



PRINCIPAL - COMPONENT ANALYSIS

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PRINCIPAL COMPONENT ANALYSIS **AND LOGISTIC REGRESSION** USING PYTHON PROGRAMMING

The Breast Cancer Wisconsin (Diagnostic) dataset is a widely used multivariate dataset in machine learning, primarily for classification tasks. Each instance in the dataset represents a patient, and the goal is to classify the tumor as either **malignant (cancerous) or benign (non-cancerous)**.

The dataset contains 30 numerical features, which describe various characteristics of the cell nuclei present in the image.

They comprise **10 core measurements** each reported as a **mean, standard error, and "worst" (largest) value**. The 10 core characteristics of the cell nuclei are:

Radius, Texture, Perimeter, Area, Smoothness, Compactness, Concavity, Concave points, Symmetry, Fractal dimension.

Its clear separation into two classes and the availability of diverse, well-defined features make it an excellent resource for learning and applying various machine learning algorithms, particularly in areas like classification, dimensionality reduction (e.g., PCA), and model evaluation.

```
import pandas as pd
import numpy as np
from sklearn.preprocessing import StandardScaler
from sklearn.decomposition import PCA
import matplotlib.pyplot as plt
import seaborn as sns
from sklearn.datasets import load_breast_cancer
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score, classification_report
```

```
cancer = load_breast_cancer()
df = pd.DataFrame(data=cancer.data, columns=cancer.feature_names)
print(cancer.DESCR)
```

:Number of Instances: 569

:Number of Attributes: 30 numeric, predictive attributes and the class

:Attribute Information:

- radius (mean of distances from center to points on the perimeter)
- texture (standard deviation of gray-scale values)
- perimeter
- area
- smoothness (local variation in radius lengths)
- compactness (perimeter² / area - 1.0)
- concavity (severity of concave portions of the contour)
- concave points (number of concave portions of the contour)
- symmetry
- fractal dimension ("coastline approximation" - 1)

The mean, standard error, and "worst" or largest (mean of the three worst/largest values) of these features were computed for each image, resulting in 30 features. For instance, field 0 is Mean Radius, field 10 is Radius SE, field 20 is Worst Radius.

- class:
 - WDBC-Malignant
 - WDBC-Benign

:Summary Statistics:

	Min	Max
radius (mean):	6.981	28.11
texture (mean):	9.71	39.28
perimeter (mean):	43.79	188.5
area (mean):	143.5	2501.0
smoothness (mean):	0.053	0.163
compactness (mean):	0.019	0.345
concavity (mean):	0.0	0.427
concave points (mean):	0.0	0.201
symmetry (mean):	0.106	0.304
fractal dimension (mean):	0.05	0.097
radius (standard error):	0.112	2.873
texture (standard error):	0.36	4.885
perimeter (standard error):	0.757	21.98
area (standard error):	6.802	542.2
smoothness (standard error):	0.002	0.031
compactness (standard error):	0.002	0.135
concavity (standard error):	0.0	0.396
concave points (standard error):	0.0	0.053
symmetry (standard error):	0.008	0.079
fractal dimension (standard error):	0.001	0.03
radius (worst):	7.93	36.04
texture (worst):	12.02	49.54
perimeter (worst):	50.41	251.2
area (worst):	185.2	4254.0
smoothness (worst):	0.071	0.223
compactness (worst):	0.027	1.058
concavity (worst):	0.0	1.252
concave points (worst):	0.0	0.291
symmetry (worst):	0.156	0.664
fractal dimension (worst):	0.055	0.208

```
# Step 1: Standardize the data
```

```
scaler = StandardScaler()
```

```
scaled_data = scaler.fit_transform(df)
```

```
pca = PCA()
```

```
res_pca = pca.fit(scaled_data)
```

```
explained_variance_ratio = pca.explained_variance_ratio_
```

