
Supplementary material

Appendix 1. Code for data processing and analyses.
Appendix 2. Additional analyses and results.
Appendix 1

**R code for data processing and analyses 2019-10-07**

This document contains the code used to process and analyse the data used in the paper Block et al. 2019. Phenological plasticity is a poor predictor of subalpine plant population performance following experimental climate change. Oikos. doi:10.1111/oik.06667.

Many species shift their phenology in response to changing climates, but we still ignore if these shifts have consistent consequences for species population performance. Here we analyse the relationship between phenological shifts and cover changes following transplantation of intact subalpine plant communities from a site at 2000 m elevation to a similar site at 1400 m elevation in the Swiss Alps, thereby imposing ca. 3 K of warming.

Before going on with the data processing and analysis, these are the details of the operating system and R session in which the following code was run.

```r
sessionInfo()
```

```
## R version 3.3.0 (2016-05-03)
## Platform: x86_64-apple-darwin13.4.0 (64-bit)
## Running under: OS X 10.13.6 (unknown)
##
## locale:
## [1] C

## attached base packages:
## [1] stats graphics grDevices utils datasets methods base
##
## loaded via a namespace (and not attached):
## [1] backports_1.1.2 magrittr_1.5 rprojroot_1.3-2 tools_3.3.0
## [5] htmltools_0.3.6 yaml_2.1.16 Rcpp_0.12.14 stringi_1.1.6
## [9] rmarkdown_1.8 knitr_1.18 stringr_1.2.0 digest_0.6.13
## [13] evaluate_0.10.1
```

**Prepare species cover data**

**3-year experiment**

We start by loading and cleaning the cover data from our main experiment.

```r
# First we load the raw data
releves <- read.csv("data/3y_cover_data.csv")

# Now data cleaning
# This solves an inconsistency in species naming
releves$Species_Name <- gsub(" Trifolium", "Trifolium", releves$Species_Name)

# Eliminates an experimental manipulation irrelevant for current study
releves <- subset(releves, Species_Name != "Focal Trifolium" | Species_Name != "")

# Remove rows without turf ID, and makes ID a factor for easier manipulation below
releves <- subset(releves, Plot_ID != "")
releves$Plot_ID <- factor(releves$Plot_ID)
```
The next step is to calculate the changes in cover of each species in every turf. We measured cover changes as the natural logarithm of the ratio between the final cover (summer 2016) and the initial cover (summer 2014). We added a constant (0.25) to both the final and initial covers to be able to calculate the logarithm in cases where the final cover was 0. Estimations of cover changes for species with very low values of percent cover in a turf are difficult and relatively unreliable. Therefore, we analysed the data including only species with various minimum values of initial or final cover (min.cov). These variations in the analysis produce qualitatively consistent results, so here we don’t exclude species with low cover values.

```r
# Define values required in the calculations and data filtering below.
# Our results are robust to variation in these values.
cr.con <- 0.25 # constant added to cover values to take the log of their ratio
min.cov <- 0 # minimum cover of a species in a plot to be considered in the analysis
min.n <- 3 # minimum number of plots a species must be in both treatments

# Make lists of species in the warming treatment, control treatment, and both
# These lists will help us to extract data from the `releves` dataset.
warmSp <- levels(factor(subset(releves, Site == "Nes")$Species_Name)) # Warming
coldSp <- levels(factor(subset(releves, Site == "Cal")$Species_Name)) # Control
sharedSp <- coldSp[coldSp %in% warmSp] # Species present in both treatments

# Create empty vectors to store information we will need in the analysis
Species <- character()
Plot <- character()
Treatment <- character()
Initial.Cover <- numeric()
Final.Cover <- numeric()

# This loop extracts relevant data from `releves`
for (s in sharedSp) {
  sp.s <- subset(releves, Species_Name == s) # subset data for only that species
  for (p in levels(factor(sp.s$Plot_ID))) { # and for each turf
    sp.s.p <- subset(sp.s, Plot_ID == p) # subset data for that plot
    if (nrow(sp.s.p) > 1) { # if there is more than one observation...
      Species = c(Species, s)
      Plot = c(Plot, p)
      Treatment = c(Treatment, ifelse(sp.s.p$Site[1] == "Nes", "Warming", "Control"))
      Initial.Cover = c(Initial.Cover, subset(sp.s.p, year == min(sp.s.p$year))$Cov[1])
    # if there is no data for 2016, the species final cover was 0
      Final.Cover = c(Final.Cover, ifelse(max(sp.s.p$year) == 2016, subset(sp.s.p, year == 2016)$Cov[1], 0))
    }
    if (nrow(sp.s.p) == 1 & sp.s.p$year != 2016) {
      # Add any necessary steps here
    }
  }
}
```
# if there is only one observation and it’s prior to 2016, 
# the final cover is 0
Species = c(Species, s)
Plot = c(Plot, p)
Treatment = c(Treatment,
  ifelse(sp.s.p$Site[1] == "Nes", 
    "Warming", "Control"))
Initial.Cover = c(Initial.Cover, sp.s.p$Cov[1])
Final.Cover = c(Final.Cover, 0)
}
}
rm(p, s)

# Now we combine the individual vectors into a data frame
dynamics <- data.frame(Species = Species, Plot = Plot,
  Treatment = Treatment, Initial.Cover = Initial.Cover,
  Final.Cover = Final.Cover)
rm(Species, Plot, Treatment, Initial.Cover, Final.Cover)

# And calculate the cover changes
dynamics$log.CR <- log((dynamics$Final.Cover+cr.con)/(dynamics$Initial.Cover+cr.con))

# Excludes cases low initial and final cover values
dynamics <- dynamics[dynamics$Initial.Cover > min.cov | dynamics$Final.Cover > min.cov,]
dynamics$Species <- factor(dynamics$Species)

4-year experiment

Now let us load, clean, and process the data from the 4-year transplant experiment. Of the 10 turfs in
the warming treatment of this experiment, two suffered severe disturbance by moles in 2016 and had to be
excluded from the analyses.

# Load data
ot.releve <- read.csv("data/4y_cover_data.csv")

# Make cover variable numeric instead of factor
ot.releve$Cov_Rel1 <- as.numeric(as.character(ot.releve$Cov_Rel1))

# Create new variable of cover with simpler name
ot.releve$Cov <- ot.releve$Cov_Rel1
    ot.releve$Cov_Rel2[ot.releve$Cov_Rel2 == ""] <- NA
    ot.releve$Cov_Rel2[ot.releve$Cov_Rel2 == "NF"] <- NA
    ot.releve$Cov_Rel2 <- as.numeric(as.character(ot.releve$Cov_Rel2))
    ot.releve$Cov[is.na(ot.releve$Cov_Rel2)] <- ot.releve$Cov_Rel2[is.na(ot.releve$Cov_Rel2)]
    ot.releve$Cov[is.na(ot.releve$Cov)] <- 0

# Exclude records without any cover measurements
ot.releve <- subset(ot.releve, !is.na(Cov))

# Exclude plots that suffered severe damage in 2016
ot.releve <- subset(ot.releve, !(Plot_ID == "NesBl3Sub1" | Plot_ID == "NesBl5Sub1"))
# Create Treatment column

```
ot.releve$Treatment <- ifelse(not.releve$Site == "Nes", "Warming", "Control")
```

The calculations of cover changes are exactly the same as for the 3-year experiment.

```
# Make lists of species in the warming treatment, control treatment, and both
# These lists will help us to extract data from the `releves` dataset.
not.warmSp <- levels(factor(subset(not.releve, Treatment == "Warming")$Species_Name))
not.coldSp <- levels(factor(subset(not.releve, Treatment == "Control")$Species_Name))
not.sharedSp <- coldSp[coldSp %in% warmSp]
```

