**Supplementary Information**

**Insights from regional and short-term biodiversity monitoring datasets are valuable: a Reply to Daskalova *et al.* 2021**

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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