

# Python Scripts to process hyperspectral images

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**Key Words:** Hyperspectral imaging, Spectra, Classification model, Random forest

## Part 1: Scripts used to process hyperspectral images

### Importing libraries

```
In [1]: import os
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import cv2
from spectral.io import envi
```

### Importing images

```
In [1]: folder_path = r'path to hyperspectral images (.raw and .hdr)'

## Image dimensions
# x = dimension if it differs from one image to another, take the min)
# y = dimension (all our images are 640)
# z = dimension, number of spectral variables (in all our images this is 244)
target_shape = (x, y, z)

# List for storing imported data
data_list = []

# Loop to browse files in folder
for file_name in os.listdir(folder_path):
    # Check if the file is an .hdr file
    if file_name.endswith(".hdr"):
        base_name = file_name[:-4] # Remove ".hdr"

        # Correspondence with raw file
        raw_file = base_name + ".raw"
        raw_path = os.path.join(folder_path, raw_file)
        hdr_path = os.path.join(folder_path, file_name)

        # Checks whether the corresponding .raw file exists
        if os.path.exists(raw_path):
            try:
                # Load hyperspectral data
                data = envi.open(hdr_path, raw_path)
                data_nparr = np.array(data.load(), dtype=np.float16)

                if data_nparr.shape == target_shape:
                    print(f"Original dimensions of {file_name} : {data_nparr.shape}")

                if data_nparr.shape[0] > target_shape[0]:
                    data_nparr = data_nparr[:target_shape[0], :, :]
                    print(f"Image {file_name} resized to {data_nparr.shape}")

                elif data_nparr.shape[0] < target_shape[0]:
                    print(f"Image {file_name} is too small to fit.")
                    continue # Go to next image

                # Adds adjusted data to the list
                data_list.append(data_nparr)
                print(f"Successfully imported : {file_name} & {raw_file}")

            except Exception as e:
                print(f"Error when importing {file_name} & {raw_file} : {e}")
            else:
                print(f"Missing RAW file for : {file_name}")

        Reflectance correction
```

### Reflectance correction

```
In [1]: dark_ref = envi.open('black reference .hdr path', 'black reference .raw path')
white_ref = envi.open('white reference .hdr path', 'white reference .raw path')
dark_nparr = np.array(dark_ref.load(), dtype=np.float16)
white_nparr = np.array(white_ref.load(), dtype=np.float16)

In [1]: # Resizing references
example_shape = data_list[0].shape

white_nparr_resized = np.zeros(example_shape, dtype=white_nparr.dtype)
for band in range(white_nparr.shape[2]):
    white_nparr_resized[:, :, band] = cv2.resize(white_nparr[:, :, band], example_shape[1], example_shape[0], interpolation=cv2.INTER_NEAREST)

dark_nparr_resized = np.zeros(example_shape, dtype=dark_nparr.dtype)
for band in range(dark_nparr.shape[2]):
    dark_nparr_resized[:, :, band] = cv2.resize(dark_nparr[:, :, band], example_shape[1], example_shape[0], interpolation=cv2.INTER_NEAREST)

2. Apply correction to each image in data_list
```

```
In [1]: corrected_images = [] # List for storing corrected images

# Loop to browse each image in data_list
for i, data_nparr in enumerate(data_list):
    # Checking dimensions
    if data_nparr.shape != white_nparr_resized.shape:
        print(f"Error: Incompatible image dimensions ({i}).")
        continue

    # Correction
    corrected_nparr = np.divide(
        np.subtract(data_nparr, dark_nparr_resized),
        np.subtract(white_nparr_resized, dark_nparr_resized))
    corrected_nparr = np.clip(corrected_nparr, 0, 1)
    corrected_images.append(corrected_nparr)
```