# Create empty vectors to store information we will need in the analysis

```
Species <- character()
Plot <- character()
Treatment <- character()
Initial.Cover <- numeric()
Final.Cover <- numeric()
```

```
for (s in not.sharedSp) {
  sp.s <- subset(not.releve, Species_Name == s)  # subset data for only that species
  for (p in levels(factor(sp.s$Plot_ID))) {  # and for each of the turfs
    sp.s.p <- subset(sp.s, Plot_ID == p)  # subset data for that turf
    if (nrow(sp.s.p) > 1) {  # if there is more than one observation...
      Species = c(Species, s)
      Plot = c(Plot, p)
      Treatment = c(Treatment,
                    ifelse(sp.s.p$Site[1] == "Nes", "Warming", "Control"))
      Initial.Cover = c(Initial.Cover,
                        subset(sp.s.p, year == min(sp.s.p$year))$Cov[1])
    # if there is no data for 2016, the species final cover was 0
    Final.Cover = c(Final.Cover,
                    ifelse(max(sp.s.p$year) == 2016,
                           subset(sp.s.p, year == 2016)$Cov[1], 0))
    }
    if (nrow(sp.s.p) == 1 & sp.s.p$year != 2016) {
      Species = c(Species, s)
      Plot = c(Plot, p)
      Treatment = c(Treatment,
                    ifelse(sp.s.p$Site[1] == "Nes", "Warming", "Control"))
      Initial.Cover = c(Initial.Cover, sp.s.p$Cov[1])
    }
    Final.Cover = c(Final.Cover, 0)
  }
}
```

```
rm(p, s, sp.s, sp.s.p)
```
# Now we combine the individual vectors into a data frame

```r
ot.dynamics <- data.frame(Species = Species, Plot = Plot, Treatment = Treatment,
Initial.Cover = Initial.Cover, Final.Cover = Final.Cover)
```

```r
ot.dynamics <- subset(ot.dynamics, Initial.Cover != 0 | Final.Cover != 0)
```

```r
ot.dynamics$Initial.Cover <- ifelse(ot.dynamics$Initial.Cover == 0,
0.5, ot.dynamics$Initial.Cover)
```

```r
ot.dynamics$log.CR <- log((ot.dynamics$Final.Cover+cr.con)/(ot.dynamics$Initial.Cover+
cr.con))
```

```r
rm(Species, Plot, Treatment, Initial.Cover, Final.Cover)
```

Prepare phenology data

As usual, we start by loading the data.

```r
# Load phenology data from 3-year transplant experiment
phenology <- read.csv("data/phenology_data.csv")
```

Next, we need to correct several typos and inconsistencies in the data. The most notorious inconsistency is that, in some turfs, species were recorded as developing seeds before they were recorded in the flowering stage. Since angiosperms must flower before producing seeds, we assumed that flowering must have been observed (at least) during the survey previous to the survey in which developing seeds were observed.

```r
# Correct a typo in the date column
phenology$Date <- as.character(phenology$Date)
phenology$Date <- ifelse(phenology$Date == "21.09.20014", "21.09.14", phenology$Date)
```

```r
## Surveys in Calanda on weeks 28, 31, and 31 have missing values of date.
## When only some of the plots have a date, I assume all the plots at the site where
## surveyed on that date.
## When in one week only Nesselboden plots have a date, I assume the survey in Calanda
## happened one day after the survey in Nesselboden, as it commonly did.
phenology$Date <- ifelse(is.na(phenology$Date) & phenology$Week == 28,
"07.07.14", phenology$Date)
phenology$Date <- ifelse(is.na(phenology$Date) & phenology$Week == 30,
"24.07.14", phenology$Date)
phenology$Date <- ifelse(is.na(phenology$Date) & phenology$Week == 31,
"30.07.14", phenology$Date)
phenology$Date <- as.Date(phenology$Date, "%d.%m.%y")
```

```r
## Correct seeding before flowering anomaly
all.plots <- levels(factor(phenology$Plot))
```

```r
mistake <- logical()
species <- character()
turf <- character()
```

```r
# We will look for mistakes only for those species which we will analyse
# (i.e., those with enough cover dynamics data)
# Let's make a list of those species both in the 3-year and the 4-year experiments
useful.species <- unique(c(sharedSp, ot.sharedSp))
```
for (j in 1:length(useful.species)) {

    # Create a character string to select the required columns in the phenology data
    n.names <- length(strsplit(useful.species[j], " ")[1])
    sp.i.name <- strsplit(useful.species[j], " ")[1][1]

    ## This loop replaces spaces with points in the species name
    for (i in 2:n.names) {
        sp.i.name <- paste(sp.i.name,
            strsplit(useful.species[j], " ")[1][i], sep = ".")
    }

    sp.i.name.flower <- paste(sp.i.name, ",C", sep = "")
    sp.i.name.seed <- paste(sp.i.name, ",D", sep = "")

    # Find and correct mistakes
    for (i in 1:length(all.plots)) {
        x <- subset(phenology, Plot == all.plots[i])
        date.flower <- min(x$Date[which(!is.na(x[, which(names(x) == sp.i.name.flower)))]))
        date.seed <- min(x$Date[which(!is.na(x[, which(names(x) == sp.i.name.seed)))]])
        mistake <- c(mistake,
            ifelse(date.flower > date.seed & !is.infinite(date.flower),
                TRUE, FALSE))
        species <- c(species, useful.species[j])
        turf <- c(turf, all.plots[i])

        # Correct mistakes
        if (date.flower > date.seed & !is.infinite(date.flower)) {
            week.correction <- x$Week[x$Date == date.seed] - 1
            id.code <- paste('2014W',
                week.correction, all.plots[i],
                'Plot', sep = 't')
            sp.column <- which(names(phenology) == sp.i.name.flower)
            phenology[phenology$ID_Code == id.code, sp.column] <- 990
        }
    }
}

rm(x, date.flower, date.seed)
rm(sp.i.name.flower, sp.i.name.seed)

mistake.report <- data.frame(Species = species, Plot = turf, Mistake = mistake)
rm(species, turf, mistake)

# The following object indicates which species in which turfs were identified as
# mistakes, and corrected accordingly
mistake.report <- mistake.report[mistake.report$Mistake == T,]

Now that the data is clean, we can estimate the time of first flowering of each species in every turf.

# Create a data frame to store the flowering times of each species in every turf
flowering.times <- data.frame(Species = character(),
Plot = character(),
Treatment = character(),
Flowering.Time = character()

for (j in 1:length(useful.species)) { # For each species with enough cover data...
  # Create a character string to select the relevant columns in the phenology data
  n.names <- length(strsplit(useful.species[j], " ")[[1]])
  sp.i.name <- strsplit(useful.species[j], " ")[[1]][1]

  ## This loop replaces spaces with points in the species name
  for (i in 2:n.names) {
    sp.i.name <- paste(sp.i.name,
      strsplit(useful.species[j], " ")[[1]][i], sep = ".")
  }

  sp.i.name.ps <- paste(sp.i.name, "_C", sep = "")

  # Now, for each of the 20 turfs...
  for (i in 1:length(levels(phenology$Plot))) {
    # Subset data for that turf
    x <- subset(phenology, Plot == levels(phenology$Plot)[i])

    # And look when flowering in turf 'i' was first observed
    date.obs <- min(
      x$Date[which(!is.na(x[, which(names(x) == sp.i.name.ps)))]))

    # But flowering must have happened before it was observed,
    # so we need to estimate the time of first flowering
    index.pd <- which(x$Date == date.obs) - 1
    if (length(index.pd) > 0) {
      if (index.pd != 0) {
        last.survey <- x[index.pd,]$Date
        date.event <- date.obs - ((date.obs - last.survey) / 2)
      }
    }
    if (index.pd == 0) {
      date.event <- date.obs - 3.5
    }
    else {
      date.event <- NA
    }

    # Now we can add this information to the `flowering.times` dataframe
    new.row <- data.frame(Species = useful.species[j],
      Plot = levels(phenology$Plot)[i],
      Treatment = ifelse(x$Site[1] == "Cal", "Control", "Warming"),
      Flowering.Time = date.event)

    flowering.times <- rbind(flowering.times, new.row)
  }
}
The observed time of first flowering of a species in a plot could depend on the abundance of the species in that plot. Therefore, we will use the initial and final cover of species in each plot where they were observed as covariates when estimating the magnitude of their phenological shifts.

```
flowering.times$iCover <- numeric(nrow(flowering.times))
flowering.times$fCover <- numeric(nrow(flowering.times))

for (i in 1:nrow(flowering.times)) {
    sp.i <- as.character(flowering.times[i,]$Species)
    plot.i <- as.character(flowering.times[i,]$Plot)
    icov.i <- subset(dynamics, Species == sp.i & Plot == plot.i)$Initial.Cover
    fcov.i <- subset(dynamics, Species == sp.i & Plot == plot.i)$Final.Cover
    flowering.times$iCover[i] <- ifelse(length(icov.i) == 0, 0.5, icov.i)
    flowering.times$fCover[i] <- ifelse(length(fcov.i) == 0, 0, fcov.i)
}
```

