Insights from regional and short-term biodiversity monitoring datasets are valuable. A Reply to Daskalova et al. 2020 EcoEvoRxiv doi:10.32942/osf.io/cg3zs

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This manuscript is a reply to Daskalova, G. N., Phillimore, A. B. & Myers-Smith, I. H. Accounting for year effects and sampling error in temporal analyses of population and biodiversity change. Response to Seibold et al. 2019 "Arthropod decline in grasslands and forests is associated with landscape-level drivers". Nature, 574(7780), 671-674. EcoEvoRxiv (2020). doi:10.32942/osf.io/cg3zs. Both were under review at Nature for two rounds with reviews from four experts including one who was brought in in the second round due his/her statistical expertise. Finally, Nature decided not to publish both comments which we interpret as approval of our original approach as well as our response presented her.

Summary

Reports of major losses in biodiversity have stimulated an increasing interest in temporal population changes, particularly in insects, which had received little attention in the past. Existing long-term datasets are often limited to a small number of study sites, few points in time, a narrow range of land-use intensities and only some taxonomic groups, or they lack standardized sampling. While new multi-site monitoring programs have been initiated, most of them still cover rather short time periods. Daskalova et al. 2020[1] argue that temporal trends of insect populations derived from short time series are biased towards extreme trends, while their own analysis of an assembly of shorter- and longer-term time series does not support an overall insect decline. With respect to the results of Seibold et al.[2] based on a 10-year multi-site time series, they claim that the analysis suffers from not accounting for temporal pseudoreplication. In this note, we explain why the criticism of missing statistical rigour in the analysis of Seibold et al.[2] is not warranted. Models that include 'year' as random effect, as suggested by Daskalova et al. 2020, fail to detect non-linear trends and assume that consecutive years are independent samples which is questionable for insect time-series data. We agree with Daskalova et al. 2020 that the assembly and analysis of larger datasets is urgently needed, but it will take time until such datasets are available. Thus, short-term datasets like ours are highly valuable, should be extended and analysed continually to provide a more detailed understanding of how insect populations are changing under the influence of global change, and to trigger immediate conservation actions.

Appropriate statistical analysis

We would like to thank Daskalova et al. 2020 for critically reanalysing our published data set. The credibility and public acceptance of science depends on a culture of rigorous peer review, both before and after publication of a study. In essence, the critique of Daskalova et al. 2020 hinges on the point whether the variable 'year', which Seibold et al.[2] included as a continuous variable to test for linear changes over time and for analysing effects of land-use measures on temporal trends, should also be included as a random effect. In principle, adding a random term for time (i.e. year) would account for the fact that several

measurements taken in the same year are simultaneously affected by year-to-year variation in environmental conditions. Daskalova et al. 2020 re-analyzed the data of Seibold et al.[2] using a modelling approach presented in VanLeeuwen et al.[3], which includes a normal random intercept with a common variance to each year. However, the units of random terms in this model are assumed to be independent from each other[3]. This assumption is questionable for insect time-series data. Yearly changes in insect population size have been shown to depend on density-independent factors such as winter and spring temperature[4,5], but there is also substantial evidence for density-dependent effects[6]. Thus, consecutive years do not represent a random set of samples[7]. In addition, the model presented in VanLeeuwen et al.[3] was developed to deal with multiple observations from the same site in the same year, in contrast to the analysis of Seibold et al.[2] with only one observation per site and year. Therefore, applying such a model to the data of Seibold et al.[2] is inappropriate. Rather than using a random effect for each year, the models presented by Seibold et al.[2] adjust for year-to-year variation in environmental conditions directly, by including annual and site-specific temperature and precipitation, two major drivers of insect populations. Compared with the model in Daskalova et al. 2020 (their Extended Data Fig. 1) the models in Seibold et al.[2] (their Fig. 1) show a better model fit, indicating that weather conditions and land-use parameters indeed explain considerably more variation than simply including year as random factor.

