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Task 1 If you were asked to build a model for predicting arousal and valence, using the provided audio features as explanatory variables:

1. Which performance metrics would you use to evaluate your model's predictions?

To evaluate our model's performance given this would be a regression problem, we would use the metrics Mean Squared Error and Root Mean Squared Error for measuring the differences between the predicted and the actual values, the root of MSE expresses this error in the same units as the target variable, allowing for more intuitive interpretation. We would also make use of Median Absolute Error, which is similar to MSE and focuses on the median of the absolute errors, we included it as it aligns well with our goal of predicting the medians. Lastly we chose the R^2 score, as it tells us the proportion of variance in the predicted values explained by the model, indicating how well the model captures underlying patterns in the data.

2. Does the selection of the performance metric depend on the type of the response variables? Explain your reasoning.

Yes, naturally different performance metrics are more accustomed to different responses, given if our response variable is regressive or catergorical would result in different performance metrics being used. For example we particularly chose Median Absolute Error when considering the response variable as it conceptually aligns with our predicted target. Especially for continous variables, regression metrics Mean Absolute Error and R^2 are well-suited for evaluating how accurately the continuous predictions approximate the actual values and insight into the model's ability to capture the underlying variability.

On the other hand for the binarized versions of the response variables, where we classify arousal and valence into categories, classification metrics such as Accuracy, Precision, Recall and F1-score are more appropriate. These metrics assess how effectively the model can distinguish between discrete categories rather than predicting exact numerical values.

3. Which validation protocol (e.g., holdout set, k-fold cross-validation, etc.) would you use given that the objective is to build a predictive model able to generalise across participants (i.e., make accurate predictions for unseen participants)? Justify your choice.

For the validation protocol, it is essential to select an approach that ensures the predictive model can generalize to new, unseen participants. Given this we chose to implement a random participant holdout strategy, a cross-validation technique that aligns with our dataset. With it we exclude (hold out) the entire data of participants from the training data to be used exclusively for testing, this ensures that during the test set it mirrors a real-world scenario where the model, where we would be expected to predict arousal and valence levels for entirely new unseen participant.

This approach would give us a strict separation between training and testing data at the participant level, preventing data leakage and overfitting that could occur if information from the same individual appeared in both sets. Other cross-validation techniques would simply discard the participant id and shuffle the data, this method is well suited for a dataset with subsequent participants.

Task 2 Using the provided audio features, build predictive models for arousal and valence:

1. Develop a predictive model for each response variable (arousal and valence) using some or all of the provided audio features as explanatory variables

First we preprocessed the dataset using feature selection; separating the target variables, median_arousal and median_valence, from the feature set. These will serve as the outputs our models aim to predict and therefore they should not be included in the training dataset. We also excluded the Participant ID as this is a categorical identifier unique to each individual, including this as a feature would make sense for a regreseeive model.

We implemented random participant holdout as a validation technique, by randomly setting aside a subset of participants during model training. The Participant ID played a crucial role for implementing this as we could set aside participants in their entirity. With this method we could be sure that no data leakage could occur during training, if we simply split a participants recordings into a training and test sets the model may easily perform unrealisitically well (given it already has training knowledge regarding them), rather than a real life scenario where an unseen participant would need to be identified.

We then used the standard scaler to scale the data, naturally we didnt need to use Label Encoding or One-Hot Encoding as there are no catergorical values in the resulting dataset.

[2]:
```
import pandas as pd
from sklearn.preprocessing import StandardScaler
import random

df = pd.read_csv("project_data.csv")
scaler = StandardScaler()

y_arousal = pd.concat([df['Participant'], df['median_arousal']], axis=1)
y_valence = pd.concat([df['Participant'], df['median_valence']], axis=1)
df = df.drop(columns=['median_arousal', 'median_valence'])

# Get participant list
last_participant = df.iloc[[-1]]
participant_list = list(range(1, int(last_participant['Participant']) + 1))

# 80/20 test-train split
test_participants_index = random.sample(participant_list, 2)
train_participants_index = [item for item in participant_list if item not in␣
 ↪test_participants_index]

x_test = pd.concat([df[df['Participant'] == index] for index in␣
 ↪test_participants_index])
x_train = pd.concat([df[df['Participant'] == index] for index in␣
 ↪train_participants_index])
```

```
y_test_arousal = pd.concat([y_arousal[y_arousal['Participant'] == index] for␣
 ↪index in test_participants_index])
y_test_valence = pd.concat([y_valence[y_valence['Participant'] == index] for␣
 ↪index in test_participants_index])
y_train_arousal = pd.concat([y_arousal[y_arousal['Participant'] == index] for␣
 ↪index in train_participants_index])
y_trian_valence = pd.concat([y_valence[y_valence['Participant'] == index] for␣
 ↪index in train_participants_index])

x_test = x_test.drop(columns=['Participant'])
x_train = x_train.drop(columns=['Participant'])
y_test_arousal = y_test_arousal.drop(columns=['Participant'])
y_test_valence = y_test_valence.drop(columns=['Participant'])
y_train_arousal = y_train_arousal.drop(columns=['Participant'])
y_trian_valence = y_trian_valence.drop(columns=['Participant'])

x_test_scaled = scaler.fit_transform(x_test)
x_train_scaled = scaler.fit_transform(x_train)
```

```
C:\Users\gianm\AppData\Local\Temp\ipykernel_190388\1980572450.py:14:
FutureWarning: Calling int on a single element Series is deprecated and will
raise a TypeError in the future. Use int(ser.iloc[0]) instead
  participant_list = list(range(1, int(last_participant['Participant']) + 1))
```

The first task when selecticg a model is to identify if the problem is a regression or classification problem, given that we have to predict the scaler values of median valence and arousal this is clearly a regression problem. Given this dataset presents a high-dimensionality problem, which traditional machine learning methods often struggle to handle, we made use of a regularization method Least Absolute Shrinkage and Selection Operator. Lasso regularization penalizes features to effectively exclude temselves by reducing them to zero, making it an ideal fit for this dataset.

[ ]:
```
from sklearn.linear_model import LassoCV

lasso_cv_arousal = LassoCV(cv=10, random_state=0,max_iter=5000)
lasso_cv_arousal.fit(x_train_scaled, y_train_arousal.values.ravel())
selected_features_mask_arousal = lasso_cv_arousal.coef_ != 0
x_train_selected_arousal = x_train_scaled[:, selected_features_mask_arousal]
x_test_selected_arousal = x_test_scaled[:, selected_features_mask_arousal]

lasso_cv_valence = LassoCV(cv=10, random_state=0,max_iter=5000)
lasso_cv_valence.fit(x_train_scaled, y_trian_valence.values.ravel())
selected_features_mask_valence = lasso_cv_valence.coef_ != 0
x_train_selected_valence = x_train_scaled[:, selected_features_mask_valence]
x_test_selected_valence = x_test_scaled[:, selected_features_mask_valence]
```

For our model here we used Iterative Generalized Linear Models. Compared to other models like Random Forests and Support Vector Machines, which often function as black-box models with limited transparency, Iterative GLMs provide explicit model coefficients that quantify the relationship between each input feature and the target variable, this makes them quite good for evaluation.

They are also more flexible and stable in handling different distributions, unlike Linear Regression, they can provide more reliable estimates in certain cases essential to this is the iterative fitting process. The iterative fitting process is inherent to GLMs, at each iteration, the algorithm recalculates weights for each observation based on how well the current model fits the data, essentially giving more importance to observations that align better with the model assumptions and less to those that do not. This ensures more reliable convergence to multicollinearity compared to simple linear regressio and particularly suited in a high-dimensional setting like ours, where the dataset contains features certainly correlate in one way or another.

