS.n$Disturbance,
      MegaS.n$pH_,MegaS.n$Tun,MegaS.n$Humidity,
      MegaS.n$RD,MegaS.n$Larvae,MegaS.n$Carabidae)
colnames(Coll) <- c("Date","Strip", "Plot", "[H+]", "SOM","Disturbance",
                  "Temperature", "Humidity", "Rain", "Larvae", "Carabidae")

# Running collinearity + automatically saving the scatterplot
png(file = 'Directory\\Name.png', width = 800, height = 600,res=100)
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,font.labels = 2,gap = 0.5, main="Carabidae S.n")
dev.off()
graphics.off()

#-----
# ### Collinearity inter-plot aka inter-Buffer (B), e/w
# Carabidae B.w
Coll <- cbind(MegaB.w$Date,MegaB.w$Strip,MegaB.w$pH_log,MegaB.w$OM_x,
              MegaB.w$Disturbance,MegaB.w$Treatment.num,
              MegaB.w$Tun,MegaB.w$Humidity,
              MegaB.w$RD,MegaB.w$Carabidae)
colnames(Coll) <- c("Date","Strip","[H+]", "SOM","Disturbance","Treatment",
                  "Temperature", "Humidity", "Rain", "Carabidae")

# Running collinearity + automatically saving the scatterplot
png(file = 'Directory\\Name.png', width = 800, height = 600,res=100)
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,font.labels = 2,gap = 0.5, main="Carabidae S.n")
dev.off()
graphics.off()

```

```

# Carabidae B.e
Coll <- cbind(MegaB.e$Date,MegaB.e$Strip,MegaB.e$pH_log,MegaB.e$OM_x,
              MegaB.e$Disturbance,MegaB.e$Treatment.num,
              MegaB.e$Tun,MegaB.e$Humidity,
              MegaB.e$RD,MegaB.e$Carabidae)
colnames(Coll) <- c("Date","Strip","[H+]", "SOM","Disturbance","Treatment",
                  "Temperature", "Humidity", "Rain", "Carabidae")

# Running collinearity + automatically saving the scatterplot
png(file = 'Directory\\Name.png', width = 800, height = 600,res=100)
pairs(Coll,    lower.panel=panel.smooth,    upper.panel=panel.cor,diag.panel    =
panel.hist,font.labels = 2,gap = 0.5, main="Carabidae S.n")
dev.off()
graphics.off()

# Araneae B.w
Coll <- cbind(MegaB.w$Date,MegaB.w$Strip,MegaB.w$pH_log,MegaB.w$OM_x,
              MegaB.w$Disturbance,MegaB.w$Treatment.num,
              MegaB.w$Tun,MegaB.w$Humidity,
              MegaB.w$RD,MegaB.w$Araneae,MegaB.w$Carabidae)
colnames(Coll) <- c("Date","Strip","[H+]", "SOM","Disturbance","Treatment",
                  "Temperature", "Humidity", "Rain","Araneae","Carabidae")
pairs(Coll,    lower.panel=panel.smooth,    upper.panel=panel.cor,diag.panel    =
panel.hist,
      font.labels = 2,gap = 0.5, main="Araneae B.w")
# Code for automatically saving the scatterplot erased for simplicity

# Araneae B.e
Coll <- cbind(MegaB.e$Date,MegaB.e$Strip,MegaB.e$pH_log,MegaB.e$OM_x,
              MegaB.e$Disturbance,MegaB.e$Treatment.num,
              MegaB.e$Tun,MegaB.e$Humidity,
              MegaB.e$RD,MegaB.e$Araneae,MegaB.e$Carabidae)
colnames(Coll) <- c("Date","Strip","[H+]", "SOM","Disturbance","Treatment",
                  "Temperature", "Humidity", "Rain","Araneae","Carabidae")
pairs(Coll,    lower.panel=panel.smooth,    upper.panel=panel.cor,diag.panel    =
panel.hist,
      font.labels = 2,gap = 0.5, main="Araneae B.e")

# Staphylinidae B.w
Coll <- cbind(MegaB.w$Date,MegaB.w$Strip,MegaB.w$pH_log,MegaB.w$OM_x,
              MegaB.w$Disturbance,MegaB.w$Treatment.num,
              MegaB.w$Tun,MegaB.w$Humidity,
              MegaB.w$RD,MegaB.w$Staphylinidae,MegaB.w$Carabidae)
colnames(Coll) <- c("Date","Strip","[H+]", "SOM","Disturbance","Treatment",
                  "Temperature", "Humidity", "Rain","Staphylinidae","Carabidae")
pairs(Coll,    lower.panel=panel.smooth,    upper.panel=panel.cor,diag.panel    =
panel.hist,
      font.labels = 2,gap = 0.5, main="Staphylinidae B.w")

```

```

# Staphylinidae B.e
Coll <- cbind(MegaB.e$Date,MegaB.e$Strip,MegaB.e$pH_log,MegaB.e$OM_x,
              MegaB.e$Disturbance,MegaB.e$Treatment.num,
              MegaB.e$Tun,MegaB.e$Humidity,
              MegaB.e$RD,MegaB.e$Staphylinidae,MegaB.e$Carabidae)
colnames(Coll) <- c("Date","Strip","[H+]", "SOM","Disturbance","Treatment",
                   "Temperature", "Humidity",
                   "Rain","Staphylinidae","Carabidae")
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,
      font.labels = 2,gap = 0.5, main="Staphylinidae B.e")

# Larvae B.w
Coll <- cbind(MegaB.w$Date,MegaB.w$Strip,MegaB.w$pH_log,MegaB.w$OM_x,
              MegaB.w$Disturbance,MegaB.w$Treatment.num,
              MegaB.w$Tun,MegaB.w$Humidity,
              MegaB.w$RD,MegaB.w$Larvae,MegaB.w$Carabidae)
colnames(Coll) <- c("Date","Strip","[H+]", "SOM","Disturbance","Treatment",
                   "Temperature", "Humidity", "Rain","Larvae","Carabidae")
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,
      font.labels = 2,gap = 0.5, main="Larvae B.w")

# Larvae B.e
Coll <- cbind(MegaB.e$Date,MegaB.e$Strip,MegaB.e$pH_log,MegaB.e$OM_x,
              MegaB.e$Disturbance,MegaB.e$Treatment.num,
              MegaB.e$Tun,MegaB.e$Humidity,
              MegaB.e$RD,MegaB.e$Larvae,MegaB.e$Carabidae)
colnames(Coll) <- c("Date","Strip","[H+]", "SOM","Disturbance","Treatment",
                   "Temperature", "Humidity", "Rain","Larvae","Carabidae")
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,
      font.labels = 2,gap = 0.5, main="Larvae B.e")

#-----
# PLOT aka BUFFERS per STRIP
# Resetting doomies
MegaB.w <- subset(Mega,Direction=="w" & Edge=="buffer")
MegaB.w <- MegaB.w[c(-9:-16)]
MegaB.w <- na.omit(MegaB.w)

MegaB.e <- subset(Mega,Direction=="e" & Edge=="buffer")
MegaB.e <- MegaB.e[c(-9:-16)]
MegaB.e <- na.omit(MegaB.e)

# Specifying strip (2, 3 or 4):
MegaB.w <- MegaB.w[which(MegaB.w$Strip==4),]
MegaB.e <- MegaB.e[which(MegaB.e$Strip==4),]

# Carabidae B.w1

```

```

# Remove "Disturbance" variable for strips 3 and 4 because it is absent
Coll <- cbind(MegaB.w$Date,
              MegaB.w$Treatment.num,
              MegaB.w$Tun,
              MegaB.w$Humidity,
              MegaB.w$RD,
              MegaB.w$Carabidae)
colnames(Coll) <- c("Date", "Treatment",
                  "Temperature", "Humidity", "Rain", "Carabidae")
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor, diag.panel =
panel.hist, font.labels = 2, gap = 0.5, main="Carabidae B.w")

# Carabidae B.e
Coll <- cbind(MegaB.e$Date, MegaB.e$Strip, MegaB.e$pH_log, MegaB.e$OM_x,
              MegaB.e$Treatment.num,
              MegaB.e$Tun, MegaB.e$Humidity,
              MegaB.e$RD, MegaB.e$Carabidae)
colnames(Coll) <- c("Date", "Strip", "[H+]", "SOM", "Treatment",
                  "Temperature", "Humidity", "Rain", "Carabidae")
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor, diag.panel =
panel.hist, font.labels = 2, gap = 0.5, main="Carabidae B.e")

# Araneae B.w
Coll <- cbind(MegaB.w$Date, MegaB.w$Strip, MegaB.w$pH_log, MegaB.w$OM_x,
              MegaB.w$Treatment.num,
              MegaB.w$Tun, MegaB.w$Humidity,
              MegaB.w$RD, MegaB.w$Araneae, MegaB.w$Carabidae)
colnames(Coll) <- c("Date", "Strip", "[H+]", "SOM", "Treatment",
                  "Temperature", "Humidity", "Rain", "Araneae", "Carabidae")
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor, diag.panel =
panel.hist,
      font.labels = 2, gap = 0.5, main="Araneae B.w")

# Araneae B.e
Coll <- cbind(MegaB.e$Date, MegaB.e$Strip, MegaB.e$pH_log, MegaB.e$OM_x,
              MegaB.e$Treatment.num,
              MegaB.e$Tun, MegaB.e$Humidity,
              MegaB.e$RD, MegaB.e$Araneae, MegaB.e$Carabidae)
colnames(Coll) <- c("Date", "Strip", "[H+]", "SOM", "Treatment",
                  "Temperature", "Humidity", "Rain", "Araneae", "Carabidae")
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor, diag.panel =
panel.hist,
      font.labels = 2, gap = 0.5, main="Araneae B.e")

# Staphylinidae B.w
Coll <- cbind(MegaB.w$Date, MegaB.w$Strip, MegaB.w$pH_log, MegaB.w$OM_x,
              MegaB.w$Treatment.num,
              MegaB.w$Tun, MegaB.w$Humidity,
              MegaB.w$RD, MegaB.w$Staphylinidae, MegaB.w$Carabidae)

```

```

colnames(Coll) <- c("Date","Strip","[H+]", "SOM","Treatment",
                  "Temperature", "Humidity",
                  "Rain","Staphylinidae","Carabidae")
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,
      font.labels = 2,gap = 0.5, main="Staphylinidae B.w")

# Staphylinidae B.e
Coll <- cbind(MegaB.e$Date,MegaB.e$Strip,MegaB.e$pH_log,MegaB.e$OM_x,
              MegaB.e$Treatment.num,
              MegaB.e$Tun,MegaB.e$Humidity,
              MegaB.e$RD,MegaB.e$Staphylinidae,MegaB.e$Carabidae)
colnames(Coll) <- c("Date","Strip","[H+]", "SOM","Treatment",
                  "Temperature", "Humidity",
                  "Rain","Staphylinidae","Carabidae")
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,
      font.labels = 2,gap = 0.5, main="Staphylinidae B.e")

# Larvae B.w
Coll <- cbind(MegaB.w$Date,MegaB.w$Strip,MegaB.w$pH_log,MegaB.w$OM_x,
              MegaB.w$Treatment.num,
              MegaB.w$Tun,MegaB.w$Humidity,
              MegaB.w$RD,MegaB.w$Larvae,MegaB.w$Carabidae)
colnames(Coll) <- c("Date","Strip","[H+]", "SOM","Treatment",
                  "Temperature", "Humidity", "Rain","Larvae","Carabidae")
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,
      font.labels = 2,gap = 0.5, main="Larvae B.w")