If a model includes 'year' both as continuous fixed effect and as random effect, as suggested by Daskalova et al. 2020, potential nonlinear developments over time are subsumed by the random effect. It is not surprising that such models fail to detect temporal trends, if nonlinear developments over time occurred. To investigate the occurrence of nonlinear effects, we fitted a model using fixed treatment contrasts, comparing each year to the reference 2008 instead of the random intercepts and including land-use and weather variables as in the original models of Seibold et al.[2] (Supplementary information). We used 95% sequential confidence intervals for each of the six models, which compare the mean change between two subsequent years, either directly or on the log scale for Poisson models. In line with the descriptive analysis (Fig. 1 in Seibold et al.[2]), a decrease from 2008 to 2009 and further from 2009 to 2010 can be observed for the grassland models (Fig. 1). This shows that nonlinear developments over time occurred and that high arthropod numbers in 2008 contributed to the overall decline in grasslands, but are not solely responsible for it. No indication could be found that high arthropod numbers in 2008 were caused by some kind of artefact (Supplementary Information S3 in Seibold et al.[2]). Our reanalysis shows that biomass and species numbers in forests also decreased over time, although in later years (Fig. 1). We would also like to point out that the analysis of gamma diversity in Seibold et al.[2], which showed a decline in overall species number across all study sites for forests and grasslands, is not affected by these considerations, as the bootstrapping approach allows comparisons between individual years and inference based on comparison of confidence intervals[8]. Thus, both the more complex reanalyses presented here and the analysis of gamma diversity in Seibold et al.[2] confirm that arthropods declined in both grasslands and forests, in all but one metric, i.e. arthropod abundance in forests. Finally, we want to stress that even the reanalyses of Daskalova et al. 2020, with limited power to detect temporal trends, found significant declines in arthropods in at least one metric in both grasslands and forests, supporting the overall finding of arthropod decline in both habitats.
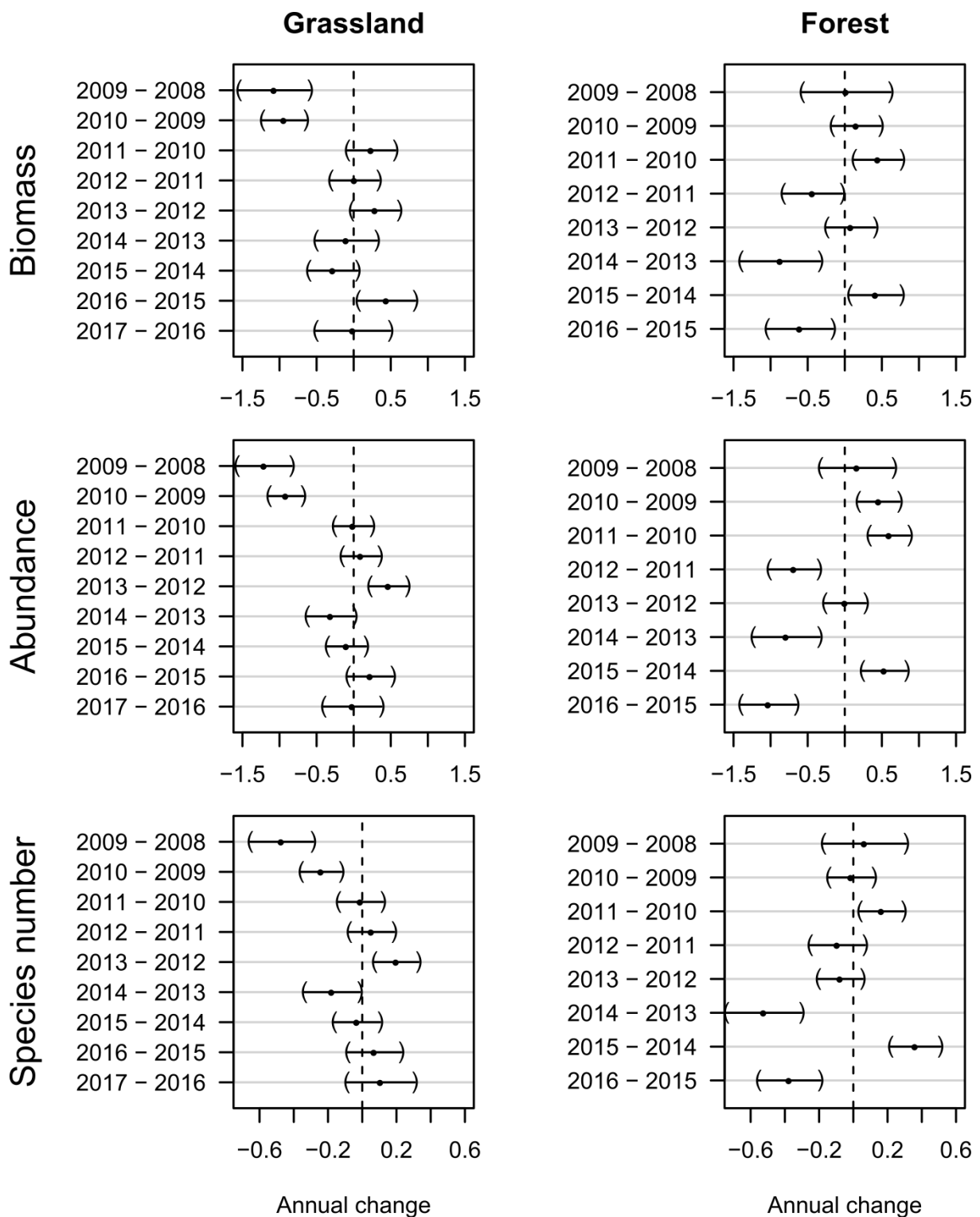
Figure 1: Temporal patterns of arthropods in 150 grasslands and 30 forests in Germany based on data from Seibold et al.[2].