[67]:
```
import statsmodels.api as sm

x_train_glm_valence = sm.add_constant(x_train_selected_valence)
x_test_glm_valence = sm.add_constant(x_test_selected_valence)
x_train_glm_arousal = sm.add_constant(x_train_selected_arousal)
x_test_glm_arousal = sm.add_constant(x_test_selected_arousal)

glm_model_arousal = sm.GLM(y_train_arousal.values.ravel(), x_train_glm_arousal,␣
  ↪family=sm.families.Gaussian())
glm_results_arousal = glm_model_arousal.fit()
glm_model_valence = sm.GLM(y_trian_valence.values.ravel(), x_train_glm_valence,␣
  ↪family=sm.families.Gaussian())
glm_results_valence = glm_model_valence.fit()


glm_predictions_valence = glm_results_valence.predict(x_test_glm_valence)
glm_predictions_arousal = glm_results_arousal.predict(x_test_glm_arousal)
```

We then generated all the metrics discussed previously to evalutate the model. In the snippet below, we can see the previously discussed evaluation of the GLM model performance using the regression metrics. The snippet also outputs detailed summaries, providing insights into model coefficients and p-values (among others), allowing use to interpret and compare the predictive performance of the GLMs.

[68]:
```
from sklearn.metrics import mean_squared_error, r2_score, median_absolute_error
import numpy as np

glm_mse_valence = mean_squared_error(y_test_valence, glm_predictions_valence)
glm_mse_arousal = mean_squared_error(y_test_arousal, glm_predictions_arousal)
glm_rmse_valence =  np.sqrt(glm_mse_valence)
glm_rmse_arousal =  np.sqrt(glm_mse_arousal)
r2_valence = r2_score(y_test_valence, glm_predictions_valence)
r2_arousal = r2_score(y_test_arousal, glm_predictions_arousal)
medae_valence = median_absolute_error(y_test_valence, glm_predictions_valence)
medae_arousal = median_absolute_error(y_test_arousal, glm_predictions_arousal)
```

```python
print(glm_results_arousal.summary())
print(f"\nGLM MSE (arousal): {glm_mse_arousal:.4f}")
print(f"\nGLM RMSE (arousal): {glm_rmse_arousal:.4f}")
print(f"\nGLM R^2 (arousal): {r2_arousal:.4f}")
print(f"\nGLM MedAE (arousal): {medae_arousal:.4f}")
print(glm_results_valence.summary())
print(f"\nGLM MSE (valence): {glm_mse_valence:.4f}")
print(f"\nGLM RMSE (valence): {glm_rmse_valence:.4f}")
print(f"\nGLM R^2 (valence): {r2_valence:.4f}")
print(f"\nGLM MedAE (valence): {medae_valence:.4f}")
```

```
                 Generalized Linear Model Regression Results
==============================================================================
Dep. Variable:                      y   No. Observations:                 5789
Model:                            GLM   Df Residuals:                     5737
Model Family:                Gaussian   Df Model:                           51
Link Function:               Identity   Scale:                        0.023753
Method:                          IRLS   Log-Likelihood:                 2637.4
Date:                Mon, 02 Jun 2025   Deviance:                       136.27
Time:                        22:57:38   Pearson chi2:                     136.
No. Iterations:                     3   Pseudo R-squ. (CS):             0.2659
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          z      P>|z|      [0.025      0.975]
------------------------------------------------------------------------------
const          0.0105      0.002      5.169      0.000       0.006       0.014
x1             0.0163      0.005      3.128      0.002       0.006       0.027
x2             0.0012      0.003      0.445      0.656      -0.004       0.006
x3             0.0573      0.009      6.391      0.000       0.040       0.075
x4            -0.0202      0.004     -5.417      0.000      -0.027      -0.013
x5             0.0144      0.004      3.263      0.001       0.006       0.023
x6            -0.0137      0.005     -2.616      0.009      -0.024      -0.003
x7             0.0051      0.004      1.409      0.159      -0.002       0.012
x8            -0.0143      0.009     -1.569      0.117      -0.032       0.004
x9            -0.0105      0.004     -2.676      0.007      -0.018      -0.003
x10            0.0050      0.003      1.590      0.112      -0.001       0.011
x11           -0.0126      0.007     -1.791      0.073      -0.026       0.001
x12            0.0505      0.008      6.540      0.000       0.035       0.066
x13           -0.0065      0.008     -0.778      0.437      -0.023       0.010
x14            0.0031      0.003      0.909      0.363      -0.004       0.010
x15            0.0376      0.010      3.619      0.000       0.017       0.058
x16           -0.0243      0.005     -5.104      0.000      -0.034      -0.015
x17           -0.0276      0.004     -7.772      0.000      -0.035      -0.021
x18            0.0012      0.004      0.311      0.755      -0.006       0.009
x19           -0.0166      0.004     -3.953      0.000      -0.025      -0.008
x20            0.0107      0.003      3.070      0.002       0.004       0.017
x21            0.0078      0.004      2.242      0.025       0.001       0.015
x22           -0.0147      0.004     -3.883      0.000      -0.022      -0.007
```

```
x23             0.0148      0.003      4.511      0.000       0.008       0.021
x24            -0.0075      0.004     -2.005      0.045      -0.015      -0.000
x25             0.0102      0.003      3.508      0.000       0.005       0.016
x26            -0.0023      0.003     -0.743      0.458      -0.008       0.004
x27            -0.0059      0.002     -2.522      0.012      -0.010      -0.001
x28             0.0037      0.002      1.611      0.107      -0.001       0.008
x29            -0.0041      0.002     -1.845      0.065      -0.009       0.000
x30            -0.0040      0.002     -1.825      0.068      -0.008       0.000
x31            -0.0383      0.006     -6.237      0.000      -0.050      -0.026
x32             0.0013      0.003      0.425      0.671      -0.005       0.007
x33             0.0084      0.006      1.406      0.160      -0.003       0.020
x34             0.0034      0.008      0.404      0.686      -0.013       0.020
x35             0.0053      0.006      0.901      0.368      -0.006       0.017
x36             0.0036      0.004      0.825      0.409      -0.005       0.012
x37             0.0026      0.005      0.502      0.616      -0.008       0.013
x38             0.0083      0.005      1.768      0.077      -0.001       0.018
x39            -0.0018      0.006     -0.316      0.752      -0.013       0.010
x40            -0.0030      0.007     -0.452      0.651      -0.016       0.010
x41            -0.0029      0.005     -0.581      0.561      -0.012       0.007
x42             0.0094      0.003      3.296      0.001       0.004       0.015
x43            -0.0134      0.003     -4.134      0.000      -0.020      -0.007
x44             0.0069      0.003      2.292      0.022       0.001       0.013
x45            -0.0095      0.003     -3.773      0.000      -0.014      -0.005
x46            -0.0107      0.004     -2.670      0.008      -0.019      -0.003
x47             0.0028      0.003      1.043      0.297      -0.003       0.008
x48             0.0234      0.003      7.096      0.000       0.017       0.030
x49            -0.0026      0.003     -0.939      0.348      -0.008       0.003
x50            -0.0011      0.003     -0.439      0.661      -0.006       0.004
x51            -0.0022      0.002     -0.931      0.352      -0.007       0.002
==============================================================================

GLM MSE (arousal): 0.0332

GLM RMSE (arousal): 0.1821

GLM R^2 (arousal): 0.2369

GLM MedAE (arousal): 0.1388
                 Generalized Linear Model Regression Results
==============================================================================
Dep. Variable:                      y   No. Observations:                 5789
Model:                            GLM   Df Residuals:                     5777
Model Family:                Gaussian   Df Model:                           11
Link Function:               Identity   Scale:                        0.010494
Method:                          IRLS   Log-Likelihood:                 4981.9
Date:                Mon, 02 Jun 2025   Deviance:                       60.624
Time:                        22:57:38   Pearson chi2:                     60.6
No. Iterations:                     3   Pseudo R-squ. (CS):            0.08110
```

