UPWINS_Prepare_Veg_Data

July 8, 2024

[1]:
```
from spectral import *
import numpy as np
import matplotlib.pyplot as plt
import matplotlib
from lazypredict.Supervised import LazyClassifier
import warnings
warnings.filterwarnings('ignore')
import seaborn as sns
from collections import Counter
from scipy.stats import reciprocal
from sklearn.metrics import accuracy_score
from skopt.space import Real, Categorical, Integer
from skopt.plots import plot_objective, plot_histogram, plot_evaluations
import pandas as pd
import skopt
from sklearn.model_selection import train_test_split
import tqdm
print(f'numpy Version: {np. __version__}')

# set parameters
sns.set(style="white")
plt.set_cmap('jet')
```

```
numpy Version: 1.24.3
```

```
<Figure size 640x480 with 0 Axes>
```

1 Load the UPWINS spectral library and metadata csv

[2]:
```
# Read the spectral library using the spectral package
lib = envi.open('data/UPWINS_spectral_library_6_25_2024.hdr')
print(f'Number of spectra in libary: {len(lib.names)}')
print(f'Number of bands in library: {len(lib.bands.centers)}')

# remove spectra with large derivate, which are the spectra collected using␣
 ↪sunlight
derivitive = np.mean(np.abs(lib.spectra[:,1:]-lib.spectra[:,:-1]), axis=1)
select_indices = np.where(derivitive<0.0025)[0]
```

```
# create variables for the library data
names = np.asarray(lib.names)[select_indices]
spectra = lib.spectra[select_indices,:]
wl = np.asarray(lib.bands.centers)
# create variables for the library metadata
nSpec = len(names)
nBands = len(wl)

print(' ')
print('...remove spectra collected using outdoor solar illumination...')
print(' ')
print(f'Number of spectra: {nSpec}')
print(f'Number of bands: {nBands}')
```

```
Number of spectra in libary: 1069
Number of bands in library: 2151

…remove spectra collected using outdoor solar illumination…

Number of spectra: 917
Number of bands: 2151
```

[3]:
```
# read the metadata dataframe and extract the metadata as numpy arrays
df = pd.read_csv('data/UPWINS_spectra_metadata_6_25_2024.csv',␣
 ↪keep_default_na=False)
genus = []
species = []
principle_part = []
health = []
growth_stage = []
DateTimeId = []
month = []
plant_type = []
name = []
name_full_category = []
name_genus_species = []
select_indices = []
for i in range(len(names)):
    row = df.loc[df['ASD UPWINS base_fname'] == names[i]+'.asd']
    # if the spectrum has a corresponding row in the csv
    if (row['sub-category'].values[0] not in ['NA','backrounds']) &␣
 ↪(row['category'].values[0] in␣
 ↪['vegetation','target_vegetation','soil','road']):
        select_indices.append(i)
        plant_type.append(row['sub-category'].values[0])
        genus.append(row['genus'].values[0])
        species.append(row['species'].values[0])
```

```
        principle_part.append(row['principal_part'].values[0])
        health.append(row['health'].values[0])
        growth_stage.append(row['growth_stage'].values[0])
        name_genus_species.append(row['genus'].values[0]+'_'+row['species'].
 ↪values[0])
        DateTimeId.append(row['DateTimeUniqueIdentifier'].values[0])
        month.append(row['DateTimeUniqueIdentifier'].values[0][4:6])
        if row['genus'].values[0]=='NA':
            #not in our primary target vegetation library
            name.append(row['sub-category'].values[0])
            name_full_category.append(row['sub-category'].
 ↪values[0]+'_'+row['principal_part'].values[0]+'_'+row['health'].
 ↪values[0]+'_'+row['growth_stage'].values[0])
        else:
            name.append(row['genus'].values[0]+'_'+row['species'].values[0])
            name_full_category.append(row['genus'].values[0]+'_'+row['species'].
 ↪values[0]+'_'+row['principal_part'].values[0]+'_'+row['health'].
 ↪values[0]+'_'+row['growth_stage'].values[0])

names = np.asarray(lib.names)[select_indices]
spectra = spectra[select_indices,:]
# create variables for the library metadata
nSpec = len(names)
nBands = len(wl)

print(f'Number of spectra: {nSpec}')
print(f'Number of bands: {nBands}')
genus = np.asarray(genus)
species = np.asarray(species)
principle_part = np.asarray(principle_part)
health = np.asarray(health)
growth_stage = np.asarray(growth_stage)
DateTimeId = np.asarray(DateTimeId)
month = np.asarray(month)
name = np.asarray(name)
name_genus_species = np.asarray(name_genus_species)
name_full_category = np.asarray(name_full_category)
plant_type = np.asarray(plant_type)
```

