	In this task, we are asked to identify relationship between albedo and composition by dividing the data into two equal halves (left and right). We are required to train our models on the left half and predict the right. The task can be viewed as a standard regression one which aims to predict the brightness of each pixel. Finally, we create a framework for combining outputs of constituent models using the stacking framework.  # Load essential libraries import pandas as pd import numpy as np import matplotlib.pyplot as plt import seaborn as sns  from sklearn.linear_model import LinearRegression, ElasticNet, Lasso from sklearn.metrics import mean_absolute_error, mean_squared_error from sklearn.ensemble import GradientBoostingRegressor from sklearn.model_selection import KFold, cross_val_score from sklearn.preprocessing import StandardScaler, RobustScaler
	from sklearn.preprocessing import StandardScaler, RobustScaler from sklearn.base import BaseEstimator, TransformerMixin, RegressorMixin, clone from sklearn.pipeline import make_pipeline from sklearn.pipeline import XGBRegressor from keras.models import LGBMRegressor from keras.models import Sequential from keras.layers import Dense from keras.wrappers.scikit_learn import KerasRegressor  plt.style.use('fivethirtyeight') # For better style %matplotlib inline
]:	Read the datasets provided at the github link  BASE_URL = "https://raw.githubusercontent.com/ML4SCI/ML4SCI_GSoC/main/Messenger/Moon/"  # Load albedo map albedo_map = pd.read_csv(BASE_URL + "Albedo_Map.csv", header=None)  NUM_ROWS = albedo_map.shape[0]  NUM_COLS = albedo_map.shape[1]  CENTER_HALF = NUM_COLS // 2  # Load iron map lpfe_map = pd.read_csv(BASE_URL + "LPFe_Map.csv", header=None)
]:	# Load potassium map lpk_map = pd.read_csv(BASE_URL + "LPTh_Map.csv", header=None)  # Load thorium map lpth_map = pd.read_csv(BASE_URL + "LPTh_Map.csv", header=None)  # Load titanium map lpti_map = pd.read_csv(BASE_URL + "LPTi_Map.csv", header=None)  Plotting the albedo map to confirm if we are reading the file correctly as a sanity check.  fig, (ax1,ax2,ax3) = plt.subplots(nrows=1, ncols=3, figsize=(24, 8), gridspec_kw={'width_ratios': [2,1,1]})  sns.heatmap(albedo_map, cmap="gray", xticklabels=False, yticklabels=False, ax=ax1)
	ax1.set_title("Mercury Albedo")  sns.heatmap(albedo_map.iloc[:, :CENTER_HALF], cmap="gray", xticklabels=False, yticklabels=False, ax=ax2)  ax2.set_title("left half of Mercury Albedo")  sns.heatmap(albedo_map.iloc[:, CENTER_HALF:], cmap="gray", xticklabels=False, yticklabels=False, ax=ax3)  ax3.set_title("right half of Mercury Albedo")  plt.suptitle("Albedo Map", fontsize=20) plt.show()  Albedo Map  Mercury Albedo Mercury Albedo right half of Mercury Albedo right half of Mercury Albedo
	10.50
	fig, (ax1,ax2,ax3,ax4) = plt.subplots(nrows=1, ncols=4, figsize=(25, 5))  sns.heatmap(lpfe_map, cmap="jet", xticklabels=False, yticklabels=False, ax=ax1) ax1.set_title("Fe map")  sns.heatmap(lpk_map, cmap="jet", xticklabels=False, yticklabels=False, ax=ax2) ax2.set_title("K map")  sns.heatmap(lpth_map, cmap="jet", xticklabels=False, yticklabels=False, ax=ax3) ax3.set_title("Th map")  sns.heatmap(lpti_map, cmap="jet", xticklabels=False, yticklabels=False, ax=ax4) ax4.set_title("Ti map")  plt.suptitle("Chemical composition of Lunar rocks", fontsize=20)
	Fe map  Chemical composition of Lunar rocks Th map  10  15  10  15  10  15  10  10  15  10  10
]:	def add_interaction_features(data):     data['potassium_inc_interaction'] = data['potassium'] * data['inon']     data['potassium_thorium_interaction'] = data['potassium'] * data['thorium']     data['potassium_titinalium_interaction'] = data['potassium'] * data['thorium']     data['inon_thorium_interaction'] = data['inon'] * data['thorium']     data['inon_thorium_interaction'] = data['inon'] * data['thorium']     data['inon_thorium_interaction'] = data['thorium'] * data['thorium']     data['thorium_interaction'] = data['thorium'] * data['tinon']     data['thorium_interaction'] = data['thorium'] * data['tinon']  df_left_half['iotassium'] = lpie_map.iloc[; :CENTER_HALF].values.reshape(-1, 1).flatten()  df_left_half['thorium'] = lpie_map.iloc[; :CENTER_HALF].values.reshape(-1, 1).flatten()  df_left_half['tinon'] = lpie_map.iloc[; :CENTER_HALF].values.reshape(-1, 1).flatten()  df_left_half['tinon'] = lpie_map.iloc[; :CENTER_HALF].values.reshape(-1, 1).flatten()  df_left_half['tinon'] = lpie_map.iloc[; :CENTER_HALF].values.reshape(-1, 1).flatten()  df_right_half['thorium'] = lpie_map.iloc[; :CENTER_HALF].values.reshape(-1, 1).flatten()  dr_right_half['thorium'] = lpie_map.iloc[; :CENTER_HALF].values.reshape(-1, 1).flatten()  dr_right_half['thorium'] = lpie_map.iloc[; :CENTER_HALF].values.reshape(-1, 1).flatten()  dr_right_half['thorium'] =