### Binaryization, creation of a binary masks

```
In [1]: binary_masks = [] # List for storing binary masks
thresholds = [] # List for storing thresholds

# Define a small core so that the effect is not intense
kernel_3x3 = np.ones((3, 3), np.uint8) * 3 # 3x3 core
# Define a large core
kernel_11x11 = np.ones((11, 11), np.uint8) * 1 # 11x11 core

for i, corrected_image in enumerate(corrected_images):
    # Select band 41 (index 40 as NumPy uses indices starting from 0)
    gray_image = corrected_image[:, :, 40]

    # Normalize image (make sure values are between 0 and 255 for cv2)
    gray_image_normalized = (gray_image / 255).astype(np.uint8)

    # Apply Otsu's binarization method
    otsu_threshold, binary_mask = cv2.threshold(gray_image_normalized, 0, 255, cv2.THRESH_BINARY + cv2.THRESH_OTSU)

    # Apply erosion (light effect so as to not lose intensity)
    binary_mask_eroded = cv2.erode(binary_mask, kernel_3x3, iterations=2)

    # Apply dilatation (light effect to restore shapes)
    binary_mask_final = cv2.dilate(binary_mask_eroded, kernel_11x11, iterations=2)

    # Add binary mask to list
    binary_masks.append(binary_mask_final)
    thresholds.append(otsu_threshold)
```

### Application of binary masks, and creation of segmented hyperspectral cubes

```
In [1]: masked_cubes = [] # List for storing hidden hyperspectral cubes

# Browse each corrected image and its binary mask
for i, (corrected_image, binary_mask) in enumerate(zip(corrected_images, binary_masks)):
    cube_images = [] # Temporary list for masked bands in this image

    # Mask the binary mask to specific bands
    for band_idx in range(corrected_image.shape[2]):
        # Extract the current spectral band
        current_band = corrected_image[:, :, band_idx]

        # Apply binary mask (black mask zones set pixels to 0)
        masked_band = np.where(binary_mask == 255, current_band, 0)

        # Add hidden band to temporary list
        cube_images.append(masked_band)

    # Convert the list of masked images into a hyperspectral cube
    cube_hyperspectral = np.stack(cube_images, axis=1)
    masked_cubes.append(cube_hyperspectral) # Add hidden cube to main list
```

### Extraction of average spectra

```
In [1]: # Define the boundaries of the three regions in the images
regions = [{"ymin": 1, "ymax": 3, "label": "Proximal"}, {"ymin": 4, "ymax": 6, "label": "Central"}, {"ymin": 7, "ymax": 9, "label": "Distal"}]

# List of labels for the DataFrame to be trained between [], (If you know or prefer indexes for the samples, to train them, otherwise without labels will be from 1 sample to n sample)
labels = []

# Initialize une structure pour stocker les spectres moyens de toutes les images
all_spectra = []

# Loop through each hyperspectral image
for img in cube_hyperspectral:
    # Create a dictionary to store the spectra of this image
    image_spectra = {} # Dictionary to store the spectra of this image

    # Calculate the average spectrum for each region
    for region in regions:
        ymin, ymax, label = region["ymin"], region["ymax"], region["label"]

        # Extract sub-region from hyperspectral image
        subregion = img[ymin:ymax, :, :]

        # Create a mask to exclude values equal to 0
        mask = (subregion > 0)

        # Calculate the average spectrum
        spectre_moyen = np.zeros(cube_hyperspectral.shape[2])
        for band_idx in range(cube_hyperspectral.shape[2]):
            spectre_moyen[band_idx] = np.mean(subregion[:, :, band_idx][mask])

        # Store the average spectrum in the dictionary
        image_spectra[label] = spectre_moyen

    # Add the average spectra of this image to the main list
    all_spectra.append(image_spectra)

# Structuring data for the DataFrame
data = []
for idx, image_spectra in enumerate(all_spectra):
    for region_label, spectra in image_spectra.items():
        region_label_spectra = spectra
        full_label = f"({idx+1},{region_label})" if idx > 0 else f"({region_label})"

        data.append(spectra)

# Creating the DataFrame
Spectra = pd.DataFrame(data, index=labels)
```