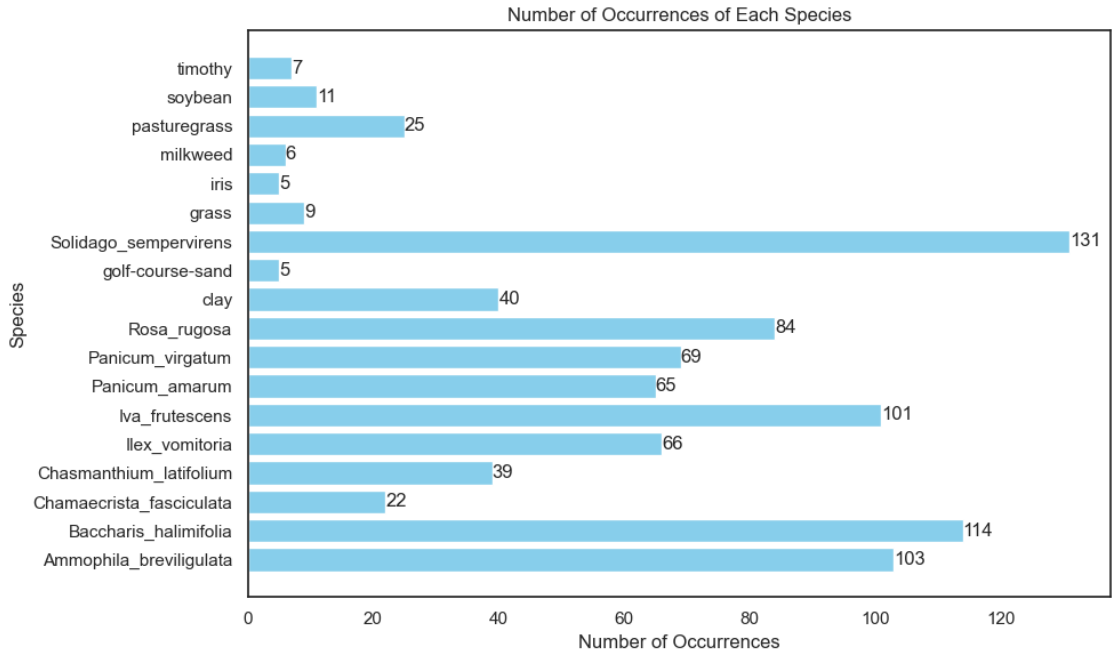
```
Number of spectra: 902
Number of bands: 2151
```

[4]:
```
# save numpy variables for the spectra and metadata
np.save('data/spectra', spectra)
np.save('data/wl', wl)
np.save('data/genus', genus)
np.save('data/species', species)
```