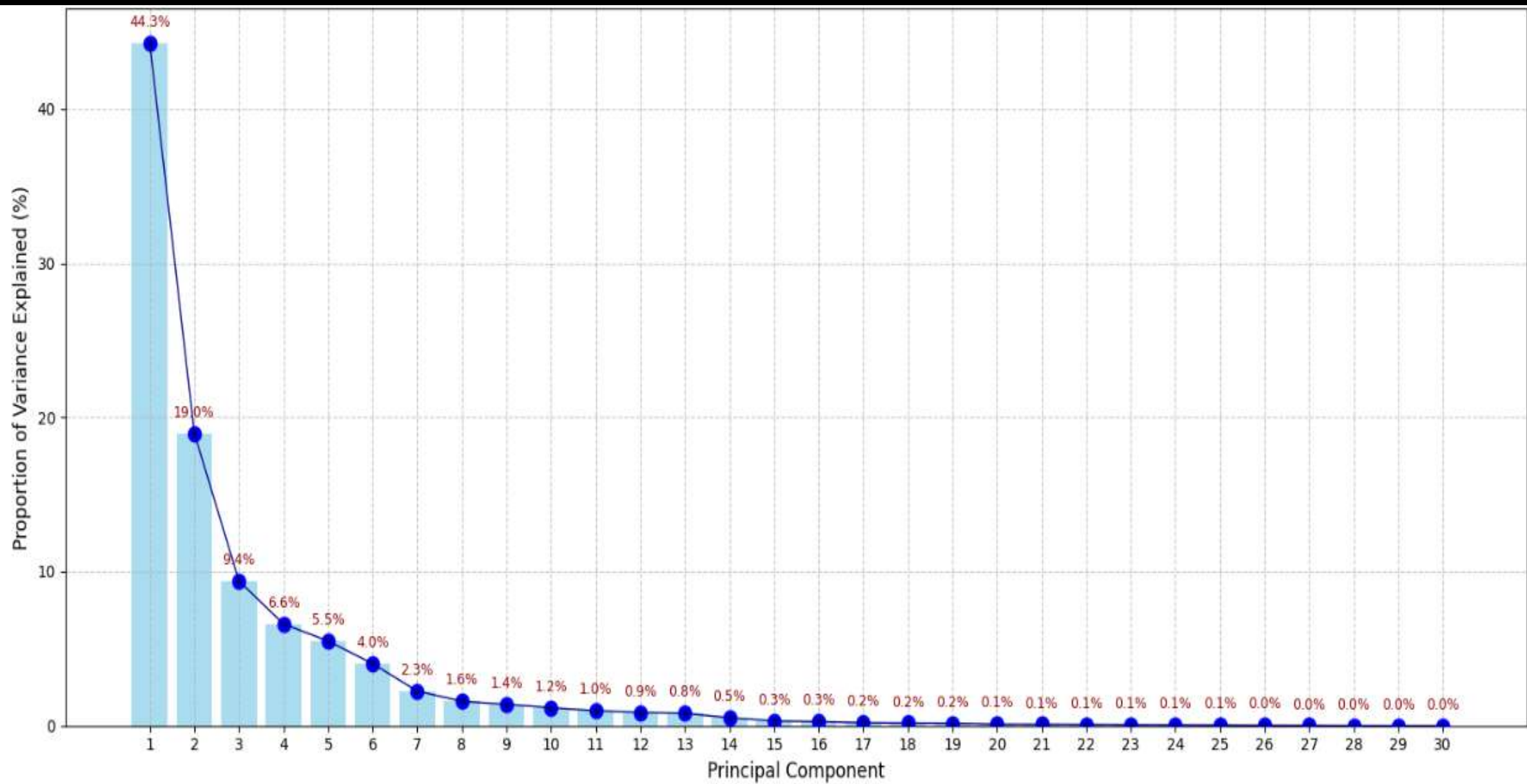
```
standard_deviation = np.sqrt(pca.explained_variance_)
```

```
cumulative_proportion = np.cumsum(explained_variance_ratio)
```

```
pca_summary = pd.DataFrame({  
    'Standard deviation': standard_deviation,  
    'Proportion of Variance': explained_variance_ratio,  
    'Cumulative Proportion': cumulative_proportion  
}, index=[f'PC{i+1}' for i in range(len(standard_deviation))])  
print("\nPCA Summary Table:")  
print(pca_summary)
```

PCA Summary Table:

	Standard deviation	Proportion of Variance	Cumulative Proportion
PC1	3.647601	0.442720	0.442720
PC2	2.387755	0.189712	0.632432
PC3	1.680152	0.093932	0.726364
PC4	1.408591	0.066021	0.792385
PC5	1.285159	0.054958	0.847343
PC6	1.099765	0.040245	0.887588
PC7	0.822441	0.022507	0.910095
PC8	0.690982	0.015887	0.925983
PC9	0.646242	0.013896	0.939879
PC10	0.592715	0.011690	0.951569
PC11	0.542617	0.009797	0.961366
PC12	0.511489	0.008705	0.970071
PC13	0.491714	0.008045	0.978117
PC14	0.396593	0.005234	0.983350
PC15	0.307084	0.003138	0.986488
PC16	0.282849	0.002662	0.989150
PC17	0.243934	0.001980	0.991130
PC18	0.229590	0.001754	0.992884
PC19	0.222631	0.001649	0.994533
PC20	0.176676	0.001039	0.995572
PC21	0.173279	0.000999	0.996571
PC22	0.165794	0.000915	0.997486
PC23	0.156153	0.000811	0.998297
PC24	0.134487	0.000602	0.998899
PC25	0.124533	0.000516	0.999415
PC26	0.090510	0.000273	0.999688
PC27	0.083142	0.000230	0.999918
PC28	0.039902	0.000053	0.999971
PC29	0.027388	0.000025	0.999996
PC30	0.011545	0.000004	1.000000



```

plt.figure(figsize=(15,7))
# 1. Bar Plot for Explained Variance
plt.bar(range(1, len(explained_variance_ratio) + 1), explained_variance_ratio * 100,
        color='skyblue', alpha=0.7, label='Explained Variance')
# 2. Scatter Plot (on top of bars) for emphasis
plt.scatter(range(1, len(explained_variance_ratio) + 1), explained_variance_ratio * 100,
            marker='o', color='blue', s=80, zorder=5) # zorder to ensure dots are on top
plt.title('Scree Plot (Variance Explained by Principal Components)', fontsize=16)
plt.xlabel('Principal Component', fontsize=12)
plt.ylabel('Proportion of Variance Explained (%)', fontsize=12)
plt.xticks(range(1, len(explained_variance_ratio) + 1)) # Ensure all PC numbers are shown
plt.plot(range(1, len(explained_variance_ratio) + 1), explained_variance_ratio * 100,
         color='darkblue', # Choose a color for the line
         linestyle='-', # Solid line
         linewidth=1, # Line thickness
         marker='o', # Add circular markers at each point
         markersize=4, # Size of the markers
         markerfacecolor='darkblue', # Fill color of the markers
         markeredgecolor='darkblue', # Edge color of the markers
         zorder=10)
# Annotate with percentage values
for i, txt in enumerate(explained_variance_ratio):
    plt.annotate(f'{txt * 100:.1f}%', # Format as percentage with one decimal place
                (i + 1, txt * 100),
                textcoords="offset points",
                xytext=(0, 10), # Offset text slightly above the point
                ha='center',
                fontsize=9,
                color='darkred') # Make annotation color stand out

plt.grid(axis='y', linestyle='--', alpha=0.7) # Grid lines only on y-axis for clarity
plt.grid(axis='x', linestyle='--', alpha=0.7) # Grid lines only on x-axis for clarity

plt.tight_layout() # Adjust layout to prevent labels from overlapping
plt.show()

