

Data Loading and Exploration

In []:

```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.preprocessing import StandardScaler, OneHotEncoder
from sklearn.compose import ColumnTransformer
from sklearn.pipeline import Pipeline
from sklearn.linear_model import LinearRegression, LogisticRegression
from sklearn.svm import SVC
from sklearn.ensemble import RandomForestRegressor
from sklearn.tree import DecisionTreeRegressor
from sklearn.metrics import mean_squared_error, mean_absolute_error, r2_score
from sklearn.metrics import accuracy_score, precision_score, recall_score, f1_score, confusion_matrix
import numpy as np

# Load the dataset
df = pd.read_csv('/content/COMP1801_CourseworkDataset1_tabular (1).csv')

# Display basic information about the dataset
print(df.info())

# Display descriptive statistics
print(df.describe())

# Check for missing values in each column
print(df.isnull().sum())

# Correlation analysis
# Compute the correlation matrix
correlation_matrix = df.corr()

# Plot the correlation matrix as a heatmap
plt.figure(figsize=(12, 8))
sns.heatmap(correlation_matrix, annot=True, cmap='coolwarm')
plt.show()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 1000 entries, 0 to 999
Data columns (total 11 columns):
#   Column          Non-Null Count  Dtype
#   :-----  :-----  :-----  :-----
```

```

---  -----
0  Lifespan      1000 non-null float64
1  partType     1000 non-null object
2  microstructure 1000 non-null object
3  coolingRate   1000 non-null int64
4  quenchTime   1000 non-null float64
5  forgeTime    1000 non-null float64
6  smallDefects 1000 non-null int64
7  largeDefects 1000 non-null int64
8  sliverDefects 1000 non-null int64
9  seedLocation 1000 non-null object
10 castType     1000 non-null object

```

dtypes: float64(3), int64(4), object(4)

memory usage: 86.1+ KB

None

| | Lifespan | coolingRate | quenchTime | forgeTime | smallDefects \ |
|-------|-------------|-------------|-------------|-------------|----------------|
| count | 1000.000000 | 1000.000000 | 1000.000000 | 1000.000000 | 1000.000000 |
| mean | 1366.373468 | 17.480000 | 2.786059 | 5.497136 | 13.37100 |
| std | 519.026551 | 7.557958 | 1.320935 | 2.613501 | 8.07047 |
| min | 115.120563 | 5.000000 | 0.501046 | 1.017799 | 0.00000 |
| 25% | 960.976320 | 11.000000 | 1.608916 | 3.203739 | 8.00000 |
| 50% | 1470.377014 | 17.000000 | 2.824488 | 5.510765 | 16.00000 |
| 75% | 1757.165684 | 24.000000 | 3.902389 | 7.735951 | 20.00000 |
| max | 2380.142759 | 30.000000 | 4.990795 | 9.988511 | 33.00000 |

| | largeDefects | sliverDefects |
|-------|--------------|---------------|
| count | 1000.000000 | 1000.000000 |
| mean | 0.117000 | 0.286000 |
| std | 0.565359 | 1.351307 |
| min | 0.000000 | 0.000000 |
| 25% | 0.000000 | 0.000000 |
| 50% | 0.000000 | 0.000000 |
| 75% | 0.000000 | 0.000000 |
| max | 4.000000 | 10.000000 |

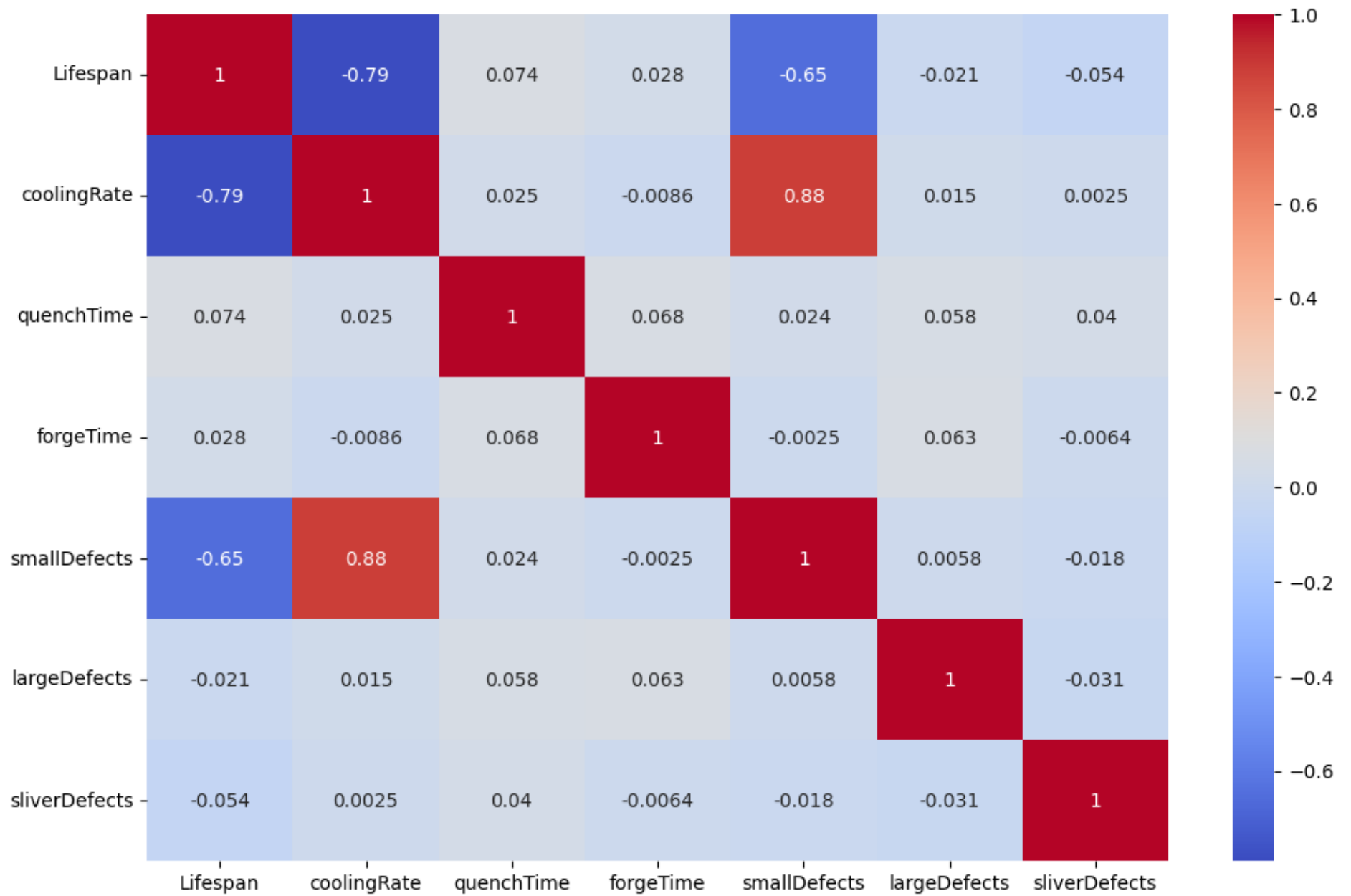
```

Lifespan      0
partType      0
microstructure 0
coolingRate   0
quenchTime    0
forgeTime     0
smallDefects  0
largeDefects  0
sliverDefects 0
seedLocation  0

```

```
castType      0  
dtype: int64
```

```
<ipython-input-1-9bab57deeb>:30: FutureWarning: The default value of numeric_only in DataFrame.corr is deprecated. In a future version, it will default to False. Select only valid columns or specify the value of numeric_only to silence this warning.  
    correlation_matrix = df.corr()
```