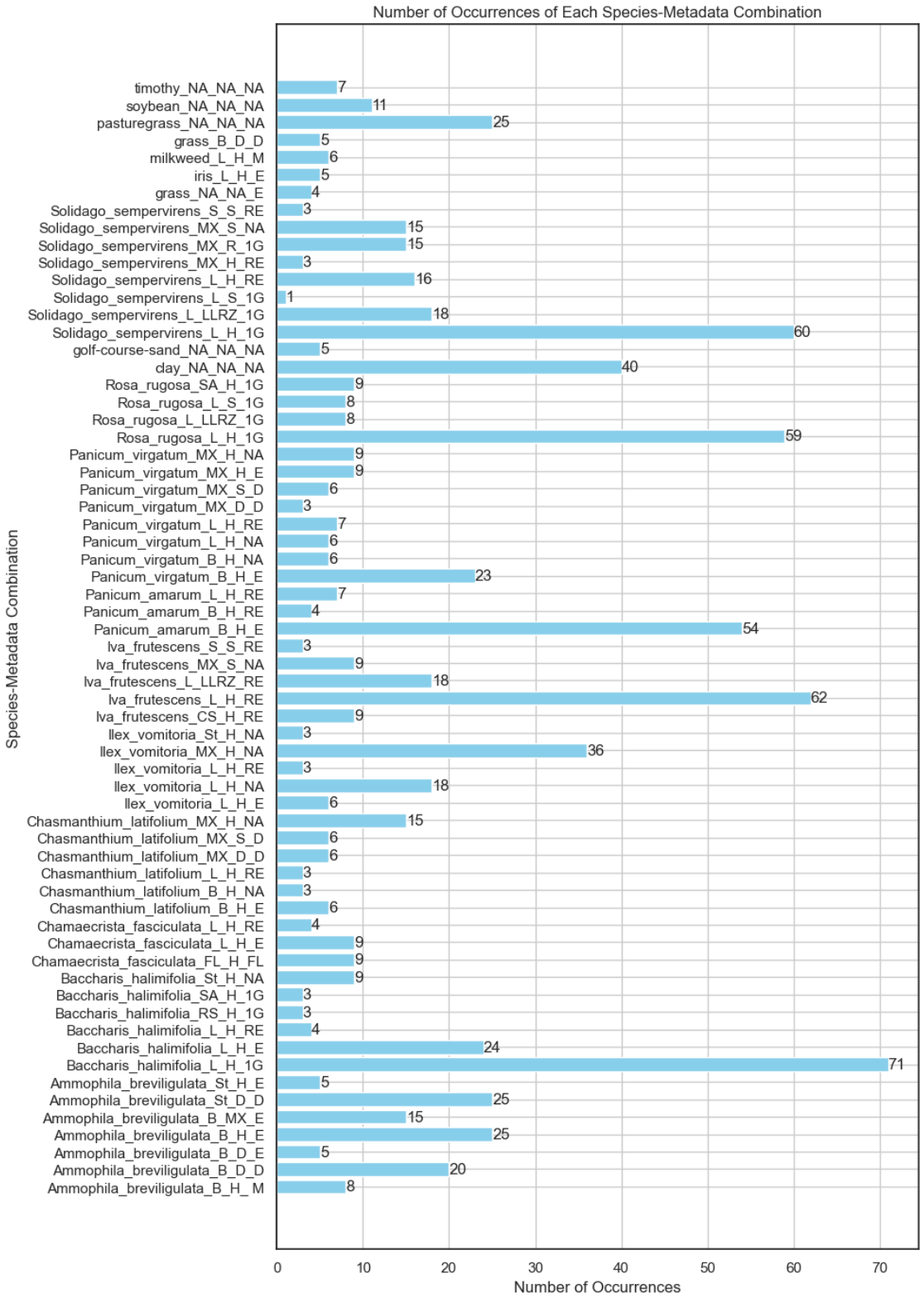
```
np.save('data/principle_part', principle_part)
np.save('data/health', health)
np.save('data/growth_stage', growth_stage)
np.save('data/DateTimeId', DateTimeId)
np.save('data/month', month)
np.save('data/name', name) # the genus and species if known, otherwise the␣
 ↪common name (or material name for soil, road, etc.)
np.save('data/name_genus_species', name_genus_species) # the genus and species␣
 ↪if known - otherwise NA
np.save('data/name_full_category', name_full_category) # all the metadata␣
 ↪available in one string
np.save('data/plant_type', plant_type) # the type of plant (tree, shrub, grass,␣
 ↪etc.) - otherwise NA
```

