

Living Data Project PREE Manuscript

Spatial distribution of saskatoon (*Amelanchier alnifolia*) in central Saskatchewan

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Abstract

Culturally significant food plants are threatened by a rapidly changing climate. It is important to understand the spatial distribution of culturally significant food plants to inform conservation decisions. In this study, we map the distribution of saskatoon (*Amelanchier alnifolia*) plants in central Saskatchewan. Although inconclusive, our results may be utilized in further studies analyzing the spatial distribution of saskatoons for conservation applications.

Introduction

Saskatoon (*Amelanchier alnifolia*) plants are an important food, medicinal, and material source for many Indigenous Peoples and settler peoples across Canada (Turner et al. 2021). However, saskatoon plants are sensitive to frost (Clavelle 1997). Climate warming effects may cause an earlier spring, which can put saskatoon blooms at risk of frost damage, thus damaging that year's crop of saskatoon berries. This in turn places the security of traditional foods of many Indigenous groups at risk. The distribution of saskatoon patches in central-saskatchewan, straddling the boreal forest, aspen parkland, and prairie ecosystems, is of interest in this study for long-term monitoring of these important food plants.

Methods

We utilized open-source occurrence records from the Global Biodiversity Information Facility (GBIF) for saskatoon plant occurrences in central Saskatchewan, in a rectangular area between 52 and 56°N and -110 and 103°W. This area consists of boreal forest, aspen parkland, and prairie grassland ecosystems, representing a diverse array of habitats in

22 which saskatoon plants are known to grow. We attempted to plot these occurrences in R using the ggplot2 package
23 (Wickham 2016; R Core Team 2022).

24 ## Skipping install of 'grateful' from a github remote, the SHA1 (ba9b003e) has not changed since last

25 ## Use `force = TRUE` to force installation

26 ## pkg version citekeys

27 ## 1 base 4.2.1 base

28 ## 2 grateful 0.1.11 grateful

29 ## 3 groundhog 2.0.1 groundhog

30 ## 4 knitr 1.40 knitr2022, knitr2015, knitr2014

31 ## 5 remotes 2.4.2 remotes

32 ## 6 rmarkdown 2.16 rmarkdown2022, rmarkdown2018, rmarkdown2020

33 ## Warning in dir.create("data/"): 'data' already exists

34 ## Warning in dir.create("data/raw"): 'data/raw' already exists

35 ## Warning in dir.create("data/clean"): 'data/clean' already exists

36 {knitr::opts_chunk\$set(echo = TRUE)}

```
#create an object for the GBIF data for the species of interest
```

```
saskatoon_occ <- ("Amelanchier alnifolia")
```

```
#download GBIF occurrence records within a specified window of coordinates:
```

```
#list coordinates small first, large second
```

```
gbif_data <- occ_data(scientificName = saskatoon_occ, hasCoordinate = TRUE,  
                      limit = 20000, decimalLongitude = "-110,-103",  
                      decimalLatitude = "52, 56")
```

```
#get a map of Saskatchewan from mapcan data by specifying the boundaries of the province
```

```
sask_map <- mapcan(boundaries = province,  
                   province = SK,  
                   type = standard)
```

```

#get the columns that are relevant for mapping saskatoon's distribution
#since these are presence data, we can get rid of the occurrence status column
#select the longitude and latitude columns
gbif_data_relevant <- gbif_data$data[, c("decimalLongitude", "decimalLatitude")]

#check the data to confirm only the relevant columns are included
view(gbif_data_relevant) #or
head(gbif_data_relevant)

```

```

37 ## # A tibble: 6 x 2
38 ##   decimalLongitude decimalLatitude
39 ##   <dbl>          <dbl>
40 ## 1    -107.         52.2
41 ## 2    -107.         52.1
42 ## 3    -107.         52.0
43 ## 4    -107.         52.0
44 ## 5   -109.         53.4
45 ## 6    -107.         52.2

```

```

#the relevant data are now in a dataframe, save it as a .csv file in the clean data folder
write.csv(gbif_data_relevant, file = "data/clean/gbif-saskatoon-occurrences.csv")