# Larvae B.e
Coll <- cbind(MegaB.e$Date,MegaB.e$Strip,MegaB.e$pH_log,MegaB.e$OM_x,
              MegaB.e$Treatment.num,
              MegaB.e$Tun,MegaB.e$Humidity,
              MegaB.e$RD,MegaB.e$Larvae,MegaB.e$Carabidae)
colnames(Coll) <- c("Date","Strip","[H+]", "SOM","Treatment",
                  "Temperature", "Humidity", "Rain","Larvae","Carabidae")
pairs(Coll, lower.panel=panel.smooth, upper.panel=panel.cor,diag.panel =
panel.hist,
      font.labels = 2,gap = 0.5, main="Larvae B.e")

#-----

#Collinearity among NEs
# NEs S.s
Coll <- cbind(MegaS.s$Carabidae,MegaS.s$Araneae,MegaS.s$Staphylinidae,
              MegaS.s$Larvae)
colnames(Coll) <- c("Carabidae", "Araneae","Staphylinidae", "Larvae")

# Running collinearity + automatically saving the scatterplot
png(file = 'Directory\\Name.png', width = 800, height = 600,res=100)

```

```

pairs(Coll,    lower.panel=panel.smooth,    upper.panel=panel.cor,diag.panel    =
panel.hist,font.labels = 2,gap = 0.5, main="NE-NE S.s")
dev.off()
graphics.off()

# NEs S.n
Coll <- cbind(MegaS.n$Carabidae,MegaS.n$Araneae,MegaS.n$Staphylinidae,
              MegaS.n$Larvae)
colnames(Coll) <- c("Carabidae", "Araneae","Staphylinidae", "Larvae")

# Running collinearity + automatically saving the scatterplot
png(file = 'Directory\\Name.png', width = 800, height = 600,res=100)
pairs(Coll,    lower.panel=panel.smooth,    upper.panel=panel.cor,diag.panel    =
panel.hist,font.labels = 2,gap = 0.5, main="NE-NE S.s")
dev.off()
graphics.off()

# NEs B.w
Coll <- cbind(MegaB.w$Carabidae,MegaB.w$Araneae,MegaB.w$Staphylinidae,
              MegaB.w$Larvae)
colnames(Coll) <- c("Carabidae", "Araneae","Staphylinidae", "Larvae")
pairs(Coll,    lower.panel=panel.smooth,    upper.panel=panel.cor,diag.panel    =
panel.hist,
      font.labels = 2,gap = 0.5, main="NE-NE B.w")

Coll <- cbind(MegaB.e$Carabidae,MegaB.e$Araneae,MegaB.e$Staphylinidae,
              MegaB.e$Larvae)
colnames(Coll) <- c("Carabidae", "Araneae","Staphylinidae", "Larvae")
pairs(Coll,    lower.panel=panel.smooth,    upper.panel=panel.cor,diag.panel    =
panel.hist,
      font.labels = 2,gap = 0.5, main="NE-NE B.e")

###-----END-----

```

GLMs Inter-plot

```
# -----  
# Script for Generalized Linear Models (GLMs) (GLM.1, GLM.2 &  
# GLM.3) of NEs between PLOTS  
# Vladimir Shlevkov 22/03/16  
# vladimir.shlevkovpronskiy@wur.nl  
# -----  
  
# change to the new directory  
setwd("Directory")  
  
# clean up workspace  
rm(list=ls())  
graphics.off()  
gc(FALSE)  
cat("\014")  
  
# load the necessary libraries  
# install.packages(c("stats", "MASS", "MuMIn"), dependencies=F) -> Installed  
library(stats)  
library(MASS)      # glm.bn model  
library(MuMIn)     # for Multi Model Inference, dredge#  
library(norm)  
  
# load the dataset  
Mega <- read.csv("Megadata.csv", header=T, sep=";", dec=".", fill=T, skip=3)  
  
# get a table with the variables names  
objects(Mega)  
  
# GLM formula (simple):  
# glm.nb(formula, family=familytype(link=linkfunction), data=dataframe)  
  
# GLM formula (extended):  
# glm.nb(formula, family = poisson, data, weights, subset,  
#       na.action, start = NULL, etastart, mustart, offset,  
#       control = list(...), model = TRUE, method = "glm.fit",  
#       x = FALSE, y = TRUE, contrasts = NULL, ...)  
  
# Defining type of variable  
Mega$Id <- as.numeric(Mega$Id)  
Mega$Date <- as.Date(Mega$Date, "%d/%m/%Y")  
Mega$Strip <- as.factor(Mega$Strip)  
Mega$Plot <- as.factor(Mega$Plot)  
Mega$Disturbance <- as.factor(Mega$Disturbance)  
Mega$Direction <- as.factor(Mega$Direction)
```

```

Mega$Direction.num <- as.numeric(Mega$Direction.num)
Mega$Column <- as.factor(Mega$Column)
Mega$FieldX <- as.numeric(Mega$FieldX)
Mega$FieldY <- as.numeric(Mega$FieldY)
Mega$RD_X <- as.factor(Mega$RD_X)
Mega$RD_Y <- as.factor(Mega$RD_Y)
Mega$ID2 <- as.factor(Mega$ID2)
Mega$Quadrant <- as.numeric(Mega$Quadrant)
Mega$Edge <- as.factor(Mega$Edge)
Mega$Days <- as.numeric(Mega$Days)
Mega$NEs <- as.numeric(Mega$NEs)
Mega$IntNEs <- as.numeric(Mega$IntNEs)
Mega$Carabidae <- as.numeric(Mega$Carabidae)
Mega$Staphylinidae <- as.numeric(Mega$Staphylinidae)
Mega$Araneae <- as.numeric(Mega$Araneae)
Mega$Larvae <- as.numeric(Mega$Larvae)
Mega$Coccinelidae <- as.numeric(Mega$Coccinelidae)
Mega$Chilopoda <- as.numeric(Mega$Chilopoda)
Mega$Hymenoptera <- as.numeric(Mega$Hymenoptera)
Mega$TotalNEs <- as.numeric(Mega$TotalNEs)
Mega$TotalIntNEs <- as.numeric(Mega$TotalIntNEs)
Mega$TotalCar <- as.numeric(Mega$TotalCar)
Mega$TotalSta <- as.numeric(Mega$TotalSta)
Mega$TotalAra <- as.numeric(Mega$TotalAra)
Mega$TotalLar <- as.numeric(Mega$TotalLar)
Mega$TotalCoc <- as.numeric(Mega$TotalCoc)
Mega$TotalChi <- as.numeric(Mega$TotalChi)
Mega$pH <- as.numeric(Mega$pH)
Mega$pH_log <- as.numeric(Mega$pH_log)
Mega$OM_x <- as.numeric(Mega$OM_x)
Mega$Ntot <- as.numeric(Mega$Ntot)
Mega$pH_fit_KCl <- as.numeric(Mega$pH_fit_KCl)
Mega$pH_fit_KCl_log <- as.numeric(Mega$pH_fit_KCl_log)
Mega$nw_correct <- as.numeric(Mega$nw_correct)
Mega$g_m2 <- as.numeric(Mega$g_m2)
Mega$Tun <- as.numeric(Mega$Tun)
Mega$Tvai <- as.numeric(Mega$Tvai)
Mega$Humidity <- as.numeric(Mega$Humidity)
Mega$RD <- as.numeric(Mega$RD)
Mega$TundG <- as.numeric(Mega$TundG)

# Absolute values:
Mega$NEs <- abs(Mega$NEs)
Mega$IntNEs <- abs(Mega$IntNEs)
Mega$Carabidae <- abs(Mega$Carabidae)
Mega$Staphylinidae <- abs(Mega$Staphylinidae)
Mega$Araneae <- abs(Mega$Araneae)
Mega$Larvae <- abs(Mega$Larvae)
Mega$Coccinelidae <- abs(Mega$Coccinelidae)
Mega$Chilopoda <- abs(Mega$Chilopoda)

```

```

Mega$Hymenoptera <- abs(Mega$Hymenoptera)
Mega$TotalNEs <- abs(Mega$TotalNEs)
Mega$TotalIntNEs <- abs(Mega$TotalIntNEs)
Mega$TotalCar <- abs(Mega$TotalCar)
Mega$TotalSta <- abs(Mega$TotalSta)
Mega$TotalAra <- abs(Mega$TotalAra)
Mega$TotalLar <- abs(Mega$TotalLar)
Mega$TotalCoc <- abs(Mega$TotalCoc)
Mega$TotalChi <- abs(Mega$TotalChi)

# Removing outliers (NE Mega) by removing extreme percentiles
library(scales)
Mega$IntNEs<-squish(Mega$IntNEs,quantile(Mega$IntNEs, c(.01, .99), na.rm=T))
Mega$NEs<-squish(Mega$NEs,quantile(Mega$NEs, c(.01, .99), na.rm=T))
Mega$Carabidae<-squish(Mega$Carabidae,quantile(Mega$Carabidae, c(.01, .99),
na.rm=T))
Mega$Staphylinidae<-squish(Mega$Staphylinidae,quantile(Mega$Staphylinidae,
c(.01, .99), na.rm=T))
Mega$Araneae<-squish(Mega$Araneae,quantile(Mega$Araneae, c(.01, .99), na.rm=T))
Mega$Larvae<-squish(Mega$Larvae,quantile(Mega$Larvae, c(.01, .99), na.rm=T))
Mega$TotalNEs<-squish(Mega$TotalNEs,quantile(Mega$TotalNEs, c(.01, .99),
na.rm=T))
Mega$TotalIntNEs<-squish(Mega$TotalIntNEs,quantile(Mega$TotalIntNEs, c(.01,
.99), na.rm=T))
Mega$TotalCar<-squish(Mega$TotalCar,quantile(Mega$TotalCar, c(.01, .99),
na.rm=T))
Mega$TotalSta<-squish(Mega$TotalSta,quantile(Mega$TotalSta, c(.01, .99),
na.rm=T))
Mega$TotalAra<-squish(Mega$TotalAra,quantile(Mega$TotalAra, c(.01, .99),
na.rm=T))
Mega$TotalLar<-squish(Mega$TotalLar,quantile(Mega$TotalLar, c(.01, .99),
na.rm=T))

# Dividing by the trap length (NE/m)
## Take variables to be divided and divide them:
myvars <- c("NEs", "IntNEs","Carabidae", "Staphylinidae", "Araneae", "Larvae",
"TotalNEs","TotalIntNEs","TotalCar",
"TotalSta", "TotalAra", "TotalLar",
"TotalCoc","TotalChi","TotalHym")
MegaNEs <- Mega[myvars]
MegaNEs<-sweep(MegaNEs, MARGIN=2, STATS= 1.5, FUN="/")
## Merge divided variables with original dataset:
Mega <- cbind(Mega,MegaNEs)
## Eliminate old non-divided variables:
Mega <- Mega[c(-22:-38)]

# Subset data corresponding to Strips only
MegaBw <- Mega[which(Mega$Direction == "w"),]
MegaBe <- Mega[which(Mega$Direction == "e"),]
MegaB <- (rbind(MegaBw, MegaBe))

```

```

na.omit(MegaB)

# Selecting strip 2, 3 and 4 only for analysis
MegaB.4 <- MegaB[which(MegaB$Strip == 4),]
MegaB.3 <- MegaB[which(MegaB$Strip == 3),]
MegaB.2 <- MegaB[which(MegaB$Strip == 2),]