2 Examine Counts of the various Categories

[5]:
```
# Count the occurrences of each unique value
name_counts = Counter(name)
# Extract the labels and values
labels, values = zip(*name_counts.items())
# Create the horizontal bar plot
plt.figure(figsize=(10, 6))
bars = plt.barh(labels, values, color='skyblue')
# Add text labels on the bars
for bar, value in zip(bars, values):
    plt.text(bar.get_width(), bar.get_y() + bar.get_height() / 2, str(value),␣
 ↪ha='left', va='center')
# Set the labels and title
plt.ylabel('Species')
plt.xlabel('Number of Occurrences')
plt.title('Number of Occurrences of Each Species')
plt.tight_layout()
plt.show()
```



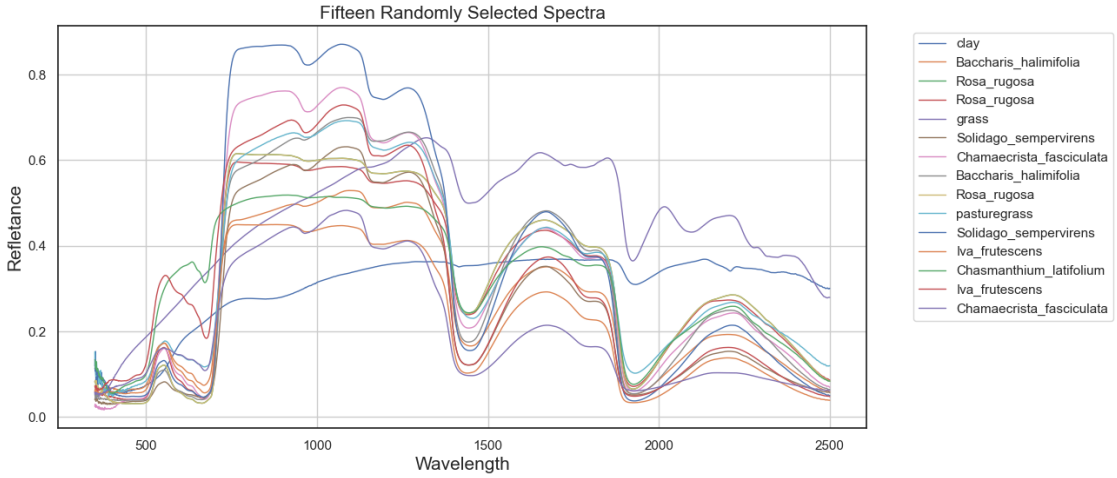
[6]:
```
# Count the occurrences of each unique value
name_full_category_counts = Counter(name_full_category)
# Extract the labels and values
labels, values = zip(*name_full_category_counts.items())
# Create the horizontal bar plot
plt.figure(figsize=(10, 14))
bars = plt.barh(labels, values, color='skyblue')
plt.grid(True)
# Add text labels on the bars
for bar, value in zip(bars, values):
    plt.text(bar.get_width(), bar.get_y() + bar.get_height() / 2, str(value),␣
 ↪ha='left', va='center')
# Set the labels and title
plt.ylabel('Species-Metadata Combination')
plt.xlabel('Number of Occurrences')
plt.title('Number of Occurrences of Each Species-Metadata Combination')
plt.tight_layout()
plt.show()
```