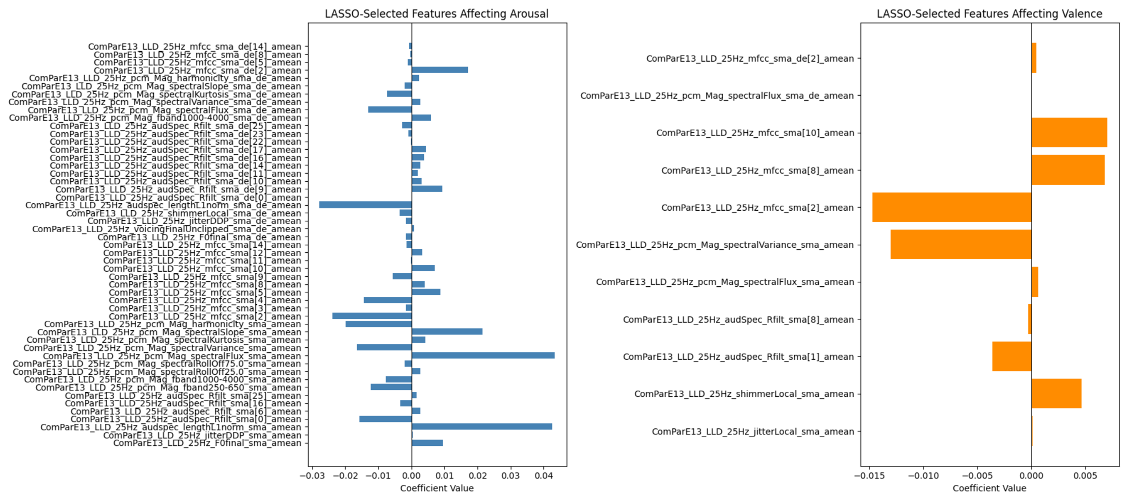
```
Covariance Type:            nonrobust
==============================================================================
                 coef    std err          z      P>|z|      [0.025      0.975]
------------------------------------------------------------------------------
const          0.0763      0.001     56.685      0.000       0.074       0.079
x1             0.0022      0.002      1.025      0.305      -0.002       0.007
x2             0.0076      0.003      2.787      0.005       0.002       0.013
x3            -0.0043      0.002     -1.874      0.061      -0.009       0.000
x4            -0.0112      0.003     -4.139      0.000      -0.016      -0.006
x5             0.0069      0.002      3.453      0.001       0.003       0.011
x6            -0.0188      0.002     -8.457      0.000      -0.023      -0.014
x7            -0.0241      0.002    -12.821      0.000      -0.028      -0.020
x8             0.0075      0.002      4.676      0.000       0.004       0.011
x9             0.0118      0.002      7.776      0.000       0.009       0.015
x10           -0.0001      0.001     -0.081      0.935      -0.003       0.003
x11            0.0043      0.001      3.014      0.003       0.001       0.007
==============================================================================

GLM MSE (valence): 0.0145

GLM RMSE (valence): 0.1202

GLM R^2 (valence): -0.0553

GLM MedAE (valence): 0.0728
```

From running the above multiple times we noticed that valence often generated with a negative R^2 score which suggests a level of underfitting in the features used. It should be known that when peforming LASSO for valence (in code below) the resulting feature set was always considerably smaller than that of arousal. In addition to this, valence always scores a better MSE and RMSE, this could be as theyre absolute measures unlike r^2 which is a relative measure that sees how the model performs versus a naive model that simply predicts the mean. We opted to be relatively skeptical of the r^2 value given it relativness to other values could cause it to swing drastically depending on the variables. Below we plotted the features selected by LASSO and their resulting coefficients.

The model summaries also highlight the explicit feature coefficients, revealing which audio features have a statistically significant effect on the predictions. With most of our p-values are low (effectively 0) meaning we can very confidently reject the null hypothesis that the coefficient is zero. This shows us that the GLMs consistently identify influential audio features and provide a transparent framework for understanding the feature relationship of our features and target.

Subsequently we indentify and plot the specific audio features that were selected by the LASSO regularization process. These selected features are then visualized using horizontal bar plots, where the magnitude and direction of each coefficient illustrate the feature's impact on the respective target variable. This visual helps us understand which audio features play the most significant role in predicting emotional states, and shows how our inclusing of LASSO is an asset in high-dimensional modelling tasks.

```
[69]: import matplotlib.pyplot as plt
      lasso_coef_arousal = lasso_cv_arousal.coef_
      lasso_coef_valence = lasso_cv_valence.coef_
      feature_names = x_train.columns
      selected_features_arousal = np.array(feature_names)[lasso_coef_arousal != 0]
      selected_coefs_arousal = lasso_coef_arousal[lasso_coef_arousal != 0]
      selected_features_valence = np.array(feature_names)[lasso_coef_valence != 0]
      selected_coefs_valence = lasso_coef_valence[lasso_coef_valence != 0]

      fig, axes = plt.subplots(1, 2, figsize=(18, 8), sharey=False)
      axes[0].barh(selected_features_arousal, selected_coefs_arousal,␣
       ↪color='steelblue')
      axes[0].axvline(0, color='black', linewidth=0.8)
      axes[0].set_title("LASSO-Selected Features Affecting Arousal")
      axes[0].set_xlabel("Coefficient Value")
      axes[1].barh(selected_features_valence, selected_coefs_valence,␣
       ↪color='darkorange')
      axes[1].axvline(0, color='black', linewidth=0.8)
      axes[1].set_title("LASSO-Selected Features Affecting Valence")
      axes[1].set_xlabel("Coefficient Value")
      plt.tight_layout()
      plt.show()

      print(f"Number of Features used for Arousal:␣
       ↪{len(x_train_selected_arousal[0])}")
      print(f"Number of Features used for Valence:␣
       ↪{len(x_train_selected_valence[0])}")
```



```
Number of Features used for Arousal: 51
Number of Features used for Valence: 11
```

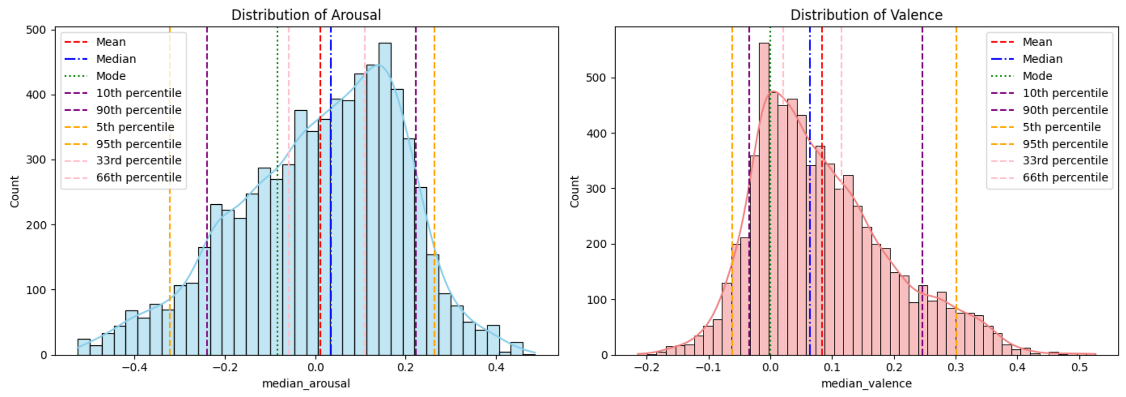
1. Select and justify appropriate threshold values for binarizing both arousal and valence annotations (the threshold for binarizing arousal should not necessarily be equal to the threshold for binarizing valence).

Our first step was to plot the distribution of the variables to see if anything may be discerned from them, we were curious if perhaps a multimodal distribution would appear. We also drew the lines of the mode, median and mean to discern the skew of the distributions. Included also is the lines of the for the percentiles, we used this to gauge what will be binarized if we use the percentiles as the threshold.

From this we discerned that both plots were unimodal with a right skew, with valence giving a prominent right distribution and arousal giving a more subtle one.