# GLM.1: Performing GLMs on the whole field (Plots only) with directionality
inside
#the formula (several combinations of variables tried, remains the one with
# lower AIC number):
glm1 <- glm.nb(Carabidae ~ Treatment+Direction.num+(Disturbance*Date), data =
MegaB, link = "log",na.action=na.omit)
summary(glm1)
# AIC: 889.26

glm1 <- glm.nb(Araneae ~ Treatment+Direction.num+(Disturbance*Date), data =
MegaB, link = "log",na.action=na.omit)
summary(glm1)

glm1 <- glm.nb(Staphylinidae ~ Treatment+Direction.num+(Disturbance*Date), data
= MegaB, link = "log",na.action=na.omit)
summary(glm1)

glm1 <- glm.nb(Larvae ~ Treatment+Direction.num+(Disturbance*Date), data =
MegaB, link = "log",na.action=na.omit)
summary(glm1)

# GLM.1 for strip X (type in "2", "3", or "4" in "X")
#("Disturbance" variable removed in strips 3 and 4 because absent):
glm1 <- glm.nb(Carabidae ~ Treatment+Direction.num*Date,
               data = MegaB.4, link = "log",na.action=na.omit)
summary(glm1)

glm1 <- glm.nb(Araneae ~ Treatment+Direction.num*Date,
               data = MegaB.4, link = "log",na.action=na.omit)
summary(glm1)

glm1 <- glm.nb(Staphylinidae ~ Treatment+Direction.num*Date,
               data = MegaB.4, link = "log",na.action=na.omit)
summary(glm1)

glm1 <- glm.nb(Larvae ~ Treatment+Direction.num*Date,
               data = MegaB.3, link = "log",na.action=na.omit)
summary(glm1)

# GLM.2: Performing GLMs on the whole field (strips only) with weather factors:

```

```

glm2 <- glm.nb(Carabidae ~ (Tun*RD*Humidity)/Date, data = MegaB, link =
"log",na.action=na.omit)
summary(glm2)

glm2 <- glm.nb(Araneae ~ (Tun*RD*Humidity)/Date, data = MegaB, link =
"log",na.action=na.omit)
summary(glm2)

glm2 <- glm.nb(Staphylinidae ~ (Tun*RD*Humidity)/Date, data = MegaB, link =
"log",na.action=na.omit)
summary(glm2)

glm2 <- glm.nb(Larvae ~ (Tun*RD*Humidity)/Date, data = MegaB, link =
"log",na.action=na.omit)
summary(glm2)

# GLM.3: Performing GLMs on the whole field (Plots only) with soil factors:
glm3 <- glm.nb(Carabidae ~ (pH_log+OM_x)*(Date*Disturbance), data = MegaB, link
= "log",na.action=na.omit)
summary(glm3)

glm3 <- glm.nb(Araneae ~ (pH_log+OM_x)*(Date*Disturbance), data = MegaB, link =
"log",na.action=na.omit)
summary(glm3)

glm3 <- glm.nb(Staphylinidae ~ (pH_log+OM_x)*(Date*Disturbance), data = MegaB,
link = "log",na.action=na.omit)
summary(glm3)

glm3 <- glm.nb(Larvae ~ (pH_log+OM_x)*(Date*Disturbance), data = MegaB, link =
"log",na.action=na.omit)
summary(glm3)

###-----END-----

```

GLMs Inter-strip

```
# -----
# Script for Generalized Linear Models (GLMs) (GLM.1, GLM.2 &
# GLM.3) of NES between STRIPS
# Model selection among GLMs left as example
# Vladimir Shlevkov 22/03/16
# vladimir.shlevkovpronskiy@wur.nl
# -----

# change to the new directory
setwd("Directory")

# clean up workspace
rm(list=ls())
graphics.off()
gc(FALSE)
cat("\014")

# load the necessary libraries
# install.packages(c("stats", "MASS", "MuMIn"), dependencies=F) -> Installed
library(stats)
library(MASS)      # glm.bm model
library(MuMIn)     # for Multi Model Inference, dredge#
library(norm)

# load the dataset
Mega <- read.csv("Megadata.csv", header=T, sep=";", dec=".", fill=T, skip=3)

# get a table the variables names
objects(Mega)

# GLM formula (simple):
# glm.nb(formula, family=familytype(link=linkfunction), data=dataframe)

# GLM formula (extended):
# glm.nb(formula, family = poisson, data, weights, subset,
#       na.action, start = NULL, etastart, mustart, offset,
#       control = list(...), model = TRUE, method = "glm.fit",
#       x = FALSE, y = TRUE, contrasts = NULL, ...)

# Abbreviated variables (general and specific ones - selected from
# observations):

# Defining type of variable
Mega$Id <- as.numeric(Mega$Id)
```

```

Mega$Date <- as.Date(Mega$Date,"%d/%m/%Y")
Mega$Strip <-as.factor(Mega$Strip)
Mega$Plot <- as.factor(Mega$Plot)
Mega$Disturbance <- as.factor(Mega$Disturbance)
Mega$Direction <- as.factor(Mega$Direction)
Mega$Direction.num <- as.numeric(Mega$Direction.num)
Mega$Column <- as.factor(Mega$Column)
Mega$FieldX <- as.numeric(Mega$FieldX)
Mega$FieldY <- as.numeric(Mega$FieldY)
Mega$RD_X <- as.factor(Mega$RD_X)
Mega$RD_Y <- as.factor(Mega$RD_Y)
Mega$ID2 <- as.factor(Mega$ID2)
Mega$Quadrant <- as.numeric(Mega$Quadrant)
Mega$Edge <- as.factor(Mega$Edge)
Mega$Days <- as.numeric(Mega$Days)
Mega$NEs <- as.numeric(Mega$NEs)
Mega$IntNEs <- as.numeric(Mega$IntNEs)
Mega$Carabidae <- as.numeric(Mega$Carabidae)
Mega$Staphylinidae <- as.numeric(Mega$Staphylinidae)
Mega$Araneae <- as.numeric(Mega$Araneae)
Mega$Larvae <- as.numeric(Mega$Larvae)
Mega$Coccinelidae <- as.numeric(Mega$Coccinelidae)
Mega$Chilopoda <- as.numeric(Mega$Chilopoda)
Mega$Hymenoptera <- as.numeric(Mega$Hymenoptera)
Mega$TotalNEs <- as.numeric(Mega$TotalNEs)
Mega$TotalIntNEs <- as.numeric(Mega$TotalIntNEs)
Mega$TotalCar <- as.numeric(Mega$TotalCar)
Mega$TotalSta <- as.numeric(Mega$TotalSta)
Mega$TotalAra <- as.numeric(Mega$TotalAra)
Mega$TotalLar <- as.numeric(Mega$TotalLar)
Mega$TotalCoc <- as.numeric(Mega$TotalCoc)
Mega$TotalChi <- as.numeric(Mega$TotalChi)
Mega$pH <- as.numeric(Mega$pH)
Mega$pH_log <- as.numeric(Mega$pH_log)
Mega$OM_x <- as.numeric(Mega$OM_x)
Mega$Ntot <- as.numeric(Mega$Ntot)
Mega$pH_fit_KCl <- as.numeric(Mega$pH_fit_KCl)
Mega$pH_fit_KCl_log <- as.numeric(Mega$pH_fit_KCl_log)
Mega$nw_correct <- as.numeric(Mega$nw_correct)
Mega$g_m2 <- as.numeric(Mega$g_m2)
Mega$Tun <- as.numeric(Mega$Tun)
Mega$Tvai <- as.numeric(Mega$Tvai)
Mega$Humidity <- as.numeric(Mega$Humidity)
Mega$RD <- as.numeric(Mega$RD)
Mega$TundG <- as.numeric(Mega$TundG)

# Absolute values:
Mega$NEs <- abs(Mega$NEs)
Mega$IntNEs <- abs(Mega$IntNEs)
Mega$Carabidae <- abs(Mega$Carabidae)
Mega$Staphylinidae <- abs(Mega$Staphylinidae)

```

```

Mega$Araneae <- abs(Mega$Araneae)
Mega$Larvae <- abs(Mega$Larvae)
Mega$Coccinelidae <- abs(Mega$Coccinelidae)
Mega$Chilopoda <- abs(Mega$Chilopoda)
Mega$Hymenoptera <- abs(Mega$Hymenoptera)
Mega$TotalNEs <- abs(Mega$TotalNEs)
Mega$TotalIntNEs <- abs(Mega$TotalIntNEs)
Mega$TotalCar <- abs(Mega$TotalCar)
Mega$TotalSta <- abs(Mega$TotalSta)
Mega$TotalAra <- abs(Mega$TotalAra)
Mega$TotalLar <- abs(Mega$TotalLar)
Mega$TotalCoc <- abs(Mega$TotalCoc)
Mega$TotalChi <- abs(Mega$TotalChi)

# Removing outliers (NE Mega) by removing extreme percentiles
library(scales)
Mega$IntNEs<-squish(Mega$IntNEs,quantile(Mega$IntNEs, c(.01, .99), na.rm=T))
Mega$NEs<-squish(Mega$NEs,quantile(Mega$NEs, c(.01, .99), na.rm=T))
Mega$Carabidae<-squish(Mega$Carabidae,quantile(Mega$Carabidae, c(.01, .99),
na.rm=T))
Mega$Staphylinidae<-squish(Mega$Staphylinidae,quantile(Mega$Staphylinidae,
c(.01, .99), na.rm=T))
Mega$Araneae<-squish(Mega$Araneae,quantile(Mega$Araneae, c(.01, .99), na.rm=T))
Mega$Larvae<-squish(Mega$Larvae,quantile(Mega$Larvae, c(.01, .99), na.rm=T))
Mega$TotalNEs<-squish(Mega$TotalNEs,quantile(Mega$TotalNEs, c(.01, .99),
na.rm=T))
Mega$TotalIntNEs<-squish(Mega$TotalIntNEs,quantile(Mega$TotalIntNEs, c(.01,
.99), na.rm=T))
Mega$TotalCar<-squish(Mega$TotalCar,quantile(Mega$TotalCar, c(.01, .99),
na.rm=T))
Mega$TotalSta<-squish(Mega$TotalSta,quantile(Mega$TotalSta, c(.01, .99),
na.rm=T))
Mega$TotalAra<-squish(Mega$TotalAra,quantile(Mega$TotalAra, c(.01, .99),
na.rm=T))
Mega$TotalLar<-squish(Mega$TotalLar,quantile(Mega$TotalLar, c(.01, .99),
na.rm=T))
Mega$D

# Dividing by the trap length (NE/m)
## Take variables to be divided and divide them:
myvars <- c("NEs", "IntNEs","Carabidae", "Staphylinidae", "Araneae", "Larvae",
"TotalNEs","TotalIntNEs","TotalCar",
"TotalSta", "TotalAra", "TotalLar",
"TotalCoc","TotalChi","TotalHym")
MegaNEs <- Mega[myvars]
MegaNEs<-sweep(MegaNEs, MARGIN=2, STATS= 1.5, FUN="/")
## Merge divided variables with original dataset:
Mega <- cbind(Mega,MegaNEs)
## Eliminate old non-divided variables:
Mega <- Mega[c(-20:-37)]

```

```

# Subset data corresponding to Strips only
MegaSn <- Mega[which(Mega$Direction == "n"),]
MegaSs <- Mega[which(Mega$Direction == "s"),]
MegaS <- (rbind(MegaSn, MegaSs))
na.omit(MegaS)