Data Visualization

In []:

```
# Plot histograms for all numerical features
df.hist(bins=15, figsize=(15, 10), layout=(3, 3))
plt.tight_layout()
plt.show()

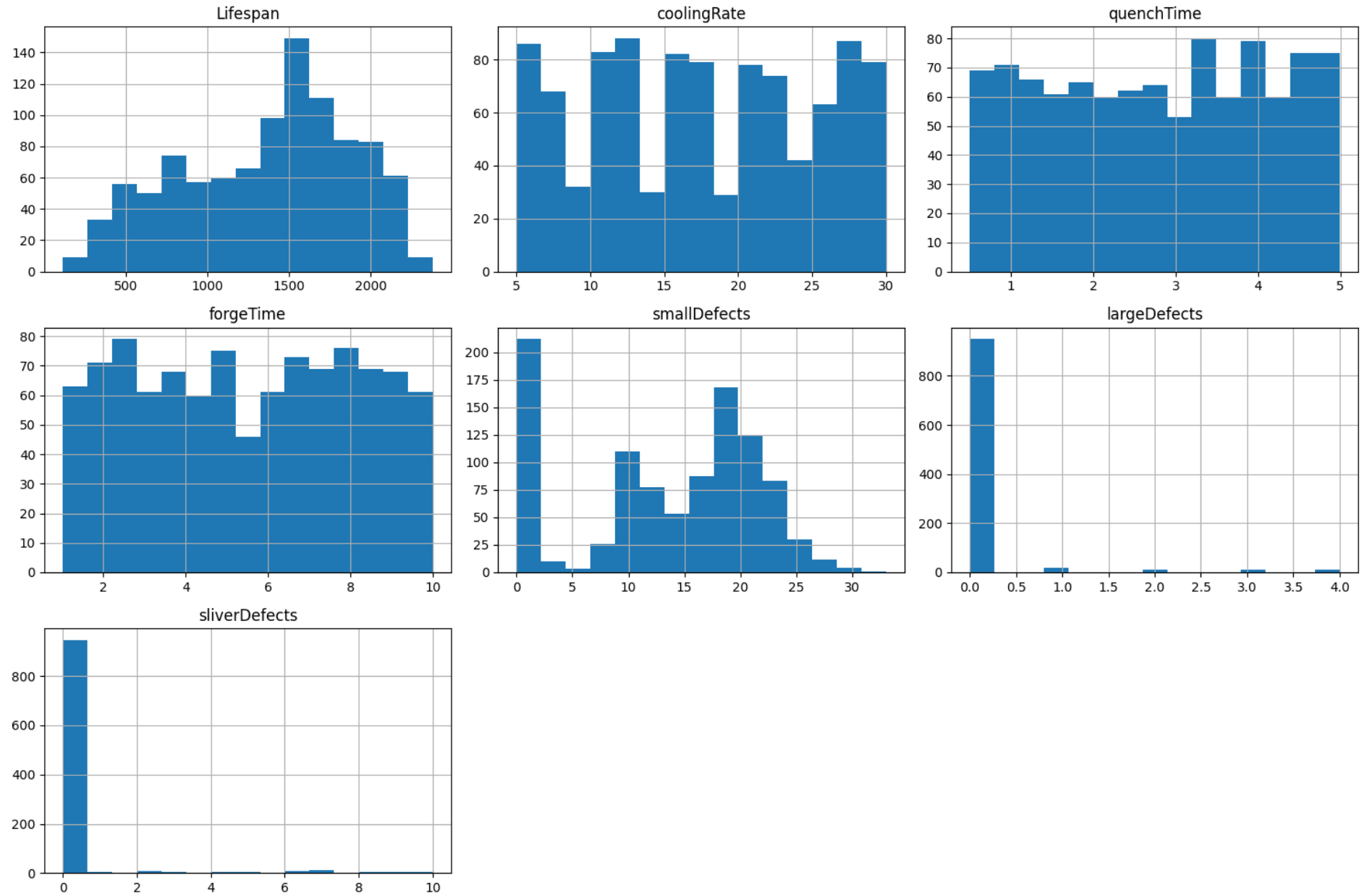
# Plot boxplots for all numerical features
df.plot(kind='box', subplots=True, layout=(3, 3), figsize=(15, 10))
plt.tight_layout()
plt.show()

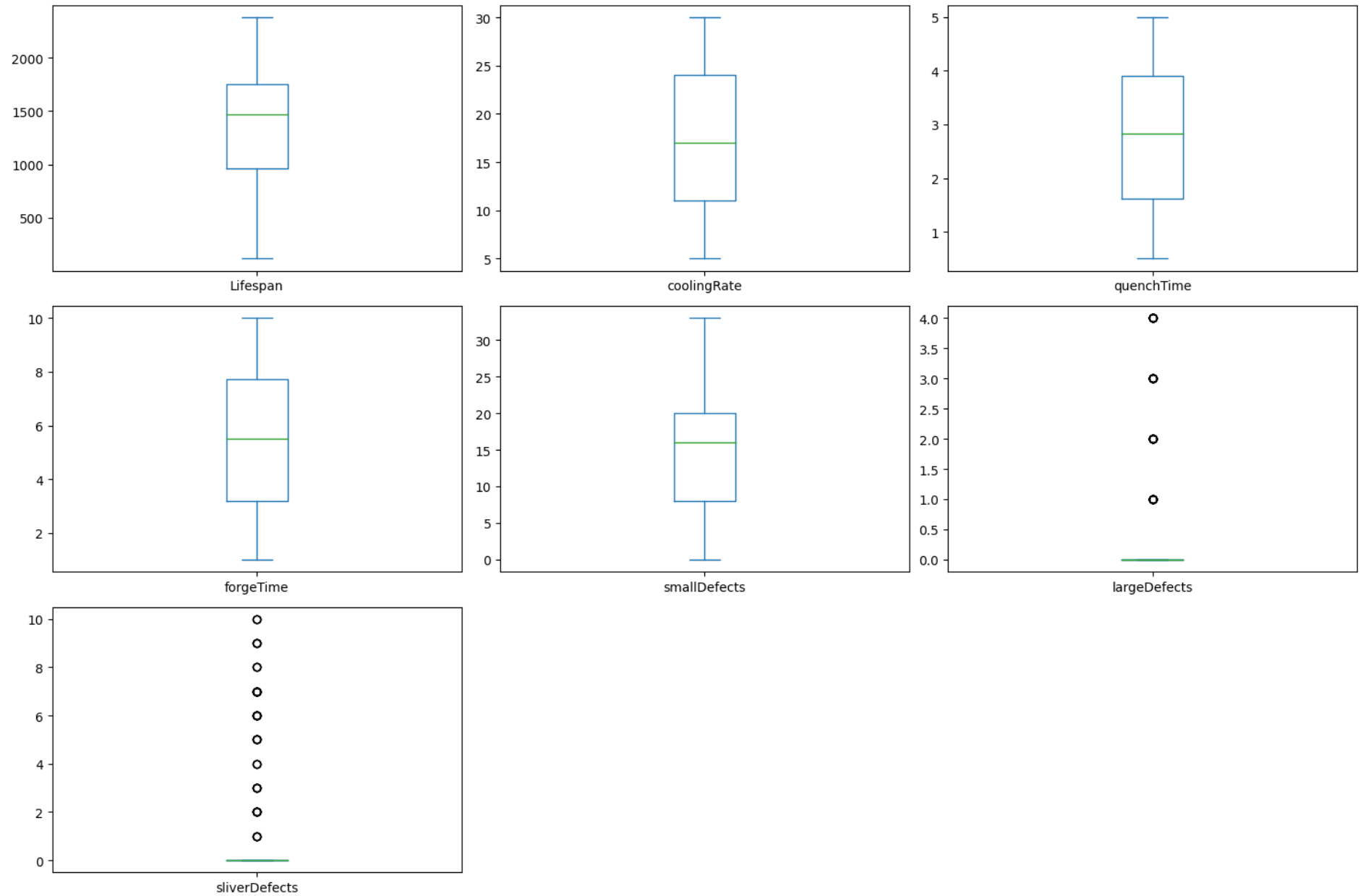
# Pair plot for a subset of features
sns.pairplot(df, diag_kind='kde')
plt.show()

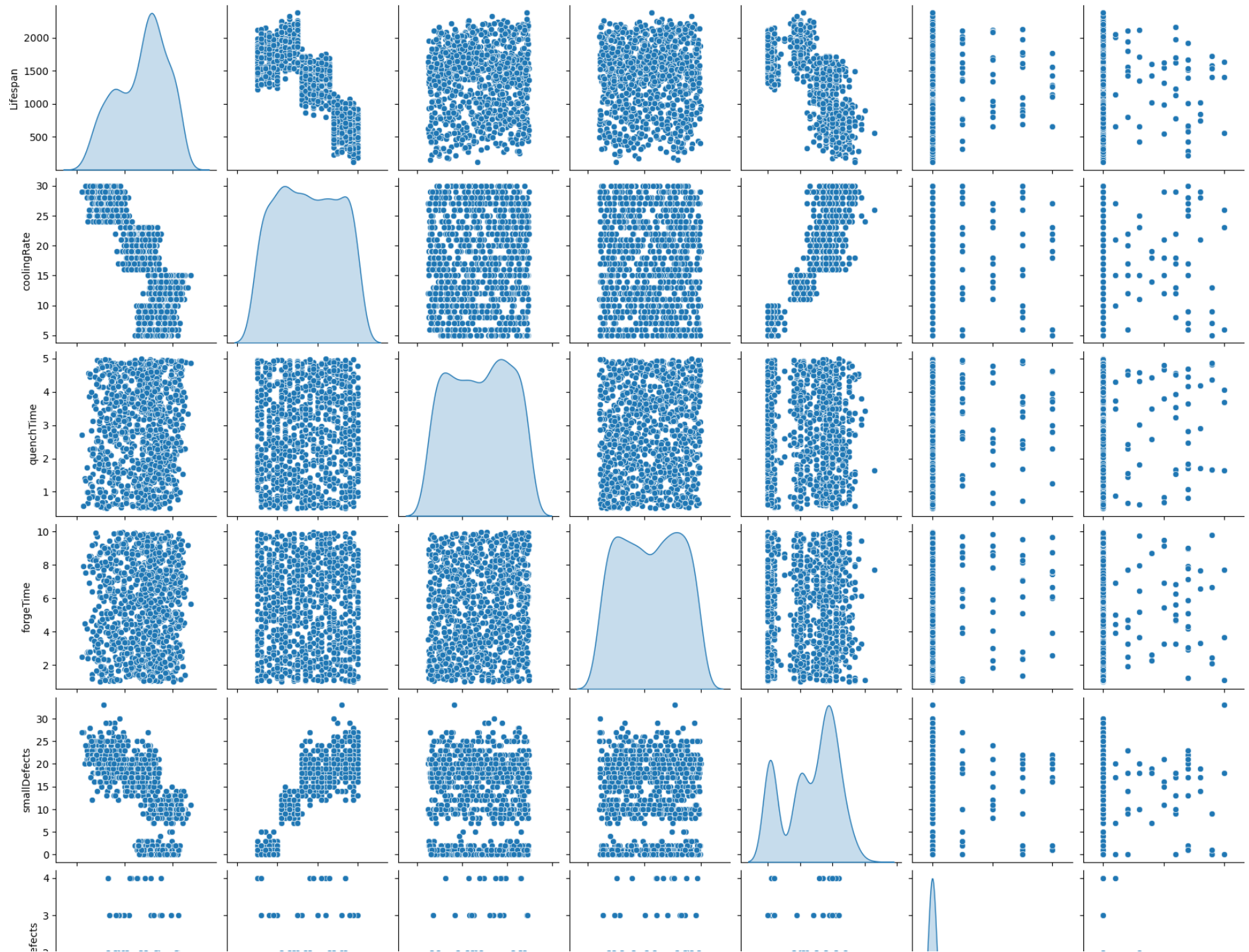