Estimate shifts in flowering time and changes in cover

Before calculating the effects of climate change on flowering time and cover changes, let’s select the species with enough replication (i.e., species present in at least three plots in both treatments) and discard those species for which we missed the start of flowering (i.e., defined as those species observed flowering in more than half the plots in which they were present at the time of the first survey in late April 2014). We will do this for the cover change data from both the 3-year and 4-year experiments.

```
## Phenology data
## Discard species without enough replication
all.useful <- logical()

for (sp in levels(flowering.times$Species)) {
    x <- subset(flowering.times, Species == sp)
    nc <- nrow(subset(x, Treatment == "Control"))
    nw <- nrow(x) - nc
    all.useful <- c(all.useful, ifelse(nw >= min.n & nc >= min.n, TRUE, FALSE))
}
rm(x, nc, nw)
```

sps.3cw <- levels(flowering.times$Species)[all.useful]
useful.ft <- flowering.times[flowering.times$Species %in% sps.3cw, ]
useful.ft$Species <- factor(useful.ft$Species)

## Exclude species for which we probably missed the start of flowering
too.early <- logical()
for (sp in levels(useful.ft$Species)) {
    median.ft <- round(summary(subset(useful.ft,
            Treatment == "Warming" &
            Species == sp)$Flowering.Time)[3])
    too.early <- c(too.early,
            ifelse(median.ft == as.Date("2014-04-20", origin = "1970-01-01"),
            FALSE, TRUE))
    rm(median.ft)
}

sps.nte <- levels(useful.ft$Species)[too.early]
useful.ft <- useful.ft[useful.ft$Species %in% sps.nte, ]
useful.ft$Species <- factor(useful.ft$Species)

## Cover changes - 3-year experiment
### Add species minimum cover (0.5) to turfs where a species was observed flowering but
### was not recorded as present
dynamics$id <- paste(dynamics$Species, dynamics$Plot, sep = ".")
flowering.times$id <- paste(flowering.times$Species, flowering.times$Plot, sep = ".")


names(dynamics)

names(flowering.times)

## [1] "Species" "Plot" "Treatment" "Flowering.Time"
## [5] "Initial.Cover" "Final.Cover" "id"

names(dynamics)

## [1] "Species" "Plot" "Treatment" "Initial.Cover"
## [5] "Final.Cover" "log.CR" "id"

dynamics$Flowering.Time <- NA
dynamics <- dynamics[,c(1:3, 8, 4:7)] # reorder columns
dynamics <- dynamics[, -7]
dynamics <- rbind(dynamics, flowering.times)
dynamics <- dynamics[, -4]
dynamics <- unique(dynamics)

dynamics$log.CR <- log(((dynamics$Final.Cover+cr.con)/(dynamics$Initial.Cover+cr.con))


dynamics$Species <- factor(dynamics$Species)

### Discard species without enough replication
all.useful <- logical()
for (sp in levels(dynamics$Species)) {
    x <- subset(dynamics, Species == sp)
    nc <- nrow(subset(x, Treatment == "Control"))
    nw <- nrow(x) - nc

    all.useful <- c(all.useful, ifelse(nw >= min.n & nc >= min.n, TRUE, FALSE))
}

sps.3cw <- levels(dynamics$Species)[all.useful]
useful.dyn <- dynamics[dynamics$Species %in% sps.3cw, ]
useful.dyn$Species <- factor(useful.dyn$Species)

## Cover changes - 4-year experiment

### Discard species without enough replication
all.useful <- logical()

for (sp in levels(ot.dynamics$Species)) {
    x <- subset(ot.dynamics, Species == sp)
    nc <- nrow(subset(x, Treatment == "Control"))
    nw <- nrow(x) - nc

    all.useful <- c(all.useful, ifelse(nw >= min.n & nc >= min.n, TRUE, FALSE))
}

sps.3cw <- levels(ot.dynamics$Species)[all.useful]
useful.ot <- ot.dynamics[ot.dynamics$Species %in% sps.3cw, ]
useful.ot$Species <- factor(useful.ot$Species)

Now, to quantify the effects of climate change (i.e, transplantation to lower elevation) we will fit a linear model of the effect of treatment on flowering time and cover change. This allows us to incorporate a species’ initial cover as a covariate, since the abundance of a species in a plot can influence the observed time of first flowering as well as the likelihood to observe a change in cover.

# Model-based estimation of flowering shifts
sps <- levels(useful.ft$Species) # vector with species names
phenshift.est <- numeric(length(sps))
phenshift.se <- numeric(length(sps))
phenshift.pval <- numeric(length(sps))

for (i in 1:length(sps)) {
    sal <- subset(useful.ft, Species == sps[i])
    sal$Flowering.Time <- as.numeric(sal$Flowering.Time)
    phen.model <- lm(Flowering.Time ~ Treatment + iCover, sal)
    phenshift.est[i] <- summary(phen.model)$coefficients[2,1]
    phenshift.se[i] <- summary(phen.model)$coefficients[2,2]
    phenshift.pval[i] <- summary(phen.model)$coefficients[2,4]
    rm(sal)
}

phenshifts <- data.frame(sps, phenshift.est, phenshift.se, pval = phenshift.pval)
We classified species as early or late flowering depending on whether their median flowering time in the control treatment was before or after the 1st of June, 2014.

phengroup <- character()

for (sp in levels(flowering.times$Species)) {
  sp.ft <- median(subset(flowering.times, Treatment == "Control" & Species == sp)$Flowering.Time)
  phengroup <- c(phengroup, ifelse(sp.ft < as.Date("2014-06-01", origin = "1970-01-01"),}
Fitting models

After merging phenology and cover dynamics data, we are ready to fit models to test for the effects of phenological shifts on cover responses to climate change, and see whether these effects differ among early- and late-flowering species. First we look at data from the 3-year experiment.

# Combine data sets with phenological shifts and cover change data
mod.pd <- merge(phenshifts, covresps)
mod.pd <- merge(mod.pd, phengroups)

# Load data with species' Landolt indicator values (from infoflora.ch)
species_landolt <- read.csv("data/species_landolt.csv")
names(species_landolt)[1] <- "sps"
mod.pd <- merge(mod.pd, species_landolt, all.x = T)

# Multiple regression to test for effect of phenological shift, phenological group,
# and their interaction
library(car)
model <- lm(covresp.est ~ phenshift.est * phengroup, mod.pd)
Anova(model)

## Anova Table (Type II tests)
## Response: covresp.est
## Sum Sq Df F value Pr(>F)
## phenshift.est 0.0839 1 0.1425 0.7115
## phengroup 0.0188 1 0.0320 0.8607
## phenshift.est:phengroup 0.0000 1 0.0001 0.9935
## Residuals 8.2463 14

model2 <- lm(covresp.est ~ phenshift.est + T, mod.pd)
Anova(model2)

## Anova Table (Type II tests)
## Response: covresp.est
## Sum Sq Df F value Pr(>F)
## phenshift.est 0.0064 1 0.0109 0.9185
## T 0.1121 1 0.1898 0.6702
## Residuals 7.6791 14

# Plot the results
plot(covresp.est ~ phenshift.est, mod.pd, ylim=range(c(mod.pd$covresp.est-mod.pd$covresp.se, mod.pd$covresp.est+mod.pd$covresp.se)), xlim=range(c(mod.pd$phenshift.est-mod.pd$phenshift.se, mod.pd$phenshift.est+mod.pd$phenshift.se),)

mod.pd$phenshift.est+mod.pd$phenshift.se)),
pch=19, xlab="Phenological shift (days)",
ylab="Cover response to climate change", col = "gray")

with(mod.pd,

    arrows(phen.shift.est, covresp.est-covresp.se,
            phen.shift.est, covresp.est+covresp.se,
            length=0.025, angle=90, code=3, col = "gray")
)

with(mod.pd,

    arrows(phen.shift.est-phen.shift.se, covresp.est,
            phen.shift.est+phen.shift.se, covresp.est,
            length=0.025, angle=90, code=3, col = "gray")
)

gc.cols <- ifelse(mod.pd$phengroup == "Early", "blue", "red")

points(mod.pd$phenshift.est, mod.pd$covresp.est, col = gc.cols)
abline(lm(covresp.est ~ phenshift.est, subset(mod.pd, phengroup == "Early")),
       col = "blue", lwd = 1.5)
abline(lm(covresp.est ~ phenshift.est, subset(mod.pd, phengroup == "Late")),
       col = "red", lwd = 1.5)