Mean change between two subsequent years, either directly for biomass or on the log scale for abundance and species number, based on models using fixed-treatment contrasts comparing each year to the reference 2008 and presenting simultaneous 95% sequential confidence intervals. Models contained temperature, precipitation, local land-use intensity, cover of arable field and cover of grasslands within 1000 m radius as covariates and site

nested in region as random effects to account for the nested structure of study sites within three regions. Poisson models contained an observation-specific random effect to account for overdispersion.

Regional and global patterns

Daskalova et al. 2020 2020 proceed by analysing a heterogeneous global dataset of aquatic and terrestrial time series from the BioTIME database[9] and by reanalysing the data compilation from the meta-analysis by van Klink et al.[10]. From these analyses, they report declines in abundance of terrestrial insects in the data of van Klink et al.[10], and in biomass of aquatic invertebrates in the BioTIME data. Although Daskalova et al. 2020 acknowledge that declines "could potentially be occurring in certain parts of the world and/or for specific taxa", their main conclusion is that there was no evidence for an overall decline of invertebrates. It is not surprising that there are places where invertebrate biomass, abundance or species numbers have not declined, as reported also by Van Klink et al.[10]. But it is also important to analyse such datasets in more detail with regard to differences between regions, habitat types and taxa instead of focussing only on overall trends. Seibold et al.[2] were careful in drawing conclusions from their dataset and neither extrapolated results beyond a Central European perspective nor beyond the studied time period (2008-2017). Regional observations should be taken seriously and conservation measures should be implemented in regions where insects are declining[11], even if this might not reflect a global trend. For taxa such as birds and mammals, for which long-term, standardized and global datasets exist, major losses in biodiversity are undisputed[12,13], but such datasets do not exist for invertebrates. Nevertheless, there is an increasing number of studies that reported declines in the long[14,15], medium[16,17] and short[2] term and investigated their drivers. Short-term studies may be more likely to find extreme trends, as pointed out by Daskalova et al. 2020, but long-term studies often suffer from less standardized sampling or opportunistic site selection limiting their ability to detect trends and underlying drivers[14,18]. The strength of the data of Seibold et al.[2] is the well-selected underlying gradient of land-use intensity at local and landscape scale, replicated in three regions, which allowed inferences about the drivers of the observed declines. The fact that an increasing number of studies is now published, which differ in study system, results and insights, suggests that the scientific process is intact. Seibold et al.[2] have been very careful in phrasing their findings, as did e.g. Hallmann et al.[16] and many others. Thus, we disagree with Daskalova et al. 2020 that studies reporting a decline have been alarmist. However, as put succinctly by Lindenmayer et al.[19], the purpose of monitoring cannot be the passive observation of species decline until extinction. Instead, monitoring should inform actions, and in a first step this includes publishing and discussion of results.