# Scatter plots showing relationship with Lifespan
sns.scatterplot(data=df, x='coolingRate', y='Lifespan')
plt.title('Relationship between Cooling Rate and Lifespan')
plt.show()

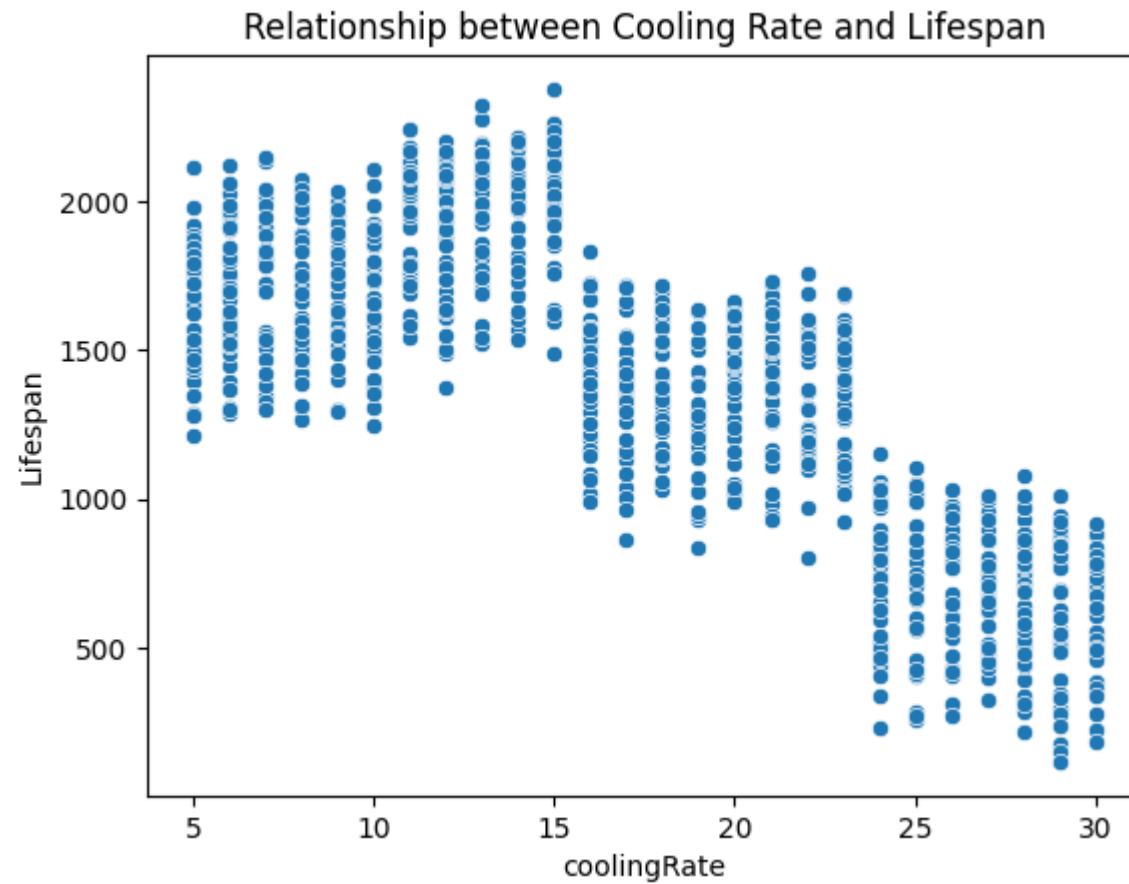
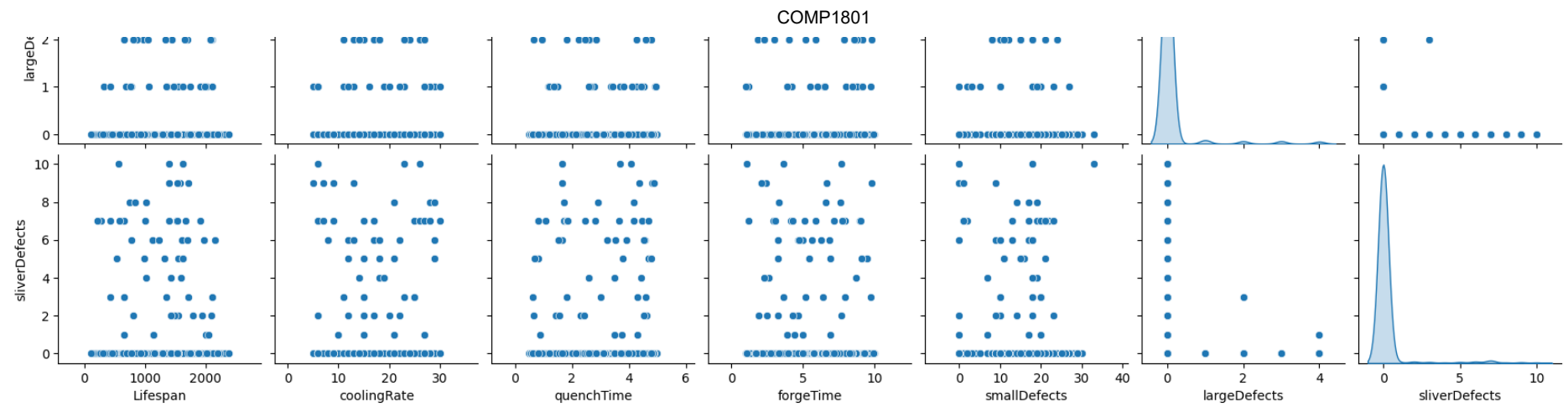
sns.scatterplot(data=df, x='quenchTime', y='Lifespan')
plt.title('Relationship between Quench Time and Lifespan')
plt.show()

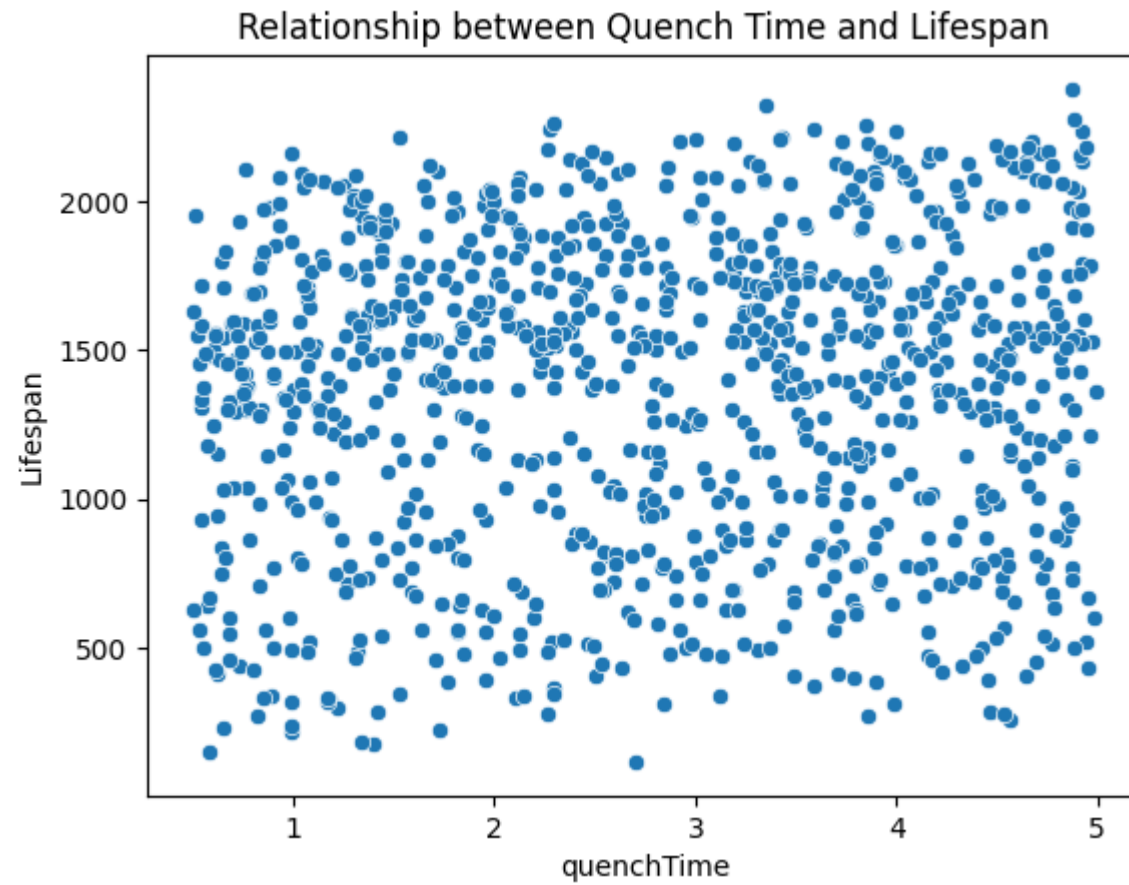
sns.scatterplot(data=df, x='forgeTime', y='Lifespan')
plt.title('Relationship between Forge Time and Lifespan')
plt.show()
```