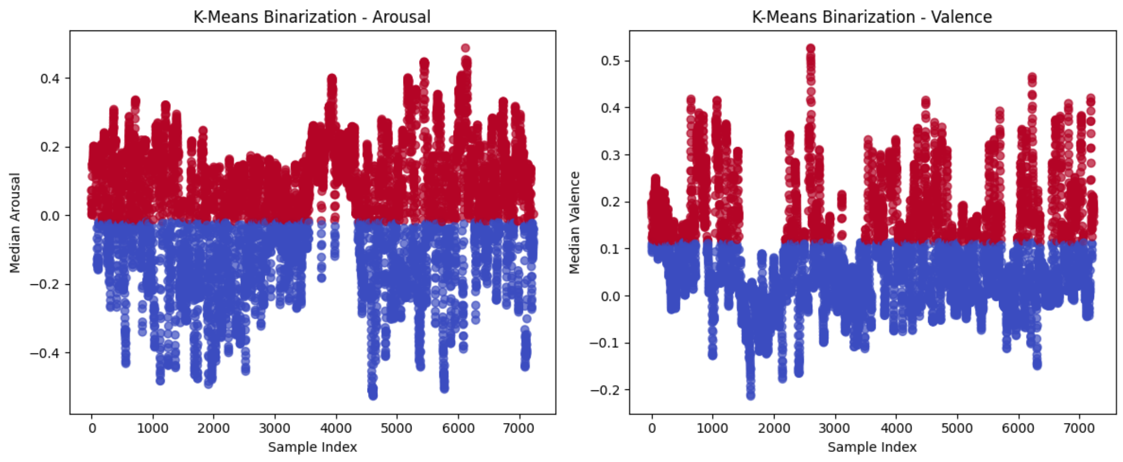
[70]:
```python
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns

arousal_10 = np.percentile(y_arousal['median_arousal'], 10)
arousal_90 = np.percentile(y_arousal['median_arousal'], 90)
arousal_5 = np.percentile(y_arousal['median_arousal'], 5)
arousal_95 = np.percentile(y_arousal['median_arousal'], 95)
arousal_33 = np.percentile(y_arousal['median_arousal'], 33)
arousal_66 = np.percentile(y_arousal['median_arousal'], 66)
valence_10 = np.percentile(y_valence['median_valence'], 10)
valence_90 = np.percentile(y_valence['median_valence'], 90)
valence_5 = np.percentile(y_valence['median_valence'], 5)
valence_95 = np.percentile(y_valence['median_valence'], 95)
valence_33 = np.percentile(y_valence['median_valence'], 33)
valence_66 = np.percentile(y_valence['median_valence'], 66)

fig, axes = plt.subplots(1, 2, figsize=(14, 5))

sns.histplot(y_arousal['median_arousal'], kde=True, ax=axes[0], color='skyblue')
axes[0].axvline(y_arousal['median_arousal'].mean(), color='red',␣
 ↪linestyle='--', label='Mean')
axes[0].axvline(y_arousal['median_arousal'].median(), color='blue',␣
 ↪linestyle='-.', label='Median')
axes[0].axvline(y_arousal['median_arousal'].mode().iloc[0], color='green',␣
 ↪linestyle=':', label='Mode')
axes[0].axvline(arousal_10, color='purple', linestyle='--', label='10th␣
 ↪percentile')
axes[0].axvline(arousal_90, color='purple', linestyle='--', label='90th␣
 ↪percentile')
axes[0].axvline(arousal_5, color='orange', linestyle='--', label='5th␣
 ↪percentile')
axes[0].axvline(arousal_95, color='orange', linestyle='--', label='95th␣
 ↪percentile')
```

```
axes[0].axvline(arousal_33, color='pink', linestyle='--', label='33rd␣
    ↪percentile')
axes[0].axvline(arousal_66, color='pink', linestyle='--', label='66th␣
    ↪percentile')
axes[0].set_title("Distribution of Arousal")
axes[0].legend()
sns.histplot(y_valence['median_valence'], kde=True, ax=axes[1],␣
    ↪color='lightcoral')
axes[1].axvline(y_valence['median_valence'].mean(), color='red',␣
    ↪linestyle='--', label='Mean')
axes[1].axvline(y_valence['median_valence'].median(), color='blue',␣
    ↪linestyle='-.', label='Median')
axes[1].axvline(y_valence['median_valence'].mode().iloc[0], color='green',␣
    ↪linestyle=':', label='Mode')
axes[1].axvline(valence_10, color='purple', linestyle='--', label='10th␣
    ↪percentile')
axes[1].axvline(valence_90, color='purple', linestyle='--', label='90th␣
    ↪percentile')
axes[1].axvline(valence_5, color='orange', linestyle='--', label='5th␣
    ↪percentile')
axes[1].axvline(valence_95, color='orange', linestyle='--', label='95th␣
    ↪percentile')
axes[1].axvline(valence_33, color='pink', linestyle='--', label='33rd␣
    ↪percentile')
axes[1].axvline(valence_66, color='pink', linestyle='--', label='66th␣
    ↪percentile')
axes[1].set_title("Distribution of Valence")
axes[1].legend()

plt.tight_layout()
plt.show()
```



We then went for a K-Means Clustering approach to see if we could descern anything from the data, unfortunately we could not realise anything from this data and wasen't of much aid.

[71]:
```python
from sklearn.cluster import KMeans

arousal_values = y_arousal['median_arousal'].values.reshape(-1, 1)
valence_values = y_valence['median_valence'].values.reshape(-1, 1)
kmeans_arousal = KMeans(n_clusters=2, random_state=42).fit(arousal_values)
kmeans_valence = KMeans(n_clusters=2, random_state=42).fit(valence_values)

# Masked so 1 is the higher value
if kmeans_arousal.cluster_centers_[0] > kmeans_arousal.cluster_centers_[1]:
    kmeans_arousal.labels_ = 1 - kmeans_arousal.labels_
if kmeans_valence.cluster_centers_[0] > kmeans_valence.cluster_centers_[1]:
    kmeans_valence.labels_ = 1 - kmeans_valence.labels_

fig, axes = plt.subplots(1, 2, figsize=(12, 5))
axes[0].scatter(range(len(arousal_values)),y_arousal['median_arousal'],␣
 ↪c=kmeans_arousal.labels_, cmap='coolwarm', alpha=0.7)
axes[0].set_title('K-Means Binarization - Arousal')
axes[0].set_xlabel('Sample Index')
axes[0].set_ylabel('Median Arousal')
axes[1].scatter(range(len(valence_values)),y_valence['median_valence'],␣
 ↪c=kmeans_valence.labels_, cmap='coolwarm', alpha=0.7)
axes[1].set_title('K-Means Binarization - Valence')
axes[1].set_xlabel('Sample Index')
axes[1].set_ylabel('Median Valence')
plt.tight_layout()
plt.show()
```



We ultimately decided to set the theshold of binarization to the median of the distributions for perfectly balanced classes. We did attempt to use the pecentiles but decided that the significant class imbalance would not be optimal, during testing a larger imbalance often performed better as the model would overfit to simply predict the larger class.

[72]:
```
# lower_pct = 5
# upper_pct = 95
# lower_pct = 10
# upper_pct = 90
y_arousal_median_threshold = y_arousal['median_arousal'].median()
y_arousal_valence_threshold = y_valence['median_valence'].median()

# arousal_lower_threshold = np.percentile(y_arousal['median_arousal'],␣
 ↪lower_pct)
# arousal_upper_threshold = np.percentile(y_arousal['median_arousal'],␣
 ↪upper_pct)
# valence_lower_threshold = np.percentile(y_valence['median_valence'],␣
 ↪lower_pct)
# valence_upper_threshold = np.percentile(y_valence['median_valence'],␣
 ↪upper_pct)

binarized_arousal = (y_arousal['median_arousal'] >= y_arousal_median_threshold).
 ↪astype(int)
binarized_valence = (y_valence['median_valence'] >=␣
 ↪y_arousal_valence_threshold).astype(int)

y_arousal_binarized = pd.concat([y_arousal['Participant'], binarized_arousal.
 ↪rename('arousal_bin')], axis=1)
y_valence_binarized = pd.concat([y_valence['Participant'], binarized_valence.
 ↪rename('valence_bin')], axis=1)

y_test_arousal_binarized = pd.
 ↪concat([y_arousal_binarized[y_arousal_binarized['Participant'] == index] for␣
 ↪index in test_participants_index]).drop(columns=['Participant'])
y_test_valence_binarized = pd.
 ↪concat([y_valence_binarized[y_valence_binarized['Participant'] == index] for␣
 ↪index in test_participants_index]).drop(columns=['Participant'])
y_train_arousal_binarized = pd.
 ↪concat([y_arousal_binarized[y_arousal_binarized['Participant'] == index] for␣
 ↪index in train_participants_index]).drop(columns=['Participant'])
y_train_valence_binarized = pd.
 ↪concat([y_valence_binarized[y_valence_binarized['Participant'] == index] for␣
 ↪index in train_participants_index]).drop(columns=['Participant'])

print("Test Arousal Binarized:")
print(y_test_arousal_binarized)
print("\nTrain Arousal Binarized:")
print(y_train_arousal_binarized)
```

```
Test Arousal Binarized:
      arousal_bin
5076            1
5077            1
5078            1
5079            1
5080            1
…             …
1451            0
1452            0
1453            0
1454            0
1455            0

[1449 rows x 1 columns]

Train Arousal Binarized:
      arousal_bin
0               1
1               1
2               1
3               1
4               1
…             …
7233            0
7234            0
7235            0
7236            0
7237            0

[5789 rows x 1 columns]
```

2. Implement a predictive model for each binarized response variable.

For this we decided on Support Vector Machines, given they were the most approriate linear classifier for high dimensional data because they are designed to find the optimal boundary that separates the two classes.

