Larsen&Shirey_ELE2021_IndependentAnalysis

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Reanalysis of Larsen and Shirey 2021 Ecology Letters

Original technical comment of interest: https://doi.org/10.1111/ele.13731

In a response to the Larsen and Shirey (2021) technical comment, Fric et al. (2021) make the claim that "...
we replicated their [LS] procedures (Supplement S5), finding that LS confused their Onset and Termination
results."

Below is a independent reanalysis of Larsen and Shirey's (2021) analysis to see if LS did indeed confuse their
Onset and Termination results. We use the same estimated phenology metrics of as Larsen and Shirey (2021),
but generate our own independent linear model results for onset and termination coefficients.

The steps and code for this reanalysis are demonstrated below.

Read in data

```r
# Get data from Larsen & Shirey's GitHub
githubURL <- "https://github.com/RiesLabGU/Larsen-Shirey2020_EcoLettersComment/blob/master/data/phenome
load(url(githubURL))
```

Examine data

Note that the phenology data has later values for termination than for onset. This makes biological sense
and confirms that at the stage of estimating phenology metrics, there was no error.

```r
head(pheno.data)
```

```
##                            unit onset.est offset.est                 name
## 2 Anthocharis cardamines-54-2015 104.59562   188.5147 Anthocharis cardamines
## 3 Anthocharis cardamines-52-2015  95.79792   184.7230 Anthocharis cardamines
## 5 Anthocharis cardamines-54-2014 107.84247   179.9457 Anthocharis cardamines
## 6 Anthocharis cardamines-52-2014 101.60338   161.8632 Anthocharis cardamines
## 7 Anthocharis cardamines-56-2014 101.14417   303.1350 Anthocharis cardamines
## 8 Anthocharis cardamines-55-2014 104.41539   153.4493 Anthocharis cardamines
##   region rndLat year  n onset term
## 2 Europe     54 2015 20   105  189
## 3 Europe     52 2015 83    96  185
## 5 Europe     54 2014 38   108  180
## 6 Europe     52 2014 66   102  162
## 7 Europe     56 2014 58   101  303
## 8 Europe     55 2014 45   104  153
```

Write functions to generate species-specific Linear models

For each of the 22 species included in the Larsen and Shirey re-analysis, fit a linear model with latitude and year as the predictor variables. Onset and Termination are the response variables. Model coeficcients and p-values of the latitude term are extracted.

```r
# Onset
onset_coef_fun <- function(spp_name){

  mdf <- filter(pheno.data, name == spp_name) # filter to spp.
  spp_lm <- lm(onset~rndLat+year, data = mdf) # fit linear model

  out_df <- data.frame(
    name = spp_name,
    onset_coef = spp_lm$coefficients[['rndLat']], # extract latitude coef
    p_value = summary(spp_lm)$coefficients[,4][['rndLat']] # extract latitude p-value
    )

  return(out_df)
}

# Termination
offset_coef_fun <- function(spp_name){

  mdf <- filter(pheno.data, name == spp_name)
  spp_lm <- lm(term~rndLat+year, data = mdf)

  out_df <- data.frame(
    name = spp_name,
    offset_coef = spp_lm$coefficients[['rndLat']],
    p_value = summary(spp_lm)$coefficients[,4][['rndLat']]
  )

  return(out_df)
}
```

Run function on the 22 species included in reanalysis.

```r
# get a list of the 22 spp
spp_list <- unique(pheno.data$name)

### get model coef for each spp

#Onset First
onset_coef_list <- lapply(spp_list, onset_coef_fun)
onset_coef_df <- bind_rows(onset_coef_list) %>%
  mutate(slope = case_when(onset_coef > 0 & p_value < 0.05 ~ "positive",
                           onset_coef < 0 & p_value < 0.05 ~ "negative",
                           p_value >= 0.05 ~ "not-sig"))

onset_coef_sum <- onset_coef_df %>%
  group_by(slope) %>%
  summarise(slope_count = n()) %>%
  mutate(phenometric = "Onset")
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
#Offset
offset_coef_list <- lapply(spp_list, offset_coef_fun)
offset_coef_df <- bind_rows(offset_coef_list) %>%
  mutate(slope = case_when(offset_coef > 0 & p_value < 0.05 ~ "positive",
                           offset_coef < 0 & p_value < 0.05 ~ "negative",
                           p_value >= 0.05 ~ "not-sig"))

offset_coef_sum <- offset_coef_df %>%
  group_by(slope) %>%
  summarise(slope_count = n()) %>%
  mutate(phenometric = "Termination")
```

```
## `summarise()` ungrouping output (override with `.groups` argument)
# bind two datasets together
total_coef <- rbind(onset_coef_sum, offset_coef_sum)
total_coef$phenometric <- factor(total_coef$phenometric, levels = c("Onset", "Termination"))
print(total_coef)
```

```
## # A tibble: 5 x 3
##    slope      slope_count phenometric
##    <chr>            <int> <fct>
## 1 not-sig              8 Onset
## 2 positive            14 Onset
## 3 negative             7 Termination
## 4 not-sig             10 Termination
## 5 positive             5 Termination
```

Plot results

Note results of our analysis that was generated independently show the same pattern as demonstrated in Larsen and Shirey (2021), Figure 2c & Figure 2f

```
  ggplot() +
  geom_bar(total_coef,mapping = aes(x = phenometric, y = slope_count,
                                    fill = slope), stat = "identity") +
  scale_fill_manual(values = c("blue", "grey", "dark green"))
```