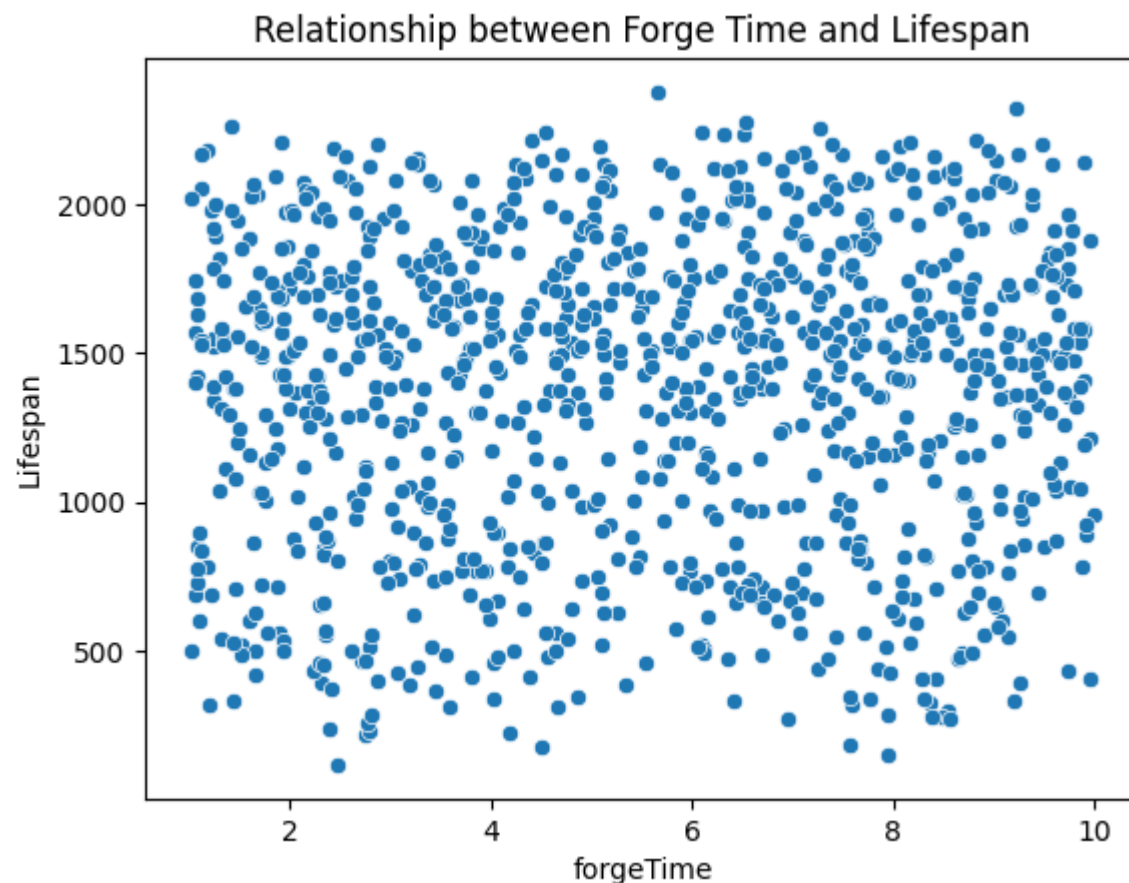












Regression Implementation

```
In [ ]: # Feature selection
X = df[['coolingRate', 'quenchTime', 'forgeTime', 'smallDefects', 'largeDefects', 'sliverDefects', 'partType', 'microstructure', '
y = df['Lifespan']]

# Train-test split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# Feature scaling and encoding
numeric_features = ['coolingRate', 'quenchTime', 'forgeTime', 'smallDefects', 'largeDefects', 'sliverDefects']
categorical_features = ['partType', 'microstructure', 'seedLocation', 'castType']

numeric_transformer = Pipeline(steps=[
```

```
    ('scaler', StandardScaler()))])

categorical_transformer = Pipeline(steps=[
    ('onehot', OneHotEncoder(handle_unknown='ignore'))])

preprocessor = ColumnTransformer(
    transformers=[
        ('num', numeric_transformer, numeric_features),
        ('cat', categorical_transformer, categorical_features)])

# Model selection and training
# Linear Regression
linear_model = Pipeline(steps=[('preprocessor', preprocessor),
                                ('regressor', LinearRegression())])

# Random Forest
rf_model = Pipeline(steps=[('preprocessor', preprocessor),
                             ('regressor', RandomForestRegressor())])

# Decision Tree
dt_model = Pipeline(steps=[('preprocessor', preprocessor),
                             ('regressor', DecisionTreeRegressor())])

# Hyperparameter tuning
param_grid = {
    'regressor__n_estimators': [100, 200],
    'regressor__max_depth': [None, 10, 20],
}

grid_search = GridSearchCV(rf_model, param_grid, cv=5)
grid_search.fit(X_train, y_train)

# Best model after tuning
best_model = grid_search.best_estimator_

# Model Evaluation
y_pred = best_model.predict(X_test)
print("Mean Squared Error:", mean_squared_error(y_test, y_pred))
print("Mean Absolute Error:", mean_absolute_error(y_test, y_pred))
print("R-squared:", r2_score(y_test, y_pred))

# Predicting using the test set
y_pred = best_model.predict(X_test)
```

```
# Calculating residuals
residuals = y_test - y_pred

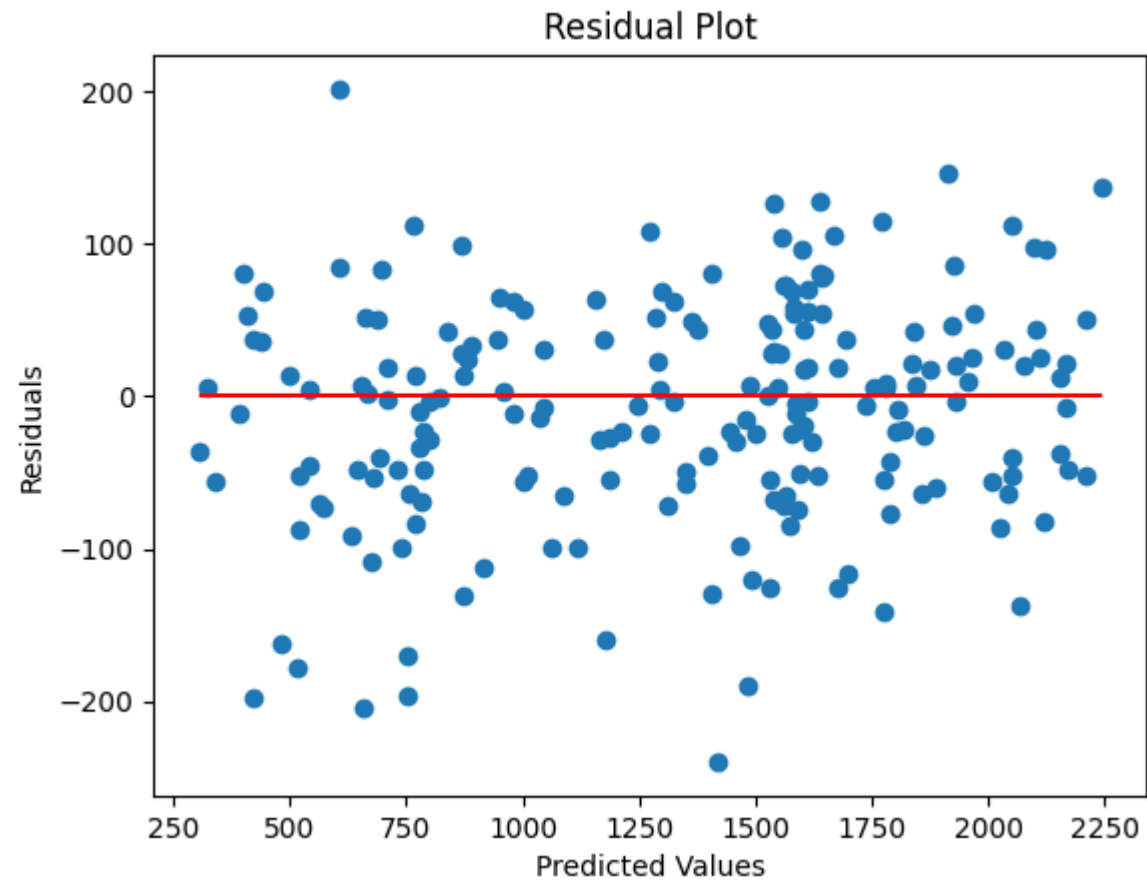
# Plotting the Residuals
plt.scatter(y_pred, residuals)
plt.hlines(y = 0, xmin = y_pred.min(), xmax = y_pred.max(), color = 'red')
plt.xlabel('Predicted Values')
plt.ylabel('Residuals')
plt.title('Residual Plot')
plt.show()

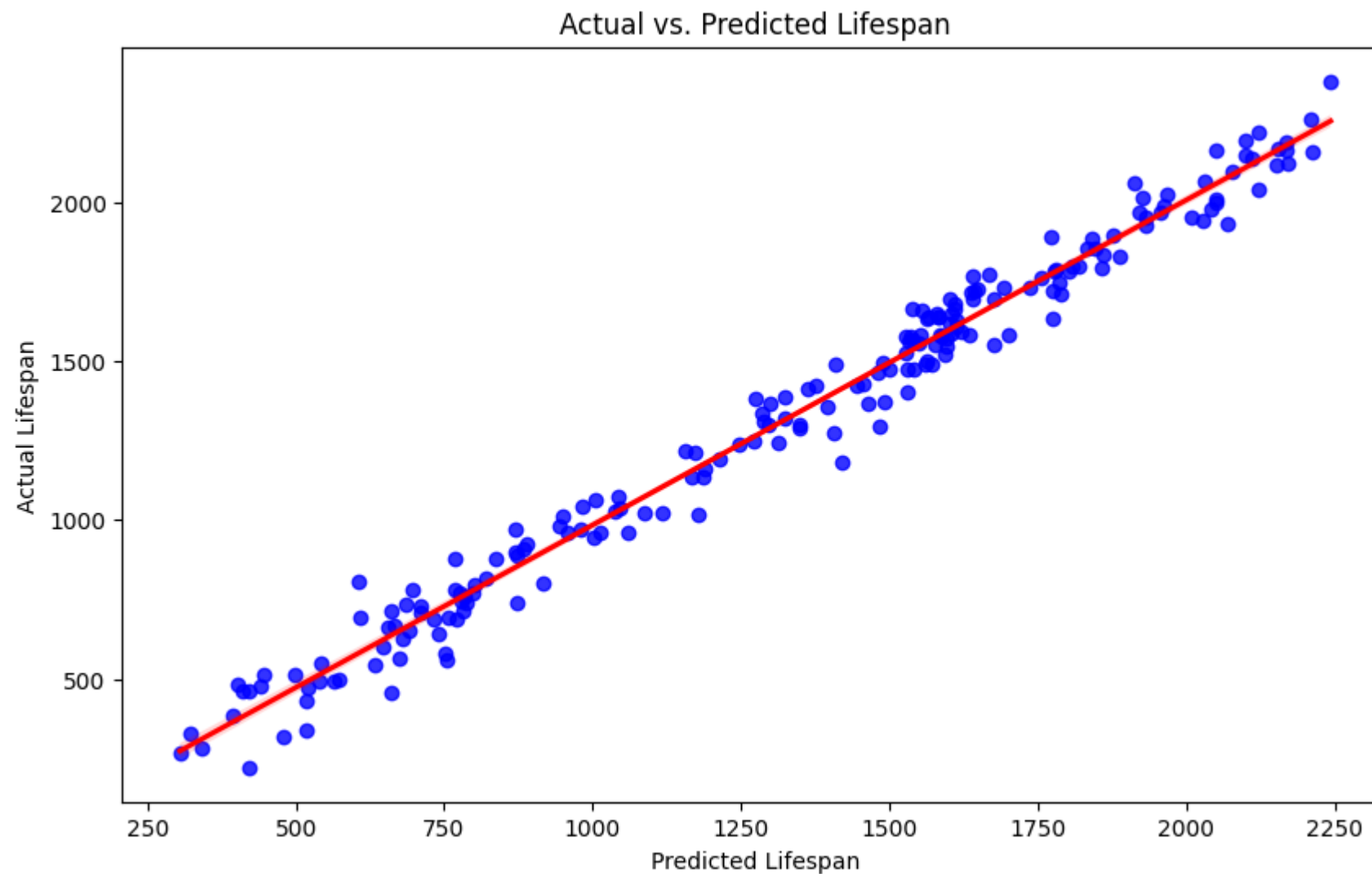
plt.figure(figsize=(10,6))
sns.regplot(x=y_pred, y=y_test, fit_reg=True, scatter_kws={"color": "blue"}, line_kws={"color": "red"})
plt.xlabel('Predicted Lifespan')
plt.ylabel('Actual Lifespan')
plt.title('Actual vs. Predicted Lifespan')
plt.show()
```

Mean Squared Error: 5505.302189210612

Mean Absolute Error: 57.80574994131826

R-squared: 0.9808131965342906





Binary Classification Implementation

```
In [ ]: from sklearn.ensemble import RandomForestClassifier
        from imblearn.over_sampling import SMOTE
        from imblearn.pipeline import Pipeline as ImbPipeline
        from sklearn.metrics import classification_report, roc_curve, auc

        # Convert 'Lifespan' to binary target
        df['is_defective'] = np.where(df['Lifespan'] < 1500, 0, 1)
```

```
# Features and target
X = df[['coolingRate', 'quenchTime', 'forgeTime', 'smallDefects', 'largeDefects', 'sliverDefects', 'partType', 'microstructure', 'is_defective']]
y = df['is_defective']

# Train-test split
X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

# Feature scaling and encoding
numeric_features = ['coolingRate', 'quenchTime', 'forgeTime', 'smallDefects', 'largeDefects', 'sliverDefects']
categorical_features = ['partType', 'microstructure', 'seedLocation', 'castType']

numeric_transformer = Pipeline(steps=[
    ('scaler', StandardScaler())])

categorical_transformer = Pipeline(steps=[
    ('onehot', OneHotEncoder(handle_unknown='ignore'))])

preprocessor = ColumnTransformer(
    transformers=[
        ('num', numeric_transformer, numeric_features),
        ('cat', categorical_transformer, categorical_features)])

# Define SMOTE for resampling
smote = SMOTE()

# Define the classifiers
classifiers = {
    'Logistic Regression': LogisticRegression(),
    'SVM': SVC(probability=True),
    'Random Forest': RandomForestClassifier()
}

# Function to run, evaluate, and visualize a model
def run_model(model_name):
    classifier = classifiers[model_name]
    pipeline = ImbPipeline(steps=[('preprocessor', preprocessor),
                                   ('smote', smote),
                                   ('classifier', classifier)])

    pipeline.fit(X_train, y_train)
    y_pred = pipeline.predict(X_test)
    y_proba = pipeline.predict_proba(X_test)[:, 1]
```



```

# Evaluation metrics
print(f"Model: {model_name}")
print(classification_report(y_test, y_pred))

# Confusion Matrix
conf_matrix = confusion_matrix(y_test, y_pred)
sns.heatmap(conf_matrix, annot=True, fmt='g')
plt.xlabel('Predicted labels')
plt.ylabel('True labels')
plt.title('Confusion Matrix')
plt.show()

# ROC Curve
fpr, tpr, _ = roc_curve(y_test, y_proba)
roc_auc = auc(fpr, tpr)
plt.figure()
plt.plot(fpr, tpr, color='darkorange', lw=2, label='ROC curve (area = %0.2f)' % roc_auc)
plt.plot([0, 1], [0, 1], color='navy', lw=2, linestyle='--')
plt.xlim([0.0, 1.0])
plt.ylim([0.0, 1.05])
plt.xlabel('False Positive Rate')
plt.ylabel('True Positive Rate')
plt.title('Receiver Operating Characteristic')
plt.legend(loc="lower right")
plt.show()

# Run and evaluate each model
for model_name in classifiers:
    run_model(model_name)

