Seeing beyond the visible: Estimating soil parameters from hyperspectral images - a starter pack

November 19, 2021

1 Introduction

How to open and understand the dataset

[1]:
```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
```

1.1 Basic information

1. Hyperspectral data:
    1. `hsi_path` contains path to hyperspectral masked numpy arrays containing hyperspectral data that underwent masking (i.e., the field area is masked, whereas all irrelevant areas are not masked)
    2. The name of the file (e.g., *'1989.npz'*) refers to the index of the corresponding training sample in the ground-truth table.
2. Ground-truth data:
    1. `gt_path` contains path to ground truth .csv file.
    2. Additionally, `wavelength_path` contains the mapping between a band number and the corresponding wavelength.

[2]:
```
hsi_path = 'train_data/1570.npz'
gt_path = 'train_gt.csv'
wavelength_path = 'wavelengths.csv'
```

[3]:
```
gt_df = pd.read_csv(gt_path)
wavelength_df = pd.read_csv(wavelength_path)
```

1.2 Ground-truth description

`gt_df` contains:

1. `sample_index` - a reference to the numpay array containing the corresponding hyperspectral data.
2. P (for simplicity, we use P while referring to P__2O__5), K, Mg, pH - soil properties levels based on laboratory measurements.

[4]:
```
gt_df[gt_df['sample_index']==1570]
```

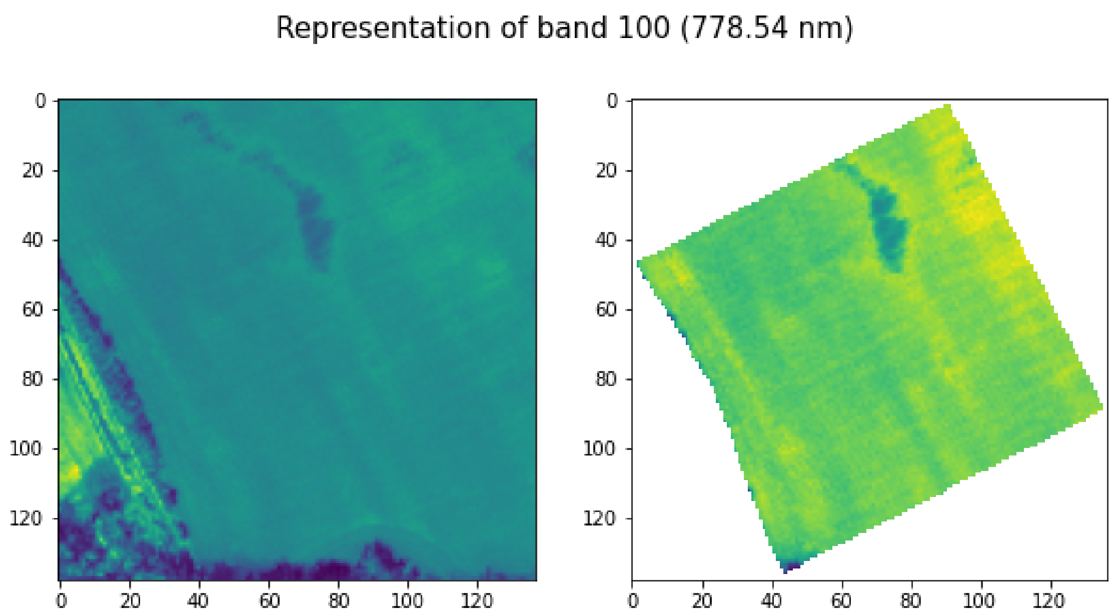
[4]:
```
      sample_index     P      K     Mg   pH
1570          1570  47.9  165.0  181.0  6.8
```