### Saving mean spectra

```
In [1]: file_path = r'path to file to save.xlsx'
```

### Data visualization (spectra and histogram of WAB value distribution)

```
In [34]: # Create figure with 2 side-by-side subplots
fig, axes = plt.subplots(1, 2, figsize=(14, 5))

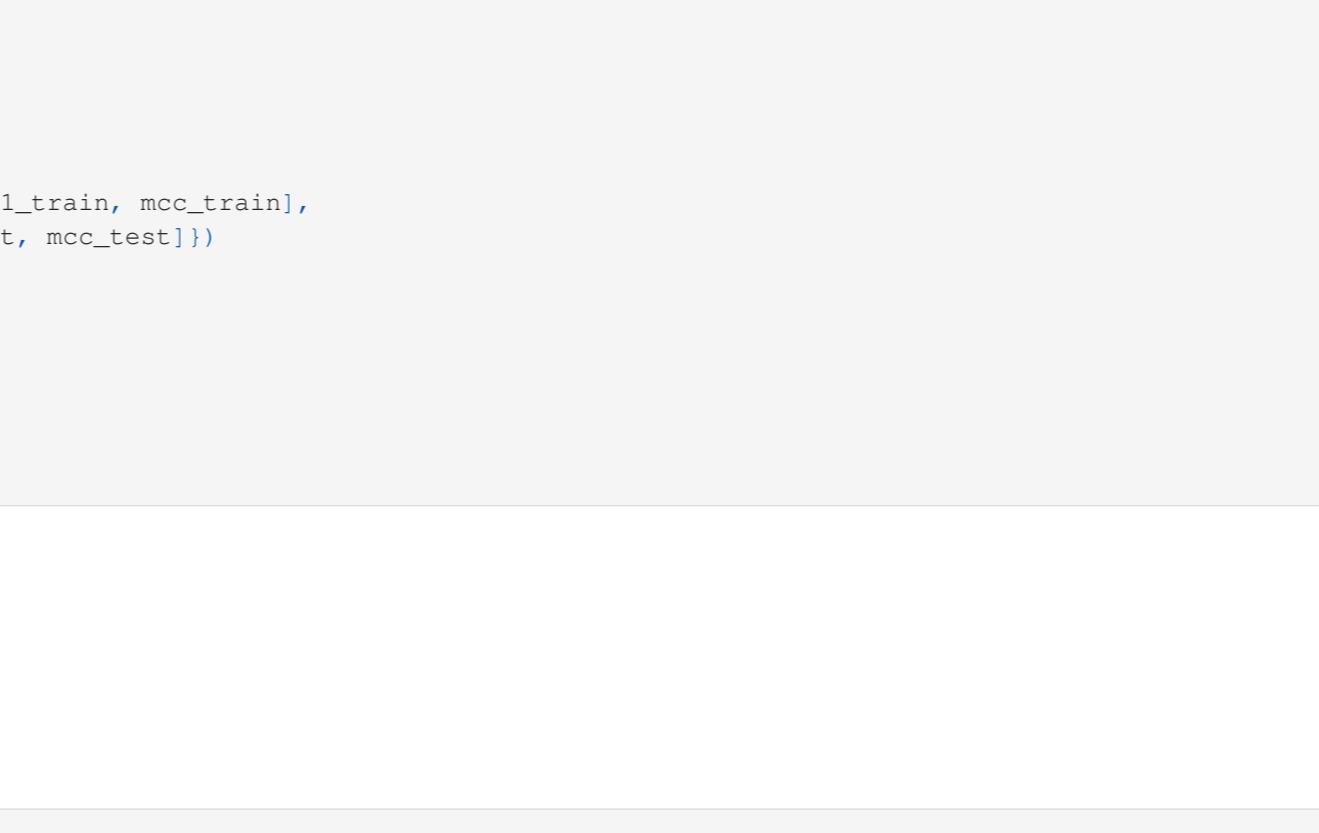
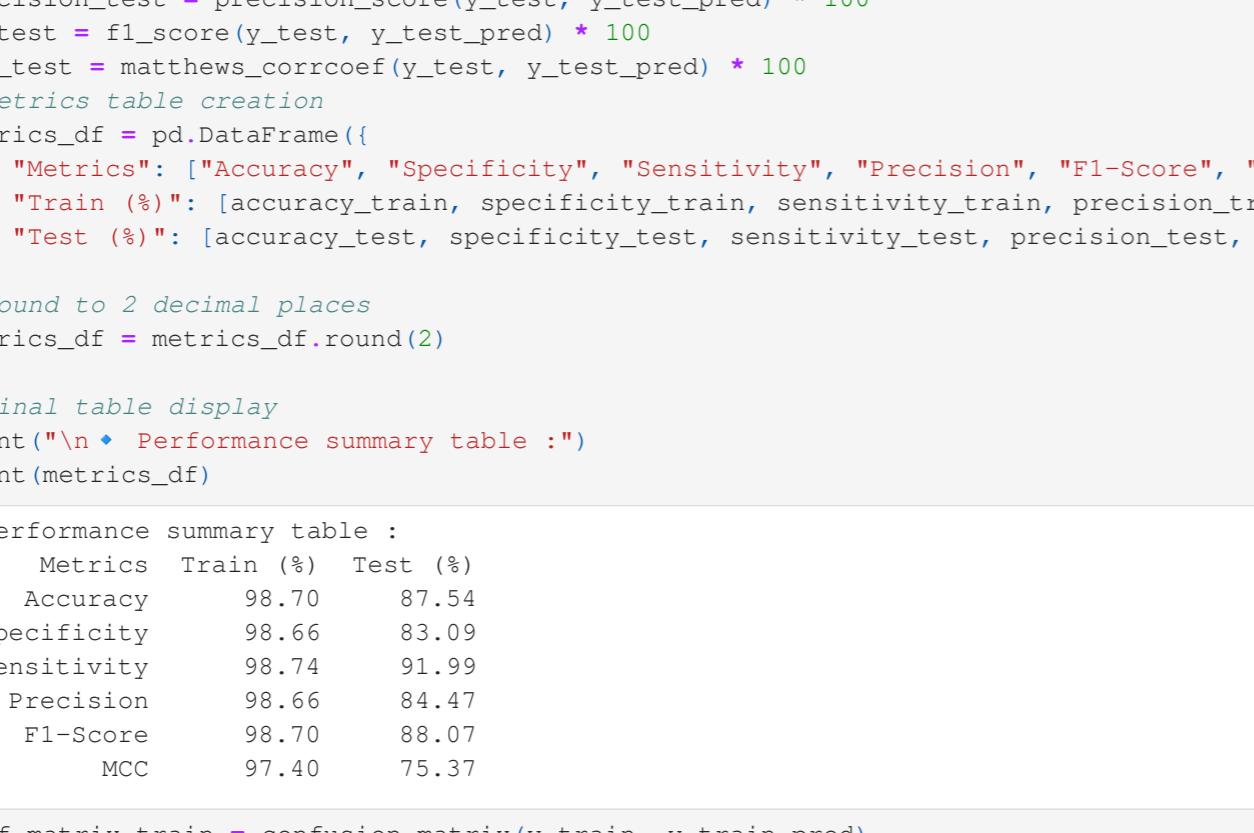
# Histogram of WAB values
sns.histplot(df_Y["WAB (%) at 30 min"], bins=30, kde=True, color="blue")
axes[0].set_title("Distribution of WAB values (%) at 30 min")
axes[0].set_xlabel("WAB (%) at 30 min")
axes[0].set_ylabel("Frequency")

# Reflectance spectra
axes[1].plot(df_spectra["Wavelength (nm)"], df_spectra["Reflectance"])
axes[1].set_title("Reflectance spectra")
axes[1].set_xlabel("Wavelength (nm)")
axes[1].set_ylabel("Reflectance")
```