	cols = df_left_half.columns.tolist() sns.pairplot(df_left_half[cols]) plt.tight_layout() plt.suptitle("Pair plot of chemical composition and albedo", fontsize=28);  Pair plot of chemical composition and albedo  Pair plot of chemical composition and albedo  1
	4900 1000 1000 1000 1000 1000 1000 1000
	As we can infer from the above plot, there are a couple of outliers (although few) for all the chemical compositions, due to the skeweness in the data. Since the spread is not that significant, we can choose to keep it in the modeling process.  Let us look for some correlations in the dataset.  Corr = df_left_half_corr() ptr.suphplots(figs1zec(8, 4)) sns.heatmap(corr, vmaxe0.9, cmap="ellues", square=True) ptr.suphplots(figs1zec(8, 4)) sns.heatmap() ptr.suphp
:	As shown above, potassium and thorium have the maximum correlation. Followed by iron and titanium which has slightly lesser correlation.  df_left_half = add_interaction_features(df_left_half) df_right_half = add_interaction_features(df_right_half)  features = ['iron', 'potassium_titanium_interaction', 'titanium', 'potassium_interaction', 'potassium_titanium_interaction', 'iron_titanium_interaction', 'thorium_interaction', 'thorium_interaction', 'thorium_interaction', 'thorium_titanium_interaction']
:	<pre>X_train = df_left_half[features] y_train = df_left_half['albedo'].values X_test = df_right_half[features] y_test = df_right_half['albedo'].values  #Validation function n_folds = 2 # 5  def mse_cv(model):     kf = KFold(n_folds, shuffle=False).get_n_splits(X_train.values)     mse = -cross_val_score(model, X_train.values, y_train, scoring="neg_mean_squared_error", cv=kf)</pre>
:	We experiment with the following set of models:  1. Linear Regression 2. Lasso Regression 3. Elastic Net Regression 4. Gradient Boosting Regression 5. XGBoost 6. LightGBM 7. Neural Network (MLP)  linear_reg = make_pipeline(StandardScaler(), LinearRegression()) lasso = make_pipeline(RobustScaler(), Lasso(alpha=0.0005, random_state=1)) ENet = make_pipeline(RobustScaler(), Lasso(alpha=0.0005, random_state=3))  GBoost = GradientBoostingRegressor(n_estimators=0.005, max_depth=4, max_features='sqrt', min_samples_lear=15, min_samples_split=10, loss="min_samples_lear=15, min_samples_lear=15, min_samples_split=10, loss="min_samples_lear=15, min_samples_lear=15, min_samples_split=10, loss="min_samples_lear=15, min_samples_split=10, loss="min_samples_lear=15, min_samples_split=10, loss="min_samples_lear=15, min_samples_split=10, loss="min_samples_lear=15, min_samples_split=10, loss="min_samples_lear=15, min_samples_split=10, loss="min_samples_lear=15, min_samples_split=10, loss="min_samples_split=10, loss="min_samples_lear=15, min_samples_split=10, loss="min_samples_split=10, loss=10, loss="min_samples_split=10, loss=10, loss=10, loss=10, loss
	1. Split the total training set into two disjoint sets, namely train and holdout.  2. Train several base models on the first part (train)  3. Test these base models on the second part (holdout)  4. Use the predictions (from 3) (called out-of-folds predictions) as the inputs, and the correct responses (target variable) as the outputs to train a higher level learner called meta-model.    Model 1
:	Learn
	<pre>self.base_models = base_models self.meta_model = meta_model self.n_folds = n_folds  # we again fit the data on clones of the original models  def fit(self, X, y):     self.base_models_ = [list() for x in self.base_models]     self.meta_model_ = clone(self.meta_model)     kfold = KFold(n_splits=self.n_folds, shuffle=False)  # Train cloned base models then create out-of-fold predictions # that are needed to train the cloned meta-model out_of_fold_predictions = np.zeros((X.shape[0], len(self.base_models))) for i, model in enumerate(self.base_models):     for train_index, holdout_index in kfold.split(X, y):         instance = clone(model)</pre>