Number of Occurrences of Each Species-Metadata Combination
Species-Metadata Combination
timothy_NA_NA_NA 7
soybean_NA_NA_NA 11
pasturegrass_NA_NA_NA 25
grass_B_D_D 5
milkweed_L_H_M 6
iris_L_H_E 5
grass_NA_NA_E 4
Solidago_sempervirens_S_S_RE 3
Solidago_sempervirens_MX_S_NA 15
Solidago_sempervirens_MX_R_1G 15
Solidago_sempervirens_MX_H_RE 3
Solidago_sempervirens_L_H_RE 16
Solidago_sempervirens_L_S_1G 1
Solidago_sempervirens_L_LLRZ_1G 18
Solidago_sempervirens_L_H_1G 60
golf-course-sand_NA_NA_NA 5
clay_NA_NA_NA 40
Rosa_rugosa_SA_H_1G 9
Rosa_rugosa_L_S_1G 8
Rosa_rugosa_L_LLRZ_1G 8
Rosa_rugosa_L_H_1G 59
Panicum_virgatum_MX_H_NA 9
Panicum_virgatum_MX_H_E 9
Panicum_virgatum_MX_S_D 6
Panicum_virgatum_MX_D_D 3
Panicum_virgatum_L_H_RE 7
Panicum_virgatum_L_H_NA 6
Panicum_virgatum_B_H_NA 6
Panicum_virgatum_B_H_E 23
Panicum_amarum_L_H_RE 7
Panicum_amarum_B_H_RE 4
Panicum_amarum_B_H_E 54
Iva_frutescens_S_S_RE 3
Iva_frutescens_MX_S_NA 9
Iva_frutescens_L_LLRZ_RE 18
Iva_frutescens_L_H_RE 62
Iva_frutescens_CS_H_RE 9
Ilex_vomitoria_St_H_NA 3
Ilex_vomitoria_MX_H_NA 36
Ilex_vomitoria_L_H_RE 3
Ilex_vomitoria_L_H_NA 18
Ilex_vomitoria_L_H_E 6
Chasmanthium_latifolium_MX_H_NA 15
Chasmanthium_latifolium_MX_S_D 6
Chasmanthium_latifolium_MX_D_D 6
Chasmanthium_latifolium_L_H_RE 3
Chasmanthium_latifolium_B_H_NA 3
Chasmanthium_latifolium_B_H_E 6
Chamaecrista_fasciculata_L_H_RE 4
Chamaecrista_fasciculata_L_H_E 9
Chamaecrista_fasciculata_FL_H_FL 9
Baccharis_halimifolia_St_H_NA 9
Baccharis_halimifolia_SA_H_1G 3
Baccharis_halimifolia_RS_H_1G 3
Baccharis_halimifolia_L_H_RE 4
Baccharis_halimifolia_L_H_E 24
Baccharis_halimifolia_L_H_1G 71
Ammophila_breviligulata_St_H_E 5
Ammophila_breviligulata_St_D_D 25
Ammophila_breviligulata_B_MX_E 15
Ammophila_breviligulata_B_H_E 25
Ammophila_breviligulata_B_D_E 5
Ammophila_breviligulata_B_D_D 20
Ammophila_breviligulata_B_H_ M 8
0
10
20
30
40
50
60
70
Number of Occurrences

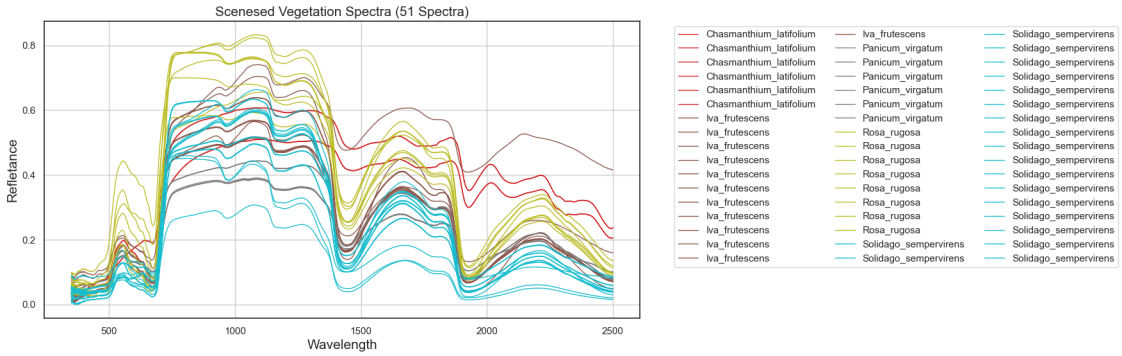
3 Plot some spectra for the library

[7]:
```
# Set the fontsize and create a function to colot plots be a specific metadata␣
 ↪category
fontsize = 15
def set_color(x, colormap_name = 'tab10'):
    # This function returns a dictionary of colors based on the input numpy x␣
 ↪of metadata values
    # The default colormap is tab10 (tableau 10), but any named colormap can be␣
 ↪used
    categories = np.unique(x)
    cmap = matplotlib.cm.get_cmap(colormap_name)
    clr = {}
    for i,category in enumerate(categories):
        clr[category] = cmap(i)
    return clr
```