Ajuster l'espace entre les graphiques

plt.tight\_layout()

plt.show()



### Application of SNV preprocessing to spectral data

```
In [36]: # definition of the snv function
def snv(input_data):
    output_data = np.zeros_like(input_data)
    for i in range(input_data.shape[0]):
        output_data[i, :] = (input_data[i, :] - np.mean(input_data[i, :])) / np.std(input_data[i, :])
    return output_data
```

### Define target variable (class)

```
In [38]: Y_df_filtered["Quality_Class"] = np.where(Y_df_filtered["WAB (%) at 30 min"] < 12, 0, 1)
```

### data oversampling with the SMOTE method

```
In [39]: # Define explanatory variables (X) and target (y)
X = df_spectra
Y = Y_df_filtered["Quality_Class"].values # Classes (0 or 1)
```

```
smote = SMOTE(random_state=42) # to fix the random effect
```

```
X_resampled, y_resampled = smote.fit_resample(X, y)
```

```
from sklearn.model_selection import train_test_split
```

```
import joblib
```

### Data import

```
In [41]: # Set file path
file_path = "path to template/12_dataset-HSI-WAB-boiled-cassava-CIAT-CIRAD-may2024-v250331.xlsx"
```

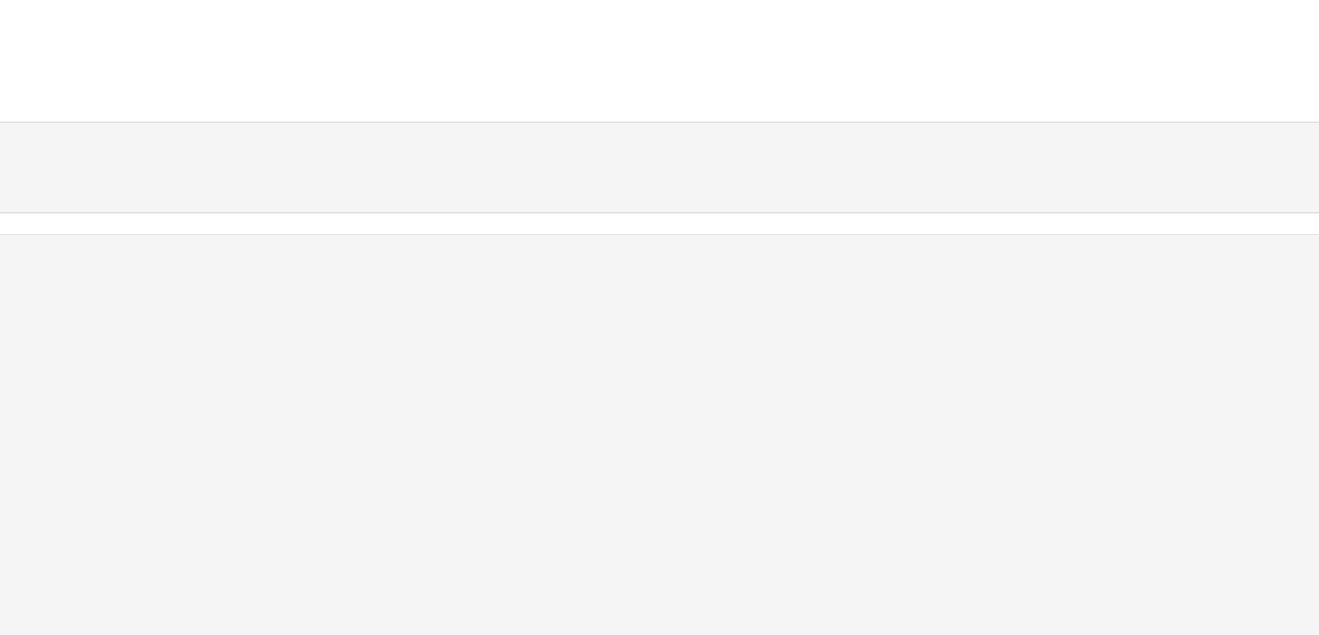
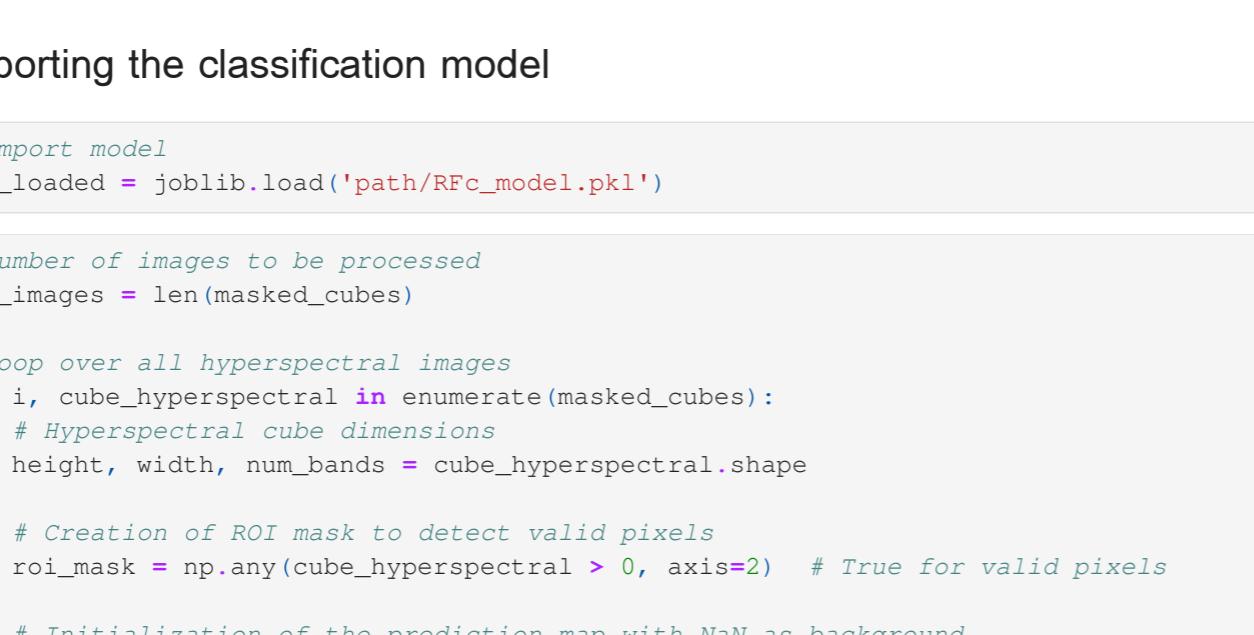
```
# Load the "Spectra" sheet and extract spectral data
df_spectra = pd.read_excel(file_path, sheet_name="Spectra", header=0, index_col=0)
```

```
# Select spectral data columns (index = 14 as Python starts at 0)
df_spectra = df_spectra.iloc[:, 14:]
```

```
# Load the "Laboratory data" sheet and extract response Y by name
df_Y = pd.read_excel(file_path, sheet_name="laboratory data", header=0, index_col=0)
```

```
# Select "WAB (%) at 30 min" column
df_Y = df_Y[['WAB (%) at 30 min']]
```

```
Data visualization (spectra and histogram of WAB value distribution)
```