```

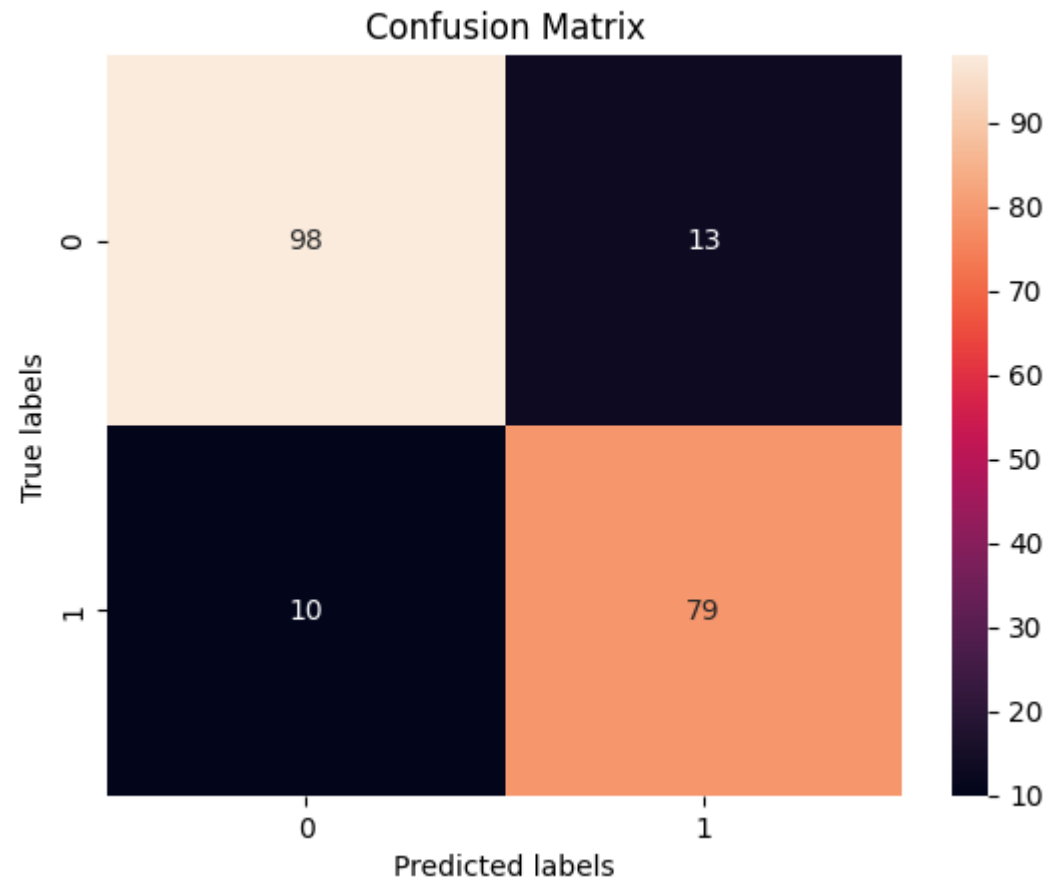
```

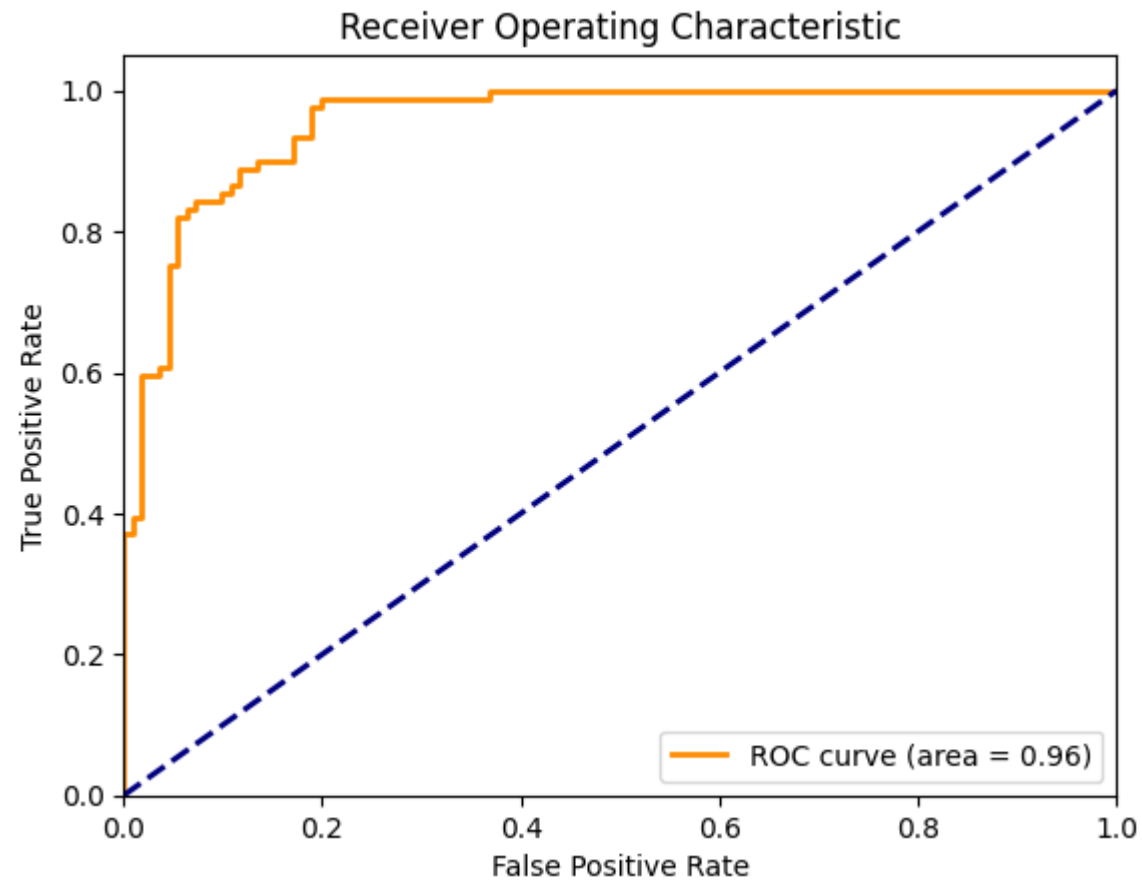
Model: Logistic Regression
      precision    recall  f1-score   support

     0       0.91      0.88      0.89        111
     1       0.86      0.89      0.87         89

 accuracy          0.89         200
 macro avg       0.88      0.89      0.88         200
 weighted avg    0.89      0.89      0.89         200

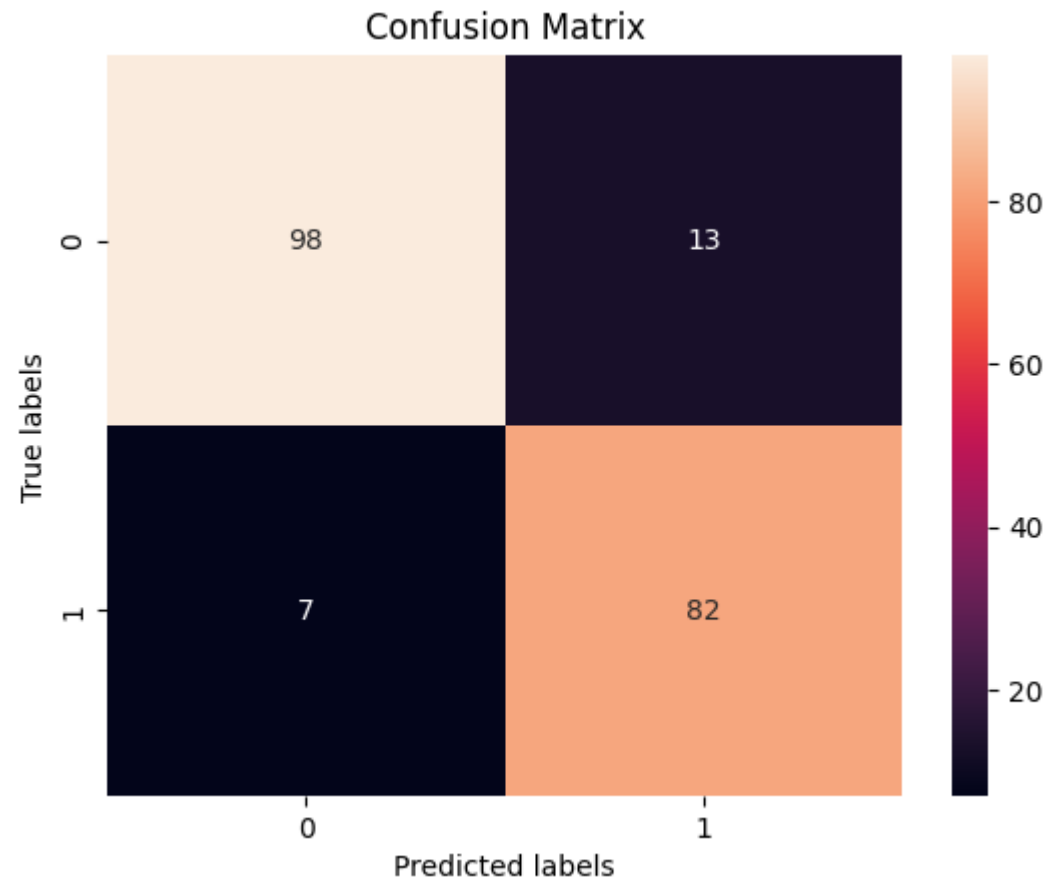
```