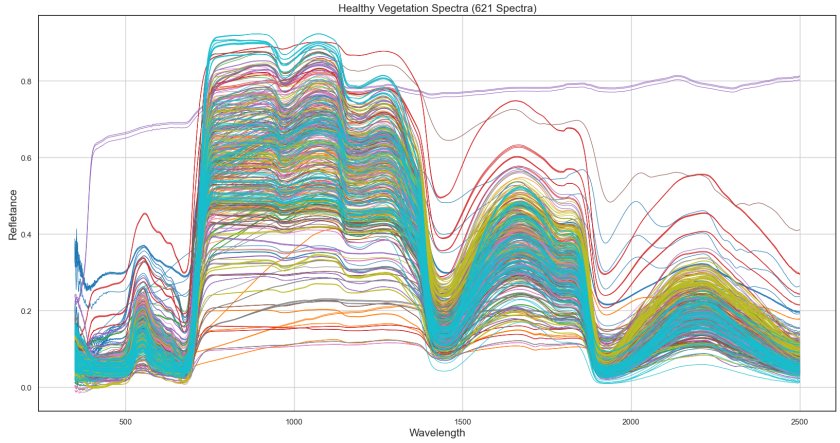
[8]:
```
# plot some random spectra
plt.figure(figsize=(12,6))
plt.grid(True)
rnd_idx = np.random.randint(0,nSpec, 15)
for idx in rnd_idx:
    plt.plot(wl, spectra[idx], label=name[idx], lw=1)
plt.xlabel('Wavelength', fontsize=fontsize)
plt.ylabel('Refletance', fontsize=fontsize)
plt.title('Fifteen Randomly Selected Spectra', fontsize=fontsize)
plt.legend(bbox_to_anchor=(1.05, 1.0), loc='upper left');
```



[9]:
```
# plot spectra satisfying some condition - note that we add 3 columns to the␣
 ↪legend because there are more labels to show
plt.figure(figsize=(12,6))
plt.grid(True)
selected_indices = np.where(health=='S')[0]
clr = set_color(name)
for idx in selected_indices:
    plt.plot(wl, spectra[idx], label=name[idx], lw=1, c=clr[name[idx]])
plt.xlabel('Wavelength', fontsize=fontsize)
plt.ylabel('Refletance', fontsize=fontsize)
plt.title(f'Scenesed Vegetation Spectra ({len(selected_indices)} Spectra)',␣
 ↪fontsize=fontsize)
plt.legend(bbox_to_anchor=(1.05, 1.0), loc='upper left', ncols=3);
```



[10]:
```
# plot spectra for healthy vegetation
plt.figure(figsize=(20,10))
plt.grid(True)
selected_indices = np.where(health=='H')[0]
for idx in selected_indices:
    plt.plot(wl, spectra[idx], label=name[idx], lw=0.75, c=clr[name[idx]])
plt.xlabel('Wavelength', fontsize=fontsize)
plt.ylabel('Refletance', fontsize=fontsize)
plt.title(f'Healthy Vegetation Spectra ({len(selected_indices)} Spectra)',␣
 ↪fontsize=fontsize)
plt.legend(bbox_to_anchor=(0.0, -0.2), loc='upper left', ncols=5);
```


Healthy Vegetation Spectra (621 Spectra)
Reflectance
0.0
0.2
0.4
0.6
0.8
500
1000
1500
2000
2500
Wavelength