Conclusions

In conclusion, we disagree with Daskalova et al. 2020 that the results of Seibold et al.[2] are based on flawed statistics and suggest that their model structure with 'year' as both fixed and random factor should be interpreted with caution. We agree, however, that observational data have to be interpreted with great care, especially when time series are short. Nevertheless, short time series also contribute important knowledge about arthropod population trends, particularly if monitoring is highly standardized, well-replicated and conducted along environmental gradients relevant for decision makers as in the case of Seibold et al.[2]. Hence, we believe that it is important to publish findings irrespective of whether observed trends are negative, positive or neutral, as long as sampling and statistical analysis are sound.

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Supplementary Information

Link to data from Seibold et al. 2019:

https://www.bexis.uni-jena.de/PublicData/PublicDataSet.aspx?DatasetId=25786

R-code used for reanalysing data from Seibold et al. 2019:

```
library(lme4)
library(multcomp)
library(vegan)


#### Load Data und subset to habitat type
data <- read.csv("25786.txt", sep = "\t", header = TRUE)

forest_140 <- subset(data, Habitat_type == "forest")
forest_30 <-subset(forest_140, Sampling_regime=="annual")
grassland <- subset(data, Habitat_type == "grassland")

# scale predictors to zero mean and unit variance
grassland$year_st <- decostand(grassland$CollectionYear, "standardize")
grassland$landuse_st <- decostand(grassland$landuse_intensity, "standardize")
grassland$grassland_st <- decostand(grassland$grassland_cover_1000, "standardize")
grassland$arable_st <- decostand(grassland$arable_cover_1000, "standardize")
grassland$temperature_st <- decostand(grassland$mean_winter_temperature, "standardize")
grassland$precipitation_st <- decostand(grassland$precipitation_sum_growing_preriod, "standardize")

forest_30$year_st <- decostand(forest_30$CollectionYear, "standardize")
forest_30$landuse_st <- decostand(forest_30$landuse_intensity, "standardize")
forest_30$grassland_st <- decostand(forest_30$grassland_cover_1000, "standardize")
forest_30$arable_st <- decostand(forest_30$arable_cover_1000, "standardize")
forest_30$temperature_st <- decostand(forest_30$mean_winter_temperature, "standardize")
forest_30$precipitation_st <- decostand(forest_30$precipitation_sum_growing_preriod, "standardize")

# create observation-specific factor
grassland$obs <- seq(1:nrow(grassland))
forest_30$obs <- seq(1:nrow(forest_30))

# create year as factor
grassland$year_f <- as.factor(grassland$CollectionYear)
forest_30$year_f <- as.factor(forest_30$CollectionYear)

##### Original models of Seibold et al. plus year as factor

### Grassland
# Biomass
m.biomass_g <-lmer(log(biomass+1)~  temperature_st*precipitation_st
                    + year_st* landuse_st + year_st*arable_st + year_st* grassland_st
                    +(1|Exploratory/PlotID) +
                    year_f - year_st,
                    data = grassland)
# Abundance
m.abundance_g <-glmer(abundance_identified~  temperature_st*precipitation_st
                    + year_st* landuse_st + year_st*arable_st + year_st* grassland_st