1.3 Displaying one hyperspectral band

[5]:
```
fig, axs = plt.subplots(1, 2, figsize=(10, 5))
band_id = 100
wavelength = wavelength_df.loc[band_id-1]

with np.load(hsi_path) as npz:
    arr = np.ma.MaskedArray(**npz)

axs[0].imshow(arr[band_id,:,:].data)
axs[1].imshow(arr[band_id,:,:])
plt.suptitle(f'Representation of band {int(wavelength["band_no"])}␣
↪({wavelength["wavelength"]} nm)', fontsize=15)
plt.show()
```



1.4 Displaying the aggregated spectral curve for a field

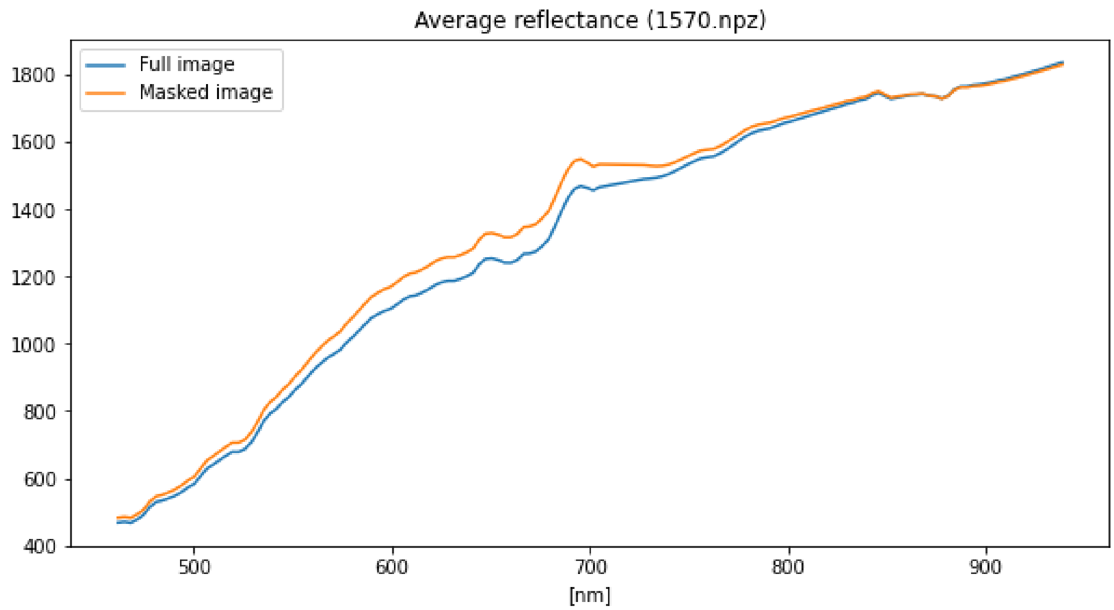
[6]:
```
fig = plt.figure(figsize=(10, 5))

masked_scene_mean_spectral_reflectance = [arr[i,:,:].mean() for i in range(arr.
↪shape[0])]
```

```
full_scene_mean_spectral_reflectance = [arr[i,:,:].data.mean() for i in␣
↪range(arr.shape[0])]

plt.plot(wavelength_df['wavelength'], full_scene_mean_spectral_reflectance,␣
↪label='Full image')
plt.plot(wavelength_df['wavelength'], masked_scene_mean_spectral_reflectance,␣
↪label='Masked image')

plt.xlabel('[nm]')
plt.legend()
plt.title(f'Average reflectance ({hsi_path.split("/")[-1]})')
plt.show()
```