	<pre>self.base_models_[i].append(instance)     instance.fit(X[train_index], y[train_index])     y_pred = instance.predict(X[holdout_index])     out_of_fold_predictions[holdout_index, i] = y_pred  # Now train the cloned meta-model using the out-of-fold predictions as new feature     self.meta_modelfit(out_of_fold_predictions, y)     return self  #Do the predictions of all base models on the test data and use the averaged predictions as #meta-features for the final prediction which is done by the meta-model  def predict(self, X):     meta_features = np.column_stack([</pre>
:	for base_models in self.base_models_]) return self.meta_modelpredict(meta_features)  stacked_averaged_models = StackingAveragedModels(base_models=(linear_reg, ENet, GBoost),
	<pre>print('MAE:', mean_absolute_error(y_test, stacked_train_pred)) print('MSE:', mean_squared_error(y_test, stacked_train_pred)) print('RMSE:', np.sqrt(mean_squared_error(y_test, stacked_train_pred)))  MAE: 0.05952097669416593 MSE: 0.006005889976332378 RMSE: 0.007749767723185243  model_xgb = XGBRegressor(colsample_bytree=0.4603, gamma=0.0468,</pre>
	<pre>model_xgb.fit(X_train, y_train) xgb_train_pred = model_xgb.predict(X_train) xgb_pred = model_xgb.predict(X_test)  print('MAE:', mean_absolute_error(y_test, xgb_train_pred)) print('MSE:', mean_squared_error(y_test, xgb_train_pred)) print('RMSE:', np.sqrt(mean_squared_error(y_test, xgb_train_pred)))  MAE: 0.059391524068225496 MSE: 0.006123035257343534</pre>
:  :	<pre>RMSE: 0.07824982592532417  model_lgb = LGBMRegressor(objective='regression', num_leaves=5,</pre>
	<pre>print('MAE:', mean_absolute_error(y_test, lgb_train_pred)) print('MSE:', mean_squared_error(y_test, lgb_train_pred)) print('RMSE:', np.sqrt(mean_squared_error(y_test, lgb_train_pred)))  MAE: 0.059377925459583335 MSE: 0.006120688434174505 RMSE: 0.07823482877960752  # define wider model def wider_model():     # create model     model = Sequential()</pre>
	<pre>model.add(Dense(32, input_dim=10, kernel_initializer='normal', activation='relu')) model.add(Dense(16, kernel_initializer='normal'), activation='relu')) model.add(Dense(1, kernel_initializer='normal')) # Compile model model.compile(loss='mean_squared_error', optimizer='adam') return model  np.random.seed(42) estimators = [] estimators.append(('standardize', StandardScaler())) estimators.append(('mlp', KerasRegressor(build_fn=wider_model, epochs=3, batch_size=32, verbose=1))) nn_model = Pipeline(estimators)  score = mse_cv(nn_model)</pre>
	Epoch 1/3 2025/2025 [====================================
:	2025/2025 [====================================
:	4050/4050 [===================================
	print('MSE:', mean_absolute_error(y_test, y_pred)) print('MSE:', mean_squared_error(y_test, y_pred)) print('MSE:', np.sqrt(mean_squared_error(y_test, y_pred)))  MAE: 0.023106635893180384 MSE: 0.0309107811937793944 RMSE: 0.030179151641147806  MSE of 0.00091 looks decent.  RIGHT_PREDICTED = y_pred.reshape(NUM_ROWS, CENTER_HALF) RIGHT_ACTUAL = albedo_map.iloc[:, CENTER_HALF:]
:	We now compare the albedo prediction to the albedo map.  fig, (ax1,ax2) = plt.subplots(nrows=1, ncols=2, figsize=(24, 10))  g1 = sns.heatmap(RIGHT_ACTUAL, cmap="gray", xticklabels=False, yticklabels=False, ax=ax1) g1.set_title("Mercury Albedo Right Half (Actual)")  g2 = sns.heatmap(RIGHT_PREDICTED, cmap="gray", xticklabels=False, yticklabels=False, ax=ax2) g2.set_title("Mercury Albedo Right Half (Predicted)")  plt.suptitle("Comparing Albedo prediction to the Albedo map", fontsize=20) plt.show();
!	Nercury Albedo Right Half (Actual)    Mercury Albedo Right Half (Actual)
	fig, ax = plt.subplots(figsize=(10, 10)) sns.distplot(residuals.values, kde=True);  //usr/local/lib/python3.7/dist_packages/seaborn/distributions.py:2557: Futurewarning: 'distplot' is a deprecated function and will be removed in a future version. Please adapt your code to use either 'displot' (a warnings.warn(msg, Futurewarning))  14  12  10  10  10  11  12  10  10  11  12  10  11  12  13  14  15  16  17  18  18  18  18  18  18  18  18  18
	As we can infer from the above image, the residues are roughly in the range ± 0.10.
	fig, ax = plt.subplots(figsize=(12, 6))  sns.residplot(x=RIGHT_ACTUAL.values.ravel(), y=residuals.values.ravel()) ax.set_xlabel("Albedo actual") ax.set_ylabel("Residuals") plt.suptitle("Residual Plot", fontsize=20) plt.show();  Residual Plot  015
	0.10