# Summing up NE at each side of the trap to quickly compare migration
# (example with Carabidae):
MegaSn.7 <- MegaSn[which(MegaSn$Strip == 7),]
MegaSs.7 <- MegaSs[which(MegaSs$Strip == 7),]
MegaSn.7[is.na(MegaSn.7)] <- 0
MegaSs.7[is.na(MegaSs.7)] <- 0
mean(MegaSn.7$Carabidae)
mean(MegaSs.7$Carabidae)

MegaSn.6 <- MegaSn[which(MegaSn$Strip == 6),]
MegaSs.6 <- MegaSs[which(MegaSs$Strip == 6),]
MegaSn.6[is.na(MegaSn.6)] <- 0
MegaSs.6[is.na(MegaSs.6)] <- 0
mean(MegaSn.6$Carabidae)
mean(MegaSs.6$Carabidae)

MegaSn.5 <- MegaSn[which(MegaSn$Strip == 5),]
MegaSs.5 <- MegaSs[which(MegaSs$Strip == 5),]
MegaSn.5[is.na(MegaSn.5)] <- 0
MegaSs.5[is.na(MegaSs.5)] <- 0
mean(MegaSn.5$Carabidae)
mean(MegaSs.5$Carabidae)

MegaSn.4 <- MegaSn[which(MegaSn$Strip == 4),]
MegaSs.4 <- MegaSs[which(MegaSs$Strip == 4),]
MegaSn.4[is.na(MegaSn.4)] <- 0
MegaSs.4[is.na(MegaSs.4)] <- 0
mean(MegaSn.4$Carabidae)
mean(MegaSs.4$Carabidae)

MegaSn.3 <- MegaSn[which(MegaSn$Strip == 3),]
MegaSs.3 <- MegaSs[which(MegaSs$Strip == 3),]
MegaSn.3[is.na(MegaSn.3)] <- 0
MegaSs.3[is.na(MegaSs.3)] <- 0
mean(MegaSn.3$Carabidae)
mean(MegaSs.3$Carabidae)

MegaSn.2 <- MegaSn[which(MegaSn$Strip == 2),]
MegaSs.2 <- MegaSs[which(MegaSs$Strip == 2),]
MegaSn.2[is.na(MegaSn.2)] <- 0
MegaSs.2[is.na(MegaSs.2)] <- 0
mean(MegaSn.2$Carabidae)
mean(MegaSs.2$Carabidae)

MegaSn.1 <- MegaSn[which(MegaSn$Strip == 1),]

```

```

MegaSs.1 <- MegaSs[which(MegaSs$Strip == 1),]
MegaSn.1[is.na(MegaSn.1)] <- 0
MegaSs.1[is.na(MegaSs.1)] <- 0
mean(MegaSn.1$Carabidae)
mean(MegaSs.1$Carabidae)

# Subsetting data for each strip
MegaS1 <- MegaS[which (MegaS$Strip == 1),]
MegaS2 <- MegaS[which (MegaS$Strip == 2),]
MegaS3 <- MegaS[which (MegaS$Strip == 3),]
MegaS4 <- MegaS[which (MegaS$Strip == 4),]
MegaS5 <- MegaS[which (MegaS$Strip == 5),]
MegaS6 <- MegaS[which (MegaS$Strip == 6),]
MegaS7 <- MegaS[which (MegaS$Strip == 7),]

# GLM.1: Performing GLMs on the whole field (strips only) with directionality
inside
#the formula (several combinations of variables tried, remains the one with
# lower AIC number):
glm1 <- glm.nb(Carabidae ~ Strip+Direction.num+(Disturbance*Date), data =
MegaS, link = "log",na.action=na.omit)
summary(glm1)

glm1 <- glm.nb(Araneae ~ Strip+Direction.num+(Disturbance*Date), data = MegaS,
link = "log",na.action=na.omit)
summary(glm1)

glm1 <- glm.nb(Staphylinidae ~ Strip+Direction.num+(Disturbance*Date), data =
MegaS, link = "log",na.action=na.omit)
summary(glm1)

glm1 <- glm.nb(Larvae ~ Strip+Direction.num+(Disturbance*Date), data = MegaS,
link = "log",na.action=na.omit)
summary(glm1)

# Performing GLMs per strip:
# (Variable "Disturbance" excluded from analyses of strips 3, 4 and 7 due to
absence of soil disturbance
# in those strips)
glm1 <- glm.nb(Carabidae ~ Disturbance*Date+Direction.num, data = MegaS1, link
= "log",na.action=na.omit)
summary(glm1)
glm1 <- glm.nb(Carabidae ~ Disturbance*Date+Direction.num, data = MegaS2,link =
"log", na.action=na.omit)
summary(glm1)
glm1 <- glm.nb(Carabidae ~ Date+Direction.num, data = MegaS3, link =
"log",na.action=na.omit)
summary(glm1)

```

```

glm1 <- glm.nb(Carabidae ~ Date+Direction.num, data = MegaS4, link =
"log",na.action=na.omit)
summary(glm1)
glm1 <- glm.nb(Carabidae ~ Disturbance*Date+Direction.num, data = MegaS5, link
= "log",na.action=na.omit)
summary(glm1)
glm1 <- glm.nb(Carabidae ~ Disturbance*Date+Direction.num, data = MegaS6, link
= "log",na.action=na.omit)
summary(glm1)
glm1 <- glm.nb(Carabidae ~ Date+Direction.num, data = MegaS7, link =
"log",na.action=na.omit)
summary(glm1)

# GLM.2: Performing GLMs on the whole field (strips only) with weather factors
# (model selection through AIC left as example):
glm2 <- glm.nb(Carabidae ~ Tun*RD*Humidity, data = MegaS, link =
"log",na.action=na.omit)
summary(glm2)
# AIC: 877.94

glm2 <- glm.nb(Carabidae ~ Tun+RD+Humidity, data = MegaS, link =
"log",na.action=na.omit)
summary(glm2)
# AIC: 890.53

glm2 <- glm.nb(Carabidae ~ Date*(Tun+RD+Humidity), data = MegaS, link =
"log",na.action=na.omit)
summary(glm2)
# AIC: 877.94

glm2 <- glm.nb(Carabidae ~ Date*(Tun*RD*Humidity), data = MegaS, link =
"log",na.action=na.omit)
summary(glm2)
# AIC: 877.94

glm2 <- glm.nb(Carabidae ~ Date/(Tun+RD+Humidity), data = MegaS, link =
"log",na.action=na.omit)
summary(glm2)
# AIC: 877.94

glm2 <- glm.nb(Carabidae ~ (Tun*RD*Humidity)/Date, data = MegaS, link =
"log",na.action=na.omit)
summary(glm2)
# AIC: 877.94 <-----SELECTED

glm2 <- glm.nb(Araneae ~ Tun*RD*Humidity/Date, data = MegaS, link =
"log",na.action=na.omit)
summary(glm2)

```

```

glm2 <- glm.nb(Staphylinidae ~ Tun*RD*Humidity/Date, data = MegaS, link =
"log",na.action=na.omit)
summary(glm2)

glm2 <- glm.nb(Larvae ~ Tun*RD*Humidity/Date, data = MegaS, link =
"log",na.action=na.omit)
summary(glm2)

# GLM.3: Performing GLMs on the whole field (strips only) with soil factors:
glm3 <- glm.nb(Carabidae ~ (pH_log+OM_x)/Disturbance, data = MegaS, link =
"log",na.action=na.omit)
summary(glm3)
# AIC: 826.38

glm3 <- glm.nb(Carabidae ~ (pH_log+OM_x)/Disturbance, data = MegaS, link =
"log",na.action=na.omit)
summary(glm3)
# 816.24

glm3 <- glm.nb(Carabidae ~ (pH_log+OM_x)/Disturbance, data = MegaS, link =
"log",na.action=na.omit)
summary(glm3)
# 646.49

glm3 <- glm.nb(Carabidae ~ (pH_log+OM_x)*(Date*Disturbance), data = MegaS, link
= "log",na.action=na.omit)
summary(glm3)
# 625.69 <-----SELECTED

glm3 <- glm.nb(Carabidae ~ (pH_log+OM_x)/Disturbance, data = MegaS, link =
"log",na.action=na.omit)
summary(glm3)
# 729.78

glm3 <- glm.nb(Carabidae ~ (pH_log+OM_x)*(Date*Disturbance), data = MegaS, link
= "log",na.action=na.omit)
summary(glm3)
# 722.76

glm3 <- glm.nb(Carabidae ~ (pH_log+OM_x)*(Date*Disturbance), data = MegaS, link
= "log",na.action=na.omit)
summary(glm3)
# 805.57

glm3 <- glm.nb(Carabidae ~ (pH_log+OM_x)*(Date*Disturbance), data = MegaS, link
= "log",na.action=na.omit)
summary(glm3)
# 718.86

###-----END-----

```

Smoothed additive graphs (Araneae and Staphylinidae)

```
# -----  
# Script for additive graphs of  
# Araneae and Staphylinidae activity between STRIP edges (NOT  
# NET FLOWS!) - log10  
# transformed scale  
# Vladimir Shlevkov 13/06/16  
# vladimir.shlevkovpronskiy@wur.nl  
# -----  
  
# Change to the new directory  
setwd("Directory")  
  
# Clean up workspace  
rm(list=ls())  
graphics.off()  
gc(FALSE)  
cat("\014")  
  
# Load necessary libraries  
  
# Load the dataset  
Mega <- read.csv("Megadata.csv", header=T, sep=";", dec=".", fill=T, skip=3)  
  
# Defining type of variable  
Mega$Id <- as.numeric(Mega$Id)  
Mega$Date <- as.Date(Mega$Date, "%d/%m/%Y")  
Mega$Date_Code <- as.numeric(Mega$Date_Code)  
Mega$Strip <- as.factor(Mega$Strip)  
Mega$Plot <- as.numeric(Mega$Plot)  
Mega$Disturbance <- as.numeric(Mega$Disturbance)  
Mega$Direction <- as.character(Mega$Direction)  
Mega$Column <- as.factor(Mega$Column)  
Mega$FieldX <- as.numeric(Mega$FieldX)  
Mega$FieldY <- as.numeric(Mega$FieldY)  
Mega$RD_X <- as.factor(Mega$RD_X)  
Mega$RD_Y <- as.factor(Mega$RD_Y)  
Mega$ID2 <- as.factor(Mega$ID2)  
Mega$Quadrant <- as.numeric(Mega$Quadrant)  
Mega$Edge <- as.factor(Mega$Edge)  
Mega$Days <- as.numeric(Mega$Days)  
Mega$NEs <- as.numeric(Mega$NEs)  
Mega$IntNEs <- as.numeric(Mega$IntNEs)  
Mega$Araneae <- as.numeric(Mega$Araneae)  
Mega$Staphylinidae <- as.numeric(Mega$Staphylinidae)  
Mega$Araneae <- as.numeric(Mega$Araneae)  
Mega$Staphylinidae <- as.numeric(Mega$Staphylinidae)  
Mega$Coccinelidae <- as.numeric(Mega$Coccinelidae)
```