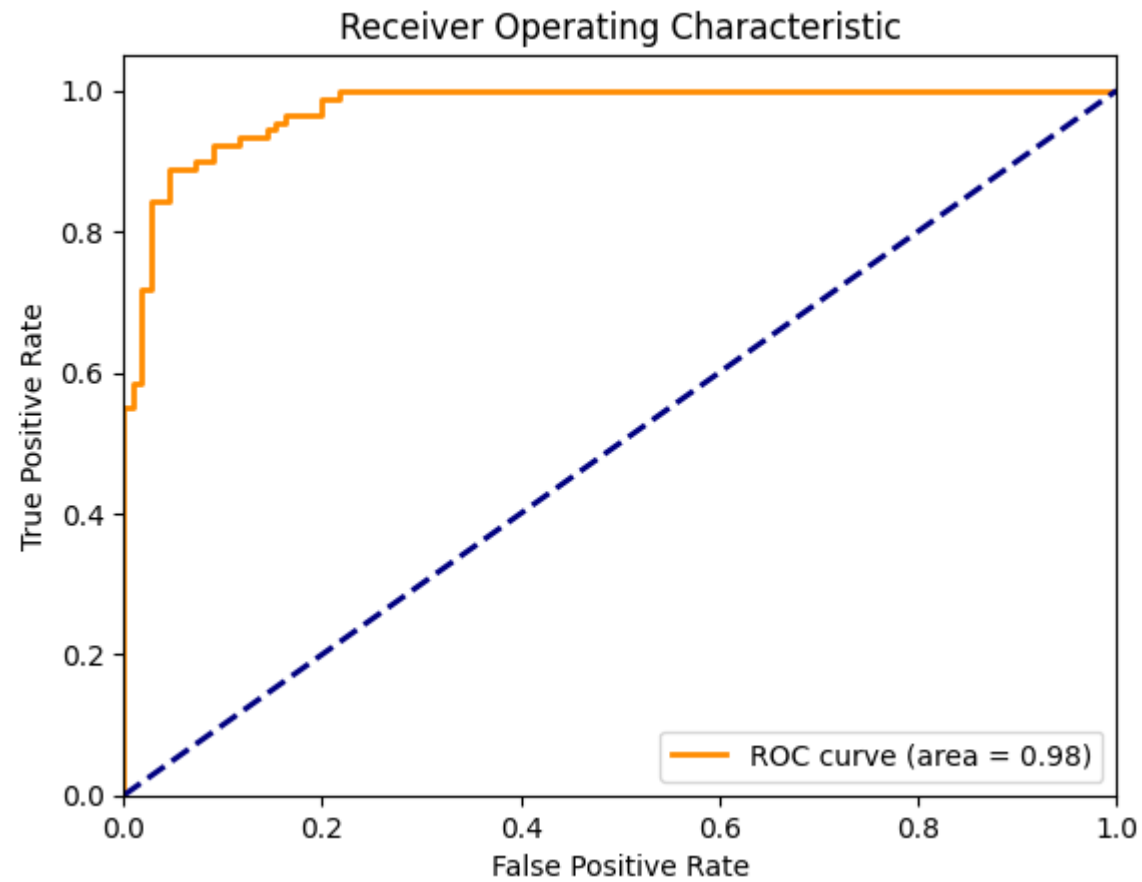




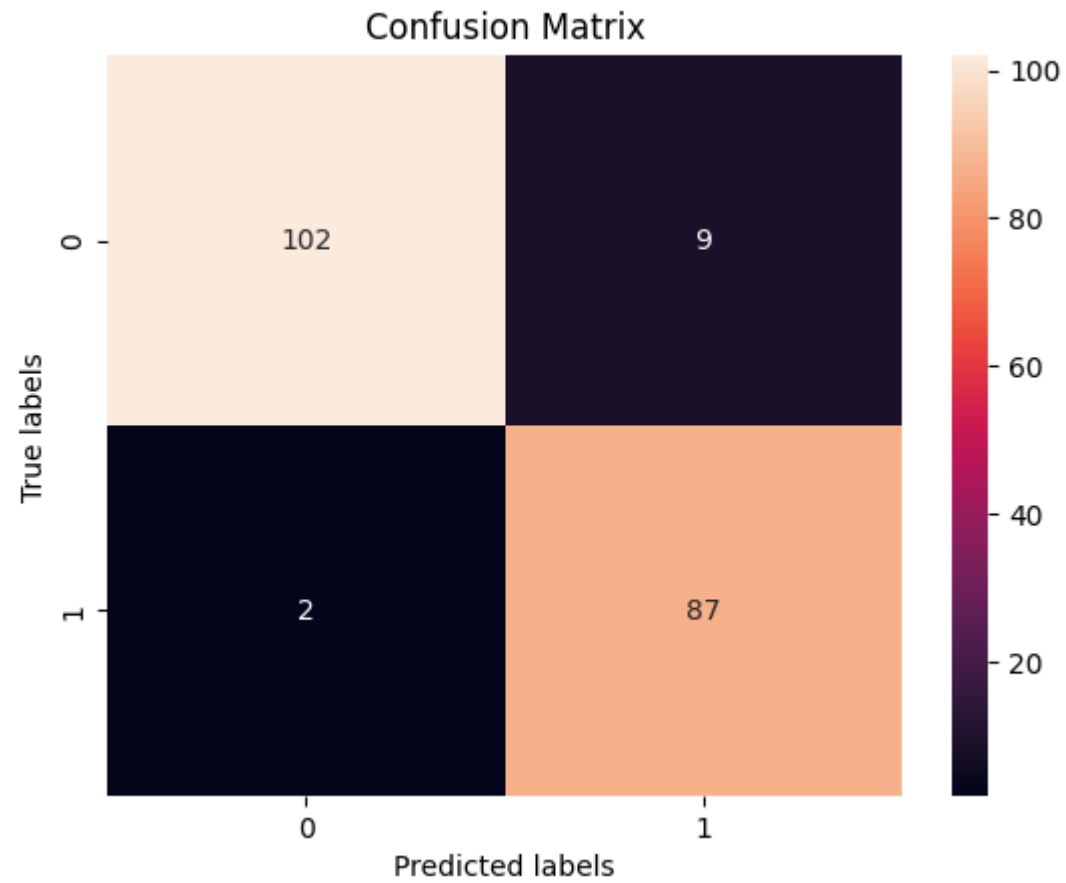
Model: SVM

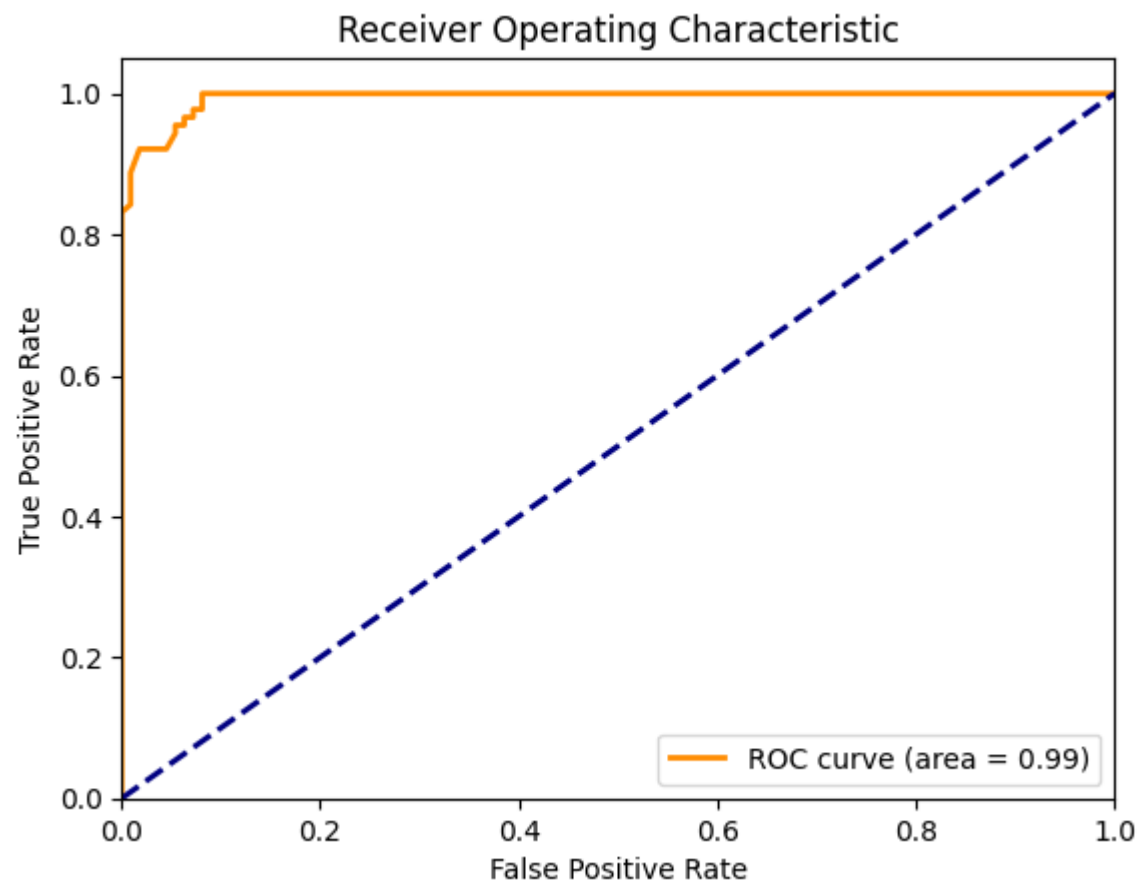
| | precision | recall | f1-score | support |
|--------------|-----------|--------|----------|---------|
| 0 | 0.93 | 0.88 | 0.91 | 111 |
| 1 | 0.86 | 0.92 | 0.89 | 89 |
| accuracy | | | 0.90 | 200 |
| macro avg | 0.90 | 0.90 | 0.90 | 200 |
| weighted avg | 0.90 | 0.90 | 0.90 | 200 |





| Model: Random Forest | | | | | |
|----------------------|-----------|--------|----------|---------|--|
| | precision | recall | f1-score | support | |
| 0 | 0.98 | 0.92 | 0.95 | 111 | |
| 1 | 0.91 | 0.98 | 0.94 | 89 | |
| accuracy | | | 0.94 | 200 | |
| macro avg | 0.94 | 0.95 | 0.94 | 200 | |
| weighted avg | 0.95 | 0.94 | 0.95 | 200 | |





Convolutional Neural Network Implementation

```
In [25]: import zipfile
import os

# Path to the zip file and extraction directory
zip_path = '/content/COMP1801_CourseworkDataset2_images (1).zip'
extract_dir = '/content/sample_data/extracted'

# Unzipping the file
with zipfile.ZipFile(zip_path, 'r') as zip_ref:
    zip_ref.extractall(extract_dir)

print("Dataset unzipped successfully to:", extract_dir)
```

Dataset unzipped successfully to: /content/sample_data/extracted

In [29]:

```
from tensorflow.keras.preprocessing.image import ImageDataGenerator
import shutil

# Load the metadata file
metadata_path = '/content/sample_data/extracted/COMP1801_CourseworkDataset2_images/COMP1801_CourseworkDataset2_images_metadata.csv'
metadata = pd.read_csv(metadata_path)

# Display the first few rows of the dataframe
print(metadata.head())

# Load the metadata file
metadata_path = '/content/COMP1801_CourseworkDataset2_images/COMP1801_CourseworkDataset2_images/COMP1801_CourseworkDataset2_images_metadata.csv'
metadata = pd.read_csv(metadata_path)

# Directory containing the unorganized images
image_dir = '/content/COMP1801_CourseworkDataset2_images/COMP1801_CourseworkDataset2_images'

# Base directory for the organized images
base_dir = '/content/organized_images'
os.makedirs(base_dir, exist_ok=True)

# Iterate over the metadata and organize images
for index, row in metadata.iterrows():
    # Get the defect type (create a 'No Defect' directory for 'None')
    defect_type = row['Type'] if row['Defect'] == 'Yes' else 'No Defect'

    # Create a directory for the defect type if it doesn't exist
    defect_dir = os.path.join(base_dir, defect_type)
    os.makedirs(defect_dir, exist_ok=True)

    # Source and destination paths
    src_path = os.path.join(image_dir, row['Image Filename'])
    dst_path = os.path.join(defect_dir, row['Image Filename'])

    # Copy the image to the new directory
    shutil.copy(src_path, dst_path)

print("Images organized successfully.")
```


| | Image Filename | Defect | Type |
|---|----------------|--------|----------|
| 0 | scan_0.png | Yes | Splinter |
| 1 | scan_1.png | No | None |
| 2 | scan_2.png | Yes | Multiple |
| 3 | scan_3.png | No | None |
| 4 | scan_4.png | No | None |

Images organized successfully.

In [31]:

```
# Base directory where images are currently organized
base_dir = '/content/organized_images'

# New directories for training and validation sets
train_dir = '/content/train'
validation_dir = '/content/validation'
os.makedirs(train_dir, exist_ok=True)
os.makedirs(validation_dir, exist_ok=True)

# Get the list of defect types (subdirectories in base_dir)
defect_types = [d for d in os.listdir(base_dir) if os.path.isdir(os.path.join(base_dir, d))]

# Split images for each defect type into train and validation sets
for defect in defect_types:
    # Paths for defect type in base, train, and validation directories
    defect_base_dir = os.path.join(base_dir, defect)
    defect_train_dir = os.path.join(train_dir, defect)
    defect_validation_dir = os.path.join(validation_dir, defect)

    # Create subdirectories in train and validation directories
    os.makedirs(defect_train_dir, exist_ok=True)
    os.makedirs(defect_validation_dir, exist_ok=True)

    # List of images for this defect type
    images = [f for f in os.listdir(defect_base_dir) if os.path.isfile(os.path.join(defect_base_dir, f))]

    # Splitting images into train and validation sets
    train_imgs, val_imgs = train_test_split(images, test_size=0.2, random_state=42)

    # Copy images to respective directories
    for img in train_imgs:
        shutil.copy(os.path.join(defect_base_dir, img), os.path.join(defect_train_dir, img))
    for img in val_imgs:
        shutil.copy(os.path.join(defect_base_dir, img), os.path.join(defect_validation_dir, img))
```

```
print("Images split into train and validation directories.")
```

Images split into train and validation directories.

In [32]:

```
from tensorflow.keras.preprocessing.image import ImageDataGenerator

# Data augmentation for training data and rescaling
train_datagen = ImageDataGenerator(
    rescale=1./255,
    rotation_range=40,
    width_shift_range=0.2,
    height_shift_range=0.2,
    shear_range=0.2,
    zoom_range=0.2,
    horizontal_flip=True)

# Rescaling for validation data
validation_datagen = ImageDataGenerator(rescale=1./255)

# Data generators for training and validation sets
train_generator = train_datagen.flow_from_directory(
    train_dir,
    target_size=(150, 150),
    batch_size=32,
    class_mode='categorical')

validation_generator = validation_datagen.flow_from_directory(
    validation_dir,
    target_size=(150, 150),
    batch_size=32,
    class_mode='categorical')
```

Found 799 images belonging to 4 classes.

Found 201 images belonging to 4 classes.

