# Course M-GFP3: Imaging and non-imaging spectroscopy: Term Paper

# Strategies to enhance predictive modeling of soil organic carbon (SOC) using the LUCAS topsoil spectral library.

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# **Table of contents**

1	Packages	1
2	Data           2.1 Load and Clean	<b>2</b>
	2.2 Sampling and Splitting	3
	2.3 Preprocessing	
3	Basemodel	5
	3.1 Finding optimal number of commponents	6
	3.2 Evaluating Base Model	
4	Model Improvement Strategies (5 P per strategy):	8
	4.1 Varying Preprocessing Strategy	9
	4.1.1 Savitzgy-Golay	
	4.1.2 Standard Normal Variate	
	4.2 Testing Different Models	13
	4.2.1 Pytorch LSTM	
5	Discussion of Results (5 P):	18

# 1 Packages

```
# Use autoreload to automatically reload modules
%load_ext autoreload
%autoreload

import matplotlib.pyplot as plt
import numpy as np
```

```
import pandas as pd
import torch
import torch.nn as nn
import torch.optim as optim
from scipy.signal import savgol_filter
from scipy.stats import pearsonr
from sklearn.cross_decomposition import PLSRegression
from sklearn.decomposition import PCA
from sklearn.metrics import mean_squared_error, pairwise_distances
from sklearn.model_selection import cross_val_score, train_test_split
from sklearn.preprocessing import StandardScaler

import own_functions
```

# 2 Data

Data splitting (5 P):

- Split your data into a calibration data set  $(\sim 70\%)$  and an independent test data set  $(\sim 30\%)$ .
- Show that both are representative of the full data set.
- For procedures with randomized approaches, please define and note the seed (in R: set.seed( ) ) to make the split reproducible for the instructors.
- From this point onward, the composition of the test data set must remain constant and unchanged for all subsequent tasks

#### 2.1 Load and Clean

```
# Load data
data = pd.read_csv('France_spc.csv')

# Remove unnecessary column
data = data.drop(columns=['Unnamed: 0'])

print(f"Data rows: {data.shape[0]}, columns: {data.shape[1]}")
display(data.head())
```

Data rows: 2807, columns: 1000

	500	502	504	506	508	510	512	514	516	518
0	0.137399	0.139045	0.140758	0.142544	0.144388	0.146281	0.148221	0.150205	0.152239	0.154322
1	0.141740	0.142851	0.144007	0.145208	0.146450	0.147726	0.149025	0.150348	0.151702	0.153081
2	0.140713	0.142216	0.143778	0.145392	0.147053	0.148756	0.150488	0.152257	0.154059	0.155892

 500	502	504	506	508	510	512	514	516	518
0.128922	0000	0000-0	00-000	0000-0	000-	0.20020	00000,	0.20120	0000
0	0000	$0.130919 \\ 0.164741$	00-000	0000-0	000-	0.20020	00000,		,

```
target = pd.read_csv('France_lab.csv')
target = target['SOC']
print(f"Target rows: {target.shape[0]}")
```

Target rows: 2807

# 2.2 Sampling and Splitting

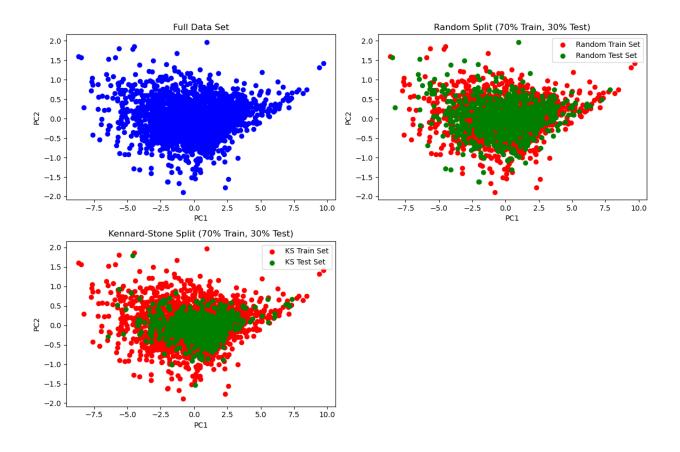
```
# Extract features and target as numpy array
X = data.values
y = target.values
# Extract features and target as numpy array
X = data.values
y = target.values
### Sampling strategies
# Step 1: Generate or Load Data
np.random.seed(100) # Set seed for reproducibility
# Step 2: Random Split (70% Calibration, 30% Test)
X_train_random, X_test_random, y_train_random, y_test_random = train_test_split(X, y, test_s
\# Step 3: Apply Kennard-Stone to select 70% of the data
n_{train} = int(0.7 * X.shape[0])
# Get indices
ks_indices = own_functions.kennard_stone(X, n_train)
# Select Training data
X_train_ks = X[ks_indices,:]
y_train_ks = y[ks_indices]
# Select Test
test_indices = np.setdiff1d(np.arange(X.shape[0]), ks_indices)
X_test_ks = X[test_indices]
y_test_ks = y[test_indices]
# Step 4: PCA for Visualization
```