# Do results differ if we include species' mean initial cover as a covariate? They don't
## (Since the bounded nature of the percentage cover variable means that
## abundant species are more likely to show large decreases in cover)
spcovs <- with(dynamics, tapply(Initial.Cover, Species, mean))

mod.pd$spcovs <- spcovs[.names(spcovs) %in% levels(mod.pd$sps)]
plot(covresp.est ~ spcovs, mod.pd)

summary(lm(covresp.est ~ phenshift.est * phengroup + spcovs, mod.pd))

# Call:
# lm(formula = covresp.est ~ phenshift.est * phengroup + spcovs, 
#     data = mod.pd)
#
# Residuals:
# Min 1Q Median 3Q Max
# -1.50160 -0.21824 0.07986 0.45923 0.86339
#
# Coefficients:
# Estimate Std. Error t value Pr(>|t|)
# (Intercept) -0.193917 0.519213 -0.373 0.715
# phenshift.est -0.001019 0.014960 -0.068 0.947
# phengroupLate -0.354487 0.692954 -0.512 0.618
# spcovs -0.044292 0.049345 -0.898 0.386
# phenshift.est:phengroupLate -0.008126 0.032426 -0.251 0.806
#
# Residual standard error: 0.7729 on 13 degrees of freedom
# Multiple R-squared: 0.06861, Adjusted R-squared: -0.218
# F-statistic: 0.2394 on 4 and 13 DF, p-value: 0.911

Anova(lm(covresp.est ~ phenshift.est * phengroup + spcovs, mod.pd))

# Anova Table (Type II tests)
#
# Response: covresp.est
# Sum Sq Df F value Pr(>F)
# phenshift.est 0.0299 1 0.0501 0.8264
# phengroup 0.1627 1 0.2724 0.6105
Cover responses to climate change were uncorrelated to the magnitude of phenological shifts and did not depend on whether species flowered early or late. These results were replicated in the analysis of the 4-year experiment.

```r
# Combine data sets with phenological shifts and cover change data
mod.pd.ot <- merge(phenshifts, covresps.ot)
mod.pd.ot <- merge(mod.pd.ot, phengroups)
mod.pd.ot <- merge(mod.pd.ot, species_landolt, all.x = T)

# Multiple regression to test for effect of phenological shift, phenological group, # and their interaction
library(car)
model.ot <- lm(covresp.est ~ phenshift.est * phengroup, mod.pd.ot)
Anova(model.ot)

## Anova Table (Type II tests)
##
## Response: covresp.est
## Sum Sq Df F value Pr(>F)
## phenshift.est 0.6107 1 0.5399 0.4755
## phengroup 0.0035 1 0.0031 0.9567
## phenshift.est:phengroup 1.1304 1 0.9993 0.3357
## Residuals 14.7048 13

model.ot2 <- lm(covresp.est ~ phenshift.est + T, mod.pd.ot)
Anova(model.ot2)

## Anova Table (Type II tests)
##
## Response: covresp.est
## Sum Sq Df F value Pr(>F)
## phenshift.est 2.5625 1 3.6618 0.07982 .
## T 4.1362 1 5.9106 0.03166 *
## Residuals 8.3976 12
## ---
## Signif. codes: 0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

# Plot the results
plot(covresp.est ~ phenshift.est, mod.pd.ot, 
 ylim=range(c(mod.pd.ot$covresp.est-mod.pd.ot$covresp.se, 
 mod.pd.ot$covresp.est+mod.pd.ot$covresp.se)),
 xlim=range(c(mod.pd.ot$phenshift.est-mod.pd.ot$phenshift.se, 
 mod.pd.ot$phenshift.est+mod.pd.ot$phenshift.se)),
 pch=19, xlab="Phenological shift (days)",
 ylab="Cover response to climate change", col = "gray")
# add error bars (+/- 1 standard error)
with(mod.pd.ot,

 arrows(phenshift.est, covresp.est-covresp.se, 
 phenshift.est, covresp.est+covresp.se, 
 length=0.025, angle=90, code=3, col = "gray")
)
```
with(mod.pd.ot,  

    arrows(phenshift.est-phenshift.se, covresp.est,  
    phenshift.est+phenshift.se, covresp.est,  
    length=0.025, angle=90, code=3, col = "gray")  
)

pg.cols <- ifelse(mod.pd.ot$phengroup == "Early", "blue", "red")

points(mod.pd.ot$phenshift.est, mod.pd.ot$covresp.est, col = pg.cols)
abline(lm(covresp.est ~ phenshift.est, subset(mod.pd.ot, phengroup == "Early")),  
    col = "blue", lwd = 1.5)
abline(lm(covresp.est ~ phenshift.est, subset(mod.pd.ot, phengroup == "Late")),  
    col = "red", lwd = 1.5)

# Do results differ if we include species' mean initial cover as a covariate? They don't
## (Since the bounded nature of the percentage cover variable means that
## abundant species are more likely to show large decreases in cover)
spcovs <- with(ot.dynamics, tapply(Initial.Cover, Species, mean))

mod.pd.ot$spcovs <- spcovs[names(spcovs) %in% levels(factor(mod.pd.ot$sps))]

plot(covresp.est ~ spcovs, mod.pd.ot)
```r
summary(lm(covresp.est ~ phenshift.est * phengroup + spcovs, mod.pd.ot))
```

```r
# Call:
# lm(formula = covresp.est ~ phenshift.est * phengroup + spcovs, data = mod.pd.ot)
#
# Residuals:
# Min 1Q Median 3Q Max
# -1.9035 -0.5351 -0.1091 0.6764 1.3218
#
# Coefficients:
# (Intercept) phenshift.est phengroupLate spcovs phenshift.est:phengroupLate
# Estimate 0.07466 0.02424 -1.09368 -0.17735 -0.04998
# Std. Error 0.62915 0.01908 0.86886 0.12157 0.04151
# t value 0.119 1.270 -1.259 -1.459 -1.204
# Pr(>|t|) 0.908 0.228 0.232 0.170 0.252
#
# Residual standard error: 1.02 on 12 degrees of freedom
# Multiple R-squared: 0.2423, Adjusted R-squared: -0.01024
# F-statistic: 0.9595 on 4 and 12 DF, p-value: 0.4643
```

```r
Anova(lm(covresp.est ~ phenshift.est * phengroup + spcovs, mod.pd.ot))
```

```r
# Anova Table (Type II tests)
#
# Response: covresp.est
# Sum Sq Df F value Pr(>F)
# phenshift.est 0.6685 1 0.6423 0.4385
# phengroup 0.2714 1 0.2607 0.6189
# spcovs 2.2149 1 2.1280 0.1703
# phenshift.est:phengroup 1.5087 1 1.4495 0.2518
```
The multiple regression analysis showed that species' phenological shifts are uncorrelated to their cover responses to climate change. However, error in our estimates of species phenological shift bias the estimated slope of the regression towards zero. As an alternative way of analysing the data while accounting for the uncertainty in both the independent and dependent variables of our model, we did a resampling analysis.