In [33]:

```
from tensorflow.keras.models import Sequential
from tensorflow.keras.layers import Conv2D, MaxPooling2D, Flatten, Dense, Dropout

# CNN architecture
model = Sequential([
    Conv2D(32, (3, 3), activation='relu', input_shape=(150, 150, 3)),
    MaxPooling2D(2, 2),
```

```

Conv2D(64, (3, 3), activation='relu'),
MaxPooling2D(2, 2),
Conv2D(128, (3, 3), activation='relu'),
MaxPooling2D(2, 2),
Flatten(),
Dense(128, activation='relu'),
Dropout(0.5),
Dense(4, activation='softmax') # 4 classes
])

model.compile(optimizer='adam', loss='categorical_crossentropy', metrics=['accuracy'])

# Training the CNN Model
history = model.fit(
    train_generator,
    steps_per_epoch=25, # 799 images = batch_size * steps
    epochs=20, # Start with 20 epochs, adjust based on performance
    validation_data=validation_generator,
    validation_steps=6) # 201 images = batch_size * steps

```

```

Epoch 1/20
25/25 [=====] - 67s 3s/step - loss: 1.1140 - accuracy: 0.5632 - val_loss: 0.8045 - val_accuracy: 0.6719
Epoch 2/20
25/25 [=====] - 46s 2s/step - loss: 0.7349 - accuracy: 0.7922 - val_loss: 0.5681 - val_accuracy: 0.8177
Epoch 3/20
25/25 [=====] - 58s 2s/step - loss: 0.6153 - accuracy: 0.8160 - val_loss: 0.9455 - val_accuracy: 0.6510
Epoch 4/20
25/25 [=====] - 49s 2s/step - loss: 0.6496 - accuracy: 0.8110 - val_loss: 0.5165 - val_accuracy: 0.8438
Epoch 5/20
25/25 [=====] - 47s 2s/step - loss: 0.5639 - accuracy: 0.8310 - val_loss: 0.5088 - val_accuracy: 0.8281
Epoch 6/20
25/25 [=====] - 46s 2s/step - loss: 0.5184 - accuracy: 0.8423 - val_loss: 0.5151 - val_accuracy: 0.8021
Epoch 7/20
25/25 [=====] - 47s 2s/step - loss: 0.5079 - accuracy: 0.8498 - val_loss: 0.5930 - val_accuracy: 0.7969
Epoch 8/20
25/25 [=====] - 49s 2s/step - loss: 0.4519 - accuracy: 0.8623 - val_loss: 0.2814 - val_accuracy: 0.9062
Epoch 9/20
25/25 [=====] - 48s 2s/step - loss: 0.4314 - accuracy: 0.8736 - val_loss: 0.3094 - val_accuracy: 0.8958
Epoch 10/20
25/25 [=====] - 48s 2s/step - loss: 0.3200 - accuracy: 0.8911 - val_loss: 0.1955 - val_accuracy: 0.9219
Epoch 11/20
25/25 [=====] - 46s 2s/step - loss: 0.2814 - accuracy: 0.9099 - val_loss: 0.2130 - val_accuracy: 0.9167
Epoch 12/20
25/25 [=====] - 46s 2s/step - loss: 0.2650 - accuracy: 0.9212 - val_loss: 0.2248 - val_accuracy: 0.9219

```

```

Epoch 13/20
25/25 [=====] - 47s 2s/step - loss: 0.2401 - accuracy: 0.9224 - val_loss: 0.1450 - val_accuracy: 0.9531
Epoch 14/20
25/25 [=====] - 48s 2s/step - loss: 0.2131 - accuracy: 0.9212 - val_loss: 0.1822 - val_accuracy: 0.9427
Epoch 15/20
25/25 [=====] - 46s 2s/step - loss: 0.2531 - accuracy: 0.9049 - val_loss: 0.2388 - val_accuracy: 0.9323
Epoch 16/20
25/25 [=====] - 46s 2s/step - loss: 0.2908 - accuracy: 0.9124 - val_loss: 0.1593 - val_accuracy: 0.9479
Epoch 17/20
25/25 [=====] - 46s 2s/step - loss: 0.1846 - accuracy: 0.9412 - val_loss: 0.2277 - val_accuracy: 0.9167
Epoch 18/20
25/25 [=====] - 48s 2s/step - loss: 0.2763 - accuracy: 0.9161 - val_loss: 0.1612 - val_accuracy: 0.9427
Epoch 19/20
25/25 [=====] - 46s 2s/step - loss: 0.2711 - accuracy: 0.9099 - val_loss: 0.1073 - val_accuracy: 0.9635
Epoch 20/20
25/25 [=====] - 46s 2s/step - loss: 0.2043 - accuracy: 0.9337 - val_loss: 0.1132 - val_accuracy: 0.9531

```

In [34]:

```

# Evaluate the model
val_loss, val_accuracy = model.evaluate(validation_generator)
print(f'Validation accuracy: {val_accuracy:.2f}')

# Plot training & validation accuracy values
plt.plot(history.history['accuracy'])
plt.plot(history.history['val_accuracy'])
plt.title('Model accuracy')
plt.ylabel('Accuracy')
plt.xlabel('Epoch')
plt.legend(['Train', 'Validation'], loc='upper left')
plt.show()

# Plot training & validation loss values
plt.plot(history.history['loss'])
plt.plot(history.history['val_loss'])
plt.title('Model loss')
plt.ylabel('Loss')
plt.xlabel('Epoch')
plt.legend(['Train', 'Validation'], loc='upper left')
plt.show()

# Predictions
predictions = model.predict(validation_generator)
predicted_classes = np.argmax(predictions, axis=1)
true_classes = validation_generator.classes

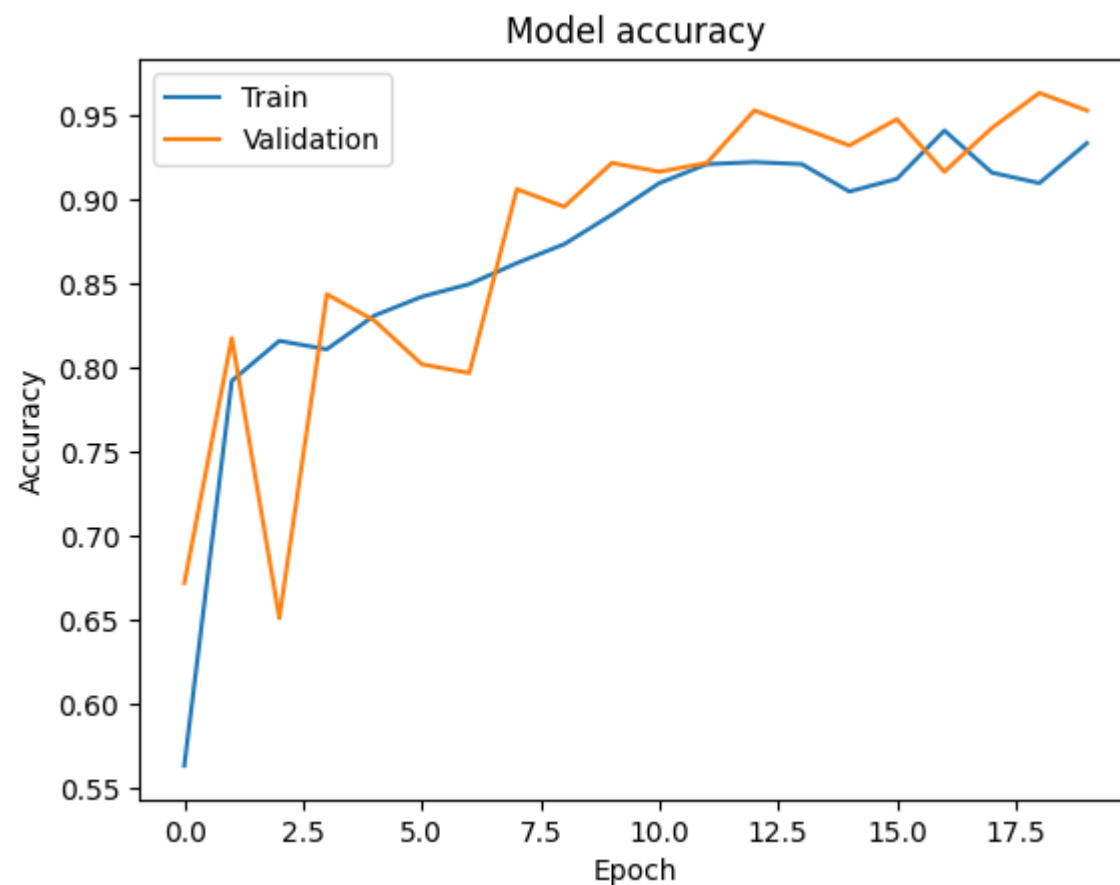
```

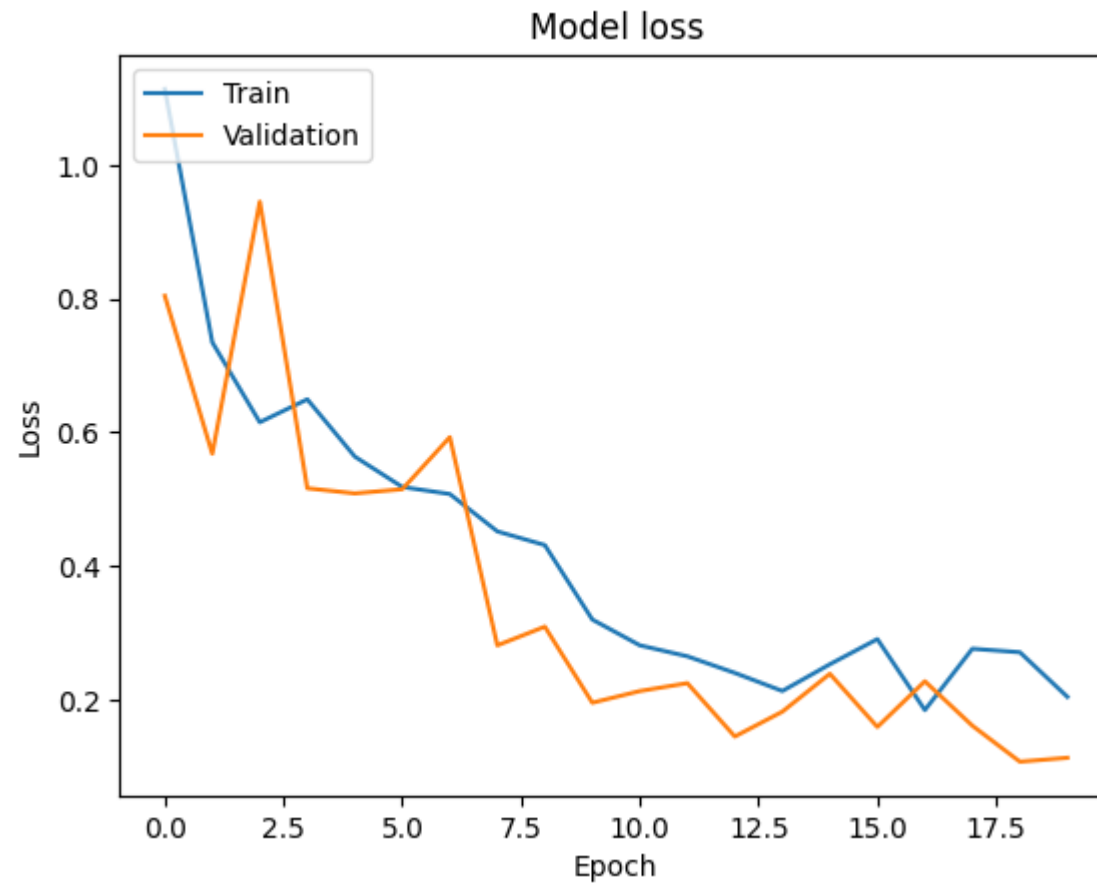
```
class_labels = list(validation_generator.class_indices.keys())

# Classification report
report = classification_report(true_classes, predicted_classes, target_names=class_labels)
print(report)

# Confusion matrix
conf_matrix = confusion_matrix(true_classes, predicted_classes)
sns.heatmap(conf_matrix, annot=True, fmt='g', xticklabels=class_labels, yticklabels=class_labels)
plt.xlabel('Predicted')
plt.ylabel('True')
plt.show()
```

7/7 [=====] - 3s 343ms/step - loss: 0.1108 - accuracy: 0.9552
Validation accuracy: 0.96