### Model performance parameters

#### Function for calculating specificity and sensitivity

```
In [42]: def specificity_sensitivity(y_true, y_pred):
    tp = np.sum(y_true == y_pred == 1)
    fp = np.sum(y_true == 0 & y_pred == 1)
    tn = np.sum(y_true == y_pred == 0)
    fn = np.sum(y_true == 1 & y_pred == 0)

    specificity = tp / (tp + fp)
    sensitivity = tp / (tp + fn)

    return specificity, sensitivity
```

#### Metrics calculation

```
In [43]: # Metrics calculation
metrics_df = pd.DataFrame({
    "Train (%)": [accuracy_train, specificity_train, sensitivity_train, precision_train, f1_score_train, mcc_train],
    "Test (%)": [accuracy_test, specificity_test, sensitivity_test, precision_test, f1_score_test, mcc_test]
})
```

#### Round to 2 decimal places

```
metrics_df = metrics_df.round(2)
```

#### Final table display

```
print("Performance summary table :")
```

```
print(metrics_df)
```

#### Performance summary table :

```
accuracy
```

```
specificity
```

```
sensitivity
```

```
precision
```

```
f1 score
```

```
mcc
```

```
accuracy
```

```
specificity
```

```
sensitivity
```

```
precision
```

```
f1 score
```

```
mcc
```

```
accuracy
```

```
specificity
```

```
sensitivity
```

```
precision
```

```
f1 score
```

```
mcc
```

```
accuracy
```

```
specificity
```

```
sensitivity
```

```
precision
```

```
f1 score
```

```
mcc
```

```
accuracy
```

```
specificity
```

```
sensitivity
```

```
precision
```

```
f1 score
```

```
mcc
```

```
accuracy
```

```
specificity
```

```
sensitivity
```

```
precision
```

```
f1 score
```

```
mcc
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accuracy
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specificity
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sensitivity
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precision
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f1 score
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```
mcc
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```
accuracy
```

```
specific
```