[73]:
```
from sklearn.svm import SVC

svm_arousal_binarized = SVC(kernel='rbf', random_state=42)
svm_arousal_binarized.fit(x_train_selected_arousal, y_train_arousal_binarized.
  ↪values)
svm_valence_binarized = SVC(kernel='rbf', random_state=42)
svm_valence_binarized.fit(x_train_selected_valence, y_train_arousal_binarized.
  ↪values)

y_pred_svm_arousal = svm_arousal_binarized.predict(x_test_selected_arousal)
```

```
y_pred_svm_valence = svm_valence_binarized.predict(x_test_selected_valence)
```

```
c:\Users\gianm\Documents\GitHub\ARI5102-Data_Analysis_Techniques\.venv\lib\site-
packages\sklearn\utils\validation.py:1408: DataConversionWarning: A column-
vector y was passed when a 1d array was expected. Please change the shape of y
to (n_samples, ), for example using ravel().
  y = column_or_1d(y, warn=True)
c:\Users\gianm\Documents\GitHub\ARI5102-Data_Analysis_Techniques\.venv\lib\site-
packages\sklearn\utils\validation.py:1408: DataConversionWarning: A column-
vector y was passed when a 1d array was expected. Please change the shape of y
to (n_samples, ), for example using ravel().
  y = column_or_1d(y, warn=True)
```

3. Select appropriate metrics to evaluate the performance of the model in this scenario using the validation protocol you proposed in Task 1.

We then evaluate the predictive performance of our SVM models using the previously discussed classification metrics being Accuracy, Precision, Recall, and F1-Score. They provide insight into the model's overall accuracy, its ability to avoid false positives and its effectiveness in identifying true positives with the F1-Score giving us a balanced metric. The overall performance of the classification metrics suggests that the SVM classifiers for both arousal and valence exhibit reasonably balanced predictive capability, demonstrating a moderate to strong ability to create meaningful distinctions between high and low states.

We also included the regression metrics to juxtapose, as noted previously choosing the proper performence metric given the target response is critical as they offer little practical insight in this context. For example, the R^2 scores for both arousal and valence are negative, indicating that these metrics are not meaningful here because they assess fit for continuous targets—not categorical classes. Similarly, the median absolute error either ends up being zero or one, reflecting the binary nature of the labels but ultimately failing to offer any nuanced understanding of the model's classification accuracy or errors. Ultimately we included these regression metrics below to illustrate their inadequacy.

[74]:
```
from sklearn.metrics import␣
 ↪mean_squared_error,r2_score,median_absolute_error,accuracy_score,precision_score,recall_sco

svm_mse_valence = mean_squared_error(y_test_valence_binarized,␣
 ↪y_pred_svm_valence)
svm_mse_arousal = mean_squared_error(y_test_arousal_binarized,␣
 ↪y_pred_svm_arousal)
svm_rmse_valence =  np.sqrt(svm_mse_valence)
svm_rmse_arousal =  np.sqrt(svm_mse_arousal)
svm_r2_valence = r2_score(y_test_valence_binarized, y_pred_svm_valence)
svm_r2_arousal = r2_score(y_test_arousal_binarized, y_pred_svm_arousal)
svm_medae_valence = median_absolute_error(y_test_valence_binarized,␣
 ↪y_pred_svm_valence)
svm_medae_arousal = median_absolute_error(y_test_arousal_binarized,␣
 ↪y_pred_svm_arousal)
```

```
print(f"\nSVM Regression Metrics for Arousal:")
print(f"SVM MSE (arousal): {svm_mse_arousal:.4f}")
print(f"SVM RMSE (arousal): {svm_rmse_arousal:.4f}")
print(f"SVM R^2 (arousal): {svm_r2_arousal:.4f}")
print(f"SVM MedAE (arousal): {svm_medae_arousal:.4f}")

print(f"\nSVM Regression Metrics for Valence:")
print(f"SVM MSE (valence): {svm_mse_valence:.4f}")
print(f"SVM RMSE (valence): {svm_rmse_valence:.4f}")
print(f"SVM R^2 (valence): {svm_r2_valence:.4f}")
print(f"SVM MedAE (valence): {svm_medae_valence:.4f}")

svm_accuracy_arousal = accuracy_score(y_test_arousal_binarized,␣
 ↪y_pred_svm_arousal)
svm_accuracy_valence = accuracy_score(y_test_valence_binarized,␣
 ↪y_pred_svm_valence)
svm_precision_arousal = precision_score(y_test_arousal_binarized,␣
 ↪y_pred_svm_arousal)
svm_precision_valence = precision_score(y_test_valence_binarized,␣
 ↪y_pred_svm_valence)
svm_recall_arousal = recall_score(y_test_arousal_binarized, y_pred_svm_arousal)
svm_recall_valence = recall_score(y_test_valence_binarized, y_pred_svm_valence)
svm_f1_arousal = f1_score(y_test_arousal_binarized, y_pred_svm_arousal)
svm_f1_valence = f1_score(y_test_valence_binarized, y_pred_svm_valence)

print(f"\nSVM Classification Metrics for Arousal:")
print(f"Accuracy: {svm_accuracy_arousal:.4f}")
print(f"Precision: {svm_precision_arousal:.4f}")
print(f"Recall: {svm_recall_arousal:.4f}")
print(f"F1-Score: {svm_f1_arousal:.4f}")

print(f"\nSVM Classification Metrics for Valence:")
print(f"Accuracy: {svm_accuracy_valence:.4f}")
print(f"Precision: {svm_precision_valence:.4f}")
print(f"Recall: {svm_recall_valence:.4f}")
print(f"F1-Score: {svm_f1_valence:.4f}")
```

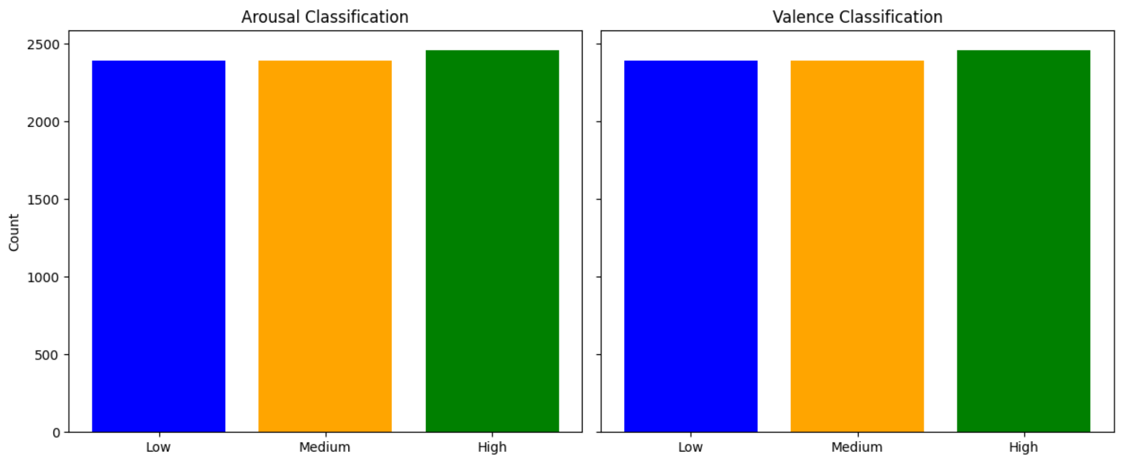
```
SVM Regression Metrics for Arousal:
SVM MSE (arousal): 0.2823
SVM RMSE (arousal): 0.5313
SVM R^2 (arousal): -0.1298
SVM MedAE (arousal): 0.0000

SVM Regression Metrics for Valence:
SVM MSE (valence): 0.3568
SVM RMSE (valence): 0.5973
SVM R^2 (valence): -0.4587
SVM MedAE (valence): 0.0000

SVM Classification Metrics for Arousal:
Accuracy: 0.7177
Precision: 0.7213
Recall: 0.6856
F1-Score: 0.7030

SVM Classification Metrics for Valence:
Accuracy: 0.6432
Precision: 0.7453
Recall: 0.5740
F1-Score: 0.6485
```

1. Select and justify appropriate threshold values for discretising (“high”, “neutral”, “low”) both arousal and valence annotations (the threshold for discretising arousal should not necessarily be equal to the threshold for discretising valence).