```

Results

The results of this study are inconclusive, as we were unable to perform analyses on the distribution of saskatoon plants (Fig. 1).

```

#plot the Saskatchewan data and create a polygon to outline and fill the province using the ggplot2 package
ggplot(data = sask_map, mapping = aes(x = long, y = lat)) +
  geom_polygon(data = sask_map, mapping = aes(group = group), fill = "grey75",
              colour = "black", show.legend = FALSE) +
  #next step is to plot the occurrences of saskatoon plants, but need to adjust the...
  #coordinate reference system so it's consistent between sask_map and gbif_data_relevant data

```

```
#this is why the axes are not in decimal degrees and the occurrences are not plotting on the actual pro
geom_jitter(data = gbif_data_relevant, aes(x = decimalLongitude, y = decimalLatitude),
            alpha = 0.5, size = 2, colour = "forestgreen", show.legend = FALSE) +
labs(x = 'Longitude', y = 'Latitude') #create more informative axes labels
```

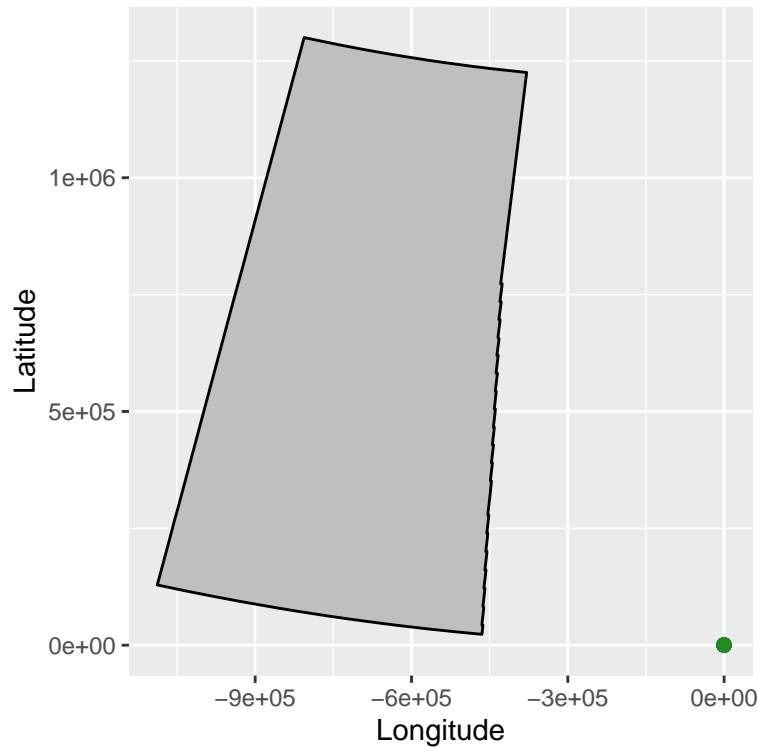


Figure 1: Spatial distribution (presences) of saskatoon (*Amelanchier alnifolia*) in central Saskatchewan, with coordinates in decimal degrees (long, lat)

Discussion

Once these occurrences are plotted, the resultant maps can be archived and used in future analyses, such as predictive species distribution modelling, analyzing the proximity and accessibility of First Nations and Métis communities to saskatoon populations, and long-term monitoring of saskatoon populations. This important plant used for food, medicinal, and technological purposes by many peoples is also likely to have niche overlap with species of similar use, due to human translocations (Cardillo and Warren 2016; Turner 2021). Quantifying the overlap in spatial distribution between culturally significant plants can help to inform conservation efforts, ultimately leading to economic savings and cultural preservation.

57 **References**

```
cite_packages(output = "paragraph", citation.style = ecology-letters)
```

58 **##** We used R version 4.2.1 [base] and the following R packages: grateful v. 0.1.11 [grateful], ground

59 Note that the echo = FALSE parameter was added to the code chunk to prevent printing of the R code that generated

60 the plot.