```

Mega$Chilopoda <- as.numeric(Mega$Chilopoda)
Mega$Hymenoptera <- as.numeric(Mega$Hymenoptera)
Mega$TotalNEs <- as.numeric(Mega$TotalNEs)
Mega$TotalIntNEs <- as.numeric(Mega$TotalIntNEs)
Mega$TotalCar <- as.numeric(Mega$TotalCar)
Mega$TotalSta <- as.numeric(Mega$TotalSta)
Mega$TotalAra <- as.numeric(Mega$TotalAra)
Mega$TotalLar <- as.numeric(Mega$TotalLar)
Mega$TotalCoc <- as.numeric(Mega$TotalCoc)
Mega$TotalChi <- as.numeric(Mega$TotalChi)
Mega$pH <- as.numeric(Mega$pH)
Mega$pH_log <- as.numeric(Mega$pH_log)
Mega$OM_x <- as.numeric(Mega$OM_x)
Mega$Ntot <- as.numeric(Mega$Ntot)
Mega$pH_fit_KCl <- as.numeric(Mega$pH_fit_KCl)
Mega$pH_fit_KCl_log <- as.numeric(Mega$pH_fit_KCl_log)
Mega$nw_correct <- as.numeric(Mega$nw_correct)
Mega$g_m2 <- as.numeric(Mega$g_m2)
Mega$Tun <- as.numeric(Mega$Tun)
Mega$Tvai <- as.numeric(Mega$Tvai)
Mega$Humidity <- as.numeric(Mega$Humidity)
Mega$RD <- as.numeric(Mega$RD)
Mega$TundG <- as.numeric(Mega$TundG)

# Dividing by the trap length (NE/m)
## Take variables to be divided and divide them:
myvars <- c("NEs", "IntNEs", "Araneae", "Staphylinidae",
            "TotalNEs", "TotalIntNEs", "TotalCar",
            "TotalSta", "TotalAra", "TotalLar",
            "TotalCoc", "TotalChi", "TotalHym")
MegaNEs <- Mega[myvars]
MegaNEs<-sweep(MegaNEs, MARGIN=2, STATS= 1.5, FUN="/")
MegaNEs<-sweep(MegaNEs, MARGIN=2, STATS= 100, FUN="*")

## Merge divided variables with original dataset:
Mega <- cbind(Mega, MegaNEs)
## Eliminate old non-divided variables:
Mega <- Mega[c(-20:-37)]

Mega$Araneae<- log10(Mega$Araneae)
Mega$Staphylinidae<- log10(Mega$Staphylinidae)

# Substitute Inf and -Inf by 0
Mega$Araneae[Mega$Araneae == "Inf"] <- 0
Mega$Araneae[Mega$Araneae == "-Inf"] <- 0

Mega$Staphylinidae[Mega$Staphylinidae == "Inf"] <- 0
Mega$Staphylinidae[Mega$Staphylinidae == "-Inf"] <- 0

# Functions to create smoothed and additive graphs:

```

```

## Gives count, mean, standard deviation, standard error of the mean, and
confidence interval (default 95%).
## data: a data frame.
## measurevar: the name of a column that contains the variable to be
summarized
## groupvars: a vector containing names of columns that contain grouping
variables
## na.rm: a boolean that indicates whether to ignore NA's
## conf.interval: the percent range of the confidence interval (default is
95%)
summarySE <- function(data=NULL, measurevar, groupvars=NULL, na.rm=FALSE,
                      conf.interval=.95, .drop=TRUE) {
  library(plyr)

  # New version of length which can handle NA's: if na.rm==T, don't count them
  length2 <- function (x, na.rm=FALSE) {
    if (na.rm) sum(!is.na(x))
    else      length(x)
  }

  # This does the summary. For each group's data frame, return a vector with
  # N, mean, and sd
  datac <- ddply(data, groupvars, .drop=.drop,
                .fun = function(xx, col) {
                  c(N      = length2(xx[[col]], na.rm=na.rm),
                    median = median  (xx[[col]], na.rm=na.rm),
                    sd     = sd      (xx[[col]], na.rm=na.rm),
                    min    = min     (xx[[col]], na.rm=na.rm),
                    max    = max     (xx[[col]], na.rm=na.rm),
                    quantile=quantile (xx[[col]], na.rm=na.rm)
                  )
                },
                measurevar
  )

  # Rename the "mean" column
  datac <- rename(datac, c("median" = measurevar))

  datac$se <- datac$sd / sqrt(datac$N) # Calculate standard error of the mean

  # Confidence interval multiplier for standard error
  # Calculate t-statistic for confidence interval:
  # e.g., if conf.interval is .95, use .975 (above/below), and use df=N-1
  datac$ci <- (datac$sd * 0.75)/2

  return(datac)
}

# Selecting inter-Strip migration for each NE
sumarydatNE<-summarySE(data = Mega[Mega$Edge=="inter",],measurevar = "IntNEs",

```

```

groupvars = c("Strip", "Direction", "Date"), na.rm=T)

sumarydatA<-summarySE(data = Mega[Mega$Edge=="inter",],measurevar = "Araneae",
groupvars = c("Strip", "Direction", "Date"), na.rm=T)

sumarydatS<-summarySE(data      =      Mega[Mega$Edge=="inter",],measurevar      =
"Staphylinidae",
groupvars = c("Strip", "Direction", "Date"), na.rm=T)

# Omitting NAs to allow calculations:
#sumarydatA <- na.omit(sumarydatA)
#sumarydatS <- na.omit(sumarydatS)

sumarydatA      <-      rename(sumarydatA,      c("quantile.25%"="firstq",
"quantile.50%"="median", "quantile.75%"="thirdq"))
sumarydatS      <-      rename(sumarydatS,      c("quantile.25%"="firstq",
"quantile.50%"="median", "quantile.75%"="thirdq"))

# Converting "n" traps as negative to indicate directionlity (from North to
South):
sumarydatA$Araneae[sumarydatA$Direction=="n"]<-
sumarydatA$Araneae[sumarydatA$Direction=="n"]*-1
sumarydatS$Staphylinidae[sumarydatS$Direction=="n"]<-
sumarydatS$Staphylinidae[sumarydatS$Direction=="n"]*-1

# "Mirroring" quantiles for N
sumarydatA$firstq[sumarydatA$Direction=="n"]<-
sumarydatA$firstq[sumarydatA$Direction=="n"]*-1
sumarydatA$thirdq[sumarydatA$Direction=="n"]<-
sumarydatA$thirdq[sumarydatA$Direction=="n"]*-1
sumarydatA$max[sumarydatA$Direction=="n"]<-
sumarydatA$max[sumarydatA$Direction=="n"]*-1

sumarydatS$firstq[sumarydatS$Direction=="n"]<-
sumarydatS$firstq[sumarydatS$Direction=="n"]*-1
sumarydatS$thirdq[sumarydatS$Direction=="n"]<-
sumarydatS$thirdq[sumarydatS$Direction=="n"]*-1
sumarydatS$max[sumarydatS$Direction=="n"]<-
sumarydatS$max[sumarydatS$Direction=="n"]*-1

# Making the figures
require(ggplot2)

## Araneae
### STRIP 1

```

```

AraS1 <- ggplot(sumarydatA[sumarydatA$Strip==1,], aes(x=Date, y=Araneae,
group=Direction)) +
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq), colour="hotpink4", width=2)
  geom_line(size=1, colour="hotpink4", alpha=0.9, alpha=0.9) +
  geom_point(size=3, shape=17, colour="hotpink4", alpha=0.7) +
  #geom_point(aes(x=Date, y=max), colour="hotpink4", shape=17, size=3, alpha=0.9)
+
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="hotpink4"), alpha=0.2) +
  theme_bw()+
  #ggtitle("Araneae Strip 2")+
  expand_limits(y=c(-2.5, 2.5)) +
  scale_y_continuous(breaks = c(-2, -1, 0, 1, 2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("hotpink4"="hotpink4"))
AraS1

```

STRIP 2

```

AraS2 <- ggplot(sumarydatA[sumarydatA$Strip==2,], aes(x=Date, y=Araneae,
group=Direction)) +
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq), colour="hotpink4", width=2)
  geom_line(size=1, colour="hotpink4", alpha=0.9) +
  geom_point(size=3, shape=17, colour="hotpink4", alpha=0.7) +
  #geom_point(aes(x=Date, y=max), colour="hotpink4", shape=17, size=3, alpha=0.9)
+
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="hotpink4"), alpha=0.2) +
  theme_bw()+
  #ggtitle("Araneae Strip 2")+
  expand_limits(y=c(-2.5, 2.5)) +
  scale_y_continuous(breaks = c(-2, -1, 0, 1, 2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("hotpink4"="hotpink4"))
AraS2

```

STRIP 3

```

AraS3 <- ggplot(sumarydatA[sumarydatA$Strip==3,], aes(x=Date, y=Araneae,
group=Direction)) +
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq), colour="hotpink4", width=2)
  geom_line(size=1, colour="hotpink4", alpha=0.9) +
  geom_point(size=3, shape=17, colour="hotpink4", alpha=0.7) +
  #geom_point(aes(x=Date, y=max), colour="hotpink4", shape=17, size=3, alpha=0.9)
+
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="hotpink4"), alpha=0.2) +
  theme_bw()+
  #ggtitle("Araneae Strip 3")+

```

```

expand_limits(y=c(-2.5,2.5)) +
scale_y_continuous(breaks = c(-2,-1,0,1,2))+
theme(panel.background = element_rect(fill = NA),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      legend.position="none")+
scale_fill_manual(values=c("hotpink4"="hotpink4"))
AraS3

### STRIP 4
AraS4 <- ggplot(summarydatA[summarydatA$Strip==4,], aes(x=Date, y=Araneae,
group=Direction)) +
  geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="hotpink4",width=2)
  geom_line(size=1, colour="hotpink4",alpha=0.9) +
  geom_point(size=3, shape=17,colour="hotpink4",alpha=0.7) +
  geom_point(aes(x=Date, y=max), colour="hotpink4",shape=17,size=3,alpha=0.9)
+
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="hotpink4"),alpha=0.2) +
  theme_bw()+
  ggtitle("Araneae Strip 4")+
  expand_limits(y=c(-2.5,2.5)) +
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("hotpink4"="hotpink4"))
AraS4

### STRIP 5
AraS5 <- ggplot(summarydatA[summarydatA$Strip==5,], aes(x=Date, y=Araneae,
group=Direction)) +
  geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="hotpink4",width=2)
  geom_line(size=1, colour="hotpink4",alpha=0.9) +
  geom_point(size=3, shape=17,colour="hotpink4",alpha=0.7) +
  geom_point(aes(x=Date, y=max), colour="hotpink4",shape=17,size=3,alpha=0.9)
+
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="hotpink4"),alpha=0.2) +
  theme_bw()+
  ggtitle("Araneae Strip 5")+
  expand_limits(y=c(-2.5,2.5)) +
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("hotpink4"="hotpink4"))
AraS5

### STRIP 6

```

```

AraS6 <- ggplot(sumarydatA[sumarydatA$Strip==6,], aes(x=Date, y=Araneae,
group=Direction)) +
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="hotpink4",width=2)
  geom_line(size=1, colour="hotpink4",alpha=0.9) +
  geom_point(size=3, shape=17,colour="hotpink4",alpha=0.7) +
  #geom_point(aes(x=Date, y=max), colour="hotpink4",shape=17,size=3,alpha=0.9)
+
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="hotpink4"),alpha=0.2) +
  theme_bw()+
  #ggtitle("Araneae Strip 6")+
  expand_limits(y=c(-2.5,2.5)) +
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("hotpink4"="hotpink4"))

```

AraS6

STRIP 7