To establish meaningful thresholds for this categorization, we leveraged the 33rd and 66th percentiles of the respective distributions, a common practice for partitioning data into roughly equal-sized groups that preserve the natural spread of the data. This method ensures that each category contains a balanced number of observations, which is particularly valuable for downstream ranking tasks that depend on capturing nuanced differences in emotional state intensity. We tested different percentiles for thresholding them, given our previous distribution plot containing a variaty of percentiles, but the resulting class imbalance proved to be detremental to learning. To provide a clear visual summary of the resulting class distributions, we plotted bar charts showing the counts of low, medium, and high categories for both arousal and valence.

[94]:
```
arousal_low_thresh = np.percentile(y_arousal['median_arousal'], 33)
arousal_high_thresh = np.percentile(y_arousal['median_arousal'], 66)
valence_low_thresh = np.percentile(y_valence['median_valence'], 33)
valence_high_thresh = np.percentile(y_valence['median_valence'], 66)



arousal_conditions = [ y_arousal['median_arousal'] <=␣
 ↪arousal_low_thresh,y_arousal['median_arousal'] >= arousal_high_thresh]
ranked_arousal = np.select(arousal_conditions, [0, 2], default=1)
valence_conditions = [y_valence['median_valence'] <=␣
 ↪valence_low_thresh,y_valence['median_valence'] >= valence_high_thresh]
ranked_valence = np.select(valence_conditions, [0, 2], default=1)

y_arousal_ranked = pd.concat([y_arousal['Participant'], pd.
 ↪Series(ranked_arousal, name='arousal_rank')], axis=1)
y_valence_ranked = pd.concat([y_valence['Participant'], pd.
 ↪Series(ranked_valence, name='valence_rank')], axis=1)
```

```
y_test_arousal_ranked = pd.
  ↪concat([y_arousal_ranked[y_arousal_ranked['Participant'] == index] for index␣
  ↪in test_participants_index]).drop(columns=['Participant'])
y_train_arousal_ranked = pd.
  ↪concat([y_arousal_ranked[y_arousal_ranked['Participant'] == index] for index␣
  ↪in train_participants_index]).drop(columns=['Participant'])
y_test_valence_ranked = pd.
  ↪concat([y_valence_ranked[y_valence_ranked['Participant'] == index] for index␣
  ↪in test_participants_index]).drop(columns=['Participant'])
y_train_valence_ranked = pd.
  ↪concat([y_valence_ranked[y_valence_ranked['Participant'] == index] for index␣
  ↪in train_participants_index]).drop(columns=['Participant'])


fig, axs = plt.subplots(1, 2, figsize=(12, 5), sharey=True)
axs[0].bar(
    ['Low', 'Medium', 'High'],
    [np.sum(ranked_arousal == 0), np.sum(ranked_arousal == 1), np.
  ↪sum(ranked_arousal == 2)],
    color=['blue', 'orange', 'green']
)
axs[0].set_title('Arousal Classification')
axs[0].set_ylabel('Count')
axs[1].bar(
    ['Low', 'Medium', 'High'],
    [np.sum(ranked_valence == 0), np.sum(ranked_valence == 1), np.
  ↪sum(ranked_valence == 2)],
    color=['blue', 'orange', 'green']
)
axs[1].set_title('Valence Classification')

plt.tight_layout()
plt.show()
```



High is slightly larger as it has the residual values of the classification.

2. Implement a ranking predictive model for each response variable.

We decided to use an ordinal regression model, as we jave adjacent catagorical states with sequential order (each category flows into the next one).

We decided to implement an ordinal regression model to handle the ranked labels. We decided on this model as it is specifically suitable for ordinal outcomes, explicitly accounting for the ordered nature of these classes (each category flows into the next one {low,medium,high}), rather than treating them as purely categorical and seperate. By doing so, it can produce predictions that better respect the inherent hierarchy in the classifications.

[95]:
```
from mord import LogisticAT

ordinal_arousal_model = LogisticAT()
ordinal_arousal_model.fit(x_train_selected_arousal, y_train_arousal_ranked.
 ↪values.ravel())
y_pred_ordinal_arousal = ordinal_arousal_model.predict(x_test_selected_arousal)
ordinal_valence_model = LogisticAT()
ordinal_valence_model.fit(x_train_selected_valence, y_train_valence_ranked.
 ↪values.ravel())
y_pred_ordinal_valence = ordinal_valence_model.predict(x_test_selected_valence)
```

3. Select appropriate metrics to evaluate the performance of the models in this scenario using the validation protocol you proposed in Task 1.

We evaluated the performance of the ordinal logistic regression models using the same classification metrics discussed earlier: accuracy, precision, recall, and F1-score. Since the predictions are ordinal labels and classification-based, we did not include the regression-style metrics here, as discussd they do not provide meaningful insights into the quality of these ranked classifications.

[96]:
```
# Classification metrics for the ordinal (ranked) predictions
ordinal_accuracy_arousal = accuracy_score(y_test_arousal_ranked,␣
 ↪y_pred_ordinal_arousal)
ordinal_accuracy_valence = accuracy_score(y_test_valence_ranked,␣
 ↪y_pred_ordinal_valence)
ordinal_precision_arousal = precision_score(y_test_arousal_ranked,␣
 ↪y_pred_ordinal_arousal, average='weighted')
ordinal_precision_valence = precision_score(y_test_valence_ranked,␣
 ↪y_pred_ordinal_valence, average='weighted')
ordinal_recall_arousal = recall_score(y_test_arousal_ranked,␣
 ↪y_pred_ordinal_arousal, average='weighted')
ordinal_recall_valence = recall_score(y_test_valence_ranked,␣
 ↪y_pred_ordinal_valence, average='weighted')
ordinal_f1_arousal = f1_score(y_test_arousal_ranked, y_pred_ordinal_arousal,␣
 ↪average='weighted')
```

```
ordinal_f1_valence = f1_score(y_test_valence_ranked, y_pred_ordinal_valence,␣
 ↪average='weighted')

# Print classification metrics
print(f"\nOrdinal Logistic Regression Metrics for Arousal:")
print(f"Accuracy: {ordinal_accuracy_arousal:.4f}")
print(f"Precision: {ordinal_precision_arousal:.4f}")
print(f"Recall: {ordinal_recall_arousal:.4f}")
print(f"F1-Score: {ordinal_f1_arousal:.4f}")

print(f"\nOrdinal Logistic Regression Metrics for Valence:")
print(f"Accuracy: {ordinal_accuracy_valence:.4f}")
print(f"Precision: {ordinal_precision_valence:.4f}")
print(f"Recall: {ordinal_recall_valence:.4f}")
print(f"F1-Score: {ordinal_f1_valence:.4f}")
```

```
Ordinal Logistic Regression Metrics for Arousal:
Accuracy: 0.3872
Precision: 0.6259
Recall: 0.3872
F1-Score: 0.3747

Ordinal Logistic Regression Metrics for Valence:
Accuracy: 0.3575
Precision: 0.6042
Recall: 0.3575
F1-Score: 0.2516
```

Task 3 In this task, you will identify similar observations captured from the first participant (participant ID = 1). Complete the following steps:

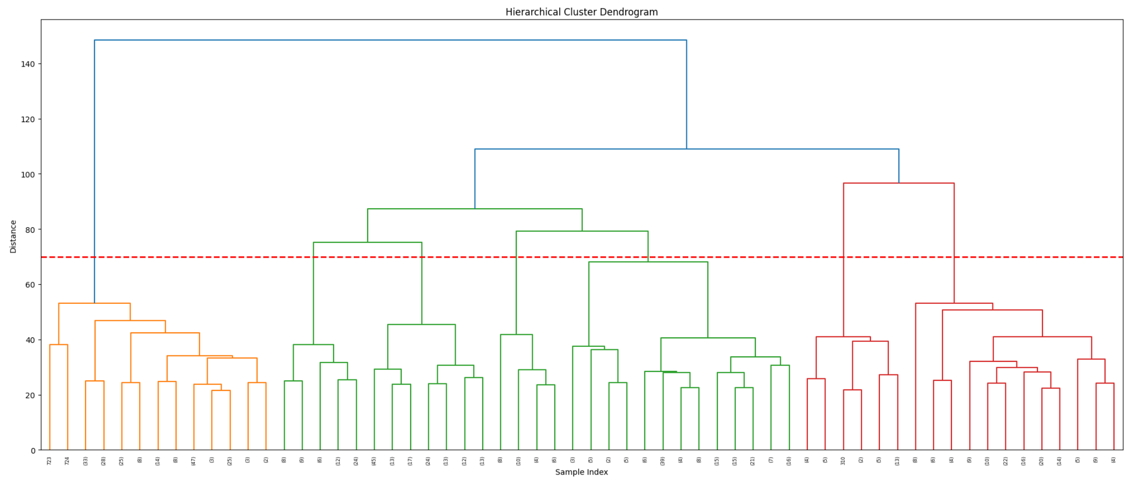
1. Create groups of similar observations from the first participant by proposing and implementing two suitable algorithms.

We created a subset of the dataset by selecting only participant 1's data, we subsequently dropped the partipants column as this data is uneccassary. We also removed the median_arousal and median_variance as this section is based on creating groups of similar observations (features) and these last two columns are annotations/scores.

[97]:
```
df = pd.read_csv("project_data.csv")

participant_df = df[df["Participant"] == 1]
participant_df = participant_df.drop(columns=["Participant",'median_arousal',␣
 ↪'median_valence'])
participant_df = scaler.fit_transform(participant_df)
```

For clustering we performed Hierarchical clustering using Ward's method to minimize the variance within the clusters and K-mediods with random initialization to further minimize the optimization criterion along with forward step wise assignment.

[98]:
```
from scipy.cluster.hierarchy import dendrogram, linkage

plt.figure(figsize=(25,10))
link = linkage(participant_df,'ward')
dn = dendrogram(link,truncate_mode='lastp',p=60)
plt.axhline(y=70, color='red', linestyle='--', linewidth=2)
plt.title('Hierarchical Cluster Dendrogram')
plt.xlabel('Sample Index')
plt.ylabel('Distance')
plt.show()
```



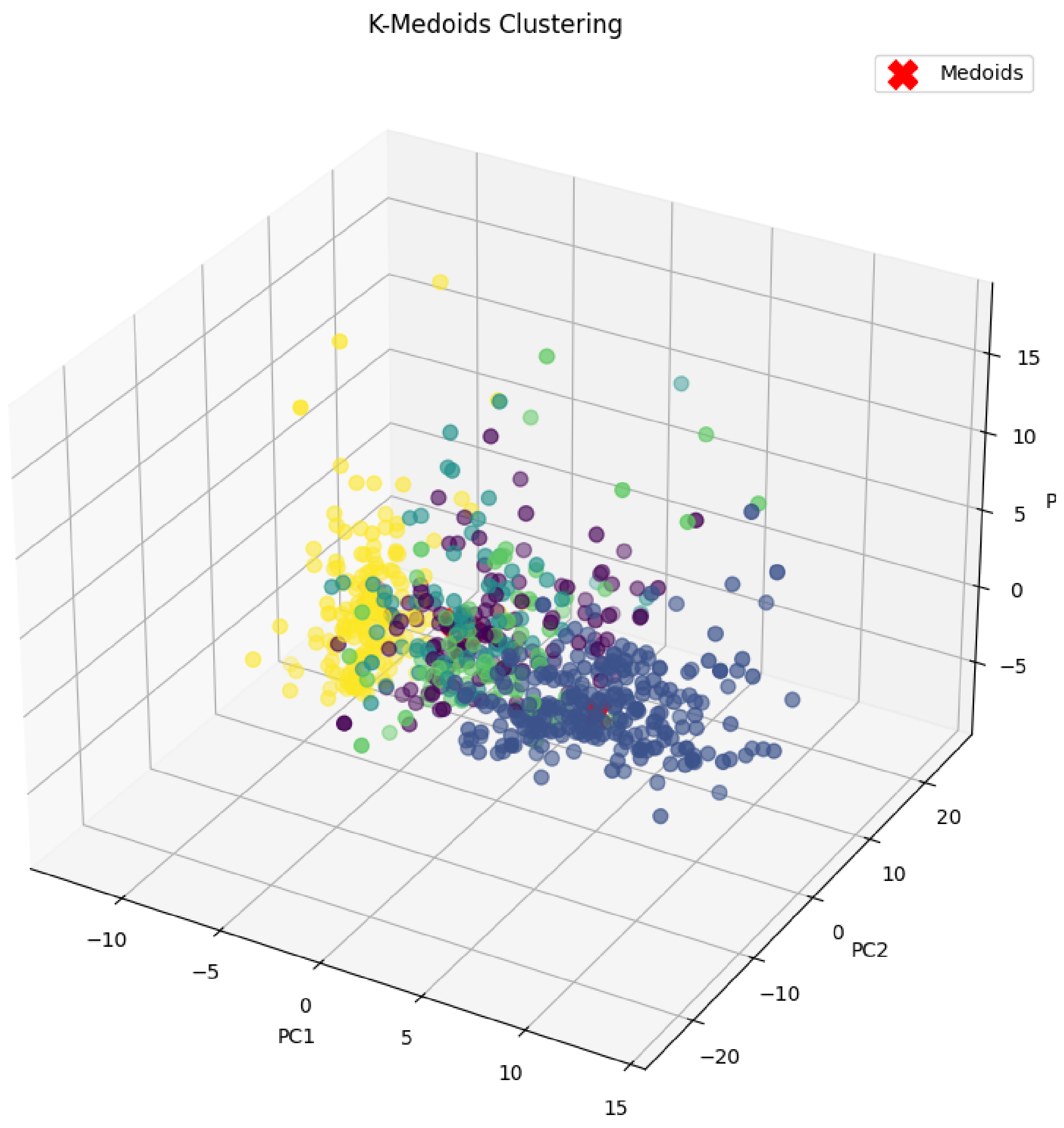
From this we can see at the 70 distance mark, shown by the dashed red line, around 5 clusters form. Hence we set the threshold for clustering to 5 clusters.