```

```

# Perform PCA on the standardized features (no n_components specified to get all for full Cos2 calculation)
pca = PCA()
pca.fit(X_scaled_df)

# Calculate Cos2 (Quality of Representation)
components_df = pd.DataFrame(pca.components_, columns=X_scaled_df.columns, index=[f'PC{i+1}' for i in range(pca.n_components_)])
cos2_matrix = components_df**2
cos2_matrix_sum = cos2_matrix.sum(axis=0)
cos2_normalized = cos2_matrix.divide(cos2_matrix_sum, axis=1)

# Ensure the index for PC selection is correct
pc_indices_to_plot = [f'PC{i+1}' for i in range(5)] # Select PC1 to PC5

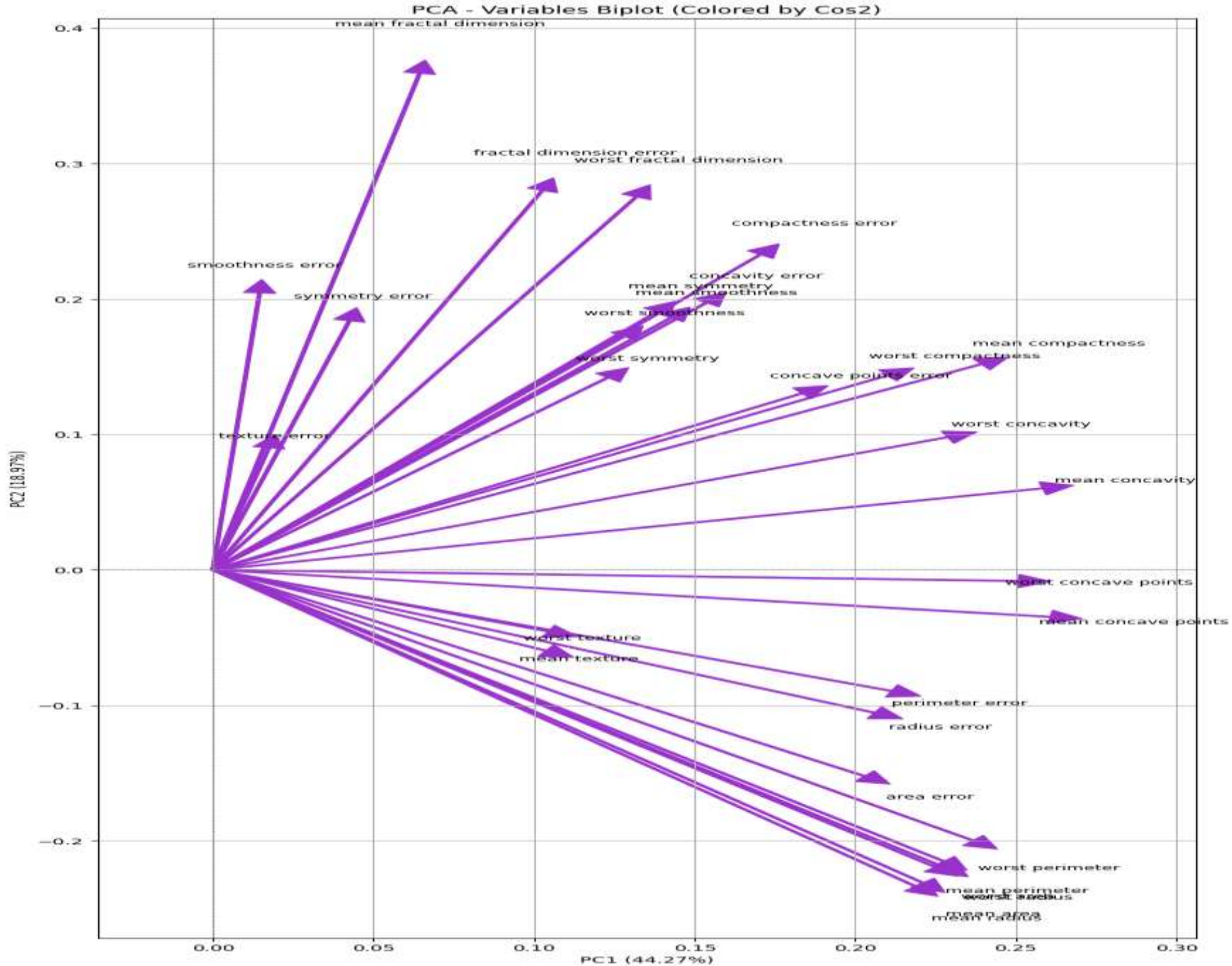
# Generate the heatmap for the first 5 PCs
plt.figure(figsize=(20, 10)) # Adjusted figsize for better readability with 5 PCs
sns.heatmap(cos2_normalized.loc[pc_indices_to_plot],
            annot=True,
            cmap='viridis',
            fmt=".2f", # Format to two decimal places
            linewidths=.5)
plt.title(' (Quality of Representation) of Variables on PC1 to PC5', fontsize=16)
plt.xlabel('Variables', fontsize=12)
plt.ylabel('Principal Components', fontsize=12)
plt.xticks(rotation=45, ha='right') # Rotate x-axis labels for better readability
plt.yticks(rotation=0) # Keep y-axis labels horizontal
plt.tight_layout()
plt.show()