Random Split:

Train set shape: (1964, 1000) Test set shape: (843, 1000)

Kennard-Stone Split:

Train set shape: (1964, 1000) Test set shape: (843, 1000)



## 2.3 Preprocessing

```
# Function to calculate RMSE using cross-validation
def calculate_rmse(n_components, X_train, y_train):
    pls = PLSRegression(n_components=n_components)
    # Use negative mean squared error as cross-validation scoring
    mse = cross_val_score(pls, X_train, y_train, cv=5, scoring='neg_mean_squared_error')
    rmse = np.sqrt(-mse).mean() # Take square root of MSE and average it across folds
    return rmse
```

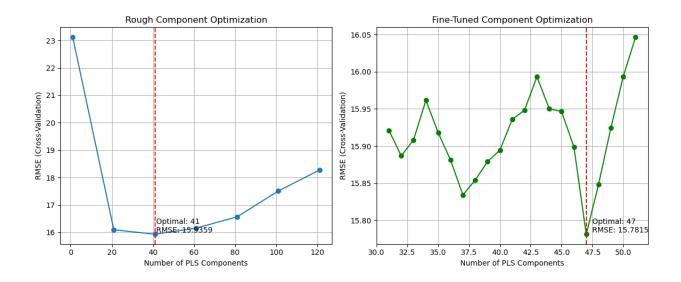
# 3 Basemodel

Baseline model (5 P): - Develop a global baseline PLSR model using the calibration dataset - (entire VNIR range from 500 nm to 2499 nm in steps of 2 nm) - without applying any spectral preprocessing. - The target variable is soil organic carbon (SOC). - Perform internal optimization to determine the optimal number of latent PLS variables - report your selected value. - Apply the optimized model\* to the independent test set. - Compute the validation metrics (R², RMSE, bias, and RPD) - visualize\* the results in a scatter plot (observed vs. predicted values) - and assess the model's performance.

# 3.1 Finding optimal number of commponents

Rough Optimization: 0% | | 0/7 [00:00<?, ?it/s]

Fine Tuning: 0%| | 0/21 [00:00<?, ?it/s]



