Automating map generation for Montana Watersheds data

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This document is a summary of work and code being developed for the CDI project "Automated Mapping of SB OBjects"

Loading Libraries

R libraries required - sbtools, sp, gdalUtils, RCurl, RColorBrewer, maps, mapdata Functions are a part of package specificed (sbtools::item_get item_get is function in sbtools library) Functions utilizing the libraries maps and mapdata need to have libraries loaded to access the databases

```
# sb tools is the CIDA developed ScienceBase access library
#suppressWarnings(suppressMessages(library(sbtools)))
suppressWarnings(suppressMessages(library(maps)))
suppressWarnings(suppressMessages(library(mapdata)))
```

Calling up items from ScienceBase

sbtools::item list files(test item)

I've set up a test page with Kathy's segments, watersheds, and data. To access the information for the SBase item, use the following code which utilizes an items Science Base ID **57114f7be4b0ef3b7ca554e8**. The function *list_files* shows the data files associated with the SB item as well as the download urls.

```
test_item=sbtools::item_get("57114f7be4b0ef3b7ca554e8")
## Setting endpoint to www.sciencebase.gov
names(test_item)
    [1] "link"
                             "relatedItems"
                                                  "id"
   [4] "title"
                             "provenance"
                                                  "hasChildren"
  [7] "parentId"
                             "browseCategories"
                                                  "browseTypes"
## [10] "systemTypes"
                             "facets"
                                                  "files"
## [13] "distributionLinks" "previewImage"
#parent<-item_get(test_item$parentId)</pre>
#item_list_children(parent)
```

```
## fname size
## 1 Streamsegments_Qchange_Buffer.csv 31750
##
## 1 https://www.sciencebase.gov/catalog/file/get/57114f7be4b0ef3b7ca554e8?f=_disk__e4%2Fc5%2Fe6%2Fe4c
```

The function $item_get_wfs$ retrieves the web feature service that is featured on the SB item's front page. The map can then be displayed.

```
layer<-sbtools::item_get_wfs("57114f7be4b0ef3b7ca554e8")

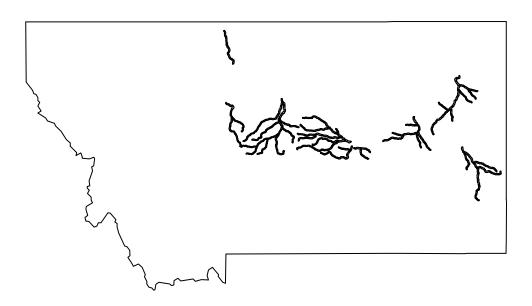
## Loading required namespace: rgdal

## Loading required namespace: xml2

## OGR data source with driver: ESRI Shapefile
## Source: "C:\Users\abock\AppData\Local\Temp\1\Rtmpkp12kd/file1bd018e95db3", layer: "StreamBuffer"

## with 185 features
## It has 11 fields

# re-project layer to decimal degrees, WGS84
layer_dd<-sp::spTransform(layer,"+init=epsg:4326")
map('state','montana')
sp::plot(layer_dd,add=TRUE)</pre>
```



Retrieving SB Data

Next step is to retrieve the environmental data/variables and map them to the WFS. The function getURL from the RCurl library retrieves the URL for each file, and downloads and opens the file to a local directory.

```
sbfiles<-sbtools::item_list_files(test_item)</pre>
print(sbfiles)
##
                                   fname size
## 1 Streamsegments_Qchange_Buffer.csv 31750
## 1 https://www.sciencebase.gov/catalog/file/get/57114f7be4b0ef3b7ca554e8?f=__disk__e4%2Fc5%2Fe6%2Fe4c
data <- RCurl::getURL(sbfiles$url[1])</pre>
data2 <- read.csv(text=data)</pre>
names(data2)
##
   [1] "FID"
                      "OBJECTID"
                                    "POI_ID"
                                                  "MAX_SO"
                                                                "K_coef"
   [6] "Basin"
                      "Segment"
                                    "COMID"
                                                                "Thirties"
                                                  "Years"
## [11] "FiftyFives" "Eighties"
```

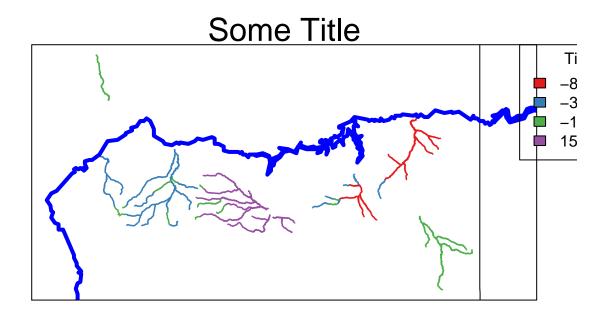
Setting up the plot

Next we set up the plotting. We can use the library RColorBrewer to automatically assign a 4-color symbology; alternatively this is something we can decide ourselves (such as in Roy's example maps). Then accessing the properties of one of environmental variables, bound these colors by the min/max and three quartiles. The base plotting function op assigns a font for title, legend, and axes. The mar function creates space along the plotting margins, so a legend can be partially fit.

```
colPal<-RColorBrewer::brewer.pal(4,"Set1")
# hard breaks for symbology
#fixedBreaks=c(-30,-15,0,15,30)
fixedBreaks=c(min(data2$FiftyFives), quantile(data2$FiftyFives,.25),median(data2$FiftyFives),quantile(dsymb<-cut(data2$FiftyFives,breaks=fixedBreaks,include.lowest=TRUE,right=TRUE)

op<-par(family="serif")
par(mar=c(0,0,0,16))</pre>
```

This next set of code is similar to the code that generates Roy's locations and data. The function par(xpd=TRUE) will add the legend (on the following line) partially outside the plotting area. Right now the legend is being cut off of the right side; I need to update my Rstudio version to see if there is a fix for this.



par(op)