```

AraS7 <- ggplot(sumarydatA[sumarydatA$Strip==7,], aes(x=Date, y=Araneae,
group=Direction)) +
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="hotpink4",width=2)
  geom_line(size=1, colour="hotpink4",alpha=0.9) +
  geom_point(size=3, shape=17,colour="hotpink4", alpha = 0.7) +
  #geom_point(aes(x=Date, y=max), colour="hotpink4",shape=17,size =3) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="hotpink4"),alpha=0.2) +
  theme_bw()+
  #ggtitle("Araneae Strip 7")+
  expand_limits(y=c(-2.5,2.5)) +
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("hotpink4"="hotpink4"))

```

AraS7

#-----

Staphylinidae

STRIP 1

```

Staphylinidae1 <- ggplot(sumarydatS[sumarydatS$Strip==1,], aes(x=Date,
y=Staphylinidae, group=Direction)) +
  geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="hotpink4",width=2)
  geom_line(size=1, colour="springgreen3",alpha=0.7) +
  geom_point(size=3, shape=15,colour="springgreen3") +
  #geom_point(aes(x=Date, y=max), colour="springgreen3",shape=15,size=3,alpha=0.9) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="springgreen3"),alpha=0.2) +

```

```

theme_bw()+
ggtitle("Staphylinidae Strip 1")+
expand_limits(y=c(-2.5,2.5))+
scale_y_continuous(breaks = c(-2,-1,0,1,2))+
theme(panel.background = element_rect(fill = NA),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      legend.position="none")+
scale_fill_manual(values=c("springgreen3"="springgreen3"))
Staphylinidae1

### STRIP 2
Staphylinidae2 <- ggplot(sumarydatS[sumarydatS$Strip==2,], aes(x=Date,
y=Staphylinidae, group=Direction)) +
  geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="hotpink4",width=2)
  geom_line(size=1, colour="springgreen3",alpha=0.9) +
  geom_point(size=3, shape=15,colour="springgreen3",alpha=0.7) +
  #geom_point(aes(x=Date, y=max),
colour="springgreen3",shape=15,size=3,alpha=0.9) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="springgreen3"),alpha=0.2) +
  theme_bw()+
  ggtitle("Staphylinidae Strip 2")+
  expand_limits(y=c(-2.5,2.5))+
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("springgreen3"="springgreen3"))
Staphylinidae2

### STRIP 3
Staphylinidae3 <- ggplot(sumarydatS[sumarydatS$Strip==3,], aes(x=Date,
y=Staphylinidae, group=Direction)) +
  geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="hotpink4",width=2)
  geom_line(size=1, colour="springgreen3",alpha=0.9) +
  geom_point(size=3, shape=15,colour="springgreen3",alpha=0.7) +
  #geom_point(aes(x=Date, y=max),
colour="springgreen3",shape=15,size=3,alpha=0.9) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="springgreen3"),alpha=0.2) +
  theme_bw()+
  ggtitle("Staphylinidae Strip 3")+
  expand_limits(y=c(-2.5,2.5))+
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+

```

```

scale_fill_manual(values=c("springgreen3"="springgreen3"))
Staphylinidae3

### STRIP 4
Staphylinidae4 <- ggplot(sumarydatS[sumarydatS$Strip==4,], aes(x=Date,
y=Staphylinidae, group=Direction)) +
  geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="hotpink4",width=2)
  geom_line(size=1, colour="springgreen3",alpha=0.9) +
  geom_point(size=3, shape=15,colour="springgreen3",alpha=0.7) +
  #geom_point(aes(x=Date, y=max),
colour="springgreen3",shape=15,size=3,alpha=0.9) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="springgreen3"),alpha=0.2) +
  theme_bw()+
  ggtitle("Staphylinidae Strip 4")+
  expand_limits(y=c(-2.5,2.5))+
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("springgreen3"="springgreen3"))
Staphylinidae4

### STRIP 5
Staphylinidae5 <- ggplot(sumarydatS[sumarydatS$Strip==5,], aes(x=Date,
y=Staphylinidae, group=Direction)) +
  geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="hotpink4",width=2)
  geom_line(size=1, colour="springgreen3",alpha=0.9) +
  geom_point(size=3, shape=15,colour="springgreen3",alpha=0.7) +
  #geom_point(aes(x=Date, y=max),
colour="springgreen3",shape=15,size=3,alpha=0.9) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="springgreen3"),alpha=0.2) +
  theme_bw()+
  ggtitle("Staphylinidae Strip 5")+
  expand_limits(y=c(-2.5,2.5))+
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("springgreen3"="springgreen3"))
Staphylinidae5

### STRIP 6
Staphylinidae6 <- ggplot(sumarydatS[sumarydatS$Strip==6,], aes(x=Date,
y=Staphylinidae, group=Direction)) +
  geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="hotpink4",width=2)
  geom_line(size=1, colour="springgreen3",alpha=0.9) +

```

```

geom_point(size=3, shape=15, colour="springgreen3", alpha=0.7) +
#geom_point(aes(x=Date,                                     y=max),
colour="springgreen3", shape=15, size=3, alpha=0.9) +
geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="springgreen3"), alpha=0.2) +
theme_bw()+
ggtitle("Staphylinidae Strip 6")+
expand_limits(y=c(-2.5, 2.5))+
scale_y_continuous(breaks = c(-2, -1, 0, 1, 2))+
theme(panel.background = element_rect(fill = NA),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      legend.position="none")+
scale_fill_manual(values=c("springgreen3"="springgreen3"))
Staphylinidae6

```

```

### STRIP 7
Staphylinidae7 <- ggplot(summarydatS[summarydatS$Strip==7,], aes(x=Date,
y=Staphylinidae, group=Direction)) +
geom_hline(aes(yintercept = 0), size=1, alpha=0.7)+
#geom_errorbar(aes(ymin=firstq, ymax=thirdq), colour="hotpink4", width=2)
geom_line(size=1, colour="springgreen3", alpha=0.9) +
geom_point(size=3, shape=15, colour="springgreen3", alpha=0.7) +
#geom_point(aes(x=Date,                                     y=max),
colour="springgreen3", shape=15, size=3, alpha=0.9) +
geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="springgreen3"), alpha=0.2) +
theme_bw()+
ggtitle("Staphylinidae Strip 7")+
expand_limits(y=c(-2.5, 2.5))+
scale_y_continuous(breaks = c(-2, -1, 0, 1, 2))+
theme(panel.background = element_rect(fill = NA),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      legend.position="none")+
scale_fill_manual(values=c("springgreen3"="springgreen3"))

```

Staphylinidae7

#-----

```

#Double ggplot:
#install.packages('gtable')
#install.packages("grid")
library(gtable)
library(grid)
grid.newpage()

```

```

# Strip 1
# extract gtable
g1 <- ggplot_gtable(ggplot_build(AraS1))
g2 <- ggplot_gtable(ggplot_build(Staphylinidae1))

```

```

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315, res=120)
grid.draw(g)
dev.off()
graphics.off()

#-----
# Strip 2
# extract gtable
g1 <- ggplot_gtable(ggplot_build(AraS2))
g2 <- ggplot_gtable(ggplot_build(Staphylinidae2))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315, res=120)
grid.draw(g)
dev.off()
graphics.off()

```

```

#-----
# Strip 3
# extract gtable
g1 <- ggplot_gtable(ggplot_build(AraS3))
g2 <- ggplot_gtable(ggplot_build(Staphylinidae3))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l, length(g$widths) - 1])
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315, res=120)
grid.draw(g)
dev.off()
graphics.off()

#-----
# Strip 4
# extract gtable
g1 <- ggplot_gtable(ggplot_build(AraS4))
g2 <- ggplot_gtable(ggplot_build(Staphylinidae4))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l, length(g$widths) - 1])
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it

```

```

grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315,res=120)
grid.draw(g)
dev.off()
graphics.off()

#-----
# Strip 5
# extract gtable
g1 <- ggplot_gtable(ggplot_build(AraS5))
g2 <- ggplot_gtable(ggplot_build(Staphylinidae5))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315,res=120)
grid.draw(g)
dev.off()
graphics.off()

#-----
# Strip 6
# extract gtable
g1 <- ggplot_gtable(ggplot_build(AraS6))
g2 <- ggplot_gtable(ggplot_build(Staphylinidae6))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]

```

```

ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315, res=120)
grid.draw(g)
dev.off()
graphics.off()

#-----
# Strip 7
# extract gtable
g1 <- ggplot_gtable(ggplot_build(AraS7))
g2 <- ggplot_gtable(ggplot_build(Staphylinidae7))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315, res=120)
grid.draw(g)
dev.off()
graphics.off()

###-----END-----

```

Smoothed additive graphs (Carabidae and Larvae)

```
# -----  
# Script for additive graphs of  
# Carabidae and Larvae activity between STRIP edges (NOT  
# NET FLOWS!) - log10  
# transformed scale  
# Vladimir Shlevkov 13/06/16  
# vladimir.shlevkovpronskiy@wur.nl  
# -----  
  
# Change to the new directory  
setwd("Directory")  
  
# Clean up workspace  
rm(list=ls())  
graphics.off()  
gc(FALSE)  
cat("\014")  
  
# Load necessary libraries  
  
# Load the dataset  
Mega <- read.csv("Megadata.csv", header=T, sep=";", dec=".", fill=T, skip=3)  
  
# Defining type of variable  
Mega$Id <- as.numeric(Mega$Id)  
Mega$Date <- as.Date(Mega$Date, "%d/%m/%Y")  
Mega$Date_Code <- as.numeric(Mega$Date_Code)  
Mega$Strip <- as.factor(Mega$Strip)  
Mega$Plot <- as.numeric(Mega$Plot)  
Mega$Disturbance <- as.numeric(Mega$Disturbance)  
Mega$Direction <- as.character(Mega$Direction)  
Mega$Column <- as.factor(Mega$Column)  
Mega$FieldX <- as.numeric(Mega$FieldX)  
Mega$FieldY <- as.numeric(Mega$FieldY)  
Mega$RD_X <- as.factor(Mega$RD_X)  
Mega$RD_Y <- as.factor(Mega$RD_Y)  
Mega$ID2 <- as.factor(Mega$ID2)  
Mega$Quadrant <- as.numeric(Mega$Quadrant)  
Mega$Edge <- as.factor(Mega$Edge)  
Mega$Days <- as.numeric(Mega$Days)  
Mega$NEs <- as.numeric(Mega$NEs)  
Mega$IntNEs <- as.numeric(Mega$IntNEs)  
Mega$Carabidae <- as.numeric(Mega$Carabidae)  
Mega$Larvae <- as.numeric(Mega$Larvae)  
Mega$Carabidae <- as.numeric(Mega$Carabidae)  
Mega$Larvae <- as.numeric(Mega$Larvae)
```

```

Mega$Coccinellidae <- as.numeric(Mega$Coccinellidae)
Mega$Chilopoda <- as.numeric(Mega$Chilopoda)
Mega$Hymenoptera <- as.numeric(Mega$Hymenoptera)
Mega$TotalNEs <- as.numeric(Mega$TotalNEs)
Mega$TotalIntNEs <- as.numeric(Mega$TotalIntNEs)
Mega$TotalCar <- as.numeric(Mega$TotalCar)
Mega$TotalSta <- as.numeric(Mega$TotalSta)
Mega$TotalAra <- as.numeric(Mega$TotalAra)
Mega$TotalLar <- as.numeric(Mega$TotalLar)
Mega$TotalCoc <- as.numeric(Mega$TotalCoc)
Mega$TotalChi <- as.numeric(Mega$TotalChi)
Mega$pH <- as.numeric(Mega$pH)
Mega$pH_log <- as.numeric(Mega$pH_log)
Mega$OM_x <- as.numeric(Mega$OM_x)
Mega$Ntot <- as.numeric(Mega$Ntot)
Mega$pH_fit_KCl <- as.numeric(Mega$pH_fit_KCl)
Mega$pH_fit_KCl_log <- as.numeric(Mega$pH_fit_KCl_log)
Mega$nw_correct <- as.numeric(Mega$nw_correct)
Mega$g_m2 <- as.numeric(Mega$g_m2)
Mega$Tun <- as.numeric(Mega$Tun)
Mega$Tvai <- as.numeric(Mega$Tvai)
Mega$Humidity <- as.numeric(Mega$Humidity)
Mega$RD <- as.numeric(Mega$RD)
Mega$TundG <- as.numeric(Mega$TundG)