```

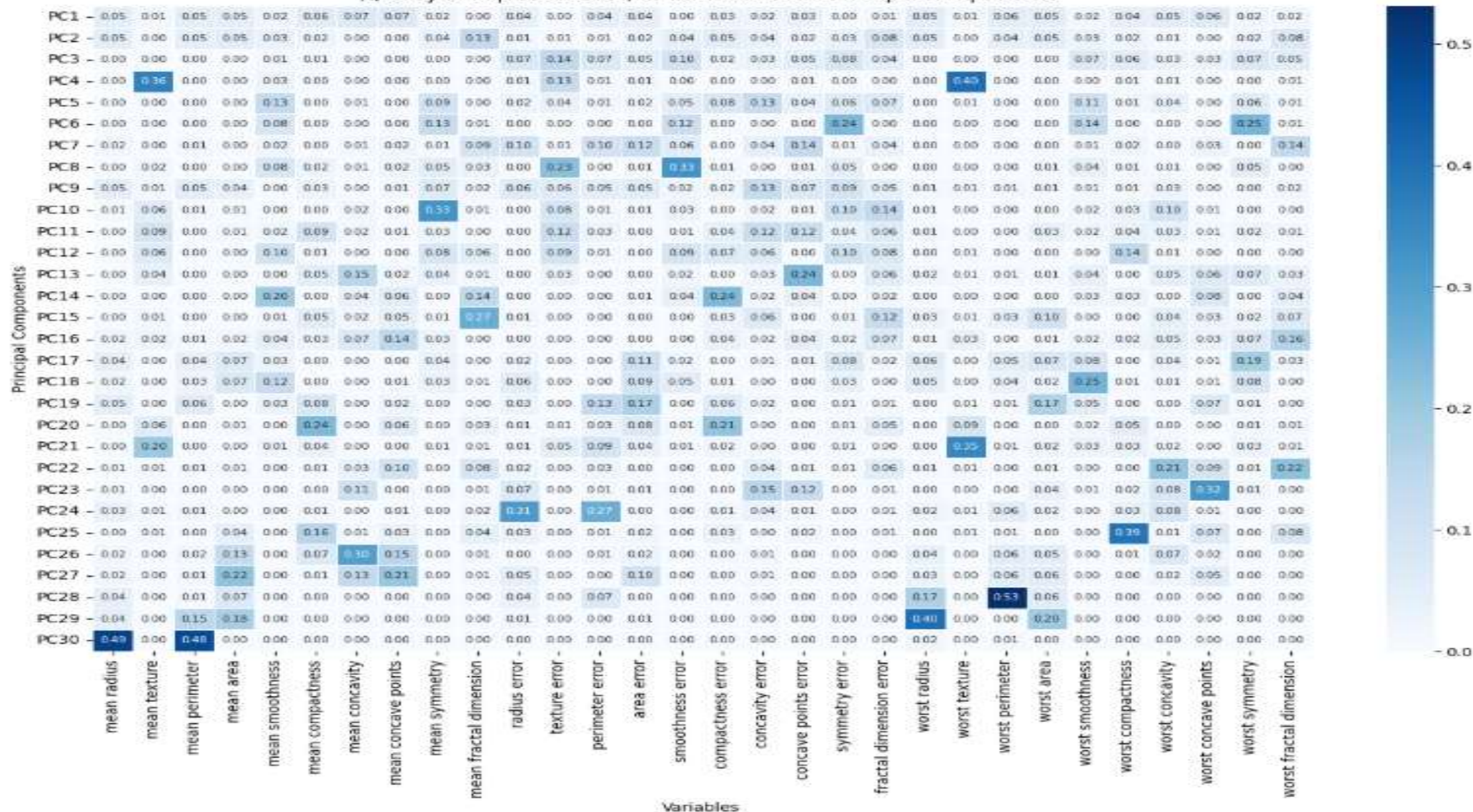
```

plt.figure(figsize=(16, 10)) # Increased size for better readability with more features
sns.heatmap(cos2_normalized, annot=True, cmap='Blues', fmt=".2f", linewidths=.5, annot_kws={"size": 7})
plt.title(' (Quality of Representation) of Variables on All Principal Components')
plt.xlabel('Variables')
plt.ylabel('Principal Components')
plt.show()

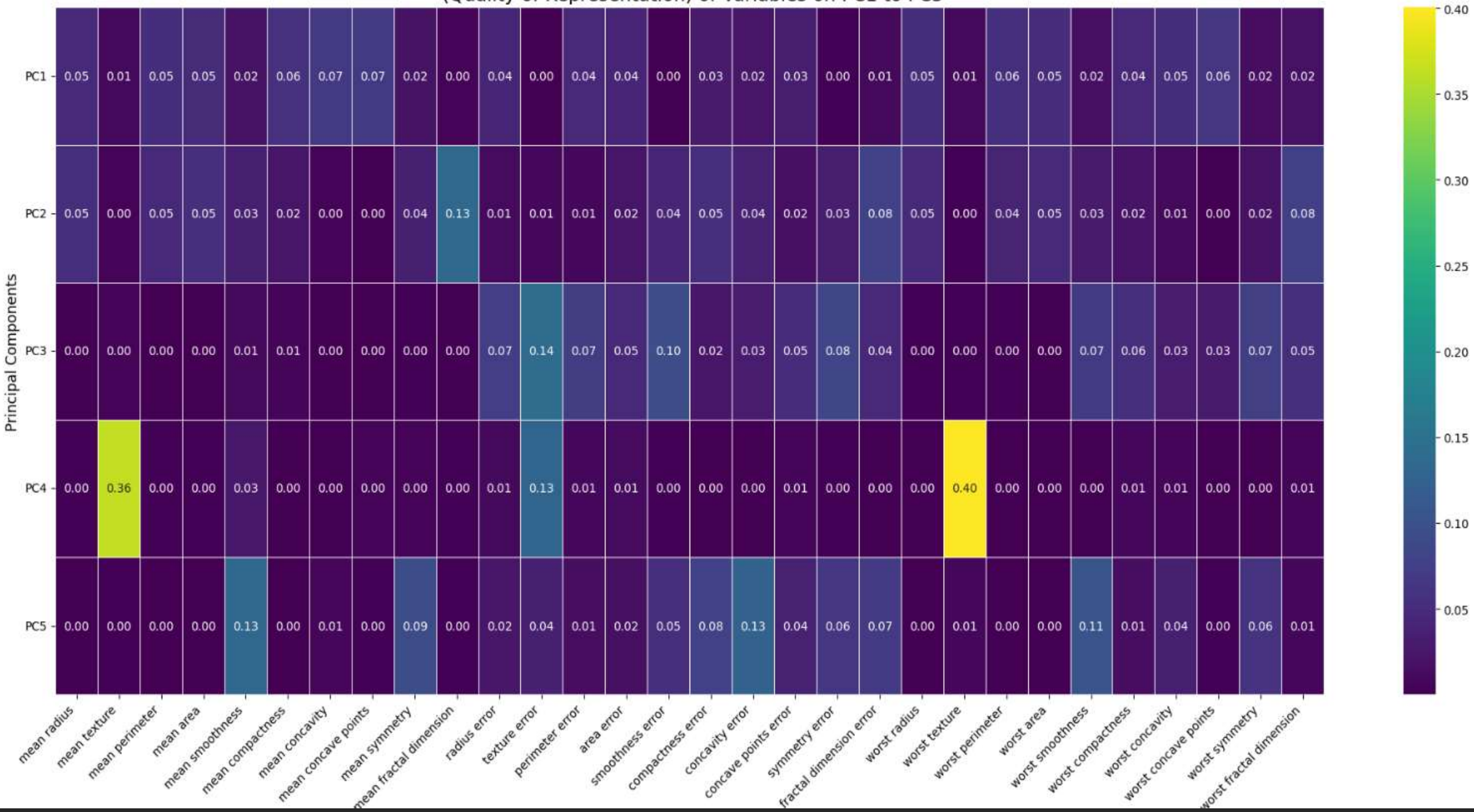
```