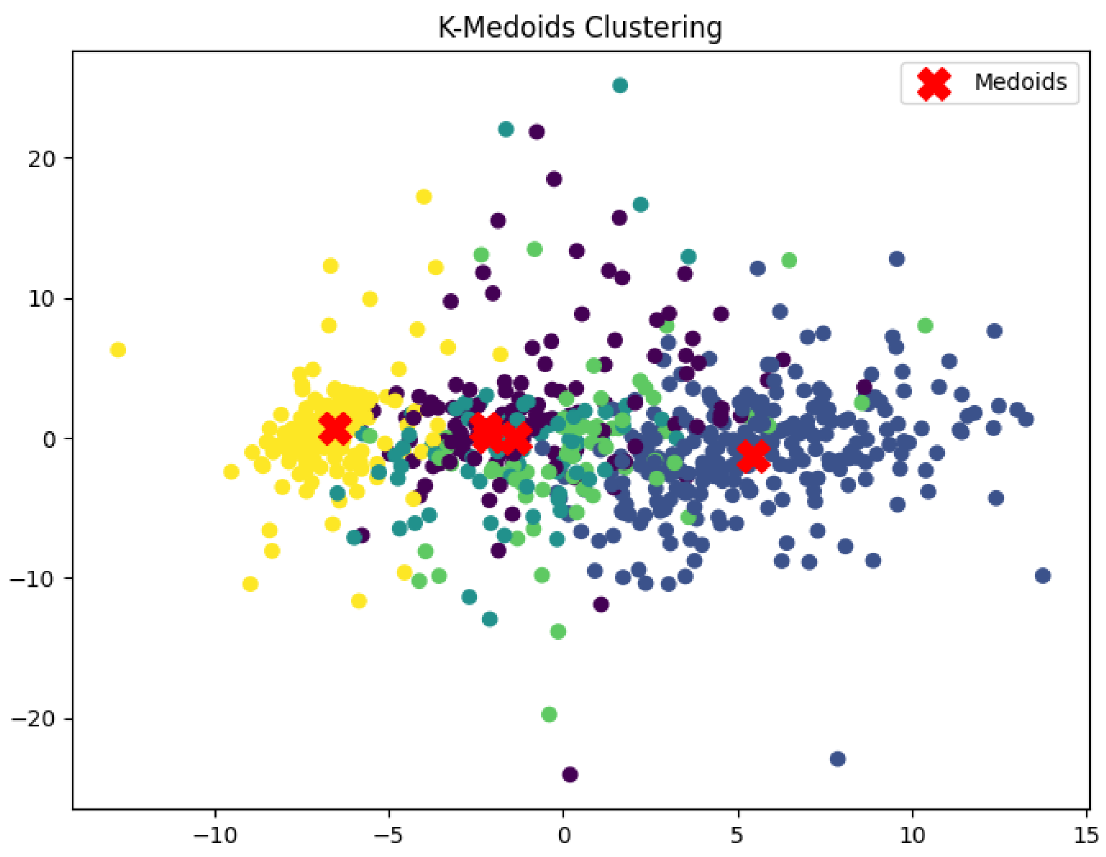
[99]:
```
from scipy.cluster.hierarchy import fcluster
from sklearn.metrics import silhouette_score, calinski_harabasz_score,␣
  ↪davies_bouldin_score
labels_hr = fcluster(link,t=5, criterion='maxclust')
```

We then implemented K-Medoids clustering on the participant data to identify five representative clusters, it is more robust against outliers, unlike k-means which uses centroids, due to its use of medians. To better visualize the results in a reduced feature space, we applied Principal Component Analysis (PCA) to project the high-dimensional data intoprincipal components to allow use to illustrate the data in 3D and 2D scatter plots. These plots show the cluster medoids which are highlighted with red large markers.

[100]:
```
from sklearn_extra.cluster import KMedoids
from sklearn.decomposition import PCA
import matplotlib.pyplot as plt
```

```
kmedoids = KMedoids(n_clusters=5, random_state=42)
labels_md = kmedoids.fit_predict(participant_df)
pca = PCA(n_components=3)
X_pca = pca.fit_transform(participant_df)
fig = plt.figure(figsize=(10, 8))
ax = fig.add_subplot(111, projection='3d')
scatter = ax.scatter(X_pca[:, 0], X_pca[:, 1], X_pca[:, 2], c=labels_md,␣
 ↪cmap='viridis', s=50)
ax.scatter(X_pca[kmedoids.medoid_indices_, 0],
           X_pca[kmedoids.medoid_indices_, 1],
           X_pca[kmedoids.medoid_indices_, 2],
           c='red', marker='X', s=200, label='Medoids')
ax.set_title('K-Medoids Clustering')
ax.set_xlabel('PC1')
ax.set_ylabel('PC2')
ax.set_zlabel('PC3')
ax.legend()
plt.tight_layout()
plt.show()
plt.figure(figsize=(8, 6))
plt.scatter(X_pca[:, 0], X_pca[:, 1], c=labels_md, cmap='viridis')
plt.scatter(X_pca[kmedoids.medoid_indices_, 0], X_pca[kmedoids.medoid_indices_,␣
 ↪1], c='red', marker='X', s=200, label='Medoids')
plt.title('K-Medoids Clustering')
plt.legend()
plt.show()
```


K-Medoids Clustering
Medoids
PC1
PC2
P
−10
−5
0
5
10
15
−20
−10
0
10
20
−5
0
5
10
15



2. Evaluate the clusters quality using appropriate metrics.

To assess the effectiveness of the hierarchical clustering and K-Medoids clustering models, we utilized the Silhouette Score, Davies-Bouldin Index, and Calinski-Harabasz Score.The Silhouette Score measures how well each observation fits within its assigned cluster compared to other clusters, how tightly grouped points are within the same cluster and show distinctly different one cluster is from another. We observed that the Silhouette Scores for both methods were relatively low, suggesting that while there is some clustering structure present, it is not strongly defined

We the applied the Davies-Bouldin Index to evaluate evaluates the similarity between each cluster and its most similar neighboring cluster with lower values implying greater separation between clusters and less overlap. In this metric hierarchical clustering generally produced a slightly lower index value.This was also true for the Calinski-Harabasz Score, which compares the dispersion of data points between clusters to the dispersion within clusters. Where hierarchical clustering scored higher as well indicating its clusters were both dense and well-separated

[101]:
```
sil_score_hr = silhouette_score(participant_df, labels_hr)
db_score_hr = davies_bouldin_score(participant_df, labels_hr)
ch_score_hr = calinski_harabasz_score(participant_df, labels_hr)
```

```
print(f"Silhouette Score: {sil_score_hr:.3f}")
print(f"Davies-Bouldin Index: {db_score_hr:.3f}")
print(f"Calinski-Harabasz Score: {ch_score_hr:.3f}")
```

```
Silhouette Score: 0.083
Davies-Bouldin Index: 2.484
Calinski-Harabasz Score: 66.584
```

[102]:
```
sil_score_md = silhouette_score(participant_df, labels_md)
db_score_md = davies_bouldin_score(participant_df, labels_md)
ch_score_md = calinski_harabasz_score(participant_df, labels_md)

print(f"Silhouette Score: {sil_score_md:.3f}")
print(f"Davies-Bouldin Index: {db_score_md:.3f}")
print(f"Calinski-Harabasz Score: {ch_score_md:.3f}")
```

```
Silhouette Score: 0.068
Davies-Bouldin Index: 3.922
Calinski-Harabasz Score: 49.035
```

3. Compare the algorithms you implemented and select the best one.

When comparing the two clustering algorithms we implemented the best algorithim becomes evident, the hierarchical clustering using Ward's method clearly performed better in all of our evaluation metrics.

Hierarchical clustering likely outperformed K-Medoids because it can naturally capture nested and progressive patterns present in spontaneous human behavior. Ward linkage minimizes intra-cluster variance, making it well-suited for high-dimensional affective data. Furthermore, hierarchical clustering does not rely on initial cluster centers, which can lead to more stable and interpretable results in this context.

5. How would you assign a new observation from the first participant to an existing group?

Since hierarchical clustering does not provide a direct way to classify new observations, we would need to train a classifier with the labels generated from clustering and have it predict the cluster of the new observaion.

2.4. Task 4 Based on the results obtained from Task 3:

1. Explain whether the clustering information could be used to build more accurate models for Task 2 and describe what you would do to build such models.

The clustering information we obtained, may be leveraged to build more accurate models for due to their ability to reveal unkown structures in the feaure space, potentially capturing local patterns that the standard regression or classification models might overlook.

We highlight one approach in particular to incorporate this information into new predictive models, being to treat the cluster assignments as an additional feature in the model. This would allow the model to differentiate between observations that come from different naturally occurring subgroups, helping to tailor predictions to the specific patterns within each cluster. These new categorical features could be easily incorporated into the existing SVM and GLM models making it easy to compare the affects with our baseline models.

Alternatively but in a similar vein, we could build separate predictive models for each cluster. This would involve splitting the dataset according to the cluster assignments and training individual models within each subgroup. We dont particularly endorse this approach as it leaves the possibility for data sparsity, meaning we have less datapoints than featurs. Despite this there are some advantages that arise from pooling all observations into a single, global model, such as reducing bias and variance.