# Dividing by the trap length (NE/m)
## Take variables to be divided and divide them:
myvars <- c("NEs", "IntNEs", "Carabidae", "Larvae",
            "TotalNEs", "TotalIntNEs", "TotalCar",
            "TotalSta", "TotalAra", "TotalLar",
            "TotalCoc", "TotalChi", "TotalHym")
MegaNEs <- Mega[myvars]
MegaNEs<-sweep(MegaNEs, MARGIN=2, STATS= 1.5, FUN="/")
MegaNEs<-sweep(MegaNEs, MARGIN=2, STATS= 100, FUN="*")

## Merge divided variables with original dataset:
Mega <- cbind(Mega, MegaNEs)
## Eliminate old non-divided variables:
Mega <- Mega[c(-20:-37)]

Mega$Carabidae<- log10(Mega$Carabidae)
Mega$Larvae<- log10(Mega$Larvae)

# Substitute Inf and -Inf by 0
Mega$Carabidae[Mega$Carabidae == "Inf"] <- 0
Mega$Carabidae[Mega$Carabidae == "-Inf"] <- 0

Mega$Larvae[Mega$Larvae == "Inf"] <- 0
Mega$Larvae[Mega$Larvae == "-Inf"] <- 0

```

```

# Functions to create smoothed and additive graphs:
## Gives count, mean, standard deviation, standard error of the mean, and
confidence interval (default 95%).
## data: a data frame.
## measurevar: the name of a column that contains the variable to be
summarized
## groupvars: a vector containing names of columns that contain grouping
variables
## na.rm: a boolean that indicates whether to ignore NA's
## conf.interval: the percent range of the confidence interval (default is
95%)
summarySE <- function(data=NULL, measurevar, groupvars=NULL, na.rm=FALSE,
                      conf.interval=.95, .drop=TRUE) {
  library(plyr)

  # New version of length which can handle NA's: if na.rm==T, don't count them
  length2 <- function (x, na.rm=FALSE) {
    if (na.rm) sum(!is.na(x))
    else      length(x)
  }

  # This does the summary. For each group's data frame, return a vector with
  # N, mean, and sd
  datac <- ddply(data, groupvars, .drop=.drop,
    .fun = function(xx, col) {
      c(N      = length2(xx[[col]], na.rm=na.rm),
        median = median  (xx[[col]], na.rm=na.rm),
        sd     = sd      (xx[[col]], na.rm=na.rm),
        min    = min     (xx[[col]], na.rm=na.rm),
        max    = max     (xx[[col]], na.rm=na.rm),
        quantile=quantile (xx[[col]], na.rm=na.rm)
      )
    },
    measurevar
  )

  # Rename the "mean" column
  datac <- rename(datac, c("median" = measurevar))

  datac$se <- datac$sd / sqrt(datac$N) # Calculate standard error of the mean

  # Confidence interval multiplier for standard error
  # Calculate t-statistic for confidence interval:
  # e.g., if conf.interval is .95, use .975 (above/below), and use df=N-1
  datac$ci <- (datac$sd * 0.75)/2

  return(datac)
}

# Selecting inter-Strip activity for each NE

```

```

sumarydatNE<-summarySE(data = Mega[Mega$Edge=="inter",],measurevar = "IntNEs",
                      groupvars = c("Strip", "Direction", "Date"), na.rm=T)

sumarydatC<-summarySE(data      =      Mega[Mega$Edge=="inter",],measurevar      =
"Carabidae",
                      groupvars = c("Strip", "Direction", "Date"), na.rm=T)

sumarydatL<-summarySE(data = Mega[Mega$Edge=="inter",],measurevar = "Larvae",
                      groupvars = c("Strip", "Direction", "Date"), na.rm=T)

# Omitting NAs to allow calculations:
#sumarydatC <- na.omit(sumarydatC)
#sumarydatL <- na.omit(sumarydatL)

sumarydatC      <-      rename(sumarydatC,      c("quantile.25%"="firstq",
"quantile.50%"="median", "quantile.75%"="thirdq"))
sumarydatL      <-      rename(sumarydatL,      c("quantile.25%"="firstq",
"quantile.50%"="median", "quantile.75%"="thirdq"))

# Converting "n" traps as negative to indicate directionlity (from North to
South):
sumarydatC$Carabidae[sumarydatC$Direction=="n"]<-
sumarydatC$Carabidae[sumarydatC$Direction=="n"]*-1
sumarydatL$Larvae[sumarydatL$Direction=="n"]<-
sumarydatL$Larvae[sumarydatL$Direction=="n"]*-1

# "Mirroring" quantiles for N
sumarydatC$firstq[sumarydatC$Direction=="n"]<-
sumarydatC$firstq[sumarydatC$Direction=="n"]*-1
sumarydatC$thirdq[sumarydatC$Direction=="n"]<-
sumarydatC$thirdq[sumarydatC$Direction=="n"]*-1
sumarydatC$max[sumarydatC$Direction=="n"]<-
sumarydatC$max[sumarydatC$Direction=="n"]*-1

sumarydatL$firstq[sumarydatL$Direction=="n"]<-
sumarydatL$firstq[sumarydatL$Direction=="n"]*-1
sumarydatL$thirdq[sumarydatL$Direction=="n"]<-
sumarydatL$thirdq[sumarydatL$Direction=="n"]*-1
sumarydatL$max[sumarydatL$Direction=="n"]<-
sumarydatL$max[sumarydatL$Direction=="n"]*-1

# Omitting NAs
sumarydatC$Carabidae[sumarydatC$Carabidae == "Inf" ] <- NA
sumarydatC$Carabidae[sumarydatC$Carabidae == "-Inf" ] <- NA

sumarydatC$firstq[sumarydatC$firstq == "Inf" ] <- NA
sumarydatC$firstq[sumarydatC$firstq == "-Inf" ] <- NA

```

```

sumarydatC$thirdq[sumarydatC$thirdq == "Inf" ] <- NA
sumarydatC$thirdq[sumarydatC$thirdq == "-Inf" ] <- NA

sumarydatL$Larvae[sumarydatL$Larvae == "Inf" ] <- NA
sumarydatL$Larvae[sumarydatL$Larvae == "-Inf" ] <- NA

sumarydatL$firstq[sumarydatL$firstq == "Inf" ] <- NA
sumarydatL$firstq[sumarydatL$firstq == "-Inf" ] <- NA

sumarydatL$thirdq[sumarydatL$thirdq == "Inf" ] <- NA
sumarydatL$thirdq[sumarydatL$thirdq == "-Inf" ] <- NA

```

```

# Making the figures
require(ggplot2)

```

```

## Carabidae
### STRIP 1

```

```

CarS1 <- ggplot(sumarydatC[sumarydatC$Strip==1,], aes(x=Date, y=Carabidae,
group=Direction)) +
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="darkblue",width=2)
  geom_line(size=1, colour="darkblue") +
  geom_point(size=4, shape=20,colour="darkblue",alpha=0.7) +
  #geom_point(aes(x=Date, y=max), colour="darkblue",shape=20,size=4) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkblue"),alpha=0.2) +
  theme_bw()+
  #ggtitle("Carabidae Strip 1")+
  expand_limits(y=c(-2.5,2.5)) +
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("darkblue"="darkblue"))
CarS1

```

```

### STRIP 2

```

```

CarS2 <- ggplot(sumarydatC[sumarydatC$Strip==2,], aes(x=Date, y=Carabidae,
group=Direction)) +
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="darkblue",width=2)
  geom_line(size=1, colour="darkblue") +
  geom_point(size=4, shape=20,colour="darkblue",alpha=0.7) +
  #geom_point(aes(x=Date, y=max), colour="darkblue",shape=20,size=4) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkblue"),alpha=0.2) +
  theme_bw()+
  #ggtitle("Carabidae Strip 2")+
  expand_limits(y=c(-2.5,2.5)) +

```

```

scale_y_continuous(breaks = c(-2,-1,0,1,2))+
theme(panel.background = element_rect(fill = NA),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      legend.position="none")+
scale_fill_manual(values=c("darkblue"="darkblue"))
CarS2

### STRIP 3
CarS3 <- ggplot(sumarydatC[sumarydatC$Strip==3,], aes(x=Date, y=Carabidae,
group=Direction)) +
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="darkblue",width=2)
  geom_line(size=1, colour="darkblue") +
  geom_point(size=4, shape=20,colour="darkblue",alpha=0.7) +
  #geom_point(aes(x=Date, y=max), colour="darkblue",shape=20,size=4) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkblue"),alpha=0.2) +
  theme_bw()+
  #ggtitle("Carabidae Strip 3")+
  expand_limits(y=c(-2.5,2.5)) +
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("darkblue"="darkblue"))
CarS3

### STRIP 4
CarS4 <- ggplot(sumarydatC[sumarydatC$Strip==4,], aes(x=Date, y=Carabidae,
group=Direction)) +
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="darkblue",width=2)
  geom_line(size=1, colour="darkblue") +
  geom_point(size=4, shape=20,colour="darkblue",alpha=0.7) +
  #geom_point(aes(x=Date, y=max), colour="darkblue",shape=20,size=4) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkblue"),alpha=0.2) +
  theme_bw()+
  #ggtitle("Carabidae Strip 4")+
  expand_limits(y=c(-2.5,2.5)) +
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("darkblue"="darkblue"))
CarS4

### STRIP 5
CarS5 <- ggplot(sumarydatC[sumarydatC$Strip==5,], aes(x=Date, y=Carabidae,
group=Direction)) +
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="darkblue",width=2)
  geom_line(size=1, colour="darkblue") +

```

```

geom_point(size=4, shape=20, colour="darkblue", alpha=0.7) +
#geom_point(aes(x=Date, y=max), colour="darkblue", shape=20, size=4) +
geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkblue"), alpha=0.2) +
theme_bw()+
#ggtitle("Carabidae Strip 5")+
expand_limits(y=c(-2.5, 2.5)) +
scale_y_continuous(breaks = c(-2, -1, 0, 1, 2))+
theme(panel.background = element_rect(fill = NA),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      legend.position="none")+
scale_fill_manual(values=c("darkblue"="darkblue"))
CarS5

```

STRIP 6

```

CarS6 <- ggplot(sumarydatC[sumarydatC$Strip==6,], aes(x=Date, y=Carabidae,
group=Direction)) +
#geom_errorbar(aes(ymin=firstq, ymax=thirdq), colour="darkblue", width=2)
geom_line(size=1, colour="darkblue") +
geom_point(size=4, shape=20, colour="darkblue", alpha=0.7) +
#geom_point(aes(x=Date, y=max), colour="darkblue", shape=20, size=4) +
geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkblue"), alpha=0.2) +
theme_bw()+
#ggtitle("Carabidae Strip 6")+
expand_limits(y=c(-2.5, 2.5)) +
scale_y_continuous(breaks = c(-2, -1, 0, 1, 2))+
theme(panel.background = element_rect(fill = NA),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      legend.position="none")+
scale_fill_manual(values=c("darkblue"="darkblue"))
CarS6

```

STRIP 7