# 3.2 Evaluating Base Model

```
print_metrics=True,
show_plot=True
)
```

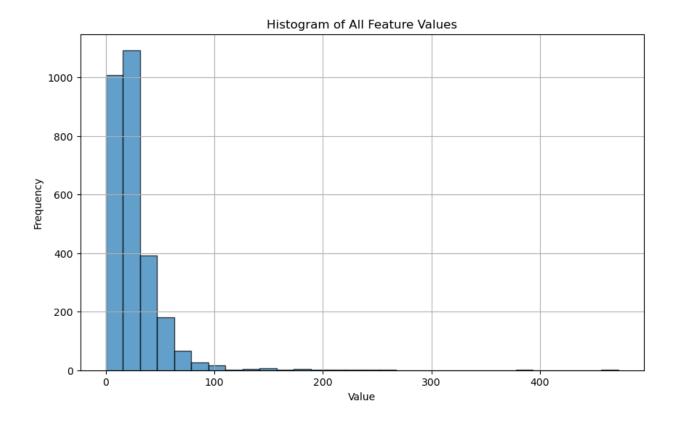
Root Mean Squared Error (RMSE): 10.0547

 $R^2$ : 0.6552 Bias: -0.1772 RPD: 1.7030

# Actual vs Predicted Values (Model) 250 200 150 50 0 50 100 150 200 250 Actual Values

```
all_values = y.flatten()

# Plot histogram of all feature values
plt.figure(figsize=(10, 6))
plt.hist(all_values, bins=30, edgecolor='k', alpha=0.7)
plt.title('Histogram of All Feature Values')
plt.xlabel('Value')
plt.ylabel('Frequency')
plt.grid(True)
plt.show()
```



# 4 Model Improvement Strategies (5 P per strategy):

- Develop and evaluate three distinct strategies to improve the baseline model,
  - using the same independent test set for validation.
- For each strategy, report the validation metrics
  - ( $R^2$ , RMSE, bias, and RPD),
  - visualize the best result in a scatter plot (observed vs.predicted values)
  - assess the performance of these alternative models.
  - Use the same independent test set for all strategies to ensure that validation metrics are directly comparable.

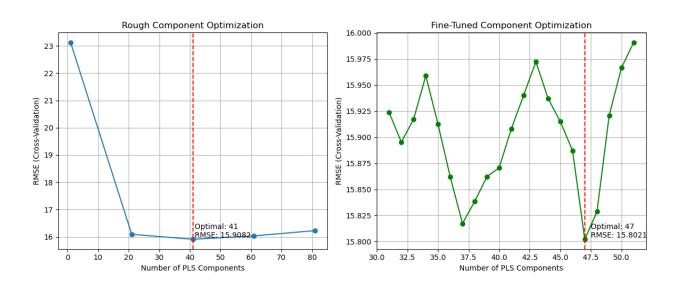
IMPORTANT: Testing two or more spectral preprocessing methods is considered one strategy, not multiple strategies. Similarly, testing one or more alternative regression algorithms counts as one strategy, not multiple.

# 4.1 Varying Preprocessing Strategy

## 4.1.1 Savitzgy-Golay

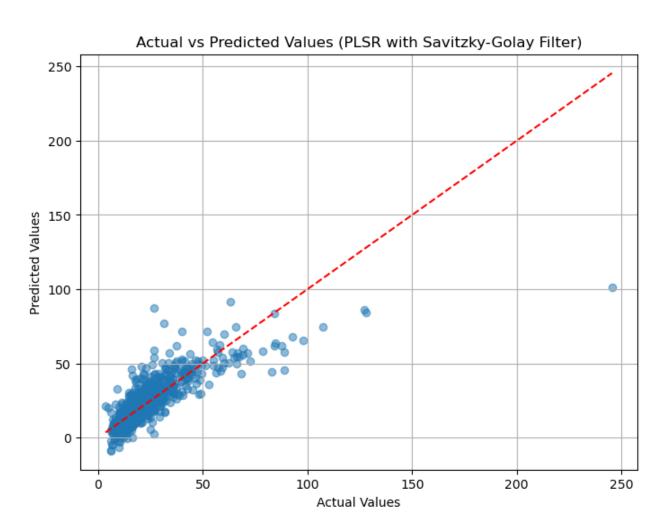
Rough Optimization: 0% | 0/5 [00:00<?, ?it/s]

Fine Tuning: 0% | 0/21 [00:00<?, ?it/s]