2 Generating baseline solution

[7]:
```
class BaselineRegressor:
    """
    Baseline regressor, which calculates the mean value of the target from the␣
↪training
    data and returns it for each testing sample.
    """
    def __init__(self):
        self.mean = 0

    def fit(self, X_train: np.ndarray, y_train: np.ndarray):
```

```python
        self.mean = np.mean(y_train, axis=0)
        self.classes_count = y_train.shape[1]
        return self

    def predict(self, X_test: np.ndarray):
        return np.full((len(X_test), self.classes_count), self.mean)


class SpectralCurveFiltering():
    """
    Create a histogram (a spectral curve) of a 3D cube, using the merge_function
    to aggregate all pixels within one band. The return array will have
    the shape of [CHANNELS_COUNT]
    """

    def __init__(self, merge_function = np.mean):
        self.merge_function = merge_function

    def __call__(self, sample: np.ndarray):
        return self.merge_function(sample, axis=(1, 2))
```

2.1 Load the data

[8]:
```python
import os
from glob import glob

def load_data(directory: str):
    """Load each cube, reduce its dimensionality and append to array.

    Args:
        directory (str): Directory to either train or test set
    Returns:
        [type]: A list with spectral curve for each sample.
    """
    data = []
    filtering = SpectralCurveFiltering()
    all_files = np.array(
        sorted(
            glob(os.path.join(directory, "*.npz")),
            key=lambda x: int(os.path.basename(x).replace(".npz", "")),
        )
    )
    for file_name in all_files:
        with np.load(file_name) as npz:
            arr = np.ma.MaskedArray(**npz)
        arr = filtering(arr)
        data.append(arr)
```

```python
    return np.array(data)


def load_gt(file_path: str):
    """Load labels for train set from the ground truth file.
    Args:
        file_path (str): Path to the ground truth .csv file.
    Returns:
        [type]: 2D numpy array with soil properties levels
    """
    gt_file = pd.read_csv(file_path)
    labels = gt_file[["P", "K", "Mg", "pH"]].values
    return labels


X_train = load_data("train_data")
y_train = load_gt("train_gt.csv")
X_test = load_data("test_data")

print(f"Train data shape: {X_train.shape}")
print(f"Test data shape: {X_test.shape}")
```

```
Train data shape: (1732, 150)
Test data shape: (1154, 150)
```

2.2 Make predictions and generate submission file

[9]:
```python
baseline_reg = BaselineRegressor()
baseline_reg = baseline_reg.fit(X_train, y_train)
predictions = baseline_reg.predict(X_test)

submission = pd.DataFrame(data = predictions, columns=["P", "K", "Mg", "pH"])
submission.to_csv("submission.csv", index_label="sample_index")
```

2.3 Calculating the metric

For the purpose of presenting the final metric calculation, we will extract a small *test_set* from the training set.

[10]:
```python
X_test = X_train[1500:]
y_test = y_train[1500:]

X_train_new = X_train[:1500]
y_train_new = y_train[:1500]

# Fit the baseline regressor once again on new training set
baseline_reg = baseline_reg.fit(X_train_new, y_train_new)
```

```
baseline_predictions = baseline_reg.predict(X_test)

# Generate baseline values to be used in score computation
baselines = np.mean((y_test - baseline_predictions) ** 2, axis=0)


# Generate random predictions, different from baseline predictions
np.random.seed(0)
predictions = np.zeros_like(y_test)
for column_index in range(predictions.shape[1]):
    class_mean_value = baseline_reg.mean[column_index]
    predictions[:, column_index] = np.random.uniform(low=class_mean_value -␣
 ↪class_mean_value * 0.05,
                                                     high=class_mean_value +␣
 ↪class_mean_value * 0.05,
                                                     size=len(predictions))

# Calculate MSE for each class
mse = np.mean((y_test - predictions) ** 2, axis=0)

# Calculate the score for each class individually
scores = mse / baselines

# Calculate the final score
final_score = np.mean(scores)

for score, class_name in zip(scores, ["P", "K", "Mg", "pH"]):
    print(f"Class {class_name} score: {score}")

print(f"Final score: {final_score}")
```

```
Class P score: 0.9896068600445717
Class K score: 1.004900913045855
Class Mg score: 1.0228518828521695
Class pH score: 1.6431314552511207
Final score: 1.1651227777984292
```