# Main experiment

```r
n <- 10000

bootPD <- data.frame(slope = numeric(n),
                      intercept = numeric(n),
                      pval = numeric(n))

for (i in 1:n) {

  PDi <- data.frame(phenshift = numeric(nrow(mod.pd)),
                    covresp = numeric(nrow(mod.pd))
  
  PDi$phenshift <- rnorm(nrow(PDi), mod.pd$phenshift.est, mod.pd$phenshift.se)
  PDi$covresp <- rnorm(nrow(PDi), mod.pd$covresp.est, mod.pd$covresp.se)

  modi <- lm(covresp ~ phenshift, PDi)

  bootPD$slope[i] <- summary(modi)$coefficients[2,1]
  bootPD$intercept[i] <- summary(modi)$coefficients[1,1]
  bootPD$pval[i] <- summary(modi)$coefficients[2,4]
}
```

# 4-year experiment

```r
bootPD.ot <- data.frame(slope = numeric(n),
                        intercept = numeric(n),
                        pval = numeric(n))

for (i in 1:n) {

  PDi <- data.frame(phenshift = numeric(nrow(mod.pd.ot)),
                    covresp = numeric(nrow(mod.pd.ot))
  
  PDi$phenshift <- rnorm(nrow(PDi), mod.pd.ot$phenshift.est, mod.pd.ot$phenshift.se)
  PDi$covresp <- rnorm(nrow(PDi), mod.pd.ot$covresp.est, mod.pd.ot$covresp.se)

  modi <- lm(covresp ~ phenshift, PDi)

  bootPD.ot$slope[i] <- summary(modi)$coefficients[2,1]
  bootPD.ot$intercept[i] <- summary(modi)$coefficients[1,1]
  bootPD.ot$pval[i] <- summary(modi)$coefficients[2,4]
}
```

```r
plot(density(bootPD$slope), main = "",
     xlab = "Effect of phenological shift on cover change",
     lwd = 2, ylim = range(c(density(bootPD$slope)$y, density(bootPD.ot$slope)$y)))
```
Effect of phenological shift on cover change

Density

-0.06 −0.04 −0.02 0.00 0.02 0.04 0.06
0 10 20 30 40

Site temperature data

We recorded temperature at the sites every 30 minutes with Onset HOBO Pendant Temperature/Light 64K Data Loggers. From these data we calculated daily mean temperatures at the high and low elevation sites. Temperature data can also be used to identify the time of snowmelt at each site.

First we need to load and process the temperature logger data.

```r
daily.means <- function (dat) {
  daily <- data.frame(date = levels(factor(dat$date)),
                     temp = tapply(dat$temp, dat$date, mean, na.rm = T))

  daily$date <- as.Date(as.character(daily$date))

  return(daily)
}
```
```r
all.cal <- read.csv("data/temp2000.csv")
all.cal$date <- as.Date(all.cal$date)

all.nes <- read.csv("data/temp1400.csv")
all.nes$date <- as.Date(all.nes$date)

# Subset data from Nov 2013 to Aug 2014
cal14 <- subset(all.cal, date > "2013-10-31" & date < "2014-09-01")
nes14 <- subset(all.nes, date > "2013-10-31" & date < "2014-09-01")

# Correct over-heated records by setting looking for the
# maximum temperature recorded under low light conditions at each site
lt <- 50
maxTcal <- max(subset(all.cal, light < lt)$temp)
maxTnes <- max(subset(all.nes, light < lt)$temp)

cal14$temp[cal14$temp > maxTcal] <- maxTcal
nes14$temp[nes14$temp > maxTnes] <- maxTnes

# Calculate mean daily temperatures
cal.daily <- daily.means(cal14)
nes.daily <- daily.means(nes14)

plot(temp ~ date, cal.daily, type = "n",
     ylim = range(c(cal.daily$temp, nes.daily$temp)),
     ylab = expression(-degree-C),
     xlab = "")

with(cal.daily, lines(date, temp, col = rgb(0,0,1,0.75), lwd = 1.5 ))
with(nes.daily, lines(date, temp, col = rgb(1,0,0,0.75), lwd = 1.5 ))
mtext("Mean daily temperatures (Nov 2013 to Aug 2014)", cex = 0.9, adj = 0,
      line = 0.1)
legend("bottomright", bty = "n", legend = c("2,000 m", "1,400 m"),
       lwd = 2, col = c(rgb(0,0,1,0.75), rgb(1,0,0,0.75)),
       title = "Elevation", title.adj = 0.2, cex = 0.8)
```
Frost damage analysis

Earlier snowmelt at lower elevations can increase the risk of frost damage during spring. We can calculate the daily minimum temperatures at both sites, and look at how often they were below \(-4.5^{\circ}\)C, the temperature at which alpine species start experiencing leaf frost damage.

# Calculate daily minimum temperatures
nes.daily <- daily.means(all.nes)
cal.daily <- daily.means(all.cal)

# Function to calculate daily minimum temperatures
daily.mins <- function (dat) {
    daily <- data.frame(date = levels(factor(dat$date)),
                        temp = tapply(dat$temp,
                                      dat$date, min, na.rm = T))

    daily$date <- as.Date(as.character(daily$date))

    return(daily)
}

# Calculate daily minimum temperatures
nes.daily.mins <- daily.mins(all.nes)
cal.daily.mins <- daily.mins(all.cal)

## Calculate onset of growth
gdd.thr <- 5
ac.gdd <- 5
### for Calanda

### for Calanda

cal.daily.14 <-.subset(cal.daily, date < "2014-06-01" & date > "2014-03-01")
cal.daily.14$gdd <- numeric(nrow(cal.daily.14))

for (i in 2:nrow(cal.daily.14)) {
    if (cal.daily.14$temp[i] > gdd.thr) {
    } else{
        cal.daily.14$gdd[i] <- cal.daily.14$gdd[i-1]
    }
}
cal.daily.14.og <- as.numeric(cal.daily.14$date[min(which(cal.daily.14$gdd >= ac.gdd))])

### and for Nesselboden

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nes.daily.14 <- subset(nes.daily, date < "2014-06-01" & date > "2014-03-01")
nes.daily.14$gdd <- numeric(nrow(nes.daily.14))
for (i in 2:nrow(nes.daily.14)) {
  if (nes.daily.14$temp[i] > gdd.thr) {
    nes.daily.14$gdd[i] <- nes.daily.14$temp[i] + nes.daily.14$gdd[i-1]
  } else{
    nes.daily.14$gdd[i] <- nes.daily.14$gdd[i-1]
  }
}
nes.daily.14.og <- as.numeric(nes.daily.14$date[min(which(nes.daily.14$gdd >= ac.gdd))])
nes.daily.15 <- subset(nes.daily, date < "2015-06-01" & date > "2015-03-01")
nes.daily.15$gdd <- numeric(nrow(nes.daily.15))
for (i in 2:nrow(nes.daily.15)) {
  if (nes.daily.15$temp[i] > gdd.thr) {
    nes.daily.15$gdd[i] <- nes.daily.15$temp[i] + nes.daily.15$gdd[i-1]
  } else{
    nes.daily.15$gdd[i] <- nes.daily.15$gdd[i-1]
  }
}
nes.daily.15.og <- as.numeric(nes.daily.15$date[min(which(nes.daily.15$gdd >= ac.gdd))])
nes.daily.16 <- subset(nes.daily, date < "2016-06-01" & date > "2016-03-01")
nes.daily.16$gdd <- numeric(nrow(nes.daily.16))
for (i in 2:nrow(nes.daily.16)) {
  if (nes.daily.16$temp[i] > gdd.thr) {
    nes.daily.16$gdd[i] <- nes.daily.16$temp[i] + nes.daily.16$gdd[i-1]
  } else{
    nes.daily.16$gdd[i] <- nes.daily.16$gdd[i-1]
  }
}
nes.daily.16.og <- as.numeric(nes.daily.16$date[min(which(nes.daily.16$gdd >= ac.gdd))])

## Plot results

par(mfrow = c(2,3), mar = c(0,0,1.5,0), oma = c(4,6,2,2))
plot(temp ~ date, subset(cal.daily, date < "2014-06-01" & date > "2014-03-01"),
     type = "l", col = "blue", lwd = 2, ylim = c(-5, 20),
     ylab = "Mean daily temperature", xlab = "", xaxt = "n")