Root Mean Squared Error (RMSE): 10.0590

 $R^2$ : 0.6549 Bias: -0.1640 RPD: 1.7023

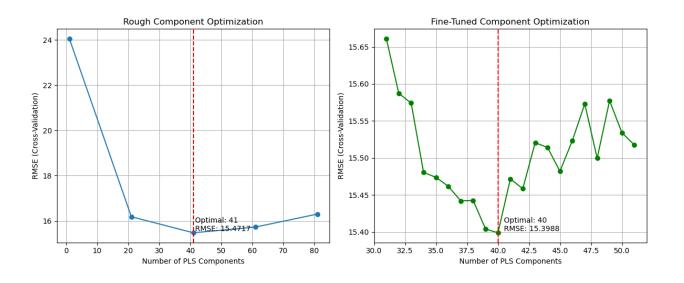


#### 4.1.2 Standard Normal Variate

```
import own_functions
# Applying Savitzky-Golay filter to calibration and test data
X_train_ks_snv = own_functions.standard_normal_variate(X_train_ks)
X_test_ks_snv = own_functions.standard_normal_variate(X_test_ks)
# Standardize data
scaler_ks_snv = StandardScaler()
X_train_ks_snv_scaled = scaler_ks_snv.fit_transform(X_train_ks_snv)
X_test_ks_snv_scaled = scaler_ks_snv.transform(X_test_ks_snv)
plsr_snv_components = own_functions.optimize_pls_components(X_train=X_train_ks_snv_scaled,
                                      y_train=y_train_ks,
                                      max_components=100,
                                      step=20,
                                      fine_tune=True,
                                      show_progress=True,
                                      plot_results=True
                                      )
```

Rough Optimization: 0%| | 0/5 [00:00<?, ?it/s]

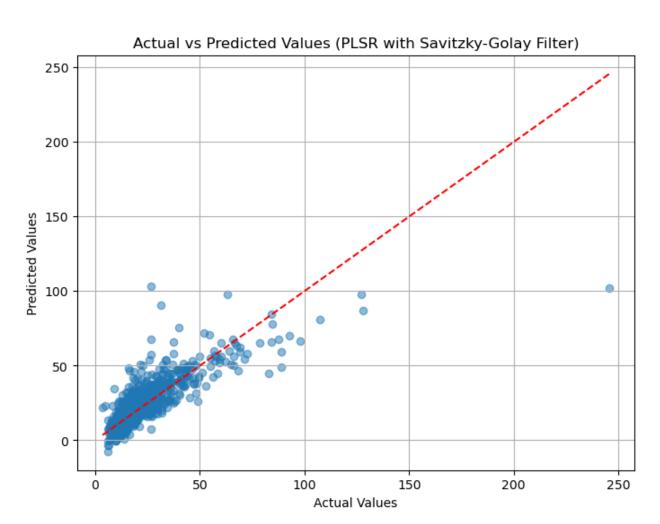
Fine Tuning: 0% | 0/21 [00:00<?, ?it/s]



```
plsr_snv_model = PLSRegression(n_components=plsr_snv_components["optimal_n"])
plsr_snv_model.fit(X_train_ks_snv, y_train_ks)
```