(Quality of Representation) of Variables on All Principal Components



(Quality of Representation) of Variables on PC1 to PC5

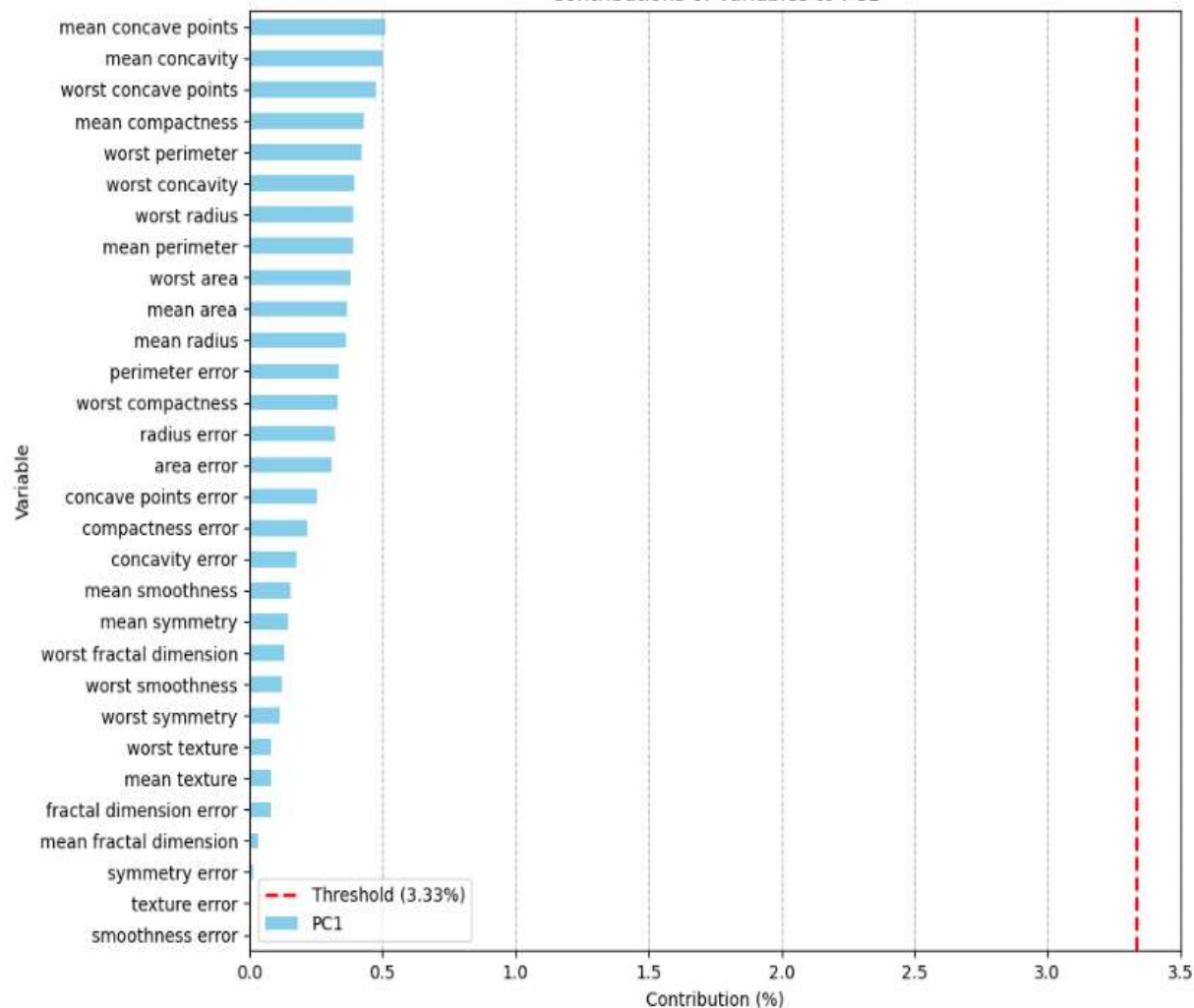


Threshold for equal contribution: 3.33%

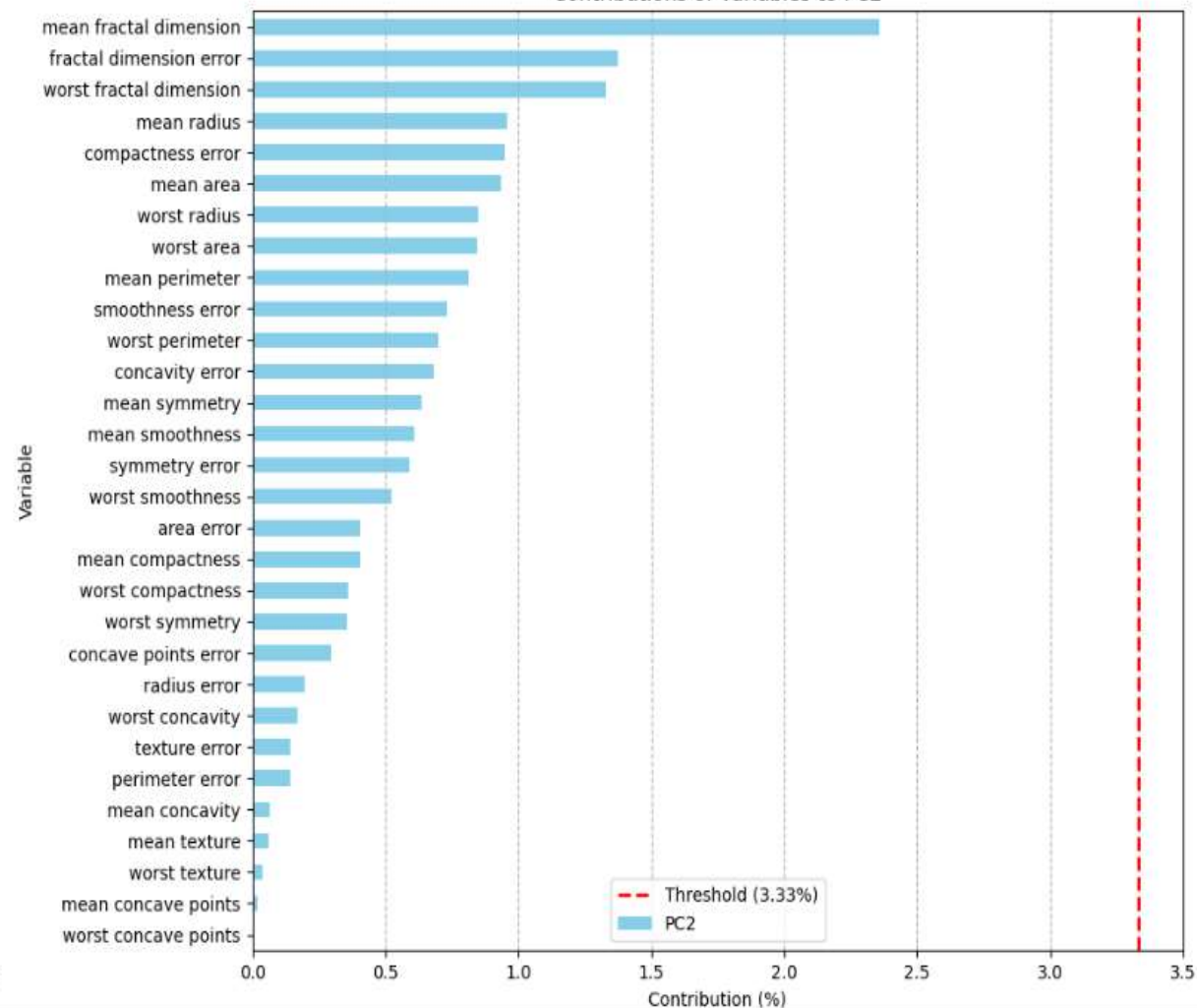


Contribution of Variables to First 5 Principal Components

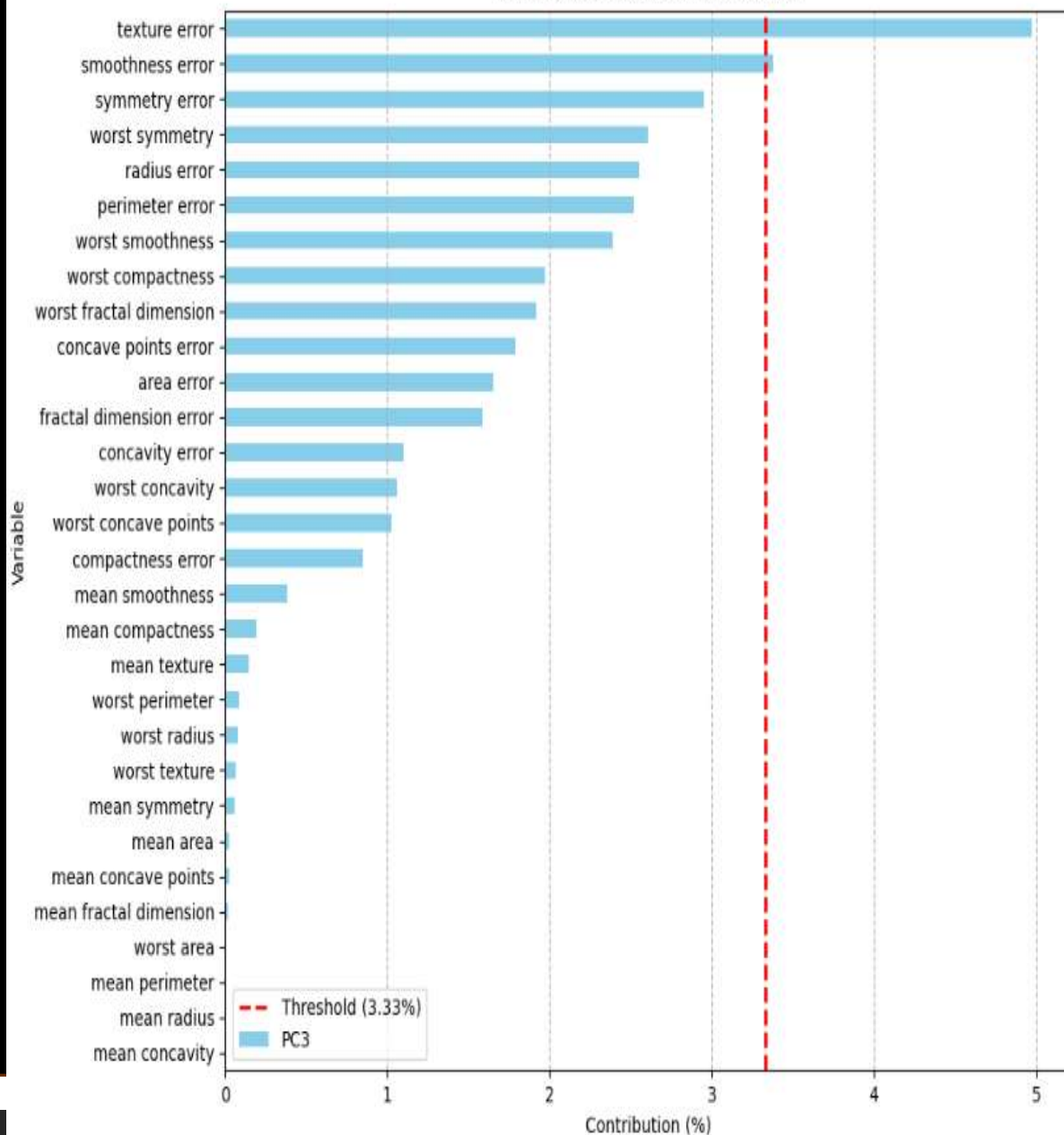
Contributions of Variables to PC1



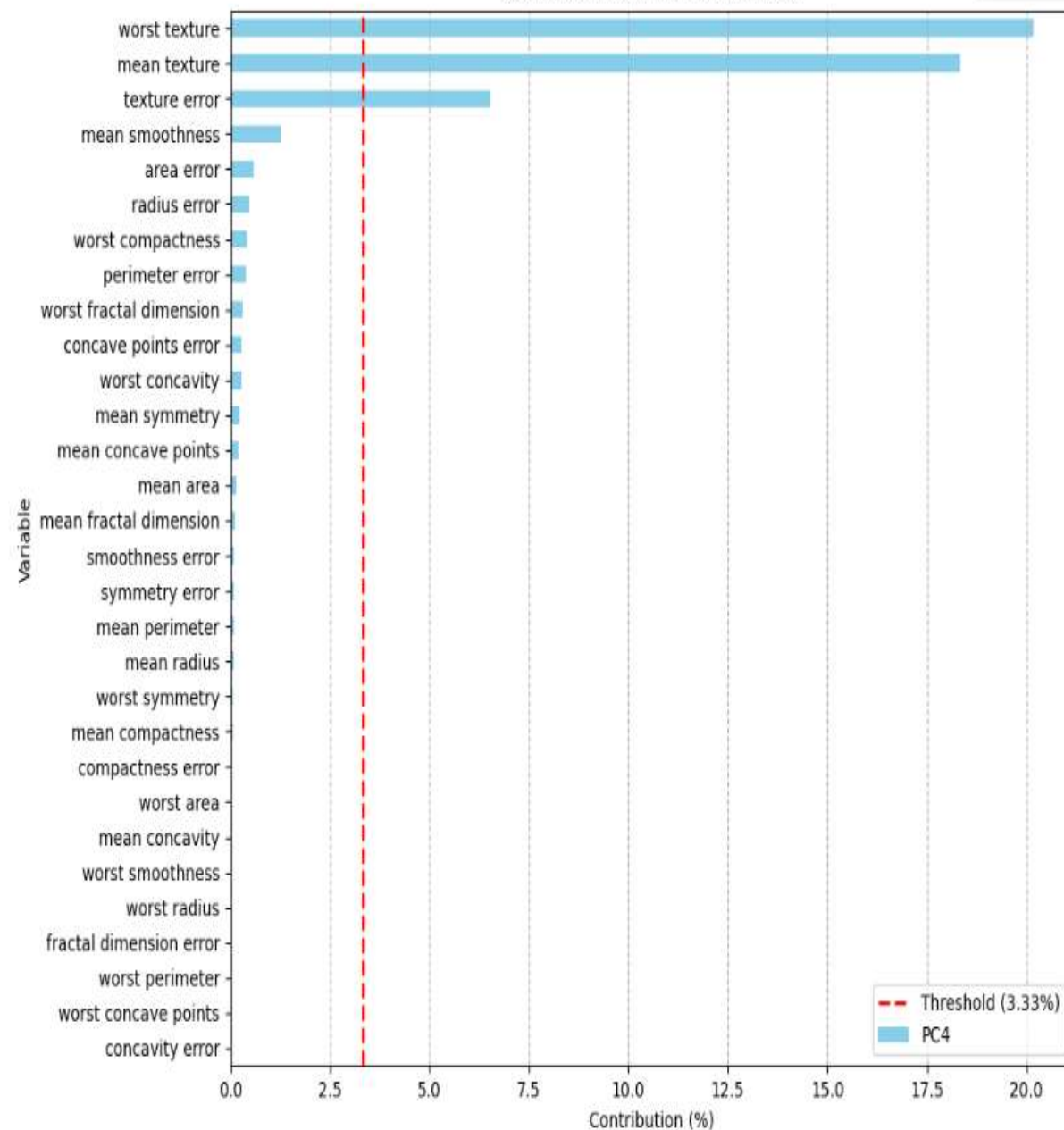
Contributions of Variables to PC2



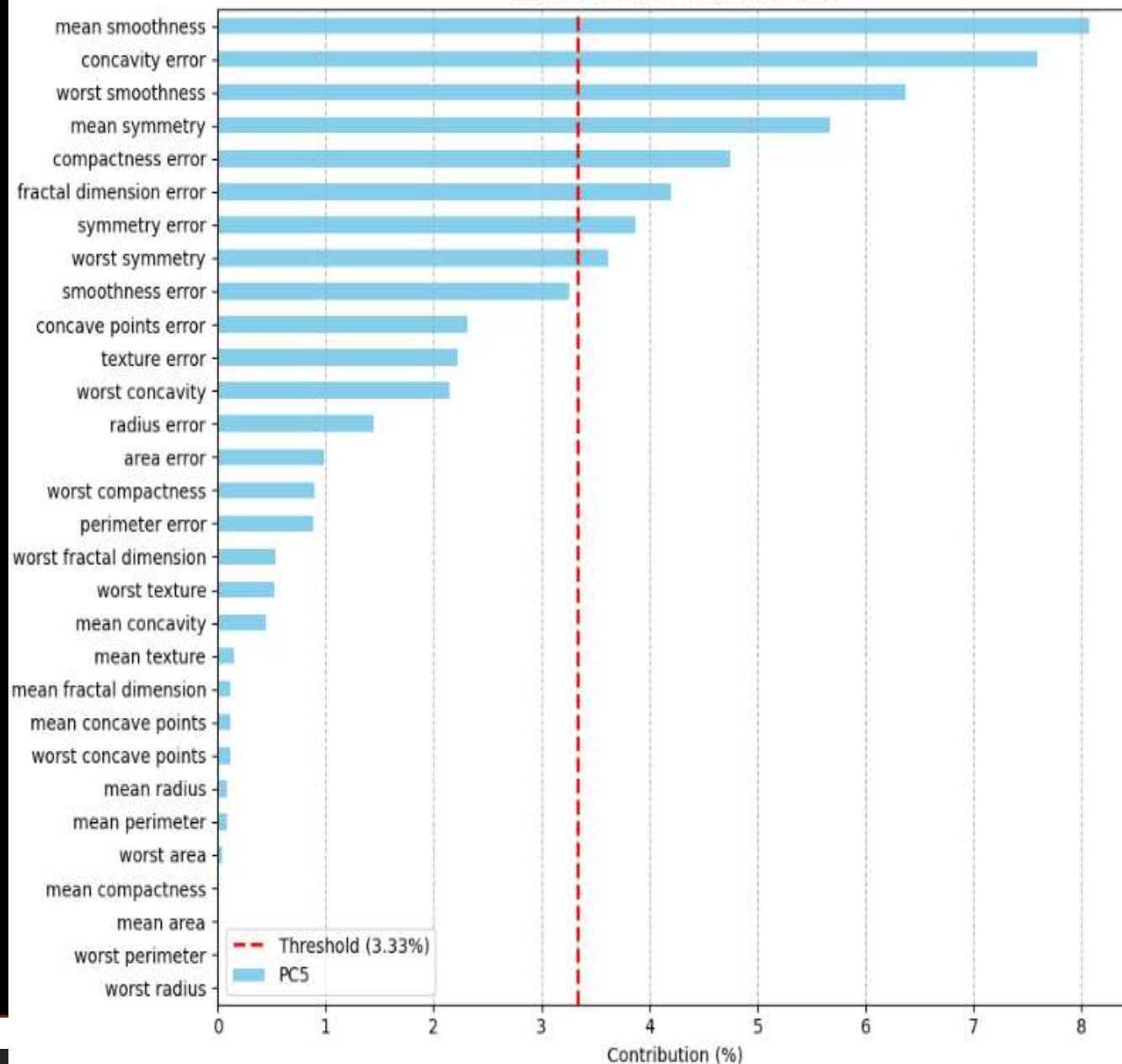
Contributions of Variables to PC3