```

CarS7 <- ggplot(sumarydatC[sumarydatC$Strip==7,], aes(x=Date, y=Carabidae,
group=Direction)) +
#geom_errorbar(aes(ymin=firstq, ymax=thirdq), colour="darkblue", width=2)
geom_line(size=1, colour="darkblue") +
geom_point(size=4, shape=20, colour="darkblue", alpha=0.7) +
#geom_point(aes(x=Date, y=max), colour="darkblue", shape=20, size =4) +
geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkblue"), alpha=0.2) +
theme_bw()+
#ggtitle("Carabidae Strip 7")+
expand_limits(y=c(-2.5, 2.5)) +
scale_y_continuous(breaks = c(-2, -1, 0, 1, 2))+
theme(panel.background = element_rect(fill = NA),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      legend.position="none")+
scale_fill_manual(values=c("darkblue"="darkblue"))
CarS7

```

```

#-----
## Larvae
### STRIP 1
Larvae1 <- ggplot(sumarydatL[sumarydatL$Strip==1,], aes(x=Date, y=Larvae,
group=Direction)) +
  geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="darkblue",width=2)
  geom_line(size=1, colour="darkorange4") +
  geom_point(size=4, shape=18,colour="darkorange4", alpha = 0.7) +
  #geom_point(aes(x=Date, y=max), colour="darkorange4",shape=18,size=4) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkorange4"),alpha=0.2) +
  theme_bw()+
  ggtitle("Larvae Strip 1")+
  expand_limits(y=c(-2.5,2.5))+
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("darkorange4"="darkorange4"))
Larvae1

### STRIP 2
Larvae2 <- ggplot(sumarydatL[sumarydatL$Strip==2,], aes(x=Date, y=Larvae,
group=Direction)) +
  geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="darkblue",width=2)
  geom_line(size=1, colour="darkorange4") +
  geom_point(size=4, shape=18,colour="darkorange4",alpha=0.7) +
  #geom_point(aes(x=Date, y=max), colour="darkorange4",shape=18,size=4) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkorange4"),alpha=0.2) +
  theme_bw()+
  ggtitle("Larvae Strip 2")+
  expand_limits(y=c(-2.5,2.5))+
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("darkorange4"="darkorange4"))
Larvae2

### STRIP 3
Larvae3 <- ggplot(sumarydatL[sumarydatL$Strip==3,], aes(x=Date, y=Larvae,
group=Direction)) +
  geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="darkblue",width=2)

```

```

geom_line(size=1, colour="darkorange4") +
geom_point(size=4, shape=18, colour="darkorange4", alpha=0.7) +
#geom_point(aes(x=Date, y=max), colour="darkorange4", shape=18, size=4) +
geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkorange4"), alpha=0.2) +
theme_bw()+
ggtitle("Larvae Strip 3")+
expand_limits(y=c(-2.5,2.5))+
scale_y_continuous(breaks = c(-2,-1,0,1,2))+
theme(panel.background = element_rect(fill = NA),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      legend.position="none")+
scale_fill_manual(values=c("darkorange4"="darkorange4"))
Larvae3

### STRIP 4
Larvae4 <- ggplot(sumarydatL[sumarydatL$Strip==4,], aes(x=Date, y=Larvae,
group=Direction)) +
geom_hline(aes(yintercept = 0), size=1, alpha=0.7)+
#geom_errorbar(aes(ymin=firstq, ymax=thirdq), colour="darkblue", width=2)
geom_line(size=1, colour="darkorange4") +
geom_point(size=4, shape=18, colour="darkorange4", alpha=0.7) +
#geom_point(aes(x=Date, y=max), colour="darkorange4", shape=18, size=4) +
geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkorange4"), alpha=0.2) +
theme_bw()+
ggtitle("Larvae Strip 4")+
expand_limits(y=c(-2.5,2.5))+
scale_y_continuous(breaks = c(-2,-1,0,1,2))+
theme(panel.background = element_rect(fill = NA),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),
      legend.position="none")+
scale_fill_manual(values=c("darkorange4"="darkorange4"))
Larvae4

### STRIP 5
Larvae5 <- ggplot(sumarydatL[sumarydatL$Strip==5,], aes(x=Date, y=Larvae,
group=Direction)) +
geom_hline(aes(yintercept = 0), size=1, alpha=0.7)+
#geom_errorbar(aes(ymin=firstq, ymax=thirdq), colour="darkblue", width=2)
geom_line(size=1, colour="darkorange4") +
geom_point(size=4, shape=18, colour="darkorange4", alpha=0.7) +
#geom_point(aes(x=Date, y=max), colour="darkorange4", shape=18, size=4) +
geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkorange4"), alpha=0.2) +
theme_bw()+
ggtitle("Larvae Strip 5")+
expand_limits(y=c(-2.5,2.5))+
scale_y_continuous(breaks = c(-2,-1,0,1,2))+
theme(panel.background = element_rect(fill = NA),
      panel.grid.major = element_blank(),
      panel.grid.minor = element_blank(),

```

```

        legend.position="none")+
  scale_fill_manual(values=c("darkorange4"="darkorange4"))
Larvae5

### STRIP 6
Larvae6 <- ggplot(summarydatL[summarydatL$Strip==6,], aes(x=Date, y=Larvae,
group=Direction)) +
  geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="darkblue",width=2)
  geom_line(size=1, colour="darkorange4") +
  geom_point(size=4, shape=18,colour="darkorange4",alpha=0.7) +
  #geom_point(aes(x=Date, y=max), colour="darkorange4",shape=18,size=4) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkorange4"),alpha=0.2) +
  theme_bw()+
  ggtitle("Larvae Strip 6")+
  expand_limits(y=c(-2.5,2.5))+
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("darkorange4"="darkorange4"))
Larvae6

### STRIP 7
Larvae7 <- ggplot(summarydatL[summarydatL$Strip==7,], aes(x=Date, y=Larvae,
group=Direction)) +
  geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="darkblue",width=2)
  geom_line(size=1, colour="darkorange4") +
  geom_point(size=4, shape=18,colour="darkorange4",alpha=0.7) +
  #geom_point(aes(x=Date, y=max), colour="darkorange4",shape=18,size=4) +
  geom_ribbon(aes(ymin=firstq, ymax=thirdq, fill="darkorange4"),alpha=0.2) +
  theme_bw()+
  ggtitle("Larvae Strip 7")+
  expand_limits(y=c(-2.5,2.5))+
  scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("darkorange4"="darkorange4"))

Larvae7

#-----

#Double ggplot:
#install.packages('gtable')
#install.packages("grid")

```

```

library(gtable)
library(grid)
grid.newpage()

# Strip 1
# extract gtable
g1 <- ggplot_gtable(ggplot_build(CarS1))
g2 <- ggplot_gtable(ggplot_build(Larvae1))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315, res=120)
grid.draw(g)
dev.off()
graphics.off()

#-----
# Strip 2
# extract gtable
g1 <- ggplot_gtable(ggplot_build(CarS2))
g2 <- ggplot_gtable(ggplot_build(Larvae2))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

```

```

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315,res=120)
grid.draw(g)
dev.off()
graphics.off()

#-----
# Strip 3
# extract gtable
g1 <- ggplot_gtable(ggplot_build(CarS3))
g2 <- ggplot_gtable(ggplot_build(Larvae3))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315,res=120)
grid.draw(g)
dev.off()
graphics.off()

#-----
# Strip 4
# extract gtable
g1 <- ggplot_gtable(ggplot_build(CarS4))
g2 <- ggplot_gtable(ggplot_build(Larvae4))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")

```

```

ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315, res=120)
grid.draw(g)
dev.off()
graphics.off()

#-----
# Strip 5
# extract gtable
g1 <- ggplot_gtable(ggplot_build(CarS5))
g2 <- ggplot_gtable(ggplot_build(Larvae5))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315, res=120)
grid.draw(g)
dev.off()
graphics.off()

#-----
# Strip 6
# extract gtable
g1 <- ggplot_gtable(ggplot_build(CarS6))
g2 <- ggplot_gtable(ggplot_build(Larvae6))

```

```

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315, res=120)
grid.draw(g)
dev.off()
graphics.off()

#-----
# Strip 7
# extract gtable
g1 <- ggplot_gtable(ggplot_build(CarS7))
g2 <- ggplot_gtable(ggplot_build(Larvae7))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315, res=120)
grid.draw(g)
dev.off()

```

```

graphics.off()

#-----

### Temperature panel
require(ggplot2)

Temp <- ggplot(Mega, aes(x=Date, y=Tun)) +
  #geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="darkblue",width=2)
  geom_line(size=1, colour="darkred") +
  geom_point(size=3, shape=25,colour="darkred",alpha=0.7) +
  theme_bw()+
  #ggtitle("Temperature")+
  expand_limits(y=c(0,15))+
  #scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("darkred"="darkred"))
Temp

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315,res=120)
grid.draw(g)
dev.off()
graphics.off()

Rain <- ggplot(Mega, aes(x=Date, y=RD)) +
  #geom_hline(aes(yintercept = 0),size=1,alpha=0.7)+
  #geom_errorbar(aes(ymin=firstq, ymax=thirdq),colour="darkblue",width=2)
  geom_line(size=1, colour="cyan4") +
  geom_point(size=3, shape=24,colour="cyan4",alpha=0.7) +
  #theme_bw()+
  #ggtitle("Rain")+
  expand_limits(y=c(0,15))+
  #scale_y_continuous(breaks = c(-2,-1,0,1,2))+
  theme(panel.background = element_rect(fill = NA),
        panel.grid.major = element_blank(),
        panel.grid.minor = element_blank(),
        legend.position="none")+
  scale_fill_manual(values=c("cyan4"="cyan4"))
Rain

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315,res=120)
grid.draw(g)
dev.off()
graphics.off()

```

```

#Double ggplot:
#install.packages('gtable')
#install.packages("grid")
library(gtable)
library(grid)
grid.newpage()

# Merging temperature and rain into one figure
# extract gtable
g1 <- ggplot_gtable(ggplot_build(Temp))
g2 <- ggplot_gtable(ggplot_build(Rain))

# overlap the panel of 2nd plot on that of 1st plot
pp <- c(subset(g1$layout, name == "panel", se = t:r))
g <- gtable_add_grob(g1, g2$grobs[[which(g2$layout$name == "panel")]], pp$t,
                    pp$l, pp$b, pp$l)

# axis tweaks
ia <- which(g2$layout$name == "axis-l")
ga <- g2$grobs[[ia]]
ax <- ga$children[[2]]
ax$widths <- rev(ax$widths)
ax$grobs <- rev(ax$grobs)
ax$grobs[[1]]$x <- ax$grobs[[1]]$x - unit(1, "npc") + unit(0.15, "cm")
g <- gtable_add_cols(g, g2$widths[g2$layout[ia, ]$l], length(g$widths) - 1)
g <- gtable_add_grob(g, ax, pp$t, length(g$widths) - 1, pp$b)

# draw it
grid.draw(g)

# Automatically saving the plot
png(file = 'Directory\\Name.png', width = 850, height = 315, res=120)
grid.draw(g)
dev.off()
graphics.off()

###-----END-----

```