Root Mean Squared Error (RMSE): 10.1517

R<sup>2</sup>: 0.6485 Bias: 0.3009 RPD: 1.6867



#### 4.2 Testing Different Models

## 4.2.1 Pytorch LSTM

```
#TODO: Changed learning rate for less epochs, original: 0.001, 3000, new: 0.005, 500
X_train = X_train_ks
X_test = X_test_ks
y_train = y_train_ks
y_test = y_test_ks
# Define the PLS Regression model for dimensionality reduction
n_components = min(40, X_train.shape[1]) # Adjust based on your data; 10 is an example
pls = PLSRegression(n_components=n_components)
# Fit PLSR on the training data and transform both training and test sets
#X train pls = pls.fit transform(X train, y train)[0]
#X_test_pls = pls.transform(X_test)# check using traning data
# Fit PLSR on the training data and transform the training set
X_train_pls, _ = pls.fit_transform(X_train, y_train)
# Transform the test set using the fitted model (trained on the training set)
X_test_pls = pls.transform(X_test)
#pls scores loading regression coefficient latent variables,
# Convert to PyTorch tensors
X_train_tensor = torch.tensor(X_train_pls, dtype=torch.float32)
y_train_tensor = torch.tensor(y_train, dtype=torch.float32)
X_test_tensor = torch.tensor(X_test_pls, dtype=torch.float32)
y_test_tensor = torch.tensor(y_test, dtype=torch.float32)
# Define LSTM model
class LSTMModel(nn.Module):
    def __init__(self, input_size, hidden_size, output_size, num_layers):
        super(LSTMModel, self).__init__()
        self.hidden_size = hidden_size
        self.num_layers = num_layers
        # LSTM layers
```

```
self.lstm = nn.LSTM(input_size, hidden size, num_layers, batch_first=True)
        # Fully connected layer
        self.fc = nn.Linear(hidden_size, output_size)
    def forward(self, x):
        # Initialize hidden and cell states
        h0 = torch.zeros(self.num_layers, x.size(0), self.hidden_size).to(x.device)
        c0 = torch.zeros(self.num_layers, x.size(0), self.hidden_size).to(x.device)
        # Forward pass through LSTM layer
        out, _ = self.lstm(x, (h0, c0))
        # Select the last time step
        out = out[:, -1, :]
        # Forward pass through fully connected layer
        out = self.fc(out)
        return out
# Hyperparameters
input_size = X_train_pls.shape[1] # Number of features after PLSR
hidden_size = 256
output_size = 1 # For regression
num_layers = 5
num_epochs = 500
learning_rate = 0.005
# Initialize the model, loss function, and optimizer
model = LSTMModel(input_size, hidden_size, output_size, num_layers)
criterion = nn.MSELoss()
optimizer = optim.Adam(model.parameters(), lr=learning_rate)
# Training loop
for epoch in range(num_epochs):
   model.train()
    # Forward pass
    outputs = model(X_train_tensor.unsqueeze(1))  # Add sequence dimension
    loss = criterion(outputs.squeeze(), y_train_tensor)
    # Backward pass and optimization
    optimizer.zero_grad()
    loss.backward()
    optimizer.step()
```

```
if (epoch + 1) \% 10 == 0:
        print(f'Epoch [{epoch + 1}/{num_epochs}], Loss: {loss.item():.4f}')
# Evaluate the model
model.eval()
with torch.no_grad():
    # Make predictions on the test set
    predictions = model(X_test_tensor.unsqueeze(1)).squeeze()
    # Calculate test loss
    test_loss = criterion(predictions, y_test_tensor)
    print(f'Test Loss: {test_loss.item():.4f}')
    # Convert predictions and y_test to numpy arrays
    y_pred_np = predictions.numpy()
    y_test_np = y_test_tensor.numpy()
    # Calculate RMSE
    rmse = np.sqrt(mean_squared_error(y_test_np, y_pred_np))
    print(f'Root Mean Squared Error (RMSE): {rmse:.4f}')
    # Calculate correlation coefficient
    correlation, _ = pearsonr(y_test_np, y_pred_np)
    print(f'Correlation coefficient: {correlation:.4f}')
    # Plot actual vs. predicted values
    plt.figure(figsize=(10, 5))
    plt.scatter(y_test_np, y_pred_np, alpha=0.5)
    plt.plot([min(y_test_np), max(y_test_np)], [min(y_test_np), max(y_test_np)], color='red'
   plt.xlabel('Actual Values')
    plt.ylabel('Predicted Values')
   plt.title('Actual vs Predicted Values (PLSR + LSTM)')
    plt.grid(True)
   plt.show()
```