Contributions of Variables to PC4



Contributions of Variables to PC5



```
cancer = load_breast_cancer()
X = pd.DataFrame(data=cancer.data, columns=cancer.feature_names)
y = pd.Series(cancer.target, name='target')
print("Shape of original features (X):", X.shape)
print("Shape of target (y):", y.shape)
```

```
Shape of original features (X): (569, 30)
Shape of target (y): (569,)
```

```
X_train, X_test, y_train, y_test = train_test_split(X_pca_selected, y, test_size=0.3, random_state=42, stratify=y)
```

```
print(f"\nTraining set shape - Features: {X_train.shape}, Target: {y_train.shape}")
```

```
print(f"\nTesting set shape - Features: {X_test.shape}, Target: {y_test.shape}")
```

```
Training set shape - Features: (398, 5), Target: (398,)
```

```
Testing set shape - Features: (171, 5), Target: (171,)
```

7. Conduct Logistic Regression

```
logistic_model = LogisticRegression(random_state=42, max_iter=200)
```

```
logistic_model.fit(X_train, y_train)
```

LogisticRegression

LogisticRegression(max_iter=200, random_state=42)

Make predictions on the test set

```
y_pred = logistic_model.predict(X_test)
```

8. Evaluate the model

```
accuracy = accuracy_score(y_test, y_pred)
```

```
class_report = classification_report(y_test, y_pred)
```

```
print(f"\nLogistic Regression Model Accuracy: {accuracy:.4f}")
```

```
print("\nClassification Report:")
```

```
print(class_report)
```

Logistic Regression Model Accuracy: 0.9766

Classification Report:

	precision	recall	f1-score	support
0	0.97	0.97	0.97	64
1	0.98	0.98	0.98	107
accuracy			0.98	171
macro avg	0.98	0.98	0.98	171
weighted avg	0.98	0.98	0.98	171