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legend("topleft", bty = "n", lwd = 2, col = c("blue", "red"),
        legend = c("High elevation", "Low elevation"), cex = 0.75)

lines(temp ~ date, subset(nes.daily, date < "2014-06-01" & date > "2014-03-01"),
        col = "red", lwd = 2)

mtext("Spring 2014", line = 0.5, cex = 0.8, font = 2)

mtext(expression(paste("daily temperature (" , degree,"C")")),
        side = 2, line = 2.5, font = 2, cex = 0.75)

mtext("Mean", font = 2,
        side = 2, line = 4, cex = 0.8)

plot(temp ~ date,
        subset(cal.daily, date < "2015-06-01" & date > "2015-03-01"),
        type = "l", col = "blue", lwd = 2,
        ylim = c(-5, 20), yaxt = "n", xaxt = "n")

lines(temp ~ date,
        subset(nes.daily, date < "2015-06-01" & date > "2015-03-01"),
        col = "red", lwd = 2)

mtext("Spring 2015", line = 0.5, cex = 0.8, font = 2)

plot(temp ~ date,
        subset(cal.daily, date < "2016-06-01" & date > "2016-03-01"),
        type = "l", col = "blue", lwd = 2,
        ylim = c(-5, 20), yaxt = "n", xaxt = "n")

lines(temp ~ date,
        subset(nes.daily, date < "2016-06-01" & date > "2016-03-01"),
        col = "red", lwd = 2)

mtext("Spring 2016", line = 0.5, cex = 0.8, font = 2)

### Minimum temps

plot(temp ~ date,
        subset(cal.daily.mins, date < "2014-06-01" & date > "2014-03-01"),
        type = "l", col = "blue", lwd = 2, xlab = "", ylab = "", ylim = c(-10, 10))

lines(temp ~ date,
        subset(nes.daily.mins, date < "2014-06-01" & date > "2014-03-01"),
        col = "red", lwd = 2)

abline(h = -4.5, lty = 2)

mtext(expression(paste("daily temperature (" , degree,"C")")),
        side = 2, line = 2.5, font = 2, cex = 0.75)

mtext("Minimum", font = 2,
        side = 2, line = 4, cex = 0.8)

plot(temp ~ date,
Now let’s calculate the accumulation of freezing temperatures over the growing season.

```r
### Frost damage degree days

cal.daily.mins.14 <- subset(cal.daily.mins, date < "2014-06-01" & date > "2014-03-01")
nes.daily.mins.14 <- subset(nes.daily.mins, date < "2014-06-01" & date > "2014-03-01")

cal.daily.mins.15 <- subset(cal.daily.mins, date < "2015-06-01" & date > "2015-03-01")
nes.daily.mins.15 <- subset(nes.daily.mins, date < "2015-06-01" & date > "2015-03-01")

cal.daily.mins.16 <- subset(cal.daily.mins, date < "2016-06-01" & date > "2016-03-01")
nes.daily.mins.16 <- subset(nes.daily.mins, date < "2016-06-01" & date > "2016-03-01")
```
## Frost degree days

### 2014

fddg_cal14 <- numeric(nrow(subset(cal.daily.14, date > cal.daily.14.og)) + 1)

fd.thr <- -4.5

for (i in 2:(length(fddg_cal14) - 1)) {
  if (subset(cal.daily.mins.14, date > cal.daily.14.og)$temp[i] <= fd.thr) {
    fddg_cal14[i] <- subset(cal.daily.mins.14,
                            date > cal.daily.14.og)$temp[i]+ fddg_cal14[i-1]
  } else{
    fddg_cal14[i] <- fddg_cal14[i-1]
  }
}

fddg_nes14 <- numeric(nrow(subset(nes.daily.14, date > nes.daily.14.og)) + 1)

fd.thr <- -4.5

for (i in 2:(length(fddg_nes14) - 1)) {
  if (subset(nes.daily.mins.14, date > nes.daily.14.og)$temp[i] <= fd.thr) {
    fddg_nes14[i] <- subset(nes.daily.mins.14,
                         date > nes.daily.14.og)$temp[i]+ fddg_nes14[i-1]
  } else{
    fddg_nes14[i] <- fddg_nes14[i-1]
  }
}

### 2015

fddg_cal15 <- numeric(nrow(subset(cal.daily.15, date > cal.daily.15.og)) + 1)

fd.thr <- -4.5

for (i in 2:(length(fddg_cal15) - 1)) {

}
if (subset(cal.daily.mins.15, date > cal.daily.15.og)$temp[i] <= fd.thr) {
    fddg_cal15[i] <- subset(cal.daily.mins.15, date > cal.daily.15.og)$temp[i]+ fddg_cal15[i-1]
} else{
    fddg_cal15[i] <- fddg_cal15[i-1]
}
}

fddg_nes15 <- numeric(nrow(subset(nes.daily.15, date > nes.daily.15.og)) + 1)

fd.thr <- -4.5
for (i in 2:(length(fddg_nes15) - 1)) {
    if (subset(nes.daily.mins.15, date > nes.daily.15.og)$temp[i] <= fd.thr) {
        fddg_nes15[i] <- subset(nes.daily.mins.15, date > nes.daily.15.og)$temp[i]+ fddg_nes15[i-1]
    } else{
        fddg_nes15[i] <- fddg_nes15[i-1]
    }
}

fddg_cal16 <- numeric(nrow(subset(cal.daily.16, date > cal.daily.16.og)) + 1)

fd.thr <- -4.5
for (i in 2:(length(fddg_cal16) - 1)) {
    if (subset(cal.daily.mins.16, date > cal.daily.16.og)$temp[i] <= fd.thr) {
        fddg_cal16[i] <- subset(cal.daily.mins.16, date > cal.daily.16.og)$temp[i]+ fddg_cal16[i-1]
    } else{
        fddg_cal16[i] <- fddg_cal16[i-1]
    }
}

fddg_nes16 <- numeric(nrow(subset(nes.daily.16, date > nes.daily.16.og)) + 1)

fd.thr <- -4.5
for (i in 2:(length(fddg_nes16) - 1)) {
    if (subset(nes.daily.mins.16, date > nes.daily.16.og)$temp[i] <= fd.thr) {
        fddg_nes16[i] <- subset(nes.daily.mins.16, date > nes.daily.16.og)$temp[i]+ fddg_nes16[i-1]
    } else{
        fddg_nes16[i] <- fddg_nes16[i-1]
    }
}
Graminoid analysis

Graminoid species tend to be more frost resistant than forbs, and therefore could be more likely to benefit from advanced phenology. Let us look at the relationship between phenological shifts and changes in cover for the only three graminoids species in the analysis.

```r
# This logical vector indicates which species in mod.pd are graminoids
gramin <- c(T, F, F, T,
            F, F, F, T,
            F, F, F, F,
            F, F, F, F,
            F, F)

# And the same for mod.pd.ot (4-year experiment)
gramin.ot <- gramin[mod.pd$sps %in% mod.pd.ot$sps]

# Let's look at the effect of plasticity on the cover changes averaged across
```
# the two experiments

```r
plot(mod.pd[gramin,]$phenshift.est,
     apply(matrix(c(mod.pd[gramin,]$covresp.est, mod.pd.ot[gramin.ot,]$covresp.est),
              nrow = 3, ncol = 2), 1, mean),
     xlab = "Phenological shift (days)",
     ylab = "Mean cover response to climate change")
```

# and fit a model to the data

```r
model.gram <- lm(apply(matrix(c(mod.pd[gramin,]$covresp.est, mod.pd.ot[gramin.ot,]$covresp.est),
                          nrow = 3, ncol = 2), 1, mean) ~ mod.pd[gramin,]$phenshift.est)
```

```r
summary(model.gram)
```

```r
##
## Call:
## lm(formula = apply(matrix(c(mod.pd[gramin,]$covresp.est, mod.pd.ot[gramin.ot,]$covresp.est),
##                      nrow = 3, ncol = 2), 1, mean) ~ mod.pd[gramin,]$phenshift.est)
##
## Residuals:
## 1      2      3
## 0.03524 -0.11956  0.08432
##
## Coefficients:             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.476708   0.135875  -10.868  0.0584 .
## mod.pd[gramin,]$phenshift.est -0.053712   0.006654   -8.072  0.0785 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1505 on 1 degrees of freedom
## Multiple R-squared:  0.9849, Adjusted R-squared:  0.9698
## F-statistic: 65.16 on 1 and 1 DF,  p-value: 0.07847
```

```r
abline(model.gram)
```
Making figures for the paper