## KeyboardInterrupt:

```
# Normalize features
scaler = StandardScaler()

#X_pca_scaled = scaler.fit_transform(X)

# Split data into training and test sets

X_train = scaler.fit_transform(X_train)
```

```
X_test = scaler.transform(X_test)
# Convert to PyTorch tensors
X_train = torch.tensor(X_train, dtype=torch.float32)
y_train = torch.tensor(y_train, dtype=torch.float32)
X test = torch.tensor(X test, dtype=torch.float32)
y_test = torch.tensor(y_test, dtype=torch.float32)
# Define LSTM model
class LSTMModel(nn.Module):
    def __init__(self, input_size, hidden_size, output_size, num_layers):
        super(LSTMModel, self).__init__()
        self.hidden_size = hidden_size
        self.num_layers = num_layers
        # LSTM layers
        self.lstm = nn.LSTM(input_size, hidden size, num_layers, batch_first=True)
        # Fully connected layer
        self.fc = nn.Linear(hidden_size, output_size)
    def forward(self, x):
        # Initialize hidden and cell states
        h0 = torch.zeros(self.num_layers, x.size(0), self.hidden_size).to(x.device)
        c0 = torch.zeros(self.num_layers, x.size(0), self.hidden_size).to(x.device)
        # Forward pass through LSTM layer
        out, _ = self.lstm(x, (h0, c0))
        # Select the last time step
        out = out[:, -1, :]
        # Forward pass through fully connected layer
        out = self.fc(out)
        return out
# Hyperparameters
input_size = X_train.shape[1] # Number of features after PCA and scaling
hidden_size = 256
output_size = 1 # For regression
num_layers = 5
num_epochs = 2000
learning_rate = 0.001
# Initialize the model, loss function, and optimizer
model = LSTMModel(input_size, hidden_size, output_size, num_layers)
criterion = nn.MSELoss()
optimizer = optim.Adam(model.parameters(), lr=learning_rate)
```

```
# Training loop
for epoch in range(num_epochs):
    model.train()
    # Forward pass
    outputs = model(X_train.unsqueeze(1)) # Add sequence dimension
    loss = criterion(outputs.squeeze(), y_train)
    # Backward pass and optimization
    optimizer.zero_grad()
    loss.backward()
    optimizer.step()
    if (epoch + 1) \% 10 == 0:
        print(f'Epoch [{epoch + 1}/{num_epochs}], Loss: {loss.item():.4f}')
# Evaluate the model
model.eval()
with torch.no_grad():
    # Make predictions on the test set
   predictions = model(X_test.unsqueeze(1)).squeeze()
    # Calculate test loss
    test_loss = criterion(predictions, y_test)
    print(f'Test Loss: {test_loss.item():.4f}')
    # Convert predictions and y_test to numpy arrays
    y_pred_np = predictions.numpy()
    y_test_np = y_test.numpy()
    # Calculate RMSE
    rmse = np.sqrt(mean_squared_error(y_test_np, y_pred_np))
    print(f'Root Mean Squared Error (RMSE): {rmse:.4f}')
    # Calculate correlation coefficient
    correlation, _ = pearsonr(y_test_np, y_pred_np)
    print(f'Correlation coefficient: {correlation:.4f}')
    # Plot actual vs. predicted values
    plt.figure(figsize=(10, 5))
    plt.scatter(y_test_np, y_pred_np, alpha=0.5)
    plt.plot([min(y_test_np), max(y_test_np)], [min(y_test_np), max(y_test_np)], color='red'
   plt.xlabel('Actual Values')
    plt.ylabel('Predicted Values')
   plt.title('Actual vs Predicted Values')
    plt.grid(True)
```

```
plt.show()
```

NameError: name 'torch' is not defined

# 5 Discussion of Results (5 P):

- Briefly discuss your results and interpret them based on the validation metrics for the test set.
- Compare your findings with those of published studies in a similar context.
- Evaluate whether soil VNIR reflectance spectroscopy could serve as a complementary approach for large-scale soil organic carbon assessment in Earth (system) science.

#### **Additional Information:**

The length of the discussion section really depends on your results, but as a general guideline, I would expect it to be around one page.

#### • Focus on:

- directly comparing your different modeling approaches
- interpreting which performed best based on the validation metrics
- If the results are not as good as expected:
  - consider discussing possible reasons and suggesting ways to improve them
  - (you might find 1-2 examples from the literature helpful here).
- Additionally, you could compare your findings with similar studies that have attempted to model SOC (or related properties) at national or continental scales using spectroscopy—ideally referencing 2-3 relevant publications.
- Finally, reflect on whether and how soil VNIR spectroscopy could contribute to large-scale soil information systems.
  - This is a more theoretical aspect, and you are free in how you approach this point.
  - Important aspects to consider might include:
    - \* a) Model accuracy (What would be considered a good accuracy in this context?)
    - \* b) Data harmonization (Challenges when combining datasets from different providers)
    - \* c) Practical usability (Would end users require programming skills, etc.?)

A recent publication that could provide a useful overview is: Peng et al. (2025): Spectroscopic solutions for generating new global soil information (Link: https://www.sciencedirect.com/science/article/pii/S2666678