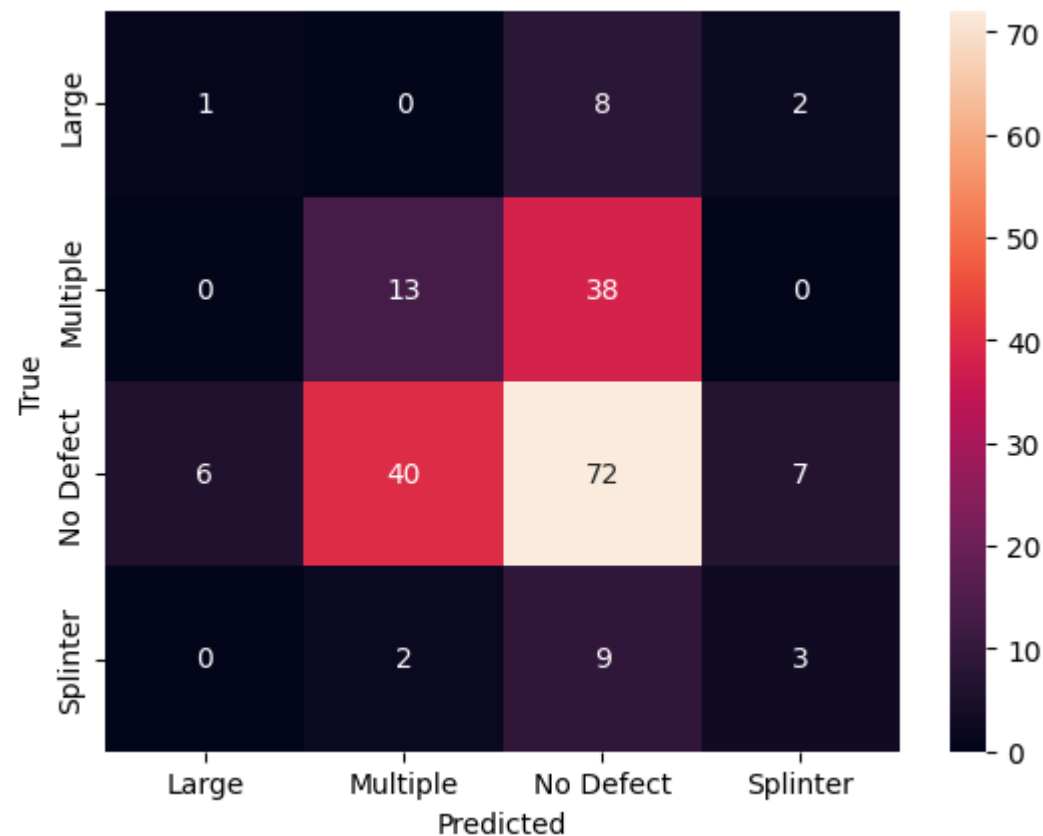




7/7 [=====] - 4s 590ms/step

| | precision | recall | f1-score | support |
|--|-----------|--------|----------|---------|
|--|-----------|--------|----------|---------|

| | | | | |
|--------------|------|------|------|-----|
| Large | 0.14 | 0.09 | 0.11 | 11 |
| Multiple | 0.24 | 0.25 | 0.25 | 51 |
| No Defect | 0.57 | 0.58 | 0.57 | 125 |
| Splinter | 0.25 | 0.21 | 0.23 | 14 |
| accuracy | | | 0.44 | 201 |
| macro avg | 0.30 | 0.28 | 0.29 | 201 |
| weighted avg | 0.44 | 0.44 | 0.44 | 201 |



Clustering Implementation

In [36]:

```
from sklearn.cluster import KMeans
from sklearn.metrics import silhouette_score

# Select relevant features for clustering
selected_features = df[['lifespan', 'coolingRate', 'quenchTime', 'forgeTime']]

# Applying K-Means Clustering
kmeans = KMeans(n_clusters=3, random_state=42) # Starting with 3 clusters
clusters = kmeans.fit_predict(selected_features)
df['Cluster'] = clusters

# Elbow Method to find the optimal number of clusters
sse = []
for k in range(1, 11): # Testing k from 1 to 10
```

```

kmeans = KMeans(n_clusters=k, random_state=42)
kmeans.fit(selected_features)
sse.append(kmeans.inertia_)

plt.plot(range(1, 11), sse)
plt.title('Elbow Method')
plt.xlabel('Number of Clusters')
plt.ylabel('SSE')
plt.show()

# Silhouette Score to validate the cluster number
silhouette_scores = []
for k in range(2, 11): # Silhouette Score needs at least 2 clusters
    kmeans = KMeans(n_clusters=k, random_state=42)
    cluster_labels = kmeans.fit_predict(selected_features)
    score = silhouette_score(selected_features, cluster_labels)
    silhouette_scores.append(score)

plt.plot(range(2, 11), silhouette_scores)
plt.title('Silhouette Scores')
plt.xlabel('Number of Clusters')
plt.ylabel('Silhouette Score')
plt.show()

```

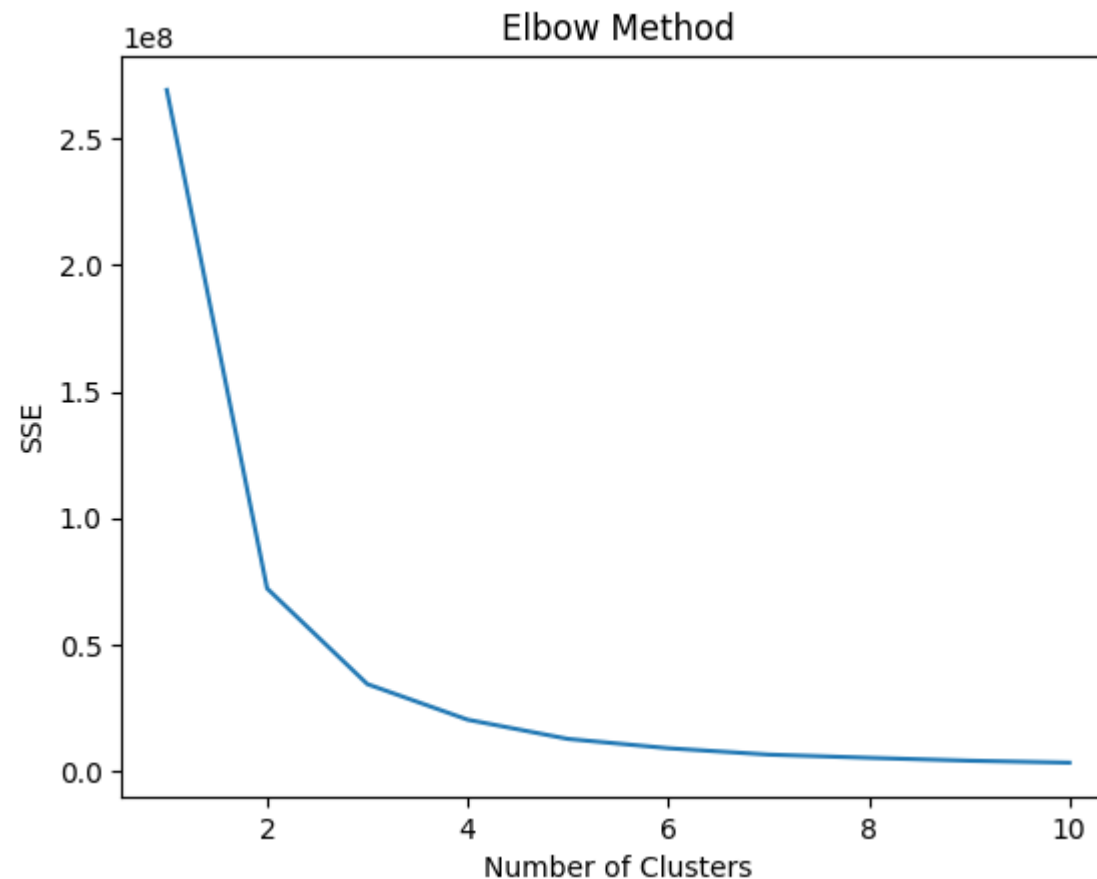
```

/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
  warnings.warn(
/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
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/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
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  warnings.warn(

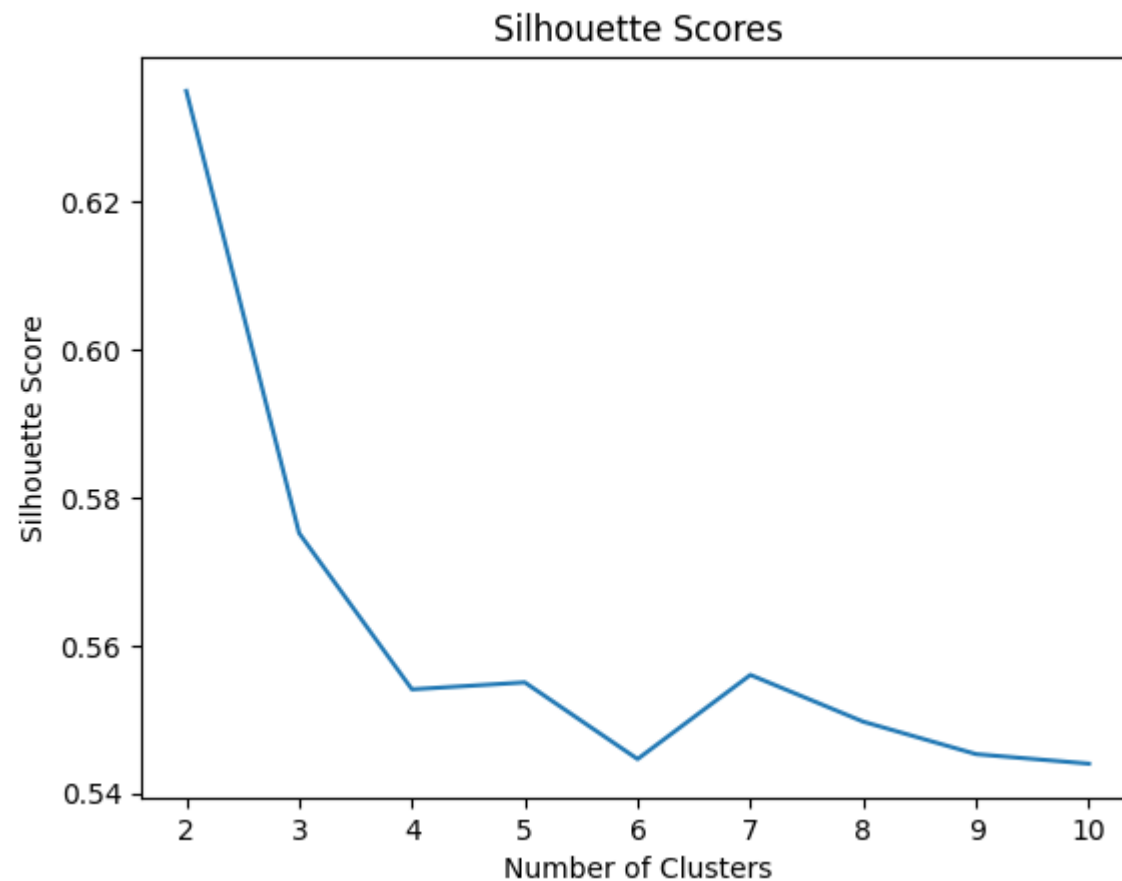
```



```
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om 10 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
warnings.warn(
```



[illegible]



```
In [37]: # Finding the optimal k based on Silhouette Scores
optimal_k_silhouette = range(2, 11)[silhouette_scores.index(max(silhouette_scores))]
print("Optimal number of clusters based on Silhouette Score:", optimal_k_silhouette)

# Final decision on optimal k
optimal_k = optimal_k_silhouette # Replace or adjust as necessary
print("Chosen optimal number of clusters:", optimal_k)
```

Optimal number of clusters based on Silhouette Score: 2
Chosen optimal number of clusters: 2

```
In [38]: # Re-run K-Means with the optimal number of clusters
optimal_k = 4
```

```
kmeans = KMeans(n_clusters=optimal_k, random_state=42)
clusters = kmeans.fit_predict(selected_features)
df['Cluster'] = clusters

# Scatter plot visualization
sns.scatterplot(data=df, x='coolingRate', y='Lifespan', hue='Cluster', palette='viridis')
plt.title('Clustering of Lifespan against Cooling Rate')
plt.show()
```

/usr/local/lib/python3.10/dist-packages/sklearn/cluster/_kmeans.py:870: FutureWarning: The default value of `n_init` will change from 10 to 'auto' in 1.4. Set the value of `n_init` explicitly to suppress the warning
warnings.warn(