We used the following code to make figure 2 in our paper.

```
# Figure 2
# Make a new data frame combining turf.offsets, wd, and ot.wd
# Make a figure with 3 panels: (a) phenology, (b) cover changes 3y, (c) cover changes 4y
figure.a.dat <- useful.ft
figure.a.dat$Species <- factor(figure.a.dat$Species)

## Ordering species' factor levels
figure.a.dat$Species <- as.character(figure.a.dat$Species)
figure.a.dat$Species <- gsub("Alchemilla conjuncta nitida",
                           "Alchemilla conjuncta", figure.a.dat$Species)
figure.a.dat$Species <- gsub("Alchemilla xanthochlora pratensis",
                           "Alchemilla xanthochlora", figure.a.dat$Species)
figure.a.dat$Species <- gsub("Thymus praecoxy polytrichus",
                           "Thymus praecoxy", figure.a.dat$Species)
figure.a.dat$Species <- gsub("Campanula scheuchzerii",
                           "Campanula scheuchzeri", figure.a.dat$Species)
figure.a.dat$Species <- factor(figure.a.dat$Species)
ftc <- subset(figure.a.dat, Treatment == "Control")
species.ordered <- levels(figure.a.dat$Species)[order(tapply(ftc$Flowering.Time,
                                                                     ftc$Species, median,
                                                                     na.rm = T),
                                     decreasing = T)]
figure.a.dat$Species <- as.character(figure.a.dat$Species)
figure.a.dat$Species <- factor(figure.a.dat$Species, levels = species.ordered)

dat.a.con <- subset(figure.a.dat, Treatment == "Control")
dat.a.war <- subset(figure.a.dat, Treatment == "Warming")
```
median.dat.a <- data.frame(  
  Species = factor(levels(dat.a.war$Species),  
    levels = species.ordered),  
  FTcon = as.numeric(tapply(dat.a.con$Flowering.Time,  
    dat.a.con$Species, median, na.rm = T)),  
  FTwar = as.numeric(tapply(dat.a.war$Flowering.Time,  
    dat.a.war$Species, median, na.rm = T)))

phenshifts2 <- phenshifts  
phenshifts2$sps <- gsub("chzerii", "chzeri", phenshifts2$sps)  
phenshifts2$sps <- gsub("conjuncta nitida", "conjuncta", phenshifts2$sps)  
phenshifts2$sps <- gsub("xanthochlora pratensis", "xanthochlora", phenshifts2$sps)

psh <- numeric()  
for(s in levels(dat.a.war$Species)) {  
  psh <- c(psh, subset(phenshifts2, sps == s)$phenshift.est)  
}
median.dat.a$psh <- psh

#  
figure.b.dat <- mod.pd.ot  
names(figure.b.dat)[1] <- "Species"  
figure.b.dat$Species <- as.character(figure.b.dat$Species)  
figure.b.dat$Species <- gsub("Alchemilla conjuncta nitida",  
  "Alchemilla conjuncta", figure.b.dat$Species)  
figure.b.dat$Species <- gsub("Alchemilla xanthochlora pratensis",  
  "Alchemilla xanthochlora", figure.b.dat$Species)  
figure.b.dat$Species <- gsub("Thymus praecox polytrichus",  
  "Thymus praecox", figure.b.dat$Species)  
figure.b.dat$Species <- gsub("Campanula scheuchzerii",  
  "Campanula scheuchzeri", figure.b.dat$Species)  
figure.b.dat$Species <- factor(figure.b.dat$Species, levels = species.ordered)  
figure.b.dat <- figure.b.dat[!is.na(figure.b.dat$Species),]

###########

#  
figure.c.dat <- mod.pd  
names(figure.c.dat)[1] <- "Species"  
figure.c.dat$Species <- gsub("Alchemilla conjuncta nitida",  
  "Alchemilla conjuncta", figure.c.dat$Species)  
figure.c.dat$Species <- gsub("Alchemilla xanthochlora pratensis",  
  "Alchemilla xanthochlora", figure.c.dat$Species)  
figure.c.dat$Species <- gsub("Thymus praecox polytrichus",  
  "Thymus praecox", figure.c.dat$Species)  
figure.c.dat$Species <- gsub("Campanula scheuchzerii",  
  "Campanula scheuchzeri", figure.c.dat$Species)  
figure.c.dat$Species <- factor(figure.c.dat$Species, levels = species.ordered)  
figure.c.dat <- figure.c.dat[!is.na(figure.c.dat$Species),]

###########

31
# par(mfrow = c(1,3))
## Figure 1a - Phenological offsets
par(mar = c(5,0,2.5,0.5), oma = c(0,18,0,0), cex.axis = 1.75, cex.lab = 2.5)
stripchart(Flowering.Time ~ Species, data = figure.a.dat, horizontal = T, yaxt = "n",
xlab = "", col = "lightgray", type = "n", xaxt = "n",
xlim = c(16175, 16330))

## Add arrows showing phenological shifts
with(median.dat.a,
    arrows(FTcon, y0 = as.numeric(median.dat.a$Species),
x1 = FTcon + psh, length = 0.1, lwd = 8, col = rgb(0.5,0.5,0.5,1)))

# Add points showing first flowering time in control and warmed turfs
points(dat.a.con$Flowering.Time, jitter(as.numeric(dat.a.con$Species), factor = 1),
col = "black", cex = 1.75, pch = 21, bg = rgb(0,0,1,0.5))
points(dat.a.war$Flowering.Time, jitter(as.numeric(dat.a.war$Species), factor = 1),
col = "black", cex = 1.75, pch = 24, bg = rgb(1,0,0,0.5))

axis(2, at = 1:length(species.ordered), labels = species.ordered, font = 3, las = 1, cex = 4)
axis(1, at = c(16191, 16222, 16252, 16283, 16314), labels = c("May", "Jun", "Jul", "Aug", "Sep"))
mtext("(a)", adj = 0, font = 2, cex = 1.25, line = 0.5)
mtext("Phenological shifts", adj = 0.11, cex = 1.25, line = 0.5)

mtext("Flowering time", adj = 0.125, cex = 1.75, side = 1, line = -1.75, outer = T)

## Figure 1b - Cover response to climate change in 4-year experiment

stripchart(covresp.est ~ Species, data = figure.b.dat, horizontal = T, yaxt = "n",las = 1, xlab = "",col = "lightgray", type = "n",
xlim = c(min(figure.b.dat$covresp.est - figure.b.dat$covresp.se),
max(figure.b.dat$covresp.est + figure.b.dat$covresp.se)))
abline(v=0, lwd = 1.5, lty = 2, col = "gray")

with(figure.b.dat,
    arrows(covresp.est - covresp.se,
y0 = as.numeric(figure.b.dat$Species), covresp.est + covresp.se,
length=0.025, angle=90, code=3, col = "gray", lwd = 3)
)

points(figure.b.dat$covresp.est, figure.b.dat$Species,
col = "black", cex = 1.5, pch = 21, bg = rgb(0.7,0.7,0.7,0.8))
mtext("(b)", adj = 0, font = 2, cex = 1.25, line = 0.5)
mtext("Demographic response in main experiment", adj = 0.6, cex = 1.25, line = 0.5)
# Figure 1c - Cover response to climate change in 3-year experiment

```r
stripchart(covresp.est ~ Species, data = figure.c.dat, horizontal = T,
    yaxt = "n", las = 1, xlab = "", col = "lightgray", type = "n",
    xlim = c(min(figure.c.dat$covresp.est - figure.c.dat$covresp.se),
    max(figure.c.dat$covresp.est + figure.c.dat$covresp.se)))
abline(v=0, lwd = 1.5, lty = 2, col = "gray")

with(figure.c.dat,

    arrows(covresp.est - covresp.se,
               y0 = as.numeric(figure.c.dat$Species),
               covresp.est + covresp.se,
               length=0.025, angle=90, code=3, col = "gray", lwd = 3)
)

points(figure.c.dat$covresp.est, figure.c.dat$Species,
        col = "black", cex = 1.5, pch = 21, bg = rgb(0.7,0.7,0.7,0.8))

mtext(quote(c), adj = 0, font = 2, cex = 1.25, line = 0.5)
mtext(quote(Demographic response in 4-year experiment), adj = 0.9, cex = 1.25, line = 0.5)
mtext(quote(Log cover ratio), adj = 0.70, cex = 1.75, side = 1, line = -1.75, outer = T)
```

