Spider Diagrams

Jade Bowers

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Abstract

Introduction

The R Markdown document is designed as a template for open source use and contains five code chunks necessary for recreate a spider diagram on your own in a separate R script.

The Code

1. Required package(s)

```
library(tidyverse)
library(tidyr)
library(dplyr)
library(ggpubr)
library(ggthemes)
```

Sequencing the elements creates an index that plots the elements in the correct order on the x axis rather than R's default alphabetical order. The character vector, *traditional*, is a vector of the traditional trace elements plotted on a multi-element diagram in the common order. This vector, or a new vector, can be modified to include or remove any elements based on your plotting needs. Just delete them from the character vector. Their sequencing will update based on the changes when you run line 8 of the code.

```
#list of traditional TEs for filtering
traditional = c("Rb","Ba", "Th" ,"U","Nb", "La",
                "Ce","Pb","Sr", "Nd","Zr","Hf",
                "Sm", "Eu", "Gd", "Tb", "Dy", "Y",
                "Ho", "Er", "Yb", "Lu")
#creates a df to join with your data
TE_seq = data.frame(elements = traditional,
                    seq = seq(1:length(traditional)))
```

```
example_data <- read_csv("../data/spider_example_data.csv")
example_data <- example_data %>%
  select(sample, Cs:Lu) %>%
  gather(key = "element", value = "value", -sample)
sequenced_data <- example_data %>% inner_join(TE_seq, by = c("element" = "elements"))
```

Multi-element diagrams exist on a log-scale, next we create the base ggplot object that you will plot your data on top of.

```
spider_diagram <- ggplot() +
 aes(x = seq, y = value) +
  scale_x_continuous(name = "",
                     breaks = sequenced_data$seq,
                     labels =sequenced_data$element) +
  ylab("Sample") +
  scale_y_log10(breaks = c(0.01, 0.1, 1, 10, 100),
               labels = c(0.01, 0.1, 1, 10, 100)) +
  theme_stata()
```

Add your data to the base plot. Make sure your data has a "sample" column to group your data buy. Without it, R will connect your data in its default hierarchical order and the plot will not look correct.

```
spider_diagram +
  geom_line(data = sequenced_data, aes(group = sample, color = sample)) +
  guides(col = guide_legend(nrow = 3)) +
  theme(axis.text.y = element_text(angle = 0))
```