                    +(1|Exploratory/PlotID)+(1|obs) +
                    year_f - year_st,
                    family=poisson,data = grassland,
                    control=glmerControl(optimizer="bobyqa",optCtrl=list(maxfun=10000)))


# Species
m.species_g <-glmer(species~  temperature_st*precipitation_st
                    + year_st* landuse_st + year_st*arable_st + year_st* grassland_st
                    +(1|Exploratory/PlotID)+(1|obs) +
                    year_f - year_st,
                    family=poisson,data = grassland,
                    control=glmerControl(optimizer="bobyqa",optCtrl=list(maxfun=10000)))
```

```
### Forest
# Biomass
m.biomass_f <-lmer(log(biomass+1)~  temperature_st*precipitation_st
                    + year_st* landuse_st + year_st*arable_st + year_st* grassland_st
                    +(1|Exploratory/PlotID) +
                    year_f - year_st,
                    data = forest_30)
# Abundance
m.abundance_f <-glmer(abundance_identified~  temperature_st*precipitation_st
                    + year_st* landuse_st + year_st*arable_st + year_st* grassland_st
                    +(1|Exploratory/PlotID)+(1|obs) +
                    year_f - year_st,
                    family=poisson,data = forest_30,
                    control=glmerControl(optimizer="bobyqa",optCtrl=list(maxfun=10000)))


# Species
m.species_f <-glmer(species~  temperature_st*precipitation_st
                    + year_st* landuse_st + year_st*arable_st + year_st* grassland_st
                    +(1|Exploratory/PlotID)+(1|obs) +
                    year_f - year_st,
                    family=poisson,data = forest_30,
                    control=glmerControl(optimizer="bobyqa",optCtrl=list(maxfun=10000)))




pdf(file = "Figure1.pdf",width = 4.7, height = 6)

par(mfcol=c(3,2),mai=c(0.2,1.1,0.4,0.01))
plot(confint(glht(m.biomass_g , linfct = mcp("year_f" = "Sequen"))), main="Grassland", xlab="");mtext("Biomass",2,line=7)

par(mai=c(0.4,1.1,0.2,0.01))
plot(confint(glht(m.abundance_g, linfct = mcp("year_f" = "Sequen"))), main="", xlab="");mtext("Abundance",2,line=7)

par(mai=c(0.6,1.1,0.0,0.01))
plot(confint(glht(m.species_g, linfct = mcp("year_f" = "Sequen"))), main="", xlab="Annual change");mtext("Species",2,line=7)

par(mai=c(0.2,1.1,0.4,0.01))
plot(confint(glht(m.biomass_f , linfct = mcp("year_f" = "Sequen"))), main="Forest", xlab="")

par(mai=c(0.4,1.1,0.2,0.01))
plot(confint(glht(m.abundance_f, linfct = mcp("year_f" = "Sequen"))), main="", xlab="")

par(mai=c(0.6,1.1,0.0,0.01))
plot(confint(glht(m.species_f, linfct = mcp("year_f" = "Sequen"))), main="", xlab="Annual change")


dev.off(); system("open Figure1.pdf")
```

Citation for public data set:
Seibold, S. Goßner, M.M., Simons, N., Blüthgen, N., Müller, J., Ambarli, D., Ammer, C., Bauhus, J., Fischer, M., Fürstenau, C., Habel, J.C., Linsenmair, K.E., Nauss, T., Ostrowski, A., Penone, C., Prati, D., Schall, P., Schulze, E.-D., Vogt, J., Wöllauer, S. & Weisser, W. (2020): Arthropod data from 150 grassland plots, 2008-2017, and 140 forest plots, 2008-2016, used in "Arthropod decline in grasslands and forests is associated with drivers at landscape level", Nature. v1.3.11. Biodiversity Exploratories Information System. Dataset. https://doi.org/10.25829/bexis.25786-1.3.11