And this code to make figure 3.

```r
par(mar = c(0,0,2,0), mfrow = c(1,2), oma = c(6, 6, 0, 1), cex.axis = 1.5)

# 3-year experiment
# Plot the results
pg.col <- ifelse(mod.pd$phengroup == "Early", "black", "gray")

plot(covresp.est - phenshift.est, mod.pd,
     ylim=range(c(mod.pd$covresp.est-mod.pd$covresp.se, mod.pd$covresp.est+mod.pd$covresp.se, mod.pd$phenshift.est+mod.pd$phenshift.se, mod.pd$phenshift.est-mod.pd$phenshift.se, mod.pd$phenshift.est),
     xlab="Phenological shift (days)", ylab="Cover response to climate change", col = pg.col, cex = 1.5)
```
# hack: we draw arrows but with very special "arrowheads"

with(mod.pd,

    arrows(phenshift.est, covresp.est-covresp.se,
            phenshift.est, covresp.est+covresp.se,
            length=0.025, angle=90, code=3, col = pg.col)
)

with(mod.pd,

    arrows(phenshift.est-phenshift.se, covresp.est,
            phenshift.est+phenshift.se, covresp.est,
            length=0.025, angle=90, code=3, col = pg.col)
)

with(subset(mod.pd, phengroup == "Late"),

    points(phenshift.est, covresp.est, cex = 1.5))

mtext(`/quotesingle.ts1(a)/quotesingle.ts1`,adj = 0, font = 2, cex = 1.5, line = 0.5)

mtext(`/quotesingle.ts1Main experiment/quotesingle.ts1`,adj = 0.075, cex = 1.5, line = 0.5)

mtext("Cover response to climate change", cex = 2, side = 2, outer = T, line = 3.5)

# 4-year experiment
# Plot the results

go.col <- ifelse(mod.pd.ot$phengroup == "Early", "black", "gray")

plot(covresp.est ~ phenshift.est, mod.pd.ot,
    ylim=range(c(mod.pd$covresp.est-mod.pd$covresp.se, mod.pd$covresp.est+mod.pd$covresp.se, mod.pd.ot$covresp.est-mod.pd.ot$covresp.se, mod.pd.ot$covresp.est+mod.pd.ot$covresp.se)),
    xlim=range(c(mod.pd$phenshift.est-mod.pd$phenshift.se, mod.pd$phenshift.est+mod.pd$phenshift.se, mod.pd.ot$phenshift.est-mod.pd.ot$phenshift.se, mod.pd.ot$phenshift.est+mod.pd.ot$phenshift.se)),
    pch=19, yaxt = "n", col = pg.col, cex = 1.5
)

# hack: we draw arrows but with very special "arrowheads"

with(mod.pd.ot,

    arrows(phenshift.est, covresp.est-covresp.se,
            phenshift.est, covresp.est+covresp.se,
            length=0.025, angle=90, code=3, col = pg.col)
)

with(mod.pd.ot,

    arrows(phenshift.est-phenshift.se, covresp.est,
            phenshift.est+phenshift.se, covresp.est,
            length=0.025, angle=90, code=3, col = pg.col)
)

with(subset(mod.pd.ot, phengroup == "Late"),

    points(phenshift.est, covresp.est, cex = 1.5))
Phenological shift (days)

(a) Main experiment

(b) 4-year experiment

Cover response to climate change

Phenological shift (days)
Appendix 2
Results from additional analyses

1. Sensitivity analysis on value of constant added to cover ratio
We added a constant to the recorded covers to handle cases in which a species final cover was 0. In the analyses described in the main manuscript we used 0.25 as such constant, but using different values produced consistent results (Table A1).

<table>
<thead>
<tr>
<th>Constant value</th>
<th>p analysis main experiment</th>
<th>p analysis 4-year experiment</th>
</tr>
</thead>
<tbody>
<tr>
<td>0.10</td>
<td>0.77</td>
<td>0.63</td>
</tr>
<tr>
<td>0.25</td>
<td>0.78</td>
<td>0.63</td>
</tr>
<tr>
<td>0.50</td>
<td>0.77</td>
<td>0.64</td>
</tr>
<tr>
<td>0.75</td>
<td>0.77</td>
<td>0.64</td>
</tr>
<tr>
<td>1.00</td>
<td>0.75</td>
<td>0.65</td>
</tr>
</tbody>
</table>

2. Results when only including species present in at least half of the turfs
Limiting the analyses to species occurring in at least five turfs in a given treatment resulted in the inclusion of only 10 species, but produced similar results and did not change the answer to our research question (Table A2–A3).

Table A2. Analysis of variance type II table for main experiment data

<table>
<thead>
<tr>
<th></th>
<th>Sum of squares</th>
<th>df</th>
<th>F-value</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phenological plasticity</td>
<td>0.575</td>
<td>1</td>
<td>0.946</td>
<td>0.37</td>
</tr>
<tr>
<td>Phenological group</td>
<td>0.048</td>
<td>1</td>
<td>0.080</td>
<td>0.79</td>
</tr>
<tr>
<td>(early versus late flowering)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Interaction plasticity and group</td>
<td>0.353</td>
<td>1</td>
<td>0.581</td>
<td>0.47</td>
</tr>
<tr>
<td>Residuals</td>
<td>3.649</td>
<td>6</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Table A3. Analysis of variance type II table for 4-year experiment data

<table>
<thead>
<tr>
<th></th>
<th>Sum of squares</th>
<th>df</th>
<th>F-value</th>
<th>p</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phenological plasticity</td>
<td>0.378</td>
<td>1</td>
<td>0.257</td>
<td>0.63</td>
</tr>
<tr>
<td>Phenological group</td>
<td>2.039</td>
<td>1</td>
<td>1.386</td>
<td>0.29</td>
</tr>
<tr>
<td>(early versus late flowering)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Interaction plasticity and group</td>
<td>0.340</td>
<td>1</td>
<td>0.231</td>
<td>0.65</td>
</tr>
<tr>
<td>Residuals</td>
<td>7.356</td>
<td>5</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

3. Effects of phenological plasticity on cover changes of grasses

Figure A1. Relationship between phenological shifts and cover response to climate change (averaged across main and 4-year experiments) for the three graminoid species included in the analysis. Phenological shift is the effect of climate change on species first flowering time estimated with a multiple regression including species initial cover as a covariate. Cover response to climate change is the effect of downslope transplantation on the logarithm of the ratio of final to initial cover of a species in a turf. This effect was estimated with a multiple regression including species’ initial cover as covariate. The solid line was fitted with a linear regression.
4. Results of resampling analysis

Figure A2. Distribution of estimated effects of phenological shifts on cover responses to climate change obtained from resampling analysis. We fitted linear regressions to data sampled from a normal distribution based on the mean and standard error of species’ phenological shifts and cover changes estimated from experimental data. The black solid line corresponds to data from the main experiment, and the grey dashed line to data from the 4-year experiment.

5. Frost damage potential

To compare the potential for frost damage between the sites at high (2000 m) and low (1400 m) elevations, we calculated the sum of daily minimum temperatures below -4.5°C threshold, the temperature at which alpine species start experiencing leaf frost damage (Taschler and Neuner 2004). We calculated this sum for the spring months (March till end of May), starting after the onset of plant growth, defined as the first date in which mean daily temperature was ≥ 5°C. In this way, we calculated potential frost damage during the springs of 2014, 2015, and 2016, the three growing seasons that could have influenced the cover changes detected between the initial survey in 2013 (2014 for the main experiment) and the final survey in early June 2016. The difference between the onset of growth at the two elevations varied among years, being almost simultaneous in 2014 and more than a month apart in 2015 (Fig A3).

The total potential for frost damage also varied between years but was consistently higher at the low elevation site (Fig. A4), especially in 2016. Also, the difference in total potential frost damage at the two elevations increases when considering data from the spring
of 2014, which could have affected the cover changes in the 4-year experiment only. This could partially explain why the early-flowering species benefited less from advancing phenology in the 4-year experiment compared to the main experiment.

Figure A3. Mean (top panels) and minimum (bottom panels) daily temperatures recorded at the low- (red lines) and high-elevation (blue lines) sites during the meteorological spring of 2014, 2015, and 2016. The dashed line in the bottom panels indicates -4.5°C, the temperature at which alpine species start suffering leaf frost damage.
Figure A4. Accumulated frost potential (sum of minimum daily temperatures below -4.5°C threshold) during spring at high and low elevation sites.

References